Table S2. List of peptides identified, separated by mouse pair

Mouse Pair 1

GI #	Sequence	Modifications	Protein Name	M/z	Highest Mascot score	Average Ratio (15N:14N), non-Log-transformed
7657429	AAAITSDLLESLGR		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	1416.7731	19.27	0
33859506	AADKDTCFSTEGPNLVTR		albumin 1 [Mus musculus]	1924.9149	124.11	1.748454424
29789080	AAESLADPTEYENLFPGLK		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	2065.0203	27.28	0
6753036	AAFQLGSPWR		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1132.5916	31.37	1.850253591
6680606	AALEGTLAETEAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1331.6868	45.13	1.946867252
23597151	AALLAELASLEADALR		PREDICTED: similar to UDP-N-acteylglucosamine pyrophosphorylase 1-like 1 [Mus musculus]	1626.9125	38.05	0
30911099	AAMLGQEDPPQHGLPR		fatty acid synthase [Mus musculus]	1716.8521	20.74	1.010052458
29126205	AANEAGYFNEEMAPIEVK		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1982.9471	36.33	0
13385006	AANNGALPPDLSYIVR		cytochrome c-1 [Mus musculus]	1670.8717	33.57	0
31542559	AAPAAAAAMAPPGPR		dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) [Mus musculus	1319.692	35.96	1.600571321
27754065	AAPFTLEYR		pyrophosphatase [Mus musculus]	1067.5548	31.38	1.983167435
6677995	AAQSPQQHSSGDPTEEESPV		solute carrier family 16, member 1 [Mus musculus]	2080.9148	78.94	2.036634345
8567336	AASATLPPITVTPVVNK		chloride channel calcium activated 3 [Mus musculus]	1678.9786	70.58	0
8567336	AASATLPPITVTPVVNK	Deamidation (NQ)	chloride channel calcium activated 3 [Mus musculus]	1679.9833	41.58	0
63474405	AASDGQYENQSPEATSPR		PREDICTED: tensin [Mus musculus]	1907.8406	100.83	1.119306144
7304889	AASGFNATEDAQTLR		annexin A4 [Mus musculus]	1551.7515	54.55	1.339182794
31981826	AAVDAGFVPNDMQVGQTGK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1904.9116	54.82	1.428393755
31543051	AAVENLPTFLVELSR		karyopherin (importin) beta 1 [Mus musculus]	1658.9127	27.17	1.453431189
51770896	AAVPSGASTGIYEALELR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1804.9473	91.8	1.508144649
27413160	AAVQQLQAEGLSPR		carbonyl reductase 3 [Mus musculus]	1467.8007	40.97	1.704257775
22094075	AAYFGIYDTAK		solute carrier family 25, member 5 [Mus musculus]	1219.5991	63.05	1.230805451
6671539	ADDGRPFPQVIK		aldolase 1, A isoform [Mus musculus]	1342.7185	50.15	1.503449941
34328489	ADFDNTVAIHPTSSEELVTLR		glutathione reductase 1 [Mus musculus]	2315.1514	65.24	0
6754084	ADIVENQVMDTR		glutathione S-transferase, mu 1 [Mus musculus]	1390.673	55.37	0
547749	ADLEMQIESLTEELAYLK	Oxidation (M)	Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	2112.0452	72.65	0.502564139
31981086	ADLNQGIGEPQSPSR		EF hand domain containing 2 [Mus musculus]	1568.7697	28.33	0
33859811	ADMVIEAVFEDLGVK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1635.8286	65.61	1.540787
31981100	ADRDESSPYAAMLAAQDVAQR		ribosomal protein S14 [Mus musculus]	2265.0635	50.72	1.171532721
31560731	ADYAQLLEDMQNAFR		ATPase, H+ transporting, V1 subunit A, isoform 1 [Mus musculus]	1784.8309	19.07	0.769881287
63562743	AEACVFWR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	981.4664	32.47	0.799718322
6679237	AEAEAQAEELSFPR		pyruvate carboxylase [Mus musculus]	1547.7443	42.99	3.125514103
6996913	AEDGSVIDYELIDQDAR		annexin A2 [Mus musculus]	1908.8898	95.7	1.46794125
31982030	AEEYEFLTPMEEAPK		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1783.8206	53.51	0
31981562	AEGSDVANAVLDGADCIMLSGETAK		pyruvate kinase 3 [Mus musculus]	2437.1377	48.73	0
6755372	AELNEFLTR		ribosomal protein S3 [Mus musculus]	1092.5664	41.92	0.825494104
6678483	AENYDISPADR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1250.5663	33.93	1.648496234
20149726	AETAPLPTSVDDTPEVLNR		phosphatidate cytidylyltransferase 2 [Mus musculus]	2024.9946	59.83	0.938696251
33859506	AETFTFHSDICTLPEK		albumin 1 [Mus musculus]	1838.8676	19	0
63746482	AEVGVPAEFGIWTR		PREDICTED: filamin, alpha [Mus musculus]	1531.8037	72.98	0.899624951
6671702	AFADALEVIPMALSENSGMNPIQTMTEVR		chaperonin subunit 5 (epsilon) [Mus musculus]	3135.5125	31.43	1.33792349
6753322	AFADAMEVIPSTLAENAGLNPISTVTELR		chaperonin subunit 4 (delta) [Mus musculus]	3030.522	27.04	1.922773395
63746482	AFGPGLQGGNAGSPAR		PREDICTED: filamin, alpha [Mus musculus]	1456.7424	99.87	0.716342152
13384888	AFIFPQESSTAYVSLIPK		hypothetical protein LOC66289 [Mus musculus]	1998.0714	106.61	0
10092608	AFLSSPEHVNRPINGNGK		glutathione S-transferase, pi 1 [Mus musculus]	1937.0073	21.93	1.437877403
7710086	AFLTLAEDILR		RAB10, member RAS oncogene family [Mus musculus]	1261.7212	44.01	1.85983522
51491845	AFMTADLPNELIELLEK		clathrin, heavy polypeptide (Hc) [Mus musculus]	1947.0134	57.07	1.454923603
37674269	AFQEQGQGQEQSEPGMSSTPR		slingshot-like 3 [Mus musculus]	2278.9978	24.19	0
6677991	AFYAPVHADDLR		solute carrier family 12, member 2 [Mus musculus]	1374.6866	42.16	3.867316772
31982186	AGAGSATLSMAYAGAR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1454.7196	39.62	1.825701457
6671507	AGFAGDDAPR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	976.4539	66.87	0.759976235
6671509	AGFAGDDAPR		actin, beta, cytoplasmic [Mus musculus]	976.4539	66.87	0.759976235
33859811	AGLEQGSDAGYLAESQK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1723.8195	80.71	1.316868272
20799907	AGLQFPVGR		histone 2, H2aa1 [Mus musculus]	944.5438	52.67	0.934136691

63562740	AGLSLMWNR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1047.5377	33.37	0.4826663
6677775	AGNLGGGVVTIER		ribosomal protein L22 [Mus musculus]	1242.6871	61.54	1.819635003
63746482	AGNNMLLVGVHGPR		PREDICTED: filamin, alpha [Mus musculus]	1434.7634	30.1	2.008057944
41322904	AGTLSITEFADMLSGNAGGFR		plectin 1 isoform 1 [Mus musculus]	2115.0173	24.59	1.017949288
11230802	AGTQIENIDEDFR		actinin alpha 4 [Mus musculus]	1507.707	19.23	1.153383395
41322904	AGVGAPVTQVTLQSTQR		plectin 1 isoform 1 [Mus musculus]	1712.9348	72.88	1.112459611
31980648	AHGGYSVFAGVGER		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1406.6902	57.73	1.636197132
31980648	AIAELGIYPAVDPLDSTSR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1988.0414	90.42	1.472744266
39652626	AIAGIINQPYYNYQAGPDAALGR		bisphosphate 3'-nucleotidase 1 [Mus musculus]	2436.2415	40.44	5.362848485
6678177	AIEPQKEEADENYNSVNTR		syntaxin 4A (placental) [Mus musculus]	2207.0251	47.2	0
12963615	AILVDLEPGTMDSVR		tubulin, beta 3 [Mus musculus]	1615.8434	66.96	0.978428372
7106439	AILVDLEPGTMDSVR		tubulin, beta 5 [Mus musculus]	1615.8434	66.96	0.978428372
21746161	AILVDLEPGTMDSVR		tubulin, beta [Mus musculus]	1615.8434	66.96	0.978428372
6755198	AINQGGLTSVAVR		proteasome (prosome, macropain) subunit, alpha type 6 [Mus musculus]	1285.7263	35.49	1.455107694
31543942	AIPDLTAPVAAVQAAVSNLVR		vinculin [Mus musculus]	2076.1794	83.32	0.714293169
6753864	AIVAGDQNVEYK		four and a half LIM domains 1 [Mus musculus]	1306.6613	81.68	0.820573647
31560560	AIVAIENPADVSVISSR		laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1740.9509	79.94	1.267327189
29789343	AKPAAQSEEETATSPAASPTPQSAER		eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]	2612.2441	79	1.061103417
9845257	ALAAAGYDVEK		histone 1, H1c [Mus musculus]	1107.5712	79.42	0.728827847
34328365	ALAAAGYDVEK		histone 1, H1d [Mus musculus]	1107.5712	79.42	0.728827847
13430890	ALAAAGYDVEK		histone 1, H1e [Mus musculus]	1107.5712	79.42	0.728827847
21426893	ALAAGGYDVEK		histone 1, H1b [Mus musculus]	1093.5504	48.69	1.050268291
7709980	ALDIAENEMPGLMR		S-adenosylhomocysteine hydrolase [Mus musculus]	1559.7571	19.91	0.606700398
547749	ALEESNYELEGK		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1381.652	55.17	0
33598964	ALELDPNLYR		myosin heavy chain 10, non-muscle [Mus musculus]	1203.6382	33.1	0.758637071
7305295	ALELDPNLYR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1203.6382	33.1	0.758637071
20137006	ALELDSNLYR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1193.6116	38.08	1.016048466
23956212	ALEPEEGNPQTEAQENGPER		HIV TAT specific factor 1 [Mus musculus]	2194.9807	51.55	1.099834295
6680606	ALEQANGELEVK		keratin complex 1, acidic, gene 19 [Mus musculus]	1300.6704	71.67	1.867101699
6679687	ALEQFLQEYFDGNLK		glucose regulated protein [Mus musculus]	1814.902	58.04	1.296711023
6678573	ALGMTPAAFSALPR		villin 1 [Mus musculus]	1402.7356	27.34	2.703180662
13385942	ALGVLAQLIWSR		citrate synthase [Mus musculus]	1326.796	22.33	1.338032463
6753322	ALIAGGGAPEIELALR		chaperonin subunit 4 (delta) [Mus musculus]	1550.8934	31.86	1.415066276
63489754	ALINADELANDVAGAEALLDR		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	2154.0955	59.25	0.868917665
6671666	ALLATASQCQQPAGNK		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1600.8123	41.41	1.197899438
33859482	ALLELQLEPEELYQTFQR		eukaryotic translation elongation factor 2 [Mus musculus]	2220.1553	50.97	1.212975289
34328489	ALLTPVAIAAGR		glutathione reductase 1 [Mus musculus]	1152.7064	31.59	1.824695297
63476037	ALNLGYALDYALR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1452.7864	35.95	0.828806353
63476037	ALNLGYALDYALR	Deamidation (NQ)	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1453.796	21.44	0
34328204	ALNPLEDWLR		valyl-tRNA synthetase 2 [Mus musculus]	1226.658	19.13	1.494723889
63506192	ALPFWNEEIVPQIK		PREDICTED: similar to phosphoglycerate mutase (EC 5.4.2.1) B chain - rat [Mus musculus]	1683.9099	35.17	1.364136323
21704020	ALSEIAGITLPYDTLDQVR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	2075.1021	54.39	1.682938057
22165384	ALTVPELTQQMFDAK		tubulin, beta, 2 [Mus musculus]	1691.8682	53.93	1.122638561
12963615	ALTVPELTQQMFDAK		tubulin, beta 3 [Mus musculus]	1691.8682	53.93	1.122638561
31981939	ALTVPELTQQMFDAK		tubulin, beta 4 [Mus musculus]	1691.8682	53.93	1.122638561
27754056	ALTVPELTQQMFDAK		tubulin, beta 6 [Mus musculus]	1691.8682	53.93	1.122638561
6754556	ALYETELADAR		lamin B1 [Mus musculus]	1251.6277	29.22	0
19526818	ALYSNILGEENTYLWR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1941.9689	28.48	2.647568663
14389431	AMADPEVQQIMSDPAMR		stress-induced phosphoprotein 1 [Mus musculus]	1889.8594	23.49	1.354401801
20874851	AMGIMNSFVNDIFER		PREDICTED: similar to histone H2b-616 [Mus musculus]	1743.8346	25.76	0.688710601
20874851	AMGIMNSFVNDIFER	Deamidation (NQ)	PREDICTED: similar to histone H2b-616 [Mus musculus]	1744.821	54.68	0
20874851	AMGIMNSFVNDIFER	Oxidation (M)	PREDICTED: similar to histone H2b-616 [Mus musculus]	1759.8138	21.85	0.707080737
21312712	AMLSGPGQFAENETNEVNFR		transcription elongation factor B (SIII), polypeptide 1 [Mus musculus]	2211.0232	25.89	0
31981549	ANIIFNTALGTIFGVK		sulfide quinone reductase-like [Mus musculus]	1678.9368	83.03	1.375106503
63746482	ANLPQSFQVDTSK		PREDICTED: filamin, alpha [Mus musculus]	1434.7219	73.5	0.731627954
20137006	ANLQIDQINTDLNLER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1869.9647	61.78	1.152503
19745150	APDAWDYSQGFVNEEMIR		diaphorase 1 [Mus musculus]	2127.9548	40.66	1.539835252
6754750	APDFVFYAPR		moesin [Mus musculus]	1182.5973	59.21	0.967006469
6678571	APDFVFYAPR		villin 2 [Mus musculus]	1182.5973	59.21	0.967006469
6681157	APILIATDVASR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1226.713	39.42	2.080570587

40068493	APILIATDVASR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1226.713	39.42	2.080570587
33859506	APQVSTPTLVEAAR		albumin 1 [Mus musculus]	1439.799	75.45	2.155585092
33563250	APSYGAGELLDFSLADAVNQEFLATR		desmin [Mus musculus]	2755.3611	59.9	0.678317293
7106435	APTAQVESFR		tenascin C [Mus musculus]	1105.5635	26.84	1.709436908
13384888	APTNLPDPAR		hypothetical protein LOC66289 [Mus musculus]	1051.5559	22.78	0
6671664	APVPTGEVYFADSFDR		calnexin [Mus musculus]	1770.8397	45.32	1.347343854
6679515	AQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLR		polypyrimidine tract binding protein 1 [Mus musculus]	3680.8481	28.82	1.305968821
41322904	AQAEAQQPVFNTLR		plectin 1 isoform 1 [Mus musculus]	1572.8198	35.41	1.650723581
41322904	AQAEAQQPVFNTLR	Deamidation (NQ)	plectin 1 isoform 1 [Mus musculus]	1573.8135	36.53	1.412951163
41322904	AQAELEAQELQR		plectin 1 isoform 1 [Mus musculus]	1385.7056	24.5	1.294236217
31982520	AQDTAELFFEDVR		acetyl-Coenzyme A dehydrogenase, long-chain [Mus musculus]	1540.7344	39.42	1.934407463
51828444	AQEAAAEEPPPAVTPAASVSALDLGEQR		PREDICTED: proline-rich polypeptide 6 [Mus musculus]	2775.375	55.29	1.959808375
29789289	AQFGQPEILLGTIPGAGGTQR		enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Mus musculus]	2111.1248	63.48	1.765881621
6679583	AQIWDTAGQER		RAB11B, member RAS oncogene family [Mus musculus]	1274.6198	48.58	1.215591311
6754482	AQMEQLNGVLLHLESELAQTR		keratin complex 1, acidic, gene 18 [Mus musculus]	2380.2217	31.49	1.289061127
33468857	AQVAQPGGDTIFGK		histidine triad nucleotide binding protein 1 [Mus musculus]	1388.7142	57.65	1.49185782
63489759	ASAFNSWFENAEEDLTDPVR		PREDICTED: spectrin alpha 2 [Mus musculus]	2298.0459	33.86	1.859035106
34328206	ASEDFVDPWTVR		tryptophanyl-tRNA synthetase [Mus musculus]	1421.6758	29.2	3.850738128
6755358	ASGNYATVISHNPETK		ribosomal protein L8 [Mus musculus]	1688.8256	78.59	1.110295763
63746482	ASGPGLNTTGVPASLPVEFTIDAK		PREDICTED: filamin, alpha [Mus musculus]	2342.207	44.35	0
9845257	ASGPPVSELITK		histone 1, H1c [Mus musculus]	1198.6692	51.27	0
34328365	ASGPPVSELITK		histone 1, H1d [Mus musculus]	1198.6692	51.27	0
23943876	ASGTSFNAVPLHPNTVLR		zymogen granule membrane protein 16 [Mus musculus]	1881.0039	56.84	0.949886088
13624315	ASLEAAIADAEQR		keratin complex 2, basic, gene 8 [Mus musculus]	1344.6844	91.62	1.881826801
6679931	ASLGTLNTLADVPDDEVQGR		UDP-N-acetyl-alpha-D-galactosamine: (N-acetylneuraminyl)-galactosyl-N- acetylglucosaminylpolypeptid	2071.0293	36.06	1.269967628
31543605	ASSFVLALEPELESR		ribophorin I [Mus musculus]	1647.8611	71.07	1.245366072
21313526	ASTPDWPSQDPQPGLQR		hypothetical protein LOC78906 [Mus musculus]	1879.8956	22.66	1.974841505
8567336	ASVTALIESVNGK		chloride channel calcium activated 3 [Mus musculus]	1288.7263	37.06	0
9845283	ASYVAPLTAQPATYR		RNA binding motif protein 14 [Mus musculus]	1608.8451	25.79	1.354573903
7305163	ATAGDTHLGGEDFDNR		heat shock protein 1-like [Mus musculus]	1675.7471	89.54	0
63704924	ATAGDTHLGGEDFDNR		PREDICTED: heat shock protein 1B [Mus musculus]	1675.7471	89.54	0
6754976	ATAVMPDGQFK		peroxiredoxin 1 [Mus musculus]	1164.571	75.5	1.26051304
6679567	ATEMVEVGPEDDEVGAER		polymerase I and transcript release factor [Mus musculus]	1932.8552	99.71	1.336811705
10946928	ATENDIYNFFSPLNPVR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1996.9789	77.37	1.286382575
6677871	ATEVPLSWESFNK		scinderin [Mus musculus]	1507.7341	37.37	0
7305295	ATLQAEQLSNELATER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1773.8992	76.83	0.986784305
6753492	ATPEPSGTPSSDTVSR		coronin, actin binding protein 1A [Mus musculus]	1588.752	85.02	0.247717557
21450625	ATQALVLAPTR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1140.6801	32.57	1.035391038
33859650	ATYSTNSPVWEEAFR		membrane bound C2 domain containing protein [Mus musculus]	1757.818	19.82	0
6753320	AVAQALEVIPR		chaperonin subunit 3 (gamma) [Mus musculus]	1166.689	29.6	1.830179519
22267442	AVAQGNLSSADVQAAK		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1529.7981	55.21	0
6680748	AVDSLVPIGR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1026.5939	30.81	1.495388587
25020120	AVEASNAYSSILQAVQAAEDAAGQALR		PREDICTED: laminin, alpha 5 [Mus musculus]	2704.3533	59.77	0.58027614
18079351	AVFPQNGLVVSSVDVQSVEPVDQR		major vault protein [Mus musculus]	2569.3245	24.81	2.079499749
6671507	AVFPSIVGRPR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1198.7131	29.39	0.840528143
6671509	AVFPSIVGRPR		actin, beta, cytoplasmic [Mus musculus]	1198.7131	29.39	0.840528143
21450277	AVFQANQENLPILK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1584.8723	48.66	1.764951201
6678467	AVFVDLEPTVIDEIR		tubulin, alpha 4 [Mus musculus]	1715.9214	87.7	1.685522375
6755901	AVFVDLEPTVIDEVR		tubulin, alpha 1 [Mus musculus]	1701.9095	96.94	1.292640562
34740335	AVFVDLEPTVIDEVR		tubulin, alpha 2 [Mus musculus]	1701.9095	96.94	1.292640562
6678469	AVFVDLEPTVIDEVR		tubulin, alpha 6 [Mus musculus]	1701.9095	96.94	1.292640562
28916673	AVITSLLDQIPEMFADTR		SEC24 related gene family, member C [Mus musculus]	2020.0369	34.45	1.098952625
22165384	AVLVDLEPGTMDSVR		tubulin, beta, 2 [Mus musculus]	1601.8221	67.78	1.686475363
31981939	AVLVDLEPGTMDSVR		tubulin, beta 4 [Mus musculus]	1601.8221	67.78	1.686475363
30578429	AVPVSNIAPAAVGR		hypothetical protein LOC94184 [Mus musculus]	1321.7675	41.64	1.625443939
7305085	AVQTLQMELQQIMK		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1660.8646	62.14	1.375245678
7305085	AVQTLQMELQQIMK	Deamidation (NQ)	glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1661.8654	38.98	1.856750136
6756039	AVTEQGAELSNEER		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Mus musc	1532.7262	94.43	1.077769116
7305173	AVTQSAEITIPVTFEAR		heat shock protein 1 [Mus musculus]	1832.9688	52.08	0.641271262
63746482	AWGPGLEGGIVGK		PREDICTED: filamin, alpha [Mus musculus]	1240.6644	53.14	0

6753138	AYGENIGYSEK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1230.5664	88.81	1.793620974
6753138	AYGENIGYSEKDR		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1501.696	56.36	1.933344166
63746482	AYGPGIEPTGNMVK		PREDICTED: filamin, alpha [Mus musculus]	1433.7098	39.59	0.505527157
33859482	AYLPVNESFGFTADLR		eukaryotic translation elongation factor 2 [Mus musculus]	1799.8955	34.13	1.308099657
63746482	CGQSAAVASPGGSIDSR		PREDICTED: filamin, alpha [Mus musculus]	1562.73	66.61	0.845112316
6679759	CPPGFYTSPDGTR		fibrillin 1 [Mus musculus]	1397.6311	23.25	0
547749	DAEAWFNEK		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1109.4869	19.32	0
6755478	DAEDAMDAMDGAVLDGR		splicing factor, arginine/serine-rich 2 [Mus musculus]	1751.7358	107.74	1.050955919
21450277	DAFQNAYLELGGLGER		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1752.8666	51.51	0.945402167
63746482	DAGEGLLAVQITDPEGKPK	Deamidation (NQ)	PREDICTED: filamin, alpha [Mus musculus]	1938.9908	26.9	0
6754036	DAGMQLQGYR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1138.5382	23.5	1.459355648
6754256	DAGQISGLNVLR		heat shock protein 9A [Mus musculus]	1242.6766	48.23	0
6754256	DAGQISGLNVLR	Deamidation (NQ)	heat shock protein 9A [Mus musculus]	1243.6626	23.45	2.523078797
31981690	DAGTIAGLNVLR		heat shock protein 8 [Mus musculus]	1199.689	59.88	1.427085163
63664182	DAGTIAGLNVLR		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1199.689	59.88	1.427085163
31981722	DAGTIAGLNVMR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1217.6335	68.24	1.233038044
30424898	DALVNAVIDSLSAYR		SEC24 related gene family, member A [Mus musculus]	1606.8512	31.31	0
31542602	DANLYISGLPR		ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) [Mus musculus]	1218.6418	32.86	0
41322904	DAPDGPSVEAEPEYTFEGLR		plectin 1 isoform 1 [Mus musculus]	2178.9922	62.41	1.284382972
21592285	DAQVQNAQCVLR		keratin 20 [Mus musculus]	1344.6714	36.78	2.43186246
30348966	DASVAEAWLLGQEPYLSSR		spectrin beta 2 isoform 1 [Mus musculus]	2092.021	26.97	1.600737077
31542333	DAVIYPILVEFTR		hypoxia up-regulated 1 [Mus musculus]	1535.8491	28.52	1.078406003
31981562	DAVLNAWAEDVDLR		pyruvate kinase 3 [Mus musculus]	1586.7854	83.75	1.529892526
31981562	DAVLNAWAEDVDLR	Deamidation (NQ)	pyruvate kinase 3 [Mus musculus]	1587.7896	20.12	0
6755809	DDILNGSHPVSFDK		talin 1 [Mus musculus]	1543.7416	28.86	0
6754036	DDNGKPYVLPSVR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1459.757	35.41	1.278433076
33859506	DDNPSLPPFERPEAEAMCTSFK		albumin 1 [Mus musculus]	2481.0977	24.86	1.639239322
19072792	DDTESLEIFQNEVAR		thioredoxin domain containing 4 [Mus musculus]	1765.8329	35.5	0
6681027	DDTYQSYSSPSPR		deleted in malignant brain tumors 1 [Mus musculus]	1502.6542	47.28	2.211931104
31981100	DESSPYAAMLAAQDVAQR		ribosomal protein S14 [Mus musculus]	1922.8931	112.58	0
6680047	DETNYGIPQR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1192.5647	54.03	1.328071585
22203747	DFDSLAQPSFFDR		procollagen, type VI, alpha 2 [Mus musculus]	1544.7072	40.28	0
8393150	DFEQPLAISR		carboxyl terminal LIM domain protein 1 [Mus musculus]	1175.5983	24.69	1.033817838
31981282	DFLLQQTMLR		glyoxalase 1 [Mus musculus]	1264.6796	20.88	0
6755142	DFMIQGGDFTR		peptidylprolyl isomerase B [Mus musculus]	1286.5879	50.6	1.0250242
58037117	DFPLTGYVELR		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Mus musculus]	1309.6783	32.33	0
20137006	DFSALESQLQDTQELLQEENR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2493.1753	76.34	1.195647936
6755714	DFTDSQLQEGK		transgelin [Mus musculus]	1267.5826	74.33	0.921271027
10181184	DFTPSGIAGAFR		ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 [Mus musculus]	1238.6161	33.53	1.49909538
6681233	DGAFDFFPVLR		solute carrier family 26 (sulfate transporter), member 2 [Mus musculus]	1283.6479	24.5	2.006394475
58037267	DGELPVEDDIDLSDVELDDLEKDEL		protein disulfide isomerase-associated 6 [Mus musculus]	2830.2896	82.6	0
33563250	DGEVVSEATQQQHEVL		desmin [Mus musculus]	1768.8423	101.66	0.579028415
22164798	DGFNPAHVEAGLYGSR		selenium binding protein 1 [Mus musculus]	1689.8083	94.9	2.823733985
27754067	DGMEYPFIGEGEPHVDGEPGDLR		DnaJ (Hsp40) homolog, subfamily B, member 11 [Mus musculus]	2516.1099	44.51	1.008970598
22779879	DGNGQITDKPVQQAQVQIR		desmoglein 2 [Mus musculus]	2095.0891	34.98	1.132832386
7709980	DGPLNMILDDGGDLTNLIHTK		S-adenosylhomocysteine hydrolase [Mus musculus]	2252.0955	56.61	0
30409956	DGPNALTPPPTTPEWVK		ATPase, Na+/K+ transporting, alpha 2 polypeptide [Mus musculus]	1819.9259	38.91	1.963523373
21450277	DGPNALTPPPTTPEWVK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1819.9259	38.91	1.963523373
27229048	DGQVIGIGAGQQSR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1385.7125	62.42	1.062005323
31982755	DGQVINETSQHHDDLE		vimentin [Mus musculus]	1836.8041	81.35	1.170440766
45597447	DGVANVSIEDR		superoxide dismutase 1, soluble [Mus musculus]	1174.5726	55.62	1.736065907
20806532	DGVPEGTQLQAHR		cold shock domain protein A short isoform [Mus musculus]	1407.6978	21.45	1.4983226
18079339	DGYAQILR		aconitase 2, mitochondrial [Mus musculus]	935.498	42.55	1.943722719
34328400	DGYDYDGYR		splicing factor, arginine/serine-rich 1 (ASF/SF2) [Mus musculus]	1123.436	26.32	1.662610799
6680117	DGYMPSQYNSQNWEAR	Deamidation (NQ)	glutathione synthetase [Mus musculus]	1946.8295	36.97	0
22203747	DIANSPHELYR		procollagen, type VI, alpha 2 [Mus musculus]	1314.6388	47.77	0.415829882
6756041	DICNDVLSLLEK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	1361.6997	69.04	1.41646201
63556656	DILCQALAAYAAACQAAGIK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1964.9945	122.5	0
6753374	DINDNAPVFNPSTYQGQVPENEVNAR		cadherin 1 [Mus musculus]	2888.3372	94.02	1.517500836
9790073	DINDNRPTFLQSK		cadherin 17 [Mus musculus]	1547.791	32.26	1.766140823

18079339	DINQEVYNFLATAGAK		aconitase 2, mitochondrial [Mus musculus]	1753.8767	60.24	1.348560899
18079339	DINQEVYNFLATAGAK	Deamidation (NQ)	aconitase 2, mitochondrial [Mus musculus]	1754.88	33.17	0
31981748	DISSAVQANPALTELSLR		ribonuclease/angiogenin inhibitor 1 [Mus musculus]	1885.0104	30.75	1.334632258
6755863	DISTNYYASQK		tumor rejection antigen gp96 [Mus musculus]	1289.6099	65.29	1.509177002
23956222	DITYFIQQLLR		ARP3 actin-related protein 3 homolog [Mus musculus]	1409.7874	59.04	1.248573866
19882201	DKTPVQSQQPSATTPSGADEK		proteasome 26S non-ATPase subunit 2 [Mus musculus]	2172.0493	54.03	1.088863744
6754524	DLADELALVDVMEDK		lactate dehydrogenase 1, A chain [Mus musculus]	1675.8198	94.55	1.680867789
6671549	DLAILLGMLDPVEK		peroxiredoxin 6 [Mus musculus]	1526.8458	80.69	1.74400466
30348966	DLDDFQSWLSR		spectrin beta 2 isoform 1 [Mus musculus]	1381.6479	27.62	2.01788985
27370092	DLDKPFLLPVESVYSIPGR		Tu translation elongation factor, mitochondrial [Mus musculus]	2145.123	26.91	1.649359299
6755809	DLDQASLAAVSQQLAPR		talin 1 [Mus musculus]	1782.9408	58.57	0
10946574	DLFDPIIEER		creatine kinase, brain [Mus musculus]	1246.631	58.16	0
6679687	DLFSDGHSEFLK		glucose regulated protein [Mus musculus]	1394.6545	57.91	1.120768767
25020120	DLGAQGAVAEAELAEAQR		PREDICTED: laminin, alpha 5 [Mus musculus]	1798.885	30.71	0
7305295	DLGEELEALKTELEDTLDSTATQQELR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	3047.4688	51.02	0.796681524
6753240	DLGLSESGEDVNAAILDESGKK		calcium binding protein, intestinal [Mus musculus]	2247.0981	67.01	0.846225008
31981302	DLIEDLKYELTGK		annexin A6 [Mus musculus]	1536.8075	50.38	1.789226033
38198665	DLIHDQDEEEEEEEGQR		p47 protein [Mus musculus]	2099.8687	104.56	1.234814763
7657429	DLLTQPGDWTLFAPTNDAFK		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2250.0889	22.14	0
21704100	DLMPHDLAR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1067.5328	29.96	0
6681233	DLPEEAFGFPSELPLETQR		solute carrier family 26 (sulfate transporter), member 2 [Mus musculus]	2175.0583	21.91	1.885610944
47578123	DLQLVLPDYFPER		potassium channel tetramerisation domain containing 12 [Mus musculus]	1604.8356	36.88	0.781016485
18266680	DLTAVSNNAGVDNFGLGLLLR		3-oxoacid CoA transferase 1 [Mus musculus]	2159.1392	36.17	0.858019828
6671507	DLTDYLMK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	998.4835	57.63	0.958521105
6671509	DLTDYLMK		actin, beta, cytoplasmic [Mus musculus]	998.4835	57.63	0.958521105
30425250	DLTDYLMK		hypothetical protein LOC238880 [Mus musculus]	998.4835	57.63	0.958521105
63652452	DLTDYLMK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	998.4835	57.63	0.958521105
58037465	DLTTAGAVTQCYR		Ribosomal protein L18A [Mus musculus]	1398.6791	64.97	1.086158517
34328286	DLVPDLSNFYAQYK		succinate dehydrogenase Ip subunit [Mus musculus]	1672.8037	29.35	0
29293809	DLVSSLTSGLLTIGDR		ATP citrate lyase [Mus musculus]	1646.9008	69.04	1.878840293
6671507	DLYANNVLSGGTTMYPGIADR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2228.1086	147.14	0.413817086
6671507	DLYANNVLSGGTTMYPGIADR	2 Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2230.0652	19.08	0
6671507	DLYANNVLSGGTTMYPGIADR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2229.0518	118.28	0
6671507	DLYANNVLSGGTTMYPGIADR	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2244.063	39.17	0.411398634
6671509	DLYANTVLSGGTTMYPGIADR		actin, beta, cytoplasmic [Mus musculus]	2215.0906	131.49	1.024873223
63652452	DLYANTVLSGGTTMYPGIADR		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2215.0906	131.49	1.024873223
6671509	DLYANTVLSGGTTMYPGIADR	Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	2231.0759	26.92	0.932840687
63652452	DLYANTVLSGGTTMYPGIADR	Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2231.0759	26.92	0.932840687
20137006	DMFQETMEAMR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1388.5675	30.45	1.535778082
6755626	DMLYQVLAAEEPSVR		sepiapterin reductase [Mus musculus]	1720.8597	50.76	1.098106876
21450277	DMTSEELDDILR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1436.6592	45.55	1.174477905
8567336	DMVTQASPYLFEATGK		chloride channel calcium activated 3 [Mus musculus]	1757.8477	98.59	0.354127862
8567336	DMVTQASPYLFEATGK	Oxidation (M)	chloride channel calcium activated 3 [Mus musculus]	1773.8328	69.15	0
8567336	DNCVFVPDPHQNEK		chloride channel calcium activated 3 [Mus musculus]	1641.7434	80.45	0.136042175
6681219	DNFTAIPEGTNGVEER		dihydropyrimidinase-like 3 [Mus musculus]	1748.8147	60.8	1.560578644
40254595	DNFTLIPEGTNGTEER		dihydropyrimidinase-like 2 [Mus musculus]	1792.8273	54.31	1.245241376
21361209	DNIQGITKPAIR		germinal histone H4 [Mus musculus]	1325.7654	70.56	0.691764922
33563250	DNLIDDLQR		desmin [Mus musculus]	1101.5559	54.6	0.677391023
29789080	DNNQFASASLDR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1337.6088	30.2	1.51692704
6678483	DNPGVVTCLDEAR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1388.6544	26.6	0
23621467	DNTINLIHTFR		PREDICTED: actin related protein 2/3 complex, subunit 2 [Mus musculus]	1343.7095	41.58	1.979442771
31543942	DPNASPGDAGEQAIR		vinculin [Mus musculus]	1497.7013	81.35	0.696391843
31982437	DPQLVPILIDAAR		NAD(P) dependent steroid dehydrogenase-like [Mus musculus]	1420.8073	23.78	0
6755809	DPVQLNLLYVQAR		talin 1 [Mus musculus]	1528.8441	46.11	0
6680572	DQDNMQAELNR		kinesin family member 5B [Mus musculus]	1333.589	34.01	2.23429805
63481281	DQDVEPGAPSMGAK		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1401.6346	53.28	0
31980648	DQEGQDVLLFIDNIFR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1921.9677	55.18	1.424137773
33620739	DQGTYEDYVEGLR		myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Mus musculus]	1544.6912	44.98	1.024143961
6754556	DQMQQQLSDYEQLLDVK		lamin B1 [Mus musculus]	2080.9829	60	0
6754254	DQVANSAFVER		heat shock protein 1, alpha [Mus musculus]	1235.6061	71.44	2.3289529

6679058	DSGQFTDEFLPEQR		nidogen 2 [Mus musculus]	1668.7588	33.02	0
6753266	DSISLSPEQLAQLR		carbonic anhydrase 1 [Mus musculus]	1556.8344	70.03	7.886092213
6755040	DSLLQDGEFTMDLR		profilin 1 [Mus musculus]	1639.7693	80.78	1.9730787
6678682	DSNNLCLHFNPR		lectin, galactose binding, soluble 1 [Mus musculus]	1429.6724	54.17	0.719690162
28916693	DSQEEEKTEALTSAK		gelsolin [Mus musculus]	1665.7805	67.06	1.123610103
31543976	DSTLIMQLLR		3-monooxgenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide [Mus musculus]	1189.6665	66.12	1.189925243
31543974	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Mus muscu	1189.6665	66.12	1.189925243
31981925	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Mus mu	1189.6665	66.12	1.189925243
6756039	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Mus musc	1189.6665	66.12	1.189925243
6756041	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	1189.6665	66.12	1.189925243
6753374	DTANWLEINPETGAIFTR		cadherin 1 [Mus musculus]	2048.0117	37.22	2.03498559
41322904	DTHDQLSEPSEVR		plectin 1 isoform 1 [Mus musculus]	1512.7045	77.43	1.868147501
9790067	DTNGENIAESLVAEGLATR		staphylococcal nuclease domain containing 1 [Mus musculus]	1959.9623	93.5	1.029538487
6755142	DTNGSQFFITTVK		peptidylprolyl isomerase B [Mus musculus]	1457.7267	58.93	0
6680163	DTPGFIVNR		L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1018.5359	39.7	1.687557146
42476274	DTPTQEDWLVSVLPEGSR		X-prolyl aminopeptidase (aminopeptidase P) 1, soluble [Mus musculus]	2028.9816	31.74	0
7305295	DVASLGSQLQDTQELLQEETR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2360.1843	138.56	0
29150272	DVAWAPSIGLPTSTIASCSQDGR		SEC13 related gene [Mus musculus]	2332.1245	32.9	1.593195282
63746482	DVDIIDHHDNTYTVK		PREDICTED: filamin, alpha [Mus musculus]	1784.8405	31.29	0
6678726	DVDPDVAYSSIPYEK		leukotriene A4 hydrolase [Mus musculus]	1697.8202	30.27	0
7305515	DVGGNNGGSGNGGGAAFSQTR		trans-acting transcription factor 1 [Mus musculus]	1879.8306	29.82	0
7305515	DVGGNNGGSGNGGGAAFSQTR	Deamidation (NQ)	trans-acting transcription factor 1 [Mus musculus]	1880.8234	27.46	1.725718804
27804325	DVPALEITHTFLER		monoamine oxidase A [Mus musculus]	1640.8677	23.98	2.166409566
51709169	DVPNPNQVDDDDEGFR		PREDICTED: similar to 80 kDa nuclear cap binding protein (NCBP 80 kDa subunit) (CBP80) [Mus musculu	1831.7888	30.14	0
7304885	DVQELYAAGENR		annexin A11 [Mus musculus]	1364.6433	28.81	0
24429590	DVVLAYPEVR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1160.6285	37.68	3.674227215
20532346	DVYEDELVPVFETVGR		hypothetical protein LOC245945 [Mus musculus]	1866.915	48.47	2.758916706
51467513	DXSHYFKTIQDLR		PREDICTED: similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18) [Homo sapiens]	1708.8495	47.59	0
6754220	DYFEQYGK		heterogeneous nuclear ribonucleoprotein A1 [Mus musculus]	1049.4636	34.71	1.217849168
27369998	DYFLFNPVTDIEEIIR		calcium-binding transporter [Mus musculus]	1984.016	62.75	2.519092888
13384736	DYIPVDQEELR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1376.668	32.87	0.985104929
13385942	DYIWNTLNSGR		citrate synthase [Mus musculus]	1338.6522	57.26	1.473355335
7304887	DYPGFSPSVDAEAIR		annexin A3 [Mus musculus]	1623.7693	29.74	1.269670894
14149756	DYTYEELLNR		eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus]	1315.6155	24.08	0
6755809	EAAFHPEVAPDVR		talin 1 [Mus musculus]	1437.7192	58.92	0.825553017
31982290	EAAYAPPASGNQNHPGMYPVSGPK		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	2440.1475	50.3	0
42415475	EADDIVNWLK		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1202.6152	39.76	1.042916652
15426055	EAELLEPLMPAIR		coatomer protein complex, subunit beta 1 [Mus musculus]	1481.8051	22.3	1.459994787
47578123	EAEYFELPELVR		potassium channel tetramerisation domain containing 12 [Mus musculus]	1494.7455	29.86	0
63474405	EAFEEMEGTSPSSPPHSVAR		PREDICTED: tensin [Mus musculus]	2144.96	52.79	0.781040902
63492583	EAFNMIDQNR		PREDICTED: myosin regulatory light polypeptide 9 [Mus musculus]	1237.5682	44.05	1.266712622
18152793	EAINQGMDEELERDEK		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1905.8652	23.46	1.14395928
6679599	EAINVEQAFQTIAR		RAB7, member RAS oncogene family [Mus musculus]	1589.8317	38.5	0
30409988	EALNVFGDDYATEDGTGVR		galactose-4-epimerase, UDP [Mus musculus]	2028.9208	40.5	1.87032675
15808988	EALTYDGALLGDR		Williams-Beuren syndrome chromosome region 1 homolog [Mus musculus]	1393.6992	40.18	1.58104764
31981515	EANNFLWPFK		ribosomal protein L7 [Mus musculus]	1265.6323	50.48	1.066017971
6677799	EAPPMEKPEVVK		ribosomal protein S15 [Mus musculus]	1353.7126	43.64	2.840373996
29336026	EAQAGLAEAQEDLEAER		nonmuscle myosin heavy chain [Mus musculus]	1829.8575	48.79	1.397748577
7305395	EAQIFDYNEIPNFPQSTVQGHAGR		purine-nucleoside phosphorylase [Mus musculus]	2718.2842	58.36	1.360776235
6679687	EATNPPIIQEEKPK		glucose regulated protein [Mus musculus]	1593.8523	97.3	1.19333896
63746482	EATTEFSVDAR		PREDICTED: filamin, alpha [Mus musculus]	1225.5706	68.19	0.812532818
12963539	EAVLIDPVLETAHR		ETHE1 protein [Mus musculus]	1562.8641	31.88	0
6680748	EAYPGDVFYLHSR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1553.7457	77.53	1.345691766
63556656	ECGILADPEGPFR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1403.6625	40.74	0.310176326
63562740	EDALMVELDSR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1277.6083	45.91	1.026253911
46575903	EDAPVGPHLQSMPSEQIR		eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus musculus]	1990.9688	25.05	1.025907254
6756033	EDGNEEDKENQGDETQGQPPQR		nuclease sensitive element binding protein 1 [Mus musculus]	2628.1067	139.69	1.284187461
29789191	EDGTFYEFGDDIPEAPER		asparaginyl-tRNA synthetase [Mus musculus]	2086.9063	26.97	1.101352022
33859482	EDLYLKPIQR		eukaryotic translation elongation factor 2 [Mus musculus]	1274.7175	39.93	2.612074454
6754254	EDQTEYLEER		heat shock protein 1, alpha [Mus musculus]	1311.5753	62.72	1.728229389

40556608	EDQTEYLEER		heat shock protein 1, beta [Mus musculus]	1311.5753	62.72	1.728229389
31982755	EEAESTLQSFR		vimentin [Mus musculus]	1296.6112	52.87	0.888859579
6755863	EEEAIQLDGLNASQIR		tumor rejection antigen gp96 [Mus musculus]	1785.9111	76.93	0
15617203	EEFASTCPDDEEIELAYEQVAR		chloride intracellular channel 1 [Mus musculus]	2544.1262	59.45	1.252771578
21312994	EEGVPTLWR		solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11 [Mus musculus]	1086.5511	25.99	1.240695112
6753036	EEIFGPVMQILK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1403.7395	35.4	0.573309906
21312260	EEIFGPVQPLFK		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1403.7585	25.48	0
63476037	EELSSLKPILTPSTGAGVGSK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2071.1282	41.32	0
6755863	EESDDEAAVEEEEEEKKPK		tumor rejection antigen gp96 [Mus musculus]	2219.9744	86.59	0
31560222	EESGAVAAAASVPAQSTAR		PYD and CARD domain containing [Mus musculus]	1772.8829	90.13	2.112000181
7710042	EEVQAGVDAANSAAQQYQR		IQ motif containing GTPase activating protein 1 [Mus musculus]	2034.95	35.23	1.682676526
6679587	EFADSLGIPFLETSAK		RAB1, member RAS oncogene family [Mus musculus]	1724.8763	58.87	0
31542159	EFDDLSPEQQR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	1363.6304	43.08	2.339232609
6806903	EFDELSPSAQR		ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	1278.6044	56.6	1.36171662
21704156	EFDPTITDGSLSGPSR		caldesmon 1 [Mus musculus]	1678.7949	78.12	0.993999892
51491880	EFEEESKQPGVSEQQR		metastasis-associated protein 2 [Mus musculus]	1906.8868	51.66	0.936624819
31982275	EFSITDVVPYPISLR		heat shock protein 4 [Mus musculus]	1735.9281	46.87	1.65439844
21426821	EGDVLTLLESER		ribosomal protein S28 [Mus musculus]	1360.7057	61.91	1.028510452
63594458	EGDYFTQQGEFR		PREDICTED: source of immunodominant MHC-associated peptides [Mus musculus]	1476.6497	51.8	1.050190298
33859482	EGIPALDNFLDKL		eukaryotic translation elongation factor 2 [Mus musculus]	1444.7664	84.3	1.283836016
6754254	EGLELPEDEEEKKK		heat shock protein 1, alpha [Mus musculus]	1672.7954	35.45	0
40556608	EGLELPEDEEEKKK		heat shock protein 1, beta [Mus musculus]	1672.7954	35.45	0
6679439	EGMNIVEAMER		peptidylprolyl isomerase A [Mus musculus]	1278.5895	57.79	1.277044716
63650244	EGMNIVEAMER		PREDICTED: similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase) (Cyclophilin A) (Cy	1278.5895	57.79	1.277044716
31981549	EGNALFTFPNTPVK		sulfide quinone reductase-like [Mus musculus]	1534.7935	26.83	1.599130727
31980648	EGNDLYHEMIESGVINLK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2061.0042	96.29	2.493154505
63746482	EGSYSISVLYGEEEVPR		PREDICTED: filamin, alpha [Mus musculus]	1913.9089	44.36	1.053481482
6753882	EGTGTETPMIGDR		FK506 binding protein 4 [Mus musculus]	1363.6234	32.97	0
18079339	EGWPLDIR		aconitase 2, mitochondrial [Mus musculus]	985.5092	42.83	1.634486593
12963527	EHNGQVTGIDWAPESNR		actin related protein 2/3 complex, subunit 1B [Mus musculus]	1909.8871	60.6	1.114961442
51592084	EIEIAEQEMPALMALR		hypothetical protein LOC74340 [Mus musculus]	1843.9252	32.06	1.995422848
26986563	EIFAQEALAPFR		choline dehydrogenase [Mus musculus]	1391.7301	29.5	15.69436739
7305085	EIFEQPESVVNTMR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1678.8193	62.03	1.504668478
6755901	EIIDLVLDR		tubulin, alpha 1 [Mus musculus]	1085.6199	38.52	1.130250138
34740335	EIIDLVLDR		tubulin, alpha 2 [Mus musculus]	1085.6199	38.52	1.130250138
6678469	EIIDLVLDR		tubulin, alpha 6 [Mus musculus]	1085.6199	38.52	1.130250138
6680924	EILVGDVGQTVDDPYTTFVK		cofilin 1, non-muscle [Mus musculus]	2196.1125	57.31	0
27804325	EIPVDAPWQAR		monoamine oxidase A [Mus musculus]	1281.6617	50.82	2.509552517
6671507	EITALAPSTMK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1161.6219	73.57	0.795753565
6671509	EITALAPSTMK		actin, beta, cytoplasmic [Mus musculus]	1161.6219	73.57	0.795753565
63652452	EITALAPSTMK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1161.6219	73.57	0.795753565
6671507	EITALAPSTMK	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1177.606	22.88	0
6671509	EITALAPSTMK	Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	1177.606	22.88	0
63652452	EITALAPSTMK	Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1177.606	22.88	0
12963615	EIVHIQAGQCGNQIGAK		tubulin, beta 3 [Mus musculus]	1765.9036	41.15	0
7106439	EIVHIQAGQCGNQIGAK		tubulin, beta 5 [Mus musculus]	1765.9036	41.15	0
21746161	EIVHIQAGQCGNQIGAK		tubulin, beta [Mus musculus]	1765.9036	41.15	0
7949051	EKPYFPIPEDCTFIQNVPLEDR		heterogenous nuclear ribonucleoprotein U [Mus musculus]	2650.2869	35.41	1.560941651
6755372	ELAEDGYSGVEVR		ribosomal protein S3 [Mus musculus]	1423.6747	54.32	1.55868662
51712562	ELAPYDENWFYTR		PREDICTED: similar to ribosomal protein S19 [Mus musculus]	1703.7775	57.59	1.182498341
6681157	ELAQQVQQVAAEYCR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1735.8402	19.22	1.501385543
24429590	ELDALDANDELTPLGR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1741.8639	55.75	0.835092577
7305295	ELDEATESNEAMGR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1551.6761	45.1	0
19482160	ELEEDFIR		coactosin-like 1 [Mus musculus]	1050.5161	36.06	0.850258053
6677813	ELEFYLR		ribosomal protein S8 [Mus musculus]	969.5036	36.2	1.462961505
7305295	ELEGHISDLQEDLDSER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1984.9204	113.75	0.906961703
20137006	ELETQISELQEDLESER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2047.9722	102.62	1.316719813
63476037	ELGTIQQVISER		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1372.7444	62.62	0.881178443
13385878	ELILSSEPSPAVTPVTPTTLIAPR		sorting nexin 2 [Mus musculus]	2489.3777	53.48	2.838426337
13386054	ELLLQPVTISR		actin related protein 2/3 complex, subunit 4 [Mus musculus]	1268.7592	24.22	1.238508298

6679687	ELNDFISYLQR		glucose regulated protein [Mus musculus]	1397.7157	84.94	1.071328389
11230802	ELPPDQAEYCIAR		actinin alpha 4 [Mus musculus]	1504.7156	43.89	0
33563250	ELQAQLQEQQVQVEMDMSKPDLTAALR		desmin [Mus musculus]	3099.5347	52.53	0.670808552
30023842	ELQELVQYPVEHPDK		valosin containing protein [Mus musculus]	1823.9209	63.24	0
13624315	ELQSQISDTSVVLSMDNSR		keratin complex 2, basic, gene 8 [Mus musculus]	2109.0198	140.63	1.853730433
63565108	ELQSQISDTSVVLSMDNSR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	2109.0198	140.63	1.853730433
31981748	ELSLASNELKDEGAR		ribonuclease/angiogenin inhibitor 1 [Mus musculus]	1631.8119	25.73	2.364007873
29336026	ELSSAESQLHDTQELLQEETR		nonmuscle myosin heavy chain [Mus musculus]	2443.1567	40.03	0
31982755	EMEENFALEAANYQDTIGR		vimentin [Mus musculus]	2200.9888	102.26	0
7305295	EMEGLSQQYEEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1470.6537	62.83	1.407875239
6671666	EMNDAAMFYTNR		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1462.6216	33.27	1.310662261
7305295	ENADLAGELR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1087.5403	74.44	0.793013598
31560680	ENDYYTPTGEFR		intergral membrane protein 1 [Mus musculus]	1491.647	66.87	1.17711637
21450129	ENGTITAANASTLNDGAAALVLMTAEAAQR		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	2945.4478	47.94	1.516306308
31982522	ENLLGEPGMGFK		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1291.6333	32.13	1.161425772
22267442	ENMAYTVEGIR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1282.6082	26.87	0
6754508	EPAAPVSIQR		LIM and SH3 protein 1 [Mus musculus]	1067.5874	23.48	1.012870434
33469029	EPGEAAAEGAAEEAR		acyl-Coenzyme A binding domain containing 3 [Mus musculus]	1457.6556	60.61	1.313486083
31982290	EPIMPAPGQEETVR		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1553.7703	68.32	1.414915559
31981657	EPITVSSEQMSHFR		carbonic anhydrase 2 [Mus musculus]	1647.7902	113.71	2.548636147
13385268	EQAGGDATENFEDVGHSTDAR		cytochrome b-5 [Mus musculus]	2205.9436	67.92	0
13385728	EQEAEPEEQEEDSSSDPR		microfibrillar-associated protein 1 [Mus musculus]	2090.8313	54.72	0
6680836	EQFLDGDAWTNR		calreticulin [Mus musculus]	1451.6637	99.56	1.04195356
22094075	EQGVLSFWR		solute carrier family 25, member 5 [Mus musculus]	1121.5804	61.6	1.784203709
50355690	EQIVPKPEEEVAQK		ribosomal protein L17 [Mus musculus]	1623.8651	65.71	0
6678499	EQIVVDLSHPGVSADDQVSR		UDP-glucose dehydrogenase [Mus musculus]	2151.0769	65.75	2.854626256
21450277	EQPLDEELKDAFQNAYLELGGLGER		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2834.3835	114.5	1.621053021
13384736	EQPWVSVQPR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1225.6394	22.58	0
13591862	EQQEAIEHIDEVQNEIDR		SET translocation [Mus musculus]	2195.0234	45.8	1.038230658
18700024	EQTEGEYSSLEHESAK		isocitrate dehydrogenase 3, beta subunit [Mus musculus]	1823.8037	46.71	1.216669554
40556608	EQVANSAFVER		heat shock protein 1, beta [Mus musculus]	1249.6182	47.02	2.266521683
39930557	EQVNLMNAAINELNVR	2 Deamidation (NQ)	A kinase (PRKA) anchor protein (yotiao) 9 [Mus musculus]	1829.8816	22.3	0.885578005
6678752	ESPYDHQSLQTALQEAFTSR		lymphocyte antigen 74 [Mus musculus]	2308.085	20.45	1.381235578
6754994	ESTGAQVQVAGDMLPNSTER		poly(rC) binding protein 1 [Mus musculus]	2089.9912	104.44	1.249973549
42734399	ESVQLYEDEVR		desmuslin isoform H [Mus musculus]	1366.6575	23.95	0.937193063
9910482	ESVQVPDDQDFR		START domain containing 10 [Mus musculus]	1434.6688	37.33	1.533046566
20874851	ESYSVYVYK		PREDICTED: similar to histone H2b-616 [Mus musculus]	1137.547	39.1	0
6754484	ETMQFLNDR		keratin complex 1, acidic, gene 1 [Mus musculus]	1153.5388	21.09	0
31982223	ETPSWTGPGFVR		laminin, beta 2 [Mus musculus]	1333.6576	20.07	0.603971562
63492203	ETSYEEALANQR		PREDICTED: ribosome binding protein 1 [Mus musculus]	1410.6593	52.05	1.614954655
30023842	ETVVEVPQVTWEDIGGLEDVKR		valosin containing protein [Mus musculus]	2498.2646	67.83	0
6680748	EVAAFAQFGSDLDAATQQLLSR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2338.1721	125.18	1.350338536
31560449	EVAGQVGVPLQDLMVR		aspartyl aminopeptidase [Mus musculus]	1710.9169	32.68	1.079962678
22208854	EVAYLGNEVSDEECLKR		cytidine monophospho-N-acetylneuraminic acid synthetase [Mus musculus]	1953.9417	21.1	2.525927526
30348966	EVDDLEQWIAER		spectrin beta 2 isoform 1 [Mus musculus]	1502.724	33.52	1.634172209
63650229	EVDEQMLNVQNK		PREDICTED: similar to TUBULIN BETA CHAIN (T BETA-15) [Mus musculus]	1446.7034	60.54	1.204493532
22165384	EVDEQMLNVQNK		tubulin, beta, 2 [Mus musculus]	1446.7034	60.54	1.204493532
7106439	EVDEQMLNVQNK		tubulin, beta 5 [Mus musculus]	1446.7034	60.54	1.204493532
21746161	EVDEQMLNVQNK		tubulin, beta [Mus musculus]	1446.7034	60.54	1.204493532
30023842	EVDIGIPDATGR		valosin containing protein [Mus musculus]	1242.635	60.95	1.382322343
12963527	EVEERPAPTPWGSK		actin related protein 2/3 complex, subunit 1B [Mus musculus]	1582.7936	26.3	0.976962787
14149756	EVEPEPTEEKDVDADEEDSR		eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus]	2317.9822	115.56	1.721693207
46593021	EVESIGAHLNAYSTR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1646.8226	34.61	2.791851359
31543315	EVFEDAMEIR		nucleolin [Mus musculus]	1238.5793	38.49	1.553483161
31980685	EVGAFGTPVINLGTR		glucosamine [Mus musculus]	1530.8274	44.52	1.851794904
7106435	EVIVGPDTTSYSLADLSPSTHYSAR		tenascin C [Mus musculus]	2666.2922	28.04	1.366954474
7305295	EVLLQVEDER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1229.6368	19.1	0
6678573	EVQGNESETFR		villin 1 [Mus musculus]	1295.5946	21.87	1.638677047
21450129	EVYMGNVIQGGEGQAPTR		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	1905.922	93.61	1.48107968
31560611	EWIEGVTGR		calponin 1 [Mus musculus]	1046.5333	49.93	0.54207268

33563250	EYQDLLNVK		desmin [Mus musculus]	1121.5824	49	0
34328368	EYQDLLNVK		internexin neuronal intermediate filament protein, alpha [Mus musculus]	1121.5824	49	0
46275814	EYQDLLNVK		neurofilament, heavy polypeptide [Mus musculus]	1121.5824	49	0
31982755	EYQDLLNVK		vimentin [Mus musculus]	1121.5824	49	0
41054806	EYQLNDSAAYYLNDLER		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	2076.9604	43.06	1.060430265
63635087	EYSSELNAPSQESDSHPR		PREDICTED: RNA binding motif protein 25 [Mus musculus]	2032.8898	73.92	1.664077833
31560560	FAAATGATPIAGR		laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1203.6522	60.7	1.377006512
31982755	FADLSEAANR		vimentin [Mus musculus]	1093.5325	54.79	1.137617975
31560613	FAEAFEAIPR		chaperonin subunit 8 (theta) [Mus musculus]	1150.59	26.1	1.637345274
6753240	FAMEPEEFDSDTLR		calcium binding protein, intestinal [Mus musculus]	1686.7351	74.69	0.882522964
21704206	FAPPEAPEPWSGVR		carboxylesterase 2 [Mus musculus]	1539.7645	32.74	2.310633706
27370126	FAPPEAPEPWSGVR		carboxylesterase 5 [Mus musculus]	1539.7645	32.74	2.310633706
33563250	FASEANGYQDNIAR		desmin [Mus musculus]	1555.7178	105.98	0.618934088
33563250	FASEANGYQDNIAR	Deamidation (NQ)	desmin [Mus musculus]	1556.7059	73.76	1.049208403
63476037	FASEIVDTVYEDGDSIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1915.8905	55.87	0
31560611	FASQQGMTAYGTR		calponin 1 [Mus musculus]	1417.6675	107.69	0.916420337
6679299	FDAGELITQR		prohibitin [Mus musculus]	1149.5857	22.25	1.510276892
31980685	FDALALATSAALMNIR		glucosamine [Mus musculus]	1677.8997	25.11	1.136327128
6678573	FDALTMHVQPQVAAQQK		villin 1 [Mus musculus]	1911.9772	76.51	1.963677272
63638100	FDGALNVDLTEFQTNLVPYPR		PREDICTED: similar to tubulin, alpha 1 [Mus musculus]	2409.2056	60.81	1.488576928
6755901	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 1 [Mus musculus]	2409.2056	60.81	1.488576928
34740335	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 2 [Mus musculus]	2409.2056	60.81	1.488576928
6678467	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 4 [Mus musculus]	2409.2056	60.81	1.488576928
6678469	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 6 [Mus musculus]	2409.2056	60.81	1.488576928
6677805	FDTGNLCMVTGGANLGR		ribosomal protein S4, X-linked [Mus musculus]	1725.8112	35.3	1.550173895
21704020	FEAPLFNAR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	1064.5706	27.27	1.429089092
6679439	FEDENFILK		peptidylprolyl isomerase A [Mus musculus]	1154.5732	56.44	1.09927484
10092608	FEDGDLTLYQSNAILR		glutathione S-transferase, pi 1 [Mus musculus]	1854.9027	101.64	1.573953642
31981690	FEELNADLFR		heat shock protein 8 [Mus musculus]	1253.62	62.29	1.554757872
31981722	FEELNMDLFR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1313.6305	27.1	1.098449389
9790073	FEEQVYNIPIR		cadherin 17 [Mus musculus]	1407.7323	52.31	1.895830804
13385374	FEIWDTAGQER		RAB5A, member RAS oncogene family [Mus musculus]	1351.6365	35.94	1.143830256
29789257	FEIWDTAGQER		RAB5C, member RAS oncogene family [Mus musculus]	1351.6365	35.94	1.143830256
31981690	FELTGIPPAPR		heat shock protein 8 [Mus musculus]	1197.6589	26.89	1.679664631
30348966	FESLEPEMNNQASR		spectrin beta 2 isoform 1 [Mus musculus]	1651.7472	22.4	1.461129231
6678483	FEVQGLQPNGEEMTLK		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1819.8656	24.61	1.047622178
6678145	FFDEESYSLLR		signal sequence receptor, delta [Mus musculus]	1405.6532	65.85	1.825416354
8567336	FFTAFDANGR		chloride channel calcium activated 3 [Mus musculus]	1145.5439	47.29	0.340466696
8567336	FFTAFDANGR	Deamidation (NQ)	chloride channel calcium activated 3 [Mus musculus]	1146.5366	29.89	0
63746482	FGGEHVPNSPFQVTALAGDQPTVQTPLR		PREDICTED: filamin, alpha [Mus musculus]	2963.4971	44.58	0.750765239
21704096	FGGNPGGFGNQGGFGNSR		TAR DNA binding protein isoform 1 [Mus musculus]	1726.7775	48.02	1.564847476
13384736	FGNPLLVQDVESYDPVLNPVLNR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	2598.3457	25.17	1.119906302
40538823	FGQKGTLMR		GLI-Kruppel family member HKR1 [Mus musculus]	1037.5421	26.83	0
31981562	FGVEQDVDMVFASFIR		pyruvate kinase 3 [Mus musculus]	1859.91	49.39	1.709570401
27413160	FHQLDIDDPQSIR		carbonyl reductase 3 [Mus musculus]	1583.7878	28.95	0
6671690	FHQLDIDNPQSIR		carbonyl reductase 1 [Mus musculus]	1582.8038	61.4	1.961359143
52317152	FIEGPVTYSEAPR		phospholipase A2, group IVC (cytosolic, calcium-independent) [Mus musculus]	1465.7318	26.17	0
6678097	FIEWTR		serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	851.4426	33.84	1.477410397
6679687	FISDKDASVVGFFR		glucose regulated protein [Mus musculus]	1587.8179	34.26	1.746464557
18079339	FKLEAPDADELPR		aconitase 2, mitochondrial [Mus musculus]	1500.7715	54.47	1.547531498
33563250	FLEQQNAALAAEVNR		desmin [Mus musculus]	1673.8616	87.92	0
6678643	FLEQQNKVLQTK		keratin complex 2, basic, gene 1 [Mus musculus]	1475.7935	70.04	0
6755740	FLESLPEEEQQR		upstream binding transcription factor, RNA polymerase I [Mus musculus]	1504.7225	24.61	0
31981246	FLIDGFPR		UMP-CMP kinase [Mus musculus]	964.5211	34.59	1.479196868
29336026	FLTNGPSSSPGQER		nonmuscle myosin heavy chain [Mus musculus]	1476.7122	76.03	2.063359401
30348966	FMELLEPLSER		spectrin beta 2 isoform 1 [Mus musculus]	1363.7058	19.61	0
13384828	FMTEDTTDAPFR		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1430.6307	59.84	1.213611055
6671622	FNASQLITQR		B-cell receptor-associated protein 37 [Mus musculus]	1177.6294	49.06	1.420265328
63540743	FNDEHIPDSPFVVPVASLSDDAR		PREDICTED: filamin C, gamma [Mus musculus]	2527.2151	44.22	0.592599093
63660302	FNDEHIPDSPYLVPVIAPSDDAR		PREDICTED: filamin B, beta [Mus musculus]	2567.2388	53.97	1.395124575

63746482	FNEEHIPDSPFVVPVASPSGDAR		PREDICTED: filamin, alpha [Mus musculus]	2467.1951	96.74	0.620686138
63746482	FNGTHIPGSPFK		PREDICTED: filamin, alpha [Mus musculus]	1301.649	40.13	0.676761724
18079339	FNPETDFLTGK		aconitase 2, mitochondrial [Mus musculus]	1268.6332	39.4	1.169814209
6677777	FNPFVTSDR		ribosomal protein L26 [Mus musculus]	1082.5311	48.06	1.262420244
6753272	FNSANEDNVTQVR		catalase [Mus musculus]	1493.7028	59.8	1.351018852
27228985	FNVSATPEQYVPYSTTR		13kDa differentiation-associated protein [Mus musculus]	1959.9514	29.03	0
22165384	FPGQLNADLR		tubulin, beta, 2 [Mus musculus]	1130.5992	50.56	1.207159208
12963615	FPGQLNADLR		tubulin, beta 3 [Mus musculus]	1130.5992	50.56	1.207159208
31981939	FPGQLNADLR		tubulin, beta 4 [Mus musculus]	1130.5992	50.56	1.207159208
7106439	FPGQLNADLR		tubulin, beta 5 [Mus musculus]	1130.5992	50.56	1.207159208
27754056	FPGQLNADLR		tubulin, beta 6 [Mus musculus]	1130.5992	50.56	1.207159208
21746161	FPGQLNADLR		tubulin, beta [Mus musculus]	1130.5992	50.56	1.207159208
30911099	FPQLDDTSFANSR		fatty acid synthase [Mus musculus]	1497.6996	26.5	2.07047654
8567336	FPSPVTVYASIR		chloride channel calcium activated 3 [Mus musculus]	1336.7303	80.14	0.152568241
51771420	FPTLWSGAR		PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1034.5413	25.95	1.466630279
40254595	FQLTDSQIYEVLSVIR		dihydropyrimidinase-like 2 [Mus musculus]	1911.0327	32.11	0.930851465
6755863	FQSSHHSTDITSLDQYVER		tumor rejection antigen gp96 [Mus musculus]	2250.0479	67.79	0.81731602
23943876	FSHSGNQLDGPITAFR		zymogen granule membrane protein 16 [Mus musculus]	1746.8605	68.59	1.033735746
31543113	FSLVGIAGQDLNEGNR		lymphocyte cytosolic protein 1 [Mus musculus]	1689.8535	30.42	0
6671539	FSNEEIAMATVTALR		aldolase 1, A isoform [Mus musculus]	1652.8354	44.34	1.37338642
30578429	FSPLMTAEGLGTR		hypothetical protein LOC94184 [Mus musculus]	1379.6974	35.52	1.795552351
28893559	FSPPEETGPSR		melanoma inhibitory activity 3 [Mus musculus]	1203.5654	29.45	1.241576951
1346343	FSSCGGGGGSFGAGGGFGSR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1708.7263	28.99	0.449201489
33859482	FSVSPVVR		eukaryotic translation elongation factor 2 [Mus musculus]	890.5062	25.82	1.18485759
31980648	FTQAGSEVSALLGR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1435.7526	96.48	1.191416467
31980648	FTQAGSEVSALLGR	Deamidation (NQ)	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1436.7588	49.96	0
13384736	FTQDTQPHYIYSPR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1752.8468	46.02	0
9790067	FVDGEWYR		staphylococcal nuclease domain containing 1 [Mus musculus]	1071.5005	19.87	0
31982178	FVEGLPINDFSR		malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1393.7152	69.78	1.392467344
31982186	FVFSLVDAMNGK		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1327.6737	26.81	0
21704144	FVIGGPQGDAGLTGR		methionine adenosyltransferase II, alpha [Mus musculus]	1444.7561	43.99	3.538092678
40068493	FVINYDYPNSSEDYVHR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	2117.9739	30.57	1.175296374
6679687	FVMQEEFSR		glucose regulated protein [Mus musculus]	1172.5493	32.19	0.983129897
6679753	FVNVVPTFGK		Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) [Mus musc	1107.611	43.49	0
6680606	FVTSSSGSYGGVR		keratin complex 1, acidic, gene 19 [Mus musculus]	1303.6354	84.15	1.771019212
6679012	FYEEVHDLER		nucleosome assembly protein 1-like 4 [Mus musculus]	1336.6282	31.53	1.180267175
6678571	FYPEDVAEELIQDITQK		villin 2 [Mus musculus]	2038.0093	73.65	1.418100531
6754750	FYPEDVSEELIQDITQR		moesin [Mus musculus]	2082.0002	65.04	0.630479746
22122523	FYQASTSELYGK		GDP-mannose 4, 6-dehydratase [Mus musculus]	1393.6581	46.38	3.540344768
6679937	GAAQNIIPASTGAAK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1369.7462	103.01	1.185563407
20806532	GAEAANVTGPDGVPVEGSR		cold shock domain protein A short isoform [Mus musculus]	1782.8549	20.37	0
6756033	GAEAANVTGPGGVPVQGSK		nuclease sensitive element binding protein 1 [Mus musculus]	1695.8685	100.07	1.397236379
55741460	GAEEMETVIPVDVMR		DJ-1 protein [Mus musculus]	1675.8127	54.97	0
7304887	GAGTDEFTLNR		annexin A3 [Mus musculus]	1180.5687	34.99	0
63746482	GAGTGGLGLAVEGPSEAK		PREDICTED: filamin, alpha [Mus musculus]	1570.8103	73.45	1.153891489
47059123	GAGVTLNVLEMTADDLENALK		UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	2174.1387	43.28	1.738682278
29293809	GAIVPAQEVPPPTVPMDYSWAR		ATP citrate lyase [Mus musculus]	2381.1929	55.49	1.512279613
7242197	GAVYSFDPVGSYQR		proteasome (prosome, macropain) subunit, beta type 1 [Mus musculus]	1545.7368	34.43	1.207270371
31982186	GCDVVVIPAGVPR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1281.6982	63.09	1.739921236
6679715	GDATVSYEDPPTAK		Ewing sarcoma breakpoint region 1 [Mus musculus]	1450.6666	38.77	0
21644581	GDDDVFVNPTNLLEFLSDR		UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 [Mus musculus]	2166.0427	69.94	0.855326756
31543113	GDEEGIPAVVIDMSGLR		lymphocyte cytosolic protein 1 [Mus musculus]	1757.8774	81.7	0.378913118
6753484	GDEGEVGDPGEDNNDISPR		procollagen, type VI, alpha 1 [Mus musculus]	1971.8269	68.28	0
45597447	GDGPVQGTIHFEQK		superoxide dismutase 1, soluble [Mus musculus]	1512.7535	67.07	1.596321783
6755714	GDPNWFMK		transgelin [Mus musculus]	994.4498	31.05	0.602589436
30348966	GDQVSQNGLPAEQGSPR		spectrin beta 2 isoform 1 [Mus musculus]	1739.8391	78.46	1.818929438
63660302	GEAGIPAEFSIWTR		PREDICTED: filamin B, beta [Mus musculus]	1533.7715	49.49	1.189669176
6678986	GEELLSPLNLEQAAYAR		myosin IC [Mus musculus]	1873.9705	20.68	1.048854056
27370092	GEETPVIVGSALCALEQR		Tu translation elongation factor, mitochondrial [Mus musculus]	1871.955	46.77	2.196926791
45504394	GEFFNELVGQQR		integrin beta 1 (fibronectin receptor beta) [Mus musculus]	1423.6993	36.7	1.242742497

31982178	GEFITTVQQR		malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1178.6248	45.37	1.507562053
54607098	GEGGILINSQGER		succinate dehydrogenase Fp subunit [Mus musculus]	1329.672	24.43	1.741721995
29336026	GELEDTLDSTNAQQELR		nonmuscle myosin heavy chain [Mus musculus]	1918.9	56.21	2.984492862
6754524	GEMMDLQHGSLFLK		lactate dehydrogenase 1, A chain [Mus musculus]	1605.7711	29.43	0
30841031	GESLWLNLR	Deamidation (NQ)	myosin regulatory light chain interacting protein [Mus musculus]	1088.5704	39.57	0
34328108	GETGPAGPAGPIGPAGAR		procollagen, type I, alpha 1 [Mus musculus]	1532.7882	71.62	0
21592285	GFEVQVTELR		keratin 20 [Mus musculus]	1177.6212	26.69	1.832762185
7949053	GFGDGYNGYGGGPGGGNFGGSPGYGGGR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2495.0347	131.85	1.651384567
6681069	GFGFGQGAGALVHSE		cysteine and glycine-rich protein 1 [Mus musculus]	1433.6843	96.01	0.707588718
7949053	GFGFVTFDDHDPVDK		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1695.776	78.45	1.625001056
7304885	GFGTDEQAIIDCLGSR		annexin A11 [Mus musculus]	1681.7959	29.68	0
6680027	GFIGPGIDVPAPDMSTGER		glutamate dehydrogenase 1 [Mus musculus]	1915.9348	29.08	1.298570782
6679687	GFPTIYFSPANK		glucose regulated protein [Mus musculus]	1341.6696	35.81	0
13385310	GFVDDIIQPSSTR		propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]	1434.717	34.7	2.05709272
34328204	GFVPSATSKPEGHESLVDR		valyl-tRNA synthetase 2 [Mus musculus]	2013.0031	42	0
24418933	GGENIYPAELEDFFLK		hypothetical protein LOC264895 [Mus musculus]	1841.8958	41.8	1.79008314
6755252	GGGGGGGGPGGEQETQELASK		purine rich element binding protein B [Mus musculus]	1829.8319	100.02	1.332627616
1346343	GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	2383.9514	246.08	0
7949053	GGGGNFGPGPGSNFR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1377.6469	92.18	1.287443209
6755372	GGKPEPPAMPQPVPTA		ribosomal protein S3 [Mus musculus]	1573.8066	41.56	3.765510896
34328400	GGPPFAFVEFEDPR		splicing factor, arginine/serine-rich 1 (ASF/SF2) [Mus musculus]	1564.7487	24.96	1.110684326
13928672	GGQVQVVPAAADQR		tenascin XB [Mus musculus]	1395.7329	28.89	0
29789343	GHPSAGAEEEGGSDGSAAEAEPR		eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]	2167.9148	129.26	1.277810076
33859482	GHVFEESQVAGTPMFVVK		eukaryotic translation elongation factor 2 [Mus musculus]	1961.9587	28.23	1.757238306
22165384	GHYTEGAELVDSVLDVVR		tubulin, beta, 2 [Mus musculus]	1958.9666	21.31	1.052345156
12963615	GHYTEGAELVDSVLDVVR		tubulin, beta 3 [Mus musculus]	1958.9666	21.31	1.052345156
7106439	GHYTEGAELVDSVLDVVR		tubulin, beta 5 [Mus musculus]	1958.9666	21.31	1.052345156
27754056	GHYTEGAELVDSVLDVVR		tubulin, beta 6 [Mus musculus]	1958.9666	21.31	1.052345156
21746161	GHYTEGAELVDSVLDVVR		tubulin, beta [Mus musculus]	1958.9666	21.31	1.052345156
21313262	GIEQAVQSHAVAEEEAR		inner membrane protein, mitochondrial [Mus musculus]	1823.8969	34.02	2.503053163
30425250	GIHETTFNSIMK		hypothetical protein LOC238880 [Mus musculus]	1377.6744	53.78	0
21450291	GILAADESVGTMGNR		aldolase 2, B isoform [Mus musculus]	1490.7313	25.78	0
63518159	GILFVGSGVSGGEEGAR		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1591.8092	41.61	1.91506559
31543942	GILSGTSDLLLTFDEAEVR		vinculin [Mus musculus]	2036.0447	43.75	1.725135628
6679457	GINQGQVWIGGR		proteoglycan 2, bone marrow [Mus musculus]	1284.6797	44.25	0.18417914
7709980	GISEETTTGVHNLYK		S-adenosylhomocysteine hydrolase [Mus musculus]	1648.8407	39.63	0
11230802	GISQEQMQEFR		actinin alpha 4 [Mus musculus]	1352.6307	52.17	1.659917977
51592084	GIVEESVTGVHR		hypothetical protein LOC74340 [Mus musculus]	1282.6758	28.82	0
13384736	GKEDEGEEAASPMLQIQR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1987.938	70.99	1.21094498
36031080	GLDGFQGPSGPR		procollagen, type IV, alpha 2 [Mus musculus]	1187.5878	53.7	0.831668652
10946870	GLEVTAYSPLGSSDR		aldo-keto reductase family 1, member A4 (aldehyde reductase) [Mus musculus]	1551.7498	23.97	1.300708231
6755863	GLFDEYGSK		tumor rejection antigen gp96 [Mus musculus]	1015.4771	48.51	0.713869232
6753060	GLGTDEDSILNLLTSR		annexin A5 [Mus musculus]	1703.8772	31.02	0.979431474
6996913	GLGTDEDSLIEIICSR		annexin A2 [Mus musculus]	1720.8485	58.29	1.210407661
31982159	GLGTEVPGNFQGPDPYR		hypothetical protein LOC235043 [Mus musculus]	1803.873	25.11	0
6678329	GLLIEPAANSYLLAER		transglutaminase 2, C polypeptide [Mus musculus]	1729.9501	46.71	1.140282045
7710046	GLLQQVPNAHK	2 Deamidation (NQ)	kinesin family member 21A [Mus musculus]	1206.6469	19.67	0
63746482	GLVEPVDVVDNADGTQTVNYVPSR		PREDICTED: filamin, alpha [Mus musculus]	2544.2566	147.4	0.715269342
13386272	GLVYETSVLDPDEGIR		citrate synthase-like protein [Mus musculus]	1762.8864	54.38	2.685352708
13385942	GLVYETSVLDPDEGIR		citrate synthase [Mus musculus]	1762.8864	54.38	2.685352708
6680748	GMSLNLEPDNVGVVVFGNDK		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2103.9973	39.51	1.652539735
31560611	GMTVYGLPR		calponin 1 [Mus musculus]	993.5183	43.75	0.707003186
30911099	GNAGQTNYGFANSTMER		fatty acid synthase [Mus musculus]	1817.7994	36.42	1.209839864
33859580	GNDVAFHFNPR		galectin-3 [Mus musculus]	1273.6163	64.14	2.419346912
63492583	GNFNYVEFTR		PREDICTED: myosin regulatory light polypeptide 9 [Mus musculus]	1246.5905	27.7	1.104561636
21704206	GNWGYLDQAAALR		carboxylesterase 2 [Mus musculus]	1434.7162	35.4	1.898350931
19527034	GPAPLGTFQVTTPQR		lamin B receptor [Mus musculus]	1569.8458	23.77	0.86140555
31560611	GPAYGLSAEVK		calponin 1 [Mus musculus]	1091.5737	86.93	0.795271997
6755204	GPGLYYVDSEGNR		proteasome (prosome, macropain) subunit, beta type 5 [Mus musculus]	1426.6721	20.45	0
6755698	GQNDLMGTAEDFADQFLR		surfeit gene 4 [Mus musculus]	2027.9204	146.59	1.4045096

27532959	GSASSALELTEEELATAEAVR	aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	2134.0356	48.46	0
16716467	GSDHSASLEPGELAELVR	N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1866.9211	85.37	1.295503878
29788989	GSESSKPWPDATTYGAGSASR	thyroid hormone receptor associated protein 3 [Mus musculus]	2111.9739	67.49	0.95025085
58037267	GSFSEQGINEFLR	protein disulfide isomerase-associated 6 [Mus musculus]	1483.7228	44.36	1.059951443
6678573	GSLNITTPGIQIWR	villin 1 [Mus musculus]	1555.86	53.54	1.13790256
21704156	GSVFSAPSASGTPNK	caldesmon 1 [Mus musculus]	1406.6918	50.39	0
6678449	GSVNMPFMDFLTK	thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	1486.7106	26.6	0
6754186	GSYSLSHVYTPNDVR	hexosaminidase B [Mus musculus]	1694.8112	27.65	1.181256298
7657429	GSYTYFAPSNEAWENLDSDIR	osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2435.0845	52.73	0
22094075	GTDIMYTGTLDCWR	solute carrier family 25, member 5 [Mus musculus]	1631.7345	27.99	1.958587295
6680850	GTELDDGIQADSGPINDIDANPR	caspase 7 [Mus musculus]	2383.0952	36.1	1.987240867
6753428	GTGGVDTAATGSVFDISNLDR	creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	2052.9976	107.28	2.128418589
7304887	GTGTDEDALIEILTTR	annexin A3 [Mus musculus]	1704.8691	47.28	1.448902338
31560449	GTPEPGPLGATDER	aspartyl aminopeptidase [Mus musculus]	1396.6742	43.84	1.972843945
31981826	GTSFEAAATSGGSASSEK	electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1644.7307	66.57	1.081640555
31652266	GTVAAAASGAAGGGGGGAGAGAPGGGR	hypothetical protein LOC229543 [Mus musculus]	1939.9382	26.34	0
22164798	GTWEKPGDAAPMGYDFWYQPR	selenium binding protein 1 [Mus musculus]	2472.1118	20.91	3.279578784
19526818	GVAPLWMR	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	929.5062	35.4	1.447726712
6996913	GVDEVTIVNILTNR	annexin A2 [Mus musculus]	1542.8496	71.16	1.334638165
29789257	GVDLQESNPASR	RAB5C, member RAS oncogene family [Mus musculus]	1272.6211	28.72	0.865639945
13385374	GVDLTEPAQPAR	RAB5A, member RAS oncogene family [Mus musculus]	1253.6487	25.41	0.922249639
30409956	GVGIISEGNETVEDIAAR	ATPase, Na+/K+ transporting, alpha 2 polypeptide [Mus musculus]	1829.929	106.63	1.557080014
21450277	GVGIISEGNETVEDIAAR	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1829.929	106.63	1.557080014
6755863	GVVDSDDLPLNVSR	tumor rejection antigen gp96 [Mus musculus]	1485.7578	65.42	0.894371525
6754254	GVVDSEDLPLNISR	heat shock protein 1, alpha [Mus musculus]	1513.792	89.66	1.77319245
40556608	GVVDSEDLPLNISR	heat shock protein 1, beta [Mus musculus]	1513.792	89.66	1.77319245
6671539	GVVPLAGTNGETTTQGLDGLSER	aldolase 1, A isoform [Mus musculus]	2272.1511	124.27	1.539033521
31543942	GWLRDPNASPGDAGEQAIR	vinculin [Mus musculus]	2009.98	21.65	0
22122825	GYAFNHSADFETVR	actin-related protein 2 [Mus musculus]	1613.7417	59.12	0.819838263
7305085	GYDVDFPR	glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	968.4521	35.8	1.571013396
21450625	GYDVIAQAQSGTGK	eukaryotic translation initiation factor 4A1 [Mus musculus]	1394.6914	57.96	1.543435483
59709449	GYEEWLLNEIR	actinin alpha 2 [Mus musculus]	1421.7136	51.78	0
11230802	GYEEWLLNEIR	actinin alpha 4 [Mus musculus]	1421.7136	51.78	0
63487095	GYELLFQPEVVR	PREDICTED: catenin src [Mus musculus]	1449.7766	28.1	2.405161178
7949051	GYFEYIEENK	heterogenous nuclear ribonucleoprotein U [Mus musculus]	1291.595	24.56	0
6753036	GYFIQPTVFGDVK	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1470.7659	56.47	1.563680827
6681069	GYGYGQGAGTLSTDK	cysteine and glycine-rich protein 1 [Mus musculus]	1474.698	69.38	0
6681069	GYGYGQGAGTLSTDKGESLGIK	cysteine and glycine-rich protein 1 [Mus musculus]	2159.0708	164.37	0.78173788
16716467	GYPPEDIFNLAGK	N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1420.7025	61.35	0
45598381	GYPTLLLFR	thioredoxin domain containing 5 [Mus musculus]	1079.6244	24.67	1.093681677
6671509	GYSFTTTAER	actin, beta, cytoplasmic [Mus musculus]	1132.5454	64.52	1.267661568
63652452	GYSFTTTAER	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1132.5454	64.52	1.267661568
6671507	GYSFVTTAER	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1130.5693	55.27	0.742164337
22164798	HEIIQTLQMTDGLIPLEIR	selenium binding protein 1 [Mus musculus]	2220.1897	21.98	2.119793343
6680027	HGGTIPVVPTAEFQDR	glutamate dehydrogenase 1 [Mus musculus]	1723.8844	63.07	1.643367988
22122825	HIVLSGGSTMYPGLPSR	actin-related protein 2 [Mus musculus]	1771.922	51.33	0.889113883
8567336	HLPTVSAGGTSICSGLR	chloride channel calcium activated 3 [Mus musculus]	1655.8521	69.77	0
6753010	HLSPDGQYVPR	anterior gradient 2 [Mus musculus]	1268.6426	66.64	1.139952305
6671507	HQGVMVGMGQK	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1171.5806	50.09	0.665057369
6671509	HQGVMVGMGQK	actin, beta, cytoplasmic [Mus musculus]	1171.5806	50.09	0.665057369
30425250	HQGVMVGMGQK	hypothetical protein LOC238880 [Mus musculus]	1171.5806	50.09	0.665057369
33563250	HQIQSYTCEIDALK	desmin [Mus musculus]	1648.8051	63.66	0.928714645
58037267	HQSLGGQYGVQGFPTIK	protein disulfide isomerase-associated 6 [Mus musculus]	1816.9241	22.76	1.151197498
10946928	HTGPNSPDTANDGFVR	heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1684.7822	56.7	1.987137859
6678413	HVFGESDELIGQK	triosephosphate isomerase 1 [Mus musculus]	1458.7206	54.09	0
27229048	HVSPAGAAVGVPLSEDEAR	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1861.9457	65.54	1.460610383
28916693	HVVPNEVVVQR	gelsolin [Mus musculus]	1275.7238	42.01	1.300641138
63487095	HYEDGYPGGSDNYGSLSR	PREDICTED: catenin src [Mus musculus]	1973.8362	80.61	2.684353192
6755142	HYGPGWVSMANAGK	peptidylprolyl isomerase B [Mus musculus]	1474.6915	54.18	0
6754036	IAATILTSPDLR	glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1270.7218	25.99	0

21450291	IADQCPSSLAIQENANALAR		aldolase 2, B isoform [Mus musculus]	2085.0452	52.92	1.199741588
63476037	IAEGVPQLLIVLTAEPSGDDVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2292.2407	72	0
6679515	IAIPGLAGAGNSVLLVSNLNPER		polypyrimidine tract binding protein 1 [Mus musculus]	2275.2805	20.63	1.518729168
31981515	IALTDNSLIAR		ribosomal protein L7 [Mus musculus]	1186.6809	23.19	0
63746482	IANLQTDLSDGLR		PREDICTED: filamin, alpha [Mus musculus]	1415.7552	48.23	0.697543239
7305295	IAQLEEELEEEQGNMEAMSDR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2451.0693	128.64	0.783944473
7305295	IAQLEEQVEQEAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1542.7859	81.77	0.893544911
6678992	IAQNESELISDEAQGDMALR		myosin VI [Mus musculus]	2190.0381	34.43	1.577597538
41054806	IAQSDYIPTQQDVLR		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1746.9111	45.45	0.87476845
21704020	IASQVAALDLGYKPGVEAIR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	2071.1646	37.97	1.532452221
36031080	IAVQPGTLGPQGR		procollagen, type IV, alpha 2 [Mus musculus]	1293.7361	35.39	0.750836714
11230802	ICDQWDNLGSLTHSR		actinin alpha 4 [Mus musculus]	1744.8232	26.38	1.852368046
6680836	IDDPTDSKPEDWDKPEHIPDPDAK		calreticulin [Mus musculus]	2760.2769	39.64	0.892674186
13384620	IDEPLEGSEDR		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1259.5809	43.91	1.315234443
23346461	IDEVEEMLTNNR		NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Mus musculus]	1462.6921	32.73	0
6680854	IDFEDVIAEPEGTHSFDGIWK		caveolin, caveolae protein 1 [Mus musculus]	2405.1348	28.6	0
40556608	IDIIPNPQER		heat shock protein 1, beta [Mus musculus]	1194.6537	54.64	1.502237539
37202121	IDIPSFDWPIAPFPR		4-aminobutyrate aminotransferase [Mus musculus]	1770.9143	22.46	1.745664573
31982030	IDKTDYMVGSYGPR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1601.7736	58	1.554345971
31980969	IDMNLTDLLGELQR		SEC23B [Mus musculus]	1630.8511	59.76	1.192586874
9790073	IDSVTGEIFSAAPLDR		cadherin 17 [Mus musculus]	1690.8463	53.42	1.64420778
7949053	IDTIEIITDR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1188.6476	47.99	1.145916056
31981100	IEDVTPIPSDSTR		ribosomal protein S14 [Mus musculus]	1429.7207	57.74	1.930229705
6680606	IEELNTQVAVHSEQIQISK		keratin complex 1, acidic, gene 19 [Mus musculus]	2166.1489	109.05	2.341206914
37620153	IEGYPDPEVVWFK		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1578.7821	32	1.03577389
1346343	IEISELNR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	973.5298	29.4	0
33563270	IEQLSPFPFDLLLK		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1659.9302	47.36	1.566779711
33563250	IESLNEEIAFLK		desmin [Mus musculus]	1405.7482	72.25	0.633288431
31559916	IETIEVMEDR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1234.6002	47.1	1.168064632
31981722	IEWLESHQDADIEDFK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1974.9219	49.72	0
14861854	IFEAQIAGLR		keratin complex 2, basic, gene 7 [Mus musculus]	1117.6311	26.65	1.239435792
31982186	IFGVTTLDIVR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1233.7222	44.49	1.334657055
27804325	IFSVTNGGQER	Deamidation (NQ)	monoamine oxidase A [Mus musculus]	1208.5897	19.02	0
31559916	IFVGGIKEDTEEYNLR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1882.9696	63.82	1.572981676
7710042	IFYPETTDIYDR		IQ motif containing GTPase activating protein 1 [Mus musculus]	1532.7327	35.24	1.126130121
63476037	IGDLQSQIVSLLK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1413.8265	51.62	0
6671539	IGEHTPSALAIMENANVLAR		aldolase 1, A isoform [Mus musculus]	2107.0918	60.22	1.32652652
6754750	IGFPWSEIR		moesin [Mus musculus]	1104.5889	30.93	0.992323166
6678571	IGFPWSEIR		villin 2 [Mus musculus]	1104.5889	30.93	0.992323166
51873060	IGGIGTVPVGR		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	1025.6194	63.35	1.354619545
63660294	IGNLQTDLSDGLR		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	1401.7336	36.48	1.173882269
6754976	IGYPAPNFK		peroxiredoxin 1 [Mus musculus]	1006.5381	39.81	1.368302676
6680027	IIAEGANGPTTPEADK		glutamate dehydrogenase 1 [Mus musculus]	1583.7975	106.93	1.357065653
6680027	IIAEGANGPTTPEADKIFLER		glutamate dehydrogenase 1 [Mus musculus]	2242.1719	57.92	1.301022626
6671507	IIAPPER		actin, alpha 2, smooth muscle, aorta [Mus musculus]	795.4758	27.19	0.727938001
6671509	IIAPPER		actin, beta, cytoplasmic [Mus musculus]	795.4758	27.19	0.727938001
30425250	IIAPPER		hypothetical protein LOC238880 [Mus musculus]	795.4758	27.19	0.727938001
63652452	IIAPPER		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	795.4758	27.19	0.727938001
46909602	IIDTPQFQR		SAM domain- and HD domain-containing protein 1 [Mus musculus]	1117.6003	21.05	0
6677813	IIDVVYNASNNELVR		ribosomal protein S8 [Mus musculus]	1718.9076	79.07	1.105492692
63476037	IIEELDVKPDGTR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1484.8019	42.92	0.80933878
6679567	IIGAVDQIQLTQAQLEER		polymerase I and transcript release factor [Mus musculus]	2025.0983	93.86	0.931946047
20137006	IIGLDQVAGMSETALPGAFK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2018.0596	58.56	1.805047074
41054806	IIHEDGYSEEECR		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1579.6807	54.76	1.077433137
6679891	IILTAQPFR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1058.6394	23.32	1.405309341
31981722	IINEPTAAAIAYGLDK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1659.8976	84.81	1.273074013
7305163	IINEPTAAAIAYGLDK		heat shock protein 1-like [Mus musculus]	1659.8976	84.81	1.273074013
31981690	IINEPTAAAIAYGLDK		heat shock protein 8 [Mus musculus]	1659.8976	84.81	1.273074013
63664182	IINEPTAAAIAYGLDK		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1659.8976	84.81	1.273074013
31981722	IINEPTAAAIAYGLDKR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1816.0011	76.72	1.489039231

63704924	IINEPTAAAIAYGLDR		PREDICTED: heat shock protein 1B [Mus musculus]	1687.9027	32.62	1.443775552
6679439	IIPGFMCQGGDFTR		peptidylprolyl isomerase A [Mus musculus]	1541.7091	77.57	1.358668365
136429	IITHPNFNGNTLDNDIMLIK		Trypsin precursor	2283.1948	135.62	0
136429	IITHPNFNGNTLDNDIMLIK	Oxidation (M)	Trypsin precursor	2299.1697	85.99	0
13384620	IITITGTQDQIQNAQYLLQNSVK		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	2589.4023	36.78	0
6680836	IKDPDAAKPEDWDER		calreticulin [Mus musculus]	1784.8551	99.76	0.993718388
6678359	ILATPPQEDAPSVDIANIR		transketolase [Mus musculus]	2020.0781	96.41	1.106966401
13937395	ILEQEEEEEQAGK		arsenate resistance protein 2 [Mus musculus]	1531.7111	26.36	0
6680748	ILGADTSVDLEETGR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1575.7968	54.53	1.03259392
31982755	ILLAELEQLK		vimentin [Mus musculus]	1169.7081	47.33	0
6680067	ILLANFLAQTEALMK		glucose phosphate isomerase 1 [Mus musculus]	1675.9438	70.07	1.976836372
31981679	ILQSSSEVGYDAMLGDFVNMVEK		heat shock protein 1 (chaperonin) [Mus musculus]	2532.2334	58.49	0
13384620	ILSISADIETIGEILK		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1714.9906	75.41	1.853582826
58037117	ILTDYGFEGHPFR		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Mus musculus]	1551.7582	19.41	0.80294957
6677771	ILTFDQLALESPK		ribosomal protein L18 [Mus musculus]	1474.8118	72.25	1.368565235
31980648	IMDPNIVGNEHYDVAR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1842.8937	66.95	1.451464091
13385310	IMDQAITVGAPVIGLNDSGGAR		propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]	2155.0833	25.77	1.323201859
18152793	IMEGPAFNFLDAPAVR		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1747.895	46.62	1.137800058
20137006	IMGIPEDEQMGLLR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1601.8076	51.84	1.464351347
31980648	IMNVIGEPIDER		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1385.722	39.96	0
6724311	INEAFDLLR		alcohol dehydrogenase 1 (class I) [Mus musculus]	1090.5936	56.14	1.880053718
51772556	INFDDNAEFR		PREDICTED: similar to Succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	1240.5638	38.51	1.702499035
6754822	INIDILPAERR	Deamidation (NQ)	NIMA (never in mitosis gene a)-related expressed kinase 4 [Mus musculus]	1310.7545	22.14	0
6754994	INISEGNCPER		poly(rC) binding protein 1 [Mus musculus]	1231.5785	27.67	1.179188899
63562740	INKPEVQCEDPEAVQEPESCSEHR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	2753.21	96.75	0.491762924
33563250	INLPIQTFSALNFR		desmin [Mus musculus]	1633.9097	80.81	0.62364535
33563250	INLPIQTFSALNFR	Deamidation (NQ)	desmin [Mus musculus]	1634.9099	34.59	0
9903607	INPDGSQSVVEVPYAR		transmembrane protein 4 [Mus musculus]	1730.8779	37.41	1.161076883
27804325	INVLVLEAR		monoamine oxidase A [Mus musculus]	1026.6274	26.05	2.120158109
21704066	INVNEIFYDLVR		RAS-related protein-1a [Mus musculus]	1494.8044	64.98	0.89470507
22165384	INVYYNEATGGK		tubulin, beta, 2 [Mus musculus]	1328.6515	64.03	2.858943884
31980648	IPSAVGYQPTLATDMGTMQER		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2266.092	92.21	1.606227937
20137008	IQAIELEDLLR		biglycan [Mus musculus]	1312.7533	47.57	1.19498066
46593021	IQEVDAQMLR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1202.6198	47.5	1.432153328
6753498	IQFNESFAEMNR		cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	1485.6903	36.8	1.724049241
31559981	IQIWDTAGQER		RAB15, member RAS oncogene family [Mus musculus]	1316.6682	77.51	1.119171359
31982223	IQNVVTSFAPQR		laminin, beta 2 [Mus musculus]	1359.7382	29.48	0
21314832	IQRPPEDSIQPYEK		UDP-glucose pyrophosphorylase 2 [Mus musculus]	1699.8704	40.14	1.240712575
19526818	IQTQPGYANTLR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1361.7269	58.41	1.606962353
31981246	IQTYLESTKPIIDLYEEMGK		UMP-CMP kinase [Mus musculus]	2371.1802	21.3	0
63476037	ISCSGNQLPTVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1274.6552	38.67	0.532180162
22165384	ISEQFTAMFR		tubulin, beta, 2 [Mus musculus]	1229.6132	70.21	1.234454262
12963615	ISEQFTAMFR		tubulin, beta 3 [Mus musculus]	1229.6132	70.21	1.234454262
31981939	ISEQFTAMFR		tubulin, beta 4 [Mus musculus]	1229.6132	70.21	1.234454262
7106439	ISEQFTAMFR		tubulin, beta 5 [Mus musculus]	1229.6132	70.21	1.234454262
21746161	ISEQFTAMFR		tubulin, beta [Mus musculus]	1229.6132	70.21	1.234454262
22122523	ISFDLAEYTADVDGVGTLR		GDP-mannose 4, 6-dehydratase [Mus musculus]	2042.0051	38	0
34328206	ISFPAVQAAPSFSNSFPK		tryptophanyl-tRNA synthetase [Mus musculus]	1894.9628	43.19	2.292456119
21361209	ISGLIYEETR		germinal histone H4 [Mus musculus]	1180.6243	65	0.763074096
31982755	ISLPLPTFSSLNLR		vimentin [Mus musculus]	1557.9039	47.6	1.215236995
63476037	ISLSPEYVYSVSTFR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1747.8965	49.69	0.62312095
29244556	ISMSHEEEPLGTAGPLALAR		GDP-mannose pyrophosphorylase B [Mus musculus]	2079.0605	30.13	0
33563256	ISQTNYIPTQQDVLR		guanine nucleotide binding protein, alpha inhibiting 3 [Mus musculus]	1775.9348	27.33	1.250420434
6678499	ISSINSISALCEATGADVEEVATAIGMDQR		UDP-glucose dehydrogenase [Mus musculus]	3051.4585	47.2	3.120976195
6677813	ISSLLEEQFQQGK		ribosomal protein S8 [Mus musculus]	1506.7709	55.1	1.097101856
31981679	ISSVQSIVPALEIANAHR		heat shock protein 1 (chaperonin) [Mus musculus]	1905.0544	41.49	1.539819259
6753320	ISTPVDVNNR		chaperonin subunit 3 (gamma) [Mus musculus]	1114.5883	32	1.086736845
31543113	ISTSLPVLDLIDAIQPGSINYDLLK		lymphocyte cytosolic protein 1 [Mus musculus]	2698.4827	32.24	1.137038489
7106439	ISVYYNEATGGK		tubulin, beta 5 [Mus musculus]	1301.6416	59.91	3.18479669
31982522	ITEIYEGTSEIQR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1538.7563	42.47	1.474029348

6679291	ITLPVDFVTADKFDENAK		phosphoglycerate kinase 1 [Mus musculus]	2023.0303	46.03	1.341277301
34328204	ITPAHDQNDYEVGQR		valyl-tRNA synthetase 2 [Mus musculus]	1742.816	57.17	0.950180776
31981722	ITPSYVAFTPEGER		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1566.7898	74.96	1.037069572
6755787	IVAERPGTNSTGPGPMAPPR		tripartite motif protein 28 [Mus musculus]	2005.0403	34.61	1.383218888
21450277	IVEIPFNSTNK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1261.6621	34.08	1.43142364
33598964	IVFQEFR		myosin heavy chain 10, non-muscle [Mus musculus]	938.5105	24.56	0.95599647
7305295	IVFQEFR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	938.5105	24.56	0.95599647
6753010	IVFVDPSLTVR		anterior gradient 2 [Mus musculus]	1245.7207	50.41	1.041578728
7305619	IVILPDYLEIAR		ubiquitin specific protease 5 (isopeptidase T) [Mus musculus]	1414.8289	22.17	0
51491845	IVLDNSVFSEHR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1415.7275	46.98	1.319194681
6754482	IVLQIDNAR		keratin complex 1, acidic, gene 18 [Mus musculus]	1041.6074	37.17	1.79187737
6680606	IVLQIDNAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1041.6074	37.17	1.79187737
24418919	IVNGWQVEEADDWLR		brain glycogen phosphorylase [Mus musculus]	1829.8833	27.66	1.959270338
63746482	IVSPSGAAVPCK		PREDICTED: filamin, alpha [Mus musculus]	1128.6106	35.29	0
18079339	IVYGHLDDPANQEIER		aconitase 2, mitochondrial [Mus musculus]	1868.9226	49.98	1.504568438
8567336	IWALGGVTSDR		chloride channel calcium activated 3 [Mus musculus]	1174.6373	74.91	0.243298564
6678483	IYDDDFFQNLDGVANALDNIDAR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	2614.2122	59.85	1.258659754
33859554	IYELAAGGTAVGTGLNTR		fumarate hydratase 1 [Mus musculus]	1763.9337	28.93	1.922123377
22164798	IYVVDVGSEPR		selenium binding protein 1 [Mus musculus]	1233.6523	32.5	2.804196821
7305295	KATLQAEQLSNELATER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1901.9949	105.76	0.846684596
6671507	KDLYANNVLSGGTTMYPGIADR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2356.1931	157.65	0.396156614
6671507	KDLYANNVLSGGTTMYPGIADR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2357.1589	84.07	0
6671509	KDLYANTVLSGGTTMYPGIADR		actin, beta, cytoplasmic [Mus musculus]	2343.1694	161.91	0.959265713
29789191	KEDGTFYEFGDDIPEAPER		asparaginyl-tRNA synthetase [Mus musculus]	2214.9995	66.78	1.460324723
30425112	KEEEEEEEEYDEGSNLKR		hypothetical protein LOC109154 [Mus musculus]	2241.9685	59.4	0
20874851	KESYSVYVYK		PREDICTED: similar to histone H2b-616 [Mus musculus]	1265.6444	57.59	0.456888266
33598964	KFDQLLAEEK		myosin heavy chain 10, non-muscle [Mus musculus]	1220.644	40.87	0
7305295	KFDQLLAEEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1220.644	40.87	0
20137006	KFDQLLAEEK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1220.644	40.87	0
29336026	KFDQLLAEEK		nonmuscle myosin heavy chain [Mus musculus]	1220.644	40.87	0
31543942	KIDAAQNWLADPNGGPEGEEQIR		vinculin [Mus musculus]	2508.2124	67.31	0.703959722
6753262	KLEVEANNAFDQYR		capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1696.8225	25.77	0.914374122
6679567	KLEVNEAELLR		polymerase I and transcript release factor [Mus musculus]	1313.7406	29.18	0
7305295	KLEVQLQDLQSK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1428.803	65.68	0
6753066	KLLETEEEAAFPLGGATPR		amine oxidase, copper containing 3 [Mus musculus]	2029.0302	27.82	0
31981246	KNPDSQYGELIEK		UMP-CMP kinase [Mus musculus]	1520.766	39.83	0
6680836	KPEDWDEEMDGEWEPPVIQNPEYK		calreticulin [Mus musculus]	2960.3015	60.66	1.039955851
6677871	KPELPDGDNDDDVVADISNR		scinderin [Mus musculus]	2184.0088	102.48	0.595674987
31981722	KSDIDEIVLVGGSTR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1588.8564	33.29	0
8567336	KYPTDGSEIVLLTDGEDNTISSCFDLVK		chloride channel calcium activated 3 [Mus musculus]	3059.4844	34.51	0
50355692	LADALQELR		lamin A isoform A [Mus musculus]	1028.569	30.14	1.478371519
31982522	LADMALALESAR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1260.6581	32.57	0
13624315	LAELEAALQR		keratin complex 2, basic, gene 8 [Mus musculus]	1113.6292	60.51	1.732069853
51491845	LAELEEFINGPNNAHIQQVGDR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2464.2036	25.57	0
31560731	LAEMPADSGYPAYLGAR		ATPase, H+ transporting, V1 subunit A, isoform 1 [Mus musculus]	1781.8676	28.77	0
6753010	LAEQFVLLNLVYETTDK		anterior gradient 2 [Mus musculus]	1996.0712	50.53	1.748129451
6678483	LAGTQPLEVLEAVQR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1623.9061	58.64	1.3052502
23956166	LALSQNQQSSGAAGPTGK		cisplatin resistance-associated overexpressed protein [Mus musculus]	1714.8773	71.43	45.64949826
51770896	LAMQEFMILPVGASSFR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1896.9668	56.58	1.429799366
6679687	LAPEYEAAATR		glucose regulated protein [Mus musculus]	1191.5892	36.52	0
31981562	LAPITSDPTEAAAVGAVEASFK		pyruvate kinase 3 [Mus musculus]	2145.1099	111.7	1.579746237
19527018	LAQDFLDSQNLSAYNTR		dipeptidylpeptidase III [Mus musculus]	1955.9553	21.45	0
51770896	LAQSNGWGVMVSHR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1541.7662	64.27	1.345658964
51770896	LAQSNGWGVMVSHR	Deamidation (NQ)	PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1542.7671	58.94	1.55025085
11230802	LASDLLEWIR		actinin alpha 4 [Mus musculus]	1215.6799	49.53	1.054408789
33186863	LATQLTGPVMPIR		ribosomal protein L13 [Mus musculus]	1396.8054	28.33	1.245334613
10946574	LAVEALSSLDGDLSGR		creatine kinase, brain [Mus musculus]	1602.822	38.78	0
63650229	LAVNMVPFPR		PREDICTED: similar to TUBULIN BETA CHAIN (T BETA-15) [Mus musculus]	1143.6359	36.7	1.329418206
22165384	LAVNMVPFPR		tubulin, beta, 2 [Mus musculus]	1143.6359	36.7	1.329418206
12963615	LAVNMVPFPR		tubulin, beta 3 [Mus musculus]	1143.6359	36.7	1.329418206

31981939	LAVNMVPFPR		tubulin, beta 4 [Mus musculus]	1143.6359	36.7	1.329418206
7106439	LAVNMVPFPR		tubulin, beta 5 [Mus musculus]	1143.6359	36.7	1.329418206
27754056	LAVNMVPFPR		tubulin, beta 6 [Mus musculus]	1143.6359	36.7	1.329418206
21746161	LAVNMVPFPR		tubulin, beta [Mus musculus]	1143.6359	36.7	1.329418206
33859506	LCAIPNLR		albumin 1 [Mus musculus]	899.5132	29.86	2.061104066
6671507	LCYVALDFENEMATAASSSSLEK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2479.1545	29.43	0
6671507	LCYVALDFENEMATAASSSSLEK	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2480.1567	21.59	0
6671509	LCYVALDFEQEMATAASSSSLEK		actin, beta, cytoplasmic [Mus musculus]	2493.1416	33.84	0
63652452	LCYVALDFEQEMATAASSSSLEK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2493.1416	33.84	0
6671509	LCYVALDFEQEMATAASSSSLEK	Deamidation (NQ)	actin, beta, cytoplasmic [Mus musculus]	2494.1653	24.21	0
63652452	LCYVALDFEQEMATAASSSSLEK	Deamidation (NQ)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2494.1653	24.21	0
7305295	LDAFLVLEQLR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1316.7612	41.65	0.99233475
21312950	LDDLINWAR		NADH dehydrogenase (ubiquinone) Fe-S protein 7 [Mus musculus]	1115.5795	27.66	1.055840433
30794450	LDELYGTWR		ribosomal protein L4 [Mus musculus]	1152.5707	20.48	1.293874842
31981562	LDIDSAPITAR		pyruvate kinase 3 [Mus musculus]	1171.6342	56.88	0
6677819	LDILDTAGQEEFGAMR		Harvey rat sarcoma oncogene, subgroup R [Mus musculus]	1765.8473	26.84	0
6678359	LDNLVAIFDINR		transketolase [Mus musculus]	1402.7736	62.83	0
14389431	LDPQNHVLYSNR		stress-induced phosphoprotein 1 [Mus musculus]	1455.7375	35.67	1.64283191
33859686	LDQETAQWLR		phosphoglucomutase 1 [Mus musculus]	1259.6617	26.92	1.798638461
33563238	LEAAVAEAEQQGEAALNDAK	Deamidation (NQ)	keratin complex 2, basic, gene 16 [Mus musculus]	2028.9833	41.28	1.738102645
13624315	LEAELGNMQGLVEDFK		keratin complex 2, basic, gene 8 [Mus musculus]	1792.8784	76.12	1.5355386
63565108	LEAELGNMQGLVEDFK		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1792.8784	76.12	1.5355386
6755817	LEDKDDLDVTELSNEELLDQLVR		thymopoietin [Mus musculus]	2701.3191	47.45	0.783902842
6679261	LEEGPPVTTVLTR		pyruvate dehydrogenase E1 alpha 1 [Mus musculus]	1411.7826	35.57	1.506920671
13624315	LEGLTDEINFLR		keratin complex 2, basic, gene 8 [Mus musculus]	1419.7581	82.5	1.691685502
63565108	LEGLTDEINFLR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1419.7581	82.5	1.691685502
547749	LENEIQTYR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1165.5826	46.38	0.384365916
21592285	LEQEIATYR		keratin 20 [Mus musculus]	1122.5836	47.17	1.663790979
6680606	LEQEIATYR		keratin complex 1, acidic, gene 19 [Mus musculus]	1122.5836	47.17	1.663790979
27370460	LEQEIATYR		RIKEN cDNA 6330509G02 [Mus musculus]	1122.5836	47.17	1.663790979
21704156	LEQYTNAIEGTK		caldesmon 1 [Mus musculus]	1366.6771	22.59	0
63565108	LEVDPNIQAVR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1253.7026	62.5	1.784437233
30911099	LFDHPEVPTPPESASVSR		fatty acid synthase [Mus musculus]	1964.9691	36.27	1.70769832
7305173	LFDQAFGVPR		heat shock protein 1 [Mus musculus]	1149.6073	51.87	0.805691007
55742711	LFELEEQDLFR		EH-domain containing 2 [Mus musculus]	1438.725	73.25	1.251211176
12963531	LFVGNLPPDITEEEMR		non-POU-domain-containing, octamer binding protein [Mus musculus]	1859.9202	32.6	1.133092983
12963531	LFVGNLPPDITEEEMR	Deamidation (NQ)	non-POU-domain-containing, octamer binding protein [Mus musculus]	1860.9269	23.36	0
38198665	LGAAPEEESAYVAGER		p47 protein [Mus musculus]	1648.7877	55.31	2.025351139
6680163	LGAGYPMGPFELLDYVGLDTTK		L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	2357.1726	40.04	2.838620649
54607098	LGANSLLDLVVFGR		succinate dehydrogenase Fp subunit [Mus musculus]	1473.8451	20.88	0
31982755	LGDLYEEEMR		vimentin [Mus musculus]	1254.5714	57.31	1.436972905
6679291	LGDVYVNDAFGTAHR		phosphoglycerate kinase 1 [Mus musculus]	1634.7905	89.04	1.814441012
136429	LGEHNIDVLEGNEQFINAAK		Trypsin precursor	2211.1255	133.32	0
6678439	LGEHNINVLEGNEQFVDSAK	2 Deamidation (NQ)	protease, serine, 2 [Mus musculus]	2215.0791	37.15	0
6755893	LGEHNINVLEGNEQFVNSAK	Deamidation (NQ)	trypsin 4 [Mus musculus]	2213.0938	23.21	0
6680720	LGEIVTTIPTIGFNVETVEYK		ADP-ribosylation factor 4 [Mus musculus]	2323.2312	64.06	1.502966322
33859506	LGEYGFQNAILVR		albumin 1 [Mus musculus]	1479.7974	53.36	1.985687037
10946574	LGFSEVELVQMVVDGVK		creatine kinase, brain [Mus musculus]	1848.9788	36.84	2.114176565
33859514	LGGNYGPTVAVQR	Deamidation (NQ)	branched chain aminotransferase 2, mitochondrial [Mus musculus]	1332.6667	21.47	0
6754254	LGLGIDEDDPTVDDTSAAVTEEMPPLEGDDDTSR		heat shock protein 1, alpha [Mus musculus]	3575.5293	100.69	1.465199217
40556608	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR		heat shock protein 1, beta [Mus musculus]	3535.6418	98.75	1.520898496
6678097	LGMTDAFGGR		serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	1024.4916	27.49	2.030175247
6678359	LGQSDPAPLQHQVDIYQK		transketolase [Mus musculus]	2037.0483	52.43	1.336305156
25020120	LGSQATGVQGQAGQLLDTTESTLGR		PREDICTED: laminin, alpha 5 [Mus musculus]	2488.2537	38.44	0
7305505	LGSVTHVTTFSHASPGNR		smoothelin [Mus musculus]	1867.9495	33.18	0.866030144
31560611	LGTDQPLDQATISLQMGTNK		calponin 1 [Mus musculus]	2131.0361	58.13	0
6753428	LGYILTCPSNLGTGLR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	1677.9033	30.79	2.540280914
31542159	LHEFTISGTTYTPEGEVR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	2036.9818	39.8	0.602968696
6755901	LIGQIVSSITASLR		tubulin, alpha 1 [Mus musculus]	1457.8799	79.4	1.103708969
6678573	LIIQWNGPESNR		villin 1 [Mus musculus]	1426.7501	33.19	1.671286402

22164798	LILPGLISSR		selenium binding protein 1 [Mus musculus]	1068.6782	29.96	3.439664517
34740335	LISQIVSSITASLR		tubulin, alpha 2 [Mus musculus]	1487.8843	48.93	1.43421943
6678467	LISQIVSSITASLR		tubulin, alpha 4 [Mus musculus]	1487.8843	48.93	1.43421943
6678469	LISQIVSSITASLR		tubulin, alpha 6 [Mus musculus]	1487.8843	48.93	1.43421943
6679937	LISWYDNEYGYSNR		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1779.8013	72.77	1.151184048
547749	LKYENEVALR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1234.6862	24.66	0.354791497
27370092	LLDAVDTYIPVPTR		Tu translation elongation factor, mitochondrial [Mus musculus]	1572.8685	52.67	1.581420001
9790261	LLDSLEPPGEPGPSTSIPENDTVDGR		Trk-fused gene [Mus musculus]	2692.2837	29.46	1.453764206
31981828	LLELGPKPEVAQQTR		coatomer protein complex subunit alpha [Mus musculus]	1678.9454	34.79	1.444173113
6753066	LLETEEEAAFPLGGATPR		amine oxidase, copper containing 3 [Mus musculus]	1900.9595	69.79	0
17647499	LLGNAIVIVLGHHLGK		hemoglobin, beta adult minor chain [Mus musculus]	1654.0262	88.52	2.757237796
31982300	LLGNMIVIVLGHHLGK		hemoglobin, beta adult major chain [Mus musculus]	1714.0223	24.8	0
6671672	LLLNNDNLLR		capping protein (actin filament) muscle Z-line, alpha 2 [Mus musculus]	1197.6995	32.04	1.954498693
20874851	LLLPGELAK		PREDICTED: similar to histone H2b-616 [Mus musculus]	953.6169	56.31	0.609843635
63556656	LLNPQGAIR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	981.5872	38.5	0.28669183
63704924	LLQDFFNGR		PREDICTED: heat shock protein 1B [Mus musculus]	1109.5746	24.71	0.978132989
31982755	LLQDSVDFSLADAINTEFK		vimentin [Mus musculus]	2126.0603	25.97	0
24418919	LLSLVDDEAFIR		brain glycogen phosphorylase [Mus musculus]	1390.754	41.82	1.184071534
63562740	LLTSAAFEDCQTR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1454.7085	28.6	0.538511667
31982300	LLVVYPWTQR		hemoglobin, beta adult major chain [Mus musculus]	1274.7285	27.03	0
17647499	LLVVYPWTQR		hemoglobin, beta adult minor chain [Mus musculus]	1274.7285	27.03	0
51491845	LLYNNVSNFGR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1296.6693	42.92	1.321539539
6755809	LNEAAAGLNQAATELVQASR		talin 1 [Mus musculus]	2027.0511	72.51	0.954252086
45387933	LNIQPSETDYAVDIR		UDP-glucose ceramide glucosyltransferase-like 1 [Mus musculus]	1733.8677	45.27	1.425989304
63476037	LNLLDLDYELAEQLDNIAEK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2332.1914	96.39	0.852385803
22164798	LNPNFLVDFGK		selenium binding protein 1 [Mus musculus]	1263.6559	42.43	2.765830204
13384736	LNTQEIFDDWAR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1507.7297	21.66	1.145732254
6754484	LNVEVDAAPTVDLNR		keratin complex 1, acidic, gene 1 [Mus musculus]	1625.8539	71.87	0
33859811	LPAKPEVSSDEDVQYR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1832.9106	106.24	1.567211483
33859506	LPCVEDYLSAILNR		albumin 1 [Mus musculus]	1605.843	102.8	1.964816302
29789080	LPEAAFLAR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	987.5557	24.33	1.280287922
56119103	LPGQPPASMGR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1110.5726	24.29	1.20780605
31982472	LPIGDVATQYFADR		chaperonin subunit 7 (eta) [Mus musculus]	1565.7946	23.86	1.594860257
51873060	LPLQDVYK		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	975.5494	48.44	0
63746482	LPQLPITNFSR		PREDICTED: filamin, alpha [Mus musculus]	1285.734	70.67	0.761963349
19526818	LPRPPPPEMPESLK		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1587.8596	29.85	5.866661955
21450325	LPSEGPQPAHVVVGDVR		biliverdin reductase B (flavin reductase (NADPH)) [Mus musculus]	1756.9424	60.53	0
63738313	LPSGSGPASPTTGSAVDIR		PREDICTED: similar to AHNAK [Mus musculus]	1769.877	28.21	1.09865094
7949051	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR		heterogenous nuclear ribonucleoprotein U [Mus musculus]	2980.4146	30.53	1.141842541
31982755	LQDEIQNMKEEMAR		vimentin [Mus musculus]	1734.8197	66.41	1.26031052
34328286	LQDPFSVYR		succinate dehydrogenase Ip subunit [Mus musculus]	1124.5753	30.92	1.755145386
6678573	LQEENQVITPR		villin 1 [Mus musculus]	1326.7096	42.57	1.768956405
50355692	LQEKEDLQELNDR		lamin A isoform A [Mus musculus]	1629.8119	53.35	1.122513493
8393988	LQEQLGNDVVEK		phosphomannomutase 2 [Mus musculus]	1371.6978	29.41	5.30523652
34594657	LQGPQTSAEVYR		glycerol-3-phosphate dehydrogenase 1-like [Mus musculus]	1348.6824	24.7	1.554148156
10946940	LQIWDTAGQESFR		RAB2, member RAS oncogene family [Mus musculus]	1550.7612	74.11	1.157106661
21450625	LQMEAPHIIVGTPGR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1618.8771	52.63	1.375565003
7305295	LQNEVESVTGMLNEAEGK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1947.9384	100.2	0.70004259
38089265	LQNTGVADGYPVR		PREDICTED: palladin [Mus musculus]	1389.707	42.53	1.228434259
20137006	LQQELDDLLVDLDHQR	Deamidation (NQ)	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1950.9907	20.8	2.258281482
7305295	LQQELDDLVVDLDNQR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1912.9648	131.99	0.895032163
19527026	LQQLPADFGR		hypothetical protein LOC98238 [Mus musculus]	1144.6122	25.08	1.424133143
63489754	LQVASDENYKDPTNLQGK		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	2019.9921	32.41	1.989508429
63746482	LQVEPAVDTSGVQCYGPGIEGQGVFR		PREDICTED: filamin, alpha [Mus musculus]	2706.3164	35.61	0.642195206
31980942	LQVSQQEDITK		Inositol (myo)-1(or 4)-monophosphatase 1 [Mus musculus]	1288.6746	68.92	0
63476037	LSDAGITPLFLTSQEDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1862.9458	83.7	0.504561092
63489759	LSDDNTIGQEEIQQR		PREDICTED: spectrin alpha 2 [Mus musculus]	1745.8164	37.31	0
6754206	LSDEILIDILTR		hexokinase 1 [Mus musculus]	1400.8051	54.15	1.689574736
6671666	LSDLLAPISEQIQEVITFR		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	2172.1917	87.14	1.320525587
13385006	LSDYFPKPYPNPEAAR		cytochrome c-1 [Mus musculus]	1864.9257	48.32	1.491135024

23956150	LSFYETGEIPR		nucleolar protein 5A [Mus musculus]	1311.6459	25.19	0
7948997	LSGGIDFNQPLVITR		PDZ and LIM domain 3 [Mus musculus]	1629.9019	30.52	1.038303854
11230802	LSGSNPYTTVTPQIINSK		actinin alpha 4 [Mus musculus]	1920.0022	40.89	1.524073256
6671549	LSILYPATTGR		peroxiredoxin 6 [Mus musculus]	1191.6813	42.06	3.010867926
21450277	LSLDELHR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	982.5327	26.12	2.297925566
63641940	LSLQDAVNQGLIDQDMATR		PREDICTED: desmoplakin [Mus musculus]	2088.0393	22.81	1.770206419
11230802	LSNRPAFMPSEGR		actinin alpha 4 [Mus musculus]	1461.7306	27.8	0.773954353
6755787	LSPPYSSPQEFAQDVGR		tripartite motif protein 28 [Mus musculus]	1877.9098	37.48	1.069983548
6755967	LSQNNFALGYK		voltage-dependent anion channel 3 [Mus musculus]	1254.6482	44.06	2.443712797
33859506	LSQTFPNADFAEITK		albumin 1 [Mus musculus]	1681.8491	74.48	2.374850388
6754556	LSSEMNTSTVNSAR		lamin B1 [Mus musculus]	1496.7085	69.79	1.007314983
136429	LSSPATLNSR		Trypsin precursor	1045.5686	33.16	0
7305085	LSTDHIPILYR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1327.7391	28.04	1.375279385
51491845	LTDQLPLIIVCDR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1498.8295	59.02	1.171819291
6755963	LTFDSSFSPNTGK		voltage-dependent anion channel 1 [Mus musculus]	1400.6647	66.02	1.376298457
51765915	LTLIDPETLLPR		PREDICTED: TBP-interacting protein [Mus musculus]	1380.8085	29.21	1.070939112
63501125	LTQQAGDLTVPAGGQR		PREDICTED: ADP-ribosylation factor interacting protein 1 [Mus musculus]	1611.8505	39.01	1.816200941
22165384	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta, 2 [Mus musculus]	2651.321	110.01	1.056968074
31981939	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta 4 [Mus musculus]	2651.321	110.01	1.056968074
7106439	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta 5 [Mus musculus]	2651.321	110.01	1.056968074
21746161	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta [Mus musculus]	2651.321	110.01	1.056968074
51556274	LVAGEMGQNEPDQGGQR		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	1785.8263	65.2	1.391064936
13385472	LVAIVDVIDQNR		ribosomal protein L14 [Mus musculus]	1354.7668	39.89	1.198380353
6679805	LVIPSELGYGER		FK506 binding protein 2 [Mus musculus]	1332.7261	25.87	0.685444572
6755100	LVKPGNQNTQVTEAWNK		proliferation-associated 2G4 [Mus musculus]	1927.0083	41.89	1.768096463
31980648	LVLEVAQHLGESTVR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1650.9167	30.81	0.994708014
6755714	LVNSLYPEGSKPVK		transgelin [Mus musculus]	1530.8572	55.26	0.611087443
31981273	LVPDMIPEVVSEQVSSYLSK		CNDP dipeptidase 2 (metallopeptidase M20 family) [Mus musculus]	2220.1423	58.16	0.464012862
63518159	LVPLLDTGDIIIDGGNSEYR		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	2160.1062	89.73	1.597638129
31543942	LVQAAQMLQSDPYSVPAR		vinculin [Mus musculus]	1974.0101	29.59	0.651594003
6754976	LVQAFQFTDK		peroxiredoxin 1 [Mus musculus]	1196.6277	45.32	0
31981679	LVQDVANNTNEEAGDGTTTATVLAR		heat shock protein 1 (chaperonin) [Mus musculus]	2560.2476	144.47	1.646669269
33859506	LVQEVTDFAK		albumin 1 [Mus musculus]	1149.616	28.58	1.813751776
24418919	LVTSIGDVVNHDPVVGDR		brain glycogen phosphorylase [Mus musculus]	1891.9678	31.56	0
6680047	LWDLTTGTTTR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1264.6547	67.47	1.066421587
6753010	LYAYEPSDTALLYDNMK		anterior gradient 2 [Mus musculus]	2006.9292	65.28	0.770753682
19525729	LYDIEQQQITDALENIR		crystallin, lamda 1 [Mus musculus]	2062.0269	40.87	1.412483716
6753304	LYGPSSVSFADDFVR		serine (or cysteine) proteinase inhibitor, clade H, member 1 [Mus musculus]	1659.7998	41.03	1.25849943
31981722	LYGSGGPPPTGEEDTSEKDEL		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	2177.9875	68.76	0.955727245
6753266	LYPIANGNNQSPIDIK		carbonic anhydrase 1 [Mus musculus]	1756.9203	27.86	7.26330031
6753428	LYPPSAEYPDLR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	1420.7195	53.08	2.049292202
31542333	LYQPEYQEVSTEEQR		hypoxia up-regulated 1 [Mus musculus]	1898.8798	63.53	0.874241944
31981939	MAATFIGNSTAIQELFK	Oxidation (M)	tubulin, beta 4 [Mus musculus]	1857.9453	49.27	1.221165288
63530525	MADAIILAIAGGQELLAQTQK		PREDICTED: SEC31-like 1 [Mus musculus]	2155.1709	34.25	1.886764922
20336740	MAHLFKEK		ret finger protein-like 4 [Mus musculus]	1003.5573	26.1	1.249403326
7305295	MAQQMLDLEEQLEEEEAAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2263.0417	145.24	0.986599253
40068507	MDENQFVAVTSTNAAK		collapsin response mediator protein 1 [Mus musculus]	1725.8175	50.48	0.784839875
40254595	MDENQFVAVTSTNAAK		dihydropyrimidinase-like 2 [Mus musculus]	1725.8175	50.48	0.784839875
6681219	MDENQFVAVTSTNAAK		dihydropyrimidinase-like 3 [Mus musculus]	1725.8175	50.48	0.784839875
7305505	MEPDPAEPPSTTVEAANGAEQAR		smoothelin [Mus musculus]	2368.0864	71.08	5.942382732
47578123	MFTQQQPQELAR		potassium channel tetramerisation domain containing 12 [Mus musculus]	1476.7366	28.48	0.580926503
21450625	MFVLDEADEMLSR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1555.728	34.55	1.495330608
23956214	MGGGGTMNMGDPYGSGGQK		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1801.7487	63.38	0
31980685	MIEQDDFDINTR		glucosamine [Mus musculus]	1496.6721	32.18	2.118709093
11230802	MLDAEDIVNTARPDEK		actinin alpha 4 [Mus musculus]	1816.8738	41.75	1.30814779
6681157	MLDMGFEPQIR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1336.6436	34.45	1.156483116
40068493	MLDMGFEPQIR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1336.6436	34.45	1.156483116
6753620	MLDMGFEPQIR		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1336.6436	34.45	1.156483116
7305505	MLDQTTNFEER		smoothelin [Mus musculus]	1383.6332	31.77	1.251003254
6679891	MLDYLQGSGETPQTDIR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1923.9174	63.95	1.928082292

7305395	MLGADAVGMSTVPEVIVAR		purine-nucleoside phosphorylase [Mus musculus]	1915.9951	24.2	0.809089689
31543942	MLGQMTDQVADLR		vinculin [Mus musculus]	1477.7133	24.15	0.932307338
10092608	MLLADQGQSWK		glutathione S-transferase, pi 1 [Mus musculus]	1276.6335	37.92	1.018589571
31982290	MLYDMENPPADDYFGR		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1933.8224	71.7	0.881448212
8567336	MNPPRPETSYVQDK		chloride channel calcium activated 3 [Mus musculus]	1661.8044	27.56	0
63556656	MPDGSMLVHQK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1242.6118	30	0
6679465	MPPYDEETQAIIDAAQEAR		protein kinase C substrate 80K-H [Mus musculus]	2147.9937	63.11	1.309731153
10946972	MQDQDEDATLTQLATAWVNLAVGGEK		epsilon subunit of coatomer protein complex [Mus musculus]	2804.3464	57.83	0
63489759	MQHNLEQQIQAR		PREDICTED: spectrin alpha 2 [Mus musculus]	1495.7488	22.3	1.222916265
21704156	MQNDSAENETAEGEEKR	Deamidation (NQ)	caldesmon 1 [Mus musculus]	1938.806	51.62	0
31982373	MQQENMKPQEQLTLEPYER		fibrillarin [Mus musculus]	2392.1252	64.87	1.076422637
8394269	MQQFDDLFR		ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltra	1199.5573	31.33	1.647960364
20137006	MQQNIQELEEQLEEEESAR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2333.0623	96.81	1.368140889
50355692	MQQQLDEYQELLDIK		lamin A isoform A [Mus musculus]	1893.9316	73.14	1.153583975
31560689	MSPEEFTEIMNQR		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	1611.7034	38.87	7.226964661
6679108	MSVQPTVSLGGFEITPPVVLR		nucleophosmin 1 [Mus musculus]	2227.2158	41.04	1.225872667
6679108	MTDQEAIQDLWQWR		nucleophosmin 1 [Mus musculus]	1819.8568	35.1	0.937928043
56119103	MTGSEFDFEEMKR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1606.7002	43.79	1.418575559
6755995	MTVNESEQLVSCSMDDTVR		WD repeat domain 1 [Mus musculus]	2143.9294	21.52	0.729583088
6678573	MVDDGSGEVQVWR		villin 1 [Mus musculus]	1477.6829	57.01	1.668454836
33859811	MVGVPAAFDMMLTGR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1595.776	32.5	2.235469648
40254595	MVIPGGIDVHTR		dihydropyrimidinase-like 2 [Mus musculus]	1294.6711	26.7	0.922396194
8393144	MYDSVLALPGALQATR		claudin 7 [Mus musculus]	1705.8899	38.74	1.485351808
13384828	MYGADLAPVDFLHASEDAR		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	2077.9685	60.37	1.477043346
6677871	MYLETDPSGR		scinderin [Mus musculus]	1168.5322	26.53	0.316536746
51766008	MYQAVLDATQR		PREDICTED: myosin IA [Mus musculus]	1295.6418	22.45	0
13937355	MYSYVTEELPQLINANFPVDPQR		esterase D/formylglutathione hydrolase [Mus musculus]	2724.333	29.62	1.48789715
8567336	NADVLVSTTSPLGNDEPYTEHIGACGEK		chloride channel calcium activated 3 [Mus musculus]	2917.3665	121.83	0.220055152
63476037	NAGPEFQYIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1194.5955	57.91	0.552932123
22267442	NALANPLYCPDYR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1509.7179	35.68	1.435861207
46593021	NALVSHLDGTTPVCEDIGR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1996.9719	29.98	0
63476037	NANPSELEQIVLSPAFILAAESLPK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2651.4233	88.56	0
30023842	NAPAIIFIDELDAIAPK		valosin containing protein [Mus musculus]	1810.9907	104.07	0.942462177
6754256	NAVITVPAYFNDSQR		heat shock protein 9A [Mus musculus]	1694.8558	70.46	1.366066202
18079339	NAVTQEFGPVPDTAR		aconitase 2, mitochondrial [Mus musculus]	1601.814	48.2	1.621225782
18079339	NDANPETHAFVTSPEIVTALAIAGTLK		aconitase 2, mitochondrial [Mus musculus]	2780.4446	55.03	1.941601824
31712036	NDFQLIGIQDGYLSLLQDSGEVR		eukaryotic translation initiation factor 5A [Mus musculus]	2580.2778	36.64	1.866255168
31560543	NDFTEEEEAQVR		S-phase kinase-associated protein 1A [Mus musculus]	1466.6508	45.47	1.293715178
9790067	NDISSHPPVEGSYAPR		staphylococcal nuclease domain containing 1 [Mus musculus]	1725.8287	51.37	1.822876483
9790247	NDVFDSLGISPDLLPDDFVR		ubiquitin-like 1 (sentrin) activating enzyme subunit 1 [Mus musculus]	2234.106	28.05	0.765238372
9790247	NDVFDSLGISPDLLPDDFVR	Deamidation (NQ)	ubiquitin-like 1 (sentrin) activating enzyme subunit 1 [Mus musculus]	2235.0979	30.46	0
21313536	NDVITVQTPAFAESVTEGDVR		dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]	2248.0977	43.41	1.527405087
6755929	NEAIQAAHDSVAQKGQCR	Deamidation (NQ)	ubiquitin carboxy-terminal hydrolase L1 [Mus musculus]	1926.8763	26.51	1.471693836
6678483	NEEDATELVGLAQAVNAR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1899.9403	100.58	1.288995102
7305443	NFGIGQDIQPK		ribosomal protein L7a [Mus musculus]	1216.6262	61.24	0
7949051	NFILDQTNVSAAAQR		heterogenous nuclear ribonucleoprotein U [Mus musculus]	1647.8513	74.4	1.159541585
51556274	NFLASQVPFPSR		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	1362.7164	27.22	1.025710563
33859490	NFLTEDSADLDSIEAVANEVLK		laminin B1 subunit 1 [Mus musculus]	2393.155	28.35	0.573736062
7305295	NFMNSPMAQADWVAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1709.7881	86.07	0.414285769
22203747	NFVINVVNR		procollagen, type VI, alpha 2 [Mus musculus]	1074.6003	42.94	0.74857625
6681157	NFYQEHPDLAR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1389.6591	49.24	2.057490473
40068493	NFYVEHPEVAR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1360.66	23.41	1.5236363
34328108	NGDRGETGPAGPAGPIGPAGAR		procollagen, type I, alpha 1 [Mus musculus]	1974.9796	73.7	0
6754854	NGFSITGGEFTR		nidogen 1 [Mus musculus]	1285.6259	24.86	0.848321259
13385078	NGMMESQLPGR		RIKEN cDNA 2210417D09 [Mus musculus]	1219.5726	20.26	0
63487095	NGNGGPGPYVGQAGTATLPR		PREDICTED: catenin src [Mus musculus]	1883.9443	69.15	2.69810789
46358078	NGQEETVGVSSTQLIR		response to metastatic cancers 1 [Mus musculus]	1717.8768	55.32	0
63746482	NGQHVASSPIPVVISQSEIGDASR		PREDICTED: filamin, alpha [Mus musculus]	2448.2351	38.9	0
8567336	NHNQEAPNDQNQR		chloride channel calcium activated 3 [Mus musculus]	1564.6909	21.3	0
31560611	NIIGLQMGTNK		calponin 1 [Mus musculus]	1188.6283	55.19	0

27229048	NIPEDAADMAR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1202.5519	19.05	1.080258018
31543605	NIQVDSPYDISR		ribophorin I [Mus musculus]	1406.6954	56.97	1.276075445
33563250	NISEAEEWYK		desmin [Mus musculus]	1268.5837	66.94	0.512989666
34996495	NIVEEIEDLVAR		ribophorin II [Mus musculus]	1399.7578	47.25	1.183297323
33620739	NKDQGTYEDYVEGLR		myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Mus musculus]	1786.8286	31.97	0
6755901	NLDIERPTYTNLNR		tubulin, alpha 1 [Mus musculus]	1718.8983	49.93	1.177602611
34740335	NLDIERPTYTNLNR		tubulin, alpha 2 [Mus musculus]	1718.8983	49.93	1.177602611
6678467	NLDIERPTYTNLNR		tubulin, alpha 4 [Mus musculus]	1718.8983	49.93	1.177602611
6678469	NLDIERPTYTNLNR		tubulin, alpha 6 [Mus musculus]	1718.8983	49.93	1.177602611
58037267	NLEPEWAAAATEVK		protein disulfide isomerase-associated 6 [Mus musculus]	1528.7657	42.91	0
40254595	NLHQSGFSLSGAQIDDNIPR		dihydropyrimidinase-like 2 [Mus musculus]	2169.0723	59.34	0.993561099
6755863	NLLHVTDTGVGMTR		tumor rejection antigen gp96 [Mus musculus]	1513.7751	35.34	1.302222477
20137006	NLPIYSEEIVEMYK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1727.8474	42.37	1.237574491
31982755	NLQEAEEWYK		vimentin [Mus musculus]	1309.6156	31.49	0
6678365	NLQYYDISAK		RAN, member RAS oncogene family [Mus musculus]	1214.618	27.87	1.640857325
23956214	NLSPYVSNELLEEAFSQFGPIER	Deamidation (NQ)	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	2640.3076	33.37	0
6678359	NMAEQIIQEIYSQVQSK		transketolase [Mus musculus]	2009.006	93.42	1.742602813
29336026	NMDPLNDNVAALLHQSTDR		nonmuscle myosin heavy chain [Mus musculus]	2124.0242	19.25	1.849040514
7305295	NMDPLNDNVTSLLNASSDK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2047.9492	88.65	0.771890494
7949053	NMGGPYGGGNYGPGGSGGSGGYGGR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2189.9224	184.34	1.372544153
7949053	NMGGPYGGGNYGPGGSGGSGGYGGR	Oxidation (M)	heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2205.916	69.94	1.205242496
30409956	NMVPQQALVIR		ATPase, Na+/K+ transporting, alpha 2 polypeptide [Mus musculus]	1268.7208	40.73	1.62920184
21450277	NMVPQQALVIR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1268.7208	40.73	1.62920184
6678145	NNEDVSIIPPLFTVSVDHR		signal sequence receptor, delta [Mus musculus]	2152.1038	36.53	1.143162364
31980868	NNFLEDEPSAQHR		kallikrein 6 [Mus musculus]	1556.7281	32.34	0.532267101
51491845	NNLAGAEELFAR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1304.662	52.14	1.478768288
22203747	NNYATMRPDSTEIDQDTINR		procollagen, type VI, alpha 2 [Mus musculus]	2354.0813	60.81	0.532344387
22203747	NNYATMRPDSTEIDQDTINR	Deamidation (NQ)	procollagen, type VI, alpha 2 [Mus musculus]	2355.0618	44.83	0
6754254	NPDDITNEEYGEFYK		heat shock protein 1, alpha [Mus musculus]	1833.792	97.66	2.342881851
40556608	NPDDITQEEYGEFYK		heat shock protein 1, beta [Mus musculus]	1847.8033	102.75	1.534746666
63518159	NPELQNLLLDDFFK		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1705.8774	79.96	1.137444861
6678329	NPLSDPLYDCIFTVEGAGLTK		transglutaminase 2, C polypeptide [Mus musculus]	2253.1084	48.11	0
63556656	NPNDDLTAVGGKPEGWK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1797.8839	109.25	0.37575701
8567402	NPPGFAFVEFEDPR		splicing factor, arginine/serine-rich 3 (SRp20) [Mus musculus]	1621.7756	23.32	1.226417834
22122585	NPPGFAFVEFEDPR		splicing factor, arginine/serine-rich 7 [Mus musculus]	1621.7756	23.32	1.226417834
42734399	NQALELEQLR		desmuslin isoform H [Mus musculus]	1213.6538	32.95	0.720515522
63489759	NQALNTDNYGHDLASVQALQR		PREDICTED: spectrin alpha 2 [Mus musculus]	2328.1418	98.02	1.394829923
18875324	NQAPGQPGASQWGSR		DAZ associated protein 1 [Mus musculus]	1540.7319	49.49	1.112693927
33563270	NQGYYDYVKPR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1402.6831	23.29	1.702602571
547749	NQILNLTTDNANILLQIDNAR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	2367.2407	24.06	0
31981722	NQLTSNPENTVFDAK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1677.8146	78.43	0.904499745
6754482	NQNINLENSLGDVEAR		keratin complex 1, acidic, gene 18 [Mus musculus]	1785.8734	123.28	1.517498769
19526884	NQQDGQLEESPGSWPGAGTIR		GDP-mannose pyrophosphorylase A [Mus musculus]	2227.0437	48.92	1.258984382
31981690	NQVAMNPTNTVFDAK		heat shock protein 8 [Mus musculus]	1649.7915	65.8	0.952995184
33563282	NQYDNDVTVWSPQGR		proteasome (prosome, macropain) subunit, alpha type 1 [Mus musculus]	1778.8153	47.55	2.064047905
46849705	NSFMNGSWGAEER		lectin, galactose binding, soluble 4 [Mus musculus]	1484.6396	101.59	1.90393062
31543942	NSKNQGIEEALKNR	3 Deamidation (NQ)	vinculin [Mus musculus]	1603.8137	24	0
31981690	NSLESYAFNMK		heat shock protein 8 [Mus musculus]	1303.621	41.8	1.260662503
33598964	NSLQEQQEEEEEAR		myosin heavy chain 10, non-muscle [Mus musculus]	1718.7411	23.99	0
50355692	NSNLVGAAHEELQQSR		lamin A isoform A [Mus musculus]	1752.8701	107.93	1.196595596
22165384	NSSYFVEWIPNNVK		tubulin, beta, 2 [Mus musculus]	1696.8464	29.19	0.216183658
12963615	NSSYFVEWIPNNVK		tubulin, beta 3 [Mus musculus]	1696.8464	29.19	0.216183658
31981939	NSSYFVEWIPNNVK		tubulin, beta 4 [Mus musculus]	1696.8464	29.19	0.216183658
7106439	NSSYFVEWIPNNVK		tubulin, beta 5 [Mus musculus]	1696.8464	29.19	0.216183658
27754056	NSSYFVEWIPNNVK		tubulin, beta 6 [Mus musculus]	1696.8464	29.19	0.216183658
21746161	NSSYFVEWIPNNVK		tubulin, beta [Mus musculus]	1696.8464	29.19	0.216183658
31981562	NTGIICTIGPASR		pyruvate kinase 3 [Mus musculus]	1302.6848	38.46	1.319061727
33563270	NTNAGAPPGTAYQSPLSLSR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	2002.0042	50.47	1.447018412
33859560	NTNDANSCQIIIPQNQVNR		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	2142.0405	63.08	1.123462692
56119103	NTNDANSCQIIIPQNQVNR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	2142.0405	63.08	1.123462692

6754556	NTSEQDQPMGGWEMIR		lamin B1 [Mus musculus]	1878.8177	72.95	0.657305958
8567336	NVAILIPESWK		chloride channel calcium activated 3 [Mus musculus]	1269.7192	63.46	0.119026001
6753364	NVFDEAILAALEPPEPK		cell division cycle 42 homolog [Mus musculus]	1852.9323	60.37	0.761503845
6678986	NVLDTSWPTPPPALR		myosin IC [Mus musculus]	1663.8597	26.92	1.175863082
27370276	NVLPSLDK		hypothetical protein LOC240960 [Mus musculus]	885.5111	19.24	0
11968166	NVNGVNYASVTR		cathepsin Z preproprotein [Mus musculus]	1293.6655	26.42	0.486063462
26986563	NVPVYKPQTLDTQR		choline dehydrogenase [Mus musculus]	1658.8936	23.5	1.383469879
31543976	NVTELNEPLSNEER		3-monooxgenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide [Mus musculus]	1643.7933	36.45	0
13385168	NVVSQFVSSMSASADVLAMSK		ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Mus musculus]	2158.0579	44.93	0
7305295	NWQWWR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	975.4615	25.5	0.858468843
20137006	NWQWWR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	975.4615	25.5	0.858468843
29336026	NWQWWR		nonmuscle myosin heavy chain [Mus musculus]	975.4615	25.5	0.858468843
6756033	NYQQNYQNSESGEKNEGSESAPEGQAQQR		nuclease sensitive element binding protein 1 [Mus musculus]	3257.3828	112.2	1.362078327
7949053	NYYEQWGK		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1087.4883	43.13	1.122688706
51771420	NYYGYQGYR		PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1183.5244	46.62	1.326033475
6671549	PGGLLLGDEAPNFEANTTIGR		peroxiredoxin 6 [Mus musculus]	2142.0828	106.46	2.240140005
16716467	PLELELCPGR		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1126.5922	24.5	0
10092608	PPYTIVYFPVR		glutathione S-transferase, pi 1 [Mus musculus]	1351.7399	21.35	2.356412702
30409956	QAADMILLDDNFASIVTGVEEGR		ATPase, Na+/K+ transporting, alpha 2 polypeptide [Mus musculus]	2464.2039	94.99	0
21450277	QAADMILLDDNFASIVTGVEEGR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2464.2039	94.99	0
6680842	QAALQVADGFISR		gelsolin-like capping protein [Mus musculus]	1375.7311	28.54	1.444062579
7305295	QADLEKEELAEELASSLSGR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2175.0828	126.31	0.876269352
6753294	QALQDLLSEYMGNAGR		catenin alpha 1 [Mus musculus]	1765.875	32.13	1.650706486
6754482	QAQEYEALLNIK		keratin complex 1, acidic, gene 18 [Mus musculus]	1419.7465	42.53	0
20137006	QAQQERDELADEIANSSGK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2088.9861	43.77	1.132938965
51492007	QAQVATGGGPGAPPGSQPDYSAAWAEYYR		KH-type splicing regulatory protein [Mus musculus]	2952.3477	38.1	1.671271991
6754256	QAVTNPNNTFYATK		heat shock protein 9A [Mus musculus]	1568.7551	34.04	0
6996913	QDIAFAYQR		annexin A2 [Mus musculus]	1111.561	49.19	1.498029444
31791057	QDIAVISDSYFPR		laminin, gamma 1 [Mus musculus]	1510.755	23.13	0.691701309
6754854	QDLGSPEGIALDHLGR		nidogen 1 [Mus musculus]	1677.8547	26.69	0
6680720	QDLPNAMAISEMTDK		ADP-ribosylation factor 4 [Mus musculus]	1663.7721	54.81	0
55742711	QEELESVEAGVQGGAFEGTR		EH-domain containing 2 [Mus musculus]	2092.9836	58.78	0
21450129	QEQDTYALSSYTR		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	1561.7236	69.44	1.450345148
7304993	QEWESAGQQAPHPR		drebrin-like [Mus musculus]	1620.7554	35.76	1.371522908
6671507	QEYDEAGPSIVHR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1501.699	43.59	0
63476037	QFGVAPLTIAR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1172.6819	50.3	1.841056722
21450625	QFYINVER		eukaryotic translation initiation factor 4A1 [Mus musculus]	1068.5504	38.15	1.547441376
22164798	QFYPDLIR		selenium binding protein 1 [Mus musculus]	1051.5627	47.88	3.973170211
30409956	QGAIVAVTGDGVNDSPALK		ATPase, Na+/K+ transporting, alpha 2 polypeptide [Mus musculus]	1811.9325	51.64	0
21450277	QGAIVAVTGDGVNDSPALK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1811.9325	51.64	0
31982233	QGEDNSHTQDTEDLEKDTR		LYRIC [Mus musculus]	2217.9563	22.27	1.839434538
7106451	QGIETPEDQNDLRK		zinc finger protein 162 [Mus musculus]	1642.8048	33.94	1.525279914
15147224	QGIVPAGLTENELWR		sideroflexin 1 [Mus musculus]	1682.8827	19.37	2.175906449
6680748	QGQYSPMAIEEQVAVIYAGVR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2309.1628	52.42	1.740761941
9845299	QGTFHSQQALEYGTK		succinate-CoA ligase, GDP-forming, alpha subunit [Mus musculus]	1694.8204	87.02	1.482734367
6753294	QIIVDPLSFSEER		catenin alpha 1 [Mus musculus]	1532.793	37.27	1.254936481
33563270	QILLPFR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	886.5481	24.84	1.732029774
18250296	QINWTVLYR		ribosomal protein L24 [Mus musculus]	1192.649	36.14	1.186549685
31982526	QIQEEITGNTEALSGR		parvin, alpha [Mus musculus]	1745.8757	68.79	1.294808167
1346343	QISNLQQSISDAEQR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1716.8538	110.95	0.048356331
6754976	QITINDLPVGR		peroxiredoxin 1 [Mus musculus]	1225.6992	47.65	1.380241606
31560539	QITVNDLPVGR		peroxiredoxin 2 [Mus musculus]	1211.676	29.42	1.49958686
21704156	QKEFDPTITDGSLSGPSR		caldesmon 1 [Mus musculus]	1934.9489	52.84	0.897539167
6755354	QLDSGLLLVTGPLVINR		ribosomal protein L6 [Mus musculus]	1808.071	63.69	1.314474759
6755901	QLFHPEQLITGK		tubulin, alpha 1 [Mus musculus]	1410.7765	77.08	1.098366137
34740335	QLFHPEQLITGK		tubulin, alpha 2 [Mus musculus]	1410.7765	77.08	1.098366137
6678467	QLFHPEQLITGK		tubulin, alpha 4 [Mus musculus]	1410.7765	77.08	1.098366137
6678469	QLFHPEQLITGK		tubulin, alpha 6 [Mus musculus]	1410.7765	77.08	1.098366137
7305295	QLHEYETELEDER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1690.7708	77.87	0.685742899
7305295	QLHEYETELEDERK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1818.858	86.47	0.61763947

16716607	QLHGESPTR	Deamidation (NQ)	regulating synaptic membrane exocytosis 2 [Mus musculus]	1025.5088	22.3	0
7305295	QLLQANPILEAFGNAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1726.9501	97.26	0.736197251
20137006	QLLQANPILEAFGNAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1726.9501	97.26	0.736197251
29336026	QLLQANPILEAFGNAK		nonmuscle myosin heavy chain [Mus musculus]	1726.9501	97.26	0.736197251
6678571	QLLTLSNELSQAR		villin 2 [Mus musculus]	1472.8113	55.35	1.386704945
22122569	QLSQNFLLDLR	3 Deamidation (NQ)	transcription factor B1, mitochondrial [Mus musculus]	1349.7111	24.38	0
56605979	QLTEMLPSILNQLGADSLTSLR		basic transcription factor 3 [Mus musculus]	2400.2791	21.7	1.541029393
13385718	QLVEQVEQIQK		transmembrane emp24 protein transport domain containing 9 [Mus musculus]	1341.7332	40.71	0
6753262	QMEKDETVSDCSPHIANIGR		capping protein (actin filament) muscle Z-line, beta [Mus musculus]	2230.0083	26.95	0
30519911	QMEQISQFLQAAER		transgelin 2 [Mus musculus]	1678.8342	23.76	2.827518783
6678483	QMNPYIQVTSHQNR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1715.8356	20.45	2.812877168
63746482	QMQLENVSVALEFLDR		PREDICTED: filamin, alpha [Mus musculus]	1891.9592	38.02	0.80603564
51712333	QNGVLNSWTDQDSK		PREDICTED: similar to anti-PRSV coat protein monoclonal antibody PRSV-L 3-8 immunoglobulin light ch	1591.7419	63.73	0
29789245	QNQLLLER	Deamidation (NQ)	centrosomal colon cancer autoantigen [Mus musculus]	1014.5422	20.13	0
63487095	QPELPEVIAMLGFR		PREDICTED: catenin src [Mus musculus]	1599.8586	45.81	1.310983433
30794450	QPYAVSELAGHQTSAESWGTGR		ribosomal protein L4 [Mus musculus]	2332.1038	76.79	1.323678744
13507628	QQEQTAQGTAPDAVDQQR		LPS-responsive beige-like anchor [Mus musculus]	1970.9241	138.11	1.883439657
14861854	QQLETLQLDGGR		keratin complex 2, basic, gene 7 [Mus musculus]	1357.7159	38.44	1.855766574
6755763	QQLSAEELDAQLDAYNAR		THO complex 4 [Mus musculus]	2034.988	53.08	1.416105217
22550094	QQPPDLVDFAVEYFTR		protein kinase, cAMP dependent regulatory, type II alpha [Mus musculus]	1924.9542	25.37	1.779655206
21312968	QQSEEDLLLQDFSR		signal sequence receptor, gamma [Mus musculus]	1707.8256	74.26	1.141212364
63476037	QQSLETAMSFVAR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1467.7247	38.63	0
51767143	QRPGQGLEWIGEIDPSDSYTNYNQK		PREDICTED: similar to immunoglobulin heavy chain [Mus musculus]	2895.3574	31.5	0.342605696
41322904	QSAEEQAQAQAQAQAAAEK		plectin 1 isoform 1 [Mus musculus]	1957.9202	102.02	2.221631922
33859580	QSAFPFESGKPFK		galectin-3 [Mus musculus]	1469.7426	64.52	4.153805947
6754508	QSFTMVADTPENLR		LIM and SH3 protein 1 [Mus musculus]	1608.7823	22.32	1.620683406
547749	QSLEASLAETEGR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1390.6851	55.92	0
13385084	QSNGTFYEFR	Deamidation (NQ)	nipsnap homolog 3A [Mus musculus]	1249.5688	19.05	0
30794412	QSSYGQQSYNNQGQQNTESSGGQGGR		TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Mus musculus]	2747.1592	121.18	1.273138849
30023842	QTNPSAMEVEEDDPVPEIR		valosin containing protein [Mus musculus]	2155.9856	91.04	1.401645423
7305291	QTPAAPETEEEPYR		metaxin 1 [Mus musculus]	1617.7426	29.26	2.269229188
7305163	QTQIFTTYSDNQPGVLIQVYEGER		heat shock protein 1-like [Mus musculus]	2786.3315	22.67	0
31981690	QTQTFTTYSDNQPGVLIQVYEGER		heat shock protein 8 [Mus musculus]	2774.3223	97.3	1.468009483
63704924	QTQTFTTYSDNQPGVLIQVYEGER		PREDICTED: heat shock protein 1B [Mus musculus]	2774.3223	97.3	1.468009483
6680606	QTSAMSSFGGTGGGSVR		keratin complex 1, acidic, gene 19 [Mus musculus]	1586.7441	109.71	1.495030518
8567336	QTTPMTAQPPAPTFSLLQIGQR		chloride channel calcium activated 3 [Mus musculus]	2383.2681	74.64	0.227897252
8567336	QTTPMTAQPPAPTFSLLQIGQR	Oxidation (M)	chloride channel calcium activated 3 [Mus musculus]	2399.2542	56.67	0.236857053
22267442	QVAEQFLNMR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1235.6237	30.76	1.678036832
6753864	QVIGTGSFFPK		four and a half LIM domains 1 [Mus musculus]	1180.6409	39.2	0
22122789	QVLLSEPQEAAALYR		acylpeptide hydrolase [Mus musculus]	1687.9059	21.46	1.591351824
63562723	QVVNIPSFIVR		PREDICTED: similar to 40S ribosomal protein S9 [Mus musculus]	1271.7485	32.25	1.133587287
6678573	QVVVEGQEPANFWMALGGK		villin 1 [Mus musculus]	2060.0032	24.84	0
50355690	QWGWTQGR		ribosomal protein L17 [Mus musculus]	1018.4848	27.9	1.147847012
6677813	QWYESHYALPLGR		ribosomal protein S8 [Mus musculus]	1619.7941	63.05	1.164576628
21592285	QWYETNAPSTIR		keratin 20 [Mus musculus]	1465.7125	30.35	1.840231061
6996913	RAEDGSVIDYELIDQDAR		annexin A2 [Mus musculus]	2064.9863	51.9	1.098069066
31981690	RFDDAVVQSDMK		heat shock protein 8 [Mus musculus]	1410.6724	43.63	1.729605492
63664182	RFDDAVVQSDMK		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1410.6724	43.63	1.729605492
6753240	RFDVSGYPTLK		calcium binding protein, intestinal [Mus musculus]	1282.6819	21.33	0
13384620	RPAEDMEEEQAFKR		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1735.8123	47.27	1.646878581
51491845	RPISADSAIMNPASK		clathrin, heavy polypeptide (Hc) [Mus musculus]	1557.8131	23.37	1.140206806
27532959	RPQPEEGATYEGIQK		aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	1702.8544	46.33	0.981382913
31542159	SAAEMVLSDDNFASIVAAVEEGR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	2381.1213	23.16	1.102672385
63489754	SADESGQALLAASHYASDEVR		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	2177.012	20.52	1.255235277
6754524	SADTLWGIQK		lactate dehydrogenase 1, A chain [Mus musculus]	1118.5743	42.39	0
63746482	SAGQGEVLVYVEDPAGHQEEAK		PREDICTED: filamin, alpha [Mus musculus]	2313.1016	60.62	0
34328108	SAGVSVPGPMGPSGPR		procollagen, type I, alpha 1 [Mus musculus]	1452.7366	25.08	0
8394027	SALASVIMGLSPILGK		alpha isoform of regulatory subunit A, protein phosphatase 2 [Mus musculus]	1556.8914	29.05	0
63476037	SALLDSIQNLQVALTSK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1800.9987	56.61	0
30348966	SALPAQSAATLPAR		spectrin beta 2 isoform 1 [Mus musculus]	1353.7493	20.65	1.905958309

6754206	SANLVAATLGAILNR	hexokinase 1 [Mus musculus]	1483.8679	69.09	1.426299499
31982290	SAQPSPHYMAGPSSGQIYGPGPR	LIM domain containing preferred translocation partner in lipoma [Mus musculus]	2342.1033	53.24	0.959987732
63518159	SAVDNCQDSWR	PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1280.5426	30.6	2.405774775
29293809	SAYDSTMETMNYAQIR	ATP citrate lyase [Mus musculus]	1880.8182	38.77	2.105483463
14861854	SAYGGPVGAGIR	keratin complex 2, basic, gene 7 [Mus musculus]	1104.5834	32.75	1.506816396
54020676	SDAAPTPVPQSAPR	hypothetical protein LOC229317 [Mus musculus]	1393.7161	43.06	1.383290612
33667042	SDALETLGFLNHYQMK	heterogeneous nuclear ribonucleoprotein L [Mus musculus]	1866.9033	27.03	1.298566009
18079339	SDFDPGQDTYQHPPK	aconitase 2, mitochondrial [Mus musculus]	1731.7659	64.63	1.299710448
31981722	SDIDEIVLVGGSTR	heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1460.7633	29.38	0
58037546	SDYLNTFEFMDK	isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	1509.6801	38.55	2.093822839
9845257	SEAAPAAPAAAPPAEK	histone 1, H1c [Mus musculus]	1448.7396	62.89	0
63738313	SEDGVEGDLGETQSR	PREDICTED: similar to AHNAK [Mus musculus]	1578.7072	23.3	1.002750259
31982290	SEGDTAYGQQVQPNTWK	LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1908.8793	75.13	1.090698678
6755817	SELVANNVTLPAGEQR	thymopoietin [Mus musculus]	1697.8868	65.53	0
6679687	SEPIPESNEGPVK	glucose regulated protein [Mus musculus]	1382.6852	79.29	1.244134878
6755566	SEQAEPPAAADTHEAGDQNEAEK	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1 [Mus musculus]	2395.0437	80.6	1.798976227
13430890	SETAPAAPAAPAPAEK	histone 1, H1e [Mus musculus]	1478.7521	59.52	0.749640786
34328365	SETAPAAPAAPAPVEK	histone 1, H1d [Mus musculus]	1506.7806	65.12	1.10949604
21426893	SETAPAETAAPAPVEK	histone 1, H1b [Mus musculus]	1568.7805	52.87	0.656666791
6671690	SETITEEELVGLMNK	carbonyl reductase 1 [Mus musculus]	1692.8368	39.44	1.173310504
21314832	SFENSLGINVPR	UDP-glucose pyrophosphorylase 2 [Mus musculus]	1332.6908	69.52	1.496440201
6679567	SFTPDHVVYAR	polymerase I and transcript release factor [Mus musculus]	1291.647	37.47	1.033035644
31981690	SFYPEEVSSMVLTK	heat shock protein 8 [Mus musculus]	1616.7925	62.15	2.630959386
51873060	SGDAAIVDMVPGKPMCVESFSDYPPLGR	eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2938.3855	77.53	1.120197824
51770896	SGETEDTFIADLVVGLCTGQIK	PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	2296.1365	68.68	1.289584121
40254244	SGSMDSPMSTENNSQLR	loss of heterozygosity, 11, chromosomal region 2, gene A homolog [Mus musculus]	1840.8048	21.34	0.911411893
13937355	SGYQQAASEHGLVVIAPDTSPR	esterase D/formylglutathione hydrolase [Mus musculus]	2283.1382	54.47	1.178211454
8567338	SIATLAITTLLK	coatomer protein complex, subunit gamma [Mus musculus]	1244.7821	25.73	0.780101102
41322904	SIITYVSSLYDAMPR	plectin 1 isoform 1 [Mus musculus]	1715.8741	24.81	0
6755863	SILFVPTSAPR	tumor rejection antigen gp96 [Mus musculus]	1187.6807	45.01	0
31981690	SINPDEAVAYGAAVQAAILSGDK	heat shock protein 8 [Mus musculus]	2260.1294	66.19	1.661862556
13384736	SIPLDEGEDEAQR	dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1458.6791	63.44	0
31982030	SIQEIQELDKDDESLR	Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1917.9484	70.69	1.018584007
31982030	SIQEIQELDKDDESLRK	Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	2046.04	35.74	0.840613046
34740335	SIQFVDWCPTGFK	tubulin, alpha 2 [Mus musculus]	1527.7346	56.13	2.233531907
6678467	SIQFVDWCPTGFK	tubulin, alpha 4 [Mus musculus]	1527.7346	56.13	2.233531907
38090003	SISTSLPVLDLIDAIAPNAVR	PREDICTED: expressed sequence AI427122 [Mus musculus]	2165.2214	73.75	1.611493611
31981657	SIVNNGHSFNVEFDDSQDNAVLK	carbonic anhydrase 2 [Mus musculus]	2549.1572	20.45	1.838266369
63556656	SLAAYTAACQAAGAAVKPWR	PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	2006.0352	55.59	0.445230105
13624315	SLDMDGIIAEVR	keratin complex 2, basic, gene 8 [Mus musculus]	1318.6737	95.99	1.913791581
63565108	SLDMDGIIAEVR	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1318.6737	95.99	1.913791581
7305295	SLEADLMQLQEDLAAAER	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2002.9836	107.19	0.81315369
31981302	SLEDALSSDTSGHFR	annexin A6 [Mus musculus]	1621.7513	39.14	0
6754556	SLETENSALQLQVTER	lamin B1 [Mus musculus]	1817.9216	36.52	0
22507391	SLGYAYVNFQQPADAER	poly(A) binding protein, cytoplasmic 4 isoform 2 [Mus musculus]	1928.9199	22.31	2.720950625
6680606	SLLEGQEAHYNNLPTPK	keratin complex 1, acidic, gene 19 [Mus musculus]	1910.9753	49.06	1.613846934
1346343	SLNNQFASFIDK	Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1383.6907	82.19	0
6754524	SLNPELGTDADKEQWK	lactate dehydrogenase 1, A chain [Mus musculus]	1830.8939	68.61	3.468001987
33859811	SLNSEMDNILANLR	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1589.8002	55.77	1.598796744
6680572	SLSALGNVISALAEGSTYVPYR	kinesin family member 5B [Mus musculus]	2268.1782	46.46	2.009247205
21592285	SLSSSSQGPALSMSGSLYR	keratin 20 [Mus musculus]	1914.9297	22.2	3.167693111
40556608	SLTNDWEDHLAVK	heat shock protein 1, beta [Mus musculus]	1527.746	50.11	1.225377269
31982755	SLYSSSPGGAYVTR	vimentin [Mus musculus]	1444.7135	69.92	1.078345926
22267442	SMAASGNLGHTPFLDEL	ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1759.8459	31.05	0
20137006	SMEAEMIQLQEELAAAER	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2048.9697	52.98	1.529371936
22122825	SMLEVNYPMENGIVR	actin-related protein 2 [Mus musculus]	1751.8582	39.01	1.216921766
50355692	SNEDQSMGNWQIR	lamin A isoform A [Mus musculus]	1564.6886	67.2	1.119948169
33469063	SNLVGMGVIPLEYLPGETADSLGLTGR	aconitase 1 [Mus musculus]	2759.4116	43.57	0
13624315	SNMDNMFESYINNLR	keratin complex 2, basic, gene 8 [Mus musculus]	1847.8213	101.92	1.774123744
63565108	SNMDNMFESYINNLR	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1847.8213	101.92	1.774123744

21450277	SPDFTNENPLETR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1519.7122	59.36	1.436011644
6679761	SPFETDMLTLTR		fructose bisphosphatase 2 [Mus musculus]	1410.699	38.36	1.294955366
63746482	SPFSVGVSPSLDLSK		PREDICTED: filamin, alpha [Mus musculus]	1519.7981	88.62	0
18087805	SPYQEFTDHLVK		ribosomal protein S2 [Mus musculus]	1463.7246	36.17	2.404451612
12746446	SQDVGFWEGEVVR		epithelial protein lost in neoplasm [Mus musculus]	1507.72	59.81	2.255714026
6678571	SQEQLAAELAEYTAK		villin 2 [Mus musculus]	1651.8229	36.13	1.028097066
6678571	SQEQLAAELAEYTAK	Deamidation (NQ)	villin 2 [Mus musculus]	1652.8151	30.16	1.336510114
6755354	SQFSLTNGMYPHK		ribosomal protein L6 [Mus musculus]	1509.7172	53.26	0
18079339	SQFTITPGSEQIR		aconitase 2, mitochondrial [Mus musculus]	1463.7573	48.64	1.762210934
31981722	SQIFSTASDNQPTVTIK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1836.938	83.77	0.983258375
31981690	SQIHDIVLVGGSTR		heat shock protein 8 [Mus musculus]	1481.8137	53	1.298436175
6677871	SQLIVVEEGSEPSELMK		scinderin [Mus musculus]	1874.9353	65.16	0
63487095	SQSSHSYDDSTLPLIDR		PREDICTED: catenin src [Mus musculus]	1920.8944	23.44	1.28946559
547749	SQYEQLAEQNR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1365.6462	68.63	0
6680606	SRLEQEIATYR		keratin complex 1, acidic, gene 19 [Mus musculus]	1365.7112	29.92	1.254818591
6671666	SSEMNVLIPTEGGDFNEFPVPEQFK		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	2811.3267	42.83	0
6755040	SSFFVNGLTLGGQK		profilin 1 [Mus musculus]	1454.7559	79.94	1.12202064
31559916	SSGSPYGGGYGSGGGSGGYGSR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1910.8058	174.21	1.387852751
136429	SSGSSYPSLLQCLK		Trypsin precursor	1469.7335	49.27	0
12083691	SSGTGASVGPPQPSDQDTLVQR		PDZ and LIM domain 5 isoform ENH1 [Mus musculus]	2184.0515	36.99	0
28416440	SSHELGNQDQGIPQLR		GTPase, IMAP family member 4 isoform a [Mus musculus]	1778.8799	24.3	0
6755354	SSITPGTVLIILTGR		ribosomal protein L6 [Mus musculus]	1527.9177	66.19	1.300319525
22779912	SSLLDDLLTESEDMAQR		dynamin 1-like [Mus musculus]	1922.9215	59.46	1.184788936
46195798	SSLNPILFR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1046.6021	31.7	1.622468616
8567338	SSPEPVALTESETEYVIR		coatomer protein complex, subunit gamma [Mus musculus]	2006.9954	22.87	1.7657849
31981690	STAGDTHLGGEDFDNR		heat shock protein 8 [Mus musculus]	1691.7456	130.07	1.260073445
33859482	STAISLFYELSENDLNFIK		eukaryotic translation elongation factor 2 [Mus musculus]	2204.1155	43.59	0.681027328
6754256	STNGDTFLGGEDFDQALLR		heat shock protein 9A [Mus musculus]	2055.9663	86.02	1.563678278
30425112	STPEDQILYQTER		hypothetical protein LOC109154 [Mus musculus]	1579.7693	25.92	0
8567336	STWEVIQESEDFK		chloride channel calcium activated 3 [Mus musculus]	1597.7372	65.79	0.324114496
6678573	SVEDLPEGVDPSR		villin 1 [Mus musculus]	1399.6514	31.6	1.764950594
19705424	SVFPEQANNNEWAR		proteasome 26S non-ATPase subunit 3 [Mus musculus]	1661.7679	27.24	1.179862812
27370510	SVNDIVVLGPEQFYATR		paraoxonase 3 [Mus musculus]	1907.9736	22.16	2.619070016
51491845	SVNESLNNLFITEEDYQALR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2355.1462	68.12	1.138424284
6678359	SVPMSTVFYPSDGVATEK		transketolase [Mus musculus]	1914.9019	35.25	1.395426532
6753658	SVSTPSEAGSQDSGDGAVGSR		dynein, cytoplasmic, intermediate chain 2 [Mus musculus]	1950.8684	98.03	1.189898133
6756041	SVTEQGAELSNEER		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	1548.7263	87.67	1.034713797
13385310	SVTNEDVTQEQLGGAK		propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]	1675.8064	47.68	0
6753138	SYEAYVLNIIR		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1340.7264	36.56	1.64107705
6671507	SYELPDGQVITIGNER		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1790.9016	110.62	0.77243777
6671509	SYELPDGQVITIGNER		actin, beta, cytoplasmic [Mus musculus]	1790.9016	110.62	0.77243777
30425250	SYELPDGQVITIGNER		hypothetical protein LOC238880 [Mus musculus]	1790.9016	110.62	0.77243777
63652452	SYKLPDGQVITIGNER	Deamidation (NQ)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1790.9385	33.87	0
6996913	SYSPYDMLESIK		annexin A2 [Mus musculus]	1432.6819	62.46	1.073570458
31543974	TAFDEAIAELDTLNEESYK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Mus muscu	2159.0205	19.88	0
6756041	TAFDEAIAELDTLSEESYK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	2131.9983	93.13	1.335479482
6806903	TASEMVLADDNFSTIVAAVEEGR		ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	2425.1687	43.6	1.717795738
63489754	TATDEAYKDPSNLQGK		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1737.8396	45.22	0.802207801
6671664	TDAPQPDVKDEEGKEEEK		calnexin [Mus musculus]	2043.9392	78.1	1.374627668
22550094	TDEHVIDQGDDGDNFYVIER		protein kinase, cAMP dependent regulatory, type II alpha [Mus musculus]	2337.0422	42.73	0
6677805	TDITYPAGFMDVISIDK		ribosomal protein S4, X-linked [Mus musculus]	1885.9183	52.54	1.581968051
6678331	TDLGPTYNGWQVLDATPQER		transglutaminase 3, E polypeptide [Mus musculus]	2261.0867	20.31	2.912198511
10946574	TDLNPDNLQGGDDLDPNYVLSSR		creatine kinase, brain [Mus musculus]	2518.1729	74.8	0
63476037	TDLQTITNDPR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1273.6409	34.57	0
6755714	TDMFQTVDLYEGK		transgelin [Mus musculus]	1546.7236	64.77	16.3392396
63540743	TDTYVTDNGDGTYR		PREDICTED: filamin C, gamma [Mus musculus]	1577.6791	20.42	0
31982030	TDYMVGSYGPR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1245.5721	61.61	0.901637037
13384620	TDYNASVSVPDSSGPER		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1780.812	86.47	1.436581146
63540743	TEAAEIVEGEDSAYSVR		PREDICTED: filamin C, gamma [Mus musculus]	1825.8622	33.41	0
6755534	TEEPESPESVDQTSPTPGDGNPR		solute carrier family 12, member 7 [Mus musculus]	2426.0547	59.26	0

63481281	TELAEPIAIRPTSETVMYPAYAK	PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	2551.3069	26.61	1.442151059
7305295	TELEDTLDSTATQQELR	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1949.9332	106.08	1.10724875
13624315	TEMENEFVLIK	keratin complex 2, basic, gene 8 [Mus musculus]	1352.656	45.68	1.156045647
63565108	TEMENEFVLIK	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1352.656	45.68	1.156045647
6755863	TETVEEPLEEDEAAKEEK	tumor rejection antigen gp96 [Mus musculus]	2075.9668	50.88	0
33859482	TFCQLILDPIFK	eukaryotic translation elongation factor 2 [Mus musculus]	1437.7815	44.75	1.287893472
33563250	TFGGAPGFSLGSPLSSPVFPR	desmin [Mus musculus]	2078.0759	110.54	0.715092558
6679078	TFIAIKPDGVQR	nucleoside-diphosphate kinase 2 [Mus musculus]	1344.7699	27.23	0
21312260	TFPTVNPTTGEVIGHVAEGDR	aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	2197.0908	67.5	1.645855489
63746482	TFSVWYVPEVTGTHK	PREDICTED: filamin, alpha [Mus musculus]	1750.8778	55.86	2.556884586
6753036	TFVQENVYDEFVER	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1774.8352	56.09	1.718020211
6755040	TFVSITPAEVGVLVGK	profilin 1 [Mus musculus]	1616.9252	101.02	1.205136455
6680748	TGAIVDVPVGEELLGR	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1624.8989	104.81	1.530807763
58037267	TGEAIVDAALSALR	protein disulfide isomerase-associated 6 [Mus musculus]	1386.7617	62.24	1.522391103
6755004	TGGLEIDSDFGGFR	programmed cell death 8 [Mus musculus]	1470.6917	37.97	2.685667084
6681095	TGQAAGFSYTDANK	cytochrome c, somatic [Mus musculus]	1430.6534	78.51	1.482998946
6680748	TGTAEMSSILEER	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1423.6819	58.76	1.395203139
31560517	TGVAPIIDVVR	ribosomal protein L27a [Mus musculus]	1139.6801	55.82	1.269947361
63746482	TGVAVNKPAEFTVDAK	PREDICTED: filamin, alpha [Mus musculus]	1646.8812	92.92	0.4948992
7305295	TGVLAHLEEER	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1253.6564	37.79	2.640397973
6754576	TGVPSQTPNPYANQR	lymphocyte antigen 64 [Mus musculus]	1629.8036	24.57	1.341591794
21644581	THYQQLLAYEDR	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 [Mus musculus]	1536.7482	33.32	0.798110037
29293809	TIAIIAEGIPEALTR	ATP citrate lyase [Mus musculus]	1567.9093	45.61	1.148095977
31980648	TIAMDGTEGLVR	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1262.6456	52.07	1.564618409
6754976	TIAQDYGVLK	peroxiredoxin 1 [Mus musculus]	1107.592	30.19	1.002649346
6755901	TIGGGDDSFNTFFSETGAGK	tubulin, alpha 1 [Mus musculus]	2007.8962	136.29	1.536863624
34740335	TIGGGDDSFNTFFSETGAGK	tubulin, alpha 2 [Mus musculus]	2007.8962	136.29	1.536863624
6678469	TIGGGDDSFNTFFSETGAGK	tubulin, alpha 6 [Mus musculus]	2007.8962	136.29	1.536863624
31981909	TIGVSNFNPLQIER	aldo-keto reductase family 1, member B3 (aldose reductase) [Mus musculus]	1587.8385	33.23	1.742897626
31543605	TILPAAAQDVYYR	ribophorin I [Mus musculus]	1480.785	47.24	1.146089657
11230802	TINEVENQILTR	actinin alpha 4 [Mus musculus]	1429.7743	73.91	0.884526928
63638100	TIQFVDWCPTGFK	PREDICTED: similar to tubulin, alpha 1 [Mus musculus]	1541.7429	56.02	0
6755901	TIQFVDWCPTGFK	tubulin, alpha 1 [Mus musculus]	1541.7429	56.02	0
6678469	TIQFVDWCPTGFK	tubulin, alpha 6 [Mus musculus]	1541.7429	56.02	0
9845265	TITLEVEPSDTIENVK	ubiquitin A-52 residue ribosomal protein fusion product 1 [Mus musculus]	1787.9286	77.56	0
31981828	TLDLPIYVTR	coatomer protein complex subunit alpha [Mus musculus]	1190.6816	30.27	1.593829118
7710042	TLINAEDPPMIVVR	IQ motif containing GTPase activating protein 1 [Mus musculus]	1567.8539	21.16	1.208023599
33563236	TLLGDVPVVADPTVPNVTVTR	Rho, GDP dissociation inhibitor (GDI) beta [Mus musculus]	2163.2043	45.91	0
31981657	TLNFNEEGDAEEAMVDNWRPAQPLK	carbonic anhydrase 2 [Mus musculus]	2874.3237	39.88	2.438295419
8393988	TMPGGNDHEIFTDPR	phosphomannomutase 2 [Mus musculus]	1686.7659	23.9	1.384797121
31542602	TNLIVNYLPQNMTQEELR	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) [Mus musculus]	2176.0964	26.97	1.276792311
29126205	TNVSGGAIALGHPLGGSGSR	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1807.9524	83	1.604382306
6754570	TPAQFDADELR	annexin A1 [Mus musculus]	1262.6078	41.75	0
29336026	TPNVGGPGGPQVEWTAR	nonmuscle myosin heavy chain [Mus musculus]	1722.8625	31.86	2.033332176
30023814	TPSPPEPEPAGTAQK	breast carcinoma amplified sequence 1 [Mus musculus]	1506.7452	42.52	0
6677935	TPVDYIDLPYSSSPSR	sorbin and SH3 domain containing 1 [Mus musculus]	1796.8605	23	0
19527174	TPVEEVPAAIAPFQGR	splicing factor 3b, subunit 3 [Mus musculus]	1681.8884	48.1	1.673584653
13385652	TPVEPEVAIHR	ribosomal protein S20 [Mus musculus]	1247.6794	57.35	1.006513888
19882201	TPVQSQQPSATTPSGADEK	proteasome 26S non-ATPase subunit 2 [Mus musculus]	1928.9226	81.12	1.135387923
18250284	TPYTDVNIVTIR	isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	1391.7518	30.24	1.45944428
31980726	TQAYPDQKPGTSGLR	phosphoglucomutase 2 [Mus musculus]	1618.8207	45.86	1.454429659
6678752	TQDDVDIADVAYYFEK	lymphocyte antigen 74 [Mus musculus]	1891.875	88.07	1.528634476
9055214	TQGNVFATDAILATLMSCTR	eukaryotic translation initiation factor 3, subunit 7 (zeta) [Mus musculus]	2113.0488	23.48	0
16716353	TQIDHYVGIAR	reticulon 3 isoform 4 [Mus musculus]	1272.6707	20.42	0
33598964	TQLEELEDELQATEDAK	myosin heavy chain 10, non-muscle [Mus musculus]	1961.9248	99.96	0.942396463
20137006	TQLEELEDELQATEDAK	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1961.9248	99.96	0.942396463
31980636	TQQTNDIELQQEQR	mannosidase, beta A, lysosomal [Mus musculus]	1730.8357	51.78	2.74135077
63748678	TQSDKLEPSPR	PREDICTED: hypothetical protein LOC73809 [Mus musculus]	1257.6459	21.95	0
21450277	TSATWFALSR	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1139.5925	21.26	1.933553041
33563270	TSFDEMLPGTHFQR	oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1665.7761	36.95	1.254324516

51491845	TSIDAYDNFDNISLAQR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1942.9224	71.93	1.283160978
51765817	TSPNEGLSGNPADLER		PREDICTED: plasma membrane calcium ATPase 1 [Mus musculus]	1656.7913	19.76	1.916235559
6678359	TSRPENAIIYSNNEDFQVGQAK		transketolase [Mus musculus]	2481.1987	65.15	1.112357779
21313262	TSSAEMPTIPLGSAVEAIR		inner membrane protein, mitochondrial [Mus musculus]	1929.9951	45.63	1.339929492
6753294	TSVQTEDDQLIAGQSAR		catenin alpha 1 [Mus musculus]	1818.8816	46.93	1.442340004
6679761	TTEDEPSEKDALQPGR		fructose bisphosphatase 2 [Mus musculus]	1772.8347	58.76	1.612350161
40254802	TTEKNVNLKISNNK	2 Deamidation (NQ)	hypothetical protein LOC215112 [Mus musculus]	1604.8295	19.13	0
6671507	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	3196.6106	84.31	0.37461476
6671509	TTGIVMDSGDGVTHTVPIYEGYALPHAILR		actin, beta, cytoplasmic [Mus musculus]	3183.6111	122.04	0.978221853
30425250	TTGIVMDSGDGVTHTVPIYEGYALPHAILR		hypothetical protein LOC238880 [Mus musculus]	3183.6111	122.04	0.978221853
31981515	TTHFVEGGDAGNREDQINR		ribosomal protein L7 [Mus musculus]	2115.9856	44.12	1.058216216
6754556	TTIPEEEEEEEEEPIGVAVEEER		lamin B1 [Mus musculus]	2672.1995	143.67	0.688234615
7305163	TTPSYVAFTDTER		heat shock protein 1-like [Mus musculus]	1487.7081	84.28	1.521449134
31981690	TTPSYVAFTDTER		heat shock protein 8 [Mus musculus]	1487.7081	84.28	1.521449134
63704924	TTPSYVAFTDTER		PREDICTED: heat shock protein 1B [Mus musculus]	1487.7081	84.28	1.521449134
24429590	TTQVPQYILDDFIQNDR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	2066.0178	35.54	0.772641992
31981828	TTYQALPCLPSMYSYPNR		coatomer protein complex subunit alpha [Mus musculus]	2104.9812	20.62	0
6679601	TVFDEAIR		RAS-related C3 botulinum substrate 2 [Mus musculus]	950.4985	19.85	0.978218224
6753428	TVGMVAGDEETYEVFAELFDPVIQER		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	2944.4136	68.15	1.438361563
33859811	TVLGVPEVLLGILPGAGGTQR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	2047.1974	41.88	2.235264462
33859506	TVMDDFAQFLDTCCK		albumin 1 [Mus musculus]	1736.7335	92.37	2.533438091
21729786	TVQQHAGETDPVTTMR		hydroxyacyl glutathione hydrolase [Mus musculus]	1770.8474	29.72	0
21361209	TVTAMDVVYALK		germinal histone H4 [Mus musculus]	1310.6997	77.78	0.566080057
8567336	TVTLELLDNGAGADATK		chloride channel calcium activated 3 [Mus musculus]	1688.8733	108.51	0
31981690	TVTNAVVTVPAYFNDSQR		heat shock protein 8 [Mus musculus]	1982.0112	103.71	1.573181775
9625006	TVTQVVPAEGQENGQR		apoptotic chromatin condensation inducer 1 [Mus musculus]	1712.8621	27.91	0
31981722	TWNDPSVQQDIK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1430.6968	75.03	1.158553233
47059123	TYAVSHTQEDLNR		UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	1533.7346	45.31	0
29789080	TYLPSQVSR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1050.5636	21.19	1.178019222
23346461	TYLQALPYFDR		NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Mus musculus]	1386.7062	34.38	1.525194973
13384828	TYNFLPEYLASTQK		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1674.8407	47.47	1.603193345
21704128	VAAVQPPEEGPSR		eukaryotic translation initiation factor 4B [Mus musculus]	1336.6938	43.15	1.395592209
6680175	VADALASAAGHLDDLPGALSALSDLHAHK		hemoglobin alpha 1 chain [Mus musculus]	2836.4441	31.56	0.374784904
7709980	VADIGLAAWGR		S-adenosylhomocysteine hydrolase [Mus musculus]	1128.6177	46.09	1.314479574
31981549	VAELNPDENCIR		sulfide quinone reductase-like [Mus musculus]	1372.6569	31.83	1.867543936
21312260	VAEQTPLSALYLASLIK		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1817.0424	47.49	1.584786612
6753036	VAEQTPLTALYVANLIK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1844.0542	65.05	1.526680022
13385680	VAGHPDVVINNAAGNFISPSER		2,4-dienoyl CoA reductase 1, mitochondrial [Mus musculus]	2264.1448	36.14	2.117972119
63476037	VAIAQFSDDVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1220.6265	63.34	0.880258767
31980648	VALTGLTVAEYFR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1439.7972	75.47	1.546065287
18079339	VAMSHFEPSEYIR		aconitase 2, mitochondrial [Mus musculus]	1565.7487	36.96	1.712313782
31542559	VAPAPAGVFTDIPISNIR		dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) [Mus musculus	1838.0171	24.4	1.565169268
6671507	VAPEEHPTLLTEAPLNPK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1956.0693	95.18	0.415010553
6671509	VAPEEHPVLLTEAPLNPK		actin, beta, cytoplasmic [Mus musculus]	1954.0872	96.48	1.01717276
13385598	VAQLEQVYIR		small nuclear ribonucleoprotein D3 [Mus musculus]	1218.6836	30.7	1.283644367
63746482	VAQPSITDNKDGTVTVR		PREDICTED: filamin, alpha [Mus musculus]	1800.9541	64.84	1.474953801
33563270	VASSVPVENFTIHGGLSR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1869.9813	45.55	1.464301837
63746482	VATVPQHATSGPGPADVSK		PREDICTED: filamin, alpha [Mus musculus]	1818.9548	93.39	0.907604072
31982186	VAVLGASGGIGQPLSLLLK		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1793.0912	47.96	1.452973878
33859580	VAVNDAHLLQYNHR		galectin-3 [Mus musculus]	1649.8595	57.75	1.486893385
31982030	VAVSADPNVPNVIVTR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1650.9247	45.43	1.049228411
6753484	VAVVQYSGQGQQQPGR		procollagen, type VI, alpha 1 [Mus musculus]	1701.8763	81.58	0.640720765
63556656	VAYDLVYYVR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1260.6543	29.38	0.177836154
8567336	VAYLQVPGTAK		chloride channel calcium activated 3 [Mus musculus]	1146.6511	64.34	0.261521939
46849705	VAYNPFGPGQFFDLSIR		lectin, galactose binding, soluble 4 [Mus musculus]	1927.976	65.24	1.749655514
42415475	VDATEESDLAQQYGVR		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1780.8408	95.26	1.092039123
45598381	VDCTQHYAVCSEHQVR		thioredoxin domain containing 5 [Mus musculus]	1874.8312	31.56	0.917483429
6678219	VDDPAGMLLAAFR		TAP binding protein [Mus musculus]	1375.7043	26.28	1.108120457
54607098	VDEYDYSKPIQGQQK		succinate dehydrogenase Fp subunit [Mus musculus]	1797.874	87.19	1.388352956
31982186	VDFPQDQLATLTGR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1560.8032	55.37	1.436643127

63738313	VDINAPDVDVR		PREDICTED: similar to AHNAK [Mus musculus]	1212.6277	26.19	2.415544378
63556656	VDLPATVLTSVSVR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1456.84	71.63	0.21833796
20149728	VDNSSLTGESEPQAR		ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Mus musculus]	1589.752	38.66	4.436057586
9055170	VDNSSLTGESEPQTR		ATPase, H+/K+ transporting, alpha polypeptide [Mus musculus]	1619.7648	108.97	1.515222526
30409956	VDNSSLTGESEPQTR		ATPase, Na+/K+ transporting, alpha 2 polypeptide [Mus musculus]	1619.7648	108.97	1.515222526
21450277	VDNSSLTGESEPQTR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1619.7648	108.97	1.515222526
33186863	VDTWFNQPAR		ribosomal protein L13 [Mus musculus]	1233.6064	26.65	1.181056659
63746482	VDVGKDQEFTVK		PREDICTED: filamin, alpha [Mus musculus]	1364.7039	54.56	0.996622842
33859722	VDVTEQTGLSGR		thioredoxin domain containing 1 [Mus musculus]	1261.6395	50.75	1.070388468
7305295	VDYNASAWLTK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1267.632	74.1	1.35739054
7305295	VEDMAELTCLNEASVLHNLR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2257.0957	48.33	0.745460724
21313356	VEEFSLPDALNEGQVQVR		zinc binding alcohol dehydrogenase, domain containing 1 [Mus musculus]	2030.0012	29.25	1.838328048
63540743	VEESTQVGGDPFPAVFGDFLGR		PREDICTED: filamin C, gamma [Mus musculus]	2324.0952	26.95	0.549870607
31542333	VEFEELCADLFDR		hypoxia up-regulated 1 [Mus musculus]	1585.7368	23.6	1.04037842
31543315	VEGSEPTTPFNLFIGNLNPNK		nucleolin [Mus musculus]	2288.1665	61.24	1.823862775
31981722	VEIIANDQGNR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1228.6362	55.5	1.169428303
7305163	VEIIANDQGNR		heat shock protein 1-like [Mus musculus]	1228.6362	55.5	1.169428303
31981690	VEIIANDQGNR		heat shock protein 8 [Mus musculus]	1228.6362	55.5	1.169428303
63704924	VEIIANDQGNR		PREDICTED: heat shock protein 1B [Mus musculus]	1228.6362	55.5	1.169428303
63664182	VEIIANDQGNR		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1228.6362	55.5	1.169428303
33563250	VELQELNDR		desmin [Mus musculus]	1115.5737	45.5	0.672979362
31982755	VELQELNDR		vimentin [Mus musculus]	1115.5737	45.5	0.672979362
63746482	VEPGLGADNSVVR		PREDICTED: filamin, alpha [Mus musculus]	1312.6913	76.64	0.707938081
11230802	VEQIAAIAQELNELDYYDSHNVNTR		actinin alpha 4 [Mus musculus]	2905.3979	26.29	1.339027461
20373167	VEQLGAEGNVEESQK		LUC7-like 2 [Mus musculus]	1616.7791	59.97	1.19492307
30578429	VEQLSSGLEHDNLEAHSPEQPPR		hypothetical protein LOC94184 [Mus musculus]	2569.2305	57.28	1.280960191
51873060	VETGVLKPGMVVTFAPVNVTTEVK		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2515.3984	98.27	1.211575073
33859482	VFDAIMNFR		eukaryotic translation elongation factor 2 [Mus musculus]	1112.5571	47.03	0
6680067	VFEGNRPTNSIVFTK		glucose phosphate isomerase 1 [Mus musculus]	1708.9014	20.61	1.058797278
21361209	VFLENVIR		germinal histone H4 [Mus musculus]	989.5799	41.12	0.666060182
31980726	VFQSNANYAENFIQSIVSTVEPALR		phosphoglucomutase 2 [Mus musculus]	2797.4236	27.82	1.155172033
6753484	VFSVAITPDHLEPR		procollagen, type VI, alpha 1 [Mus musculus]	1580.847	67.03	0.448451991
31981549	VGAENVAIVEPSER		sulfide quinone reductase-like [Mus musculus]	1469.7654	65.6	1.675251631
6755809	VGAIPANALDDGQWSQGLISAAR		talin 1 [Mus musculus]	2310.1812	72.29	1.116652508
6755478	VGDVYIPR		splicing factor, arginine/serine-rich 2 [Mus musculus]	918.5015	39.82	1.480565265
63638100	VGINYQPPTVVPGGDLAK		PREDICTED: similar to tubulin, alpha 1 [Mus musculus]	1824.9877	46.23	1.236715243
6755901	VGINYQPPTVVPGGDLAK		tubulin, alpha 1 [Mus musculus]	1824.9877	46.23	1.236715243
34740335	VGINYQPPTVVPGGDLAK		tubulin, alpha 2 [Mus musculus]	1824.9877	46.23	1.236715243
6678467	VGINYQPPTVVPGGDLAK		tubulin, alpha 4 [Mus musculus]	1824.9877	46.23	1.236715243
6678469	VGINYQPPTVVPGGDLAK		tubulin, alpha 6 [Mus musculus]	1824.9877	46.23	1.236715243
63476037	VGLVQYNSDPTDEFFLR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1999.9796	20.36	0.969244229
63476037	VGLVQYNSDPTDEFFLR	Deamidation (NQ)	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2000.9603	59.5	0
6753620	VGNLGLATSFFNER	Deamidation (NQ)	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1525.7828	31.89	0
21312260	VGNPFELDTQQGPQVDKEQFER		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	2561.2263	87.44	1.725544121
7242148	VGQEIEVRPGIVSK		eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked [Mus musculus]	1510.8666	29.39	1.41427943
63746482	VGSAADIPINISETDLSLLTATVVPPSGR		PREDICTED: filamin, alpha [Mus musculus]	2893.552	101.1	0.767936025
16716467	VGSGDTNNFPYLEK		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1540.7268	29.22	1.50056085
46849705	VGSSGDIALHLNPR		lectin, galactose binding, soluble 4 [Mus musculus]	1435.7771	91.51	1.416511902
6679937	VGVNGFGR		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	805.4317	20.24	2.068008791
63680429	VGVSQQPEDSQQDLPGER		PREDICTED: plexin B2 [Mus musculus]	1968.9321	72.81	1.108516879
11230802	VGWEQLLTTIAR		actinin alpha 4 [Mus musculus]	1386.7798	47.83	1.173937239
6679937	VIISAPSADAPMFVMGVNHEK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	2213.1187	75.44	0
51772343	VIISASSADAPMFVMGVNHEK	Oxidation (M)	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	2219.0828	23.88	0
33469063	VILQDFTGVPAVVDFAAMR		aconitase 1 [Mus musculus]	2049.0693	19.4	1.76928236
9055170	VIMVTGDHPITAK		ATPase, H+/K+ transporting, alpha polypeptide [Mus musculus]	1381.7427	33.07	0
20149728	VIMVTGDHPITAK		ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Mus musculus]	1381.7427	33.07	0
30409956	VIMVTGDHPITAK		ATPase, Na+/K+ transporting, alpha 2 polypeptide [Mus musculus]	1381.7427	33.07	0
21450277	VIMVTGDHPITAK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1381.7427	33.07	0
20137006	VISGVLQLGNIAFK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1458.8672	70.73	1.071596497
45597447	VISLSGEHSIIGR		superoxide dismutase 1, soluble [Mus musculus]	1367.7676	58.29	1.471375922

11230802	VLAVNQENEHLMEDYER		actinin alpha 4 [Mus musculus]	2088.9641	66.38	1.316170716
33413404	VLCVINPGNPTGQVQTR	3 Deamidation (NQ)	glutamic pyruvic transaminase 1, soluble [Mus musculus]	1798.8788	19.81	0
6678449	VLDASWYSPGTR		thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	1351.6678	28.99	1.75639206
6680606	VLDELTLAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1029.5942	40.48	1.988786781
51766008	VLDNTWPAAPYR		PREDICTED: myosin IA [Mus musculus]	1402.7166	35.55	1.579284561
15617203	VLDNYLTSPLPEEVDETSAEDEGISQR		chloride intracellular channel 1 [Mus musculus]	3006.4043	120.5	1.216780622
6678359	VLDPFTIKPLDR		transketolase [Mus musculus]	1413.8038	22.11	0.955763737
31980648	VLDSGAPIKIPVGPETLGR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1919.0908	46.95	1.334558272
40068493	VLEEANQAINPK		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1325.7023	69.82	1.168320567
19923052	VLEVPPIVYLR		brain acyl-CoA hydrolase [Mus musculus]	1297.7896	29.67	1.401888017
6754854	VLFDTGLVNPR		nidogen 1 [Mus musculus]	1230.687	31.77	0
29336026	VLGLLPEEITAMLR		nonmuscle myosin heavy chain [Mus musculus]	1554.9014	32.29	2.731994885
63655455	VLGSIISSLDLLPYGLR		PREDICTED: similar to Ras GTPase-activating-like protein IQGAP2 [Mus musculus]	1816.0551	29.94	1.156472581
27804325	VLGSQEALSPVHYEEK		monoamine oxidase A [Mus musculus]	1785.9097	89.89	1.986617775
6753484	VLLFSDGNSQGATAEAIEK		procollagen, type VI, alpha 1 [Mus musculus]	1949.9597	66.3	0
6679291	VLNNMEIGTSLYDEEGAK		phosphoglycerate kinase 1 [Mus musculus]	1982.9625	24.12	0
38080000	VLNSYWVGEDSTYK		PREDICTED: similar to ribosomal protein L15 [Mus musculus]	1660.7834	24.93	1.160124482
7948997	VLQDLVNDGPDDRPAGTR		PDZ and LIM domain 3 [Mus musculus]	1937.9752	36.79	0.960588279
13384736	VLRPQVTAVAQQNQGEAPEPQDMK		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	2634.3259	25.94	1.37856784
6680748	VLSIGDGIAR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1000.5763	35.63	1.463127857
63556656	VLSPLEYFR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1123.6193	39.28	0.278591158
6671622	VLSRPNAQELPSMYQR		B-cell receptor-associated protein 37 [Mus musculus]	1888.9774	23.81	1.668438897
6755626	VLSYAPGPLDNDMQQLAR		sepiapterin reductase [Mus musculus]	1987.9971	27.94	1.669754748
10946574	VLTPELYAELR		creatine kinase, brain [Mus musculus]	1303.7273	49.81	0.67280307
7657429	VLTQIGTSIQDFLEAEDDLSSFR		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2584.2769	64.13	1.636587095
6679078	VMLGETNPADSKPGTIR		nucleoside-diphosphate kinase 2 [Mus musculus]	1785.9182	64.1	1.15137313
34576561	VMQQQQQATQQQLPQK		splicing factor 3a, subunit 1 [Mus musculus]	1911.9756	76.17	1.391025553
34576561	VMQQQQQATQQQLPQK	Oxidation (M)	splicing factor 3a, subunit 1 [Mus musculus]	1927.9689	32	0
31543113	VNDDIIVNWVNTTLK		lymphocyte cytosolic protein 1 [Mus musculus]	1743.9053	19.02	0
63517295	VNEAAPEKPQEDSGTAGGISSTSASVNR		PREDICTED: RIKEN cDNA 1810009A16 [Mus musculus]	2759.292	40.68	0
31560611	VNESTQNWHQLENIGNFIK		calponin 1 [Mus musculus]	2271.1304	58.12	0
7305085	VNFDDYTVNLGGLK		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1554.7612	34	0
33859482	VNFTVDQIR		eukaryotic translation elongation factor 2 [Mus musculus]	1091.5886	57.52	1.114007823
6678752	VNGEPLDLDPGQTLIYYVDEK	Deamidation (NQ)	lymphocyte antigen 74 [Mus musculus]	2379.1555	24.15	0
7305445	VNGRPLEMIEPR		ribosomal protein S16 [Mus musculus]	1410.755	19.7	0
63556656	VNGVLMALPVYLAGGR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1629.9163	41.71	0.347769078
9790069	VNIAFNYDMPEDSDTYLHR		HLA-B-associated transcript 1A [Mus musculus]	2300.0347	45.82	0.911708489
6755967	VNNASLIGLGYTQTLRPGVK		voltage-dependent anion channel 3 [Mus musculus]	2101.1782	44.47	1.655734998
6755963	VNNSSLIGLGYTQTLKPGIK		voltage-dependent anion channel 1 [Mus musculus]	2103.1826	70.11	2.29619861
6755965	VNNSSLIGVGYTQTLRPGVK		voltage-dependent anion channel 2 [Mus musculus]	2103.1565	77	1.257530289
6679439	VNPTVFFDITADDEPLGR		peptidylprolyl isomerase A [Mus musculus]	2005.9879	79.49	1.198167929
6679439	VNPTVFFDITADDEPLGR	Deamidation (NQ)	peptidylprolyl isomerase A [Mus musculus]	2006.9878	25.57	0
63529263	VNVQETIPYRVMHDK	Deamidation (NQ)	PREDICTED: Nedd4 binding protein 2 [Mus musculus]	1829.9215	20.3	0
31981824	VPAPEVASGPDPEEEIR		ankyrin repeat domain 25 [Mus musculus]	1791.8953	26.94	0
19525729	VPDDPEHLAAR		crystallin, lamda 1 [Mus musculus]	1219.6093	28.21	0
13385168	VPDFSDYR		ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Mus musculus]	998.4586	37.5	1.644238113
6755714	VPENPPSMVFK		transgelin [Mus musculus]	1244.6327	51.1	0
18079351	VPHNAAVQVYDYR		major vault protein [Mus musculus]	1531.772	56.69	3.191691998
6753484	VPNYQALLR		procollagen, type VI, alpha 1 [Mus musculus]	1073.6256	36.78	0.616403307
7305443	VPPAINQFTQALDR		ribosomal protein L7a [Mus musculus]	1569.8385	23	1.010990357
6754090	VPPLIASFVR		glutathione S-transferase omega 1 [Mus musculus]	1098.6705	44.51	1.848291691
51711855	VPQLPITNFNR		PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like prot	1298.7245	23.57	0.764383222
56119103	VPSTEAEALASSLMGLFEK		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1980.0006	100.63	1.198331014
6679937	VPTPNVSVVDLTCR		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1499.7942	96.78	1.133319608
37537522	VPVDVAYQR		epiplakin 1 [Mus musculus]	1046.5658	41.59	1.543299696
46849705	VPYVGALQGGLTVR		lectin, galactose binding, soluble 4 [Mus musculus]	1429.8296	107.2	1.892353667
6671700	VQDDEVGDGTTSVTVLAAELLR		chaperonin subunit 2 (beta) [Mus musculus]	2288.1543	30.27	0
63552538	VQEVEVPEDFGPVR		PREDICTED: echinoderm microtubule associated protein like 2 [Mus musculus]	1599.8104	55.15	1.390606022
6754256	VQQTVQDLFGR		heat shock protein 9A [Mus musculus]	1290.6843	61.63	2.296214557
6754482	VRPASSAASVYAGAGGSGSR		keratin complex 1, acidic, gene 18 [Mus musculus]	1807.9136	67.2	0.96167516

21312216	VSDVVDGNIQGR		gasdermin domain containing 1 [Mus musculus]	1258.6411	50.46	1.085777644
37620153	VSDVYDIEER		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1224.5806	53.33	1.201038748
30348966	VSEEAESQQWDTSK		spectrin beta 2 isoform 1 [Mus musculus]	1623.7134	41.83	1.236006361
6679439	VSFELFADK		peptidylprolyl isomerase A [Mus musculus]	1055.5443	66.62	1.447415658
31982373	VSISEGDDKIEYR		fibrillarin [Mus musculus]	1510.7401	33.12	0.901379878
28916693	VSNGAGSMSVSLVADENPFAQGALR		gelsolin [Mus musculus]	2477.21	54.54	0
28916693	VSNGAGSMSVSLVADENPFAQGALR	Deamidation (NQ)	gelsolin [Mus musculus]	2478.2078	36.49	0
63556656	VSQHGSDVVIETDFGLR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1858.9298	35.18	0
31982169	VSVVEPGNFIAATSLYSPER		3-hydroxybutyrate dehydrogenase (heart, mitochondrial) [Mus musculus]	2136.1052	44.67	1.483424318
6753086	VSYGIGEEEHDQEGR		apurinic/apyrimidinic endonuclease 1 [Mus musculus]	1704.7501	20.26	0
31543605	VTAEVVLVHPGGGSTSR		ribophorin I [Mus musculus]	1665.8988	61.46	0.88596671
63746482	VTAQGPGLEPSGNIANK		PREDICTED: filamin, alpha [Mus musculus]	1652.8651	110.21	0.802902518
63660302	VTASGPGLSAYGVPASLPVEFAIDAR		PREDICTED: filamin B, beta [Mus musculus]	2545.3325	29.25	1.124826572
31560353	VTASSENFHVGENDENQER		solute carrier family 6 (neurotransmitter transporter), member 14 [Mus musculus]	2161.9448	69.03	1.525828239
31981722	VTHAVVTVPAYFNDAQR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1887.9758	112.96	0.923333228
20799907	VTIAQGGVLPNIQAVLLPK		histone 2, H2aa1 [Mus musculus]	1931.1812	120.29	0.950250008
54607098	VTLEYRPVIDK		succinate dehydrogenase Fp subunit [Mus musculus]	1332.7532	24.15	1.500754614
6755963	VTQSNFAVGYK		voltage-dependent anion channel 1 [Mus musculus]	1213.6232	79.22	2.701657988
63746482	VTYTPMAPGSYLISIK		PREDICTED: filamin, alpha [Mus musculus]	1740.9042	37.5	1.477189991
58037117	VVAEPVELAQEFR		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Mus musculus]	1486.7961	37.03	1.435002344
6755809	VVAPTISSPVCQEQLVEAGR		talin 1 [Mus musculus]	2083.0862	49.58	0
31980648	VVDLLAPYAK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1088.6276	32.44	0
6671549	VVDSLQLTGTKPVATPVDWK		peroxiredoxin 6 [Mus musculus]	2154.1824	72.49	2.398921773
63476037	VVESLDVGPDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1185.6156	38.26	0
46849705	VVFNTMQSGQWGK		lectin, galactose binding, soluble 4 [Mus musculus]	1481.7269	65.92	2.098706389
20137006	VVFQEFR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	924.4914	30.44	1.587115466
27754118	VVHCSDLGLTSVPNNIPFDTR		asporin [Mus musculus]	2284.1194	25.9	0
34538601	VVLPMELPIR		cytochrome c oxidase subunit II [Mus musculus]	1166.7017	30.59	1.718696836
13386272	VVPGYGHAVLR		citrate synthase-like protein [Mus musculus]	1167.6732	20.83	1.618080295
13385942	VVPGYGHAVLR		citrate synthase [Mus musculus]	1167.6732	20.83	1.618080295
26006861	VVPVADIITPNQFEAELLSGR		pyridoxal (pyridoxine, vitamin B6) kinase [Mus musculus]	2268.217	21.38	1.896915633
7305295	VVSSVLQLGNIVFK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1502.8936	96.15	0.856502483
46849705	VVVNGNSFYEYGHR		lectin, galactose binding, soluble 4 [Mus musculus]	1640.7904	65.93	1.724149197
46849705	VVVNGNSFYEYGHR	Deamidation (NQ)	lectin, galactose binding, soluble 4 [Mus musculus]	1641.7762	46.1	1.846114361
6677773	VWLDPNETNEIANANSR		ribosomal protein L19 [Mus musculus]	1942.9236	27.47	1.196111582
6680047	VWQVTIGTR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1059.5958	41.34	1.376293051
31543474	VYAEANSQESADR		phosphoglucomutase 3 [Mus musculus]	1439.6467	26.88	1.305606419
21312950	VYDQMPEPR		NADH dehydrogenase (ubiquinone) Fe-S protein 7 [Mus musculus]	1134.5304	41.75	1.384364885
46593021	VYEEDAVPGLTPCR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1548.7355	29.72	1.373492797
63481281	VYEELLAIPVVR		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1400.8187	24.2	0
41322904	VYHDPSTQEPVTYSQLQQR		plectin 1 isoform 1 [Mus musculus]	2276.0977	37.22	1.091824755
8567400	VYNYNHLMPTR		ribosomal protein L27 [Mus musculus]	1407.6902	29.01	1.405030186
33859686	VYWDNGAQIISPHDR		phosphoglucomutase 1 [Mus musculus]	1770.8647	36.83	2.159201795
30023842	WALSQSNPSALR		valosin containing protein [Mus musculus]	1329.6946	21.59	1.983214644
7305085	WATHGEPNPVNSHPQR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1826.8787	22.71	1.421342055
6753498	WDYDKNEWK		cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	1283.5814	26.82	1.414801859
1346343	WELLQQVDTSTR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1475.7472	46.45	0
63746482	WGDEHIPGSPYR		PREDICTED: filamin, alpha [Mus musculus]	1413.6609	61.19	0.776757625
31559916	WGTLTDCVVMR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1280.614	33.33	1.212042685
8567336	WGVFNEYNNDEK		chloride channel calcium activated 3 [Mus musculus]	1514.662	91.17	0.275918818
31543942	WIDNPTVDDR		vinculin [Mus musculus]	1230.5824	42.68	0.780187223
33859640	WLHNEDQMAVEK		transaldolase 1 [Mus musculus]	1499.6953	65.44	1.244959848
6755963	WNTDNTLGTEITVEDQLAR		voltage-dependent anion channel 1 [Mus musculus]	2176.051	28.61	1.603288309
31980832	WQFYQNR		keratin complex 2, basic gene 18 [Mus musculus]	1041.4995	33.54	0
24762230	WQNNLLPSR		ribosomal protein S15a [Mus musculus]	1127.5959	40.56	1.235997834
13624315	WSLLQQQK		keratin complex 2, basic, gene 8 [Mus musculus]	1030.5645	41.19	1.784369334
63565108	WSLLQQQK		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1030.5645	41.19	1.784369334
27804325	WVDVGGAYVGPTQNR		monoamine oxidase A [Mus musculus]	1618.808	96.54	2.242640568
21450277	WVNDVEDSYGQQWTYEQR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2303.0061	97.07	1.500930994
18079339	WVVIGDENYGEGSSR		aconitase 2, mitochondrial [Mus musculus]	1667.7738	51.16	0

31981549	YADALQEIIR		sulfide quinone reductase-like [Mus musculus]	1191.6382	47.57	1.489171365
31981983	YAEEELEQVR		stromal interaction molecule 1 [Mus musculus]	1265.6031	35.95	1.302800966
9790219	YALYDASFETK		destrin [Mus musculus]	1307.6163	67.36	1.832648187
6680924	YALYDATYETK		cofilin 1, non-muscle [Mus musculus]	1337.6346	67.96	1.501973855
29244560	YASASEPTEIYR		hypothetical protein LOC331063 [Mus musculus]	1386.6615	52.75	0.393820489
31981828	YAVTTGDHGIIR		coatomer protein complex subunit alpha [Mus musculus]	1302.6833	40.55	1.198852354
19482160	YDGATIVPGDQGADYQHFIQQCTDDVR		coactosin-like 1 [Mus musculus]	3012.3337	19.64	0.533382462
6678483	YDGQVAVFGSDFQEK		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1689.7875	37.26	0
21704066	YDPTIEDSYR		RAS-related protein-1a [Mus musculus]	1258.5701	25.68	0.697275783
6755809	YDQATDTILTVTENIFSSMGDAGEMVR		talin 1 [Mus musculus]	2964.3601	51.2	0.826150103
37497112	YDSRPGGYGYGYGR		RNA binding motif protein 3 [Mus musculus]	1567.7035	19.1	5.00632257
9790051	YEASYDMSDSGK		phosphofructokinase, platelet [Mus musculus]	1352.5437	31.55	10.12860562
22267442	YEDSNNLGTSHLLR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1618.7863	41.78	1.253692992
27370092	YEEIDNAPEER		Tu translation elongation factor, mitochondrial [Mus musculus]	1364.6022	60.34	1.545502589
1346343	YEELQITAGR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1179.603	47.36	0
13624315	YEELQTLAGK		keratin complex 2, basic, gene 8 [Mus musculus]	1151.5957	55.06	0
13385998	YESSALPAGQLTSLPDYASR		TNF receptor-associated protein 1 [Mus musculus]	2126.0376	34.38	1.819683539
33859482	YEWDVAEAR		eukaryotic translation elongation factor 2 [Mus musculus]	1138.5178	57.98	1.530179238
22094075	YFPTQALNFAFK		solute carrier family 25, member 5 [Mus musculus]	1446.7463	57.02	1.698976432
23621467	YFQFQEEGK		PREDICTED: actin related protein 2/3 complex, subunit 2 [Mus musculus]	1175.5414	31.65	0
46593021	YFYDQCPAVAGYGPIEQLPDYNR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	2679.2329	37.66	1.645502567
34328204	YGEAGDGPGWGGPHPR		valyl-tRNA synthetase 2 [Mus musculus]	1609.7297	31.34	1.025693973
63746482	YGGDEIPFSPYR		PREDICTED: filamin, alpha [Mus musculus]	1400.6586	43.91	0.715162974
63540743	YGGPQHIVGSPFK		PREDICTED: filamin C, gamma [Mus musculus]	1386.6946	22.93	0
63746482	YGGPYHIGGSPFK		PREDICTED: filamin, alpha [Mus musculus]	1379.6807	62.02	0.831545462
21312260	YGLAAAVFTR		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1068.5885	37.55	1.822289303
6755817	YGVNPGPIVGTTR		thymopoietin [Mus musculus]	1330.7139	32.37	1.567875829
6680606	YGVQLSQIQSVISGFEAQLSDVR		keratin complex 1, acidic, gene 19 [Mus musculus]	2524.3059	116.21	1.760864094
6679687	YGVSGYPTLK		glucose regulated protein [Mus musculus]	1084.5693	45.32	0.963363122
31981246	YGYTHLSAGELLR		UMP-CMP kinase [Mus musculus]	1479.7637	61.95	1.558262915
40556608	YHTSQSGDEMTSLSEYVSR		heat shock protein 1, beta [Mus musculus]	2176.949	94.97	1.488317992
34996495	YHVPVVVVPEGSTSDTQEQAILR		ribophorin II [Mus musculus]	2524.3013	63.9	1.283284696
63746482	YIPVQQGPVGVNVTYGGDHIPK		PREDICTED: filamin, alpha [Mus musculus]	2338.2273	103.12	0.937167041
38080000	YIQELWR		PREDICTED: similar to ribosomal protein L15 [Mus musculus]	1007.5432	21.08	1.414164528
51770896	YITPDQLADLYK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1439.7252	69.33	1.201400225
21704144	YLDEDTIYHLQPSGR		methionine adenosyltransferase II, alpha [Mus musculus]	1806.871	46.33	3.187320148
6679601	YLECSALTQR		RAS-related C3 botulinum substrate 2 [Mus musculus]	1183.5823	22.69	1.096221422
63530525	YLELLGYR		PREDICTED: SEC31-like 1 [Mus musculus]	1026.5623	28.26	4.06512741
6678449	YLGTQPEPDIVGLDSGHIR		thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	2067.0432	45.47	0
6678449	YLGTQPEPDIVGLDSGHIR	Deamidation (NQ)	thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	2068.0537	70.77	0
33468931	YLIATSEQPIAALHR		seryl-aminoacyl-tRNA synthetase 1 [Mus musculus]	1682.926	29.33	0
31560645	YLLSQSSPAPLTAAEEELR		twinfilin [Mus musculus]	2075.0618	28.48	1.345963815
6753254	YLNQDYETLR		calpain 2 [Mus musculus]	1314.6547	26.14	1.108421967
33859506	YMCENQATISSK		albumin 1 [Mus musculus]	1374.6045	73.71	1.791675543
63660302	YMIGVTYGGDNIPLSPYR		PREDICTED: filamin B, beta [Mus musculus]	2015.9878	39.3	1.318725552
6678573	YNDEPVQIR		villin 1 [Mus musculus]	1133.5641	30.23	2.052843219
63746482	YNDQHIPGSPFTAR		PREDICTED: filamin, alpha [Mus musculus]	1602.7734	52.85	0.610172811
6753138	YNPNVLPVQCTGK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1432.7177	41.02	1.664612966
31981522	YNQMDSTEDAQEEFGWK		transmembrane 9 superfamily member 2 [Mus musculus]	2077.8777	64.95	0
51771420	YNVLGAETVLTQMR		PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1594.8243	40.29	1.364660806
31543918	YPEAPPSVR		ubiquitin-conjugating enzyme E2 variant 2 [Mus musculus]	1015.5297	34.39	1.090610591
6671507	YPIEHGIITNWDDMEK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1960.9352	62.56	1.023743369
6671507	YPIEHGIITNWDDMEK	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1976.9232	26.59	0.62712739
31981945	YQAVTATLEEK		ribosomal protein L13a [Mus musculus]	1252.6332	37.77	0
7549795	YQEEGPVPQPR		tight junction protein 2 [Mus musculus]	1299.6384	21.37	1.743403992
6755963	YQVDPDACFSAK		voltage-dependent anion channel 1 [Mus musculus]	1343.6003	37.07	6.283644591
6679891	YRVPDVLVADPPTAR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1668.9009	23.96	0.607737853
31982223	YSEIEPSTEGEVIYR		laminin, beta 2 [Mus musculus]	1771.8385	32.32	0
23956406	YSGGLPLPPSYVPVVMSELSDR		UDP glucuronosyltransferase 2 family, polypeptide B34 [Mus musculus]	2363.1899	23.28	1.765310843
63474405	YSMPDNSPETR		PREDICTED: tensin [Mus musculus]	1296.5612	27.38	0.893581079

33469063	YTINIPEDLKPR	aconitase 1 [Mus musculus]	1458.7938	34.92	0
6754016	YTTPEDATPEPGEDPR	guanine nucleotide binding protein alpha stimulating isoform b [Mus musculus]	1774.785	60.91	1.186762735
6680854	YVDSEGHLYTVPIR	caveolin, caveolae protein 1 [Mus musculus]	1648.8414	71.86	0.951824828
13386062	YVEEQPGNLQR	hypothetical protein LOC68117 [Mus musculus]	1332.6611	32.58	1.39726356
33859482	YVEPIEDVPCGNIVGLVGVDQFLVK	eukaryotic translation elongation factor 2 [Mus musculus]	2702.4089	24.09	1.344777716
40254244	YVQELPLETDGALR	loss of heterozygosity, 11, chromosomal region 2, gene A homolog [Mus musculus]	1603.8322	47.13	2.662466373
17432429	YVRPGGGYQPTFSLTQK	glutathione peroxidase 2 [Mus musculus]	1898.9796	22.38	0
64427157	YVVDSDTVQAHTVR	PREDICTED: synaptopodin 2 [Mus musculus]	1589.7894	65.53	0.872868972
27754118	YWEIQPATFR	asporin [Mus musculus]	1310.6581	38.39	1.173954339
6678499	YWQQVIDMNDYQR	UDP-glucose dehydrogenase [Mus musculus]	1758.7986	25.05	6.615958977
31982290	YYEPYYAAGPSYGGR	LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1713.7645	56.4	0.781091909
23943876	YYIVGLQVR	zymogen granule membrane protein 16 [Mus musculus]	1110.6317	34.62	1.054799485
6755354	YYPTEDVPR	ribosomal protein L6 [Mus musculus]	1139.5382	46.31	1.31956668
63556656	YYVLGATFYPGPECER	PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1864.8677	27.93	0.416164238
51873060	YYVTIIDAPGHR	eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	1404.7349	41.83	1.099238234

Mouse Pair 2

GI #	Sequence	Modifications	Protein Name	M/z	Highest Mascot score	Average Ratio (15N:14N), non-Log-transformed
7657429	AAAITSDLLESLGR		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	1416.7697	65.91	1.112258157
33859506	AADKDTCFSTEGPNLVTR		albumin 1 [Mus musculus]	1924.9158	98.29	3.294522749
31981925	AAFDDAIAELDTLSEESYK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Mus mu	2087.9912	43.86	1.959881332
6753036	AAFQLGSPWR		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1132.5909	24.02	2.931261288
6680606	AALEGTLAETEAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1331.6879	59.41	1.639573032
13385006	AANNGALPPDLSYIVR		cytochrome c-1 [Mus musculus]	1670.8679	42.75	0.86753387
27754065	AAPFTLEYR		pyrophosphatase [Mus musculus]	1067.5526	28.15	2.286688337
6677995	AAQSPQQHSSGDPTEEESPV		solute carrier family 16, member 1 [Mus musculus]	2080.9155	118.79	1.270836103
63474405	AASDGQYENQSPEATSPR		PREDICTED: tensin [Mus musculus]	1907.8444	71.07	0.285619877
7304889	AASGFNATEDAQTLR		annexin A4 [Mus musculus]	1551.7499	56.02	1.513946375
6755809	AATAPLLEAVDNLSAFASNPEFSSVPAQISPEGR		talin 1 [Mus musculus]	3456.7322	67.06	
31543051	AAVENLPTFLVELSR		karyopherin (importin) beta 1 [Mus musculus]	1658.9133	40.22	2.28274311
7305027	AAVPSGASTGIYEALELR		enolase 2, gamma neuronal [Mus musculus]	1804.9502	86.15	0.964245036
51770896	AAVPSGASTGIYEALELR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1804.9502	86.15	0.964245036
50355692	AAYEAELGDAR		lamin A isoform A [Mus musculus]	1165.568	32.21	0.624811951
22094075	AAYFGIYDTAK		solute carrier family 25, member 5 [Mus musculus]	1219.6029	48.61	1.049932819
13937391	ACGDSTLTQITAGLDPVGR		guanine nucleotide-binding protein, beta-2 subunit [Mus musculus]	1874.9291	20.33	0
63476037	ACNLEVILGFDGSR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1493.7495	28.18	0
6671539	ADDGRPFPQVIK		aldolase 1, A isoform [Mus musculus]	1342.7174	40.76	1.125455481
34328489	ADFDNTVAIHPTSSEELVTLR		glutathione reductase 1 [Mus musculus]	2315.1392	38.86	0
6753266	ADGLAILGVLMK		carbonic anhydrase 1 [Mus musculus]	1200.7012	88.68	0
6754084	ADIVENQVMDTR		glutathione S-transferase, mu 1 [Mus musculus]	1390.6703	35.64	0
33859811	ADMVIEAVFEDLGVK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1635.827	91.26	1.076097213
6996913	AEDGSVIDYELIDQDAR		annexin A2 [Mus musculus]	1908.8857	76.5	1.976660554
63746482	AEFTVETR		PREDICTED: filamin, alpha [Mus musculus]	952.4718	39.77	0
31981562	AEGSDVANAVLDGADCIMLSGETAK	Deamidation (NQ)	pyruvate kinase 3 [Mus musculus]	2438.1274	93.55	0
63746482	AEISFEDR		PREDICTED: filamin, alpha [Mus musculus]	966.4476	21.99	0
6678573	AELGNSGDWSQIADEVMSPK		villin 1 [Mus musculus]	2133.99	80.25	1.474480827
6678573	AELGNSGDWSQIADEVMSPK	Deamidation (NQ)	villin 1 [Mus musculus]	2134.9949	69.26	1.033154964
6755372	AELNEFLTR		ribosomal protein S3 [Mus musculus]	1092.5696	22.67	1.19316314
13386054	AENFFILR		actin related protein 2/3 complex, subunit 4 [Mus musculus]	1009.5424	22.89	1.349512292
6678483	AENYDISPADR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1250.566	39.19	1.563495984
13626040	AEVGQEGEAGQFDGEK		A kinase (PRKA) anchor protein (gravin) 12 [Mus musculus]	1650.74	56.79	0
63746482	AEVGVPAEFGIWTR		PREDICTED: filamin, alpha [Mus musculus]	1531.7869	42.3	0.288923965
46559834	AEVSTIHLQSPGR		desmuslin isoform M [Mus musculus]	1394.7445	32.5	0
6753322	AFADAMEVIPSTLAENAGLNPISTVTELR		chaperonin subunit 4 (delta) [Mus musculus]	3030.5381	58.12	1.644567751
63746482	AFGPGLQGGNAGSPAR		PREDICTED: filamin, alpha [Mus musculus]	1456.7435	100.58	0.265706355
7710086	AFLTLAEDILR		RAB10, member RAS oncogene family [Mus musculus]	1261.7209	48.51	1.393144743
6678892	AFQVWSDVTPLR	Deamidation (NQ)	matrix metalloproteinase 12 [Mus musculus]	1419.7052	19.18	0
6755901	AFVHWYVGEGMEEGEFSEAR		tubulin, alpha 1 [Mus musculus]	2330.0391	27.28	1.568922979
34740335	AFVHWYVGEGMEEGEFSEAR		tubulin, alpha 2 [Mus musculus]	2330.0391	27.28	1.568922979
6678467	AFVHWYVGEGMEEGEFSEAR		tubulin, alpha 4 [Mus musculus]	2330.0391	27.28	1.568922979
6678469	AFVHWYVGEGMEEGEFSEAR		tubulin, alpha 6 [Mus musculus]	2330.0391	27.28	1.568922979
31982186	AGAGSATLSMAYAGAR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1454.7133	61.43	1.252738723
6671507	AGFAGDDAPR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	976.4477	54.55	0.403319735
6671509	AGFAGDDAPR		actin, beta, cytoplasmic [Mus musculus]	976.4477	54.55	0.403319735
31982275	AGGIETIANEYSDR		heat shock protein 4 [Mus musculus]	1495.7202	25.93	0.806970103
33859811	AGLEQGSDAGYLAESQK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1723.8177	105.87	0.605724708
8394269	AGLMFPNMEAYAVSPAR		ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltra	1824.8827	30.92	1.390177193
20799907	AGLQFPVGR		histone 2, H2aa1 [Mus musculus]	944.5343	46.58	1.339463159
6677775	AGNLGGGVVTIER		ribosomal protein L22 [Mus musculus]	1242.6847	25.06	3.910271303
63746482	AGNNMLLVGVHGPR	2 Deamidation (NQ)	PREDICTED: filamin, alpha [Mus musculus]	1436.7406	24.22	0
31982223	AGNSLAASTAEETAGSAQSR		laminin, beta 2 [Mus musculus]	1878.8832	53.61	0
41322904	AGTLSITEFADMLSGNAGGFR		plectin 1 isoform 1 [Mus musculus]	2115.0217	81.51	1.108206952

59709449	AGTQIENIEEDFR		actinin alpha 2 [Mus musculus]	1521.7183	40.13	0.840440107
7304855	AGTQIENIEEDFR		actinin alpha 3 [Mus musculus]	1521.7183	40.13	0.840440107
59709449	AGTQIENIEEDFRNGLK	Deamidation (NQ)	actinin alpha 2 [Mus musculus]	1934.9807	25.18	1.647057329
7304855	AGTQIENIEEDFRNGLK	Deamidation (NQ)	actinin alpha 3 [Mus musculus]	1934.9807	25.18	1.647057329
41322904	AGVGAPVTQVTLQSTQR		plectin 1 isoform 1 [Mus musculus]	1712.938	30.61	0.756211992
51770896	AGYTDQVVIGMDVAASEFYR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	2192.0371	27.92	0.908296138
31980648	AHGGYSVFAGVGER		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1406.6902	70.26	0
31980648	AIAELGIYPAVDPLDSTSR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1988.0399	123	1.037630287
31542413	AIFLADGNVFTTGFSR		coronin, actin binding protein 1C [Mus musculus]	1715.8767	42.03	0
33859488	AILVDLEPGTMDSVR		tubulin, beta 2 [Mus musculus]	1615.8481	76	1.162005828
12963615	AILVDLEPGTMDSVR		tubulin, beta 3 [Mus musculus]	1615.8481	76	1.162005828
7106439	AILVDLEPGTMDSVR		tubulin, beta 5 [Mus musculus]	1615.8481	76	1.162005828
6755198	AINQGGLTSVAVR		proteasome (prosome, macropain) subunit, alpha type 6 [Mus musculus]	1285.7301	21.52	1.407512259
31543942	AIPDLTAPVAAVQAAVSNLVR		vinculin [Mus musculus]	2076.1826	49.33	0.48442928
6753864	AIVAGDQNVEYK		four and a half LIM domains 1 [Mus musculus]	1306.6667	78.44	0.517281142
31560560	AIVAIENPADVSVISSR		laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1740.9497	75.59	1.319612729
31981722	AKFEELNMDLFR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1512.7592	34.99	1.473101784
31981722	AKFEELNMDLFR	Deamidation (NQ)	heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1513.7566	20.13	0
34328365	ALAAAGYDVEK		histone 1, H1d [Mus musculus]	1107.5691	83.95	1.241050121
13430890	ALAAAGYDVEK		histone 1, H1e [Mus musculus]	1107.5691	83.95	1.241050121
21426893	ALAAGGYDVEK		histone 1, H1b [Mus musculus]	1093.5433	63.59	1.308414666
33598964	ALELDPNLYR		myosin heavy chain 10, non-muscle [Mus musculus]	1203.6376	46.68	0.151195386
7305295	ALELDPNLYR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1203.6376	46.68	0.151195386
20137006	ALELDSNLYR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1193.6151	38.75	1.47573805
6680606	ALEQANGELEVK		keratin complex 1, acidic, gene 19 [Mus musculus]	1300.6742	74.6	1.534607837
6679687	ALEQFLQEYFDGNLK		glucose regulated protein [Mus musculus]	1814.879	81.54	1.40705778
23956176	ALEQNPDDAQYYCQR		SGT1, suppressor of G2 allele of SKP1 [Mus musculus]	1813.8168	25.49	0
7305295	ALETQMEEMK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1209.5496	52.04	0.237285892
63746482	ALGALVDSCAPGLCPDWDSWDASKPVNNAR		PREDICTED: filamin, alpha [Mus musculus]	3128.4685	67.98	0
6678573	ALGMTPAAFSALPR		villin 1 [Mus musculus]	1402.7396	22.34	2.888255229
33620739	ALGQNPTNAEVLK		myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Mus musculus]	1354.7152	40.04	0
6753322	ALIAGGGAPEIELALR		chaperonin subunit 4 (delta) [Mus musculus]	1550.8914	40.48	1.613896709
29244556	ALILVGGYGTR		GDP-mannose pyrophosphorylase B [Mus musculus]	1119.6552	21.82	1.850978668
63489754	ALINADELANDVAGAEALLDR		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	2154.1023	125.2	1.227497307
6671666	ALLATASQCQQPAGNK		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1600.8116	59.71	1.448359177
46559834	ALLEGESNPEILIWTENIENVPQEPR		desmuslin isoform M [Mus musculus]	2990.5186	37.91	0
33859482	ALLELQLEPEELYQTFQR		eukaryotic translation elongation factor 2 [Mus musculus]	2220.1577	86.18	1.214100638
40556608	ALLFIPR		heat shock protein 1, beta [Mus musculus]	829.5231	33.37	1.654545423
31981679	ALMLQGVDLLADAVAVTMGPK		heat shock protein 1 (chaperonin) [Mus musculus]	2113.1436	62.01	0
63476037	ALNLGYALDYALR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1452.7915	64.83	0.270254416
63506192	ALPFWNEEIVPQIK		PREDICTED: similar to phosphoglycerate mutase (EC 5.4.2.1) B chain - rat [Mus musculus]	1683.9053	27.09	2.017808105
30578429	ALPLWLSLQYLGLDGIVER		hypothetical protein LOC94184 [Mus musculus]	2156.2131	20.1	1.353489055
31982286	ALQNAVSTFVNR	Deamidation (NQ)	HGF-regulated tyrosine kinase substrate [Mus musculus]	1320.6821	21.07	0
21704020	ALSEIAGITLPYDTLDQVR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	2075.1025	79.13	1.010453206
22165384	ALTVPELTQQMFDAK		tubulin, beta, 2 [Mus musculus]	1691.8729	57.86	1.082451621
12963615	ALTVPELTQQMFDAK		tubulin, beta 3 [Mus musculus]	1691.8729	57.86	1.082451621
31981939	ALTVPELTQQMFDAK		tubulin, beta 4 [Mus musculus]	1691.8729	57.86	1.082451621
27754056	ALTVPELTQQMFDAK		tubulin, beta 6 [Mus musculus]	1691.8729	57.86	1.082451621
9903607	ALVDELEWEIAR		transmembrane protein 4 [Mus musculus]	1443.7524	35.26	0
19526818	ALYSNILGEENTYLWR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1941.9736	60.17	1.350926231
14389431	AMADPEVQQIMSDPAMR		stress-induced phosphoprotein 1 [Mus musculus]	1889.8751	36.2	1.295657309
21704100	AMDSDWFAQNYMGR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1691.7013	38.27	0.870227973
21704100	AMDSDWFAQNYMGR	Deamidation (NQ)	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1692.6975	27.08	0
20874851	AMGIMNSFVNDIFER		PREDICTED: similar to histone H2b-616 [Mus musculus]	1743.8418	46	0
20874851	AMGIMNSFVNDIFER	Deamidation (NQ)	PREDICTED: similar to histone H2b-616 [Mus musculus]	1744.8287	84.16	0
20874851	AMGIMNSFVNDIFER	Oxidation (M)	PREDICTED: similar to histone H2b-616 [Mus musculus]	1759.8228	36.13	1.076089212
41054806	AMGNLQIDFADPQR		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1575.7677	22.17	1.345444086
41054806	AMGNLQIDFADPQRADDAR	2 Deamidation (NQ)	guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	2105.9819	19.79	0
38372905	ANINVENAFFTLAR		cell line NK14 derived transforming oncogene [Mus musculus]	1579.8282	55.14	1.55941834
63746482	ANLPQSFQVDTSK		PREDICTED: filamin, alpha [Mus musculus]	1434.7257	85.71	0.264512121

20137006	ANLQIDQINTDLNLER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1869.9568	59.99	1.50167768
7304881	ANNTTYGLAAGLFTK		aldehyde dehydrogenase family 1, subfamily A1 [Mus musculus]	1541.7832	34.51	1.49225543
19745150	APDAWDYSQGFVNEEMIR		diaphorase 1 [Mus musculus]	2127.947	32.5	1.240947151
6754750	APDFVFYAPR		moesin [Mus musculus]	1182.5948	54.75	1.452763021
6678571	APDFVFYAPR		villin 2 [Mus musculus]	1182.5948	54.75	1.452763021
6681157	APILIATDVASR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1226.7057	38.14	2.083272106
31560689	APLVLEQGLR		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	1095.6498	51.28	0.321300528
33859506	APQVSTPTLVEAAR		albumin 1 [Mus musculus]	1439.795	63.77	2.7328288
33563250	APSYGAGELLDFSLADAVNQEFLATR		desmin [Mus musculus]	2755.3733	114.28	0.2063851
7106435	APTAQVESFR		tenascin C [Mus musculus]	1105.5649	39.45	1.00770626
6671664	APVPTGEVYFADSFDR		calnexin [Mus musculus]	1770.8364	68.74	0
41322904	AQAEAQQPVFNTLR		plectin 1 isoform 1 [Mus musculus]	1572.8146	30.69	0
41322904	AQAELEAQELQR		plectin 1 isoform 1 [Mus musculus]	1385.7043	32.14	1.078395328
31982520	AQDTAELFFEDVR		acetyl-Coenzyme A dehydrogenase, long-chain [Mus musculus]	1540.7335	69.05	1.982934665
51828444	AQEAAAEEPPPAVTPAASVSALDLGEQR		PREDICTED: proline-rich polypeptide 6 [Mus musculus]	2775.3782	65.85	1.178022199
6754256	AQFEGIVTDLIK		heat shock protein 9A [Mus musculus]	1333.7314	63.62	1.809393747
29789289	AQFGQPEILLGTIPGAGGTQR		enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Mus musculus]	2111.1301	58.44	1.875314892
27229118	AQFSEVQLEWQPPPFR		hypothetical protein LOC71664 [Mus musculus]	1958.9725	23.92	0
6679583	AQIWDTAGQER		RAB11B, member RAS oncogene family [Mus musculus]	1274.6185	31.76	1.622585762
6754482	AQMEQLNGVLLHLESELAQTR		keratin complex 1, acidic, gene 18 [Mus musculus]	2380.2241	24.15	1.433569273
21536220	AQSELSGAADEAAR		ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit precursor [Mus musculus]	1375.6521	110.78	1.013263532
19526862	AQSSQDAVSSMNLFDLGGQYLR		fuse-binding protein-interacting repressor [Mus musculus]	2387.0999	19.51	0
6754556	ASAPATPLSPTR		lamin B1 [Mus musculus]	1168.6357	24.18	1.174960941
34328206	ASEDFVDPWTVR		tryptophanyl-tRNA synthetase [Mus musculus]	1421.6711	33.75	0
6755358	ASGNYATVISHNPETK		ribosomal protein L8 [Mus musculus]	1688.8252	78.05	0
63746482	ASGPGLNTTGVPASLPVEFTIDAK		PREDICTED: filamin, alpha [Mus musculus]	2342.229	84.69	0
34328365	ASGPPVSELITK		histone 1, H1d [Mus musculus]	1198.6698	31.66	0
23943876	ASGTSFNAVPLHPNTVLR		zymogen granule membrane protein 16 [Mus musculus]	1880.9993	36.38	3.14960897
13624315	ASLEAAIADAEQR		keratin complex 2, basic, gene 8 [Mus musculus]	1344.6794	67.98	1.312127502
6679931	ASLGTLNTLADVPDDEVQGR		UDP-N-acetyl-alpha-D-galactosamine: (N-acetylneuraminyl)-galactosyl-N- acetylglucosaminylpolypeptid	2071.0281	60.35	0
31543605	ASSFVLALEPELESR		ribophorin I [Mus musculus]	1647.8629	51.93	1.277140386
9845283	ASYVAPLTAQPATYR		RNA binding motif protein 14 [Mus musculus]	1608.8413	35.73	1.210263232
7305163	ATAGDTHLGGEDFDNR		heat shock protein 1-like [Mus musculus]	1675.7479	60.3	0
63704924	ATAGDTHLGGEDFDNR		PREDICTED: heat shock protein 1B [Mus musculus]	1675.7479	60.3	0
6754976	ATAVMPDGQFK		peroxiredoxin 1 [Mus musculus]	1164.5696	63.03	1.380875034
6755114	ATDLLLDDSLVSLFGNR		peroxiredoxin 5 precursor [Mus musculus]	1848.9874	44.05	2.574202111
6679567	ATEMVEVGPEDDEVGAER		polymerase I and transcript release factor [Mus musculus]	1932.8557	106.36	0.600034241
6679567	ATEMVEVGPEDDEVGAER	Oxidation (M)	polymerase I and transcript release factor [Mus musculus]	1948.8485	30.19	0
9845253	ATENDIYNFFSPLNPMR		heterogeneous nuclear ribonucleoprotein H2 [Mus musculus]	2028.9503	30.99	0.986487774
10946928	ATENDIYNFFSPLNPVR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1996.9727	78.04	1.640791374
25020120	ATGDPWLTDGSYLDGSGFAR		PREDICTED: laminin, alpha 5 [Mus musculus]	2085.97	26.92	0
55741703	ATGVLLYDLVSR		glutaminyl-tRNA synthetase [Mus musculus]	1306.7349	25.48	0
7305295	ATLQAEQLSNELATER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1773.9039	105.87	0.1822314
6753492	ATPEPSGTPSSDTVSR		coronin, actin binding protein 1A [Mus musculus]	1588.7574	65.59	5.152195039
21450625	ATQALVLAPTR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1140.674	29.25	1.79222132
6755809	AVAEQIPLLVQGVR		talin 1 [Mus musculus]	1492.8856	45.92	0
22267442	AVAQGNLSSADVQAAK		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1529.7998	49.19	0
6755901	AVCMLSNTTAIAEAWAR		tubulin, alpha 1 [Mus musculus]	1807.8944	22.44	1.123734352
34740335	AVCMLSNTTAIAEAWAR		tubulin, alpha 2 [Mus musculus]	1807.8944	22.44	1.123734352
6678467	AVCMLSNTTAIAEAWAR		tubulin, alpha 4 [Mus musculus]	1807.8944	22.44	1.123734352
6678469	AVCMLSNTTAIAEAWAR		tubulin, alpha 6 [Mus musculus]	1807.8944	22.44	1.123734352
6680748	AVDSLVPIGR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1026.5929	57.15	0.921602227
25020120	AVEASNAYSSILQAVQAAEDAAGQALR		PREDICTED: laminin, alpha 5 [Mus musculus]	2704.345	55.04	0.301952509
18079351	AVFPQNGLVVSSVDVQSVEPVDQR		major vault protein [Mus musculus]	2569.3215	67.41	1.24540746
6671507	AVFPSIVGRPR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1198.7054	27.24	0.437800529
6671509	AVFPSIVGRPR		actin, beta, cytoplasmic [Mus musculus]	1198.7054	27.24	0.437800529
21450277	AVFQANQENLPILK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1584.8759	57.32	1.244677131
6678467	AVFVDLEPTVIDEIR		tubulin, alpha 4 [Mus musculus]	1715.9268	51.65	1.662333853
6755901	AVFVDLEPTVIDEVR		tubulin, alpha 1 [Mus musculus]	1701.9135	116.28	0.967612901
34740335	AVFVDLEPTVIDEVR		tubulin, alpha 2 [Mus musculus]	1701.9135	116.28	0.967612901

6678469	AVFVDLEPTVIDEVR		tubulin, alpha 6 [Mus musculus]	1701.9135	116.28	0.967612901
28916673	AVITSLLDQIPEMFADTR		SEC24 related gene family, member C [Mus musculus]	2020.0338	51.16	2.105277472
22165384	AVLVDLEPGTMDSVR		tubulin, beta, 2 [Mus musculus]	1601.8191	66.08	1.264405525
31981939	AVLVDLEPGTMDSVR		tubulin, beta 4 [Mus musculus]	1601.8191	66.08	1.264405525
16716471	AVPVSNIAPAAVGR		hypothetical protein LOC94184 [Mus musculus]	1321.7654	44.47	1.303810106
6756039	AVTEQGAELSNEER		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Mus musc	1532.7223	57.5	1.177833896
7305173	AVTQSAEITIPVTFEAR		heat shock protein 1 [Mus musculus]	1832.9714	63.69	0.314210752
31543605	AVTSEIAVLQSR		ribophorin I [Mus musculus]	1273.7073	31.38	1.138369344
63746482	AWGPGLEGGIVGK		PREDICTED: filamin, alpha [Mus musculus]	1240.6641	82.41	0
63540743	AWGPGLETGQVGK		PREDICTED: filamin C, gamma [Mus musculus]	1299.6622	28.56	0
6753138	AYGENIGYSEK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1230.5654	71.71	1.507482101
63746482	AYGPGIEPTGNMVK		PREDICTED: filamin, alpha [Mus musculus]	1433.7113	44.21	0.337809677
6755901	AYHEQLSVAEITNACFEPANQMVK		tubulin, alpha 1 [Mus musculus]	2693.282	48.43	0.960860302
34740335	AYHEQLSVAEITNACFEPANQMVK		tubulin, alpha 2 [Mus musculus]	2693.282	48.43	0.960860302
6678467	AYHEQLSVAEITNACFEPANQMVK		tubulin, alpha 4 [Mus musculus]	2693.282	48.43	0.960860302
33859482	AYLPVNESFGFTADLR		eukaryotic translation elongation factor 2 [Mus musculus]	1799.8943	51.55	1.365482222
20137008	AYYNGISLFNNPVPYWEVQPATFR		biglycan [Mus musculus]	2846.3762	46.79	1.349264004
63746482	CAPGVVGPTEADIDFDIIR		PREDICTED: filamin, alpha [Mus musculus]	1987.9602	20.13	0
63746482	CGQSAAVASPGGSIDSR		PREDICTED: filamin, alpha [Mus musculus]	1562.731	90.85	0.238089425
26024211	CIHQSLEDNNR	2 Deamidation (NQ)	constitutive photomorphogenic protein 1 [Mus musculus]	1330.5791	24.64	0
6753484	DAEEVISQTIDTIVDMIK		procollagen, type VI, alpha 1 [Mus musculus]	2020.0264	82.47	0
6753484	DAEEVISQTIDTIVDMIK	Oxidation (M)	procollagen, type VI, alpha 1 [Mus musculus]	2036.0068	26.41	0
6754482	DAETTLTELR		keratin complex 1, acidic, gene 18 [Mus musculus]	1148.577	22.34	0.506507333
21450277	DAFQNAYLELGGLGER		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1752.8593	44.9	0.796203942
63660302	DAGEGLLAVQITDQEGKPQR		PREDICTED: filamin B, beta [Mus musculus]	2125.082	38.56	1.487495552
6754036	DAGMQLQGYR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1138.5352	33.97	0
6754256	DAGQISGLNVLR		heat shock protein 9A [Mus musculus]	1242.6794	47	0
31981690	DAGTIAGLNVLR		heat shock protein 8 [Mus musculus]	1199.6765	60.89	1.122077916
63664182	DAGTIAGLNVLR		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1199.6765	60.89	1.122077916
31981722	DAGTIAGLNVMR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1217.6285	65.19	1.146909918
31542602	DANLYISGLPR		ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) [Mus musculus]	1218.637	24.68	0.882472189
41322904	DAPDGPSVEAEPEYTFEGLR		plectin 1 isoform 1 [Mus musculus]	2178.9912	73.86	0.998748298
21592285	DAQVQNAQCVLR		keratin 20 [Mus musculus]	1344.671	57.26	1.176327632
30348966	DASVAEAWLLGQEPYLSSR		spectrin beta 2 isoform 1 [Mus musculus]	2092.0193	42.98	1.391482722
7106421	DASVAEAWLLGQEPYLSSR		spectrin beta 2 isoform 2 [Mus musculus]	2092.0193	42.98	1.391482722
6679687	DASVVGFFR		glucose regulated protein [Mus musculus]	997.5002	59.41	1.183794824
51770896	DATNVGDEGGFAPNILENK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1960.9368	49.51	0.958928702
31542333	DAVIYPILVEFTR		hypoxia up-regulated 1 [Mus musculus]	1535.854	47.51	1.252757088
31981562	DAVLNAWAEDVDLR		pyruvate kinase 3 [Mus musculus]	1586.7877	114.17	1.388842232
31981562	DAVLNAWAEDVDLR	Deamidation (NQ)	pyruvate kinase 3 [Mus musculus]	1587.7899	43.92	0
6755204	DAYSGGAVNLYHVR		proteasome (prosome, macropain) subunit, beta type 5 [Mus musculus]	1521.7313	20.9	0.409269127
6679291	DCVGPEVENACANPAAGTVILLENLR		phosphoglycerate kinase 1 [Mus musculus]	2668.291	42.79	1.475034181
56699423	DDFLGQVDVPLYPLPTENPR		neural precursor cell expressed, developmentally down-regulated gene 4 [Mus musculus]	2285.1541	44.08	0
6680027	DDGSWEVIEGYR		glutamate dehydrogenase 1 [Mus musculus]	1425.6322	33.65	0.596284264
31982122	DDLIASILSEVTPTPLEELR		phospholipase C, beta 3 [Mus musculus]	2211.1726	40.06	1.670450802
6681027	DDTYQSYSSPSPR		deleted in malignant brain tumors 1 [Mus musculus]	1502.65	39.29	1.298025684
31981100	DESSPYAAMLAAQDVAQR		ribosomal protein S14 [Mus musculus]	1922.8925	61.97	0
6680047	DETNYGIPQR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1192.5673	69.9	1.506818381
22203747	DFDSLAQPSFFDR		procollagen, type VI, alpha 2 [Mus musculus]	1544.7035	59.48	0
8393150	DFEQPLAISR		carboxyl terminal LIM domain protein 1 [Mus musculus]	1175.6063	26.39	0
6755142	DFMIQGGDFTR		peptidylprolyl isomerase B [Mus musculus]	1286.5925	50.89	0.853132194
14149647	DFNHINVELSLLGK		ribosomal protein L9 [Mus musculus]	1598.8317	64.85	0
24418919	DFNVGDYIEAVLDR		brain glycogen phosphorylase [Mus musculus]	1625.7791	53.68	0
42475998	DFNVPLSISR		PDZ and LIM domain 7 [Mus musculus]	1147.6156	40.52	0.319287102
31981657	DFPIANGDR		carbonic anhydrase 2 [Mus musculus]	1004.4788	31.77	1.336435904
20137006	DFSALESQLQDTQELLQEENR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2493.1746	159.91	1.72231268
29126205	DFSATDLTEFAAR		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1443.6792	24.94	1.334964003
6755714	DFTDSQLQEGK		transgelin [Mus musculus]	1267.5864	72.66	0.360192166
10181184	DFTPSGIAGAFR		ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 [Mus musculus]	1238.6163	30.23	1.027589282
6681233	DGAFDFFPVLR		solute carrier family 26 (sulfate transporter), member 2 [Mus musculus]	1283.6453	36.54	1.340103859

58037267	DGELPVEDDIDLSDVELDDLEKDEL		protein disulfide isomerase-associated 6 [Mus musculus]	2830.3284	51.59	2.1893621
33563250	DGEVVSEATQQQHEVL		desmin [Mus musculus]	1768.8481	100.63	0
22164798	DGFNPAHVEAGLYGSR		selenium binding protein 1 [Mus musculus]	1689.8038	69.49	1.087978076
55742711	DGMLDDEEFALASHLIEAK		EH-domain containing 2 [Mus musculus]	2104.0022	25.21	0.916145846
7709980	DGPLNMILDDGGDLTNLIHTK		S-adenosylhomocysteine hydrolase [Mus musculus]	2252.1104	41.48	0
21450277	DGPNALTPPPTTPEWVK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1819.924	36.38	1.576544377
6680047	DGQAMLWDLNEGK		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1476.6825	39.23	0
27229048	DGQVIGIGAGQQSR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1385.7159	51.33	1.146036679
31982755	DGQVINETSQHHDDLE		vimentin [Mus musculus]	1836.8029	94.02	0.717553193
45597447	DGVANVSIEDR		superoxide dismutase 1, soluble [Mus musculus]	1174.5669	58.67	1.079467023
20806532	DGVPEGTQLQAHR		cold shock domain protein A short isoform [Mus musculus]	1407.7007	43.14	1.00907926
27754099	DGWSLWYAEYR		eukaryotic translation elongation factor 1 gamma [Mus musculus]	1445.6578	30.92	1.445471065
18079339	DGYAQILR		aconitase 2, mitochondrial [Mus musculus]	935.4882	42.74	1.344313687
6680117	DGYMPSQYNSQNWEAR		glutathione synthetase [Mus musculus]	1945.8278	23.92	1.972613302
22203747	DIANSPHELYR		procollagen, type VI, alpha 2 [Mus musculus]	1314.6412	44.72	0.225619105
41350312	DIELVMSQANVSR		nascent polypeptide-associated complex alpha polypeptide [Mus musculus]	1461.7235	21.74	0
40254595	DIGAIAQVHAENGDIIAEEQQR		dihydropyrimidinase-like 2 [Mus musculus]	2377.1753	94.91	0.963663414
19745150	DILLRPELEELR		diaphorase 1 [Mus musculus]	1495.8214	21.68	0.886736114
9790073	DINDNRPTFLQSK		cadherin 17 [Mus musculus]	1547.7913	30.92	2.514685498
18079339	DINQEVYNFLATAGAK		aconitase 2, mitochondrial [Mus musculus]	1753.8781	107.98	0.728962952
18079339	DINQEVYNFLATAGAK	Deamidation (NQ)	aconitase 2, mitochondrial [Mus musculus]	1754.8748	22.1	0
24429590	DINTDFLLVVLR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1417.8042	72.75	1.343549323
6755863	DISTNYYASQK		tumor rejection antigen gp96 [Mus musculus]	1289.6025	49.47	2.614050788
23956222	DITYFIQQLLR		ARP3 actin-related protein 3 homolog [Mus musculus]	1409.7815	54.32	1.820499884
63476037	DIVFLVDGSSSLGPSNFNAIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2208.1255	53.29	0
51711847	DKDTPVSNGREPR	Deamidation (NQ)	PREDICTED: hypothetical protein LOC76224 [Mus musculus]	1471.7295	20.94	0
6754524	DLADELALVDVMEDK		lactate dehydrogenase 1, A chain [Mus musculus]	1675.8217	106.84	1.451150328
63746482	DLAEDAPWK		PREDICTED: filamin, alpha [Mus musculus]	1044.4933	37.77	0
63660294	DLAEDAPWK		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	1044.4933	37.77	0
51711855	DLAEDAPWK		PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like prot	1044.4933	37.77	0
6671549	DLAILLGMLDPVEK		peroxiredoxin 6 [Mus musculus]	1526.8538	103.62	3.525275878
30348966	DLDDFQSWLSR		spectrin beta 2 isoform 1 [Mus musculus]	1381.6437	33.72	1.19357587
7106421	DLDDFQSWLSR		spectrin beta 2 isoform 2 [Mus musculus]	1381.6437	33.72	1.19357587
27370092	DLDKPFLLPVESVYSIPGR		Tu translation elongation factor, mitochondrial [Mus musculus]	2145.1477	35.48	1.296789024
6755809	DLDQASLAAVSQQLAPR		talin 1 [Mus musculus]	1782.9434	57.79	0
45598381	DLDSLHSFVLR		thioredoxin domain containing 5 [Mus musculus]	1301.6823	40.99	0.61696084
10946574	DLFDPIIEER		creatine kinase, brain [Mus musculus]	1246.627	61.01	0.153823307
6671762	DLFDPIIQDR		creatine kinase, muscle [Mus musculus]	1231.6345	30.76	0.882067103
13242328	DLFEDELVPLFEK		NS1-associated protein 1 [Mus musculus]	1593.8026	54.63	0
6679687	DLFSDGHSEFLK		glucose regulated protein [Mus musculus]	1394.6578	68.72	1.296388794
6678413	DLGATWVVLGHSER		triosephosphate isomerase 1 [Mus musculus]	1539.8022	55.26	2.07777465
20137006	DLGEELEALKTELEDTLDSTAAQQELR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	3017.4839	76.2	8.404946133
7305295	DLGEELEALKTELEDTLDSTATQQELR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	3047.4893	104.27	0.238579413
56119103	DLGTDSQIFISR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1351.6913	78.86	1.374664543
38198665	DLIHDQDEEEEEEEGQR		p47 protein [Mus musculus]	2099.8743	113.5	1.539445521
7657429	DLLTQPGDWTLFAPTNDAFK		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2250.105	19.98	1.334297852
7657429	DLLTQPGDWTLFAPTNDAFK	Deamidation (NQ)	osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2251.1091	28.81	0.953256598
21312062	DLLVTGAYEITDQSGGAGGLR		transmembrane trafficking protein [Mus musculus]	2093.0408	31.85	0
30348966	DLMLWMEDVIR		spectrin beta 2 isoform 1 [Mus musculus]	1420.703	32.33	1.343728609
7106421	DLMLWMEDVIR		spectrin beta 2 isoform 2 [Mus musculus]	1420.703	32.33	1.343728609
63489759	DLMSWINGIR		PREDICTED: spectrin alpha 2 [Mus musculus]	1204.6155	33.78	1.363371292
6681233	DLPEEAFGFPSELPLETQR		solute carrier family 26 (sulfate transporter), member 2 [Mus musculus]	2175.0581	25.14	1.147939624
47578123	DLQLVLPDYFPER		potassium channel tetramerisation domain containing 12 [Mus musculus]	1604.835	42.03	0.917079157
6671622	DLQMVNISLR		B-cell receptor-associated protein 37 [Mus musculus]	1188.6304	27.84	0
6678726	DLSSHQLNEFLAQVLQK		leukotriene A4 hydrolase [Mus musculus]	1970.0295	29.24	1.358364358
18266680	DLTAVSNNAGVDNFGLGLLLR		3-oxoacid CoA transferase 1 [Mus musculus]	2159.1511	46.39	0.870513543
6671507	DLTDYLMK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	998.4838	58.85	0.449905466
6671509	DLTDYLMK		actin, beta, cytoplasmic [Mus musculus]	998.4838	58.85	0.449905466
30425250	DLTDYLMK		hypothetical protein LOC238880 [Mus musculus]	998.4838	58.85	0.449905466
63652452	DLTDYLMK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	998.4838	58.85	0.449905466

58037465	DLTTAGAVTQCYR		Ribosomal protein L18A [Mus musculus]	1398.6752	50.12	1.375641175
34328286	DLVPDLSNFYAQYK		succinate dehydrogenase Ip subunit [Mus musculus]	1672.804	39.08	0
29293809	DLVSSLTSGLLTIGDR		ATP citrate lyase [Mus musculus]	1646.9005	72.95	2.118237229
6671507	DLYANNVLSGGTTMYPGIADR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2228.104	159.75	0.123780892
6671507	DLYANNVLSGGTTMYPGIADR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2229.0688	132.99	0
6671507	DLYANNVLSGGTTMYPGIADR	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2244.0664	38.41	0.148080982
6671509	DLYANTVLSGGTTMYPGIADR		actin, beta, cytoplasmic [Mus musculus]	2215.093	109.19	1.252331631
63652452	DLYANTVLSGGTTMYPGIADR		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2215.093	109.19	1.252331631
6755626	DMLYQVLAAEEPSVR		sepiapterin reductase [Mus musculus]	1720.8567	44.06	1.173932583
21450277	DMTSEELDDILR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1436.6638	40.25	0.767235688
8567336	DMVTQASPYLFEATGK	Deamidation (NQ)	chloride channel calcium activated 3 [Mus musculus]	1758.8387	34.96	0
8567336	DNCVFVPDPHQNEK		chloride channel calcium activated 3 [Mus musculus]	1641.7424	43.36	1.081256137
6681219	DNFTAIPEGTNGVEER		dihydropyrimidinase-like 3 [Mus musculus]	1748.8213	44.99	0.912987591
40254595	DNFTLIPEGTNGTEER		dihydropyrimidinase-like 2 [Mus musculus]	1792.8507	47.43	1.0490122
63746482	DNGNGTYSCSYVPR		PREDICTED: filamin, alpha [Mus musculus]	1532.6433	72.05	0.300588493
31981722	DNHLLGTFDLTGIPPAPR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1934.0085	74.51	0.856483874
21361209	DNIQGITKPAIR		germinal histone H4 [Mus musculus]	1325.762	72.23	1.253632151
33563250	DNLIDDLQR		desmin [Mus musculus]	1101.5516	65.36	0.203705203
29789080	DNNQFASASLDR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1337.6095	48.81	1.125786985
6753304	DNQSGSLLFIGR		serine (or cysteine) proteinase inhibitor, clade H, member 1 [Mus musculus]	1306.6774	71.38	1.519550062
28916693	DPDQTDGPGLGYLSSHIANVER		gelsolin [Mus musculus]	2341.1101	32.13	1.737357937
31543942	DPNASPGDAGEQAIR		vinculin [Mus musculus]	1497.6993	83.7	0.523066766
6755809	DPVQLNLLYVQAR		talin 1 [Mus musculus]	1528.8474	40.75	0.112955066
6680572	DQDNMQAELNR		kinesin family member 5B [Mus musculus]	1333.5896	29.2	1.779060322
31980648	DQEGQDVLLFIDNIFR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1921.9786	75.05	1.059600542
33620739	DQGTYEDYVEGLR		myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Mus musculus]	1544.6899	47.83	0.627203772
8392847	DQLQTFSEEHPVLLTEAPLNPR		ARP1 actin-related protein 1 homolog A [Mus musculus]	2534.2947	25.99	0.970153601
6754254	DQVANSAFVER		heat shock protein 1, alpha [Mus musculus]	1235.6051	79.97	2.323833034
63476037	DSFQEVLR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	993.4935	41.05	0.236272138
21313138	DSGNQPPAMVPR		glutathione S-transferase class kappa [Mus musculus]	1268.6167	21.78	3.495428291
6679058	DSGQFTDEFLPEQR		nidogen 2 [Mus musculus]	1668.7687	49.61	0
33859811	DSIFSNLIGQLDYK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1612.8273	80.28	1.520677099
6753266	DSISLSPEQLAQLR		carbonic anhydrase 1 [Mus musculus]	1556.8364	84.86	0.239717196
6755040	DSLLQDGEFTMDLR		profilin 1 [Mus musculus]	1639.7683	85.14	1.639236028
6678682	DSNNLCLHFNPR		lectin, galactose binding, soluble 1 [Mus musculus]	1429.6709	78.45	0.538604541
6680027	DSNYHLLMSVQESLER		glutamate dehydrogenase 1 [Mus musculus]	1920.9243	20.38	1.480295245
8567338	DSPLFDFIESCLR		coatomer protein complex, subunit gamma [Mus musculus]	1541.7415	77.32	0.928058515
28916693	DSQEEEKTEALTSAK		gelsolin [Mus musculus]	1665.7865	72.97	1.21982769
31981925	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Mus mu	1189.662	63.66	1.596250806
6756039	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Mus musc	1189.662	63.66	1.596250806
6756041	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	1189.662	63.66	1.596250806
12331400	DSYIEVLLPLGTDPELR		acyl-Coenzyme A thioesterase 3, mitochondrial [Mus musculus]	1930.0074	34.18	0
54261793	DTEGMDEIDLAEMELR		plasma membrane calcium ATPase 4 [Mus musculus]	1866.8262	38.28	0
51491845	DTELAEELLQWFLQEEK		clathrin, heavy polypeptide (Hc) [Mus musculus]	2121.0415	96.02	1.215115086
10946940	DTFNHLTTWLEDAR		RAB2, member RAS oncogene family [Mus musculus]	1718.8314	50.79	2.164573354
41322904	DTHDQLSEPSEVR		plectin 1 isoform 1 [Mus musculus]	1512.6996	74.56	1.284016611
9790067	DTNGENIAESLVAEGLATR		staphylococcal nuclease domain containing 1 [Mus musculus]	1959.9686	63.2	1.14718863
6755142	DTNGSQFFITTVK		peptidylprolyl isomerase B [Mus musculus]	1457.718	43.99	0
6680163	DTPGFIVNR		L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1018.5317	36.58	0
54144620	DTPPVPVVVCDGSGR		transient receptor potential cation channel, subfamily M, member 3 [Mus musculus]	1497.7614	19.08	0
7305295	DVASLGSQLQDTQELLQEETR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2360.1631	53.79	0.182767729
63746482	DVDIIDHHDNTYTVK		PREDICTED: filamin, alpha [Mus musculus]	1784.8438	55.16	0
33859506	DVFLGTFLYEYSR		albumin 1 [Mus musculus]	1609.7899	80.97	2.457195372
18079339	DVGGIVLANACGPCIGQWDR		aconitase 2, mitochondrial [Mus musculus]	2043.9736	20.08	1.221344004
31560689	DVGILALEVYFPAQYVDQTDLEK		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	2626.322	54.96	14.70913894
6678499	DVLNLVYLCEALNLPEVAR		UDP-glucose dehydrogenase [Mus musculus]	2144.1328	72.33	0.484023235
27804325	DVPALEITHTFLER		monoamine oxidase A [Mus musculus]	1640.8702	26.47	1.532558158
20532346	DVYEDELVPVFETVGR		hypothetical protein LOC245945 [Mus musculus]	1866.9209	23.86	1.483932382
51467513	DXSHYFKTIQDLR		PREDICTED: similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18) [Homo sapiens]	1708.8579	22.94	0
6754220	DYFEQYGK		heterogeneous nuclear ribonucleoprotein A1 [Mus musculus]	1049.4629	22.53	0

63663965	DYFEQYGK	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Sin	1049.4629	22.53	0
27369998	DYFLFNPVTDIEEIIR	calcium-binding transporter [Mus musculus]	1984.0028	57.67	1.229835368
6680690	DYGVLLESAGIALR	peroxiredoxin 3 [Mus musculus]	1476.8107	22.51	0.980690129
13384736	DYIPVDQEELR	dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1376.6711	22.24	1.086483874
13385942	DYIWNTLNSGR	citrate synthase [Mus musculus]	1338.6466	54.22	1.15100432
14042921	DYIYAVTPLLEDALMDR	splicing factor 3b, subunit 1 [Mus musculus]	1997.9901	20.7	0
21592285	DYSSYYAQIK	keratin 20 [Mus musculus]	1237.572	29.69	0.58206276
7242187	DYTGEDVTPENFLAVLR	legumain [Mus musculus]	1938.9595	62.18	1.581781994
14149756	DYTYEELLNR	eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus]	1315.6169	24.62	4.846132942
6755809	EAAFHPEVAPDVR	talin 1 [Mus musculus]	1437.7162	53.62	0.847689128
31982290	EAAYAPPASGNQNHPGMYPVSGPK	LIM domain containing preferred translocation partner in lipoma [Mus musculus]	2440.1523	70.71	0
15426055	EAELLEPLMPAIR	coatomer protein complex, subunit beta 1 [Mus musculus]	1481.7985	19.31	1.061051851
6755911	EAFQEALAAAGDK	thioredoxin 1 [Mus musculus]	1320.62	26.14	1.31116828
33620739	EAFQLFDR	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Mus musculus]	1025.5033	19.67	0.61231411
58696420	EAFTDHGEEFAGR	cytochrome P450, family 2, subfamily c, polypeptide 65 [Mus musculus]	1465.6481	47.22	0.909533737
63746482	EAGAGGLAIAVEGPSK	PREDICTED: filamin, alpha [Mus musculus]	1426.7783	33.15	0
6679599	EAINVEQAFQTIAR	RAB7, member RAS oncogene family [Mus musculus]	1589.8341	48.46	1.055596398
19527306	EALMDVMPYVDILFGNETEAATFAR	adenosine kinase [Mus musculus]	2803.3091	30.78	0
30409988	EALNVFGDDYATEDGTGVR	galactose-4-epimerase, UDP [Mus musculus]	2028.9241	47.35	1.954430906
31981515	EANNFLWPFK	ribosomal protein L7 [Mus musculus]	1265.6339	37.62	1.110360083
29336026	EAQAGLAEAQEDLEAER	nonmuscle myosin heavy chain [Mus musculus]	1829.8558	45.13	0.641031579
11528504	EAQPLEAEAPGVDLGILPEGR	niban protein [Mus musculus]	2161.1035	51.09	1.744670484
33468887	EASDPQPEDVDGGLK	capping protein (actin filament) muscle Z-line, alpha 1 [Mus musculus]	1556.7156	19.29	0
31981562	EATESFASDPILYRPVAVALDTK	pyruvate kinase 3 [Mus musculus]	2493.2871	41.72	1.308651061
6679687	EATNPPIIQEEKPK	glucose regulated protein [Mus musculus]	1593.8577	97.17	1.069294415
23956084	EATQAVLDKPETLSSDASTR	acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	2119.0557	73.63	1.232020425
63746482	EATTEFSVDAR	PREDICTED: filamin, alpha [Mus musculus]	1225.5734	78.35	0.340427661
12963539	EAVLIDPVLETAHR	ETHE1 protein [Mus musculus]	1562.8499	27.93	0
6680748	EAYPGDVFYLHSR	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1553.7417	73.54	0.942038667
6677805	ECLPLIIFLR	ribosomal protein S4, X-linked [Mus musculus]	1216.7037	30.11	1.350208316
30023842	EDEEESLNEVGYDDIGGCR	valosin containing protein [Mus musculus]	2128.8667	88.94	1.354507177
6756033	EDGNEEDKENQGDETQGQQPPQR	nuclease sensitive element binding protein 1 [Mus musculus]	2628.105	102.31	1.225676594
33859482	EDLYLKPIQR	eukaryotic translation elongation factor 2 [Mus musculus]	1274.7136	38.89	3.470000311
6754254	EDQTEYLEER	heat shock protein 1, alpha [Mus musculus]	1311.5802	72.42	1.615835905
40556608	EDQTEYLEER	heat shock protein 1, beta [Mus musculus]	1311.5802	72.42	1.615835905
31982755	EEAESTLQSFR	vimentin [Mus musculus]	1296.6096	56.8	0.652960501
41322904	EEELQQTLQQEQNMLDR	plectin 1 isoform 1 [Mus musculus]	2131.9849	22.72	0.790374721
15617203	EEFASTCPDDEEIELAYEQVAR	chloride intracellular channel 1 [Mus musculus]	2544.1262	97.85	1.779075034
6753036	EEIFGPVMQILK	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1403.7334	31.87	0.823365713
21312260	EEIFGPVQPLFK	aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1403.7548	30.72	0
7305295	EELAEELASSLSGR	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1490.7328	49.27	0
31560222	EESGAVAAAASVPAQSTAR	PYD and CARD domain containing [Mus musculus]	1772.8889	26.59	1.589532016
46849812	EESPPLIGQQATVSDIPR	fibronectin 1 [Mus musculus]	1936.9974	29.68	0.79816036
13385680	EEWDIIEGLIR	2,4-dienoyl CoA reductase 1, mitochondrial [Mus musculus]	1372.7092	58.23	1.806335522
6679587	EFADSLGIPFLETSAK	RAB1, member RAS oncogene family [Mus musculus]	1724.8776	75.11	1.496653373
31542159	EFDDLSPEQQR	ATPase, Ca++ transporting, ubiquitous [Mus musculus]	1363.6234	38.75	1.401629319
6806903	EFDELSPSAQR	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	1278.5988	61.22	0.846288342
21704156	EFDPTITDGSLSGPSR	caldesmon 1 [Mus musculus]	1678.7991	100.19	0
6755863	EFEPLLNWMK	tumor rejection antigen gp96 [Mus musculus]	1306.652	67.01	1.122369945
45598381	EFPGLSDVTIAEVDCTAER	thioredoxin domain containing 5 [Mus musculus]	2051.9688	48.74	0
31982275	EFSITDVVPYPISLR	heat shock protein 4 [Mus musculus]	1735.9286	60.1	1.169417193
6806903	EFTLEFSR	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	1028.5006	44.37	0.997278798
36031132	EFTLEFSR	ATPase, Ca++ transporting, fast twitch 1 [Mus musculus]	1028.5006	44.37	0.997278798
31542159	EFTLEFSR	ATPase, Ca++ transporting, ubiquitous [Mus musculus]	1028.5006	44.37	0.997278798
6996911	EFVEEFIWPAVQSSALYEDR	argininosuccinate synthetase [Mus musculus]	2415.1533	28.15	0.973188166
21426821	EGDVLTLLESER	ribosomal protein S28 [Mus musculus]	1360.6953	70.75	1.296687056
63594458	EGDYFTQQGEFR	PREDICTED: source of immunodominant MHC-associated peptides [Mus musculus]	1476.6487	22.05	1.326567468
29789191	EGIDPAPYYWYTDQR	asparaginyl-tRNA synthetase [Mus musculus]	1873.8492	33.71	0
33859482	EGIPALDNFLDKL	eukaryotic translation elongation factor 2 [Mus musculus]	1444.7665	92.11	1.17715323
59709449	EGLLLWCQR	actinin alpha 2 [Mus musculus]	1117.5807	43.97	0.781412866

7304855	EGLLLWCQR		actinin alpha 3 [Mus musculus]	1117.5807	43.97	0.781412866
11230802	EGLLLWCQR		actinin alpha 4 [Mus musculus]	1117.5807	43.97	0.781412866
6679439	EGMNIVEAMER		peptidylprolyl isomerase A [Mus musculus]	1278.5878	57.59	1.426376667
63650244	EGMNIVEAMER		PREDICTED: similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase) (Cyclophilin A) (Cy	1278.5878	57.59	1.426376667
31981549	EGNALFTFPNTPVK		sulfide quinone reductase-like [Mus musculus]	1534.787	41.43	1.077542466
31980648	EGNDLYHEMIESGVINLK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2061.0032	106.61	1.115862491
63746482	EGSYSISVLYGEEEVPR		PREDICTED: filamin, alpha [Mus musculus]	1913.9171	84.94	0.329761715
21450339	EGVLDAMGDVAFGVPSVIVSR		hypothetical protein LOC234564 [Mus musculus]	2118.0933	53.86	0
21450339	EGYLHIGGTTQQAQR		hypothetical protein LOC234564 [Mus musculus]	1658.8359	21.75	0.29755941
12963527	EHNGQVTGIDWAPESNR		actin related protein 2/3 complex, subunit 1B [Mus musculus]	1909.8848	33.05	1.584003981
26986563	EIFAQEALAPFR		choline dehydrogenase [Mus musculus]	1391.7179	20.44	2.214494028
7305085	EIFEQPESVVNTMR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1678.8245	85.2	1.317385899
28173568	EIFLSQPILLELEAPLK		protein phosphatase 1, catalytic subunit, beta [Mus musculus]	1953.1415	72.3	1.03932375
6755901	EIIDLVLDR		tubulin, alpha 1 [Mus musculus]	1085.6182	59.35	1.129425985
34740335	EIIDLVLDR		tubulin, alpha 2 [Mus musculus]	1085.6182	59.35	1.129425985
6678469	EIIDLVLDR		tubulin, alpha 6 [Mus musculus]	1085.6182	59.35	1.129425985
6680924	EILVGDVGQTVDDPYTTFVK		cofilin 1, non-muscle [Mus musculus]	2196.1082	86.98	0
27804325	EIPVDAPWQAR		monoamine oxidase A [Mus musculus]	1281.6578	39.62	1.088765222
20137008	EISPDTTLLDLQNNDISELRK		biglycan [Mus musculus]	2414.2329	42.6	1.812821477
6671507	EITALAPSTMK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1161.6177	82.95	0.455084338
6671509	EITALAPSTMK		actin, beta, cytoplasmic [Mus musculus]	1161.6177	82.95	0.455084338
63652452	EITALAPSTMK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1161.6177	82.95	0.455084338
6671507	EITALAPSTMK	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1177.6071	30.67	0
6671509	EITALAPSTMK	Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	1177.6071	30.67	0
63652452	EITALAPSTMK	Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1177.6071	30.67	0
14861854	EITINQSLLAPLSVDIDPTIQQVR		keratin complex 2, basic, gene 7 [Mus musculus]	2663.415	27.01	0.647488882
33859488	EIVHIQAGQCGNQIGAK		tubulin, beta 2 [Mus musculus]	1765.9075	86.43	0.934300652
12963615	EIVHIQAGQCGNQIGAK		tubulin, beta 3 [Mus musculus]	1765.9075	86.43	0.934300652
7106439	EIVHIQAGQCGNQIGAK		tubulin, beta 5 [Mus musculus]	1765.9075	86.43	0.934300652
7949051	EKPYFPIPEDCTFIQNVPLEDR		heterogenous nuclear ribonucleoprotein U [Mus musculus]	2650.2886	29.2	1.385453126
6755372	ELAEDGYSGVEVR		ribosomal protein S3 [Mus musculus]	1423.6733	31.7	2.160353179
51712562	ELAPYDENWFYTR		PREDICTED: similar to ribosomal protein S19 [Mus musculus]	1703.7823	35	1.261721898
24429590	ELDALDANDELTPLGR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1741.8628	50.56	2.013381726
7305295	ELDEATESNEAMGR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1551.6782	73.74	0
20137006	ELEDATETADAMNR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1565.6864	31.75	1.031607415
7305295	ELEGHISDLQEDLDSER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1984.9174	120.72	0.191937947
7106435	ELEPGVEYFIR		tenascin C [Mus musculus]	1351.6874	25.37	0.470340769
20137006	ELETQISELQEDLESER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2047.9739	63.82	2.309039907
6680067	ELFEADPER		glucose phosphate isomerase 1 [Mus musculus]	1105.5181	30.65	1.337432806
29336026	ELFQETLESLR		nonmuscle myosin heavy chain [Mus musculus]	1364.7089	60.83	1.439827186
23956084	ELGAFGLQVPSELGGLGLSNTQYAR		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	2577.3398	29.14	0.966546374
63476037	ELGTIQQVISER		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1372.7428	52.85	0.428024581
6679687	ELNDFISYLQR		glucose regulated protein [Mus musculus]	1397.7162	70.42	1.106628046
63476037	ELPNIEER		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	999.5058	42.22	0
11230802	ELPPDQAEYCIAR		actinin alpha 4 [Mus musculus]	1504.7131	28.97	2.071238179
18079351	ELPSGVEELLNLGHDPLADR		major vault protein [Mus musculus]	2174.1116	20.79	0.9586323
33563250	ELQAQLQEQQVQVEMDMSKPDLTAALR		desmin [Mus musculus]	3099.5376	53.25	0.182803172
33563250	ELQAQLQEQQVQVEMDMSKPDLTAALR	Oxidation (M)	desmin [Mus musculus]	3115.5535	21.79	0
13624315	ELQSQISDTSVVLSMDNSR		keratin complex 2, basic, gene 8 [Mus musculus]	2109.0171	140.45	1.522237808
63565108	ELQSQISDTSVVLSMDNSR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	2109.0171	140.45	1.522237808
46275826	ELVDEEADEAQELLSQAENWQR		laminin, alpha 4 [Mus musculus]	2602.2065	41.83	0
13385076	ELWAVLNGWR		sorcin [Mus musculus]	1243.6625	25.37	1.49741238
13385076	ELWAVLNGWR	Deamidation (NQ)	sorcin [Mus musculus]	1244.6554	20.26	0
31982755	EMEENFALEAANYQDTIGR		vimentin [Mus musculus]	2200.9939	127.71	0
7305295	EMEGLSQQYEEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1470.6611	78.84	0
7305295	ENADLAGELR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1087.5354	70.13	0.179700831
31560680	ENDYYTPTGEFR		intergral membrane protein 1 [Mus musculus]	1491.644	39.57	1.104985674
13384736	ENFIPTIVNFSAEEISDAIR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	2265.1438	22.14	1.316138198
21450129	ENGTITAANASTLNDGAAALVLMTAEAAQR		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	2945.4607	51.52	1.155523021
31982522	ENLLGEPGMGFK		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1291.6295	30.96	0.961184442

18250284	ENTEGEYSGIEHVIVDGVVQSIK		isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	2502.196	19.64	0
6753484	ENYAELLDDGFLK		procollagen, type VI, alpha 1 [Mus musculus]	1526.7389	72.24	0
33469029	EPGEAAAEGAAEEAR		acyl-Coenzyme A binding domain containing 3 [Mus musculus]	1457.6583	54.9	0.953757358
31982290	EPIMPAPGQEETVR		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1553.7761	80.58	1.040573587
31981657	EPITVSSEQMSHFR		carbonic anhydrase 2 [Mus musculus]	1647.7864	110.45	1.11430657
7305295	EQADFAIEALAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1305.6753	78.79	0
20137006	EQADFAIEALAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1305.6753	78.79	0
7305295	EQADFAIEALAK	Deamidation (NQ)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1306.6766	37.85	0
20137006	EQADFAIEALAK	Deamidation (NQ)	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1306.6766	37.85	0
6680836	EQFLDGDAWTNR		calreticulin [Mus musculus]	1451.6598	83.46	0.997003049
51764087	EQGFLSFWR		PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	1169.5726	57.2	0.274346265
22094075	EQGVLSFWR		solute carrier family 25, member 5 [Mus musculus]	1121.5758	71.05	1.558510935
50355690	EQIVPKPEEEVAQK		ribosomal protein L17 [Mus musculus]	1623.8644	56.4	0
6678499	EQIVVDLSHPGVSADDQVSR		UDP-glucose dehydrogenase [Mus musculus]	2151.0754	121.02	0.355200425
6754782	EQLLQSNPVLEAFGNAK		myosin IB [Mus musculus]	1857.9592	30.47	0
51766008	EQLLQSNPVLEAFGNAK		PREDICTED: myosin IA [Mus musculus]	1857.9592	30.47	0
30725802	EQNLYRSCGQSVR	2 Deamidation (NQ)	hypothetical protein LOC106755 [Mus musculus]	1541.719	19.94	0
21450277	EQPLDEELKDAFQNAYLELGGLGER		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2834.3862	108.15	1.122278278
13384736	EQPWVSVQPR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1225.6346	19.78	0.395166373
40556608	EQVANSAFVER		heat shock protein 1, beta [Mus musculus]	1249.619	67.11	1.322429345
40556608	EQVANSAFVER	2 Deamidation (NQ)	heat shock protein 1, beta [Mus musculus]	1251.5835	21.64	0
6677935	ESDGTPGGLASLENER		sorbin and SH3 domain containing 1 [Mus musculus]	1631.7552	27.45	0
6678752	ESPYDHQSLQTALQEAFTSR		lymphocyte antigen 74 [Mus musculus]	2308.0898	120.99	1.663188888
6754994	ESTGAQVQVAGDMLPNSTER		poly(rC) binding protein 1 [Mus musculus]	2089.9905	72.84	1.264682415
46559834	ESVQLYEDEVR		desmuslin isoform M [Mus musculus]	1366.6561	42.22	0.387273458
9910482	ESVQVPDDQDFR		START domain containing 10 [Mus musculus]	1434.6613	23.43	2.139982117
20874851	ESYSVYVYK		PREDICTED: similar to histone H2b-616 [Mus musculus]	1137.5425	32.39	0
63492203	ETSYEEALANQR		PREDICTED: ribosome binding protein 1 [Mus musculus]	1410.657	38.79	1.323693946
22122523	ETTPFYPR		GDP-mannose 4, 6-dehydratase [Mus musculus]	1010.4943	26.06	1.148664665
30023842	ETVVEVPQVTWEDIGGLEDVKR		valosin containing protein [Mus musculus]	2498.283	50.05	0
6680748	EVAAFAQFGSDLDAATQQLLSR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2338.1829	108.88	1.030127292
31560449	EVAGQVGVPLQDLMVR		aspartyl aminopeptidase [Mus musculus]	1710.9231	56.24	1.147167416
30348966	EVDDLEQWIAER		spectrin beta 2 isoform 1 [Mus musculus]	1502.722	38.12	0.969291198
7106421	EVDDLEQWIAER		spectrin beta 2 isoform 2 [Mus musculus]	1502.722	38.12	0.969291198
63650229	EVDEQMLNVQNK		PREDICTED: similar to TUBULIN BETA CHAIN (T BETA-15) [Mus musculus]	1446.6964	67.24	1.254807422
22165384	EVDEQMLNVQNK		tubulin, beta, 2 [Mus musculus]	1446.6964	67.24	1.254807422
33859488	EVDEQMLNVQNK		tubulin, beta 2 [Mus musculus]	1446.6964	67.24	1.254807422
7106439	EVDEQMLNVQNK		tubulin, beta 5 [Mus musculus]	1446.6964	67.24	1.254807422
30023842	EVDIGIPDATGR		valosin containing protein [Mus musculus]	1242.6315	54.3	1.548516992
12963527	EVEERPAPTPWGSK		actin related protein 2/3 complex, subunit 1B [Mus musculus]	1582.7963	20.79	1.938374624
14149756	EVEPEPTEEKDVDADEEDSR		eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus]	2317.9854	110.56	1.690087421
46593021	EVESIGAHLNAYSTR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1646.817	23.18	1.197495471
31543315	EVFEDAMEIR		nucleolin [Mus musculus]	1238.5735	26.75	2.032658854
31980685	EVGAFGTPVINLGTR		glucosamine [Mus musculus]	1530.8234	37.52	1.761392003
7305295	EVLLQVEDER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1229.6403	63.86	0.159077285
6678573	EVQGNESETFR		villin 1 [Mus musculus]	1295.5894	31.42	0
33859811	EVQSEFIEVMNEIWANDQIR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	2450.1768	24.1	0
6680816	EVSFQATGDSEWR		complement component 1, q subcomponent binding protein [Mus musculus]	1511.682	19.67	1.294244818
21450129	EVYMGNVIQGGEGQAPTR		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	1905.9222	67.55	1.282212443
31560611	EWIEGVTGR		calponin 1 [Mus musculus]	1046.5298	55.97	0.140522785
6753066	EYQDIEEMIFHR		amine oxidase, copper containing 3 [Mus musculus]	1609.7407	37.17	0
33563250	EYQDLLNVK		desmin [Mus musculus]	1121.5812	57.76	0
34328368	EYQDLLNVK		internexin neuronal intermediate filament protein, alpha [Mus musculus]	1121.5812	57.76	0
46275814	EYQDLLNVK		neurofilament, heavy polypeptide [Mus musculus]	1121.5812	57.76	0
31982755	EYQDLLNVK		vimentin [Mus musculus]	1121.5812	57.76	0
41054806	EYQLNDSAAYYLNDLER		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	2076.9609	35.54	1.379941428
63635087	EYSSELNAPSQESDSHPR		PREDICTED: RNA binding motif protein 25 [Mus musculus]	2032.8907	37.83	2.90941961
31560560	FAAATGATPIAGR		laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1203.6525	51.86	1.807341746
6680067	FAAYFQQGDMESNGK		glucose phosphate isomerase 1 [Mus musculus]	1692.7477	46.35	0
6753254	FADDELIIDFDNFVR		calpain 2 [Mus musculus]	1828.8821	54.09	0.939348601

31982755	FADLSEAANR		vimentin [Mus musculus]	1093.525	62.64	0.671862272
31560613	FAEAFEAIPR		chaperonin subunit 8 (theta) [Mus musculus]	1150.5864	30.5	1.301835165
6755863	FAFQAEVNR		tumor rejection antigen gp96 [Mus musculus]	1081.5449	58.53	1.195893104
7710042	FALGISAINEAVDSGDVGR		IQ motif containing GTPase activating protein 1 [Mus musculus]	1890.9612	35.53	0
19482160	FALITWIGEDVSGLQR		coactosin-like 1 [Mus musculus]	1804.9528	33.51	2.348685041
6753240	FAMEPEEFDSDTLR		calcium binding protein, intestinal [Mus musculus]	1686.7401	66.25	1.290601498
21704206	FAPPEAPEPWSGVR		carboxylesterase 2 [Mus musculus]	1539.7587	46.92	0.861984328
27370126	FAPPEAPEPWSGVR		carboxylesterase 5 [Mus musculus]	1539.7587	46.92	0.861984328
23956214	FAQHGTFEYEYSQR		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1762.7927	21.96	1.542608146
33563250	FASEANGYQDNIAR		desmin [Mus musculus]	1555.7136	32.74	0.155374707
33563250	FASEANGYQDNIAR	Deamidation (NQ)	desmin [Mus musculus]	1556.708	78.39	0.303230623
63476037	FASEIVDTVYEDGDSIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1915.8853	95.4	0
31560611	FASQQGMTAYGTR		calponin 1 [Mus musculus]	1417.6727	106.4	0.60145226
10946574	FCTGLTQIETLFK		creatine kinase, brain [Mus musculus]	1500.7756	84.44	0.212043251
31980685	FDALALATSAALMNIR		glucosamine [Mus musculus]	1677.8929	43.13	1.188536109
6755901	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 1 [Mus musculus]	2409.2146	73.62	0.990588632
34740335	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 2 [Mus musculus]	2409.2146	73.62	0.990588632
6678467	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 4 [Mus musculus]	2409.2146	73.62	0.990588632
6678469	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 6 [Mus musculus]	2409.2146	73.62	0.990588632
33598964	FDQLLAEEK		myosin heavy chain 10, non-muscle [Mus musculus]	1092.5538	32.4	0
7305295	FDQLLAEEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1092.5538	32.4	0
20137006	FDQLLAEEK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1092.5538	32.4	0
29336026	FDQLLAEEK		nonmuscle myosin heavy chain [Mus musculus]	1092.5538	32.4	0
6677805	FDTGNLCMVTGGANLGR		ribosomal protein S4, X-linked [Mus musculus]	1725.8137	55.05	1.436414017
6679439	FEDENFILK		peptidylprolyl isomerase A [Mus musculus]	1154.5676	56.29	2.255368123
10092608	FEDGDLTLYQSNAILR		glutathione S-transferase, pi 1 [Mus musculus]	1854.9141	100.66	1.27593594
33563270	FEEFLQR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	968.4772	26.87	1.256010836
31981690	FEELNADLFR		heat shock protein 8 [Mus musculus]	1253.6233	58.38	1.373856651
31981722	FEELNMDLFR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1313.6244	66.07	0.88344202
9790073	FEEQVYNIPIR		cadherin 17 [Mus musculus]	1407.7375	49.02	1.88384818
13385374	FEIWDTAGQER		RAB5A, member RAS oncogene family [Mus musculus]	1351.6373	35.16	1.262707566
29789257	FEIWDTAGQER		RAB5C, member RAS oncogene family [Mus musculus]	1351.6373	35.16	1.262707566
31981690	FELTGIPPAPR		heat shock protein 8 [Mus musculus]	1197.6595	42.49	1.255637093
6678145	FFDEESYSLLR		signal sequence receptor, delta [Mus musculus]	1405.6593	51.22	1.379184518
16716471	FFQELPASDSAFK		hypothetical protein LOC94184 [Mus musculus]	1486.7279	52.02	0
8567336	FFTAFDANGR		chloride channel calcium activated 3 [Mus musculus]	1145.5393	49.47	1.436514238
6755809	FFYSDQNVDSR		talin 1 [Mus musculus]	1377.6169	57.69	0.603608975
6755372	FGFPEGSVELYAEK		ribosomal protein S3 [Mus musculus]	1572.7734	37.73	2.013762885
63746482	FGGEHVPNSPFQVTALAGDQPTVQTPLR		PREDICTED: filamin, alpha [Mus musculus]	2963.4788	80.68	0.252420295
21704096	FGGNPGGFGNQGGFGNSR		TAR DNA binding protein isoform 1 [Mus musculus]	1726.7777	58.31	2.260399723
13384736	FGNPLLVQDVESYDPVLNPVLNR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	2598.3411	47.1	1.142213599
23956214	FGQGGAGPVGGQGPR		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1341.6721	50.84	1.538060299
31981562	FGVEQDVDMVFASFIR		pyruvate kinase 3 [Mus musculus]	1859.9053	92.88	1.204061887
6671690	FHQLDIDNPQSIR		carbonyl reductase 1 [Mus musculus]	1582.8018	28.46	1.709953844
6679687	FISDKDASVVGFFR		glucose regulated protein [Mus musculus]	1587.8213	35.43	1.858226465
18079339	FKLEAPDADELPR		aconitase 2, mitochondrial [Mus musculus]	1500.7711	48.68	0
33563270	FLDTAFDLDAFK		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1402.6837	25.57	0
33563250	FLEQQNAALAAEVNR		desmin [Mus musculus]	1673.8673	92.37	0.204956253
6678643	FLEQQNKVLQTK		keratin complex 2, basic, gene 1 [Mus musculus]	1475.793	73.54	0
7305295	FLFVDK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	768.4169	36.82	0.242319227
22164798	FLHDPSATQGFVGCALSSNIQR		selenium binding protein 1 [Mus musculus]	2348.1362	20.63	1.126487851
31980648	FLSQPFQVAEVFTGHMGK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2023.0007	35.66	0
29789191	FLSWILNR		asparaginyl-tRNA synthetase [Mus musculus]	1048.588	23.03	1.067936362
29336026	FLTNGPSSSPGQER		nonmuscle myosin heavy chain [Mus musculus]	1476.7159	66.34	1.21141591
25020120	FMNQEVETQR		PREDICTED: laminin, alpha 5 [Mus musculus]	1281.5939	37.09	0.813644603
13384828	FMTEDTTDAPFR		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1430.635	41.96	1.030192952
6671622	FNASQLITQR		B-cell receptor-associated protein 37 [Mus musculus]	1177.6282	24.23	1.11837528
63540743	FNDEHIPDSPFVVPVASLSDDAR		PREDICTED: filamin C, gamma [Mus musculus]	2527.2222	61.6	0.421492466
63660302	FNDEHIPDSPYLVPVIAPSDDAR		PREDICTED: filamin B, beta [Mus musculus]	2567.2495	66.44	1.716616701
63746482	FNEEHIPDSPFVVPVASPSGDAR		PREDICTED: filamin, alpha [Mus musculus]	2467.1909	109.37	0.238895334

6677777	FNPFVTSDR	ribosomal protein L26 [Mus musculus]	1082.526	35.96	1.908867822
6753272	FNSANEDNVTQVR	catalase [Mus musculus]	1493.7002	57.12	1.035153688
6678365	FNVWDTAGQEK	RAN, member RAS oncogene family [Mus musculus]	1294.6167	43.22	1.174963031
13384736	FNYGFEYLGVQDK	dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1579.7677	19.22	0
19527018	FPEDGPELEEVLIQLAAADAR	dipeptidylpeptidase III [Mus musculus]	2283.1475	31.56	1.603538093
22165384	FPGQLNADLR	tubulin, beta, 2 [Mus musculus]	1130.595	55.37	0.952741003
33859488	FPGQLNADLR	tubulin, beta 2 [Mus musculus]	1130.595	55.37	0.952741003
12963615	FPGQLNADLR	tubulin, beta 3 [Mus musculus]	1130.595	55.37	0.952741003
31981939	FPGQLNADLR	tubulin, beta 4 [Mus musculus]	1130.595	55.37	0.952741003
7106439	FPGQLNADLR	tubulin, beta 5 [Mus musculus]	1130.595	55.37	0.952741003
27754056	FPGQLNADLR	tubulin, beta 6 [Mus musculus]	1130.595	55.37	0.952741003
33859560	FQILEGPPESMGR	guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	1460.7258	28.28	1.200679898
40254595	FQLTDSQIYEVLSVIR	dihydropyrimidinase-like 2 [Mus musculus]	1911.0173	71.31	0.781982367
40254595	FQMPDQGMTSADDFFQGTK	dihydropyrimidinase-like 2 [Mus musculus]	2150.9431	87.62	0
8394252	FSGNLLVSLLGTWSDTSSGGPAR	Sec61 alpha subunit homolog [Mus musculus]	2322.1699	25.13	1.560862473
23943876	FSHSGNQLDGPITAFR	zymogen granule membrane protein 16 [Mus musculus]	1746.8657	47.21	5.878906414
6671539	FSNEEIAMATVTALR	aldolase 1, A isoform [Mus musculus]	1652.8352	108.14	1.276827659
6756085	FSPGAPSGPGPQPNQK	zyxin [Mus musculus]	1565.7714	35.26	0
16716471	FSPLMTAEGLGTR	hypothetical protein LOC94184 [Mus musculus]	1379.7031	34.99	1.459602519
20070412	FSPLTANLMNLLAENGR	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit [Mus musculus]	1860.9705	26.69	0.921563576
28893559	FSPPEETGPSR	melanoma inhibitory activity 3 [Mus musculus]	1203.5685	26.05	0
6677775	FTLDCTHPVEDGIMDAANFEQFLQER	ribosomal protein L22 [Mus musculus]	3026.3447	25.41	1.413188542
31560560	FTPGTFTNQIQAAFR	laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1698.8551	34.81	1.320716203
31980648	FTQAGSEVSALLGR	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1435.7585	86.57	0.933471019
31543605	FVDHVFDEQVIDSLTVK	ribophorin I [Mus musculus]	1991.0327	21.18	0
31982178	FVEGLPINDFSR	malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1393.7114	68.05	1.078710674
31982186	FVFSLVDAMNGK	malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1327.6658	70.48	0
21704144	FVIGGPQGDAGLTGR	methionine adenosyltransferase II, alpha [Mus musculus]	1444.7562	25.34	2.918372307
6679687	FVMQEEFSR	glucose regulated protein [Mus musculus]	1172.5459	44.92	0.950517103
7305395	FVSILMESIPLPDR	purine-nucleoside phosphorylase [Mus musculus]	1616.8751	24.63	14.00954336
6680606	FVTSSSGSYGGVR	keratin complex 1, acidic, gene 19 [Mus musculus]	1303.6392	93.12	1.686630084
6754036	FVTVQTISGTGALR	glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1449.8075	22.58	0
58037465	FWYFVSQLK	Ribosomal protein L18A [Mus musculus]	1217.6304	46.41	1.962981225
6678571	FYPEDVAEELIQDITQK	villin 2 [Mus musculus]	2037.9921	69.51	1.455822173
6754750	FYPEDVSEELIQDITQR	moesin [Mus musculus]	2082.0039	74.4	2.334053513
22122523	FYQASTSELYGK	GDP-mannose 4, 6-dehydratase [Mus musculus]	1393.6591	51.1	2.543586428
33563266	FYSVNVDYSK	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 [Mus musculus]	1221.5776	42	1.420210072
6679937	GAAQNIIPASTGAAK	similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1369.7462	121.65	1.168063988
31981562	GADFLVTEVENGGSLGSK	pyruvate kinase 3 [Mus musculus]	1779.8737	88.41	0
6756033	GAEAANVTGPGGVPVQGSK	nuclease sensitive element binding protein 1 [Mus musculus]	1695.8727	139.44	1.41888488
63746482	GAGTGGLGLAVEGPSEAK	PREDICTED: filamin, alpha [Mus musculus]	1570.8124	84.22	0.401705265
29293809	GAIVPAQEVPPPTVPMDYSWAR	ATP citrate lyase [Mus musculus]	2381.1978	63.01	2.716775482
7242197	GAVYSFDPVGSYQR	proteasome (prosome, macropain) subunit, beta type 1 [Mus musculus]	1545.7404	25.97	1.139158858
51764087	GAWSNVLR	PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	902.477	29.11	0.913049183
22094075	GAWSNVLR	solute carrier family 25, member 5 [Mus musculus]	902.477	29.11	0.913049183
27229277	GAYIYNTLMEFIR	threonyl-tRNA synthetase [Mus musculus]	1590.7996	26.24	2.228866111
31982186	GCDVVVIPAGVPR	malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1281.7021	61.89	1.229477436
6679715	GDATVSYEDPPTAK	Ewing sarcoma breakpoint region 1 [Mus musculus]	1450.6672	33.51	0
6753484	GDEGEVGDPGEDNNDISPR	procollagen, type VI, alpha 1 [Mus musculus]	1971.8269	40.44	0
6753484	GDEGPPGPEGLR	procollagen, type VI, alpha 1 [Mus musculus]	1180.5676	55.04	0
6679078	GDFCIQVGR	nucleoside-diphosphate kinase 2 [Mus musculus]	994.4791	33.1	0.905554158
6754206	GDFIALDLGGSSFR	hexokinase 1 [Mus musculus]	1454.7297	40.88	1.795079553
45597447	GDGPVQGTIHFEQK	superoxide dismutase 1, soluble [Mus musculus]	1512.7618	66.2	0.547053797
30348966	GDQVSQNGLPAEQGSPR	spectrin beta 2 isoform 1 [Mus musculus]	1739.8374	46.57	1.185245673
7106421	GDQVSQNGLPAEQGSPR	spectrin beta 2 isoform 2 [Mus musculus]	1739.8374	46.57	1.185245673
31981562	GDYPLEAVR	pyruvate kinase 3 [Mus musculus]	1019.5139	21.68	1.180701086
63660302	GEAGIPAEFSIWTR	PREDICTED: filamin B, beta [Mus musculus]	1533.7715	44.51	1.498243305
6678986	GEELLSPLNLEQAAYAR	myosin IC [Mus musculus]	1873.9713	54.84	0.743354496
27370092	GEETPVIVGSALCALEQR	Tu translation elongation factor, mitochondrial [Mus musculus]	1871.9508	28.81	1.588853407
45504394	GEFFNELVGQQR	integrin beta 1 (fibronectin receptor beta) [Mus musculus]	1423.6962	64.5	0.637955008

31982178	GEFITTVQQR		malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1178.6257	44.71	1.273535544
54607098	GEGGILINSQGER		succinate dehydrogenase Fp subunit [Mus musculus]	1329.6744	29.92	1.159775128
29336026	GELEDTLDSTNAQQELR		nonmuscle myosin heavy chain [Mus musculus]	1918.9053	28.95	2.407045798
6754524	GEMMDLQHGSLFLK		lactate dehydrogenase 1, A chain [Mus musculus]	1605.7721	43.55	0
51592084	GESEDDFWWCIDR		hypothetical protein LOC74340 [Mus musculus]	1657.6707	44.57	0.827774649
30841031	GESLWLNLR	Deamidation (NQ)	myosin regulatory light chain interacting protein [Mus musculus]	1088.566	22.44	0
34328108	GETGPAGPAGPIGPAGAR		procollagen, type I, alpha 1 [Mus musculus]	1532.7814	63.61	0
8393544	GFAFVQYVNER		heterogeneous nuclear ribonucleoprotein C [Mus musculus]	1329.6608	32.49	2.016969218
21592285	GFEVQVTELR		keratin 20 [Mus musculus]	1177.6224	33.49	0.667091254
40556608	GFEVVYMTEPIDEYCVQQLK		heat shock protein 1, beta [Mus musculus]	2391.1418	89.01	1.786392123
31560449	GFFELFPSVSR		aspartyl aminopeptidase [Mus musculus]	1285.6615	29.55	1.442771044
7304881	GFFVQPTVFSNVTDEMR		aldehyde dehydrogenase family 1, subfamily A1 [Mus musculus]	1973.9403	60.2	0
7106242	GFFVQPTVFSNVTDEMR		aldehyde dehydrogenase family 1, subfamily A7 [Mus musculus]	1973.9403	60.2	0
7949053	GFGDGYNGYGGGPGGGNFGGSPGYGGGR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2495.0337	140.84	1.665031687
6681069	GFGFGQGAGALVHSE		cysteine and glycine-rich protein 1 [Mus musculus]	1433.6808	101.46	0.275936969
7949053	GFGFVTFDDHDPVDK		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1695.7732	67.74	3.387510017
7304885	GFGTDEQAIIDCLGSR		annexin A11 [Mus musculus]	1681.7906	24.06	0
6680027	GFIGPGIDVPAPDMSTGER		glutamate dehydrogenase 1 [Mus musculus]	1915.9385	58.13	0.908349051
27229277	GFQEVVTPNIFNSR		threonyl-tRNA synthetase [Mus musculus]	1607.8324	19.5	0
24418933	GGENIYPAELEDFFLK		hypothetical protein LOC264895 [Mus musculus]	1841.8999	81.3	0.772756539
6755252	GGGGGGGGPGGEQETQELASK		purine rich element binding protein B [Mus musculus]	1829.8339	92.01	0.816876356
1346343	GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	2383.949	172.17	
7949053	GGGGNFGPGPGSNFR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1377.6449	67.96	1.467575054
63476037	GGPGQPGFEGEQGTR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1473.6791	34.48	0.226030159
6680606	GGSFSGTLAVSDGLLSGNEK		keratin complex 1, acidic, gene 19 [Mus musculus]	1895.9275	82.42	0
24418933	GGVIAGSPAPPELIR		hypothetical protein LOC264895 [Mus musculus]	1433.8134	27	0.467687103
29789343	GHPSAGAEEEGGSDGSAAEAEPR		eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]	2167.9275	94.96	0
22165384	GHYTEGAELVDSVLDVVR		tubulin, beta, 2 [Mus musculus]	1958.9843	138.11	0.910479029
33859488	GHYTEGAELVDSVLDVVR		tubulin, beta 2 [Mus musculus]	1958.9843	138.11	0.910479029
12963615	GHYTEGAELVDSVLDVVR		tubulin, beta 3 [Mus musculus]	1958.9843	138.11	0.910479029
7106439	GHYTEGAELVDSVLDVVR		tubulin, beta 5 [Mus musculus]	1958.9843	138.11	0.910479029
27754056	GHYTEGAELVDSVLDVVR		tubulin, beta 6 [Mus musculus]	1958.9843	138.11	0.910479029
21313262	GIEQAVQSHAVAEEEAR		inner membrane protein, mitochondrial [Mus musculus]	1823.899	49.29	0.825288117
21450291	GILAADESVGTMGNR		aldolase 2, B isoform [Mus musculus]	1490.7351	27.94	0
63518159	GILFVGSGVSGGEEGAR		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1591.8136	24.63	1.743063783
31543942	GILSGTSDLLLTFDEAEVR		vinculin [Mus musculus]	2036.0466	37.97	0.632698853
6679457	GINQGQVWIGGR		proteoglycan 2, bone marrow [Mus musculus]	1284.6782	36.96	0.694872941
11230802	GISQEQMQEFR		actinin alpha 4 [Mus musculus]	1352.6282	34.12	1.912816841
6681095	GITWGEDTLMEYLENPK		cytochrome c, somatic [Mus musculus]	1995.9509	46.16	0
6756041	GIVDQSQQAYQEAFEISK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	2040.9849	19.16	0
51592084	GIVEESVTGVHR		hypothetical protein LOC74340 [Mus musculus]	1282.6765	19.09	0
23956084	GIVNEQFLLQR		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	1316.7323	21.17	0.960054173
13386034	GLAPDLPEDLYHLIK		ribosomal protein S13 [Mus musculus]	1693.9014	40.31	3.57443504
36031080	GLDGFQGPSGPR		procollagen, type IV, alpha 2 [Mus musculus]	1187.5856	47.58	0.614733376
6754088	GLELYLDLLSQPSR		glutathione S-transferase, theta 2 [Mus musculus]	1603.8621	21.73	0.937056669
6681069	GLESTTLADKDGEIYCK		cysteine and glycine-rich protein 1 [Mus musculus]	1842.8889	74.11	0
46195430	GLGMTLSYLFR		NADH dehydrogenase (ubiquinone) Fe-S protein 8 [Mus musculus]	1257.6625	29.9	0.851468969
7304889	GLGTDEDAIIGILAYR		annexin A4 [Mus musculus]	1676.8866	92.94	2.036757716
6753060	GLGTDEDSILNLLTSR		annexin A5 [Mus musculus]	1703.8824	80	1.122920076
6754570	GLGTDEDTLIEILTTR		annexin A1 [Mus musculus]	1746.8997	69.98	2.331141637
31982159	GLGTEVPGNFQGPDPYR		hypothetical protein LOC235043 [Mus musculus]	1803.8694	21.67	1.342486192
63557759	GLHRDLHR		PREDICTED: similar to polytene protein [Mus musculus]	1003.5535	19.39	0
40018610	GLIEIISNAAEYENIPIR		U5 snRNP-specific protein, 200 kDa [Mus musculus]	2015.0746	32.95	1.40438075
7948997	GLIPGSLQNEPTASVPPQSDVYR		PDZ and LIM domain 3 [Mus musculus]	2425.2322	79.73	0
6678329	GLLIEPAANSYLLAER		transglutaminase 2, C polypeptide [Mus musculus]	1729.9486	34.57	0.831164694
31981826	GLLPEELTPLILETQK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1794.0288	57	1.035027908
6671684	GLNTIPLFVQLLYSPIENIQR		catenin beta [Mus musculus]	2428.3616	24.42	2.7516677
13386034	GLSQSALPYR		ribosomal protein S13 [Mus musculus]	1091.5825	28.11	1.381742125
63746482	GLVEPVDVVDNADGTQTVNYVPSR		PREDICTED: filamin, alpha [Mus musculus]	2544.2571	139.33	0.261462206
13386272	GLVYETSVLDPDEGIR		citrate synthase-like protein [Mus musculus]	1762.8804	64.66	1.923685599

13385942	GLVYETSVLDPDEGIR		citrate synthase [Mus musculus]	1762.8804	64.66	1.923685599
6680748	GMSLNLEPDNVGVVVFGNDK		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2104.0413	84.31	1.716645864
6680748	GMSLNLEPDNVGVVVFGNDK	Deamidation (NQ)	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2105.0454	42.74	0
31560611	GMTVYGLPR		calponin 1 [Mus musculus]	993.5162	41.53	0.326264364
30911099	GNAGQTNYGFANSTMER		fatty acid synthase [Mus musculus]	1817.7958	43.1	1.485444736
63492583	GNFNYVEFTR		PREDICTED: myosin regulatory light polypeptide 9 [Mus musculus]	1246.5865	29.58	0
6754854	GNLYWTDWNR		nidogen 1 [Mus musculus]	1324.6056	38.23	0
6679058	GNLYWTDWNR		nidogen 2 [Mus musculus]	1324.6056	38.23	0
7305027	GNPTVEVDLYTAK		enolase 2, gamma neuronal [Mus musculus]	1406.7101	39.19	0
51770896	GNPTVEVDLYTAK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1406.7101	39.19	0
21704206	GNWGYLDQAAALR		carboxylesterase 2 [Mus musculus]	1434.7161	23.52	0.43800941
19527034	GPAPLGTFQVTTPQR		lamin B receptor [Mus musculus]	1569.8398	24.46	1.888300951
31560611	GPAYGLSAEVK		calponin 1 [Mus musculus]	1091.574	87.14	0.202476735
6679573	GPGLGSTQGQTIALPAQGLIEFR		purine rich element binding protein A [Mus musculus]	2311.2407	23.06	0.98038931
6755204	GPGLYYVDSEGNR		proteasome (prosome, macropain) subunit, beta type 5 [Mus musculus]	1426.6697	21.84	0.981963952
33859600	GPTEQLVSPEPEVYEIVR		protein phosphatase 1B, magnesium dependent, beta isoform [Mus musculus]	2042.0375	21.56	1.555260608
58037546	GQETSTNPIASIFAWSR		isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	1864.9189	23.1	2.257023513
6677871	GQIIYTWQGANATR		scinderin [Mus musculus]	1578.7919	24.33	0.845300768
6755698	GQNDLMGTAEDFADQFLR		surfeit gene 4 [Mus musculus]	2027.9158	88.16	1.437591231
27477057	GQNLLLTNLQTIQGILER		translocated promoter region protein [Mus musculus]	2024.1432	21.08	2.548838361
6754090	GSAPPGPVPEGQIR		glutathione S-transferase omega 1 [Mus musculus]	1361.7245	36.1	1.680060512
16716467	GSDHSASLEPGELAELVR		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1866.9253	58.09	1.379640378
58037267	GSFSEQGINEFLR		protein disulfide isomerase-associated 6 [Mus musculus]	1483.7219	44.49	0
6678573	GSLNITTPGIQIWR		villin 1 [Mus musculus]	1555.8677	37.73	1.30648214
21704156	GSVFSAPSASGTPNK		caldesmon 1 [Mus musculus]	1406.6941	91.47	0
6678449	GSVNMPFMDFLTK		thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	1486.7035	33.45	0
7657429	GSYTYFAPSNEAWENLDSDIR		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2435.083	50.7	0
22094075	GTDIMYTGTLDCWR		solute carrier family 25, member 5 [Mus musculus]	1631.7272	102.09	1.684122039
6754570	GTDVNVFTTILTSR		annexin A1 [Mus musculus]	1523.8016	35.27	2.624261913
6679761	GTGELTQLLNSMLTAIK		fructose bisphosphatase 2 [Mus musculus]	1789.9779	50.72	0.958734431
6753428	GTGGVDTAATGSVFDISNLDR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	2052.9922	73.81	5.395345596
6671762	GTGGVDTAAVGAVFDISNADR		creatine kinase, muscle [Mus musculus]	1992.9625	46.86	0
10946574	GTGGVDTAAVGGVFDVSNADR		creatine kinase, brain [Mus musculus]	1964.9475	65.31	0.2289586
13385340	GTGLDEAMEWLVETLK		ADP-ribosylation factor-like 1 [Mus musculus]	1791.887	47.89	0
7304887	GTGTDEDALIEILTTR		annexin A3 [Mus musculus]	1704.8646	55.42	3.104978089
31560449	GTPEPGPLGATDER		aspartyl aminopeptidase [Mus musculus]	1396.6738	35.09	1.200683301
31981826	GTSFEAAATSGGSASSEK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1644.7352	41.87	0
13384736	GTVGEPTYDAEFQHFLR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1966.9358	34.41	1.636600765
22164798	GTWEKPGDAAPMGYDFWYQPR		selenium binding protein 1 [Mus musculus]	2472.1167	33.51	1.356631847
63540743	GVAGVPAEFSIWTR		PREDICTED: filamin C, gamma [Mus musculus]	1489.7821	29.52	0.440199502
19526818	GVAPLWMR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	929.4997	24.28	1.093614055
23956222	GVDDLDFFIGDEAIEKPTYATK		ARP3 actin-related protein 3 homolog [Mus musculus]	2444.2039	51.99	0
6754570	GVDEATIIDILTK		annexin A1 [Mus musculus]	1387.7616	19.6	0
6996913	GVDEVTIVNILTNR		annexin A2 [Mus musculus]	1542.8542	78.87	1.9999124
6677799	GVDLDQLLDMSYEQLMQLYSAR		ribosomal protein S15 [Mus musculus]	2588.2434	41.49	1.626201546
29789257	GVDLQESNPASR		RAB5C, member RAS oncogene family [Mus musculus]	1272.6223	31.11	1.073074526
13385374	GVDLTEPAQPAR		RAB5A, member RAS oncogene family [Mus musculus]	1253.6511	19.13	0
21450277	GVGIISEGNETVEDIAAR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1829.9302	94.6	1.107105915
63562740	GVMLWGWR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1004.5128	21.73	0.710697662
6755863	GVVDSDDLPLNVSR		tumor rejection antigen gp96 [Mus musculus]	1485.7594	65.04	1.326045989
6754254	GVVDSEDLPLNISR		heat shock protein 1, alpha [Mus musculus]	1513.7903	82.49	1.327038049
40556608	GVVDSEDLPLNISR		heat shock protein 1, beta [Mus musculus]	1513.7903	82.49	1.327038049
6671539	GVVPLAGTNGETTTQGLDGLSER		aldolase 1, A isoform [Mus musculus]	2272.1414	115.59	0.893457121
6753010	GWGDQLIWTQTYEEALYR		anterior gradient 2 [Mus musculus]	2229.0603	72.26	0.432893289
22122825	GYAFNHSADFETVR		actin-related protein 2 [Mus musculus]	1613.7439	31.77	1.641090508
55742711	GYDFPAVLR		EH-domain containing 2 [Mus musculus]	1037.5353	32.28	0
7305085	GYDVDFPR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	968.4479	41.1	1.117551171
21450625	GYDVIAQAQSGTGK		eukaryotic translation initiation factor 4A1 [Mus musculus]	1394.689	47.31	2.040991438
7305019	GYDVIAQAQSGTGK		eukaryotic translation initiation factor 4A2 [Mus musculus]	1394.689	47.31	2.040991438
59709449	GYEEWLLNEIR		actinin alpha 2 [Mus musculus]	1421.7146	59.45	0.821288475

11230802	GYEEWLLNEIR		actinin alpha 4 [Mus musculus]	1421.7146	59.45	0.821288475
63487095	GYELLFQPEVVR		PREDICTED: catenin src [Mus musculus]	1449.7772	43.72	0
7949051	GYFEYIEENK		heterogenous nuclear ribonucleoprotein U [Mus musculus]	1291.5931	25.7	0
6681069	GYGYGQGAGTLSTDK		cysteine and glycine-rich protein 1 [Mus musculus]	1474.6962	74.26	0
6681069	GYGYGQGAGTLSTDKGESLGIK		cysteine and glycine-rich protein 1 [Mus musculus]	2159.0701	153.65	0.40807393
30425250	GYNFTTTAER	Deamidation (NQ)	hypothetical protein LOC238880 [Mus musculus]	1160.5265	30.58	0
45598381	GYPTLLLFR		thioredoxin domain containing 5 [Mus musculus]	1079.6243	34.57	0.781232873
45598381	GYPTLLWFR		thioredoxin domain containing 5 [Mus musculus]	1152.6228	30.37	0.673396482
6671509	GYSFTTTAER		actin, beta, cytoplasmic [Mus musculus]	1132.542	58.73	1.383861354
63652452	GYSFTTTAER		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1132.542	58.73	1.383861354
6671507	GYSFVTTAER		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1130.564	50.55	0.240024121
6754524	GYTSWAIGLSVADLAESIMK		lactate dehydrogenase 1, A chain [Mus musculus]	2112.071	89.77	1.517049302
63664186	GYTSWAIGLSVADLAESIMK		PREDICTED: similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M) [Mus mus	2112.071	89.77	1.517049302
46849705	GYVLPTAR		lectin, galactose binding, soluble 4 [Mus musculus]	876.4898	23.48	1.871755216
31981549	GYWGGPAFLR		sulfide quinone reductase-like [Mus musculus]	1123.5647	23.7	1.360405082
7305295	HESMISELEVR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1329.6395	34.18	0
9790219	HEYQANGPEDLNR		destrin [Mus musculus]	1542.7146	25.79	0
9790219	HEYQANGPEDLNR	Deamidation (NQ)	destrin [Mus musculus]	1543.6989	23.5	0
63702717	HGQWPQSSNEMVK	Deamidation (NQ); Oxidation (M)	PREDICTED: hypothetical protein XP_619435 [Mus musculus]	1544.7081	35.79	1.050243831
22122825	HIVLSGGSTMYPGLPSR		actin-related protein 2 [Mus musculus]	1771.9249	30.95	2.307011928
6753010	HLSPDGQYVPR		anterior gradient 2 [Mus musculus]	1268.6444	63.32	0.475037336
6671507	HQGVMVGMGQK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1171.5741	55.09	0.609057385
6671509	HQGVMVGMGQK		actin, beta, cytoplasmic [Mus musculus]	1171.5741	55.09	0.609057385
30425250	HQGVMVGMGQK		hypothetical protein LOC238880 [Mus musculus]	1171.5741	55.09	0.609057385
46559834	HQLVEVIGQLEETLPER		desmuslin isoform M [Mus musculus]	1990.0543	24.16	0
63746482	HTAMVSWGGVSIPNSPFR		PREDICTED: filamin, alpha [Mus musculus]	1942.9659	47.3	0
10946928	HTGPNSPDTANDGFVR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1684.7762	42.85	2.280533776
9845253	HTGPNSPDTANDGFVR		heterogeneous nuclear ribonucleoprotein H2 [Mus musculus]	1684.7762	42.85	2.280533776
7305295	HTQAVEELTEQLEQFK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1929.9614	123.01	0.256685328
6678413	HVFGESDELIGQK		triosephosphate isomerase 1 [Mus musculus]	1458.7261	74.66	0
27229048	HVSPAGAAVGVPLSEDEAR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1861.9432	19.76	1.367366663
7305295	HVSTLNIQLSDSK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1441.7648	83.88	0.335903111
28916693	HVVPNEVVVQR		gelsolin [Mus musculus]	1275.7188	45.27	1.327025553
63487095	HYEDGYPGGSDNYGSLSR		PREDICTED: catenin src [Mus musculus]	1973.8328	57.45	2.227686883
6754036	IAATILTSPDLR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1270.7347	30.59	0
18250284	IAEFAFEYAR		isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	1216.6051	21.25	1.012780212
63476037	IAEGVPQLLIVLTAEPSGDDVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2292.2402	116.64	0.215314937
31981515	IALTDNSLIAR		ribosomal protein L7 [Mus musculus]	1186.6775	27.26	0
63746482	IANLQTDLSDGLR		PREDICTED: filamin, alpha [Mus musculus]	1415.7516	62.78	0.302622749
18700004	IAQFLSGIPETVPLSTVNR		acetyl-Coenzyme A acyltransferase 1 [Mus musculus]	2042.1276	23.79	0.927329397
7305295	IAQLEEELEEEQGNMEAMSDR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2451.0833	102.39	0.181894707
20137006	IAQLEEQLDNETK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1530.78	19.27	0
7305295	IAQLEEQVEQEAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1542.7889	91.97	0.211043362
41054806	IAQSDYIPTQQDVLR		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1746.907	79.81	1.095170475
13385010	IASGLGLAWIIGR		microsomal glutathione S-transferase 3 [Mus musculus]	1326.79	26.76	1.075974601
21704020	IASQVAALDLGYKPGVEAIR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	2071.1638	52.62	1.274449139
36031080	IAVQPGTLGPQGR		procollagen, type IV, alpha 2 [Mus musculus]	1293.7355	43.91	0
13384620	IDEPLEGSEDR		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1259.5787	50.67	1.357678159
6680854	IDFEDVIAEPEGTHSFDGIWK		caveolin, caveolae protein 1 [Mus musculus]	2405.1548	54.52	0.825315901
33469063	IDFEKEPLGVNAQGR		aconitase 1 [Mus musculus]	1672.8668	35.41	0
40556608	IDIIPNPQER		heat shock protein 1, beta [Mus musculus]	1194.6541	44.31	1.508819351
31980969	IDMNLTDLLGELQR		SEC23B [Mus musculus]	1630.8514	67.05	1.120774411
6680836	IDNSQVESGSLEDDWDFLPPKK		calreticulin [Mus musculus]	2519.1885	19.83	1.317019
9790073	IDSVTGEIFSAAPLDR		cadherin 17 [Mus musculus]	1690.8661	59.04	1.567230265
7949053	IDTIEIITDR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1188.6437	40.04	1.445553652
63476037	IEDNVQQFLVLLVAGR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1814.0165	84.8	0.228480984
31981100	IEDVTPIPSDSTR		ribosomal protein S14 [Mus musculus]	1429.7244	50.57	1.983629986
63476037	IEEGVPQFLVLISSGK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1715.9624	52.97	0.586622483
6680606	IEELNTQVAVHSEQIQISK		keratin complex 1, acidic, gene 19 [Mus musculus]	2166.1511	129.15	1.558720628
37620153	IEGYPDPEVVWFK		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1578.7845	59.69	0.193695069

33563250	IESLNEEIAFLK		desmin [Mus musculus]	1405.7555	81	0.20833577
31559916	IETIEVMEDR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1234.6006	26.01	1.15495478
31981722	IEWLESHQDADIEDFK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1974.9243	55.88	2.691799637
14861854	IFEAQIAGLR		keratin complex 2, basic, gene 7 [Mus musculus]	1117.6359	28.54	1.548194061
6679421	IFELGLGDDDGNLEEDFITWR		P450 (cytochrome) oxidoreductase [Mus musculus]	2454.1577	39.07	0
31982186	IFGVTTLDIVR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1233.7216	49.33	1.103667256
31559916	IFVGGIKEDTEEYNLR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1882.9569	73.05	1.389487969
22164798	IFVWDWQR		selenium binding protein 1 [Mus musculus]	1149.5801	41.41	1.162246912
31982522	IGCFALSEPGNGSDAGAASTTAR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	2152.9927	78.4	0.780300116
63476037	IGDLQSQIVSLLK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1413.8307	75.79	0
24418919	IGEGFLTDLSQLK		brain glycogen phosphorylase [Mus musculus]	1420.7715	64.07	0
6671539	IGEHTPSALAIMENANVLAR		aldolase 1, A isoform [Mus musculus]	2107.0955	98.49	0.846628876
6754750	IGFPWSEIR		moesin [Mus musculus]	1104.5795	40.11	1.361679705
6678571	IGFPWSEIR		villin 2 [Mus musculus]	1104.5795	40.11	1.361679705
51873060	IGGIGTVPVGR		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	1025.6167	39.65	1.180814833
63660294	IGNLQTDLSDGLR		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	1401.7314	23.62	1.675430731
63476037	IGVVQFSNDVFPEFYLK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2002.0211	44.29	0.334017224
6754976	IGYPAPNFK		peroxiredoxin 1 [Mus musculus]	1006.531	33.89	1.396351576
7106242	IHGQTIPSDGNIFTYTR	Deamidation (NQ)	aldehyde dehydrogenase family 1, subfamily A7 [Mus musculus]	1920.921	24.84	0
6680027	IIAEGANGPTTPEADK		glutamate dehydrogenase 1 [Mus musculus]	1583.796	72.31	0.768056515
6680027	IIAEGANGPTTPEADKIFLER		glutamate dehydrogenase 1 [Mus musculus]	2242.1641	43.77	1.605073142
6671507	IIAPPER		actin, alpha 2, smooth muscle, aorta [Mus musculus]	795.4681	24.6	0.414279911
6671509	IIAPPER		actin, beta, cytoplasmic [Mus musculus]	795.4681	24.6	0.414279911
30425250	IIAPPER		hypothetical protein LOC238880 [Mus musculus]	795.4681	24.6	0.414279911
63652452	IIAPPER		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	795.4681	24.6	0.414279911
37620153	IIDEDFELTER		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1379.6631	50.75	0
30425168	IIDFGLAR		myosin light chain kinase [Mus musculus]	904.5195	23.72	0.223310263
6677813	IIDVVYNASNNELVR		ribosomal protein S8 [Mus musculus]	1718.9178	97.24	1.463052836
63476037	IIEELDVKPDGTR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1484.8046	47.2	0.553389032
6679567	IIGAVDQIQLTQAQLEER		polymerase I and transcript release factor [Mus musculus]	2025.0945	89.02	0.424458539
20137006	IIGLDQVAGMSETALPGAFK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2018.0645	68.66	1.823457752
13384620	IILDLISESPIK		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1340.7999	78.27	1.707979814
6679891	IILTAQPFR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1058.6333	22.96	1.409647476
31981722	IINEPTAAAIAYGLDK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1659.9032	94.75	1.08032625
7305163	IINEPTAAAIAYGLDK		heat shock protein 1-like [Mus musculus]	1659.9032	94.75	1.08032625
31981690	IINEPTAAAIAYGLDK		heat shock protein 8 [Mus musculus]	1659.9032	94.75	1.08032625
63664182	IINEPTAAAIAYGLDK		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1659.9032	94.75	1.08032625
63704924	IINEPTAAAIAYGLDR		PREDICTED: heat shock protein 1B [Mus musculus]	1687.9041	43.9	0.532618912
6679439	IIPGFMCQGGDFTR		peptidylprolyl isomerase A [Mus musculus]	1541.7198	66.6	1.643080766
41322904	IISLETYNLFR		plectin 1 isoform 1 [Mus musculus]	1368.7571	24.26	0.886194169
136429	IITHPNFNGNTLDNDIMLIK		Trypsin precursor	2283.1956	156.72	10.96802705
136429	IITHPNFNGNTLDNDIMLIK	2 Deamidation (NQ)	Trypsin precursor	2285.176	32.63	0
136429	IITHPNFNGNTLDNDIMLIK	Deamidation (NQ)	Trypsin precursor	2284.1716	58.15	0.316558595
136429	IITHPNFNGNTLDNDIMLIK	Oxidation (M)	Trypsin precursor	2299.1785	87.67	0
13384620	IITITGTQDQIQNAQYLLQNSVK		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	2589.3984	22.94	0
6680960	IIYSPTVGDPIDEYTTVPGR		procollagen, type XII, alpha 1 [Mus musculus]	2193.1108	66.91	0
6678359	ILATPPQEDAPSVDIANIR		transketolase [Mus musculus]	2020.0782	67.4	1.398268584
42415475	ILFIFIDSDHTDNQR		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1833.9088	38.18	0
6680748	ILGADTSVDLEETGR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1575.7994	91.73	0.739608483
31982755	ILLAELEQLK		vimentin [Mus musculus]	1169.7062	73.64	0.57975111
6680067	ILLANFLAQTEALMK		glucose phosphate isomerase 1 [Mus musculus]	1675.9374	67.24	1.274052846
46195430	ILMWTELIR		NADH dehydrogenase (ubiquinone) Fe-S protein 8 [Mus musculus]	1174.6627	26.89	0.995916781
51827543	ILPEIIPILEEGLR		PREDICTED: GCN1 general control of amino-acid synthesis 1-like 1 [Mus musculus]	1604.9644	34.04	0
16716471	ILSDTTLWLR		hypothetical protein LOC94184 [Mus musculus]	1217.6884	29.12	1.051331958
6677771	ILTFDQLALESPK		ribosomal protein L18 [Mus musculus]	1474.8085	51.24	1.395527183
9790069	ILVATNLFGR		HLA-B-associated transcript 1A [Mus musculus]	1103.6532	38.32	1.616827506
34538601	ILYMMDEINNPVLTVK		cytochrome c oxidase subunit II [Mus musculus]	1892.9801	47.53	0
31980648	IMDPNIVGNEHYDVAR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1842.8911	66.36	1.188007857
18152793	IMEGPAFNFLDAPAVR		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1747.8914	27.97	1.012455984
20137006	IMGIPEDEQMGLLR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1601.8022	45.9	2.21707494

31980648	IMNVIGEPIDER		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1385.7208	48.11	0
6724311	INEAFDLLR		alcohol dehydrogenase 1 (class I) [Mus musculus]	1090.5875	65.24	6.19549282
51772556	INFDDNAEFR		PREDICTED: similar to Succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	1240.564	43.6	1.280612394
33598964	INFDVTGYIVGANIETYLLEK		myosin heavy chain 10, non-muscle [Mus musculus]	2372.2349	124.01	0.786177567
7305295	INFDVTGYIVGANIETYLLEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2372.2349	124.01	0.786177567
6754994	INISEGNCPER		poly(rC) binding protein 1 [Mus musculus]	1231.576	19.35	1.418558736
33563250	INLPIQTFSALNFR		desmin [Mus musculus]	1633.9108	73.54	0.184409824
33563250	INLPIQTFSALNFR	Deamidation (NQ)	desmin [Mus musculus]	1634.8915	44.84	0
9903607	INPDGSQSVVEVPYAR		transmembrane protein 4 [Mus musculus]	1730.8746	23.09	0
27804325	INVLVLEAR		monoamine oxidase A [Mus musculus]	1026.6277	26.95	1.171763828
21704066	INVNEIFYDLVR		RAS-related protein-1a [Mus musculus]	1494.7955	73.91	0.833511867
33859488	INVYYNEAAGNK		tubulin, beta 2 [Mus musculus]	1355.6835	40.78	0
22165384	INVYYNEATGGK		tubulin, beta, 2 [Mus musculus]	1328.6516	34.73	5.214574617
31980648	IPSAVGYQPTLATDMGTMQER		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2266.0911	109.4	1.426023409
20137008	IQAIELEDLLR		biglycan [Mus musculus]	1312.748	46.94	0.734569881
46593021	IQEVDAQMLR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1202.6154	47.87	0.919031284
6753498	IQFNESFAEMNR		cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	1485.6836	53.26	1.676661748
31559981	IQIWDTAGQER		RAB15, member RAS oncogene family [Mus musculus]	1316.666	77.54	1.578773833
21314832	IQRPPEDSIQPYEK		UDP-glucose pyrophosphorylase 2 [Mus musculus]	1699.874	38.38	0.571729621
19526818	IQTQPGYANTLR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1361.7268	54.59	1.18798004
31981246	IQTYLESTKPIIDLYEEMGK		UMP-CMP kinase [Mus musculus]	2371.2136	69.53	1.390473065
63476037	ISCSGNQLPTVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1274.6555	28.35	0
22165384	ISEQFTAMFR		tubulin, beta, 2 [Mus musculus]	1229.6042	54.56	0.918390119
33859488	ISEQFTAMFR		tubulin, beta 2 [Mus musculus]	1229.6042	54.56	0.918390119
12963615	ISEQFTAMFR		tubulin, beta 3 [Mus musculus]	1229.6042	54.56	0.918390119
31981939	ISEQFTAMFR		tubulin, beta 4 [Mus musculus]	1229.6042	54.56	0.918390119
7106439	ISEQFTAMFR		tubulin, beta 5 [Mus musculus]	1229.6042	54.56	0.918390119
22122523	ISFDLAEYTADVDGVGTLR		GDP-mannose 4, 6-dehydratase [Mus musculus]	2042.0118	84.91	0.87138893
51491845	ISGETIFVTAPHEATAGIIGVNR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2353.2495	32.55	1.237155805
21361209	ISGLIYEETR		germinal histone H4 [Mus musculus]	1180.6256	63.59	1.300645282
31982755	ISLPLPTFSSLNLR		vimentin [Mus musculus]	1557.9076	79.54	0.808475559
63476037	ISLSPEYVYSVSTFR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1747.8966	46.03	0.254187918
33563256	ISQTNYIPTQQDVLR		guanine nucleotide binding protein, alpha inhibiting 3 [Mus musculus]	1775.9346	23.83	1.363130611
6678499	ISSINSISALCEATGADVEEVATAIGMDQR		UDP-glucose dehydrogenase [Mus musculus]	3051.4509	94.82	0.483793636
6677813	ISSLLEEQFQQGK		ribosomal protein S8 [Mus musculus]	1506.7754	72.97	1.727523307
31981679	ISSVQSIVPALEIANAHR		heat shock protein 1 (chaperonin) [Mus musculus]	1905.0566	31.68	1.347833718
6753320	ISTPVDVNNR		chaperonin subunit 3 (gamma) [Mus musculus]	1114.5864	22.2	1.700683234
40254595	ISVGSDADLVIWDPDSVK		dihydropyrimidinase-like 2 [Mus musculus]	1915.9398	22.51	0
7106439	ISVYYNEATGGK		tubulin, beta 5 [Mus musculus]	1301.6398	84.8	1.657882387
7106435	ITAQGQYELR		tenascin C [Mus musculus]	1178.6127	21.16	0.567197365
31982522	ITEIYEGTSEIQR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1538.7709	67.33	0.756935917
50355692	ITESEEVVSR		lamin A isoform A [Mus musculus]	1148.5828	22.9	0
12963691	ITGWGEETLPDGR		tubulointerstitial nephritis antigen-like [Mus musculus]	1430.6989	24.87	0
6679291	ITLPVDFVTADKFDENAK		phosphoglycerate kinase 1 [Mus musculus]	2023.0356	69.19	1.625497216
6680606	ITMQNLNDR		keratin complex 1, acidic, gene 19 [Mus musculus]	1104.5466	48.91	1.43859135
34328204	ITPAHDQNDYEVGQR		valyl-tRNA synthetase 2 [Mus musculus]	1742.8192	64.59	1.043385486
31981722	ITPSYVAFTPEGER		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1566.7847	62.65	1.086686489
9790073	ITQVQWNDPGAQYSLVNK		cadherin 17 [Mus musculus]	2061.0557	44.57	0
6680960	ITYQPSTGEGNEQTITVGGR		procollagen, type XII, alpha 1 [Mus musculus]	2108.0339	76.81	0
21450277	IVEIPFNSTNK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1261.6687	28.97	1.007978272
63476037	IVEYLDIGFDTTR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1541.7887	80.03	0.201376834
33598964	IVFQEFR		myosin heavy chain 10, non-muscle [Mus musculus]	938.5127	35.14	0.205642308
7305295	IVFQEFR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	938.5127	35.14	0.205642308
6753010	IVFVDPSLTVR		anterior gradient 2 [Mus musculus]	1245.7229	64.91	0.452175912
7305619	IVILPDYLEIAR		ubiquitin specific protease 5 (isopeptidase T) [Mus musculus]	1414.8322	25.23	1.326880697
33859580	IVLDFR		galectin-3 [Mus musculus]	762.442	39.37	0
40254595	IVLEDGTLHVTEGSGR		dihydropyrimidinase-like 2 [Mus musculus]	1682.8696	65	0
6754482	IVLQIDNAR		keratin complex 1, acidic, gene 18 [Mus musculus]	1041.6035	33.68	1.5072317
6680606	IVLQIDNAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1041.6035	33.68	1.5072317
417200	IVLQIDNAR		Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1041.6035	33.68	1.5072317

24418919	IVNGWQVEEADDWLR		brain glycogen phosphorylase [Mus musculus]	1829.8788	47.09	0.947455659
31981246	IVPVEITISLLK		UMP-CMP kinase [Mus musculus]	1324.8466	66.38	1.121362811
6679937	IVSNASCTTNCLAPLAK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1705.8606	80.28	1.275004977
6679937	IVSNASCTTNCLAPLAK	Deamidation (NQ)	similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1706.8462	45.66	1.839173166
63746482	IVSPSGAAVPCK		PREDICTED: filamin, alpha [Mus musculus]	1128.6057	37.54	0
30023842	IVSQLLTLMDGLK		valosin containing protein [Mus musculus]	1430.827	72.27	0.884394552
18079339	IVYGHLDDPANQEIER		aconitase 2, mitochondrial [Mus musculus]	1868.922	65.67	1.007600791
8567336	IWALGGVTSDR		chloride channel calcium activated 3 [Mus musculus]	1174.6268	59.42	1.113715356
33859482	IWCFGPDGTGPNILTDITK		eukaryotic translation elongation factor 2 [Mus musculus]	2048.0117	51.18	1.304904496
6678483	IYDDDFFQNLDGVANALDNIDAR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	2614.2058	53.69	1.099515311
33859554	IYELAAGGTAVGTGLNTR		fumarate hydratase 1 [Mus musculus]	1763.9386	66.73	1.255212737
8567390	IYIDDGLISLVVR		pyruvate kinase liver and red blood cell [Mus musculus]	1475.8456	36.88	0
51491845	IYIDSNNNPER		clathrin, heavy polypeptide (Hc) [Mus musculus]	1334.6416	49.16	1.432447723
22122523	IYLGQLECFSLGNLDAK		GDP-mannose 4, 6-dehydratase [Mus musculus]	1883.9419	34.73	1.630261241
6671622	IYLTADNLVLNLQDESFTR		B-cell receptor-associated protein 37 [Mus musculus]	2225.1506	34.39	0
6680618	IYQIYEGTAQIQR		acetyl-Coenzyme A dehydrogenase, medium chain [Mus musculus]	1582.828	35.2	7.060047097
22164798	IYVVDVGSEPR		selenium binding protein 1 [Mus musculus]	1233.6526	37.43	1.122275164
7305295	KATLQAEQLSNELATER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1902.0002	104.23	0.269498462
7304901	KCYEAGMTLGARK	Oxidation (M)	androgen receptor [Mus musculus]	1443.7054	19.01	0
6671507	KDLYANNVLSGGTTMYPGIADR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2356.1814	144.99	0.108131737
6671507	KDLYANNVLSGGTTMYPGIADR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2357.1565	96.38	1.555102718
6671507	KDLYANNVLSGGTTMYPGIADR	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2372.1565	31.12	0.175775945
6671509	KDLYANTVLSGGTTMYPGIADR		actin, beta, cytoplasmic [Mus musculus]	2343.1692	107.41	1.101917086
63694749	KDLYANTVLSGGTTMYPGIADR		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2343.1692	107.41	1.101917086
6671509	KDLYANTVLSGGTTMYPGIADR	Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	2359.1738	29.23	1.109087149
63694749	KDLYANTVLSGGTTMYPGIADR	Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2359.1738	29.23	1.109087149
7305295	KEEELQAALAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1257.6841	65.96	0
20137006	KEEELQAALAR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1257.6841	65.96	0
33598964	KFDQLLAEEK		myosin heavy chain 10, non-muscle [Mus musculus]	1220.6458	62.8	0
7305295	KFDQLLAEEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1220.6458	62.8	0
20137006	KFDQLLAEEK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1220.6458	62.8	0
29336026	KFDQLLAEEK		nonmuscle myosin heavy chain [Mus musculus]	1220.6458	62.8	0
7305295	KLEGDASDFHEQIADLQAQIAELK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2669.321	30.05	0
7305295	KLEVQLQDLQSK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1428.8076	95.98	0
6753066	KLLETEEEAAFPLGGATPR		amine oxidase, copper containing 3 [Mus musculus]	2029.0574	23.39	0
6680836	KPEDWDEEMDGEWEPPVIQNPEYK		calreticulin [Mus musculus]	2960.3064	43.6	0
33695080	KPGLLNSSNKEQSELR	3 Deamidation (NQ)	protein kinase C binding protein 1 [Mus musculus]	1802.9156	21.99	0
31982099	LAAIQESGVER		proteasome (prosome, macropain) subunit, beta type 6 [Mus musculus]	1172.6277	23.12	1.638084442
6678499	LAANAFLAQR		UDP-glucose dehydrogenase [Mus musculus]	1074.6038	33.21	0.426064054
31982522	LADMALALESAR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1260.6567	41.99	0
13624315	LAELEAALQR		keratin complex 2, basic, gene 8 [Mus musculus]	1113.6301	65.59	1.399057281
6753010	LAEQFVLLNLVYETTDK		anterior gradient 2 [Mus musculus]	1996.0645	77.77	0
6678483	LAGTQPLEVLEAVQR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1623.9059	80.35	1.254844842
13624315	LALDIEITTYR		keratin complex 2, basic, gene 8 [Mus musculus]	1307.7224	59.15	1.78427987
23956396	LALQQDLTSMAPGLVIQAVR		SPFH domain family, member 2 [Mus musculus]	2124.1843	33.08	2.555058071
51770896	LAMQEFMILPVGASSFR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1896.9757	77.02	1.008157849
31543942	LANVMMGPYR		vinculin [Mus musculus]	1151.569	21.85	0
6679687	LAPEYEAAATR		glucose regulated protein [Mus musculus]	1191.6046	45.08	0.932583808
31981562	LAPITSDPTEAAAVGAVEASFK		pyruvate kinase 3 [Mus musculus]	2145.1077	104.19	2.792808959
6755809	LAQAAQSSVATITR		talin 1 [Mus musculus]	1416.7837	25.89	2.732768584
19527018	LAQDFLDSQNLSAYNTR		dipeptidylpeptidase III [Mus musculus]	1955.9498	19.19	0.922713908
18079351	LAQDPFPLYPGELLEK		major vault protein [Mus musculus]	1829.9683	35.54	1.136816162
41322904	LAQGHTTVAELTQR		plectin 1 isoform 1 [Mus musculus]	1524.8202	30.75	0.627609285
51770896	LAQSNGWGVMVSHR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1541.7667	34.3	1.364933841
51770896	LAQSNGWGVMVSHR	Deamidation (NQ)	PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1542.7671	65.18	1.303173387
11230802	LASDLLEWIR		actinin alpha 4 [Mus musculus]	1215.6747	65.06	0.826812415
10946574	LAVEALSSLDGDLSGR		creatine kinase, brain [Mus musculus]	1602.8406	92.23	0
63650229	LAVNMVPFPR		PREDICTED: similar to TUBULIN BETA CHAIN (T BETA-15) [Mus musculus]	1143.6293	42.2	0.947684509
22165384	LAVNMVPFPR		tubulin, beta, 2 [Mus musculus]	1143.6293	42.2	0.947684509
33859488	LAVNMVPFPR		tubulin, beta 2 [Mus musculus]	1143.6293	42.2	0.947684509

12963615	LAVNMVPFPR		tubulin, beta 3 [Mus musculus]	1143.6293	42.2	0.947684509
31981939	LAVNMVPFPR		tubulin, beta 4 [Mus musculus]	1143.6293	42.2	0.947684509
7106439	LAVNMVPFPR		tubulin, beta 5 [Mus musculus]	1143.6293	42.2	0.947684509
27754056	LAVNMVPFPR		tubulin, beta 6 [Mus musculus]	1143.6293	42.2	0.947684509
56090513	LCAEVPTR		hypothetical protein LOC434285 [Mus musculus]	888.4442	21.27	0
6671507	LCYVALDFENEMATAASSSSLEK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2479.1753	21.6	0.227317214
6671507	LCYVALDFENEMATAASSSSLEK	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2480.1479	51.91	0
6671509	LCYVALDFEQEMATAASSSSLEK		actin, beta, cytoplasmic [Mus musculus]	2493.1777	27.88	0
63652452	LCYVALDFEQEMATAASSSSLEK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2493.1777	27.88	0
6671509	LCYVALDFEQEMATAASSSSLEK	Deamidation (NQ)	actin, beta, cytoplasmic [Mus musculus]	2494.1704	40.74	0
63652452	LCYVALDFEQEMATAASSSSLEK	Deamidation (NQ)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2494.1704	40.74	0
7305295	LDAFLVLEQLR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1316.7654	69.06	0.251821797
30794450	LDELYGTWR		ribosomal protein L4 [Mus musculus]	1152.5707	22.3	1.052946081
31981562	LDIDSAPITAR		pyruvate kinase 3 [Mus musculus]	1171.6311	55.17	0
6677819	LDILDTAGQEEFGAMR		Harvey rat sarcoma oncogene, subgroup R [Mus musculus]	1765.8508	52.68	0
54607112	LDLGSNEFTEVPEVLEQLSGLR		Erbb2 interacting protein isoform 2 [Mus musculus]	2445.2334	19.02	0
22779912	LDLMDAGTDAMDVLMGR		dynamin 1-like [Mus musculus]	1823.8621	35.14	0
6678359	LDNLVAIFDINR		transketolase [Mus musculus]	1402.7732	95.72	1.382712485
33859686	LDQETAQWLR		phosphoglucomutase 1 [Mus musculus]	1259.6484	22.09	1.464068096
30023842	LDQLIYIPLPDEK		valosin containing protein [Mus musculus]	1556.8501	49.3	2.033145058
6754482	LEAEIATYR		keratin complex 1, acidic, gene 18 [Mus musculus]	1065.5581	27.17	1.707599297
13624315	LEAELGNMQGLVEDFK		keratin complex 2, basic, gene 8 [Mus musculus]	1792.8859	88.12	1.698009511
63565108	LEAELGNMQGLVEDFK		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1792.8859	88.12	1.698009511
18079339	LEAPDADELPR		aconitase 2, mitochondrial [Mus musculus]	1225.6028	26.93	0
6755817	LEDKDDLDVTELSNEELLDQLVR		thymopoietin [Mus musculus]	2701.3096	84.76	1.164418932
6679261	LEEGPPVTTVLTR		pyruvate dehydrogenase E1 alpha 1 [Mus musculus]	1411.7842	22.99	1.03638696
7305295	LEGDASDFHEQIADLQAQIAELK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2541.2498	76.33	0
55742711	LEGHGLPTNLPR		EH-domain containing 2 [Mus musculus]	1303.7104	33.78	0.779121181
13624315	LEGLTDEINFLR		keratin complex 2, basic, gene 8 [Mus musculus]	1419.7576	73.17	1.380227042
63565108	LEGLTDEINFLR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1419.7576	73.17	1.380227042
55742711	LEISDEFSEAIGALR		EH-domain containing 2 [Mus musculus]	1649.8401	79.84	0.898946798
6680748	LELAQYR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	892.4811	24.92	1.098372846
51711855	LENVSVALEFLER		PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like prot	1518.8217	51.66	0.923226419
21592285	LEQEIATYR		keratin 20 [Mus musculus]	1122.5808	37.26	1.476098617
7106335	LEQEIATYR		keratin complex 1, acidic, gene 17 [Mus musculus]	1122.5808	37.26	1.476098617
6680606	LEQEIATYR		keratin complex 1, acidic, gene 19 [Mus musculus]	1122.5808	37.26	1.476098617
547751	LEQEIATYR		Keratin, type I cytoskeletal 17 (Cytokeratin 17) (K17) (CK 17) (39.1)	1122.5808	37.26	1.476098617
417200	LEQEIATYR		Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1122.5808	37.26	1.476098617
63517295	LEQVSSDEGIGTLAENLLEALR		PREDICTED: RIKEN cDNA 1810009A16 [Mus musculus]	2357.2019	23.26	1.377066248
21704156	LEQYTNAIEGTK		caldesmon 1 [Mus musculus]	1366.6869	47.31	0
13624315	LESGMQNMSIHTK		keratin complex 2, basic, gene 8 [Mus musculus]	1475.7079	72.65	1.650822567
63565108	LEVDPNIQAVR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1253.7021	46.8	1.539362028
6753262	LEVEANNAFDQYR		capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1568.7404	41.05	0
7305295	LEVQLQDLQSK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1300.6924	64.98	0
7305173	LFDQAFGVPR		heat shock protein 1 [Mus musculus]	1149.6029	58.92	0.355787626
55742711	LFELEEQDLFR		EH-domain containing 2 [Mus musculus]	1438.719	73.88	0.556058262
31559916	LFIGGLSFETTDDSLR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1770.8922	125.08	1.441372522
7949053	LFIGGLSFETTEESLR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1798.9221	56.45	1.442347627
38198665	LGAAPEEESAYVAGER		p47 protein [Mus musculus]	1648.7878	37.76	2.3595537
21592285	LGAAPSVYGGAGGHGTR		keratin 20 [Mus musculus]	1527.7792	29.27	0.8840977
54607098	LGANSLLDLVVFGR		succinate dehydrogenase Fp subunit [Mus musculus]	1473.85	96	1.034661351
30725863	LGDAVEQGVINNSVLGYFIGR		glycyl-tRNA synthetase [Mus musculus]	2221.1614	20.58	2.015247781
31982755	LGDLYEEEMR		vimentin [Mus musculus]	1254.5687	36.83	0.758216295
6679291	LGDVYVNDAFGTAHR		phosphoglycerate kinase 1 [Mus musculus]	1634.7938	91.85	2.252070148
136429	LGEHNIDVLEGNEQFINAAK		Trypsin precursor	2211.1301	120.92	0
6671571	LGEIVTTIPTIGFNVETVEYK		ADP-ribosylation factor 2 [Mus musculus]	2323.2598	109.85	1.583899646
10181184	LGELPSWIMMR		ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 [Mus musculus]	1332.6849	30.34	1.061876818
33859506	LGEYGFQNAILVR		albumin 1 [Mus musculus]	1479.7976	44.93	3.118937632
6755714	LGFQVWLK		transgelin [Mus musculus]	990.5727	23.19	0.306286712
10946574	LGFSEVELVQMVVDGVK		creatine kinase, brain [Mus musculus]	1848.9772	67.82	0.38816225

33859514	LGGNYGPTVAVQR		branched chain aminotransferase 2, mitochondrial [Mus musculus]	1331.7085	19.06	0.902956322
6754084	LGLDFPNLPYLIDGSHK		glutathione S-transferase, mu 1 [Mus musculus]	1898.9993	46.3	3.08074437
40556608	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR		heat shock protein 1, beta [Mus musculus]	3535.6187	115.94	
6677811	LGMPQFLSTEAQSLLR		ribosomal protein S6 kinase polypeptide 1 [Mus musculus]	1790.9427	21.29	1.753119421
6678359	LGQSDPAPLQHQVDIYQK		transketolase [Mus musculus]	2037.0498	57.19	1.466021721
25020120	LGSQATGVQGQAGQLLDTTESTLGR		PREDICTED: laminin, alpha 5 [Mus musculus]	2488.272	78.32	0
31560611	LGTDQPLDQATISLQMGTNK		calponin 1 [Mus musculus]	2131.0776	103.42	0.229986946
31560611	LGTDQPLDQATISLQMGTNK	Oxidation (M)	calponin 1 [Mus musculus]	2147.0652	78.19	0
6753428	LGYILTCPSNLGTGLR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	1677.8993	31.49	6.6679941
63746482	LIALLEVLSQK		PREDICTED: filamin, alpha [Mus musculus]	1226.7675	66.52	0.370022341
63660294	LIALLEVLSQK		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	1226.7675	66.52	0.370022341
51711855	LIALLEVLSQK		PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like prot	1226.7675	66.52	0.370022341
19745150	LIDKEVISPDTR		diaphorase 1 [Mus musculus]	1385.7611	25.95	3.425408642
6755901	LIGQIVSSITASLR		tubulin, alpha 1 [Mus musculus]	1457.8729	70.45	0.538486545
33238874	LIIGQNGILSTPAVSCIIR		phosphoglucomutase 5 [Mus musculus]	1968.1276	21.87	0.447455738
6678573	LIIQWNGPESNR		villin 1 [Mus musculus]	1426.7524	48.91	1.309553062
22164798	LILPGLISSR		selenium binding protein 1 [Mus musculus]	1068.6774	46.78	1.374956296
58037546	LILPYVELDLHSYDLGIENR		isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	2372.2205	30.21	1.448463136
34740335	LISQIVSSITASLR		tubulin, alpha 2 [Mus musculus]	1487.8868	81.27	1.661829912
6678467	LISQIVSSITASLR		tubulin, alpha 4 [Mus musculus]	1487.8868	81.27	1.661829912
6678469	LISQIVSSITASLR		tubulin, alpha 6 [Mus musculus]	1487.8868	81.27	1.661829912
6679937	LISWYDNEYGYSNR		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1779.8079	87.87	1.164091815
6680748	LKEIVTNFLAGFEP		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1577.8574	122.99	1.174067198
7305295	LKEVLLQVEDER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1470.8221	37.07	0.422556035
13624315	LKLEAELGNMQGLVEDFK		keratin complex 2, basic, gene 8 [Mus musculus]	2034.0591	87.46	1.971985551
63565108	LKLEAELGNMQGLVEDFK		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	2034.0591	87.46	1.971985551
13624315	LKLEAELGNMQGLVEDFK	Deamidation (NQ)	keratin complex 2, basic, gene 8 [Mus musculus]	2035.0619	37.65	1.782822564
63565108	LKLEAELGNMQGLVEDFK	Deamidation (NQ)	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	2035.0619	37.65	1.782822564
27370092	LLDAVDTYIPVPTR		Tu translation elongation factor, mitochondrial [Mus musculus]	1572.8615	51.5	1.334033403
55742711	LLEALDDMLAQDIAK	Deamidation (NQ)	EH-domain containing 2 [Mus musculus]	1659.8743	48.01	14.97462594
6753066	LLETEEEAAFPLGGATPR		amine oxidase, copper containing 3 [Mus musculus]	1900.9681	79.04	0
31981017	LLHTQYHAVEKPSSGLSIR	Deamidation (NQ)	nuclear prelamin A recognition factor-like [Mus musculus]	2137.1174	19.29	1.532806529
10946574	LLIEMEQR		creatine kinase, brain [Mus musculus]	1031.5507	42.19	0.173534361
20874851	LLLPGELAK		PREDICTED: similar to histone H2b-616 [Mus musculus]	953.5967	48.73	1.482144184
51491845	LLLPWLEAR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1110.6682	26.62	1.756751711
63556656	LLNPQGAIR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	981.5788	34.27	3.122316868
6680960	LLPETPSDPFAIWQITDR		procollagen, type XII, alpha 1 [Mus musculus]	2099.0776	43.33	0.832167807
31981690	LLQDFFNGK		heat shock protein 8 [Mus musculus]	1081.5574	51.47	1.967465466
31982755	LLQDSVDFSLADAINTEFK		vimentin [Mus musculus]	2126.0542	47.18	0
24418919	LLSLVDDEAFIR		brain glycogen phosphorylase [Mus musculus]	1390.7566	59.04	0.774005143
63562740	LLTSAAFEDCQTR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1454.7037	24.71	0.795293078
33859650	LLVPLVPDLQDVAQLR		membrane bound C2 domain containing protein [Mus musculus]	1789.0643	20.91	1.985629546
17647499	LLVVYPWTQR		hemoglobin, beta adult minor chain [Mus musculus]	1274.7336	21.84	0
31981826	LLYDLADQLHAAVGASR		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1812.9611	36.1	0.653488812
51491845	LLYNNVSNFGR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1296.6648	38.91	1.464112766
7657429	LLYPADIPVGNDQLLELLNK		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2238.24	51.43	1.213404348
29336026	LMATLSNTNPSFVR		nonmuscle myosin heavy chain [Mus musculus]	1550.7988	19.05	0
33859482	LMEPIYLVEIQCPEQVVGGIYGVLNR		eukaryotic translation elongation factor 2 [Mus musculus]	2932.5344	25.7	1.937460572
31560689	LMFNDFLSSSSDK		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	1490.6899	74.84	0
59709449	LMLLLEVISGER		actinin alpha 2 [Mus musculus]	1372.7852	39.92	0.777776365
7304855	LMLLLEVISGER		actinin alpha 3 [Mus musculus]	1372.7852	39.92	0.777776365
11230802	LMLLLEVISGER		actinin alpha 4 [Mus musculus]	1372.7852	39.92	0.777776365
6755809	LNEAAAGLNQAATELVQASR		talin 1 [Mus musculus]	2027.0574	67.64	0.618386652
27370516	LNEHFLNTTDFLDTIK		isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	1920.9847	26.79	0.119002585
6679687	LNFAVASR		glucose regulated protein [Mus musculus]	877.4815	40.84	1.049663143
63492583	LNGTDPEDVIR		PREDICTED: myosin regulatory light polypeptide 9 [Mus musculus]	1228.6191	21.32	0.974982232
45387933	LNIQPSETDYAVDIR		UDP-glucose ceramide glucosyltransferase-like 1 [Mus musculus]	1733.8671	22.35	1.45839325
6679030	LNITPNSGATGNNAGPK		N-myc downstream regulated-like [Mus musculus]	1625.7991	67.92	1.695330882
63476037	LNLLDLDYELAEQLDNIAEK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2332.2002	94.47	0
6677819	LNVDEAFEQLVR		Harvey rat sarcoma oncogene, subgroup R [Mus musculus]	1432.7382	21.64	0

9790017	LNWLSVDFNNWK		telomerase binding protein, p23 [Mus musculus]	1535.7838	36.29	0.622355085
33859811	LPAKPEVSSDEDVQYR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1832.9121	88.02	0.97338481
33859506	LPCVEDYLSAILNR		albumin 1 [Mus musculus]	1605.834	61.81	2.45865446
31982472	LPIGDVATQYFADR		chaperonin subunit 7 (eta) [Mus musculus]	1565.7986	46.38	1.963976342
51873060	LPLQDVYK		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	975.5461	45.87	1.303990029
22267442	LPNGLVIASLENYAPLSR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1927.0717	36.61	1.018331717
63746482	LPQLPITNFSR		PREDICTED: filamin, alpha [Mus musculus]	1285.7256	82.81	0
63738313	LPSGSGPASPTTGSAVDIR		PREDICTED: similar to AHNAK [Mus musculus]	1769.8989	29.64	1.33341031
41322904	LPVDVAYQR		plectin 1 isoform 1 [Mus musculus]	1060.571	20.33	1.0248514
31560689	LPWDAVGR		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	913.4813	31.8	1.086199661
27370126	LPYTEEEEQLSR		carboxylesterase 5 [Mus musculus]	1493.7209	30.84	1.690443095
13624315	LQAEIEALK		keratin complex 2, basic, gene 8 [Mus musculus]	1014.5734	25.17	2.665831979
31982755	LQDEIQNMKEEMAR		vimentin [Mus musculus]	1734.8096	63.36	1.097649542
7305295	LQDFASTIEVMEEGK	Deamidation (NQ)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1697.8164	33.39	0
7305295	LQDFASTIEVMEEGK	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1712.7982	36.18	0.412197787
7305295	LQDFASTIEVMEEGKK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1824.8787	33.75	0
33563250	LQEEIQLR		desmin [Mus musculus]	1028.5802	35.53	0
6678573	LQEENQVITPR		villin 1 [Mus musculus]	1326.7102	58.52	1.451609838
50355692	LQEKEDLQELNDR		lamin A isoform A [Mus musculus]	1629.8109	49.41	1.03233907
8393988	LQEQLGNDVVEK		phosphomannomutase 2 [Mus musculus]	1371.7019	29.54	0
30525051	LQIWDTAGQESFR		RAB2B protein [Mus musculus]	1550.7689	35.54	0.719144443
10946940	LQIWDTAGQESFR		RAB2, member RAS oncogene family [Mus musculus]	1550.7689	35.54	0.719144443
21450625	LQMEAPHIIVGTPGR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1618.8732	24.81	1.791958247
7305295	LQNEVESVTGMLNEAEGK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1947.9419	114.89	0
38089265	LQNTGVADGYPVR		PREDICTED: palladin [Mus musculus]	1389.7163	67.62	0
7305295	LQQELDDLVVDLDNQR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1912.9728	117.17	0.214721381
7305295	LQQELDDLVVDLDNQR	Deamidation (NQ)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1913.9636	26.12	0.618555224
19527026	LQQLPADFGR		hypothetical protein LOC98238 [Mus musculus]	1144.6124	40.84	6.164877909
63746482	LQVEPAVDTSGVQCYGPGIEGQGVFR		PREDICTED: filamin, alpha [Mus musculus]	2706.3132	114.52	0.22148791
63476037	LSDAGITPLFLTSQEDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1862.954	84.49	0.207669015
63489759	LSDDNTIGQEEIQQR		PREDICTED: spectrin alpha 2 [Mus musculus]	1745.8192	30.11	0.986970819
6754206	LSDEILIDILTR		hexokinase 1 [Mus musculus]	1400.8068	61.36	1.302670005
6671666	LSDLLAPISEQIQEVITFR		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	2172.1946	98.49	1.694906797
12963539	LSGAQADLHIGEGDSIR		ETHE1 protein [Mus musculus]	1738.8793	90.11	0.767505782
7948997	LSGGIDFNQPLVITR		PDZ and LIM domain 3 [Mus musculus]	1629.8921	71.59	0.336550285
27229048	LSGVSVSSDAFFPFR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1615.8129	34.18	1.53513634
6753484	LSIIATDHTYR		procollagen, type VI, alpha 1 [Mus musculus]	1289.6846	20.67	0
6679166	LSLLEELTLAENQLLR		osteoglycin [Mus musculus]	1855.0587	69.59	0.475612904
63641940	LSLQDAVNQGLIDQDMATR		PREDICTED: desmoplakin [Mus musculus]	2088.0427	23.57	1.374820003
13384736	LSLSNAISTVLPLTQLR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1826.0623	22.74	0.918937109
11230802	LSNRPAFMPSEGR		actinin alpha 4 [Mus musculus]	1461.7257	22.4	0.591245463
6755967	LSQNNFALGYK		voltage-dependent anion channel 3 [Mus musculus]	1254.6476	57.36	1.445033976
33859506	LSQTFPNADFAEITK	Deamidation (NQ)	albumin 1 [Mus musculus]	1682.8452	22.7	0
6754556	LSSEMNTSTVNSAR		lamin B1 [Mus musculus]	1496.7081	25.94	1.810494926
136429	LSSPATLNSR		Trypsin precursor	1045.5658	53.68	0
6680606	LSVEADINGLR		keratin complex 1, acidic, gene 19 [Mus musculus]	1186.6459	54.97	1.38764294
547751	LSVEADINGLR		Keratin, type I cytoskeletal 17 (Cytokeratin 17) (K17) (CK 17) (39.1)	1186.6459	54.97	1.38764294
51491845	LTDQLPLIIVCDR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1498.8043	37.55	1.164828623
6755863	LTESPCALVASQYGWSGNMER		tumor rejection antigen gp96 [Mus musculus]	2299.0615	35.64	1.142198022
29789191	LTESVDVLMPNVGEIVGGSMR		asparaginyl-tRNA synthetase [Mus musculus]	2203.1218	30.42	1.138718029
6755963	LTFDSSFSPNTGK		voltage-dependent anion channel 1 [Mus musculus]	1400.6681	65.69	1.042326758
6755965	LTFDTTFSPNTGK		voltage-dependent anion channel 2 [Mus musculus]	1428.6987	21.51	0
51765915	LTLIDPETLLPR		PREDICTED: TBP-interacting protein [Mus musculus]	1380.8041	38.74	0.694828528
63476037	LTLLGGPTPNTGAALEFVLR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2040.1495	53.89	0.191227246
63501125	LTQQAGDLTVPAGGQR		PREDICTED: ADP-ribosylation factor interacting protein 1 [Mus musculus]	1611.8563	43.2	1.41184479
46575903	LTSLVPFVDAFQLER		eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus musculus]	1734.9425	35.42	1.58780253
22165384	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta, 2 [Mus musculus]	2651.3203	88.12	1.017281544
33859488	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta 2 [Mus musculus]	2651.3203	88.12	1.017281544
31981939	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta 4 [Mus musculus]	2651.3203	88.12	1.017281544
7106439	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta 5 [Mus musculus]	2651.3203	88.12	1.017281544

51556274	LVAGEMGQNEPDQGGQR		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	1785.8291	56.15	1.369783723
13385472	LVAIVDVIDQNR		ribosomal protein L14 [Mus musculus]	1354.7684	55.25	1.6264073
6755714	LVEWIVVQCGPDVGRPDR		transgelin [Mus musculus]	2038.0461	28.39	0
6754524	LVIITAGAR		lactate dehydrogenase 1, A chain [Mus musculus]	913.5762	32.39	1.477053597
6679937	LVINGKPITIFQER		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1627.9432	58.12	1.057806147
6679937	LVINGKPITIFQER	Deamidation (NQ)	similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1628.9321	22.97	1.610274551
6679805	LVIPSELGYGER		FK506 binding protein 2 [Mus musculus]	1332.7218	25.54	0
31980648	LVLEVAQHLGESTVR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1650.926	71.8	0.938512808
6755714	LVNSLYPEGSKPVK		transgelin [Mus musculus]	1530.8588	56.26	0.214411538
63518159	LVPLLDTGDIIIDGGNSEYR		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	2160.1135	61.44	1.748436942
31543942	LVQAAQMLQSDPYSVPAR		vinculin [Mus musculus]	1974.0071	50.64	0.58372608
6754976	LVQAFQFTDK		peroxiredoxin 1 [Mus musculus]	1196.624	41.25	1.672540833
31981679	LVQDVANNTNEEAGDGTTTATVLAR		heat shock protein 1 (chaperonin) [Mus musculus]	2560.252	147.1	1.296625882
33859506	LVQEVTDFAK		albumin 1 [Mus musculus]	1149.6102	42.13	3.090840526
24418919	LVTSIGDVVNHDPVVGDR		brain glycogen phosphorylase [Mus musculus]	1891.9867	37.25	0
6680047	LWDLTTGTTTR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1264.6478	64.71	1.220900509
31560517	LWTLVSEQTR		ribosomal protein L27a [Mus musculus]	1232.6614	23.75	1.622281214
6753010	LYAYEPSDTALLYDNMK		anterior gradient 2 [Mus musculus]	2006.9382	96.01	0.421710993
6753304	LYGPSSVSFADDFVR		serine (or cysteine) proteinase inhibitor, clade H, member 1 [Mus musculus]	1659.8036	106.13	1.169619559
31981722	LYGSGGPPPTGEEDTSEKDEL		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	2177.9937	68.23	1.052537999
6753266	LYPIANGNNQSPIDIK		carbonic anhydrase 1 [Mus musculus]	1756.926	89.57	0
6753266	LYPIANGNNQSPIDIK	Deamidation (NQ)	carbonic anhydrase 1 [Mus musculus]	1757.9132	78.64	0
6753428	LYPPSAEYPDLR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	1420.7179	36.15	4.973001392
31542333	LYQPEYQEVSTEEQR		hypoxia up-regulated 1 [Mus musculus]	1898.8834	75.24	0.999116956
16716589	LYTLVTYVPVTTFK		ribosomal protein L31 [Mus musculus]	1644.9158	50.32	1.966019058
33563250	MALDVEIATYR		desmin [Mus musculus]	1281.6512	60.66	0
34610207	MALELLTQEFGIPVER		alanyl-tRNA synthetase [Mus musculus]	1845.9834	28.94	0
7305295	MAQQMLDLEEQLEEEEAAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2263.0425	46.39	0.199761282
7305295	MAQQMLDLEEQLEEEEAAR	2 Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2295.0374	29.2	0
7305295	MAQQMLDLEEQLEEEEAAR	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2279.0281	67.64	0.352039864
18079351	MAVFGFEMSEDAGPDGALLPR		major vault protein [Mus musculus]	2210.0452	24.01	0
6679687	MDATANDVPSPYEVK		glucose regulated protein [Mus musculus]	1636.7621	52.39	1.285822807
63746482	MDCQECPEGYR		PREDICTED: filamin, alpha [Mus musculus]	1330.4949	44.15	0
7305505	MEPDPAEPPSTTVEAANGAEQAR		smoothelin [Mus musculus]	2368.0881	88.27	1.843019336
21450625	MFVLDEADEMLSR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1555.7192	72.02	1.980966748
7305019	MFVLDEADEMLSR		eukaryotic translation initiation factor 4A2 [Mus musculus]	1555.7192	72.02	1.980966748
25020120	MGQGSPGDALVPSGEQLR		PREDICTED: laminin, alpha 5 [Mus musculus]	1798.877	33.84	0
25020120	MGQGSPGDALVPSGEQLR	Deamidation (NQ)	PREDICTED: laminin, alpha 5 [Mus musculus]	1799.8636	35.5	2.116355252
31980685	MIEQDDFDINTR		glucosamine [Mus musculus]	1496.6755	21.07	2.03961094
21704206	MIPAVVDGEFFPR		carboxylesterase 2 [Mus musculus]	1477.7484	25.73	0.697188857
29336026	MIQALELDPNLYR		nonmuscle myosin heavy chain [Mus musculus]	1575.8204	26.93	1.18064725
6671571	MLAEDELR		ADP-ribosylation factor 2 [Mus musculus]	976.4744	30.18	1.527064176
11230802	MLDAEDIVNTARPDEK		actinin alpha 4 [Mus musculus]	1816.8718	19.32	1.359802562
6681157	MLDMGFEPQIR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1336.6403	38.14	1.925082349
6753620	MLDMGFEPQIR		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1336.6403	38.14	1.925082349
7305505	MLDQTTNFEER		smoothelin [Mus musculus]	1383.6282	57.74	0.733048113
6679891	MLDYLQGSGETPQTDIR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1923.9143	68.11	1.368045318
10092608	MLLADQGQSWK		glutathione S-transferase, pi 1 [Mus musculus]	1276.6339	37.72	0
6753320	MLLDPMGGIVMTNDGNAILR		chaperonin subunit 3 (gamma) [Mus musculus]	2131.0715	47.98	0.911630552
31982290	MLYDMENPPADDYFGR		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1933.8207	81.07	0
6996911	MPEFYNR		argininosuccinate synthetase [Mus musculus]	956.4271	29.61	0.747259715
6679465	MPPYDEETQAIIDAAQEAR		protein kinase C substrate 80K-H [Mus musculus]	2147.9929	36.61	1.398906399
6678359	MPTPPSYK		transketolase [Mus musculus]	920.4485	47.87	1.384443844
8394269	MQQFDDLFR		ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltra	1199.5574	33.34	2.130145099
20137006	MQQNIQELEEQLEEEESAR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2333.0627	107.53	2.051918218
50355692	MQQQLDEYQELLDIK		lamin A isoform A [Mus musculus]	1893.9363	82.35	1.275531652
50355692	MQQQLDEYQELLDIK	Deamidation (NQ)	lamin A isoform A [Mus musculus]	1894.9323	45.58	0
64427157	MQSSVSESSFQMGR		PREDICTED: synaptopodin 2 [Mus musculus]	1560.6898	39.93	0
22165384	MSATFIGNSTAIQELFK		tubulin, beta, 2 [Mus musculus]	1857.9504	108.3	1.146485908
33859488	MSATFIGNSTAIQELFK		tubulin, beta 2 [Mus musculus]	1857.9504	108.3	1.146485908

31560689	MSPEEFTEIMNQR		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	1611.7097	56.78	0.375417304
6679108	MSVQPTVSLGGFEITPPVVLR		nucleophosmin 1 [Mus musculus]	2227.2112	34.14	1.401230456
6679108	MTDQEAIQDLWQWR		nucleophosmin 1 [Mus musculus]	1819.8579	46.42	1.58116895
56119103	MTGSEFDFEEMKR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1606.7015	29.57	1.791111891
6678573	MVDDGSGEVQVWR		villin 1 [Mus musculus]	1477.6813	65.58	1.609296127
6755809	MVGGIAQIIAAQEEMLR		talin 1 [Mus musculus]	1829.9641	65.67	0.540563251
33859811	MVGVPAAFDMMLTGR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1595.7827	49.51	1.413379833
63600542	MWEIQNFSAIQK	3 Deamidation (NQ)	PREDICTED: similar to guanylate-binding protein 5 [Mus musculus]	1497.7046	20.92	0
8393144	MYDSVLALPGALQATR		claudin 7 [Mus musculus]	1705.8947	34.07	1.688017005
13384828	MYGADLAPVDFLHASEDAR		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	2077.9724	87.97	1.701704619
51766008	MYQAVLDATQR		PREDICTED: myosin IA [Mus musculus]	1295.6384	23.47	0
13937355	MYSYVTEELPQLINANFPVDPQR		esterase D/formylglutathione hydrolase [Mus musculus]	2724.3101	27.52	1.145198184
63476037	NAGPEFQYIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1194.5917	54.27	0.281465312
22267442	NALANPLYCPDYR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1509.7212	35.27	0.729253874
63476037	NANPSELEQIVLSPAFILAAESLPK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2651.4146	95.55	0
30023842	NAPAIIFIDELDAIAPK		valosin containing protein [Mus musculus]	1810.9962	89.97	1.05404618
21313162	NATNVEQAFMTMAAEIK		RAB1B, member RAS oncogene family [Mus musculus]	1868.8927	63.47	0
6679587	NATNVEQSFMTMAAEIK		RAB1, member RAS oncogene family [Mus musculus]	1884.895	51.84	1.013861157
6679587	NATNVEQSFMTMAAEIK	Deamidation (NQ)	RAB1, member RAS oncogene family [Mus musculus]	1885.8981	42.35	0.424808914
31982275	NAVEEYVYEMR		heat shock protein 4 [Mus musculus]	1402.6324	29.72	0
6754256	NAVITVPAYFNDSQR		heat shock protein 9A [Mus musculus]	1694.8517	75.05	1.169575252
18079339	NAVTQEFGPVPDTAR		aconitase 2, mitochondrial [Mus musculus]	1601.8119	45.15	0.987421397
6677813	NCIVLIDSTPYR		ribosomal protein S8 [Mus musculus]	1393.7097	47.74	5.52286837
63737134	NCVHVATVMDRFR	Deamidation (NQ)	PREDICTED: similar to family with sequence similarity 26, member A [Mus musculus]	1548.7673	21.32	0
31712036	NDFQLIGIQDGYLSLLQDSGEVR		eukaryotic translation initiation factor 5A [Mus musculus]	2580.2869	42.92	1.488953722
9790067	NDISSHPPVEGSYAPR		staphylococcal nuclease domain containing 1 [Mus musculus]	1725.8265	34.88	2.543752803
33667042	NDQDTWDYTNPNLSGQGDPGSNPNKR		heterogeneous nuclear ribonucleoprotein L [Mus musculus]	2890.2598	68.31	1.225304729
9790247	NDVFDSLGISPDLLPDDFVR		ubiquitin-like 1 (sentrin) activating enzyme subunit 1 [Mus musculus]	2234.0996	57.55	1.740514483
21313536	NDVITVQTPAFAESVTEGDVR		dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]	2248.0935	39.97	0.935160389
6755929	NEAIQAAHDSVAQKGQCR	Deamidation (NQ)	ubiquitin carboxy-terminal hydrolase L1 [Mus musculus]	1926.8867	29.91	0.512888421
6678483	NEEDATELVGLAQAVNAR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1899.943	106.05	1.256040058
6671684	NEGVATYAAAVLFR		catenin beta [Mus musculus]	1481.7728	56.65	1.955417464
13384720	NFDFEDVFVNIPR		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Mus musculus]	1611.7877	43.77	1.587682049
34996495	NFESLSEAFSVASAAAALSQNR		ribophorin II [Mus musculus]	2270.1138	68.31	0.789333778
7305443	NFGIGQDIQPK		ribosomal protein L7a [Mus musculus]	1216.6272	41.5	0
7949051	NFILDQTNVSAAAQR		heterogenous nuclear ribonucleoprotein U [Mus musculus]	1647.8558	69.44	1.432960545
7949051	NFILDQTNVSAAAQR	Deamidation (NQ)	heterogenous nuclear ribonucleoprotein U [Mus musculus]	1648.8439	43.49	1.440017824
20137006	NFINNPLAQADWAAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1672.8231	39.21	0
20137006	NFINNPLAQADWAAK	Deamidation (NQ)	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1673.8425	29.39	2.087114295
51556274	NFLASQVPFPSR		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	1362.7175	30.63	0.870249838
33859490	NFLTEDSADLDSIEAVANEVLK		laminin B1 subunit 1 [Mus musculus]	2393.1724	54.93	0
7305295	NFMNSPMAQADWVAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1709.785	69.27	0
22203747	NFVINVVNR		procollagen, type VI, alpha 2 [Mus musculus]	1074.5999	35.01	0.254345934
6681157	NFYQEHPDLAR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1389.6577	22.33	2.431693472
6755302	NGDGFVSLEEFLGDYR		reticulocalbin 2 [Mus musculus]	1817.8691	20.44	0.791220909
34328108	NGDRGETGPAGPAGPIGPAGAR		procollagen, type I, alpha 1 [Mus musculus]	1974.9835	66.85	0
6678483	NGFLNLALPFFGFSEPLAAPR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	2278.1909	24.42	0
63487095	NGNGGPGPYVGQAGTATLPR		PREDICTED: catenin src [Mus musculus]	1883.9423	58.87	0
63746482	NGQHVASSPIPVVISQSEIGDASR		PREDICTED: filamin, alpha [Mus musculus]	2448.2527	27.45	0
20806532	NGYGFINR		cold shock domain protein A short isoform [Mus musculus]	940.4583	34.51	1.955683844
6756033	NGYGFINR		nuclease sensitive element binding protein 1 [Mus musculus]	940.4583	34.51	1.955683844
27229204	NIIDPTFR		chitobiase, di-N-acetyl- [Mus musculus]	975.5234	26.66	1.398950995
31560611	NIIGLQMGTNK		calponin 1 [Mus musculus]	1188.6333	75.11	0
31560611	NIIGLQMGTNK	Oxidation (M)	calponin 1 [Mus musculus]	1204.6218	29.66	0
31543605	NIQVDSPYDISR		ribophorin I [Mus musculus]	1406.6967	37.05	0.880348922
33563250	NISEAEEWYK		desmin [Mus musculus]	1268.5781	67.33	0
34996495	NIVEEIEDLVAR		ribophorin II [Mus musculus]	1399.7494	67.71	1.205903213
21704100	NIVVVEGVR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	984.5803	28.98	2.909031396
33620739	NKDQGTYEDYVEGLR		myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Mus musculus]	1786.8185	24.29	0
6755901	NLDIERPTYTNLNR		tubulin, alpha 1 [Mus musculus]	1718.8997	48.01	0.983199804

34740335	NLDIERPTYTNLNR		tubulin, alpha 2 [Mus musculus]	1718.8997	48.01	0.983199804
6678467	NLDIERPTYTNLNR		tubulin, alpha 4 [Mus musculus]	1718.8997	48.01	0.983199804
6678469	NLDIERPTYTNLNR		tubulin, alpha 6 [Mus musculus]	1718.8997	48.01	0.983199804
6678499	NLFFSTNIDDAIR		UDP-glucose dehydrogenase [Mus musculus]	1525.7671	57.43	0.478990383
40254595	NLHQSGFSLSGAQIDDNIPR		dihydropyrimidinase-like 2 [Mus musculus]	2169.0645	43.67	0.464263957
20137006	NLPIYSEEIVEMYK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1727.8451	54.42	1.515655959
12963531	NLPQYVSNELLEEAFSVFGQVER		non-POU-domain-containing, octamer binding protein [Mus musculus]	2668.3149	40.82	1.642714888
31982755	NLQEAEEWYK		vimentin [Mus musculus]	1309.6183	31.67	0
6678365	NLQYYDISAK		RAN, member RAS oncogene family [Mus musculus]	1214.618	30.97	1.977173476
23956214	NLSPYVSNELLEEAFSQFGPIER		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	2639.3054	34.78	1.830639861
6678359	NMAEQIIQEIYSQVQSK		transketolase [Mus musculus]	2009.0073	81.11	2.810881253
29336026	NMDPLNDNVAALLHQSTDR		nonmuscle myosin heavy chain [Mus musculus]	2124.0298	26.89	0.778320393
7305295	NMDPLNDNVTSLLNASSDK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2047.9559	102.35	0.298627875
7305295	NMDPLNDNVTSLLNASSDK	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2063.9473	87.22	0
7949053	NMGGPYGGGNYGPGGSGGSGGYGGR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2189.9172	154.55	1.542492522
7949053	NMGGPYGGGNYGPGGSGGSGGYGGR	Oxidation (M)	heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2205.9036	20.87	1.421786468
21450277	NMVPQQALVIR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1268.7145	46.73	1.354926846
6678145	NNEDVSIIPPLFTVSVDHR		signal sequence receptor, delta [Mus musculus]	2152.1062	52.31	1.551327625
6678145	NNEDVSIIPPLFTVSVDHR	Deamidation (NQ)	signal sequence receptor, delta [Mus musculus]	2153.1077	35.33	0
6679599	NNIPYFETSAK		RAB7, member RAS oncogene family [Mus musculus]	1283.6298	30.44	1.47918128
51491845	NNLAGAEELFAR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1304.6661	58.85	1.497233377
22203747	NNYATMRPDSTEIDQDTINR		procollagen, type VI, alpha 2 [Mus musculus]	2354.075	51.26	0.273348158
22203747	NNYATMRPDSTEIDQDTINR	Deamidation (NQ)	procollagen, type VI, alpha 2 [Mus musculus]	2355.0664	64.07	0
22203747	NNYATMRPDSTEIDQDTINR	Oxidation (M)	procollagen, type VI, alpha 2 [Mus musculus]	2370.0723	23.68	0
63530525	NPAVLSAASFDGR		PREDICTED: SEC31-like 1 [Mus musculus]	1304.6631	34.81	1.39156083
6754254	NPDDITNEEYGEFYK		heat shock protein 1, alpha [Mus musculus]	1833.7954	105.01	1.291754214
40556608	NPDDITQEEYGEFYK		heat shock protein 1, beta [Mus musculus]	1847.8032	104.35	1.542881288
63518159	NPELQNLLLDDFFK		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1705.8832	58.23	1.637400105
8567402	NPPGFAFVEFEDPR		splicing factor, arginine/serine-rich 3 (SRp20) [Mus musculus]	1621.7761	45.44	1.705730211
46559834	NQALELEQLR		desmuslin isoform M [Mus musculus]	1213.6531	55.91	0.168200607
18875324	NQAPGQPGASQWGSR		DAZ associated protein 1 [Mus musculus]	1540.7279	28.35	1.350842524
33563270	NQGYYDYVKPR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1402.6827	29.16	1.116045142
547749	NQILNLTTDNANILLQIDNAR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	2367.2517	70.68	0
31981722	NQLTSNPENTVFDAK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1677.8168	85.58	0.865109508
6754482	NQNINLENSLGDVEAR		keratin complex 1, acidic, gene 18 [Mus musculus]	1785.8744	103.03	1.34630481
6754482	NQNINLENSLGDVEAR	3 Deamidation (NQ)	keratin complex 1, acidic, gene 18 [Mus musculus]	1788.8188	50.91	0
20149720	NQNLQEALQR	3 Deamidation (NQ)	oxidized low density lipoprotein (lectin-like) receptor 1 [Mus musculus]	1216.5865	24.03	0
31981690	NQVAMNPTNTVFDAK		heat shock protein 8 [Mus musculus]	1649.7949	79.94	0.933018656
63660799	NRCVLPNR	Deamidation (NQ)	PREDICTED: similar to Dual specificity protein phosphatase 13 (Testis- and skeletal-muscle-specific	972.49	19.98	0
21361250	NRLFQENSLLNSLPLNSLSR	5 Deamidation (NQ)	ATPase, H+ transporting, lysosomal accessory protein 2 [Mus musculus]	2320.1775	19.47	0
46849705	NSFMNGSWGAEER		lectin, galactose binding, soluble 4 [Mus musculus]	1484.6311	100.14	1.922969324
31542083	NSGSFSSPSISPR		mitochondrial tumor suppressor 1 isoform 2 [Mus musculus]	1322.6389	19.32	0
7305295	NSLQDQLDEEMEAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1649.7478	71.29	0.49954304
54020742	NSNILEDLETLR		archain 1 [Mus musculus]	1416.7368	45.27	1.511677877
50355692	NSNLVGAAHEELQQSR		lamin A isoform A [Mus musculus]	1752.8673	88.01	1.036119999
22165384	NSSYFVEWIPNNVK		tubulin, beta, 2 [Mus musculus]	1696.8463	41.23	0.334827824
33859488	NSSYFVEWIPNNVK		tubulin, beta 2 [Mus musculus]	1696.8463	41.23	0.334827824
12963615	NSSYFVEWIPNNVK		tubulin, beta 3 [Mus musculus]	1696.8463	41.23	0.334827824
31981939	NSSYFVEWIPNNVK		tubulin, beta 4 [Mus musculus]	1696.8463	41.23	0.334827824
7106439	NSSYFVEWIPNNVK		tubulin, beta 5 [Mus musculus]	1696.8463	41.23	0.334827824
27754056	NSSYFVEWIPNNVK		tubulin, beta 6 [Mus musculus]	1696.8463	41.23	0.334827824
31981562	NTGIICTIGPASR		pyruvate kinase 3 [Mus musculus]	1302.6801	27	1.014768825
46195798	NTLLIAGLQAR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1169.6924	38.18	0
33563270	NTNAGAPPGTAYQSPLSLSR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	2002.0035	37.51	0.926260194
33859560	NTNDANSCQIIIPQNQVNR		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	2142.0415	94.15	1.124881347
56119103	NTNDANSCQIIIPQNQVNR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	2142.0415	94.15	1.124881347
6754556	NTSEQDQPMGGWEMIR		lamin B1 [Mus musculus]	1878.823	53.6	1.209624262
18700004	NTTPDELLSAVLTAVLQDVR		acetyl-Coenzyme A acyltransferase 1 [Mus musculus]	2155.1602	29.8	1.283327662
8567336	NVAILIPESWK		chloride channel calcium activated 3 [Mus musculus]	1269.7167	38.7	2.20384122
6753364	NVFDEAILAALEPPEPK		cell division cycle 42 homolog [Mus musculus]	1852.9755	75.43	1.401118947

6678986	NVLDTSWPTPPPALR		myosin IC [Mus musculus]	1663.8625	25.35	0
547749	NVSTGDVNVEMNAAPGVDLTQLLNNMR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	2872.3884	50.74	0
6756033	NYQQNYQNSESGEKNEGSESAPEGQAQQR		nuclease sensitive element binding protein 1 [Mus musculus]	3257.3884	106.73	1.633682023
7949053	NYYEQWGK		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1087.4894	47.6	1.329937087
51771420	NYYGYQGYR		PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1183.5217	26.54	1.46850441
6671549	PGGLLLGDEAPNFEANTTIGR		peroxiredoxin 6 [Mus musculus]	2142.1096	35.47	2.922110611
16716467	PLELELCPGR		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1126.5891	24.81	1.637674622
6754084	PMILGYWNVR		glutathione S-transferase, mu 1 [Mus musculus]	1248.6559	19.17	0
21450277	QAADMILLDDNFASIVTGVEEGR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2464.2002	95.65	0
7305295	QADLEKEELAEELASSLSGR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2175.0828	129.09	0.300164455
7304881	QAFQIGSPWR		aldehyde dehydrogenase family 1, subfamily A1 [Mus musculus]	1189.6079	25.61	0.356277747
7106242	QAFQIGSPWR		aldehyde dehydrogenase family 1, subfamily A7 [Mus musculus]	1189.6079	25.61	0.356277747
6753294	QALQDLLSEYMGNAGR		catenin alpha 1 [Mus musculus]	1765.8821	20.07	1.325527009
20137006	QAQQERDELADEIANSSGK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2088.9983	19.59	0
27369806	QASLSQSIR	2 Deamidation (NQ)	rhomboid-like protein 6 [Mus musculus]	991.4896	30.65	0
6754256	QAVTNPNNTFYATK		heat shock protein 9A [Mus musculus]	1568.7754	29.4	1.067879602
63489754	QDEVNAAWQR		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1216.5748	35.16	2.238285489
6996913	QDIAFAYQR		annexin A2 [Mus musculus]	1111.5573	40.07	2.204983152
31791057	QDIAVISDSYFPR		laminin, gamma 1 [Mus musculus]	1510.7487	64.79	0.896875665
6754854	QDLGSPEGIALDHLGR		nidogen 1 [Mus musculus]	1677.8567	41.09	0
6671571	QDLPNAMNAAEITDK		ADP-ribosylation factor 2 [Mus musculus]	1630.7793	76.34	2.896322642
63487095	QDVYGPQPQVR		PREDICTED: catenin src [Mus musculus]	1286.6504	33.52	1.695266696
55742711	QEELESVEAGVQGGAFEGTR		EH-domain containing 2 [Mus musculus]	2092.9858	89.13	0
7305295	QELEEILHEMEAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1626.7874	79.25	0
21450129	QEQDTYALSSYTR		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	1561.7231	88	1.350985132
51770846	QEQLLSGRGSYPR	Deamidation (NQ)	PREDICTED: hypothetical protein XP_488848 [Mus musculus]	1491.749	28.64	0
6671507	QEYDEAGPSIVHR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1500.7261	73	0.624034859
6671507	QEYDEAGPSIVHR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1501.7206	20	0
6671509	QEYDESGPSIVHR		actin, beta, cytoplasmic [Mus musculus]	1516.7296	78.79	1.513661501
63694749	QEYDESGPSIVHR		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1516.7296	78.79	1.513661501
63476037	QFGVAPLTIAR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1172.6782	51.96	1.696338744
21450625	QFYINVER		eukaryotic translation initiation factor 4A1 [Mus musculus]	1068.5468	29.03	1.530462726
7305019	QFYINVER		eukaryotic translation initiation factor 4A2 [Mus musculus]	1068.5468	29.03	1.530462726
22164798	QFYPDLIR		selenium binding protein 1 [Mus musculus]	1051.5538	26.3	1.455118909
21450277	QGAIVAVTGDGVNDSPALK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1811.9327	25.63	0
7106451	QGIETPEDQNDLRK	Deamidation (NQ)	zinc finger protein 162 [Mus musculus]	1643.8099	43.69	0
6680748	QGQYSPMAIEEQVAVIYAGVR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2309.1626	96.18	1.06015141
9845299	QGTFHSQQALEYGTK		succinate-CoA ligase, GDP-forming, alpha subunit [Mus musculus]	1694.8237	58.44	0
51764087	QIFLGGVDR		PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	1004.5381	31.04	0
6679607	QIIQQNPSLLPALLQQIGR		RAD23b homolog [Mus musculus]	2130.2292	29.76	0
6753294	QIIVDPLSFSEER		catenin alpha 1 [Mus musculus]	1532.7921	32.24	1.549944083
18250296	QINWTVLYR		ribosomal protein L24 [Mus musculus]	1192.6492	50.05	1.448618996
31982526	QIQEEITGNTEALSGR		parvin, alpha [Mus musculus]	1745.8773	86.38	0
37620153	QISEGVEYIHK		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1302.6678	42.57	0
1346343	QISNLQQSISDAEQR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1716.8484	84.3	0
6754976	QITINDLPVGR		peroxiredoxin 1 [Mus musculus]	1225.6946	50.08	1.266707203
31560539	QITVNDLPVGR		peroxiredoxin 2 [Mus musculus]	1211.673	27.72	1.78781787
6679291	QIVWNGPVGVFEWEAFAR		phosphoglycerate kinase 1 [Mus musculus]	2105.0657	57.91	1.527380923
21704156	QKEFDPTITDGSLSGPSR		caldesmon 1 [Mus musculus]	1934.9492	82.51	0.327773805
6755354	QLDSGLLLVTGPLVINR		ribosomal protein L6 [Mus musculus]	1808.0715	82.15	1.431819194
11875203	QLEEEQQALQK		tropomyosin 2, beta [Mus musculus]	1343.687	30.06	0
6755901	QLFHPEQLITGK		tubulin, alpha 1 [Mus musculus]	1410.7808	56.35	0
34740335	QLFHPEQLITGK		tubulin, alpha 2 [Mus musculus]	1410.7808	56.35	0
6678467	QLFHPEQLITGK		tubulin, alpha 4 [Mus musculus]	1410.7808	56.35	0
6678469	QLFHPEQLITGK		tubulin, alpha 6 [Mus musculus]	1410.7808	56.35	0
7305295	QLHEYETELEDER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1690.7643	77.93	0
7305295	QLHEYETELEDERK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1818.856	69.28	0.176914114
6678571	QLLTLSNELSQAR		villin 2 [Mus musculus]	1472.7981	25.34	0.986892042
6679537	QLPDVQLLAQQLLLR		prostaglandin-endoperoxide synthase 1 [Mus musculus]	1748.047	33.9	1.09963251
29336026	QLPIYTEAIVEMYR		nonmuscle myosin heavy chain [Mus musculus]	1725.8881	24.31	2.20381661

13384736	QLQNISQAAASGGAK		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1443.7528	61.33	0
28490839	QLSNDAASVDLNPTESK	Deamidation (NQ)	PREDICTED: nuclear protein in the AT region [Mus musculus]	1789.8595	23.05	0
22122569	QLSQNFLLDLR	3 Deamidation (NQ)	transcription factor B1, mitochondrial [Mus musculus]	1349.7113	28.13	0
56605979	QLTEMLPSILNQLGADSLTSLR		basic transcription factor 3 [Mus musculus]	2400.2773	25.23	1.461060802
7304993	QLTQPETSYGR		drebrin-like [Mus musculus]	1279.6324	38.41	1.377234814
13385718	QLVEQVEQIQK		transmembrane emp24 protein transport domain containing 9 [Mus musculus]	1341.7325	36.44	2.41221246
6755714	QMEQVAQFLK		transgelin [Mus musculus]	1221.6249	57.62	0
63746482	QMQLENVSVALEFLDR		PREDICTED: filamin, alpha [Mus musculus]	1891.959	104.16	0.213545122
50355692	QNGDDPLMTYR		lamin A isoform A [Mus musculus]	1309.5878	28.87	1.847180757
51712333	QNGVLNSWTDQDSK		PREDICTED: similar to anti-PRSV coat protein monoclonal antibody PRSV-L 3-8 immunoglobulin light ch	1591.7484	47.9	0
63487095	QPELPEVIAMLGFR		PREDICTED: catenin src [Mus musculus]	1599.8524	46.06	1.699115809
30794450	QPYAVSELAGHQTSAESWGTGR		ribosomal protein L4 [Mus musculus]	2332.1011	61.99	1.517049946
29789080	QQALTVSTDPEHR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1481.7386	38.19	1.350861444
63540743	QQEGEASSQDMTAQVTSPSGK		PREDICTED: filamin C, gamma [Mus musculus]	2165.9302	49.83	0
16716509	QQEQLQLQLLQQQHAGK	3 Deamidation (NQ)	forkhead box P1 [Mus musculus]	2021.0483	25.68	0
13507628	QQEQTAQGTAPDAVDQQR		LPS-responsive beige-like anchor [Mus musculus]	1970.9293	70.94	1.829394521
46559834	QQLDELNWSTALAEGER		desmuslin isoform M [Mus musculus]	1959.951	45.94	0
14861854	QQLETLQLDGGR		keratin complex 2, basic, gene 7 [Mus musculus]	1357.7142	21.39	2.212314392
6755763	QQLSAEELDAQLDAYNAR		THO complex 4 [Mus musculus]	2034.983	36.4	2.015179959
7106421	QQMLENQMEVR		spectrin beta 2 isoform 2 [Mus musculus]	1405.6621	29.31	0
22550094	QQPPDLVDFAVEYFTR		protein kinase, cAMP dependent regulatory, type II alpha [Mus musculus]	1924.9435	65.57	1.347074483
21312968	QQSEEDLLLQDFSR		signal sequence receptor, gamma [Mus musculus]	1707.8276	55.04	1.672364974
21312968	QQSEEDLLLQDFSR	Deamidation (NQ)	signal sequence receptor, gamma [Mus musculus]	1708.8119	22.54	3.516980655
63476037	QQSLETAMSFVAR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1467.7235	34.14	0
7305295	QRYEILAANAIPK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1486.8407	30.72	0.259291238
41322904	QSAEEQAQAQAQAQAAAEK		plectin 1 isoform 1 [Mus musculus]	1957.9312	85.82	1.644634783
6754508	QSFTMVADTPENLR		LIM and SH3 protein 1 [Mus musculus]	1608.7694	37.07	1.044429005
21592285	QSQTLQQQVTVNTEELK		keratin 20 [Mus musculus]	1974.0204	68.94	0
30794412	QSSYGQQSYNNQGQQNTESSGGQGGR		TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Mus musculus]	2747.1577	140.64	1.591580595
41322904	QTNLENLDQAFSVAER		plectin 1 isoform 1 [Mus musculus]	1834.9028	45.9	0.892494214
7305291	QTPAAPETEEEPYR		metaxin 1 [Mus musculus]	1617.7419	24.55	0
31981690	QTQTFTTYSDNQPGVLIQVYEGER		heat shock protein 8 [Mus musculus]	2774.3213	79.76	1.1473841
63704924	QTQTFTTYSDNQPGVLIQVYEGER		PREDICTED: heat shock protein 1B [Mus musculus]	2774.3213	79.76	1.1473841
6680606	QTSAMSSFGGTGGGSVR		keratin complex 1, acidic, gene 19 [Mus musculus]	1586.7484	114.79	1.192578965
8567336	QTTPMTAQPPAPTFSLLQIGQR		chloride channel calcium activated 3 [Mus musculus]	2383.2312	19.21	2.395700006
22267442	QVAEQFLNMR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1235.6217	24.27	1.059594075
6677935	QVDENWYEGR		sorbin and SH3 domain containing 1 [Mus musculus]	1295.5735	26.95	0
6680726	QVELALWDTAGQEDYDR		ras homolog gene family, member B [Mus musculus]	2008.9006	31.35	1.155737349
7305085	QVLEELTELPVMVELASDFLDR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	2546.3037	125.73	1.380290168
22122789	QVLLSEPQEAAALYR		acylpeptide hydrolase [Mus musculus]	1687.9037	20.87	1.258727712
41322904	QVQVALETAQR		plectin 1 isoform 1 [Mus musculus]	1242.6818	34.9	0.977689378
63680681	QVSVGQVPGR	2 Deamidation (NQ)	PREDICTED: similar to Zinc finger protein 132 [Mus musculus]	1028.5178	19	0
63562723	QVVNIPSFIVR		PREDICTED: similar to 40S ribosomal protein S9 [Mus musculus]	1271.7487	53.51	1.375970704
21313162	QWLQEIDR		RAB1B, member RAS oncogene family [Mus musculus]	1087.5536	37.37	2.036148514
6679587	QWLQEIDR		RAB1, member RAS oncogene family [Mus musculus]	1087.5536	37.37	2.036148514
6677813	QWYESHYALPLGR		ribosomal protein S8 [Mus musculus]	1619.7866	25.44	1.497708684
21592285	QWYETNAPSTIR		keratin 20 [Mus musculus]	1465.7106	51.25	0.770439999
6996913	RAEDGSVIDYELIDQDAR		annexin A2 [Mus musculus]	2064.9895	50.98	1.137137611
31981690	RFDDAVVQSDMK		heat shock protein 8 [Mus musculus]	1410.6707	59.79	1.681665582
63664182	RFDDAVVQSDMK		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1410.6707	59.79	1.681665582
33563250	RIESLNEEIAFLK		desmin [Mus musculus]	1561.8616	62.01	0
63489754	SADESGQALLAASHYASDEVR		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	2177.011	56.64	1.084955764
34328108	SAGVSVPGPMGPSGPR		procollagen, type I, alpha 1 [Mus musculus]	1452.7323	56.42	0
6671666	SALFAQINQGESITHALK		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1928.0226	28.11	1.890980405
63476037	SALLDSIQNLQVALTSK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1801.0044	85.42	0.096469615
6754206	SANLVAATLGAILNR		hexokinase 1 [Mus musculus]	1483.8604	77.3	1.120202466
29293809	SAYDSTMETMNYAQIR		ATP citrate lyase [Mus musculus]	1880.8241	67.12	2.614236203
136429	SCAAAGTECLISGWGNTK		Trypsin precursor	1768.8038	128.14	0
54020676	SDAAPTPVPQSAPR		hypothetical protein LOC229317 [Mus musculus]	1393.7085	35.44	1.77131939
18079339	SDFDPGQDTYQHPPK		aconitase 2, mitochondrial [Mus musculus]	1731.7611	48.16	0.769357138

31981722	SDIDEIVLVGGSTR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1460.7618	55.79	0
6679567	SDQVNGVLVLSLLDK		polymerase I and transcript release factor [Mus musculus]	1599.9021	92.65	3.532556968
63738313	SEDGVEGDLGETQSR		PREDICTED: similar to AHNAK [Mus musculus]	1578.705	29.43	1.248937487
6753498	SEDYAFPTYADR		cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	1434.6228	49.14	0.946182181
31982290	SEGDTAYGQQVQPNTWK		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1908.8838	72.93	0.673005658
6755817	SELVANNVTLPAGEQR		thymopoietin [Mus musculus]	1697.8879	45.1	1.455233511
6755963	SENGLEFTSSGSANTETTK		voltage-dependent anion channel 1 [Mus musculus]	1959.8726	85.97	1.736105517
6679687	SEPIPESNEGPVK		glucose regulated protein [Mus musculus]	1382.6829	77.36	1.079889373
6755566	SEQAEPPAAADTHEAGDQNEAEK		solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1 [Mus musculus]	2395.0393	101.65	0.742654289
13430890	SETAPAAPAAPAPAEK		histone 1, H1e [Mus musculus]	1478.7516	63.66	0
34328365	SETAPAAPAAPAPVEK		histone 1, H1d [Mus musculus]	1506.783	46.57	2.207909846
7304889	SETSGSFEDALLAIVK		annexin A4 [Mus musculus]	1666.844	41.72	0
29293809	SFDELGEIIQSVYEDLVAK		ATP citrate lyase [Mus musculus]	2155.0928	92.67	3.16102367
21314832	SFENSLGINVPR		UDP-glucose pyrophosphorylase 2 [Mus musculus]	1332.6874	55.82	0.734519923
63704924	SFFPEEISSMVLTK		PREDICTED: heat shock protein 1B [Mus musculus]	1614.7982	51.78	0
51767507	SFGGGTGSGFTSLLMER		PREDICTED: similar to tubulin, alpha-like 3 [Mus musculus]	1703.814	40.69	1.59623282
6754090	SFLGGDSPSMVDYLTWPWFQR		glutathione S-transferase omega 1 [Mus musculus]	2489.168	25.41	1.696078086
51770896	SFVQNYPVVSIEDPFDQDDWGAWQK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	2970.3728	86.92	0.88614526
31981690	SFYPEEVSSMVLTK		heat shock protein 8 [Mus musculus]	1616.7947	59.99	1.803836596
51873060	SGDAAIVDMVPGKPMCVESFSDYPPLGR		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2938.3899	51.65	1.190111826
7305027	SGETEDTFIADLVVGLCTGQIK		enolase 2, gamma neuronal [Mus musculus]	2296.1511	121.59	1.152423561
51770896	SGETEDTFIADLVVGLCTGQIK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	2296.1511	121.59	1.152423561
6679793	SGIGTGDEPGPQGLNGEAGPEDPSR		protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform [Mus musculus]	2394.1116	32.03	1.102698379
6680970	SGLGSQVGLMPGSVGPVGPR	Oxidation (M)	procollagen, type V, alpha 2 [Mus musculus]	1867.9723	28.46	0
22165384	SGPFGQIFRPDNFVFGQSGAGNNWAK		tubulin, beta, 2 [Mus musculus]	2798.3457	25.99	1.010408164
33859488	SGPFGQIFRPDNFVFGQSGAGNNWAK		tubulin, beta 2 [Mus musculus]	2798.3457	25.99	1.010408164
31981939	SGPFGQIFRPDNFVFGQSGAGNNWAK		tubulin, beta 4 [Mus musculus]	2798.3457	25.99	1.010408164
7106439	SGPFGQIFRPDNFVFGQSGAGNNWAK		tubulin, beta 5 [Mus musculus]	2798.3457	25.99	1.010408164
40254244	SGSMDSPMSTENNSQLR		loss of heterozygosity, 11, chromosomal region 2, gene A homolog [Mus musculus]	1840.7836	20.9	1.542995857
6680836	SGTIFDNFLITNDEAYAEEFGNETWGVTK		calreticulin [Mus musculus]	3268.4995	82.92	0
9845263	SGTTWLSEIVDMVLNDGNVEK		dopa/tyrosine sulfotransferase [Mus musculus]	2307.0728	35.59	1.043332127
13937355	SGYQQAASEHGLVVIAPDTSPR		esterase D/formylglutathione hydrolase [Mus musculus]	2283.1279	38.52	0.991030514
41322904	SIITYVSSLYDAMPR		plectin 1 isoform 1 [Mus musculus]	1715.8695	26.73	2.428242219
6755863	SILFVPTSAPR		tumor rejection antigen gp96 [Mus musculus]	1187.6796	30.24	0
31981690	SINPDEAVAYGAAVQAAILSGDK		heat shock protein 8 [Mus musculus]	2260.1519	121.91	1.279678503
6754206	SIPDGTEHGDFLALDLGGTNFR		hexokinase 1 [Mus musculus]	2332.1318	53.22	0
13384736	SIPLDEGEDEAQR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1458.6726	50.18	0
31982030	SIQEIQELDKDDESLR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1917.9436	71.3	1.197488781
34740335	SIQFVDWCPTGFK		tubulin, alpha 2 [Mus musculus]	1527.7356	64.35	1.350915685
6678467	SIQFVDWCPTGFK		tubulin, alpha 4 [Mus musculus]	1527.7356	64.35	1.350915685
38090003	SISTSLPVLDLIDAIAPNAVR		PREDICTED: expressed sequence AI427122 [Mus musculus]	2165.2185	66.58	1.039011204
31981657	SIVNNGHSFNVEFDDSQDNAVLK		carbonic anhydrase 2 [Mus musculus]	2549.166	60.07	0.966575542
6679439	SIYGEKFEDENFILK		peptidylprolyl isomerase A [Mus musculus]	1831.905	24.84	1.519504276
6678674	SLADELALVDVLEDK		lactate dehydrogenase 2, B chain [Mus musculus]	1629.8513	58.08	0
64427157	SLASVPQQNGFSGVSETAGAQR		PREDICTED: synaptopodin 2 [Mus musculus]	2191.0767	51.08	0
64427157	SLASVPQQNGFSGVSETAGAQR	Deamidation (NQ)	PREDICTED: synaptopodin 2 [Mus musculus]	2192.0623	47	0.418618034
63476037	SLDEVSQPAQELK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1443.7408	22.92	0
63476037	SLDEVSQPAQELKR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1599.8346	40.44	0
20911031	SLDLDSIIAEVK		keratin complex 2, basic, gene 5 [Mus musculus]	1302.6921	69.61	0
1346343	SLDLDSIIAEVK		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1302.6921	69.61	0
13624315	SLDMDGIIAEVR		keratin complex 2, basic, gene 8 [Mus musculus]	1318.6741	58.17	1.585758127
63565108	SLDMDGIIAEVR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1318.6741	58.17	1.585758127
7305295	SLEADLMQLQEDLAAAER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2002.9976	107.64	0.191820883
7305295	SLEADLMQLQEDLAAAER	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2018.9702	45.23	0.312509692
6754556	SLETENSALQLQVTER		lamin B1 [Mus musculus]	1817.9269	30.97	0
29243996	SLINFDKDNISDK	2 Deamidation (NQ)	1-beta dynein [Mus musculus]	1510.7522	19.33	0
6680606	SLLEGQEAHYNNLPTPK		keratin complex 1, acidic, gene 19 [Mus musculus]	1910.9691	68.37	1.507709999
6680606	SLLEGQEAHYNNLPTPK	Deamidation (NQ)	keratin complex 1, acidic, gene 19 [Mus musculus]	1911.9528	41.92	1.696048657
12963539	SLLPGCQSVISR		ETHE1 protein [Mus musculus]	1259.6793	23.22	0.832818889
47086911	SLNNQFASFIDK		keratin Kb40 [Mus musculus]	1383.6888	73.68	0

1346343	SLNNQFASFIDK		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1383.6888	73.68	0
6754524	SLNPELGTDADKEQWK		lactate dehydrogenase 1, A chain [Mus musculus]	1830.8921	69.13	2.042114786
63664186	SLNPELGTDADKEQWK		PREDICTED: similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M) [Mus mus	1830.8921	69.13	2.042114786
33859811	SLNSEMDNILANLR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1589.7983	75.4	0.767748499
21313080	SLNYWSNLLGMK		hypothetical protein LOC67201 [Mus musculus]	1425.7139	21.98	0
31980648	SLQDIIAILGMDELSEEDKLTVSR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2675.3862	38.26	1.226146229
6680572	SLSALGNVISALAEGSTYVPYR		kinesin family member 5B [Mus musculus]	2268.1802	52.92	1.43429373
21592285	SLSSSSQGPALSMSGSLYR		keratin 20 [Mus musculus]	1914.9307	45.85	0.637214255
40556608	SLTNDWEDHLAVK		heat shock protein 1, beta [Mus musculus]	1527.7435	37.01	1.361468797
31982755	SLYSSSPGGAYVTR		vimentin [Mus musculus]	1444.7144	53.24	0.704169397
22267442	SMAASGNLGHTPFLDEL		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1759.8466	20.35	0
20137006	SMEAEMIQLQEELAAAER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2048.9697	51.26	2.202467987
22122825	SMLEVNYPMENGIVR		actin-related protein 2 [Mus musculus]	1751.8682	26.16	1.474143164
50355692	SNEDQSMGNWQIR		lamin A isoform A [Mus musculus]	1564.6915	52.81	1.045640313
31543051	SNEILTAIIQGMR		karyopherin (importin) beta 1 [Mus musculus]	1445.7833	21.78	7.574023263
6754854	SNGAYNIFANDR		nidogen 1 [Mus musculus]	1341.6257	22.47	3.234219538
33469063	SNLVGMGVIPLEYLPGETADSLGLTGR		aconitase 1 [Mus musculus]	2759.4309	56.66	1.380378878
13624315	SNMDNMFESYINNLR		keratin complex 2, basic, gene 8 [Mus musculus]	1847.8258	57.59	1.490567299
63565108	SNMDNMFESYINNLR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1847.8258	57.59	1.490567299
21450277	SPDFTNENPLETR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1519.7112	80.59	0.981682571
6679761	SPFETDMLTLTR		fructose bisphosphatase 2 [Mus musculus]	1410.7003	34.77	1.254268524
63746482	SPFEVYVDK		PREDICTED: filamin, alpha [Mus musculus]	1083.5333	57.6	0.391459575
31980969	SPFLQVFNNSPDESSYYR		SEC23B [Mus musculus]	2149.9937	39.57	0.666953669
63746482	SPFSVGVSPSLDLSK		PREDICTED: filamin, alpha [Mus musculus]	1519.8031	99.47	0
7305505	SPLSAEELTAIEDEGVLDK		smoothelin [Mus musculus]	2016.0089	78.26	0.53645309
37620153	SPSENGGNSAEVLNVK	Deamidation (NQ)	myosin, light polypeptide kinase telokin isoform [Mus musculus]	1602.7739	23.82	0
25030960	SPYAPANER	Deamidation (NQ)	PREDICTED: similar to MORF-related gene X [Mus musculus]	1005.4724	19.01	0
33859560	SPYLYPLYGLGELPQGFAR		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	2141.106	53.52	1.03720766
56119103	SPYLYPLYGLGELPQGFAR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	2141.106	53.52	1.03720766
6678571	SQEQLAAELAEYTAK		villin 2 [Mus musculus]	1651.819	33.17	1.505278087
18079339	SQFTITPGSEQIR		aconitase 2, mitochondrial [Mus musculus]	1463.759	50.12	1.013850585
31981722	SQIFSTASDNQPTVTIK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1836.9492	69.76	0.80405472
31981690	SQIHDIVLVGGSTR		heat shock protein 8 [Mus musculus]	1481.813	65.1	0.997061366
41322904	SQVEEELFSVR		plectin 1 isoform 1 [Mus musculus]	1322.6597	24.02	0
547749	SQYEQLAEQNR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1365.6464	55.81	0
6680606	SRLEQEIATYR		keratin complex 1, acidic, gene 19 [Mus musculus]	1365.72	39.1	1.331946232
417200	SRLEQEIATYR		Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1365.72	39.1	1.331946232
33859650	SSELAAALLSVFLER		membrane bound C2 domain containing protein [Mus musculus]	1605.8766	31.07	1.395155893
6755040	SSFFVNGLTLGGQK		profilin 1 [Mus musculus]	1454.7587	89.6	1.319659649
31559916	SSGSPYGGGYGSGGGSGGYGSR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1910.8035	159.69	1.64137153
136429	SSGSSYPSLLQCLK		Trypsin precursor	1469.7283	64.94	0
12083691	SSGTGASVGPPQPSDQDTLVQR		PDZ and LIM domain 5 isoform ENH1 [Mus musculus]	2184.0562	44.33	1.410667565
6755354	SSITPGTVLIILTGR		ribosomal protein L6 [Mus musculus]	1527.9176	42.79	1.711048206
22779912	SSLLDDLLTESEDMAQR		dynamin 1-like [Mus musculus]	1922.9258	32.6	1.17194107
46195798	SSLNPILFR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1046.5968	37.16	1.610955375
8567338	SSPEPVALTESETEYVIR		coatomer protein complex, subunit gamma [Mus musculus]	2006.991	49.51	1.024875044
31981690	STAGDTHLGGEDFDNR		heat shock protein 8 [Mus musculus]	1691.7413	123.26	1.214241848
33859482	STAISLFYELSENDLNFIK		eukaryotic translation elongation factor 2 [Mus musculus]	2204.1011	105.05	0.987468013
46559834	STETMIGEMINLGLK		desmuslin isoform M [Mus musculus]	1636.826	78.31	0
33469093	STGGGLMEEMNAMLAR		vasodilator-stimulated phosphoprotein [Mus musculus]	1667.772	34.95	0.977069815
6754816	STLINSLFLTDLYPER		septin 2 [Mus musculus]	1881.9941	47.85	0.884200386
31981549	STLSVIPSGVQWIQDR		sulfide quinone reductase-like [Mus musculus]	1785.9502	41.81	1.227260628
6754256	STNGDTFLGGEDFDQALLR		heat shock protein 9A [Mus musculus]	2055.9668	106.68	1.340889593
6754256	STNGDTFLGGEDFDQALLR	Deamidation (NQ)	heat shock protein 9A [Mus musculus]	2056.9683	72.2	0
51491845	SVDPTLALSVYLR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1433.806	41.76	0
6678573	SVEDLPEGVDPSR		villin 1 [Mus musculus]	1399.642	31.64	0.697149309
50355692	SVGGSGGGSFGDNLVTR		lamin A isoform A [Mus musculus]	1566.752	25.86	0
19745150	SVGMIAGGTGITPMLQVIR		diaphorase 1 [Mus musculus]	1901.0287	29.21	1.570740949
7305085	SVHFPGQAVGTR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1255.6567	21.62	0
51491845	SVNESLNNLFITEEDYQALR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2355.1484	61.09	1.199619053

6753658	SVSTPSEAGSQDSGDGAVGSR	dynein, cytoplasmic, intermediate chain 2 [Mus musculus]	1950.8593	128.13	1.181487086
6756041	SVTEQGAELSNEER	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	1548.7256	84.87	1.432691273
33563270	SWDIFFR	oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	970.4785	28.11	0.797000892
6753138	SYEAYVLNIIR	Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1340.7288	45	1.261298974
6671507	SYELPDGQVITIGNER	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1790.9003	60.74	0.516066211
6671509	SYELPDGQVITIGNER	actin, beta, cytoplasmic [Mus musculus]	1790.9003	60.74	0.516066211
30425250	SYELPDGQVITIGNER	hypothetical protein LOC238880 [Mus musculus]	1790.9003	60.74	0.516066211
63694749	SYELPDGQVITIGNER	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1790.9003	60.74	0.516066211
63652452	SYKLPDGQVITIGNER	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1789.9653	64.39	0
38090710	SYLTPVRDEESESQR	PREDICTED: protein phosphatase 1, regulatory (inhibitor) subunit 12A [Mus musculus]	1795.85	47.26	0
6753620	TAAFLLPILSQIYADGPGEALR	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	2316.2476	27.76	1.251178186
6756041	TAFDEAIAELDTLSEESYK	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	2131.9922	82.61	1.732299092
6806903	TASEMVLADDNFSTIVAAVEEGR	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	2425.1548	64.95	0.973928493
36031132	TASEMVLADDNFSTIVAAVEEGR	ATPase, Ca++ transporting, fast twitch 1 [Mus musculus]	2425.1548	64.95	0.973928493
63489754	TATDEAYKDPSNLQGK	PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1737.8376	30.85	0.865826577
6671664	TDAPQPDVKDEEGKEEEK	calnexin [Mus musculus]	2043.941	55.33	2.00718067
6754034	TDESQPWVLPVVR	glutamate oxaloacetate transaminase 1, soluble [Mus musculus]	1525.8086	31.7	2.428578369
6677805	TDITYPAGFMDVISIDK	ribosomal protein S4, X-linked [Mus musculus]	1885.9303	86.81	1.957171984
6680606	TDLEMQIESLKEELAYLK	keratin complex 1, acidic, gene 19 [Mus musculus]	2153.1201	91.62	1.715662809
10946574	TDLNPDNLQGGDDLDPNYVLSSR	creatine kinase, brain [Mus musculus]	2518.1736	96.22	0
63476037	TDLQTITNDPR	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1273.6394	47.87	0
6755714	TDMFQTVDLYEGK	transgelin [Mus musculus]	1546.7209	53.12	0
63540743	TDTYVTDNGDGTYR	PREDICTED: filamin C, gamma [Mus musculus]	1577.673	25.06	0
31982030	TDYMVGSYGPR	Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1245.5677	26.92	1.305283193
13384620	TDYNASVSVPDSSGPER	heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1780.8077	103.08	1.533965217
63540743	TEAAEIVEGEDSAYSVR	PREDICTED: filamin C, gamma [Mus musculus]	1825.8524	53.49	0
6753138	TEISFRPNDPK	Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1303.6693	21.4	1.735916574
6679931	TELDVVGGSVQGNTYQFR	UDP-N-acetyl-alpha-D-galactosamine: (N-acetylneuraminyl)-galactosyl-N- acetylglucosaminylpolypeptid	1969.9666	41.98	0
7305295	TELEDTLDSTATQQELR	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1949.9316	138.74	0.20648068
13624315	TEMENEFVLIK	keratin complex 2, basic, gene 8 [Mus musculus]	1352.6632	50.4	1.000928202
63565108	TEMENEFVLIK	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1352.6632	50.4	1.000928202
31981722	TFAPEEISAMVLTK	heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1536.7981	59.29	1.666305678
31791057	TFGEVTDLDNEVNGMLR	laminin, gamma 1 [Mus musculus]	1909.9084	70.52	0
33563250	TFGGAPGFSLGSPLSSPVFPR	desmin [Mus musculus]	2078.072	125.93	0.261868618
6679078	TFIAIKPDGVQR	nucleoside-diphosphate kinase 2 [Mus musculus]	1344.7692	22.82	0
21312260	TFPTVNPTTGEVIGHVAEGDR	aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	2197.094	63.27	1.148143428
63746482	TFSVWYVPEVTGTHK	PREDICTED: filamin, alpha [Mus musculus]	1750.8844	86.79	0
6680067	TFTTQETITNAETAK	glucose phosphate isomerase 1 [Mus musculus]	1655.8169	31.66	1.380662606
6753036	TFVQENVYDEFVER	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1774.832	94.84	2.328899481
6755040	TFVSITPAEVGVLVGK	profilin 1 [Mus musculus]	1616.9321	90.05	1.366713558
6680748	TGAIVDVPVGEELLGR	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1624.8964	84.01	1.049454298
6755965	TGDFQLHTNVNNGTEFGGSIYQK	voltage-dependent anion channel 2 [Mus musculus]	2527.1885	103.2	1.282978677
58037267	TGEAIVDAALSALR	protein disulfide isomerase-associated 6 [Mus musculus]	1386.7628	88.32	1.203077727
6755004	TGGLEIDSDFGGFR	programmed cell death 8 [Mus musculus]	1470.6855	52.49	0.755266298
64427157	TGGMAGGGPDALQTDGLR	PREDICTED: synaptopodin 2 [Mus musculus]	1673.7933	29.44	0
6681095	TGQAAGFSYTDANK	cytochrome c, somatic [Mus musculus]	1430.6545	68.63	0.490158208
6680748	TGTAEMSSILEER	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1423.6787	42.86	1.005916486
31560517	TGVAPIIDVVR	ribosomal protein L27a [Mus musculus]	1139.6772	33.56	1.125821439
63746482	TGVAVNKPAEFTVDAK	PREDICTED: filamin, alpha [Mus musculus]	1646.8795	84.88	0
7305295	TGVLAHLEEER	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1253.6501	63.99	0
6754576	TGVPSQTPNPYANQR	lymphocyte antigen 64 [Mus musculus]	1629.803	38.76	1.689328533
29293809	TIAIIAEGIPEALTR	ATP citrate lyase [Mus musculus]	1567.9034	47.91	2.434323262
31980648	TIAMDGTEGLVR	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1262.6459	52.28	0.95349535
6754976	TIAQDYGVLK	peroxiredoxin 1 [Mus musculus]	1107.5884	27.32	0
33859811	TIEYLEEVAVNFAK	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1625.8398	48.82	0
6754854	TIFWTDSQLDR	nidogen 1 [Mus musculus]	1381.6774	34.48	0
6755901	TIGGGDDSFNTFFSETGAGK	tubulin, alpha 1 [Mus musculus]	2007.8975	131.26	1.236712847
34740335	TIGGGDDSFNTFFSETGAGK	tubulin, alpha 2 [Mus musculus]	2007.8975	131.26	1.236712847
6678469	TIGGGDDSFNTFFSETGAGK	tubulin, alpha 6 [Mus musculus]	2007.8975	131.26	1.236712847
31981909	TIGVSNFNPLQIER	aldo-keto reductase family 1, member B3 (aldose reductase) [Mus musculus]	1587.8378	22.63	1.754369966

6754816	TIISYIDEQFER		septin 2 [Mus musculus]	1513.7579	21.66	0.938235145
31543605	TILPAAAQDVYYR		ribophorin I [Mus musculus]	1480.7882	37.03	1.191219049
11230802	TINEVENQILTR		actinin alpha 4 [Mus musculus]	1429.7736	60.07	0.567234083
6753036	TIPIDGDFFSYTR		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1531.7484	62.75	2.787883978
59709449	TIPWLENR		actinin alpha 2 [Mus musculus]	1028.542	31.23	0.5135482
6755901	TIQFVDWCPTGFK		tubulin, alpha 1 [Mus musculus]	1541.7451	50.25	0.898859997
6678469	TIQFVDWCPTGFK		tubulin, alpha 6 [Mus musculus]	1541.7451	50.25	0.898859997
9845265	TITLEVEPSDTIENVK		ubiquitin A-52 residue ribosomal protein fusion product 1 [Mus musculus]	1787.9337	67.74	0
6680067	TLASLSPETSLFIIASK		glucose phosphate isomerase 1 [Mus musculus]	1777.9957	59.16	0
31981828	TLDLPIYVTR		coatomer protein complex subunit alpha [Mus musculus]	1190.6744	31.98	1.166761192
51092303	TLDNDIMLIKLSSPVTLNAR	Oxidation (M)	Try10-like trypsinogen [Mus musculus]	2230.2151	27.09	0
7305295	TLLQEQLQAETELYAESEEMR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2511.2014	27.79	0
54607098	TLNEADCATVPPAIR		succinate dehydrogenase Fp subunit [Mus musculus]	1570.7845	19.12	1.176375526
31981657	TLNFNEEGDAEEAMVDNWRPAQPLK		carbonic anhydrase 2 [Mus musculus]	2874.332	43	1.137724323
6680606	TLQGLEIELQSQLSMK		keratin complex 1, acidic, gene 19 [Mus musculus]	1817.9746	87.82	2.780438226
417200	TLQGLEIELQSQLSMK		Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1817.9746	87.82	2.780438226
6680606	TLQGLEIELQSQLSMK	2 Deamidation (NQ)	keratin complex 1, acidic, gene 19 [Mus musculus]	1819.9652	34.36	0
417200	TLQGLEIELQSQLSMK	2 Deamidation (NQ)	Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1819.9652	34.36	0
6680606	TLQGLEIELQSQLSMK	Deamidation (NQ)	keratin complex 1, acidic, gene 19 [Mus musculus]	1818.9692	23.8	0.77343618
417200	TLQGLEIELQSQLSMK	Deamidation (NQ)	Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1818.9692	23.8	0.77343618
6754482	TLQTLEIDLDSMK	Deamidation (NQ)	keratin complex 1, acidic, gene 18 [Mus musculus]	1507.7371	29.81	0
46195798	TLVLLDNLNVR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1269.7529	22.54	1.739352649
29126205	TNVSGGAIALGHPLGGSGSR		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1807.9467	49.86	0.605439442
6996913	TPAQYDASELK		annexin A2 [Mus musculus]	1222.5895	54.54	0
51592084	TPELTWER		hypothetical protein LOC74340 [Mus musculus]	1031.5138	20.95	0.679935156
6753364	TPFLLVGTQIDLR		cell division cycle 42 homolog [Mus musculus]	1472.8507	37.3	1.747020129
9790061	TPLFDQIIDMLR		pyrroline-5-carboxylate synthetase [Mus musculus]	1461.7795	38.3	1.096805108
29336026	TPNVGGPGGPQVEWTAR		nonmuscle myosin heavy chain [Mus musculus]	1722.86	37.04	1.540024541
6677935	TPVDYIDLPYSSSPSR		sorbin and SH3 domain containing 1 [Mus musculus]	1796.8705	40.59	0
19527174	TPVEEVPAAIAPFQGR		splicing factor 3b, subunit 3 [Mus musculus]	1681.8831	38.09	0
13385652	TPVEPEVAIHR		ribosomal protein S20 [Mus musculus]	1247.677	52.74	1.265903446
18250284	TPYTDVNIVTIR		isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	1391.7494	30.14	1.675989149
31980726	TQAYPDQKPGTSGLR		phosphoglucomutase 2 [Mus musculus]	1618.8234	42.57	0.863783279
31981824	TQDDIETILQLFR		ankyrin repeat domain 25 [Mus musculus]	1591.8248	57.57	0
6678752	TQDDVDIADVAYYFEK		lymphocyte antigen 74 [Mus musculus]	1891.8701	107.02	1.695903621
33598964	TQLEELEDELQATEDAK		myosin heavy chain 10, non-muscle [Mus musculus]	1961.9283	119.01	0.259877692
20137006	TQLEELEDELQATEDAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1961.9283	119.01	0.259877692
31980636	TQQTNDIELQQEQR		mannosidase, beta A, lysosomal [Mus musculus]	1730.8304	22.68	0
21704096	TSDLIVLGLPWK		TAR DNA binding protein isoform 1 [Mus musculus]	1341.7716	37.56	1.736431393
33563270	TSFDEMLPGTHFQR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1665.7745	30.34	0
55742711	TSFIQYLLEQEVPGSR		EH-domain containing 2 [Mus musculus]	1866.9609	30.8	0.616438156
13430890	TSGPPVSELITK		histone 1, H1e [Mus musculus]	1228.6628	26.87	0
51491845	TSIDAYDNFDNISLAQR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1942.9207	85.41	1.358810343
27501448	TSIEDQDELSSLLQVPLVAGTVNR		integrin beta 4 binding protein [Mus musculus]	2584.3613	19.29	1.33897672
6678359	TSRPENAIIYSNNEDFQVGQAK		transketolase [Mus musculus]	2481.1973	42.72	1.075645925
21313262	TSSAEMPTIPLGSAVEAIR		inner membrane protein, mitochondrial [Mus musculus]	1929.9983	82.29	1.587152994
31982275	TSTVDLPIESQLLWQLDR		heat shock protein 4 [Mus musculus]	2114.1038	39.47	1.276242379
6753294	TSVQTEDDQLIAGQSAR		catenin alpha 1 [Mus musculus]	1818.877	53.04	0.936436232
6679761	TTEDEPSEKDALQPGR		fructose bisphosphatase 2 [Mus musculus]	1772.8385	62.19	0
6671507	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	3196.5869	82.67	0.132839482
6671509	TTGIVMDSGDGVTHTVPIYEGYALPHAILR		actin, beta, cytoplasmic [Mus musculus]	3183.613	36.47	0.914483216
30425250	TTGIVMDSGDGVTHTVPIYEGYALPHAILR		hypothetical protein LOC238880 [Mus musculus]	3183.613	36.47	0.914483216
63694749	TTGIVMDSGDGVTHTVPIYEGYALPHAILR		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	3183.613	36.47	0.914483216
6754556	TTIPEEEEEEEEEPIGVAVEEER		lamin B1 [Mus musculus]	2672.1899	119.89	1.013276072
38076180	TTPDVIFVFGFR		PREDICTED: similar to ribosomal protein S24 [Mus musculus]	1398.7417	45.21	1.580270821
7305163	TTPSYVAFTDTER		heat shock protein 1-like [Mus musculus]	1487.7142	67.3	1.286193294
31981690	TTPSYVAFTDTER		heat shock protein 8 [Mus musculus]	1487.7142	67.3	1.286193294
63704924	TTPSYVAFTDTER		PREDICTED: heat shock protein 1B [Mus musculus]	1487.7142	67.3	1.286193294
28395018	TTTYTQGVPQNQGDLEYQMSTTAR		junction plakoglobin [Mus musculus]	2690.2385	27.7	1.965233324
18875380	TVFDEAIR		RAS-related C3 botulinum substrate 3 [Mus musculus]	950.4917	22.09	1.710304834

6753428	TVGMVAGDEETYEVFAELFDPVIQER		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	2944.4019	47.01	3.285344481
33859811	TVLGVPEVLLGILPGAGGTQR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	2047.1947	19.45	0
21361209	TVTAMDVVYALK		germinal histone H4 [Mus musculus]	1310.6963	76.83	0.889812942
31981690	TVTNAVVTVPAYFNDSQR		heat shock protein 8 [Mus musculus]	1982.0059	84.98	1.155846139
6681069	TVYFAEEVQCEGNSFHK		cysteine and glycine-rich protein 1 [Mus musculus]	1987.8947	33.33	0
31981722	TWNDPSVQQDIK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1430.7036	52.86	0.921530869
31981722	TWNDPSVQQDIK	Deamidation (NQ)	heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1431.7024	37.33	0
47059123	TYAVSHTQEDLNR		UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	1533.7328	46.19	2.211312679
29789080	TYLPSQVSR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1050.5598	21.59	0.998424907
23346461	TYLQALPYFDR		NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Mus musculus]	1386.7096	21.53	1.046381077
31982755	TYSLGSALRPSTSR		vimentin [Mus musculus]	1495.796	28.58	0.77289882
18152793	TYYMSAGLQPVPIVFR		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1841.9663	20.73	1.173739857
21704128	VAAVQPPEEGPSR		eukaryotic translation initiation factor 4B [Mus musculus]	1336.6924	35.29	1.149343847
7709980	VADIGLAAWGR		S-adenosylhomocysteine hydrolase [Mus musculus]	1128.6104	55.61	1.52650539
31981549	VAELNPDENCIR		sulfide quinone reductase-like [Mus musculus]	1372.6595	37.33	1.485924716
21312260	VAEQTPLSALYLASLIK		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1817.046	88.61	0.69420831
6753036	VAEQTPLTALYVANLIK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1844.048	32.6	3.737016418
6753036	VAEQTPLTALYVANLIK	Deamidation (NQ)	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1845.0582	20.35	4.180042627
6755809	VAGSVTELIQAAEAMK		talin 1 [Mus musculus]	1617.8568	25.22	0
63476037	VAIAQFSDDVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1220.625	51.37	0.437920442
21704020	VALIGSPVDLTYR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	1403.7919	26.08	0
31980648	VALTGLTVAEYFR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1439.7992	87.43	1.118269689
63476037	VALVQYSDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1050.5538	35.67	0.445891538
18079339	VAMSHFEPSEYIR		aconitase 2, mitochondrial [Mus musculus]	1565.7443	29.84	1.073205401
63746482	VANPSGNLTDTYVQDCGDGTYK		PREDICTED: filamin, alpha [Mus musculus]	2318.0374	152.93	0
31542559	VAPAPAGVFTDIPISNIR		dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) [Mus musculus	1838.0162	28.43	0.988504312
6671507	VAPEEHPTLLTEAPLNPK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1956.0587	108.4	0.158235429
6671509	VAPEEHPVLLTEAPLNPK		actin, beta, cytoplasmic [Mus musculus]	1954.0781	89.52	1.096211168
63694749	VAPEEHPVLLTEAPLNPK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1954.0781	89.52	1.096211168
13385598	VAQLEQVYIR		small nuclear ribonucleoprotein D3 [Mus musculus]	1218.6838	23.62	2.041972296
63746482	VAQPSITDNKDGTVTVR		PREDICTED: filamin, alpha [Mus musculus]	1800.949	81.68	0.463477549
33563270	VASSVPVENFTIHGGLSR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1869.9819	25.76	1.212304092
63746482	VATVPQHATSGPGPADVSK		PREDICTED: filamin, alpha [Mus musculus]	1818.9595	99.07	0.337389351
136429	VATVSLPR		Trypsin precursor	842.5023	48.46	0.088305068
63540743	VAVGQEQAFSVNTR		PREDICTED: filamin C, gamma [Mus musculus]	1505.7786	35.58	0
31982186	VAVLGASGGIGQPLSLLLK		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1793.0942	86.28	0.858403017
31982030	VAVSADPNVPNVIVTR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1650.9258	42.68	1.15980192
6753484	VAVVQYSGQGQQQPGR		procollagen, type VI, alpha 1 [Mus musculus]	1701.8745	77.16	0.383516778
63476037	VAVVTYNNEVTTEIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1707.9003	49.9	0
63476037	VAVVTYNNEVTTEIR	Deamidation (NQ)	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1708.906	35.44	0
46849705	VAYNPFGPGQFFDLSIR		lectin, galactose binding, soluble 4 [Mus musculus]	1927.9829	76.87	1.800911
7305295	VCHLVGINVTDFTR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1573.8208	72.68	0
37497108	VCKLIYTVMENNSGR	Deamidation (NQ); Oxidation (M)	Ras and Rab interactor 2 [Mus musculus]	1743.8602	19.03	1.502491809
33238874	VDAMHGVMGPYVR		phosphoglucomutase 5 [Mus musculus]	1431.6906	24.3	0
42415475	VDATEESDLAQQYGVR		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1780.8425	115.01	1.02946283
45598381	VDCTADSDVCSAQGVR		thioredoxin domain containing 5 [Mus musculus]	1625.7036	47.38	0.937137018
21312462	VDDNVLQCLEEYLR		glucosaminyl (N-acetyl) transferase 3, mucin type [Mus musculus]	1708.8325	26.06	1.305378926
54607098	VDEYDYSKPIQGQQK		succinate dehydrogenase Fp subunit [Mus musculus]	1797.87	94.23	0.921527234
31982186	VDFPQDQLATLTGR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1560.8105	67.22	1.200699572
63738313	VDIDVPDVNIEGPDAK		PREDICTED: similar to AHNAK [Mus musculus]	1695.8491	67.9	1.195021791
63738313	VDINAPDVDVR		PREDICTED: similar to AHNAK [Mus musculus]	1212.6268	21.99	2.994515395
7106435	VDLQDHGESAYAVYDR		tenascin C [Mus musculus]	1837.8445	74.89	0.482331896
6679108	VDNDENEHQLSLR		nucleophosmin 1 [Mus musculus]	1568.7396	39.85	1.651501238
6679108	VDNDENEHQLSLR	Deamidation (NQ)	nucleophosmin 1 [Mus musculus]	1569.7369	51.33	3.31684951
21450277	VDNSSLTGESEPQTR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1619.7633	77.21	1.151914185
31543942	VDQLTAQLADLAAR		vinculin [Mus musculus]	1484.7775	72.5	0
6681087	VDQSAVGFEYQGK		cortactin [Mus musculus]	1427.6656	47.07	0
33186863	VDTWFNQPAR		ribosomal protein L13 [Mus musculus]	1233.6077	19.81	1.388720837
63746482	VDVGKDQEFTVK		PREDICTED: filamin, alpha [Mus musculus]	1364.7052	57.94	0.993094694
33859722	VDVTEQTGLSGR		thioredoxin domain containing 1 [Mus musculus]	1261.6439	19.78	1.019148158

7305295	VDYNASAWLTK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1267.6337	83.63	0.277464208
33598964	VEDMAELTCLNEASVLHNLK		myosin heavy chain 10, non-muscle [Mus musculus]	2229.0776	19.05	0.916708426
20137006	VEDMAELTCLNEASVLHNLK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2229.0776	19.05	0.916708426
63540743	VEESTQVGGDPFPAVFGDFLGR		PREDICTED: filamin C, gamma [Mus musculus]	2324.1267	60.09	0.396048675
31542333	VEFEELCADLFDR		hypoxia up-regulated 1 [Mus musculus]	1585.7244	71.95	0.94580878
21313536	VEGGTPLFTLR		dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]	1189.6594	25.57	0.992037686
7106435	VEGYSGTAGDSMNYHNGR		tenascin C [Mus musculus]	1914.8121	62.79	1.249106019
31981722	VEIIANDQGNR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1228.6317	50	1.14569942
7305163	VEIIANDQGNR		heat shock protein 1-like [Mus musculus]	1228.6317	50	1.14569942
31981690	VEIIANDQGNR		heat shock protein 8 [Mus musculus]	1228.6317	50	1.14569942
63704924	VEIIANDQGNR		PREDICTED: heat shock protein 1B [Mus musculus]	1228.6317	50	1.14569942
63664182	VEIIANDQGNR		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1228.6317	50	1.14569942
63746482	VEPGLGADNSVVR		PREDICTED: filamin, alpha [Mus musculus]	1312.6887	62.48	0.240143365
11230802	VEQIAAIAQELNELDYYDSHNVNTR		actinin alpha 4 [Mus musculus]	2905.3887	46.76	1.117091451
20373167	VEQLGAEGNVEESQK		LUC7-like 2 [Mus musculus]	1616.7842	88.37	0
51873060	VETGVLKPGMVVTFAPVNVTTEVK		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2515.3989	106.53	0.951828112
51873060	VETGVLKPGMVVTFAPVNVTTEVK	Oxidation (M)	eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2531.3901	31.81	0.838884542
33859490	VETLSQVEVILQQSAADIAR		laminin B1 subunit 1 [Mus musculus]	2170.1375	50.81	0.992802335
46849705	VFANGQHLFDFSHR		lectin, galactose binding, soluble 4 [Mus musculus]	1674.8229	37.64	2.321902539
22203747	VFAVVITDGR		procollagen, type VI, alpha 2 [Mus musculus]	1076.6007	35.52	0
33859482	VFDAIMNFR		eukaryotic translation elongation factor 2 [Mus musculus]	1112.5558	43.84	1.032901287
33620739	VFDKEGNGTVMGAEIR		myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Mus musculus]	1722.8516	53.08	0
31980669	VFEVSLADLQNDEVAFR		ribosomal protein S3a [Mus musculus]	1951.9786	29.16	1.666382395
6754254	VFIMDNCEELIPEYLNFIR		heat shock protein 1, alpha [Mus musculus]	2358.1509	37.68	1.440581116
40556608	VFIMDSCDELIPEYLNFIR		heat shock protein 1, beta [Mus musculus]	2317.1528	58.44	1.461116388
21361209	VFLENVIR		germinal histone H4 [Mus musculus]	989.5791	54.46	1.317934385
6753484	VFSVAITPDHLEPR		procollagen, type VI, alpha 1 [Mus musculus]	1580.847	56.26	0.194598777
31981549	VGAENVAIVEPSER		sulfide quinone reductase-like [Mus musculus]	1469.7634	52.57	1.045595856
6755809	VGAIPANALDDGQWSQGLISAAR		talin 1 [Mus musculus]	2310.189	51.33	0.483601114
6755478	VGDVYIPR		splicing factor, arginine/serine-rich 2 [Mus musculus]	918.4982	27.68	1.524949407
51491845	VGEQAQVVIIDMNDPSNPIR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2195.1406	34.18	1.077133673
6755901	VGINYQPPTVVPGGDLAK		tubulin, alpha 1 [Mus musculus]	1824.9908	46.71	1.267602515
34740335	VGINYQPPTVVPGGDLAK		tubulin, alpha 2 [Mus musculus]	1824.9908	46.71	1.267602515
6678467	VGINYQPPTVVPGGDLAK		tubulin, alpha 4 [Mus musculus]	1824.9908	46.71	1.267602515
6678469	VGINYQPPTVVPGGDLAK		tubulin, alpha 6 [Mus musculus]	1824.9908	46.71	1.267602515
63476037	VGLVQYNSDPTDEFFLR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1999.9791	45.15	0
63476037	VGLVQYNSDPTDEFFLR	Deamidation (NQ)	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2000.9662	60.81	0.1253609
6753620	VGNLGLATSFFNER		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1524.7905	39.85	0
21312260	VGNPFELDTQQGPQVDKEQFER		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	2561.2185	61.11	0.745449089
63746482	VGSAADIPINISETDLSLLTATVVPPSGR		PREDICTED: filamin, alpha [Mus musculus]	2893.5596	117.44	0.325844961
16716467	VGSGDTNNFPYLEK		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1540.7308	46.98	1.370206416
46849705	VGSSGDIALHLNPR		lectin, galactose binding, soluble 4 [Mus musculus]	1435.7761	92.04	1.293542535
29126205	VGVPTETGALTLNR		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1427.7941	63.98	0.881406833
63680429	VGVSQQPEDSQQDLPGER		PREDICTED: plexin B2 [Mus musculus]	1968.9282	53.38	1.24082482
11230802	VGWEQLLTTIAR		actinin alpha 4 [Mus musculus]	1386.7805	71.87	1.107353003
51491845	VGYTPDWIFLLR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1479.8088	40.38	2.318530698
46559834	VIDSLEDEKEALTLAMADR		desmuslin isoform M [Mus musculus]	2119.0569	89.5	0.200163023
30348966	VIESTQDLGNDLAGVMALQR		spectrin beta 2 isoform 1 [Mus musculus]	2130.0684	26.03	1.693563712
30348966	VIESTQDLGNDLAGVMALQR	Deamidation (NQ)	spectrin beta 2 isoform 1 [Mus musculus]	2131.0784	48.22	0
7305085	VIFLEDDDVAAVVDGR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1732.8784	84.33	0
6754524	VIGSGCNLDSAR		lactate dehydrogenase 1, A chain [Mus musculus]	1191.583	72.76	1.30364605
6678674	VIGSGCNLDSAR		lactate dehydrogenase 2, B chain [Mus musculus]	1191.583	72.76	1.30364605
63664186	VIGSGCNLDSAR		PREDICTED: similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M) [Mus mus	1191.583	72.76	1.30364605
6679937	VIISAPSADAPMFVMGVNHEK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	2213.1169	92.7	0
33469063	VILQDFTGVPAVVDFAAMR		aconitase 1 [Mus musculus]	2049.0757	34.24	1.83644156
20137006	VISGVLQLGNIAFK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1458.869	85.6	0
45597447	VISLSGEHSIIGR		superoxide dismutase 1, soluble [Mus musculus]	1367.7594	58.93	1.051804267
31982178	VIVVGNPANTNCLTASK		malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1700.9061	73.79	0
29293809	VKSINNPDMR	Oxidation (M)	ATP citrate lyase [Mus musculus]	1189.5903	21.49	0
11230802	VLAVNQENEHLMEDYER		actinin alpha 4 [Mus musculus]	2088.967	59.64	1.378760372

6678449	VLDASWYSPGTR	thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	1351.6647	48.92	1.219105186
7106335	VLDELTLAR	keratin complex 1, acidic, gene 17 [Mus musculus]	1029.5889	47.04	1.692523951
6680606	VLDELTLAR	keratin complex 1, acidic, gene 19 [Mus musculus]	1029.5889	47.04	1.692523951
547751	VLDELTLAR	Keratin, type I cytoskeletal 17 (Cytokeratin 17) (K17) (CK 17) (39.1)	1029.5889	47.04	1.692523951
417200	VLDELTLAR	Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1029.5889	47.04	1.692523951
51766008	VLDNTWPAAPYR	PREDICTED: myosin IA [Mus musculus]	1402.707	34.78	1.246827495
15617203	VLDNYLTSPLPEEVDETSAEDEGISQR	chloride intracellular channel 1 [Mus musculus]	3006.4116	74.13	1.660252537
31980648	VLDSGAPIKIPVGPETLGR	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1919.0908	27.73	0.976112595
19923052	VLEVPPIVYLR	brain acyl-CoA hydrolase [Mus musculus]	1297.7861	30.5	0.953396128
6754854	VLFDTGLVNPR	nidogen 1 [Mus musculus]	1230.6833	39.09	0.458008686
60218877	VLGELWPLFGGR	ATP-binding cassette, sub-family D, member 3 [Mus musculus]	1343.7445	53.82	0.712856886
29336026	VLGLLPEEITAMLR	nonmuscle myosin heavy chain [Mus musculus]	1554.8995	48.29	1.526056481
27804325	VLGSQEALSPVHYEEK	monoamine oxidase A [Mus musculus]	1785.9113	60.61	1.035778028
31982526	VLIDWINDVLVGER	parvin, alpha [Mus musculus]	1640.9037	53.41	0.5611612
6678499	VLIGGDETPEGQK	UDP-glucose dehydrogenase [Mus musculus]	1342.6836	70.76	0
6753484	VLLFSDGNSQGATAEAIEK	procollagen, type VI, alpha 1 [Mus musculus]	1949.9784	121.87	0
13385036	VLNSYWVGEDSTYK	ribosomal protein L15 [Mus musculus]	1660.7903	99.21	0
15426055	VLQDLVMDILR	coatomer protein complex, subunit beta 1 [Mus musculus]	1314.744	33.48	1.190750221
7948997	VLQDLVNDGPDDRPAGTR	PDZ and LIM domain 3 [Mus musculus]	1937.9764	35.94	0.147099358
6680748	VLSIGDGIAR	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1000.5732	35.91	1.106154543
6754984	VLSMAPGLTSVEIIPFR	3'-phosphoadenosine 5'-phosphosulfate synthase 2 [Mus musculus]	1830.0321	25.3	0.954045057
63556656	VLSPLEYFR	PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1123.6118	27.92	3.204341146
10946574	VLTPELYAELR	creatine kinase, brain [Mus musculus]	1303.725	47.24	0.22074433
7657429	VLTQIGTSIQDFLEAEDDLSSFR	osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2584.28	113.92	0.698760815
7657031	VLVDMDGVLADFESGLLQGFR	5',3'-nucleotidase, cytosolic [Mus musculus]	2281.1379	43.87	3.001061214
42415475	VLVGANFEEVAFDEK	prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1666.8198	80.51	1.210403871
13569841	VLVLDFVTPTPLGTR	thioredoxin reductase 1 [Mus musculus]	1627.943	30.47	1.17340251
6679078	VMLGETNPADSKPGTIR	nucleoside-diphosphate kinase 2 [Mus musculus]	1785.918	63.33	1.492933996
34576561	VMQQQQQATQQQLPQK	splicing factor 3a, subunit 1 [Mus musculus]	1911.9723	76.65	2.054622725
31560611	VNESTQNWHQLENIGNFIK	calponin 1 [Mus musculus]	2271.1384	83.27	0
7305085	VNFDDYTVNLGGLK	glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1554.7751	64.89	0.70708547
31560689	VNFSPPGDTSNLFPGTWYLER	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	2397.1553	77.57	0.122613638
33859482	VNFTVDQIR	eukaryotic translation elongation factor 2 [Mus musculus]	1091.5846	51.26	1.357506128
6678752	VNGEPLDLDPGQTLIYYVDEK	lymphocyte antigen 74 [Mus musculus]	2378.1858	71.12	2.338964765
63556656	VNGVLMALPVYLAGGR	PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1629.9178	22.39	3.184809237
9790069	VNIAFNYDMPEDSDTYLHR	HLA-B-associated transcript 1A [Mus musculus]	2300.0471	35.05	0
6755967	VNNASLIGLGYTQTLRPGVK	voltage-dependent anion channel 3 [Mus musculus]	2101.1685	29.42	0.903328326
6679439	VNPTVFFDITADDEPLGR	peptidylprolyl isomerase A [Mus musculus]	2005.9894	108.98	1.452942539
6677807	VNQAIWLLCTGAR	ribosomal protein S5 [Mus musculus]	1444.7681	23.56	3.054576239
63540743	VNQPASFAVQLNGAR	PREDICTED: filamin C, gamma [Mus musculus]	1571.8291	38.34	0
31981824	VPAPEVASGPDPEEEIR	ankyrin repeat domain 25 [Mus musculus]	1791.8811	54.49	0
19525729	VPDDPEHLAAR	crystallin, lamda 1 [Mus musculus]	1219.6071	40.95	0.935500163
13385168	VPDFSDYR	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Mus musculus]	998.4575	39.96	0.910946369
6755714	VPENPPSMVFK	transgelin [Mus musculus]	1244.6318	59.61	0
6753484	VPNYQALLR	procollagen, type VI, alpha 1 [Mus musculus]	1073.6089	54.89	0.233146948
29126205	VPPETIDSVIVGNVMQSSSDAAYLAR	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	2719.3586	44.39	0.679023754
51711855	VPQLPITNFNR	PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like prot	1298.7197	22.48	0.458060447
56119103	VPSTEAEALASSLMGLFEK	guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1979.9902	75.65	1.026674077
6679937	VPTPNVSVVDLTCR	similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1499.793	91.58	1.259604633
37537522	VPVDVAYQR	epiplakin 1 [Mus musculus]	1046.5605	56.64	1.675703876
46849705	VPYVGALQGGLTVR	lectin, galactose binding, soluble 4 [Mus musculus]	1429.8271	100.8	1.78220075
63552538	VQEVEVPEDFGPVR	PREDICTED: echinoderm microtubule associated protein like 2 [Mus musculus]	1599.8103	56.41	1.014700637
6754256	VQQTVQDLFGR	heat shock protein 9A [Mus musculus]	1290.6807	60.69	1.594154243
6754482	VRPASSAASVYAGAGGSGSR	keratin complex 1, acidic, gene 18 [Mus musculus]	1807.9116	48.58	1.055963148
54607098	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	succinate dehydrogenase Fp subunit [Mus musculus]	2929.4875	43.36	0
7305295	VSDLTTNLAEEEEK	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1577.7642	79.6	0
21312216	VSDVVDGNIQGR	gasdermin domain containing 1 [Mus musculus]	1258.637	39.63	2.155628041
37620153	VSDVYDIEER	myosin, light polypeptide kinase telokin isoform [Mus musculus]	1224.5809	67.55	0
30348966	VSEEAESQQWDTSK	spectrin beta 2 isoform 1 [Mus musculus]	1623.7203	40.84	0
7106421	VSEEAESQQWDTSK	spectrin beta 2 isoform 2 [Mus musculus]	1623.7203	40.84	0

63481281	VSETVAFTDVNSILR		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1650.8656	21.79	0
28916693	VSNGAGSMSVSLVADENPFAQGALR		gelsolin [Mus musculus]	2477.2163	36.92	1.561876658
63556656	VSQHGSDVVIETDFGLR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1858.9347	19.96	1.469796149
6755809	VSQMAQYFEPLTLAAVGAASK		talin 1 [Mus musculus]	2182.1416	27.63	1.42632745
38142460	VSVISVEEPPQR		electron transferring flavoprotein, beta polypeptide [Mus musculus]	1339.7227	20.47	0.608593399
31982169	VSVVEPGNFIAATSLYSPER		3-hydroxybutyrate dehydrogenase (heart, mitochondrial) [Mus musculus]	2136.0981	86.67	1.300348509
31543605	VTAEVVLVHPGGGSTSR		ribophorin I [Mus musculus]	1665.9	65.48	0.740955126
63746482	VTAQGPGLEPSGNIANK		PREDICTED: filamin, alpha [Mus musculus]	1652.8733	82.25	0.2345229
63660302	VTASGPGLSAYGVPASLPVEFAIDAR		PREDICTED: filamin B, beta [Mus musculus]	2545.3132	26.12	1.319955334
31981722	VTHAVVTVPAYFNDAQR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1887.973	56.4	0.89085913
20799907	VTIAQGGVLPNIQAVLLPK		histone 2, H2aa1 [Mus musculus]	1931.1863	123.67	1.515013222
34328142	VTIASLPR		lymphoid-restricted membrane protein [Mus musculus]	856.5162	23.09	0
54607098	VTLEYRPVIDK		succinate dehydrogenase Fp subunit [Mus musculus]	1332.7538	23.06	0.945830902
8393150	VTPPEGYDVVTVFR		carboxyl terminal LIM domain protein 1 [Mus musculus]	1578.8259	44.47	1.217962091
6755963	VTQSNFAVGYK		voltage-dependent anion channel 1 [Mus musculus]	1213.6213	70.53	2.040042011
6678499	VTVVDVNEAR		UDP-glucose dehydrogenase [Mus musculus]	1101.5892	34.51	0.371831868
63746482	VTYTPMAPGSYLISIK		PREDICTED: filamin, alpha [Mus musculus]	1740.9198	66.98	1.026436187
6754084	VTYVDFLAYDILDQYR		glutathione S-transferase, mu 1 [Mus musculus]	1993.9952	43.62	1.781476583
58037117	VVAEPVELAQEFR		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Mus musculus]	1486.7889	40.49	1.027906939
6755809	VVAPTISSPVCQEQLVEAGR		talin 1 [Mus musculus]	2083.0872	39.97	0
46593021	VVELLADIVQNSSLEDSQIEK		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	2329.2168	77.85	0.595713436
63476037	VVESLDVGPDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1185.613	39.21	0
46849705	VVFNTMQSGQWGK		lectin, galactose binding, soluble 4 [Mus musculus]	1481.7228	87.11	1.93513884
20137006	VVFQEFR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	924.4819	27.14	1.987490917
27754118	VVHCSDLGLTSVPNNIPFDTR		asporin [Mus musculus]	2284.1201	20.15	0
63476037	VVIHFTDGADGDMADLYR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1994.9178	46.81	0
6678413	VVLAYEPVWAIGTGK		triosephosphate isomerase 1 [Mus musculus]	1602.8861	58.73	1.154163969
6680309	VVLDDKDYFLFR		heat shock protein 1 (chaperonin 10) [Mus musculus]	1529.7722	25.59	1.435453919
34538601	VVLPMELPIR		cytochrome c oxidase subunit II [Mus musculus]	1166.6991	39.77	1.077493945
7305169	VVNVELPVEANLVWQLGR		heat shock protein 105 [Mus musculus]	2035.1144	26.41	0
7305295	VVSSVLQLGNIVFK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1502.8982	117.8	0.174097387
46849705	VVVNGNSFYEYGHR		lectin, galactose binding, soluble 4 [Mus musculus]	1640.787	68.06	1.429214849
46849705	VVVNGNSFYEYGHR	Deamidation (NQ)	lectin, galactose binding, soluble 4 [Mus musculus]	1641.7744	82.01	1.827080515
6677773	VWLDPNETNEIANANSR		ribosomal protein L19 [Mus musculus]	1942.9432	23.94	1.800591067
6680047	VWQVTIGTR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1059.5938	49.98	1.807171196
63481281	VYEELLAIPVVR		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1400.8248	34.4	0
6755142	VYFDLQIGDESVGR		peptidylprolyl isomerase B [Mus musculus]	1597.7811	79.88	0
41322904	VYHDPSTQEPVTYSQLQQR		plectin 1 isoform 1 [Mus musculus]	2276.094	55.75	0.872578107
33859686	VYWDNGAQIISPHDR		phosphoglucomutase 1 [Mus musculus]	1770.8651	23.14	0
46559834	WAEDQALYAEEAR		desmuslin isoform M [Mus musculus]	1551.7177	52.81	0
30023842	WALSQSNPSALR		valosin containing protein [Mus musculus]	1329.6884	20.86	1.991186347
31981892	WDDPYYDIAR		Rho GTPase activating protein 1 [Mus musculus]	1313.5867	25.68	2.120094565
1346343	WELLQQVDTSTR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1475.7378	64.51	0
27754099	WFLTCINQPQFR		eukaryotic translation elongation factor 1 gamma [Mus musculus]	1552.7783	27.58	1.420158623
63746482	WGDEHIPGSPYR		PREDICTED: filamin, alpha [Mus musculus]	1413.6595	70.99	0
6679937	WGEAGAEYVVESTGVFTTMEK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	2291.0691	55.28	1.367706163
31559916	WGTLTDCVVMR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1280.6102	36.25	1.478548887
8567336	WGVFNEYNNDEK		chloride channel calcium activated 3 [Mus musculus]	1514.6615	63.41	1.521920348
31543942	WIDNPTVDDR		vinculin [Mus musculus]	1230.5826	45.85	0.695109961
51491845	WLLLTGISAQQNR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1499.8314	23.9	1.258391726
6755965	WNTDNTLGTEIAIEDQICQGLK		voltage-dependent anion channel 2 [Mus musculus]	2462.2019	21.57	0
6755963	WNTDNTLGTEITVEDQLAR		voltage-dependent anion channel 1 [Mus musculus]	2176.0571	125.01	1.32572446
41322904	WQAVLAQTDVR		plectin 1 isoform 1 [Mus musculus]	1286.6829	21.54	5.799579019
24762230	WQNNLLPSR		ribosomal protein S15a [Mus musculus]	1127.5906	21.21	1.76822223
6755963	WTEYGLTFTEK		voltage-dependent anion channel 1 [Mus musculus]	1374.652	68.95	1.318854335
27804325	WVDVGGAYVGPTQNR		monoamine oxidase A [Mus musculus]	1618.8068	83.5	1.226078144
6671702	WVGGPEIELIAIATGGR		chaperonin subunit 5 (epsilon) [Mus musculus]	1738.9419	19.06	0.873703232
21450277	WVNDVEDSYGQQWTYEQR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2303.0056	85.67	1.084679297
12963633	WVPPLIGEMYGLR		genes associated with retinoid-IFN-induced mortality 19 [Mus musculus]	1530.8176	20.97	1.243345281
18079339	WVVIGDENYGEGSSR		aconitase 2, mitochondrial [Mus musculus]	1667.7748	75.74	0.933709702

6680934	WWQQEEQLGPEESR	chromogranin B [Mus musculus]	1801.819	26.34	0
31981549	YADALQEIIR	sulfide quinone reductase-like [Mus musculus]	1191.632	55.33	1.596062505
6754854	YALSNSIGPVR	nidogen 1 [Mus musculus]	1176.6343	19.64	0.549086145
9790219	YALYDASFETK	destrin [Mus musculus]	1307.6168	68.93	0
6680924	YALYDATYETK	cofilin 1, non-muscle [Mus musculus]	1337.6302	61.05	1.239303212
13195624	YAPGYNAEVGDK	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 [Mus musculus]	1283.5923	48.36	0
6755995	YAPSGFYIASGDISGK	WD repeat domain 1 [Mus musculus]	1632.7869	31.33	0
29244560	YASASEPTEIYR	hypothetical protein LOC331063 [Mus musculus]	1386.6649	22.16	1.263386034
22164770	YDGWPELLELEGCVPR	oncoprotein induced transcript 1 [Mus musculus]	1875.9022	56.14	0
6753262	YDPPLEDGAMPSAR	capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1518.6836	35.81	1.287322007
21704066	YDPTIEDSYR	RAS-related protein-1a [Mus musculus]	1258.5654	27.42	0.777904186
6755809	YDQATDTILTVTENIFSSMGDAGEMVR	talin 1 [Mus musculus]	2964.3655	90.65	0.492945801
12963769	YDQGVEPADHLDGSTEEQR	harmonin isoform a1 [Mus musculus]	2145.9202	25.55	0
22267442	YEDSNNLGTSHLLR	ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1618.7795	52.37	0
27370092	YEEIDNAPEER	Tu translation elongation factor, mitochondrial [Mus musculus]	1364.6	56.66	0.984011335
1346343	YEELQITAGR	Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1179.6024	53.22	0.221114445
13624315	YEELQTLAGK	keratin complex 2, basic, gene 8 [Mus musculus]	1151.5975	60.2	0
16716471	YEHANDDDTSLKSDPEGEK	hypothetical protein LOC94184 [Mus musculus]	2149.9233	105.8	1.366304221
7305295	YEILAANAIPK	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1202.673	50.29	0.330747509
33859482	YEWDVAEAR	eukaryotic translation elongation factor 2 [Mus musculus]	1138.5204	65.43	1.711868112
51764087	YFAGNLASGGAAGATSLCFVYPLDFAR	PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	2739.3	58.37	1.240838137
22094075	YFAGNLASGGAAGATSLCFVYPLDFAR	solute carrier family 25, member 5 [Mus musculus]	2739.3	58.37	1.240838137
27370516	YFDLGLPNR	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	1094.5612	27.07	1.179192979
31657132	YFGELLADLSR	premature ovarian failure 1B [Mus musculus]	1283.6652	33.02	1.746711213
51764087	YFPTQALNFAFK	PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	1446.7524	57.62	1.43646682
22094075	YFPTQALNFAFK	solute carrier family 25, member 5 [Mus musculus]	1446.7524	57.62	1.43646682
23621467	YFQFQEEGKEGENR	PREDICTED: actin related protein 2/3 complex, subunit 2 [Mus musculus]	1760.8049	24.1	0.926691763
47059123	YFSLPSVVFSR	UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	1301.6942	27.96	0.844328901
46593021	YFYDQCPAVAGYGPIEQLPDYNR	ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	2679.2322	83.91	1.07801037
34328204	YGEAGDGPGWGGPHPR	valyl-tRNA synthetase 2 [Mus musculus]	1609.7279	36.79	1.368332974
63746482	YGGDEIPFSPYR	PREDICTED: filamin, alpha [Mus musculus]	1400.6563	68.07	0.372965994
22203747	YGGLHFSDQVEVFSPPGSDR	procollagen, type VI, alpha 2 [Mus musculus]	2194.0347	56.58	0
21312260	YGLAAAVFTR	aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1068.5812	40.19	0.944816599
6681087	YGLFPANYVELR	cortactin [Mus musculus]	1441.7445	22.73	1.258847172
6677975	YGPIADVSIVYDQQSR	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila) [Mus musculus]	1810.8693	21.92	0.735206262
6755817	YGVNPGPIVGTTR	thymopoietin [Mus musculus]	1330.7133	26.41	2.246518412
6680606	YGVQLSQIQSVISGFEAQLSDVR	keratin complex 1, acidic, gene 19 [Mus musculus]	2524.3142	183.61	1.70240479
40556608	YHTSQSGDEMTSLSEYVSR	heat shock protein 1, beta [Mus musculus]	2176.9573	78.57	1.426160625
34996495	YHVPVVVVPEGSTSDTQEQAILR	ribophorin II [Mus musculus]	2524.2957	79.05	0.944844975
63746482	YIPVQQGPVGVNVTYGGDHIPK	PREDICTED: filamin, alpha [Mus musculus]	2338.2239	107.91	0
51770896	YITPDQLADLYK	PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1439.7288	61.27	0.914677172
16716381	YLDLILNDFVR	lysyl-tRNA synthetase [Mus musculus]	1380.7551	32.36	1.587114604
18875380	YLECSALTQR	RAS-related C3 botulinum substrate 3 [Mus musculus]	1183.5825	29.18	2.865112578
6678449	YLGTQPEPDIVGLDSGHIR	thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	2067.0339	50.49	0.805616858
31560645	YLLSQSSPAPLTAAEEELR	twinfilin [Mus musculus]	2075.0605	39.89	0.94918524
7305295	YLPIYSEK	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1012.5289	40.43	0.234802273
41322904	YLQDLLAWVEENQR	plectin 1 isoform 1 [Mus musculus]	1776.8932	58.68	1.366474982
22165384	YLTVAAVFR	tubulin, beta, 2 [Mus musculus]	1039.5938	36.49	1.100173467
31981939	YLTVAAVFR	tubulin, beta 4 [Mus musculus]	1039.5938	36.49	1.100173467
7106439	YLTVAAVFR	tubulin, beta 5 [Mus musculus]	1039.5938	36.49	1.100173467
33859506	YMCENQATISSK	albumin 1 [Mus musculus]	1374.609	73.37	2.098818486
63660302	YMIGVTYGGDNIPLSPYR	PREDICTED: filamin B, beta [Mus musculus]	2015.9944	25.01	1.58104274
6679078	YMNSGPVVAMVWEGLNVVK	nucleoside-diphosphate kinase 2 [Mus musculus]	2093.0579	36.12	0.948362222
6678573	YNDEPVQIR	villin 1 [Mus musculus]	1133.5593	31.81	1.969094576
63746482	YNDQHIPGSPFTAR	PREDICTED: filamin, alpha [Mus musculus]	1602.7739	80.41	0.36577749
19072792	YNGDNVIYKPPGR	thioredoxin domain containing 4 [Mus musculus]	1492.7568	39.95	0
6753138	YNPNVLPVQCTGK	Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1432.7258	32.49	1.584742989
51771420	YNVLGAETVLTQMR	PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1594.8214	33.59	1.532451602
42741690	YPEAPPSVR	ubiquitin-conjugating enzyme E2 variant 1 [Mus musculus]	1015.5206	35.07	1.087546281
6671507	YPIEHGIITNWDDMEK	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1960.9279	62.24	1.072204208

6755965	YQLDPTASISAK	voltage-dependent anion channel 2 [Mus musculus]	1293.6552	20.65	0
6755963	YQVDPDACFSAK	voltage-dependent anion channel 1 [Mus musculus]	1343.6036	53.82	1.329269096
13386110	YRPAAEDILLR	hypothetical protein LOC68226 [Mus musculus]	1316.7499	19.41	1.159073369
31982223	YSEIEPSTEGEVIYR	laminin, beta 2 [Mus musculus]	1771.8477	53.48	0
8394024	YSFLQFDPAPR	protein phosphatase 2a, catalytic subunit, beta isoform [Mus musculus]	1340.6699	19.92	0
23956406	YSGGLPLPPSYVPVVMSELSDR	UDP glucuronosyltransferase 2 family, polypeptide B34 [Mus musculus]	2363.2046	26.92	1.130668463
63474405	YSMPDNSPETR	PREDICTED: tensin [Mus musculus]	1296.5575	29.55	0
63746482	YSPSEAGLHEMDIR	PREDICTED: filamin, alpha [Mus musculus]	1604.7498	68.9	0
6755863	YSQFINFPIYVWSSK	tumor rejection antigen gp96 [Mus musculus]	1878.938	25.28	2.42831489
46559834	YSWQDEIAQGTWR	desmuslin isoform M [Mus musculus]	1639.745	50.05	0
6671539	YTPSGQSGAAASESLFISNHAY	aldolase 1, A isoform [Mus musculus]	2258.031	85.93	0.997273198
6754016	YTTPEDATPEPGEDPR	guanine nucleotide binding protein alpha stimulating isoform b [Mus musculus]	1774.7831	49.13	1.194628667
6680854	YVDSEGHLYTVPIR	caveolin, caveolae protein 1 [Mus musculus]	1648.8323	64.73	0.410946695
13386062	YVEEQPGNLQR	hypothetical protein LOC68117 [Mus musculus]	1332.6603	33.69	0.942658669
31543349	YVGESEANIR	N-ethylmaleimide sensitive fusion protein [Mus musculus]	1137.5559	35.96	0
31541863	YVNWIQQTIAAN	RIKEN cDNA 2210010C04 [Mus musculus]	1420.7249	79.24	0
40254244	YVQELPLETDGALR	loss of heterozygosity, 11, chromosomal region 2, gene A homolog [Mus musculus]	1603.8314	36.67	2.115125429
64427157	YVVDSDTVQAHTVR	PREDICTED: synaptopodin 2 [Mus musculus]	1589.7892	80.28	0.465509955
6681143	YWEIFPNTFR	decorin [Mus musculus]	1372.6742	25.84	0.634499736
27754118	YWEIQPATFR	asporin [Mus musculus]	1310.652	38.38	0.447558057
6678499	YWQQVIDMNDYQR	UDP-glucose dehydrogenase [Mus musculus]	1758.8051	50.13	0.949933273
31982290	YYEPYYAAGPSYGGR	LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1713.7595	69.8	0.556368756
23943876	YYIVGLQVR	zymogen granule membrane protein 16 [Mus musculus]	1110.629	37.51	3.798331932
6755354	YYPTEDVPR	ribosomal protein L6 [Mus musculus]	1139.5391	33.75	1.523438235
63556656	YYVLGATFYPGPECER	PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1864.8593	22.52	2.670763222
51873060	YYVTIIDAPGHR	eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	1404.7323	23.88	1.32459851

Mouse Pair 3

GI #	Sequence	Modifications	Protein Name	M/z	Highest Mascot score	Average Ratio (15N:14N), non-Log-transformed
33859554	AAAEVNQEYGLDPK		fumarate hydratase 1 [Mus musculus]	1504.7223	69.26	0
57634518	AAAQLLQSQAQQSGAQQTK		septin 11 [Mus musculus]	1957.0112	72.15	1.215810433
33859506	AADKDTCFSTEGPNLVTR		albumin 1 [Mus musculus]	1924.9061	49.89	1.808824086
6756033	AADPPAENSSAPEAEQGGAE		nuclease sensitive element binding protein 1 [Mus musculus]	1897.7997	85.55	1.354769357
29789080	AAESLADPTEYENLFPGLK		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	2065.0112	66.04	0.983041071
31981925	AAFDDAIAELDTLSEESYK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Mus mu	2087.978	85.84	1.102580567
6753036	AAFQLGSPWR		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1132.5895	31.3	2.139532284
6724311	AAGAARIIAVDINK	Deamidation (NQ)	alcohol dehydrogenase 1 (class I) [Mus musculus]	1383.8196	21.23	0
6680606	AALEGTLAETEAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1331.6812	64.76	1.49662011
29126205	AANEAGYFNEEMAPIEVK		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1982.9382	25.97	1.303376707
13385006	AANNGALPPDLSYIVR		cytochrome c-1 [Mus musculus]	1670.8837	28.45	1.466027529
27754065	AAPFTLEYR		pyrophosphatase [Mus musculus]	1067.5601	37.56	1.352918179
6677995	AAQSPQQHSSGDPTEEESPV		solute carrier family 16, member 1 [Mus musculus]	2080.9092	93.08	1.408448746
8567336	AASATLPPITVTPVVNK		chloride channel calcium activated 3 [Mus musculus]	1678.9706	62.13	0
63474405	AASDGQYENQSPEATSPR		PREDICTED: tensin [Mus musculus]	1907.8383	56.77	1.547021376
7304889	AASGFNATEDAQTLR		annexin A4 [Mus musculus]	1551.7439	94.01	1.719330088
6678483	AAVASLLQSVQVPEFTPK		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1885.0399	47.29	0.902248037
31981826	AAVDAGFVPNDMQVGQTGK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1904.9149	29.84	0
51770896	AAVPSGASTGIYEALELR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1804.9504	103.81	2.0694588
22094075	AAYFGIYDTAK		solute carrier family 25, member 5 [Mus musculus]	1219.6038	67.76	0.980257888
6671539	ADDGRPFPQVIK		aldolase 1, A isoform [Mus musculus]	1342.7147	39.2	1.194458855
34328489	ADFDNTVAIHPTSSEELVTLR		glutathione reductase 1 [Mus musculus]	2315.1563	52.5	2.188657304
6753598	ADFQGISPER		defender against cell death 1 [Mus musculus]	1119.545	22.27	0
31981522	ADIELFVNR		transmembrane 9 superfamily member 2 [Mus musculus]	1076.5709	24.86	1.014498875
6754084	ADIVENQVMDTR		glutathione S-transferase, mu 1 [Mus musculus]	1390.6617	60.74	1.039752452
547749	ADLEMQIESLTEELAYLK	Oxidation (M)	Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	2112.0422	86.73	0
6754254	ADLINNLGTIAK		heat shock protein 1, alpha [Mus musculus]	1242.6915	43.55	1.342167165
40556608	ADLINNLGTIAK		heat shock protein 1, beta [Mus musculus]	1242.6915	43.55	1.342167165
33859811	ADMVIEAVFEDLGVK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1635.83	80.36	1.549564867
31981100	ADRDESSPYAAMLAAQDVAQR		ribosomal protein S14 [Mus musculus]	2265.0562	42.24	2.235278843
31560731	ADYAQLLEDMQNAFR		ATPase, H+ transporting, V1 subunit A, isoform 1 [Mus musculus]	1784.8339	22.52	1.400125703
13399310	AEAGAGSATEFQFR		ribosomal protein S10 [Mus musculus]	1441.6774	39.8	0.83431684
6996913	AEDGSVIDYELIDQDAR		annexin A2 [Mus musculus]	1908.8928	61.23	1.363990223
21703832	AEFGPPGPGPGSR		arginyl aminopeptidase (aminopeptidase B) [Mus musculus]	1225.5989	22.19	1.304689494
6678573	AELGNSGDWSQIADEVMSPK		villin 1 [Mus musculus]	2133.9849	73.36	0.844094937
6755372	AELNEFLTR		ribosomal protein S3 [Mus musculus]	1092.5671	30.85	0.742891359
13386054	AENFFILR		actin related protein 2/3 complex, subunit 4 [Mus musculus]	1009.5494	35.13	0.93737522
6678483	AENYDISPADR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1250.5728	56.6	0.996018312
23956222	AEPEDHYFLLTEPPLNTPENR		ARP3 actin-related protein 3 homolog [Mus musculus]	2482.1643	68.5	1.103643882
20149726	AETAPLPTSVDDTPEVLNR		phosphatidate cytidylyltransferase 2 [Mus musculus]	2025.0079	68.86	2.616810997
14149645	AETSESSGSAPAVPEASASPK		methyl CpG binding protein 2 [Mus musculus]	1959.8849	21.07	0
63746482	AEVGVPAEFGIWTR		PREDICTED: filamin, alpha [Mus musculus]	1531.8018	68.86	1.617163351
6753294	AEVQNLGGELVVSGVDSAMSLIQAAK		catenin alpha 1 [Mus musculus]	2586.3286	28.3	1.449113902
29293809	AFDSGIIPMEFVNK		ATP citrate lyase [Mus musculus]	1567.7742	27.45	1.964736488
63746482	AFGPGLQGGNAGSPAR		PREDICTED: filamin, alpha [Mus musculus]	1456.7349	104.8	1.670095236
8567402	AFGYYGPLR		splicing factor, arginine/serine-rich 3 (SRp20) [Mus musculus]	1043.5364	27.97	1.280756456
13384888	AFIFPQESSTAYVSLIPK		hypothetical protein LOC66289 [Mus musculus]	1998.0565	111.36	0
7710086	AFLTLAEDILR		RAB10, member RAS oncogene family [Mus musculus]	1261.7227	49.25	1.326189996
51491845	AFMTADLPNELIELLEK		clathrin, heavy polypeptide (Hc) [Mus musculus]	1947.0143	54.28	1.427239585
6755781	AFSGLTQNPESIELR		thrombospondin 4 [Mus musculus]	1661.8323	37.51	0
6677991	AFYAPVHADDLR		solute carrier family 12, member 2 [Mus musculus]	1374.6862	37	2.210525536
31982186	AGAGSATLSMAYAGAR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1454.709	71.19	1.115027974
6671507	AGFAGDDAPR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	976.4518	52.96	1.029200041
6671509	AGFAGDDAPR		actin, beta, cytoplasmic [Mus musculus]	976.4518	52.96	1.029200041

18266680	AGGAGVPAFYTSTGYGTLVQEGGSPIK	3-oxoacid CoA transferase 1 [Mus musculus]	2585.2849	40.29	1.42511251
31982275	AGGIETIANEYSDR	heat shock protein 4 [Mus musculus]	1495.705	27.96	0
33859811	AGLEQGSDAGYLAESQK	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1723.8142	103.41	1.285021036
20799907	AGLQFPVGR	histone 2, H2aa1 [Mus musculus]	944.5352	52.67	0.779666653
63562740	AGLSLMWNR	PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1047.5447	20.56	0.44737913
31982223	AGNSLAASTAEETAGSAQSR	laminin, beta 2 [Mus musculus]	1878.88	46.48	0.949117888
11230802	AGTQIENIDEDFR	actinin alpha 4 [Mus musculus]	1507.7	55.82	0.959189202
59709449	AGTQIENIEEDFR	actinin alpha 2 [Mus musculus]	1521.7247	50.93	1.401465542
7106453	AGYSQGATQYTQAQQAR	zinc finger RNA binding protein [Mus musculus]	1828.86	22.86	1.27690816
31980648	AIAELGIYPAVDPLDSTSR	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1988.038	94.78	1.06708932
39652626	AIAGIINQPYYNYQAGPDAALGR	bisphosphate 3'-nucleotidase 1 [Mus musculus]	2436.25	59.36	3.880380672
6755004	AIASATEGGSVPQIR	programmed cell death 8 [Mus musculus]	1456.77	47.72	1.585249167
12963569	AIENIDTLTNLESLFLGK	protein phosphatase-1 regulatory subunit 7 [Mus musculus]	1991.0343	23.48	0
31560653	AIGVLTSGGDAQGMNAAVR	phosphofructokinase, liver, B-type [Mus musculus]	1787.8901	63.26	1.049512968
9790051	AIGVLTSGGDAQGMNAAVR	phosphofructokinase, platelet [Mus musculus]	1787.8901	63.26	1.049512968
12963615	AILVDLEPGTMDSVR	tubulin, beta 3 [Mus musculus]	1615.8369	53.05	0
7106439	AILVDLEPGTMDSVR	tubulin, beta 5 [Mus musculus]	1615.8369	53.05	0
21746161	AILVDLEPGTMDSVR	tubulin, beta [Mus musculus]	1615.8369	53.05	0
6755198	AINQGGLTSVAVR	proteasome (prosome, macropain) subunit, alpha type 6 [Mus musculus]	1285.7211	59	0.909156103
31543942	AIPDLTAPVAAVQAAVSNLVR	vinculin [Mus musculus]	2076.1863	48.59	1.192683304
6753864	AIVAGDQNVEYK	four and a half LIM domains 1 [Mus musculus]	1306.6627	68.71	1.304577602
31560560	AIVAIENPADVSVISSR	laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1740.9559	69.08	1.112331767
31981722	AKFEELNMDLFR	heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1512.7599	31.23	0
29789343	AKPAAQSEEETATSPAASPTPQSAER	eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]	2612.2388	51.41	1.091180453
9845257	ALAAAGYDVEK	histone 1, H1c [Mus musculus]	1107.5665	87.23	0.723504647
34328365	ALAAAGYDVEK	histone 1, H1d [Mus musculus]	1107.5665	87.23	0.723504647
13430890	ALAAAGYDVEK	histone 1, H1e [Mus musculus]	1107.5665	87.23	0.723504647
13386370	ALAIYESQLGPDNPNVAR	kinesin-like 8 [Mus musculus]	1927.9874	38.91	0
6755809	ALDGDFTEENR	talin 1 [Mus musculus]	1266.5776	28.59	1.839568845
63471580	ALDIAENEMPGLMR	PREDICTED: similar to S-adenosylhomocysteine hydrolase [Mus musculus]	1559.767	55.77	1.395900136
58037267	ALDLFSDNAPPPELLEIINEDIAK	protein disulfide isomerase-associated 6 [Mus musculus]	2637.3643	21.52	0.760335364
547749	ALEESNYELEGK	Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1381.6454	75.17	0
33598964	ALELDPNLYR	myosin heavy chain 10, non-muscle [Mus musculus]	1203.6425	48.56	1.572437965
7305295	ALELDPNLYR	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1203.6425	48.56	1.572437965
20137006	ALELDSNLYR	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1193.6132	61.19	0.992468961
23956212	ALEPEEGNPQTEAQENGPER	HIV TAT specific factor 1 [Mus musculus]	2194.9944	106.25	1.216330791
6680606	ALEQANGELEVK	keratin complex 1, acidic, gene 19 [Mus musculus]	1300.6733	82.99	1.269984114
6679687	ALEQFLQEYFDGNLK	glucose regulated protein [Mus musculus]	1814.8999	20.26	0.788204997
20137006	ALEQQVEEMK	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1204.5647	31.09	1.210146877
7305295	ALETQMEEMK	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1209.5547	47.06	2.092556935
36031035	ALEYTIYNQELNETR	chondroitin sulfate proteoglycan 6 [Mus musculus]	1856.8661	26.13	0.751851044
27754099	ALIAAQYSGAQVR	eukaryotic translation elongation factor 1 gamma [Mus musculus]	1347.7419	71.58	0
63489754	ALINADELANDVAGAEALLDR	PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	2154.1052	88.48	1.048535174
6671666	ALLATASQCQQPAGNK	CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1600.8027	30.77	0.909830128
33859482	ALLELQLEPEELYQTFQR	eukaryotic translation elongation factor 2 [Mus musculus]	2220.1545	54.53	0.943799146
40556608	ALLFIPR	heat shock protein 1, beta [Mus musculus]	829.5453	39.75	1.098591806
34328489	ALLTPVAIAAGR	glutathione reductase 1 [Mus musculus]	1152.7126	26.67	1.23449606
63476037	ALNLGYALDYALR	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1452.7876	39.68	0.896549352
34328204	ALNPLEDWLR	valyl-tRNA synthetase 2 [Mus musculus]	1226.6598	27.39	0.859070726
63506192	ALPFWNEEIVPQIK	PREDICTED: similar to phosphoglycerate mutase (EC 5.4.2.1) B chain - rat [Mus musculus]	1683.8973	28.33	1.160738418
31981810	ALQLGTLFSPAEALK	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase) [Mus musculus]	1558.8644	27.67	0
21704020	ALSEIAGITLPYDTLDQVR	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	2075.1038	77.56	1.487430713
21703972	ALTTQLTDAELAQGR	malic enzyme 2, NAD(+)-dependent, mitochondrial [Mus musculus]	1587.8409	45.24	1.592529654
22165384	ALTVPELTQQMFDAK	tubulin, beta, 2 [Mus musculus]	1691.8728	50.74	1.118627103
12963615	ALTVPELTQQMFDAK	tubulin, beta 3 [Mus musculus]	1691.8728	50.74	1.118627103
31981939	ALTVPELTQQMFDAK	tubulin, beta 4 [Mus musculus]	1691.8728	50.74	1.118627103
27754056	ALTVPELTQQMFDAK	tubulin, beta 6 [Mus musculus]	1691.8728	50.74	1.118627103
7106439	ALTVPELTQQVFDAK	tubulin, beta 5 [Mus musculus]	1659.8954	50.39	0.819614776
63655455	ALVGSENPPLTVIR	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP2 [Mus musculus]	1465.842	27.66	0.996105454
31980953	ALVVTVDAPVLGNR	hydroxyacid oxidase (glycolate oxidase) 3 [Mus musculus]	1423.8226	48.89	0

6754556	ALYETELADAR		lamin B1 [Mus musculus]	1251.6228	41.64	0.927996571
19526818	ALYSNILGEENTYLWR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1941.9729	44.47	1.495442144
31981983	AMAEEDNGSIGEETDSSPGR		stromal interaction molecule 1 [Mus musculus]	2051.8545	111.15	1.10340186
21704100	AMDSDWFAQNYMGR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1691.7074	57.47	1.210198578
20874851	AMGIMNSFVNDIFER		PREDICTED: similar to histone H2b-616 [Mus musculus]	1743.8285	92.49	0.666532297
20874851	AMGIMNSFVNDIFER	Deamidation (NQ)	PREDICTED: similar to histone H2b-616 [Mus musculus]	1744.8119	49.36	1.102064875
41054806	AMGNLQIDFADPQR		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1575.764	40.5	0.95136484
6753320	AMTGVEQWPYR		chaperonin subunit 3 (gamma) [Mus musculus]	1337.6542	27.08	1.155931265
31981549	ANIIFNTALGTIFGVK		sulfide quinone reductase-like [Mus musculus]	1678.9473	64.61	0.923422734
63746482	ANLPQSFQVDTSK		PREDICTED: filamin, alpha [Mus musculus]	1434.7233	75.97	1.636384995
20137006	ANLQIDQINTDLNLER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1869.964	58.58	1.057409574
19745150	APDAWDYSQGFVNEEMIR		diaphorase 1 [Mus musculus]	2127.9536	72.52	1.3547669
6754750	APDFVFYAPR		moesin [Mus musculus]	1182.6023	59	0.97851534
6677699	APDFVFYAPR		radixin [Mus musculus]	1182.6023	59	0.97851534
6678571	APDFVFYAPR		villin 2 [Mus musculus]	1182.6023	59	0.97851534
39204553	APEPPPQQVAQQQ		chromodomain helicase DNA binding protein 4 [Mus musculus]	1417.7013	86.52	1.052653888
6681157	APILIATDVASR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1226.7151	45.84	1.408898921
40068493	APILIATDVASR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1226.7151	45.84	1.408898921
63540743	APLQVAVLGPTGVAEPVEVR		PREDICTED: filamin C, gamma [Mus musculus]	2002.1263	20.57	2.957618645
31560689	APLVLEQGLR		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	1095.6569	37.72	1.743481499
38078825	APPAAPAADEPGSPGGPPR		PREDICTED: hypothetical protein LOC97130 [Mus musculus]	1711.8345	27.29	1.423665161
33859506	APQVSTPTLVEAAR		albumin 1 [Mus musculus]	1439.7861	80.26	1.79399562
33563250	APSYGAGELLDFSLADAVNQEFLATR		desmin [Mus musculus]	2755.3572	30.69	2.08280331
6671664	APVPTGEVYFADSFDR		calnexin [Mus musculus]	1770.8427	75.05	0.636353164
41322904	AQAEAQQPVFNTLR		plectin 1 isoform 1 [Mus musculus]	1572.8159	33.83	1.103164863
41322904	AQAELEAQELQR		plectin 1 isoform 1 [Mus musculus]	1385.7068	48.18	1.122520903
31126968	AQAPASPYNDYEGR		retinoic acid induced 3 [Mus musculus]	1538.6914	49.01	1.558818528
31982520	AQDTAELFFEDVR		acetyl-Coenzyme A dehydrogenase, long-chain [Mus musculus]	1540.7305	69.44	2.056403369
51828444	AQEAAAEEPPPAVTPAASVSALDLGEQR		PREDICTED: proline-rich polypeptide 6 [Mus musculus]	2775.3779	44.95	0.986553215
6754256	AQFEGIVTDLIK		heat shock protein 9A [Mus musculus]	1333.735	55.16	2.952628751
29789289	AQFGQPEILLGTIPGAGGTQR		enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Mus musculus]	2111.1301	83.96	1.402709261
6679583	AQIWDTAGQER		RAB11B, member RAS oncogene family [Mus musculus]	1274.6188	60.16	1.04915604
31560313	AQLFALTGVQPAR		ubiquitin specific protease 14 [Mus musculus]	1371.7756	27.56	1.0565302
13385998	AQLLQPTLEINPR		TNF receptor-associated protein 1 [Mus musculus]	1492.8557	33.95	0.825069812
6755404	AQQEFAAGVFSNPAVR		secretory carrier membrane protein 3 [Mus musculus]	1691.8391	23.19	1.311156276
6679809	AQQVAVQEQEIAR		flotillin 1 [Mus musculus]	1469.7727	42.93	0
33468857	AQVAQPGGDTIFGK		histidine triad nucleotide binding protein 1 [Mus musculus]	1388.7103	53.98	0.838825735
41322904	AQVEQELTTLR		plectin 1 isoform 1 [Mus musculus]	1287.6926	22.96	0
29244176	AQYEDIANR		hypothetical protein 4732456N10 [Mus musculus]	1079.5139	30.23	1.337810668
13624315	AQYEDIANR		keratin complex 2, basic, gene 8 [Mus musculus]	1079.5139	30.23	1.337810668
29789317	AQYEDIANR		keratinocyte associated protein 1 [Mus musculus]	1079.5139	30.23	1.337810668
2506774	AQYEDIANR		Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)	1079.5139	30.23	1.337810668
63565108	AQYEDIANR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1079.5139	30.23	1.337810668
21313536	ASAFALQEQPVVNAVIDDATK		dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]	2187.1157	32.65	0
34328206	ASEDFVDPWTVR		tryptophanyl-tRNA synthetase [Mus musculus]	1421.6796	43.06	1.111108026
6755358	ASGNYATVISHNPETK		ribosomal protein L8 [Mus musculus]	1688.8242	68.45	0.888798987
63746482	ASGPGLNTTGVPASLPVEFTIDAK		PREDICTED: filamin, alpha [Mus musculus]	2342.2197	40.26	1.437003536
9845257	ASGPPVSELITK		histone 1, H1c [Mus musculus]	1198.6619	83.86	0.847936298
34328365	ASGPPVSELITK		histone 1, H1d [Mus musculus]	1198.6619	83.86	0.847936298
23943876	ASGTSFNAVPLHPNTVLR		zymogen granule membrane protein 16 [Mus musculus]	1880.9989	48.89	0.801001486
13624315	ASLEAAIADAEQR		keratin complex 2, basic, gene 8 [Mus musculus]	1344.6826	85.46	1.417062707
2506774	ASLEAAIADAEQR		Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)	1344.6826	85.46	1.417062707
6679931	ASLGTLNTLADVPDDEVQGR		UDP-N-acetyl-alpha-D-galactosamine: (N-acetylneuraminyl)-galactosyl-N- acetylglucosaminylpolypeptid	2071.0293	28.52	0.451246881
31543605	ASSFVLALEPELESR		ribophorin I [Mus musculus]	1647.8639	55.74	0.824377883
38198665	ASSSILINEAEPTTNIQIR		p47 protein [Mus musculus]	2057.095	33.05	0
21313526	ASTPDWPSQDPQPGLQR		hypothetical protein LOC78906 [Mus musculus]	1879.9005	20.34	1.557949227
13385938	ASVASDPESPPGGNEPAAASGQR		RNA (guanine-7-) methyltransferase [Mus musculus]	2151.9846	33.48	0.812742132
8567336	ASVTALIESVNGK		chloride channel calcium activated 3 [Mus musculus]	1288.7087	63.75	3.470046073
6681143	ASYSAVSLYGNPVR		decorin [Mus musculus]	1483.7544	20.12	0.965632052
9845283	ASYVAPLTAQPATYR		RNA binding motif protein 14 [Mus musculus]	1608.8411	35.22	0

50080209	ATAGDTHLGGEDFDNR		heat shock protein 1A [Mus musculus]	1675.7338	103.26	0
7305163	ATAGDTHLGGEDFDNR		heat shock protein 1-like [Mus musculus]	1675.7338	103.26	0
6754976	ATAVMPDGQFK		peroxiredoxin 1 [Mus musculus]	1164.5743	61.25	1.154977606
6679567	ATEMVEVGPEDDEVGAER		polymerase I and transcript release factor [Mus musculus]	1932.8549	98.03	1.408901169
9845253	ATENDIYNFFSPLNPMR		heterogeneous nuclear ribonucleoprotein H2 [Mus musculus]	2028.9526	26.28	0
10946928	ATENDIYNFFSPLNPVR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1996.9802	78.73	0.986842829
25020120	ATGDPWLTDGSYLDGSGFAR		PREDICTED: laminin, alpha 5 [Mus musculus]	2085.9578	21.68	0.723187439
7305295	ATLQAEQLSNELATER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1773.9083	74.82	1.989771382
6753492	ATPEPSGTPSSDTVSR		coronin, actin binding protein 1A [Mus musculus]	1588.7474	69.2	0.449657981
6753320	AVAQALEVIPR		chaperonin subunit 3 (gamma) [Mus musculus]	1166.6952	23.87	0.765793338
22267442	AVAQGNLSSADVQAAK		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1529.7863	121.44	1.442898429
6680748	AVDSLVPIGR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1026.5946	45.06	1.427547195
34610207	AVFDETYPDPVR		alanyl-tRNA synthetase [Mus musculus]	1408.6768	27.57	1.181286561
18079351	AVFPQNGLVVSSVDVQSVEPVDQR		major vault protein [Mus musculus]	2569.3125	56.52	1.407123907
21450277	AVFQANQENLPILK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1584.8779	69.17	0.967416098
31981273	AVFQYIDENQDR		CNDP dipeptidase 2 (metallopeptidase M20 family) [Mus musculus]	1497.7035	26.95	0.766590631
6678467	AVFVDLEPTVIDEIR		tubulin, alpha 4 [Mus musculus]	1715.9216	63.09	1.542632944
6755901	AVFVDLEPTVIDEVR		tubulin, alpha 1 [Mus musculus]	1701.9152	95.4	1.168138401
34740335	AVFVDLEPTVIDEVR		tubulin, alpha 2 [Mus musculus]	1701.9152	95.4	1.168138401
6678469	AVFVDLEPTVIDEVR		tubulin, alpha 6 [Mus musculus]	1701.9152	95.4	1.168138401
30409988	AVGESVQKPLDYYR		galactose-4-epimerase, UDP [Mus musculus]	1624.8303	28.62	1.255409096
28916673	AVITSLLDQIPEMFADTR		SEC24 related gene family, member C [Mus musculus]	2020.0367	45.67	0
22165384	AVLVDLEPGTMDSVR		tubulin, beta, 2 [Mus musculus]	1601.8234	57.18	1.27049937
31981939	AVLVDLEPGTMDSVR		tubulin, beta 4 [Mus musculus]	1601.8234	57.18	1.27049937
6755354	AVPQLQGYLR		ribosomal protein L6 [Mus musculus]	1144.6528	30.79	1.122278633
16716471	AVPVSNIAPAAVGR		hypothetical protein LOC94184 [Mus musculus]	1321.7609	44.16	1.274122844
7305085	AVQTLQMELQQIMK		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1660.8654	55.99	0.936422956
6756039	AVTEQGAELSNEER		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Mus musc	1532.7179	68.29	0
14149750	AWDDFFPGSDR		ADP-ribosylation factor-like 6 interacting protein 5 [Mus musculus]	1312.5653	34.4	1.221016963
63746482	AWGPGLEGGIVGK		PREDICTED: filamin, alpha [Mus musculus]	1240.6661	63.34	1.059276172
7106381	AYAQQLTEWAR		protein kinase C and casein kinase substrate in neurons 2 [Mus musculus]	1336.6724	28.75	1.383845906
6753138	AYGENIGYSEK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1230.5645	72.55	1.118993691
63746482	AYGPGIEPTGNMVK		PREDICTED: filamin, alpha [Mus musculus]	1433.7043	42.2	1.29481841
33859482	AYLPVNESFGFTADLR		eukaryotic translation elongation factor 2 [Mus musculus]	1799.9008	81.38	0.915783189
6679491	DADSIHQYLLQR		aminopeptidase puromycin sensitive [Mus musculus]	1458.7323	22.69	0
547749	DAEAWFNEK		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1109.4969	51.49	0.066400034
6755478	DAEDAMDAMDGAVLDGR		splicing factor, arginine/serine-rich 2 [Mus musculus]	1751.7365	66.59	0.721246995
6753484	DAEEVISQTIDTIVDMIK	Oxidation (M)	procollagen, type VI, alpha 1 [Mus musculus]	2036.0181	23.83	0
21450277	DAFQNAYLELGGLGER		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1752.861	87.01	1.159112359
6754036	DAGMQLQGYR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1138.5396	53.73	1.114815818
6754256	DAGQISGLNVLR		heat shock protein 9A [Mus musculus]	1242.6794	35.42	1.031915154
31981690	DAGTIAGLNVLR		heat shock protein 8 [Mus musculus]	1199.6782	72.31	0.809278797
63664182	DAGTIAGLNVLR		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1199.6782	72.31	0.809278797
31981722	DAGTIAGLNVMR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1217.6305	67.57	0.822952352
31543485	DAHENGDVGAAGESPLDDTAAR		golgi associated PDZ and coiled-coil motif containing [Mus musculus]	2167.9563	35.97	1.838095851
22203755	DAHNALLDIQSSGR		eukaryotic translation initiation factor 3, subunit 8 [Mus musculus]	1496.7645	21.78	0
30424898	DALVNAVIDSLSAYR		SEC24 related gene family, member A [Mus musculus]	1606.8459	42.29	0
31542602	DANLYISGLPR		ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) [Mus musculus]	1218.6383	34.61	0
41322904	DAPDGPSVEAEPEYTFEGLR		plectin 1 isoform 1 [Mus musculus]	2179.0059	55.12	0.990307887
30348966	DASVAEAWLLGQEPYLSSR		spectrin beta 2 isoform 1 [Mus musculus]	2092.0244	43.06	1.203222763
7106421	DASVAEAWLLGQEPYLSSR		spectrin beta 2 isoform 2 [Mus musculus]	2092.0244	43.06	1.203222763
51770896	DATNVGDEGGFAPNILENK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1960.9319	76.63	1.110702868
31542333	DAVITVPAFFNQAER		hypoxia up-regulated 1 [Mus musculus]	1677.8645	30.64	1.200540654
31981562	DAVLNAWAEDVDLR		pyruvate kinase 3 [Mus musculus]	1586.7897	92.56	1.692435442
6755204	DAYSGGAVNLYHVR		proteasome (prosome, macropain) subunit, beta type 5 [Mus musculus]	1521.7524	26.95	0.952499249
56699423	DDFLGQVDVPLYPLPTENPR		neural precursor cell expressed, developmentally down-regulated gene 4 [Mus musculus]	2285.1602	52.3	1.134646132
30519911	DDGLFSGDPNWFPK		transgelin 2 [Mus musculus]	1594.7314	39.17	0.814858564
6680027	DDGSWEVIEGYR		glutamate dehydrogenase 1 [Mus musculus]	1425.6372	63.61	1.101913667
31982122	DDLIASILSEVTPTPLEELR		phospholipase C, beta 3 [Mus musculus]	2211.1721	39.62	2.265765893
19072792	DDTESLEIFQNEVAR		thioredoxin domain containing 4 [Mus musculus]	1765.8259	75.45	0.926498285

6681027	DDTYQSYSSPSPR		deleted in malignant brain tumors 1 [Mus musculus]	1502.6439	43.6	1.600452611
21389320	DESSDNFGSFFLR		leucine-rich PPR motif-containing protein [Mus musculus]	1520.6819	40.1	1.150235824
31981100	DESSPYAAMLAAQDVAQR		ribosomal protein S14 [Mus musculus]	1922.8921	84.92	0.934445738
6680047	DETNYGIPQR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1192.5653	66.26	0.926502162
22203747	DFDSLAQPSFFDR		procollagen, type VI, alpha 2 [Mus musculus]	1544.7104	53.26	1.201964025
8393150	DFEQPLAISR		carboxyl terminal LIM domain protein 1 [Mus musculus]	1175.599	44.94	1.624255452
7305075	DFFQNFGNVVELR		ras-GTPase-activating protein SH3-domain binding protein [Mus musculus]	1584.7831	45.21	0.946739234
21704100	DFIYVSQDPK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1211.5968	33.92	1.495794834
9790069	DFLLKPELLR		HLA-B-associated transcript 1A [Mus musculus]	1243.7393	27.88	1.060259464
31981282	DFLLQQTMLR		glyoxalase 1 [Mus musculus]	1264.6722	41.09	1.573204816
6755142	DFMIQGGDFTR		peptidylprolyl isomerase B [Mus musculus]	1286.5881	67.36	0.82795553
58037117	DFPLTGYVELR		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Mus musculus]	1309.6754	35.59	1.509211839
20137006	DFSALESQLQDTQELLQEENR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2493.1711	96.88	0.894668399
6755714	DFTDSQLQEGK		transgelin [Mus musculus]	1267.5804	62.9	2.710827729
10181184	DFTPSGIAGAFR		ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 [Mus musculus]	1238.6223	29.74	1.28948867
6681233	DGAFDFFPVLR		solute carrier family 26 (sulfate transporter), member 2 [Mus musculus]	1283.6426	26.82	1.512606775
33563250	DGEVVSEATQQQHEVL		desmin [Mus musculus]	1768.8326	94.47	2.002802469
22164798	DGFNPAHVEAGLYGSR		selenium binding protein 1 [Mus musculus]	1689.8042	107.64	2.216161422
7657429	DGHFTLFAPTNEAFEK		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	1823.8623	26.32	3.162783705
6680193	DGIDDESYEAIFKPVMSK		histone deacetylase 1 [Mus musculus]	2043.9432	22.88	0
27754067	DGMEYPFIGEGEPHVDGEPGDLR		DnaJ (Hsp40) homolog, subfamily B, member 11 [Mus musculus]	2516.126	28.41	0.77907318
22779879	DGNGQITDKPVQQAQVQIR		desmoglein 2 [Mus musculus]	2095.0955	47.83	0.997403923
63471580	DGPLNMILDDGGDLTNLIHTK		PREDICTED: similar to S-adenosylhomocysteine hydrolase [Mus musculus]	2252.1121	36.69	0
21450277	DGPNALTPPPTTPEWVK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1819.9224	46.9	1.25631784
6680047	DGQAMLWDLNEGK		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1476.6859	68.51	1.043152571
27229048	DGQVIGIGAGQQSR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1385.71	62.92	0.75477319
31982755	DGQVINETSQHHDDLE		vimentin [Mus musculus]	1836.7985	77.9	1.289652709
34328400	DGTGVVEFVR		splicing factor, arginine/serine-rich 1 (ASF/SF2) [Mus musculus]	1078.5582	39.27	0.302098764
45597447	DGVANVSIEDR		superoxide dismutase 1, soluble [Mus musculus]	1174.5728	66.78	1.230317168
18079339	DGYAQILR		aconitase 2, mitochondrial [Mus musculus]	935.4994	32.67	1.329469952
34328400	DGYDYDGYR		splicing factor, arginine/serine-rich 1 (ASF/SF2) [Mus musculus]	1123.4355	24.61	1.072491323
6680117	DGYMPSQYNSQNWEAR		glutathione synthetase [Mus musculus]	1945.8195	40.22	1.162509354
13384736	DHLYGTLDPNTR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1401.6785	25.75	0
22203747	DIANSPHELYR		procollagen, type VI, alpha 2 [Mus musculus]	1314.6379	45.87	0.623838007
51890205	DIFAMDDKSENEPIENEAAR		succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	2294.0432	59.09	0.833637088
58037564	DIFPIAFPR		protease, serine, 15 [Mus musculus]	1075.6018	30.94	1.172036705
27370516	DIFQEIFDK		isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	1154.5803	29.89	2.088612327
40254595	DIGAIAQVHAENGDIIAEEQQR		dihydropyrimidinase-like 2 [Mus musculus]	2377.1877	65.28	0.771701402
7305445	DILIQYDR		ribosomal protein S16 [Mus musculus]	1035.548	41.37	1.331082474
6671549	DINAYNGETPTEK	Deamidation (NQ)	peroxiredoxin 6 [Mus musculus]	1452.6628	50.29	2.024318003
6753374	DINDNAPVFNPSTYQGQVPENEVNAR		cadherin 1 [Mus musculus]	2888.3315	113.09	1.186163625
9790073	DINDNRPTFLQSK		cadherin 17 [Mus musculus]	1547.7938	20.61	1.230808464
18079339	DINQEVYNFLATAGAK		aconitase 2, mitochondrial [Mus musculus]	1753.8756	82.26	0.965488279
31543605	DIPAYSQDTFK		ribophorin I [Mus musculus]	1284.6217	20.87	0
6677809	DIPGLTDTTVPR		ribosomal protein S6 [Mus musculus]	1284.679	42	1.492468518
6680283	DIQENYGQDYVHTQK		hydroxysteroid (17-beta) dehydrogenase 2 [Mus musculus]	1837.8431	49.08	1.139082
6680159	DIQLAR		H3 histone, family 3A [Mus musculus]	715.416	25.2	0.600295943
6755863	DISTNYYASQK		tumor rejection antigen gp96 [Mus musculus]	1289.6031	90	0.775839227
23956222	DITYFIQQLLR		ARP3 actin-related protein 3 homolog [Mus musculus]	1409.7874	58	1.304102972
6755787	DIVENYFMR		tripartite motif protein 28 [Mus musculus]	1186.5662	29.77	0.938961157
22267440	DIVEVLFTQPNVELNQQNK		SH3 domain protein 3 [Mus musculus]	2228.1135	21.96	1.45616753
19882201	DKTPVQSQQPSATTPSGADEK		proteasome 26S non-ATPase subunit 2 [Mus musculus]	2172.0454	88.39	1.057741813
6754524	DLADELALVDVMEDK		lactate dehydrogenase 1, A chain [Mus musculus]	1675.8113	98.84	1.551034344
63746482	DLAEDAPWK		PREDICTED: filamin, alpha [Mus musculus]	1044.5023	35	0
63660294	DLAEDAPWK		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	1044.5023	35	0
30348966	DLDDFQSWLSR		spectrin beta 2 isoform 1 [Mus musculus]	1381.6544	24.23	1.17482555
7106421	DLDDFQSWLSR		spectrin beta 2 isoform 2 [Mus musculus]	1381.6544	24.23	1.17482555
27370092	DLDKPFLLPVESVYSIPGR		Tu translation elongation factor, mitochondrial [Mus musculus]	2145.1543	38.53	1.180171347
6755809	DLDQASLAAVSQQLAPR		talin 1 [Mus musculus]	1782.9409	40.69	0
45598381	DLDSLHSFVLR		thioredoxin domain containing 5 [Mus musculus]	1301.6962	49.65	0.941787274

6753658	DLEDKEGEIQAGAK		dynein, cytoplasmic, intermediate chain 2 [Mus musculus]	1502.7268	31.48	0
10946574	DLFDPIIEER		creatine kinase, brain [Mus musculus]	1246.6406	47.9	1.787853804
13242328	DLFEDELVPLFEK		NS1-associated protein 1 [Mus musculus]	1593.8081	31.06	0
6679687	DLFSDGHSEFLK		glucose regulated protein [Mus musculus]	1394.6644	69.09	0.90674792
25020120	DLGAQGAVAEAELAEAQR		PREDICTED: laminin, alpha 5 [Mus musculus]	1798.8816	60.2	0.759051603
27532959	DLGEAALNEYLR		aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	1363.6869	29.55	2.625994493
29336026	DLGEELEALR		nonmuscle myosin heavy chain [Mus musculus]	1144.5807	32.17	0
31541890	DLGQVAAQEAER		hypothetical protein LOC67873 [Mus musculus]	1286.6384	20.33	0
56119103	DLGTDSQIFISR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1351.6929	68.64	1.729088677
38198665	DLIHDQDEEEEEEEGQR		p47 protein [Mus musculus]	2099.8711	69.69	0.932374069
22507357	DLKPSNILYVDESGNPESIR		ribosomal protein S6 kinase polypeptide 3 [Mus musculus]	2246.1116	34.02	0
59709449	DLLLDPAWEK		actinin alpha 2 [Mus musculus]	1199.6321	54.22	1.2206527
11230802	DLLLDPAWEK		actinin alpha 4 [Mus musculus]	1199.6321	54.22	1.2206527
6679687	DLLTAYYDVDYEK		glucose regulated protein [Mus musculus]	1607.7505	46.07	0
7657429	DLLTQPGDWTLFAPTNDAFK		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2250.0945	26.96	1.833317904
6681233	DLPEEAFGFPSELPLETQR		solute carrier family 26 (sulfate transporter), member 2 [Mus musculus]	2175.0608	30.41	2.003103798
47578123	DLQLVLPDYFPER		potassium channel tetramerisation domain containing 12 [Mus musculus]	1604.835	59.22	0.711302871
6671507	DLTDYLMK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	998.495	52.66	1.155332405
6671509	DLTDYLMK		actin, beta, cytoplasmic [Mus musculus]	998.495	52.66	1.155332405
30425250	DLTDYLMK		hypothetical protein LOC238880 [Mus musculus]	998.495	52.66	1.155332405
63652452	DLTDYLMK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	998.495	52.66	1.155332405
58037465	DLTTAGAVTQCYR		Ribosomal protein L18A [Mus musculus]	1398.672	36.93	1.871362486
34328286	DLVPDLSNFYAQYK		succinate dehydrogenase Ip subunit [Mus musculus]	1672.8094	37.99	0.526291338
29293809	DLVSSLTSGLLTIGDR		ATP citrate lyase [Mus musculus]	1646.8967	52.01	1.563117878
6671507	DLYANNVLSGGTTMYPGIADR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2228.0762	146.86	1.07961248
6671507	DLYANNVLSGGTTMYPGIADR	2 Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2230.0679	20.46	0
6671507	DLYANNVLSGGTTMYPGIADR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2229.0566	141.17	0
6671507	DLYANNVLSGGTTMYPGIADR	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2244.0649	46.62	0.883665116
6671509	DLYANTVLSGGTTMYPGIADR		actin, beta, cytoplasmic [Mus musculus]	2215.075	157.93	0.98840993
63652452	DLYANTVLSGGTTMYPGIADR		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2215.075	157.93	0.98840993
6671509	DLYANTVLSGGTTMYPGIADR	Deamidation (NQ)	actin, beta, cytoplasmic [Mus musculus]	2216.0381	27.97	0
63652452	DLYANTVLSGGTTMYPGIADR	Deamidation (NQ)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2216.0381	27.97	0
6671509	DLYANTVLSGGTTMYPGIADR	Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	2231.0684	28	1.069182793
63652452	DLYANTVLSGGTTMYPGIADR	Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2231.0684	28	1.069182793
29126205	DMDLIDVNEAFAPQFLSVQK		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	2280.1055	25.55	1.976804017
20137006	DMFQETMEAMR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1388.5724	44.36	0.875237155
6677799	DMIILPEMVGSMVGVYNGK		ribosomal protein S15 [Mus musculus]	2053.0278	51.72	0
6755626	DMLYQVLAAEEPSVR		sepiapterin reductase [Mus musculus]	1720.8628	48.27	1.274906424
21450277	DMTSEELDDILR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1436.6635	88.26	1.468187913
8567336	DMVTQASPYLFEATGK		chloride channel calcium activated 3 [Mus musculus]	1757.856	70.28	0
8567336	DMVTQASPYLFEATGK	Oxidation (M)	chloride channel calcium activated 3 [Mus musculus]	1773.8336	53.7	0
6681219	DNFTAIPEGTNGVEER		dihydropyrimidinase-like 3 [Mus musculus]	1748.8153	56.05	6.127227352
40254595	DNFTLIPEGTNGTEER		dihydropyrimidinase-like 2 [Mus musculus]	1792.8151	50.69	0.728424765
21361209	DNIQGITKPAIR		germinal histone H4 [Mus musculus]	1325.7603	71.03	0.533154956
31982755	DNLAEDIMR		vimentin [Mus musculus]	1076.5129	32.54	1.442691217
29789080	DNNQFASASLDR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1337.6106	82.74	1.102336876
23621467	DNTINLIHTFR		PREDICTED: actin related protein 2/3 complex, subunit 2 [Mus musculus]	1343.7188	33.94	1.124202158
34328278	DNVDDPTGNFR		lectin, mannose-binding 2 [Mus musculus]	1249.5459	44.63	0
6679891	DPAEGNGAQPEATPGDGDKPEETQEK		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	2667.1724	56.49	0.973162809
6679891	DPAEGNGAQPEATPGDGDKPEETQEK	Deamidation (NQ)	alpha glucosidase 2 alpha neutral subunit [Mus musculus]	2668.1582	78.22	0.943315568
6680836	DPDAAKPEDWDER		calreticulin [Mus musculus]	1543.6686	61.27	0
28916693	DPDQTDGPGLGYLSSHIANVER		gelsolin [Mus musculus]	2341.1094	59.1	1.294670215
31981826	DPEAPIFQVADYGIVADLFK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	2208.1287	36.13	1.841921736
31543942	DPNASPGDAGEQAIR		vinculin [Mus musculus]	1497.6946	87.71	1.146215696
31980794	DPTSLLFPESELSIR		solute carrier family 39 (metal ion transporter), member 11 [Mus musculus]	1703.8811	40.21	1.379466749
63589703	DPVQLNLLYVQAR		PREDICTED: talin 2 [Mus musculus]	1528.851	54.13	0
6755809	DPVQLNLLYVQAR		talin 1 [Mus musculus]	1528.851	54.13	0
51768600	DQAPSEAELER		PREDICTED: LIM domain only 7 [Mus musculus]	1244.5771	26.16	0.907555397
63481281	DQDVEPGAPSMGAK		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1401.637	54.15	1.492001012
31980648	DQEGQDVLLFIDNIFR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1921.9718	88.26	1.237585222

30520375	DQEQLQAWESEGLSQISQNK		UDP-N-acteylglucosamine pyrophosphorylase 1 homolog [Mus musculus]	2318.0901	66.35	1.215294019
33620739	DQGTYEDYVEGLR		myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Mus musculus]	1544.697	33.3	1.554395706
6754556	DQMQQQLSDYEQLLDVK		lamin B1 [Mus musculus]	2080.9922	68.67	0.868280427
6754556	DQMQQQLSDYEQLLDVK	Deamidation (NQ)	lamin B1 [Mus musculus]	2081.9871	21.84	0
6753824	DQPFTILYR		fibulin 5 [Mus musculus]	1152.6025	21.46	1.404420112
63492693	DQSQWENASENAER		PREDICTED: activity-dependent neuroprotective protein [Mus musculus]	1663.7134	28.7	0.985902049
6754254	DQVANSAFVER		heat shock protein 1, alpha [Mus musculus]	1235.6002	64.78	1.880171559
63481281	DQVDSAVQELLQLK		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1585.8265	54.71	0
31982122	DREDEEEDEEEEETTDPK		phospholipase C, beta 3 [Mus musculus]	2223.8606	30.24	1.635621938
23956222	DREVGIPPEQSLETAK		ARP3 actin-related protein 3 homolog [Mus musculus]	1768.9071	24.94	0.758486958
6679058	DSGQFTDEFLPEQR		nidogen 2 [Mus musculus]	1668.7494	41.36	0
33859811	DSIFSNLIGQLDYK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1612.8143	61.3	1.264800573
6753266	DSISLSPEQLAQLR		carbonic anhydrase 1 [Mus musculus]	1556.8363	81.98	2.772666637
6755040	DSLLQDGEFTMDLR		profilin 1 [Mus musculus]	1639.7633	41.4	1.058358448
31543976	DSTLIMQLLR		3-monooxgenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide [Mus musculus]	1189.6639	51.59	1.063988304
31543974	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Mus muscu	1189.6639	51.59	1.063988304
31981925	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Mus mu	1189.6639	51.59	1.063988304
6756039	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Mus musc	1189.6639	51.59	1.063988304
6756041	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	1189.6639	51.59	1.063988304
6753514	DSTQTPAIAPQSQPAATDSSVSVQK		carnitine palmitoyltransferase 2 [Mus musculus]	2514.2209	58.81	1.663987042
6671507	DSYVGDEAQSK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1198.519	74.77	0.94564111
6671509	DSYVGDEAQSK		actin, beta, cytoplasmic [Mus musculus]	1198.519	74.77	0.94564111
6753374	DTANWLEINPETGAIFTR		cadherin 1 [Mus musculus]	2048.0151	52.49	1.332611298
41322904	DTHDQLSEPSEVR		plectin 1 isoform 1 [Mus musculus]	1512.697	58.01	0.706560938
9790067	DTNGENIAESLVAEGLATR		staphylococcal nuclease domain containing 1 [Mus musculus]	1959.9624	72.15	0.790441856
6755142	DTNGSQFFITTVK		peptidylprolyl isomerase B [Mus musculus]	1457.7305	71.91	0.925205768
6680163	DTPGFIVNR		L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1018.5351	32.06	1.365302875
42476274	DTPTQEDWLVSVLPEGSR		X-prolyl aminopeptidase (aminopeptidase P) 1, soluble [Mus musculus]	2028.9852	26.15	1.425595456
7305295	DVASLGSQLQDTQELLQEETR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2360.1572	134.21	1.461276272
63746482	DVDIIDHHDNTYTVK		PREDICTED: filamin, alpha [Mus musculus]	1784.8452	87.29	1.354179275
27804325	DVPALEITHTFLER		monoamine oxidase A [Mus musculus]	1640.863	40.26	1.568213019
7304885	DVQELYAAGENR		annexin A11 [Mus musculus]	1364.6366	21.39	0
27229048	DVSELTGFPEMLGGR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1607.7791	62.04	1.175654751
28173550	DVTNNVHYENYR		cell division cycle 10 homolog [Mus musculus]	1523.6913	81.43	0.897955889
24429590	DVVLAYPEVR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1160.6208	38.5	3.013730589
20532346	DVYEDELVPVFETVGR		hypothetical protein LOC245945 [Mus musculus]	1866.9204	83.93	1.118279888
51467513	DXSHYFKTIQDLR		PREDICTED: similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18) [Homo sapiens]	1708.8521	34.45	0
7948999	DYGVYLEDSGHTLR		peroxiredoxin 4 [Mus musculus]	1624.757	36.49	0.760694188
13385942	DYIWNTLNSGR		citrate synthase [Mus musculus]	1338.6488	51.42	1.599516839
7304887	DYPGFSPSVDAEAIR		annexin A3 [Mus musculus]	1623.7742	64.48	1.37578887
7242187	DYTGEDVTPENFLAVLR		legumain [Mus musculus]	1938.9392	24.1	1.468580775
14149756	DYTYEELLNR		eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus]	1315.6234	39.6	1.14559348
6671684	EAAEAIEAEGATAPLTELLHSR		catenin beta [Mus musculus]	2279.1472	42.33	1.08941866
6755809	EAAFHPEVAPDVR		talin 1 [Mus musculus]	1437.7163	41.02	0
6753086	EAAGEGPVLYEDPPDQK		apurinic/apyrimidinic endonuclease 1 [Mus musculus]	1814.8459	21.29	0
31982722	EAAGTTAAAGTGGTTEQPPR		squamous cell carcinoma antigen recognized by T-cells 1 [Mus musculus]	1843.8787	54.89	1.125953782
63664073	EAAPDTGAEPSPEDSDPTYSSK		PREDICTED: p30 DBC protein [Mus musculus]	2250.9453	51.08	1.546173842
31982290	EAAYAPPASGNQNHPGMYPVSGPK		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	2440.1416	35.92	0
42415475	EADDIVNWLK		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1202.6127	75.4	1.479049512
15426055	EAELLEPLMPAIR		coatomer protein complex, subunit beta 1 [Mus musculus]	1481.8096	35.53	0.962704833
47578123	EAEYFELPELVR		potassium channel tetramerisation domain containing 12 [Mus musculus]	1494.7589	26.45	0.697487595
6755911	EAFQEALAAAGDK		thioredoxin 1 [Mus musculus]	1320.6354	60.31	2.046617399
58696420	EAFTDHGEEFAGR		cytochrome P450, family 2, subfamily c, polypeptide 65 [Mus musculus]	1465.6398	51.01	1.462249438
6679599	EAINVEQAFQTIAR		RAB7, member RAS oncogene family [Mus musculus]	1589.8263	41.1	1.364292427
21311915	EALGGQAEEFSGR		cytochrome P450, family 2, subfamily s, polypeptide 1 [Mus musculus]	1350.6401	22.96	0
30409988	EALNVFGDDYATEDGTGVR		galactose-4-epimerase, UDP [Mus musculus]	2028.9222	79.95	1.358532622
15808988	EALTYDGALLGDR		Williams-Beuren syndrome chromosome region 1 homolog [Mus musculus]	1393.6969	50.87	0
31981515	EANNFLWPFK		ribosomal protein L7 [Mus musculus]	1265.6355	38.19	1.087962239
29336026	EAQAGLAEAQEDLEAER		nonmuscle myosin heavy chain [Mus musculus]	1829.8513	72.25	1.474102962
7305395	EAQIFDYNEIPNFPQSTVQGHAGR		purine-nucleoside phosphorylase [Mus musculus]	2718.3008	20.34	1.150558522

6679687	EATNPPIIQEEKPK		glucose regulated protein [Mus musculus]	1593.8495	79.69	0.895203586
23956084	EATQAVLDKPETLSSDASTR		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	2119.0552	80.23	1.85810724
63746482	EATTEFSVDAR		PREDICTED: filamin, alpha [Mus musculus]	1225.5729	70.1	1.51462512
12963539	EAVLIDPVLETAHR		ETHE1 protein [Mus musculus]	1562.8553	32.63	1.061844417
6680748	EAYPGDVFYLHSR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1553.7428	55.47	1.898616184
63562740	EDALMVELDSR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1277.6124	65.31	0.703074421
46575903	EDAPVGPHLQSMPSEQIR		eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus musculus]	1990.963	46.64	0.911576275
6756033	EDGNEEDKENQGDETQGQQPPQR		nuclease sensitive element binding protein 1 [Mus musculus]	2628.1023	121.94	0.860919865
7710014	EDGSEVGVGGAQVTGSNTR		cullin 3 [Mus musculus]	1819.8501	36.32	1.254029264
20330802	EDLIWEILK		transferrin [Mus musculus]	1158.6411	23.94	1.126217264
33859482	EDLYLKPIQR		eukaryotic translation elongation factor 2 [Mus musculus]	1274.7103	29.36	0.925286433
6754254	EDQTEYLEER		heat shock protein 1, alpha [Mus musculus]	1311.5714	68.47	1.200223906
40556608	EDQTEYLEER		heat shock protein 1, beta [Mus musculus]	1311.5714	68.47	1.200223906
51768600	EDSVVAETQLASHSPEEQR		PREDICTED: LIM domain only 7 [Mus musculus]	2111.9863	49.67	1.317127729
31982755	EEAESTLQSFR		vimentin [Mus musculus]	1296.6118	65.6	0.993721432
9790247	EEAGGGGGGGISEEEAAQYDR		ubiquitin-like 1 (sentrin) activating enzyme subunit 1 [Mus musculus]	2038.8582	59.25	1.085381622
6755863	EEEAIQLDGLNASQIR		tumor rejection antigen gp96 [Mus musculus]	1785.9004	96.27	1.062756235
30425112	EEEEEEEYDEGSNLKR		hypothetical protein LOC109154 [Mus musculus]	2113.8804	56.18	1.137534611
22208854	EEGYDSVFSVVR		cytidine monophospho-N-acetylneuraminic acid synthetase [Mus musculus]	1386.6593	41	1.148642967
6753036	EEIFGPVMQILK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1403.7655	52.62	1.179280404
21312260	EEIFGPVQPLFK		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1403.7607	56.4	1.73029191
7710042	EEIQSSISGVTAAYNR		IQ motif containing GTPase activating protein 1 [Mus musculus]	1724.8466	71.93	1.830003584
27777677	EELGDEWLTPDLFR		deoxyribose-phosphate aldolase-like [Mus musculus]	1719.8334	49.48	0.525155244
19527034	EELSPASSGNAVYDFFIGR		lamin B receptor [Mus musculus]	2058.9822	23.54	1.0475339
6755863	EESDDEAAVEEEEEEKKPK		tumor rejection antigen gp96 [Mus musculus]	2219.9685	81.25	0
31560222	EESGAVAAAASVPAQSTAR		PYD and CARD domain containing [Mus musculus]	1772.886	88.18	0
7710042	EEVQAGVDAANSAAQQYQR		IQ motif containing GTPase activating protein 1 [Mus musculus]	2034.9509	116.09	1.072370406
13385680	EEWDIIEGLIR		2,4-dienoyl CoA reductase 1, mitochondrial [Mus musculus]	1372.7081	27.38	1.608129012
20330802	EEYNGYTGAFR		transferrin [Mus musculus]	1306.587	24.16	1.4501955
6679587	EFADSLGIPFLETSAK		RAB1, member RAS oncogene family [Mus musculus]	1724.869	66.08	1.088632223
21313162	EFADSLGVPFLETSAK		RAB1B, member RAS oncogene family [Mus musculus]	1710.8534	31.6	1.417018357
31542159	EFDDLSPEQQR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	1363.6155	62	1.344818112
6806903	EFDELSPSAQR		ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	1278.6002	65.76	1.175252101
21704156	EFDPTITDGSLSGPSR		caldesmon 1 [Mus musculus]	1678.7976	91.28	1.348882744
51491880	EFEEESKQPGVSEQQR		metastasis-associated protein 2 [Mus musculus]	1906.8805	76.97	1.047593606
6755863	EFEPLLNWMK		tumor rejection antigen gp96 [Mus musculus]	1306.6554	48.69	0.46893423
13242328	EFNEDGALAVLQQFK		NS1-associated protein 1 [Mus musculus]	1708.8536	57.47	0
31982275	EFSITDVVPYPISLR		heat shock protein 4 [Mus musculus]	1735.9242	54.91	1.232310208
6677991	EGAQYLMQAAGLGR		solute carrier family 12, member 2 [Mus musculus]	1464.734	48.62	0.65959058
14161694	EGDFFFDSLR		myosin VIIb [Mus musculus]	1232.5706	25.12	1.068181013
21426821	EGDVLTLLESER		ribosomal protein S28 [Mus musculus]	1360.7009	83.19	0.843336285
63594458	EGDYFTQQGEFR		PREDICTED: source of immunodominant MHC-associated peptides [Mus musculus]	1476.6415	46.65	1.178303344
29789191	EGIDPAPYYWYTDQR		asparaginyl-tRNA synthetase [Mus musculus]	1873.8413	34.91	1.358272738
6679951	EGIQTRNR	2 Deamidation (NQ)	GATA binding protein 3 [Mus musculus]	975.4709	20.74	0
6679439	EGMNIVEAMER		peptidylprolyl isomerase A [Mus musculus]	1278.5914	70.72	1.137690104
63650244	EGMNIVEAMER		PREDICTED: similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase) (Cyclophilin A) (Cy	1278.5914	70.72	1.137690104
31981549	EGNALFTFPNTPVK		sulfide quinone reductase-like [Mus musculus]	1534.7871	46.92	0.833293188
31980648	EGNDLYHEMIESGVINLK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2060.9927	77.02	2.073467211
63746482	EGSYSISVLYGEEEVPR		PREDICTED: filamin, alpha [Mus musculus]	1913.9133	45.79	2.076080039
18079339	EGWPLDIR		aconitase 2, mitochondrial [Mus musculus]	985.519	33.79	1.01399701
12963527	EHNGQVTGIDWAPESNR		actin related protein 2/3 complex, subunit 1B [Mus musculus]	1909.8715	43.8	0.667768589
13385168	EIDQEAAVEVSQLR		ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Mus musculus]	1586.8019	62.98	1.536549501
51592084	EIEIAEQEMPALMALR		hypothetical protein LOC74340 [Mus musculus]	1843.931	57.45	1.497507659
453155	EIETYHNLLEGGQEDFESSGAGK		keratin 9 [Homo sapiens]	2510.1174	75.94	0
7305085	EIFEQPESVVNTMR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1678.8147	58	1.036890053
13994195	EIFLSQPILLELEAPLK		protein phosphatase 1, catalytic subunit, alpha [Mus musculus]	1953.1305	60.39	1.258199007
28173568	EIFLSQPILLELEAPLK		protein phosphatase 1, catalytic subunit, beta [Mus musculus]	1953.1305	60.39	1.258199007
31980772	EIFLSQPILLELEAPLK		protein phosphatase 1, catalytic subunit, gamma isoform [Mus musculus]	1953.1305	60.39	1.258199007
6755901	EIIDLVLDR		tubulin, alpha 1 [Mus musculus]	1085.6267	60.98	1.092622548
34740335	EIIDLVLDR		tubulin, alpha 2 [Mus musculus]	1085.6267	60.98	1.092622548

6678469	EIIDLVLDR		tubulin, alpha 6 [Mus musculus]	1085.6267	60.98	1.092622548
9790219	EILVGDVGATITDPFK		destrin [Mus musculus]	1674.8959	102.93	1.714043186
6680924	EILVGDVGQTVDDPYTTFVK		cofilin 1, non-muscle [Mus musculus]	2196.1042	84.36	1.300770541
27804325	EIPVDAPWQAR		monoamine oxidase A [Mus musculus]	1281.6611	47.3	1.694658295
20137008	EISPDTTLLDLQNNDISELR		biglycan [Mus musculus]	2286.1396	56.31	0.926695585
6671507	EITALAPSTMK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1161.6177	63.6	1.372892093
6671509	EITALAPSTMK		actin, beta, cytoplasmic [Mus musculus]	1161.6177	63.6	1.372892093
63652452	EITALAPSTMK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1161.6177	63.6	1.372892093
6671507	EITALAPSTMK	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1177.6077	24.02	0
6671509	EITALAPSTMK	Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	1177.6077	24.02	0
63652452	EITALAPSTMK	Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1177.6077	24.02	0
14861854	EITINQSLLAPLSVDIDPTIQQVR		keratin complex 2, basic, gene 7 [Mus musculus]	2663.4385	23.15	1.409103636
6678523	EIYTNLGPR		ubiquitin specific protease 9, X chromosome [Mus musculus]	1062.5527	24.47	0.757806104
22203747	EKDFDSLAQPSFFDR		procollagen, type VI, alpha 2 [Mus musculus]	1801.8516	53.21	0.572859293
28269703	EKEEEEEEEDEDASGGDQDQEER		RAD21 homolog [Mus musculus]	2711.0249	100.91	1.22225461
6755372	ELAEDGYSGVEVR		ribosomal protein S3 [Mus musculus]	1423.6642	54.15	0.899225966
51712562	ELAPYDENWFYTR		PREDICTED: similar to ribosomal protein S19 [Mus musculus]	1703.7758	26.84	1.256362136
24429590	ELDALDANDELTPLGR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1741.8623	78.55	0.965612103
7305295	ELDEATESNEAMGR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1551.6638	108.8	2.146409156
19482160	ELEEDFIR		coactosin-like 1 [Mus musculus]	1050.5159	40.87	1.097922052
31981722	ELEEIVQPIISK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1397.7838	39.89	0.827216584
6677813	ELEFYLR		ribosomal protein S8 [Mus musculus]	969.5076	39.24	0.913151899
7305295	ELEGHISDLQEDLDSER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1984.9077	101.51	1.828389799
20137006	ELETQISELQEDLESER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2047.9697	112.19	1.113893226
6680067	ELFEADPER		glucose phosphate isomerase 1 [Mus musculus]	1105.5215	45.4	1.43130217
29336026	ELFQETLESLR		nonmuscle myosin heavy chain [Mus musculus]	1364.7126	56.63	1.265440708
23956084	ELGAFGLQVPSELGGLGLSNTQYAR		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	2577.3198	31.92	1.38961144
6753036	ELGEYGLQAYTEVK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1599.7888	56.69	1.899930368
63476037	ELGTIQQVISER		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1372.7451	34.73	0.752415648
13386054	ELLLQPVTISR		actin related protein 2/3 complex, subunit 4 [Mus musculus]	1268.764	23.3	0.992147302
6679687	ELNDFISYLQR		glucose regulated protein [Mus musculus]	1397.7163	75.89	0.85174814
30023842	ELQELVQYPVEHPDK		valosin containing protein [Mus musculus]	1823.9097	65.49	0.789595525
13624315	ELQSQISDTSVVLSMDNSR		keratin complex 2, basic, gene 8 [Mus musculus]	2109.0193	170.94	1.316544024
2506774	ELQSQISDTSVVLSMDNSR		Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)	2109.0193	170.94	1.316544024
63565108	ELQSQISDTSVVLSMDNSR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	2109.0193	170.94	1.316544024
16716499	ELQVGIPVTDEAGQR		sideroflexin 3 [Mus musculus]	1611.8347	42.02	0
29336026	ELSSAESQLHDTQELLQEETR		nonmuscle myosin heavy chain [Mus musculus]	2443.1753	47.96	1.972558446
547749	ELTTEIDNNIEQISSYK		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1996.9554	75.33	0
31982522	ELVPIAAQLDR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1224.692	27.48	1.462187884
6679082	ELYTLLNENYVEDDDNMFR		N-myristoyltransferase 1 [Mus musculus]	2393.0698	29.58	1.004666722
31982755	EMEENFALEAANYQDTIGR		vimentin [Mus musculus]	2200.991	51.15	0
7305295	EMEGLSQQYEEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1470.6421	56.61	1.574869205
6671666	EMNDAAMFYTNR		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1462.6217	62.85	0.767535907
31560680	ENDYYTPTGEFR		intergral membrane protein 1 [Mus musculus]	1491.6432	58.44	0.784237878
39204553	ENEFSFEDNAIR		chromodomain helicase DNA binding protein 4 [Mus musculus]	1470.6674	22.44	0.995751517
63518335	ENEFSFEDNAIR		PREDICTED: chromodomain helicase DNA binding protein 5 [Mus musculus]	1470.6674	22.44	0.995751517
33859809	ENENVINEYSSILEDQR		fibrinogen, B beta polypeptide [Mus musculus]	2051.9636	32.55	1.203477856
13384736	ENFIPTIVNFSAEEISDAIR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	2265.1399	38.13	1.358707254
22267442	ENMAYTVEGIR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1282.6177	49.04	1.029053143
6753484	ENYAELLDDGFLK		procollagen, type VI, alpha 1 [Mus musculus]	1526.7389	81.51	0.692098272
6754508	EPAAPVSIQR		LIM and SH3 protein 1 [Mus musculus]	1067.5903	54.82	1.12782767
33469029	EPGEAAAEGAAEEAR		acyl-Coenzyme A binding domain containing 3 [Mus musculus]	1457.6538	58.03	1.364366024
31982290	EPIMPAPGQEETVR		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1553.7557	89.1	1.087618961
31981657	EPITVSSEQMSHFR		carbonic anhydrase 2 [Mus musculus]	1647.785	105.28	1.676228168
51708124	EPPTDVTPTFLTTGVLSTLR		PREDICTED: similar to GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase) (GMP synthe	2145.1318	20.74	0.774107369
6679891	EPWLLASQYQDAIR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1689.8622	25.82	0
13385728	EQEAEPEEQEEDSSSDPR		microfibrillar-associated protein 1 [Mus musculus]	2090.8254	49.59	1.02598415
6680836	EQFLDGDAWTNR		calreticulin [Mus musculus]	1451.6649	83.09	0.889981491
9625037	EQGQAPITPQQGQALAK		ras homolog gene family, member G [Mus musculus]	1764.9216	31.25	1.426617238
22094075	EQGVLSFWR		solute carrier family 25, member 5 [Mus musculus]	1121.5837	60.25	1.367694688

50355690	EQIVPKPEEEVAQK	ribosomal protein L17 [Mus musculus]	1623.8555	52.59	1.190897381
6678499	EQIVVDLSHPGVSADDQVSR	UDP-glucose dehydrogenase [Mus musculus]	2151.0667	83.19	1.689647137
6754782	EQLLQSNPVLEAFGNAK	myosin IB [Mus musculus]	1857.9725	25.93	1.267499104
51766008	EQLLQSNPVLEAFGNAK	PREDICTED: myosin IA [Mus musculus]	1857.9725	25.93	1.267499104
18252782	EQLQDMGLIDLFSPEK	serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1 [Mus musculus]	1862.931	66.19	0
29336026	EQMEEEVVAR	nonmuscle myosin heavy chain [Mus musculus]	1219.5691	21.69	0
21450277	EQPLDEELKDAFQNAYLELGGLGER	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2834.3857	28.11	1.146421118
13384736	EQPWVSVQPR	dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1225.6346	29.36	1.238808636
18700024	EQTEGEYSSLEHESAK	isocitrate dehydrogenase 3, beta subunit [Mus musculus]	1823.8014	70.86	0.963937455
40556608	EQVANSAFVER	heat shock protein 1, beta [Mus musculus]	1249.6134	48.37	1.208845131
30348966	EQWANLEQLSAIR	spectrin beta 2 isoform 1 [Mus musculus]	1557.8058	34.01	0.672749705
7106421	EQWANLEQLSAIR	spectrin beta 2 isoform 2 [Mus musculus]	1557.8058	34.01	0.672749705
63750688	ESNQPPEDSSPPASSESSSTR	PREDICTED: HECT, UBA and WWE domain containing 1 [Mus musculus]	2175.9402	67.04	0.8835075
6678752	ESPYDHQSLQTALQEAFTSR	lymphocyte antigen 74 [Mus musculus]	2308.0776	61.38	1.3981502
6754994	ESTGAQVQVAGDMLPNSTER	poly(rC) binding protein 1 [Mus musculus]	2089.99	76.72	1.121576245
6756049	ESVLDKSDLKK	zinc finger protein 148 [Mus musculus]	1261.7192	20.56	2.024768699
9910482	ESVQVPDDQDFR	START domain containing 10 [Mus musculus]	1434.6528	27.89	1.359858231
20874851	ESYSVYVYK	PREDICTED: similar to histone H2b-616 [Mus musculus]	1137.5431	28.99	0
22122515	ETFLTSPEELYR	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 [Mus musculus]	1484.7294	37.14	1.077358102
63691573	ETPDTLSDPQTVPEEER	PREDICTED: zinc finger protein 294 [Mus musculus]	1942.899	20.37	1.247372818
6753060	ETSGNLEQLLLAVVK	annexin A5 [Mus musculus]	1613.9056	25.13	1.861664465
7305403	ETSLHSPSNTSASHSQGGGPPTSGM	pantophysin isoform 1 [Mus musculus]	2411.0352	47.99	1.010323329
63492203	ETSYEEALANQR	PREDICTED: ribosome binding protein 1 [Mus musculus]	1410.6504	89.43	0.785958681
29825827	ETTGTGPNVYHENDTIAK	hypothetical protein LOC69091 [Mus musculus]	1946.9087	23.53	1.947927776
21450291	ETTIQGLDGLSER	aldolase 2, B isoform [Mus musculus]	1418.7205	30.43	4.254598071
22122523	ETTPFYPR	GDP-mannose 4, 6-dehydratase [Mus musculus]	1010.4973	27.12	1.17857739
30023842	ETVVEVPQVTWEDIGGLEDVKR	valosin containing protein [Mus musculus]	2498.2703	51.69	0
6753670	EVAEQLAEIYGPDR	dolichol-phosphate (beta-D) mannosyltransferase 1 [Mus musculus]	1589.7749	21.94	1.561030108
31560449	EVAGQVGVPLQDLMVR	aspartyl aminopeptidase [Mus musculus]	1710.9237	32.5	0.954963066
30348966	EVDDLEQWIAER	spectrin beta 2 isoform 1 [Mus musculus]	1502.7198	53.12	1.028519576
7106421	EVDDLEQWIAER	spectrin beta 2 isoform 2 [Mus musculus]	1502.7198	53.12	1.028519576
63650229	EVDEQMLNVQNK	PREDICTED: similar to TUBULIN BETA CHAIN (T BETA-15) [Mus musculus]	1446.6913	83.97	1.185749356
22165384	EVDEQMLNVQNK	tubulin, beta, 2 [Mus musculus]	1446.6913	83.97	1.185749356
7106439	EVDEQMLNVQNK	tubulin, beta 5 [Mus musculus]	1446.6913	83.97	1.185749356
21746161	EVDEQMLNVQNK	tubulin, beta [Mus musculus]	1446.6913	83.97	1.185749356
30023842	EVDIGIPDATGR	valosin containing protein [Mus musculus]	1242.6333	50.03	1.198883995
12963527	EVEERPAPTPWGSK	actin related protein 2/3 complex, subunit 1B [Mus musculus]	1582.791	31.77	0.889111741
29789052	EVENEQTPVSEPEEEK	erythrocyte protein band 4.1-like 2 [Mus musculus]	1872.8367	41.16	1.361066009
14149756	EVEPEPTEEKDVDADEEDSR	eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus]	2317.9797	97.31	1.184310487
46593021	EVESIGAHLNAYSTR	ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1646.8136	33.32	1.254277113
31543315	EVFEDAMEIR	nucleolin [Mus musculus]	1238.5793	32.52	1.543421319
31980685	EVGAFGTPVINLGTR	glucosamine [Mus musculus]	1530.8322	66.36	0.833283771
7305295	EVLLQVEDER	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1229.635	36.83	1.955069229
33859811	EVQSEFIEVMNEIWANDQIR	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	2450.1763	42.99	0.993285281
6679737	EVSGNELIQTYTYEGVEAK	fatty acid binding protein 2, intestinal [Mus musculus]	2130.0195	25.15	0
63589709	EVSTPQDVHTTQGVPAAR	PREDICTED: vacuolar protein sorting 13C [Mus musculus]	1892.9426	20.23	0
21450129	EVYMGNVIQGGEGQAPTR	acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	1905.9178	95.91	1.181311422
31560611	EWIEGVTGR	calponin 1 [Mus musculus]	1046.5311	59.25	1.167404265
9625037	EYIPTVFDNYSAQSAVDGR	ras homolog gene family, member G [Mus musculus]	2131.9941	66.48	1.39565887
33563250	EYQDLLNVK	desmin [Mus musculus]	1121.5828	47.2	0
34328368	EYQDLLNVK	internexin neuronal intermediate filament protein, alpha [Mus musculus]	1121.5828	47.2	0
31982755	EYQDLLNVK	vimentin [Mus musculus]	1121.5828	47.2	0
29244176	EYQELMNVK	hypothetical protein 4732456N10 [Mus musculus]	1153.5499	36	1.302866558
13624315	EYQELMNVK	keratin complex 2, basic, gene 8 [Mus musculus]	1153.5499	36	1.302866558
29789317	EYQELMNVK	keratinocyte associated protein 1 [Mus musculus]	1153.5499	36	1.302866558
1346345	EYQELMNVK	Keratin, type II cytoskeletal 6B (Cytokeratin 6B) (CK 6B) (K6b keratin)	1153.5499	36	1.302866558
2506774	EYQELMNVK	Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)	1153.5499	36	1.302866558
41054806	EYQLNDSAAYYLNDLER	guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	2076.9617	73.03	0.947236154
13384736	EYQTQLIQR	dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1178.618	30.53	1.479509289
63635087	EYSSELNAPSQESDSHPR	PREDICTED: RNA binding motif protein 25 [Mus musculus]	2032.8822	80.01	0.820713177

31560560	FAAATGATPIAGR		laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1203.6484	74.03	1.166795442
6680067	FAAYFQQGDMESNGK		glucose phosphate isomerase 1 [Mus musculus]	1692.7611	36.57	0.818989958
31982755	FADLSEAANR		vimentin [Mus musculus]	1093.5321	54.99	1.220160342
31560613	FAEAFEAIPR		chaperonin subunit 8 (theta) [Mus musculus]	1150.5944	41.87	0.940036509
6755863	FAFQAEVNR		tumor rejection antigen gp96 [Mus musculus]	1081.5485	39.07	0.770904583
7710042	FALGISAINEAVDSGDVGR		IQ motif containing GTPase activating protein 1 [Mus musculus]	1890.9474	41.24	1.152671758
6753240	FAMEPEEFDSDTLR		calcium binding protein, intestinal [Mus musculus]	1686.7411	75.09	0.979794539
21704206	FAPPEAPEPWSGVR		carboxylesterase 2 [Mus musculus]	1539.7664	39.36	0
51772153	FAQPGSFEYEYAMR		PREDICTED: similar to Non-POU-domain-containing, octamer binding protein [Mus musculus]	1695.756	32.26	1.124092796
33563250	FASEANGYQDNIAR		desmin [Mus musculus]	1555.7183	89.01	1.643656164
33563250	FASEANGYQDNIAR	Deamidation (NQ)	desmin [Mus musculus]	1556.6993	51.57	2.807427666
63476037	FASEIVDTVYEDGDSIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1915.8966	75.18	0.665294141
31560611	FASQQGMTAYGTR		calponin 1 [Mus musculus]	1417.6544	91.31	1.839249524
22203747	FAYNQLIK		procollagen, type VI, alpha 2 [Mus musculus]	996.5508	47.19	0.741501925
6679299	FDAGELITQR		prohibitin [Mus musculus]	1149.5919	26.81	1.320839734
6678573	FDALTMHVQPQVAAQQK		villin 1 [Mus musculus]	1911.9694	38.04	1.50112176
63638100	FDGALNVDLTEFQTNLVPYPR		PREDICTED: similar to tubulin, alpha 1 [Mus musculus]	2409.2073	61.29	1.248096521
6755901	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 1 [Mus musculus]	2409.2073	61.29	1.248096521
34740335	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 2 [Mus musculus]	2409.2073	61.29	1.248096521
6678467	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 4 [Mus musculus]	2409.2073	61.29	1.248096521
6678469	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 6 [Mus musculus]	2409.2073	61.29	1.248096521
63638100	FDLMYAK		PREDICTED: similar to tubulin, alpha 1 [Mus musculus]	887.4402	31.97	0.706603455
6755901	FDLMYAK		tubulin, alpha 1 [Mus musculus]	887.4402	31.97	0.706603455
34740335	FDLMYAK		tubulin, alpha 2 [Mus musculus]	887.4402	31.97	0.706603455
6678467	FDLMYAK		tubulin, alpha 4 [Mus musculus]	887.4402	31.97	0.706603455
6678469	FDLMYAK		tubulin, alpha 6 [Mus musculus]	887.4402	31.97	0.706603455
13385280	FDQLFDDESDPFEVLK		PAI-1 mRNA-binding protein [Mus musculus]	1943.8997	72.38	0.943390993
7710042	FDVPGDENAEMDAR		IQ motif containing GTPase activating protein 1 [Mus musculus]	1565.6628	39.21	1.346481214
21704020	FEAPLFNAR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	1064.5579	32.86	1.858734512
10092608	FEDGDLTLYQSNAILR		glutathione S-transferase, pi 1 [Mus musculus]	1854.9236	99.11	1.101933564
31981690	FEELNADLFR		heat shock protein 8 [Mus musculus]	1253.6136	77.43	1.147322628
31981722	FEELNMDLFR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1313.6305	53.77	0.637525005
22203755	FEELTNLIR		eukaryotic translation initiation factor 3, subunit 8 [Mus musculus]	1134.6184	25.02	0
9790073	FEEQVYNIPIR		cadherin 17 [Mus musculus]	1407.7333	61.64	1.4074148
13385374	FEIWDTAGQER		RAB5A, member RAS oncogene family [Mus musculus]	1351.646	32.61	0.689581437
34996495	FELDTSER		ribophorin II [Mus musculus]	996.4673	30.29	1.153656662
31981690	FELTGIPPAPR		heat shock protein 8 [Mus musculus]	1197.6591	43.69	1.141374354
63650244	FENENFILK	Deamidation (NQ)	PREDICTED: similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase) (Cyclophilin A) (Cy	1154.5719	60.36	0
30348966	FESLEPEMNNQASR		spectrin beta 2 isoform 1 [Mus musculus]	1651.7426	55.2	0.91968132
7106421	FESLEPEMNNQASR		spectrin beta 2 isoform 2 [Mus musculus]	1651.7426	55.2	0.91968132
6678145	FFDEESYSLLR		signal sequence receptor, delta [Mus musculus]	1405.678	70.17	0.990305048
63641940	FFDQYR		PREDICTED: desmoplakin [Mus musculus]	875.4075	21.78	0.91240129
16716471	FFQELPASDSAFK		hypothetical protein LOC94184 [Mus musculus]	1486.7212	40.57	0
8567336	FFTAFDANGR		chloride channel calcium activated 3 [Mus musculus]	1145.5455	63.14	0.254313267
8567336	FFTAFDANGR	Deamidation (NQ)	chloride channel calcium activated 3 [Mus musculus]	1146.5319	53.37	0
63594458	FGEMQLDFR		PREDICTED: source of immunodominant MHC-associated peptides [Mus musculus]	1142.5438	21.2	0
19526818	FGFYEVFK		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1036.521	41.16	1.297206395
21704096	FGGNPGGFGNQGGFGNSR		TAR DNA binding protein isoform 1 [Mus musculus]	1726.7733	109.6	1.130055787
13384736	FGNPLLVQDVESYDPVLNPVLNR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	2598.3311	20.75	1.236127966
31981562	FGVEQDVDMVFASFIR		pyruvate kinase 3 [Mus musculus]	1859.9104	52.15	1.220096704
31981562	FGVEQDVDMVFASFIR	Oxidation (M)	pyruvate kinase 3 [Mus musculus]	1875.901	35.64	1.412933148
63487095	FHPEPYGLEDDQR		PREDICTED: catenin src [Mus musculus]	1602.7449	28.8	0.863454829
6671690	FHQLDIDNPQSIR		carbonyl reductase 1 [Mus musculus]	1582.7975	53.39	1.772878662
52317152	FIEGPVTYSEAPR		phospholipase A2, group IVC (cytosolic, calcium-independent) [Mus musculus]	1465.7339	63.01	0
6679687	FISDKDASVVGFFR		glucose regulated protein [Mus musculus]	1587.8164	59	0
18079339	FKLEAPDADELPR		aconitase 2, mitochondrial [Mus musculus]	1500.7719	67.17	1.478835992
31560680	FLAEEGFYK		intergral membrane protein 1 [Mus musculus]	1103.5538	31.05	0
33563250	FLEQQNAALAAEVNR		desmin [Mus musculus]	1673.8633	89.25	1.628397356
482387	FLEQQNQVLQTK		keratin, 67K type II epidermal - human	1475.7845	95.18	0.045944367
51092293	FLEQQNQVLQTK		keratin complex 2, basic, gene 39 [Mus musculus]	1475.7845	95.18	0.045944367

1346343	FLEQQNQVLQTK		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1475.7845	95.18	0.045944367
31981246	FLIDGFPR		UMP-CMP kinase [Mus musculus]	964.5352	38.32	1.103152738
6756041	FLIPNASQPESK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	1330.6921	33.9	0
6753618	FLTEELSLDQDR		D-dopachrome tautomerase [Mus musculus]	1465.7169	23.67	1.861661146
29336026	FLTNGPSSSPGQER		nonmuscle myosin heavy chain [Mus musculus]	1476.7123	93.41	1.200905385
13384828	FMTEDTTDAPFR		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1430.6315	41.75	1.032915469
16418339	FNADEFEDMVAEK		ribosomal protein 10 [Mus musculus]	1544.665	67.01	1.50641276
6671622	FNASQLITQR		B-cell receptor-associated protein 37 [Mus musculus]	1177.634	42.07	1.374997072
63660302	FNDEHIPDSPYLVPVIAPSDDAR		PREDICTED: filamin B, beta [Mus musculus]	2567.2419	44.68	0.763038324
63746482	FNEEHIPDSPFVVPVASPSGDAR		PREDICTED: filamin, alpha [Mus musculus]	2467.1836	69.31	1.47006386
18079339	FNPETDFLTGK		aconitase 2, mitochondrial [Mus musculus]	1268.6198	57.07	1.297145128
18079339	FNPETDFLTGK	Deamidation (NQ)	aconitase 2, mitochondrial [Mus musculus]	1269.6249	22.87	0
6677777	FNPFVTSDR		ribosomal protein L26 [Mus musculus]	1082.5309	53.83	0.871430085
6753272	FNSANEDNVTQVR		catalase [Mus musculus]	1493.7173	49.24	0.822338006
27228985	FNVSATPEQYVPYSTTR		13kDa differentiation-associated protein [Mus musculus]	1959.9467	31.39	1.258094044
6678365	FNVWDTAGQEK		RAN, member RAS oncogene family [Mus musculus]	1294.6168	58.77	0.813914074
30911099	FPQLDDTSFANSR		fatty acid synthase [Mus musculus]	1497.705	57.31	0
8567336	FPSPVTVYASIR		chloride channel calcium activated 3 [Mus musculus]	1336.7299	79.64	0.21255495
51491880	FQAEIPDR		metastasis-associated protein 2 [Mus musculus]	975.4854	29.32	0.667099667
33859560	FQILEGPPESMGR		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	1460.7246	24.58	0
40254595	FQLTDSQIYEVLSVIR		dihydropyrimidinase-like 2 [Mus musculus]	1911.0239	24.21	0.885509304
40254595	FQMPDQGMTSADDFFQGTK		dihydropyrimidinase-like 2 [Mus musculus]	2150.936	61.72	1.344129261
6755863	FQSSHHSTDITSLDQYVER		tumor rejection antigen gp96 [Mus musculus]	2250.0413	44.88	0.815979141
23943876	FSHSGNQLDGPITAFR		zymogen granule membrane protein 16 [Mus musculus]	1746.8636	88.65	1.056367976
31543113	FSLVGIAGQDLNEGNR		lymphocyte cytosolic protein 1 [Mus musculus]	1689.8665	21.72	0
31541909	FSMVLPEVEAALAEIPGVR		isochorismatase domain containing 1 [Mus musculus]	2028.0895	31	3.945794529
6671539	FSNEEIAMATVTALR		aldolase 1, A isoform [Mus musculus]	1652.8365	84.31	0.941434182
16716471	FSPLMTAEGLGTR		hypothetical protein LOC94184 [Mus musculus]	1379.7079	59.63	1.431844293
28893559	FSPPEETGPSR		melanoma inhibitory activity 3 [Mus musculus]	1203.5648	44.4	1.177816252
1346343	FSSCGGGGGSFGAGGGFGSR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1708.7118	26.47	0
21450241	FSSQEAASSFGDDR		propionyl-Coenzyme A carboxylase, alpha polypeptide [Mus musculus]	1503.645	77.11	1.051674175
31982171	FSTSQSLPASQTR		murinoglobulin 1 [Mus musculus]	1409.6993	23.54	1.660989691
33859482	FSVSPVVR		eukaryotic translation elongation factor 2 [Mus musculus]	890.5168	36.46	0.966181147
31560560	FTPGTFTNQIQAAFR		laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1698.8668	36.39	2.781003785
31980648	FTQAGSEVSALLGR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1435.7628	105.98	1.062317906
13384736	FTQDTQPHYIYSPR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1752.8304	37.94	2.409300936
31982178	FVEGLPINDFSR		malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1393.7274	70.08	1.442341021
21704144	FVIGGPQGDAGLTGR		methionine adenosyltransferase II, alpha [Mus musculus]	1444.7627	61.19	1.548254258
6681157	FVINYDYPNSSEDYIHR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	2132.0095	32	0.903459032
40068493	FVINYDYPNSSEDYVHR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	2117.9546	24.86	1.251448992
6679687	FVMQEEFSR		glucose regulated protein [Mus musculus]	1172.545	35.13	0.747962885
6679753	FVNVVPTFGK		Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) [Mus musc	1107.6125	40.86	0.938618931
7305395	FVSILMESIPLPDR		purine-nucleoside phosphorylase [Mus musculus]	1616.8728	20.94	1.598791641
6680606	FVTSSSGSYGGVR		keratin complex 1, acidic, gene 19 [Mus musculus]	1303.634	81.69	1.335563412
6754036	FVTVQTISGTGALR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1449.8121	45.36	1.254472781
33859604	FVVDLSDQVAPTDIEEGMR		proteasome (prosome, macropain) 26S subunit, ATPase 2 [Mus musculus]	2121.0352	21.83	0.822269183
6678097	FYEAELEELDFQGATEESR		serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	2263.0056	41.15	1.38257208
54287684	FYEQMNGPVTSGSR		eukaryotic translation elongation factor 1 delta isoform b [Mus musculus]	1572.7172	59.26	1.074174177
6755002	FYNELTEILVR		programmed cell death 6 interacting protein [Mus musculus]	1396.7485	20.55	1.357076761
6678571	FYPEDVAEELIQDITQK		villin 2 [Mus musculus]	2038.0043	76.23	1.379878013
6754750	FYPEDVSEELIQDITQR		moesin [Mus musculus]	2082.0049	46.74	0.974004757
22122523	FYQASTSELYGK		GDP-mannose 4, 6-dehydratase [Mus musculus]	1393.6583	83.87	1.396769707
33563266	FYSVNVDYSK		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 [Mus musculus]	1221.5798	42.45	1.466887885
6679937	GAAQNIIPASTGAAK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1369.7411	111.31	1.038328955
40549395	GADVNAPPVPSSR		ankyrin repeat domain protein 17 isoform b [Mus musculus]	1266.6455	24.49	1.128293493
20806532	GAEAANVTGPDGVPVEGSR		cold shock domain protein A short isoform [Mus musculus]	1782.8628	56.47	1.189632686
6756033	GAEAANVTGPGGVPVQGSK		nuclease sensitive element binding protein 1 [Mus musculus]	1695.8605	108.08	0.912842716
55741460	GAEEMETVIPVDVMR		DJ-1 protein [Mus musculus]	1675.7985	73.93	1.304630089
47059123	GAGVTLNVLEMTADDLENALK		UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	2174.1035	49.43	1.507453838
29293809	GAIVPAQEVPPPTVPMDYSWAR		ATP citrate lyase [Mus musculus]	2381.189	36.97	1.271264629

6671700	GATQQILDEAER		chaperonin subunit 2 (beta) [Mus musculus]	1330.6564	20.36	0
26080429	GAVEAAHQAAPGWGAQSPR		aldehyde dehydrogenase 16 family, member A1 [Mus musculus]	1860.9064	21.59	0.802194947
7242197	GAVYSFDPVGSYQR		proteasome (prosome, macropain) subunit, beta type 1 [Mus musculus]	1545.7402	46.37	1.01320851
10946928	GAYGGGYGGYDDYNGYNDGYGFGSDR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	2717.0603	22.65	1.980426489
6679715	GDATVSYEDPPTAK		Ewing sarcoma breakpoint region 1 [Mus musculus]	1450.6627	62.51	0.82297465
21644581	GDDDVFVNPTNLLEFLSDR		UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 [Mus musculus]	2166.0388	87.37	0.716375915
31543113	GDEEGIPAVVIDMSGLR		lymphocyte cytosolic protein 1 [Mus musculus]	1757.8728	41.35	0.55860982
6753484	GDEGEVGDPGEDNNDISPR		procollagen, type VI, alpha 1 [Mus musculus]	1971.8282	61.71	0
6754206	GDFIALDLGGSSFR		hexokinase 1 [Mus musculus]	1454.7338	32.72	1.641920278
45597447	GDGPVQGTIHFEQK		superoxide dismutase 1, soluble [Mus musculus]	1512.7463	60.9	1.028423979
30348966	GDQVSQNGLPAEQGSPR		spectrin beta 2 isoform 1 [Mus musculus]	1739.8307	128.7	1.268948013
7106421	GDQVSQNGLPAEQGSPR		spectrin beta 2 isoform 2 [Mus musculus]	1739.8307	128.7	1.268948013
30348966	GDQVSQNGLPAEQGSPR	Deamidation (NQ)	spectrin beta 2 isoform 1 [Mus musculus]	1740.8147	42.77	1.236217008
7106421	GDQVSQNGLPAEQGSPR	Deamidation (NQ)	spectrin beta 2 isoform 2 [Mus musculus]	1740.8147	42.77	1.236217008
25141233	GDTDQASNILASFGLSAR		matrin 3 [Mus musculus]	1822.8937	25.79	1.642348236
63650187	GDVAEGDLIEHFSQFGAVEK		PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A0 [Mus musculus]	2148.022	22.67	1.133827262
31981562	GDYPLEAVR		pyruvate kinase 3 [Mus musculus]	1019.5198	25.55	1.13505513
63660302	GEAGIPAEFSIWTR		PREDICTED: filamin B, beta [Mus musculus]	1533.775	49.23	1.078039298
63618830	GEELLSPLNLEQAAYAR		PREDICTED: similar to nuclear myosin I beta [Mus musculus]	1873.9717	47.07	0.849876046
45504394	GEFFNELVGQQR		integrin beta 1 (fibronectin receptor beta) [Mus musculus]	1423.702	33.19	1.374690669
31982178	GEFITTVQQR		malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1178.6183	49.48	1.165447728
29336026	GELEDTLDSTNAQQELR		nonmuscle myosin heavy chain [Mus musculus]	1918.9038	92.56	1.5960585
63738313	GEYDVTVPR		PREDICTED: similar to AHNAK [Mus musculus]	1035.5103	35.72	1.887040739
8393544	GFAFVQYVNER		heterogeneous nuclear ribonucleoprotein C [Mus musculus]	1329.6699	25.08	0
21592285	GFEVQVTELR		keratin 20 [Mus musculus]	1177.6293	38.92	1.124959355
63641940	GFFDPNTEENLTYLQLK		PREDICTED: desmoplakin [Mus musculus]	2028.9967	23.19	0
31560449	GFFELFPSVSR		aspartyl aminopeptidase [Mus musculus]	1285.6633	33.23	1.043250205
7949053	GFGDGYNGYGGGPGGGNFGGSPGYGGGR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2495.0386	171.8	1.193434274
7949053	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	Deamidation (NQ)	heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2496.0388	98.96	1.313036022
6681069	GFGFGQGAGALVHSE		cysteine and glycine-rich protein 1 [Mus musculus]	1433.6837	104.95	1.347135824
7949053	GFGFVTFDDHDPVDK		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1695.7751	84.23	1.044886476
6680027	GFIGPGIDVPAPDMSTGER		glutamate dehydrogenase 1 [Mus musculus]	1915.9222	55.92	0.875978859
6679687	GFPTIYFSPANK		glucose regulated protein [Mus musculus]	1341.6835	28.5	0.781509114
6754508	GFSVVADTPELQR		LIM and SH3 protein 1 [Mus musculus]	1418.7352	47.85	2.671873319
15617203	GFTIPEAFR		chloride intracellular channel 1 [Mus musculus]	1037.5431	31.97	1.08930735
24418933	GGENIYPAELEDFFLK		hypothetical protein LOC264895 [Mus musculus]	1841.8954	84.6	1.02222598
6755252	GGGGGGGGPGGEQETQELASK		purine rich element binding protein B [Mus musculus]	1829.8287	85.13	1.377589699
1346343	GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	2383.9514	236.56	0
7949053	GGGGNFGPGPGSNFR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1377.6337	83.78	0.808168945
6680572	GGGSFVQNNQPVGLR		kinesin family member 5B [Mus musculus]	1529.7825	30.24	3.053924531
34328400	GGPPFAFVEFEDPR		splicing factor, arginine/serine-rich 1 (ASF/SF2) [Mus musculus]	1564.7428	44.13	0.907339825
6680606	GGSFSGTLAVSDGLLSGNEK		keratin complex 1, acidic, gene 19 [Mus musculus]	1895.9351	76.43	7.376757402
453155	GGSGGSYGGGGSGGGYGGGSGSR		keratin 9 [Homo sapiens]	1791.7382	26.91	0
28478945	GGTPPQQQQQQQQPGASPPAAPGPK		PREDICTED: glutaminase [Mus musculus]	2608.3079	34.98	1.771823004
24418933	GGVIAGSPAPPELIR		hypothetical protein LOC264895 [Mus musculus]	1433.8092	20.79	1.070016505
29789343	GHPSAGAEEEGGSDGSAAEAEPR		eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]	2167.9194	84.26	1.085670795
13385310	GHQDVEAAQAEYVEK		propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]	1673.7473	69.36	0.998153478
22165384	GHYTEGAELVDSVLDVVR		tubulin, beta, 2 [Mus musculus]	1958.9857	73.61	1.051164837
12963615	GHYTEGAELVDSVLDVVR		tubulin, beta 3 [Mus musculus]	1958.9857	73.61	1.051164837
7106439	GHYTEGAELVDSVLDVVR		tubulin, beta 5 [Mus musculus]	1958.9857	73.61	1.051164837
27754056	GHYTEGAELVDSVLDVVR		tubulin, beta 6 [Mus musculus]	1958.9857	73.61	1.051164837
21746161	GHYTEGAELVDSVLDVVR		tubulin, beta [Mus musculus]	1958.9857	73.61	1.051164837
21313520	GIADVPEWFR		acetoacetyl-CoA synthetase [Mus musculus]	1189.6135	22.64	0.730787665
21313262	GIEQAVQSHAVAEEEAR		inner membrane protein, mitochondrial [Mus musculus]	1823.8839	61.05	0
38142460	GIHVEIPGAQAESLGPLQVAR		electron transferring flavoprotein, beta polypeptide [Mus musculus]	2142.1567	37.21	1.830574375
21450291	GILAADESVGTMGNR		aldolase 2, B isoform [Mus musculus]	1490.7319	21.95	0.544334124
63518159	GILFVGSGVSGGEEGAR		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1591.8168	63.48	1.607147579
30023842	GILLYGPPGTGK		valosin containing protein [Mus musculus]	1172.6627	26.14	0
31543942	GILSGTSDLLLTFDEAEVR		vinculin [Mus musculus]	2036.0504	36.33	0
6679457	GINQGQVWIGGR		proteoglycan 2, bone marrow [Mus musculus]	1284.6862	43.75	0.734901094

6679457	GINQGQVWIGGR	2 Deamidation (NQ)	proteoglycan 2, bone marrow [Mus musculus]	1286.6733	21.74	0
27754190	GIPERLINACVENTLR	2 Deamidation (NQ)	ATP-binding cassette, sub-family A (ABC1), member 3 [Mus musculus]	1799.9225	24.85	0
16716471	GIQEAQVQLQK		hypothetical protein LOC94184 [Mus musculus]	1241.6775	52.03	1.294319805
11230802	GISQEQMQEFR		actinin alpha 4 [Mus musculus]	1352.634	52.79	1.479181254
51592084	GIVEESVTGVHR		hypothetical protein LOC74340 [Mus musculus]	1282.6744	33.75	2.700105874
23956084	GIVNEQFLLQR		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	1316.7382	35.87	1.841239137
20149756	GIYAYGFEKPSAIQQR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Mus musculus]	1827.946	31.6	1.228236743
21450625	GIYAYGFEKPSAIQQR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1827.946	31.6	1.228236743
36031080	GLDGFQGPSGPR		procollagen, type IV, alpha 2 [Mus musculus]	1187.5892	43.71	1.075484779
10946870	GLEVTAYSPLGSSDR		aldo-keto reductase family 1, member A4 (aldehyde reductase) [Mus musculus]	1551.7825	37.38	1.306230527
6755863	GLFDEYGSK		tumor rejection antigen gp96 [Mus musculus]	1015.4708	38.26	0.899738371
7304889	GLGTDEDAIIGILAYR		annexin A4 [Mus musculus]	1676.886	54.04	1.192846971
6753060	GLGTDEDSILNLLTSR		annexin A5 [Mus musculus]	1703.8806	83.74	1.05322582
6996913	GLGTDEDSLIEIICSR		annexin A2 [Mus musculus]	1720.8495	21.52	1.20910684
6678329	GLLIEPAANSYLLAER		transglutaminase 2, C polypeptide [Mus musculus]	1729.9521	38.19	1.270298656
31981826	GLLPEELTPLILETQK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1794.0292	41.2	1.502405125
13386034	GLSQSALPYR		ribosomal protein S13 [Mus musculus]	1091.5844	26.16	0.612800149
63746482	GLVEPVDVVDNADGTQTVNYVPSR		PREDICTED: filamin, alpha [Mus musculus]	2544.259	118.45	1.2134544
13386272	GLVYETSVLDPDEGIR		citrate synthase-like protein [Mus musculus]	1762.8884	56.46	1.712409791
13385942	GLVYETSVLDPDEGIR		citrate synthase [Mus musculus]	1762.8884	56.46	1.712409791
6680748	GMSLNLEPDNVGVVVFGNDK		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2104.0454	74.23	1.17366396
31560611	GMTVYGLPR		calponin 1 [Mus musculus]	993.5211	39.96	1.621639751
30911099	GNAGQTNYGFANSTMER		fatty acid synthase [Mus musculus]	1817.7938	66.49	0.818458265
33859580	GNDVAFHFNPR		galectin-3 [Mus musculus]	1273.6123	53.56	1.092366962
21313308	GNFGGSFAGSFGGAGGHAPGVAR		heterogeneous nuclear ribonucleoprotein M [Mus musculus]	2034.9509	46.06	1.013839958
51770896	GNPTVEVDLYTAK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1406.7096	69.11	1.103958714
13385994	GNSIIMLEALER		small nuclear ribonucleoprotein polypeptide G [Mus musculus]	1345.7219	22.27	0
19527034	GPAPLGTFQVTTPQR		lamin B receptor [Mus musculus]	1569.8434	32.94	0.776782008
6755204	GPGLYYVDSEGNR		proteasome (prosome, macropain) subunit, beta type 5 [Mus musculus]	1426.6672	41.05	1.514782003
6671497	GPQVPAGEPTQEASGATATK		ATP-binding cassette, sub-family D, member 1 [Mus musculus]	1896.9236	20.72	1.51592329
13626040	GPSEAPQEAEAEEGATSDGEK		A kinase (PRKA) anchor protein (gravin) 12 [Mus musculus]	2088.8928	75.82	1.623085504
7305029	GPSSQEDESGGLEDSPDR		erythrocyte protein band 4.1-like 1 isoform a [Mus musculus]	1861.7887	20.07	0
33859600	GPTEQLVSPEPEVYEIVR		protein phosphatase 1B, magnesium dependent, beta isoform [Mus musculus]	2042.0505	29.82	1.016449491
29293809	GQELIYAGMPITEVFK		ATP citrate lyase [Mus musculus]	1795.9281	28.3	2.166156308
13386370	GQGAAAAQQGGYEIPAR		kinesin-like 8 [Mus musculus]	1644.8109	48.3	1.051562771
6677871	GQIIYTWQGANATR		scinderin [Mus musculus]	1578.8054	49.99	0.899832364
6755698	GQNDLMGTAEDFADQFLR		surfeit gene 4 [Mus musculus]	2027.9246	28.06	1.577280761
6754090	GSAPPGPVPEGQIR		glutathione S-transferase omega 1 [Mus musculus]	1361.7196	54.01	1.465935118
27532959	GSASSALELTEEELATAEAVR		aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	2134.0449	68.43	1.46507067
16716467	GSDHSASLEPGELAELVR		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1866.9215	103.62	1.089187116
29788989	GSESSKPWPDATTYGAGSASR		thyroid hormone receptor associated protein 3 [Mus musculus]	2111.9639	47.85	1.187743748
547749	GSLGGGFSSGGFSGGSFSR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1707.7786	45.83	0
6678573	GSLNITTPGIQIWR		villin 1 [Mus musculus]	1555.8646	42.7	1.320826379
21704156	GSVFSAPSASGTPNK		caldesmon 1 [Mus musculus]	1406.6823	48.38	0.573064671
6678449	GSVNMPFMDFLTK		thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	1486.7133	33.35	1.672280284
1346343	GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	3312.3149	71.29	0
7657429	GSYTYFAPSNEAWENLDSDIR		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2435.0852	44.36	0.936067982
6679761	GTGELTQLLNSMLTAIK		fructose bisphosphatase 2 [Mus musculus]	1789.9752	46.11	1.058780882
6753428	GTGGVDTAATGSVFDISNLDR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	2052.9868	104.76	1.68819706
10946574	GTGGVDTAAVGGVFDVSNADR		creatine kinase, brain [Mus musculus]	1964.9357	64.8	1.825752257
7304887	GTGTDEDALIEILTTR		annexin A3 [Mus musculus]	1704.87	51.73	1.523881396
31560449	GTPEPGPLGATDER		aspartyl aminopeptidase [Mus musculus]	1396.6735	45.7	1.387238116
29789343	GTQGVVTNFEIFR		eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]	1467.7659	21.04	1.527751704
31981826	GTSFEAAATSGGSASSEK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1644.729	52.44	1.916081462
6678097	GTTASQMAQALALDK		serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	1505.7518	47.07	0
31652266	GTVAAAASGAAGGGGGGAGAGAPGGGR		hypothetical protein LOC229543 [Mus musculus]	1939.9366	30.33	1.879132185
40254595	GTVVYGEPITASLGTDGSHYWSK		dihydropyrimidinase-like 2 [Mus musculus]	2425.1619	39.87	0
19526818	GVAPLWMR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	929.5115	28.17	1.055520922
23956222	GVDDLDFFIGDEAIEKPTYATK		ARP3 actin-related protein 3 homolog [Mus musculus]	2444.1824	31.76	0
6996913	GVDEVTIVNILTNR		annexin A2 [Mus musculus]	1542.8517	93.25	1.157719377

13385374	GVDLTEPAQPAR		RAB5A, member RAS oncogene family [Mus musculus]	1253.6515	35.28	1.650250245
21450277	GVGIISEGNETVEDIAAR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1829.9209	76.85	1.077743651
31981562	GVNLPGAAVDLPAVSEK		pyruvate kinase 3 [Mus musculus]	1636.8888	56.75	1.122502775
33859482	GVQYLNEIK		eukaryotic translation elongation factor 2 [Mus musculus]	1063.5758	31.79	1.000401484
6753514	GVTLPELYQDPAYQR		carnitine palmitoyltransferase 2 [Mus musculus]	1749.8782	33.36	0
6755863	GVVDSDDLPLNVSR		tumor rejection antigen gp96 [Mus musculus]	1485.7598	49.2	0.960776483
6754254	GVVDSEDLPLNISR		heat shock protein 1, alpha [Mus musculus]	1513.7906	74.66	1.112763939
40556608	GVVDSEDLPLNISR		heat shock protein 1, beta [Mus musculus]	1513.7906	74.66	1.112763939
6671539	GVVPLAGTNGETTTQGLDGLSER		aldolase 1, A isoform [Mus musculus]	2272.146	132.53	0.93950316
6671539	GVVPLAGTNGETTTQGLDGLSER	Deamidation (NQ)	aldolase 1, A isoform [Mus musculus]	2273.1255	91.95	1.135503018
6753428	GWEFMWNER		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	1254.5452	34.38	1.881365225
6753010	GWGDQLIWTQTYEEALYR		anterior gradient 2 [Mus musculus]	2229.0657	27.7	0.908368976
22122825	GYAFNHSADFETVR		actin-related protein 2 [Mus musculus]	1613.739	47.92	0.859027714
7305085	GYDVDFPR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	968.4468	49.7	1.075627158
21450625	GYDVIAQAQSGTGK		eukaryotic translation initiation factor 4A1 [Mus musculus]	1394.6906	73.01	0.816552719
59709449	GYEEWLLNEIR		actinin alpha 2 [Mus musculus]	1421.7108	50.69	1.087345737
11230802	GYEEWLLNEIR		actinin alpha 4 [Mus musculus]	1421.7108	50.69	1.087345737
63487095	GYELLFQPEVVR		PREDICTED: catenin src [Mus musculus]	1449.7759	55.38	1.040022244
37537522	GYFDEDMNSILADPGDDTK		epiplakin 1 [Mus musculus]	2102.8904	22.17	0.814408411
41322904	GYFDEEMNR		plectin 1 isoform 1 [Mus musculus]	1160.4725	32.01	1.172439765
7949051	GYFEYIEENK		heterogenous nuclear ribonucleoprotein U [Mus musculus]	1291.5984	58.33	0.764247046
6753036	GYFIQPTVFGDVK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1470.7625	61.42	1.739603375
6681069	GYGYGQGAGTLSTDK		cysteine and glycine-rich protein 1 [Mus musculus]	1474.6831	76.33	1.531059625
6681069	GYGYGQGAGTLSTDKGESLGIK		cysteine and glycine-rich protein 1 [Mus musculus]	2159.0579	190.09	1.81932098
30425250	GYNFTTTAER	Deamidation (NQ)	hypothetical protein LOC238880 [Mus musculus]	1160.528	27.19	1.203834162
16716467	GYPPEDIFNLAGK		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1420.7096	53.02	1.231608303
45598381	GYPTLLLFR		thioredoxin domain containing 5 [Mus musculus]	1079.6311	26.43	0.931227708
6671509	GYSFTTTAER		actin, beta, cytoplasmic [Mus musculus]	1132.5355	58.92	1.192022894
63652452	GYSFTTTAER		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1132.5355	58.92	1.192022894
6671507	GYSFVTTAER		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1130.5548	56.34	1.18909026
31981549	GYWGGPAFLR		sulfide quinone reductase-like [Mus musculus]	1123.5765	23.75	1.483551768
63738313	HEVTEISNTDVETQPGK		PREDICTED: similar to AHNAK [Mus musculus]	1883.8977	50.66	0
6680027	HGGTIPVVPTAEFQDR		glutamate dehydrogenase 1 [Mus musculus]	1723.8816	57.74	1.084828038
63702717	HGQWPQSSNEMVK	Deamidation (NQ); Oxidation (M)	PREDICTED: hypothetical protein XP_619435 [Mus musculus]	1544.6976	29.26	1.104048556
22122825	HIVLSGGSTMYPGLPSR		actin-related protein 2 [Mus musculus]	1771.926	28.51	0.486960181
6753010	HLSPDGQYVPR		anterior gradient 2 [Mus musculus]	1268.6389	48.24	2.362692806
58037267	HQSLGGQYGVQGFPTIK		protein disulfide isomerase-associated 6 [Mus musculus]	1816.9314	29.34	0
10946928	HTGPNSPDTANDGFVR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1684.7762	62.95	2.667360544
9845253	HTGPNSPDTANDGFVR		heterogeneous nuclear ribonucleoprotein H2 [Mus musculus]	1684.7762	62.95	2.667360544
7305295	HTQAVEELTEQLEQFK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1929.953	59.72	2.386937562
27229048	HVSPAGAAVGVPLSEDEAR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1861.9347	37.4	0.803335167
63487095	HYEDGYPGGSDNYGSLSR		PREDICTED: catenin src [Mus musculus]	1973.8278	107.33	1.506436468
6755142	HYGPGWVSMANAGK		peptidylprolyl isomerase B [Mus musculus]	1474.6782	22.81	0
21450129	IAAFADAAVDPIDFPLAPAYAVPK		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	2443.2886	40.34	0
6754036	IAATILTSPDLR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1270.7435	20.37	1.530738504
6753296	IAEAGSRMDKLAR		catenin alpha 2 isoform 2 [Mus musculus]	1417.7407	21.42	0
63476037	IAEGVPQLLIVLTAEPSGDDVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2292.2395	60.78	0.71262065
46909602	IAGSFLPFLDEDR		SAM domain- and HD domain-containing protein 1 [Mus musculus]	1479.7561	27.65	0
6679515	IAIPGLAGAGNSVLLVSNLNPER		polypyrimidine tract binding protein 1 [Mus musculus]	2275.2751	43.79	1.104019634
31982522	IAMQTLDMGR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1135.561	31.6	1.624810039
63746482	IANLQTDLSDGLR		PREDICTED: filamin, alpha [Mus musculus]	1415.7562	70.92	1.45762163
7305295	IAQLEEELEEEQGNMEAMSDR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2451.0669	108.03	1.693000313
20137006	IAQLEEQLDNETK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1530.7654	56.22	2.208961596
7305295	IAQLEEQVEQEAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1542.778	66.87	1.224209286
41054806	IAQSDYIPTQQDVLR		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1746.9069	55.56	1.392418274
6754004	IATVGYLPTQQDVLR		guanine nucleotide binding protein, alpha 11 [Mus musculus]	1673.924	24.71	0
36031080	IAVQPGTLGPQGR		procollagen, type IV, alpha 2 [Mus musculus]	1293.7307	57.11	1.1601278
23346461	IDEVEEMLTNNR		NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Mus musculus]	1462.6926	50.46	1.346760626
38090003	IDIDNSGYVSDYELQDLFK		PREDICTED: expressed sequence AI427122 [Mus musculus]	2234.0513	48.81	2.571546488
40556608	IDIIPNPQER		heat shock protein 1, beta [Mus musculus]	1194.6451	43.21	0.682245105

31980969	IDMNLTDLLGELQR		SEC23B [Mus musculus]	1630.8406	28.88	0.804207479
50355692	IDSLSAQLSQLQK		lamin A isoform A [Mus musculus]	1430.777	54.89	1.089755216
9790073	IDSVTGEIFSAAPLDR		cadherin 17 [Mus musculus]	1690.8688	80.8	1.078748261
7949053	IDTIEIITDR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1188.6644	35.46	1.166067499
63562723	IEDFLER		PREDICTED: similar to 40S ribosomal protein S9 [Mus musculus]	921.4709	34.07	0.883682952
63476037	IEDNVQQFLVLLVAGR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1814.0208	28.98	0.852649689
31981100	IEDVTPIPSDSTR		ribosomal protein S14 [Mus musculus]	1429.7192	94.64	1.124131131
63476037	IEEGVPQFLVLISSGK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1715.9604	26.1	0
6680606	IEELNTQVAVHSEQIQISK		keratin complex 1, acidic, gene 19 [Mus musculus]	2166.1392	89.99	1.064265763
30794450	IEEVPELPLVVEDK		ribosomal protein L4 [Mus musculus]	1608.8739	26.67	0.994544896
37620153	IEGYPDPEVVWFK		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1578.7852	42.18	2.175515968
482387	IEISELNR		keratin, 67K type II epidermal - human	973.5337	41.51	0
1346343	IEISELNR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	973.5337	41.51	0
33563270	IEQLSPFPFDLLLK		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1659.9344	35.68	1.698314202
33563250	IESLNEEIAFLK		desmin [Mus musculus]	1405.7612	69.88	1.671388448
31559916	IETIEVMEDR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1234.6046	38.47	0.963559026
63621835	IETIEVMEDR		PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3 [Mus musculus]	1234.6046	38.47	0.963559026
21703972	IETQDIQALR		malic enzyme 2, NAD(+)-dependent, mitochondrial [Mus musculus]	1186.6455	40.47	1.159968577
31981722	IEWLESHQDADIEDFK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1974.9081	69.46	1.082137844
46849708	IFDLQDWSQEDER		succinate-Coenzyme A ligase, ADP-forming, beta subunit [Mus musculus]	1680.771	36.84	1.684293829
31982186	IFGVTTLDIVR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1233.7264	47.3	1.22666984
31559916	IFVGGIKEDTEEYNLR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1882.9541	45.3	0
6671602	IFVGGLSPDTPEEK		heterogeneous nuclear ribonucleoprotein D [Mus musculus]	1488.752	50.64	1.103649699
22164798	IFVWDWQR		selenium binding protein 1 [Mus musculus]	1149.5908	25.97	2.192476541
7710042	IFYPETTDIYDR		IQ motif containing GTPase activating protein 1 [Mus musculus]	1532.7356	21.07	0.843954674
6754012	IGAGDYQPTEQDILR		guanine nucleotide binding protein, alpha o [Mus musculus]	1675.8324	39.77	1.965212024
63476037	IGDLQSQIVSLLK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1413.8275	81.34	1.036649452
6671539	IGEHTPSALAIMENANVLAR		aldolase 1, A isoform [Mus musculus]	2107.105	29.18	1.037982426
6754750	IGFPWSEIR		moesin [Mus musculus]	1104.5907	34.48	0.945960401
6677699	IGFPWSEIR		radixin [Mus musculus]	1104.5907	34.48	0.945960401
6678571	IGFPWSEIR		villin 2 [Mus musculus]	1104.5907	34.48	0.945960401
51873060	IGGIGTVPVGR		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	1025.6158	47.79	0.905359513
51492007	IGQQPQQPGAPPQQDYTK		KH-type splicing regulatory protein [Mus musculus]	1980.9733	40.77	1.147895492
6754976	IGYPAPNFK		peroxiredoxin 1 [Mus musculus]	1006.5403	46.38	0
6678483	IHVSDQELQSANASVDDSR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	2070.9695	101.55	1.141117815
6680027	IIAEGANGPTTPEADK		glutamate dehydrogenase 1 [Mus musculus]	1583.7928	82.38	1.058560398
6680027	IIAEGANGPTTPEADKIFLER		glutamate dehydrogenase 1 [Mus musculus]	2242.1733	46.16	3.894495296
37620153	IIDEDFELTER		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1379.678	52.17	0
6677813	IIDVVYNASNNELVR		ribosomal protein S8 [Mus musculus]	1718.9081	91.16	0.685904564
31980706	IIEEAPAPGINPEVR		methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) [Mus musculus]	1604.8623	22.02	0
63476037	IIEELDVKPDGTR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1484.8004	69.6	0.802476006
6679567	IIGAVDQIQLTQAQLEER		polymerase I and transcript release factor [Mus musculus]	2025.1046	69.51	1.605082554
20137006	IIGLDQVAGMSETALPGAFK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2018.0576	92.61	1.165040859
31981722	IINEPTAAAIAYGLDK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1659.9058	82.61	0.846366827
7305163	IINEPTAAAIAYGLDK		heat shock protein 1-like [Mus musculus]	1659.9058	82.61	0.846366827
31981690	IINEPTAAAIAYGLDK		heat shock protein 8 [Mus musculus]	1659.9058	82.61	0.846366827
63664182	IINEPTAAAIAYGLDK		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1659.9058	82.61	0.846366827
50080209	IINEPTAAAIAYGLDR		heat shock protein 1A [Mus musculus]	1687.8922	28.55	2.654485917
41322904	IISLETYNLFR		plectin 1 isoform 1 [Mus musculus]	1368.7562	22.65	0.886914216
136429	IITHPNFNGNTLDNDIMLIK		Trypsin precursor	2283.1838	97.54	0
136429	IITHPNFNGNTLDNDIMLIK	Deamidation (NQ)	Trypsin precursor	2284.1741	62.22	0
136429	IITHPNFNGNTLDNDIMLIK	Oxidation (M)	Trypsin precursor	2299.1841	34.13	0.055592593
13384620	IITITGTQDQIQNAQYLLQNSVK		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	2589.3906	27.65	0
6680836	IKDPDAAKPEDWDER		calreticulin [Mus musculus]	1784.8492	87.72	0.841519231
7710042	ILAIGLINEALDEGDAQK		IQ motif containing GTPase activating protein 1 [Mus musculus]	1882.9789	42.72	2.316616525
7710042	ILAIGLINEALDEGDAQK	Deamidation (NQ)	IQ motif containing GTPase activating protein 1 [Mus musculus]	1883.9723	25.82	0
6678359	ILATPPQEDAPSVDIANIR		transketolase [Mus musculus]	2020.0674	89.59	1.004101595
13937395	ILEQEEEEEQAGK		arsenate resistance protein 2 [Mus musculus]	1531.6967	36.77	2.664795431
6680748	ILGADTSVDLEETGR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1575.7894	87.31	1.125147631
31982755	ILLAELEQLK		vimentin [Mus musculus]	1169.7202	58.02	0.637279571

6680067	ILLANFLAQTEALMK	glucose phosphate isomerase 1 [Mus musculus]	1675.948	74.79	1.512914993
31981679	ILQSSSEVGYDAMLGDFVNMVEK	heat shock protein 1 (chaperonin) [Mus musculus]	2532.2002	27.3	0.870177904
16716471	ILSDTTLWLR	hypothetical protein LOC94184 [Mus musculus]	1217.6973	50.07	0.960718603
13384620	ILSISADIETIGEILK	heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1714.9779	74.53	1.261224214
6677771	ILTFDQLALESPK	ribosomal protein L18 [Mus musculus]	1474.8116	78.52	1.015077557
34538601	ILYMMDEINNPVLTVK	cytochrome c oxidase subunit II [Mus musculus]	1892.9753	27.73	1.84748106
31980648	IMDPNIVGNEHYDVAR	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1842.8873	73.23	1.013243337
18152793	IMEGPAFNFLDAPAVR	pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1747.8894	56.95	0.929438712
20137006	IMGIPEDEQMGLLR	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1601.8074	53.76	1.176191683
31980648	IMNVIGEPIDER	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1385.7128	54.21	1.195146437
6678499	INAWNSPTLPIYEPGLK	UDP-glucose dehydrogenase [Mus musculus]	1913.0145	44.04	5.158620927
6724311	INEAFDLLR	alcohol dehydrogenase 1 (class I) [Mus musculus]	1090.5927	44.95	1.779550626
51890205	INFDDNAEFR	succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	1240.5618	72.38	1.19368109
21704066	INVNEIFYDLVR	RAS-related protein-1a [Mus musculus]	1494.7902	54.09	0.643281654
22165384	INVYYNEATGGK	tubulin, beta, 2 [Mus musculus]	1328.6663	25.74	0.844500405
16716467	IPAGTTLTLDMLTVK	N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1573.8773	44.64	0
22094989	IPDEFDSDPILVQQLR	translocase of inner mitochondrial membrane 50 homolog [Mus musculus]	1884.9646	63.08	0.949594836
21312062	IPDQLVILDMK	transmembrane trafficking protein [Mus musculus]	1284.718	35.43	0
6755368	IPDWFLNR	ribosomal protein S18 [Mus musculus]	1060.566	30.23	0.978757895
31980648	IPSAVGYQPTLATDMGTMQER	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2266.0889	96.78	1.342603381
9790077	IQAAASPPANATAASDTNAGDR	glycogen synthase kinase 3 beta [Mus musculus]	2069.9814	24.8	3.653963094
20137008	IQAIELEDLLR	biglycan [Mus musculus]	1312.7505	30.77	1.061536009
10946940	IQEGVFDINNEANGIK	RAB2, member RAS oncogene family [Mus musculus]	1760.8785	59.37	1.190004585
6678832	IQETQAELPR	minichromosome maintenance protein 6 [Mus musculus]	1184.6245	30.56	0
46593021	IQEVDAQMLR	ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1202.6233	49.4	1.095491705
6753498	IQFNESFAEMNR	cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	1485.6921	76.03	2.072931773
58037546	IQGGSVVEMQGDEMTR	isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	1736.8027	81.41	1.259302644
7657429	IQIEGDPDFR	osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	1189.5864	27.07	2.072418418
31559981	IQIWDTAGQER	RAB15, member RAS oncogene family [Mus musculus]	1316.6605	25.95	1.357712501
31560030	IQLVEEELDR	tropomyosin 1, alpha [Mus musculus]	1243.6512	29.86	1.796233139
40254525	IQLVEEELDR	tropomyosin 3, gamma [Mus musculus]	1243.6512	29.86	1.796233139
21314832	IQRPPEDSIQPYEK	UDP-glucose pyrophosphorylase 2 [Mus musculus]	1699.8658	41.53	0.963350665
19526818	IQTQPGYANTLR	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1361.7211	72.75	1.343265592
23956396	ISEIEDAAFLAR	SPFH domain family, member 2 [Mus musculus]	1334.6921	22.55	0
22165384	ISEQFTAMFR	tubulin, beta, 2 [Mus musculus]	1229.606	50.62	1.05912403
12963615	ISEQFTAMFR	tubulin, beta 3 [Mus musculus]	1229.606	50.62	1.05912403
31981939	ISEQFTAMFR	tubulin, beta 4 [Mus musculus]	1229.606	50.62	1.05912403
7106439	ISEQFTAMFR	tubulin, beta 5 [Mus musculus]	1229.606	50.62	1.05912403
21746161	ISEQFTAMFR	tubulin, beta [Mus musculus]	1229.606	50.62	1.05912403
22122523	ISFDLAEYTADVDGVGTLR	GDP-mannose 4, 6-dehydratase [Mus musculus]	2042.0081	76.24	1.100892998
34328206	ISFPAVQAAPSFSNSFPK	tryptophanyl-tRNA synthetase [Mus musculus]	1894.9677	61.06	1.004466652
51491845	ISGETIFVTAPHEATAGIIGVNR	clathrin, heavy polypeptide (Hc) [Mus musculus]	2353.2524	51.46	0.996967151
21361209	ISGLIYEETR	germinal histone H4 [Mus musculus]	1180.6273	76.06	0
31982755	ISLPLPTFSSLNLR	vimentin [Mus musculus]	1557.9039	66.55	1.251021917
63476037	ISLSPEYVYSVSTFR	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1747.9006	77.14	0.720517153
6677813	ISSLLEEQFQQGK	ribosomal protein S8 [Mus musculus]	1506.781	72.92	0.791363141
31981679	ISSVQSIVPALEIANAHR	heat shock protein 1 (chaperonin) [Mus musculus]	1905.0646	75.5	1.362212315
7106439	ISVYYNEATGGK	tubulin, beta 5 [Mus musculus]	1301.6368	81.54	2.555070361
31982522	ITEIYEGTSEIQR	acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1538.7739	74.67	1.348579257
31981562	ITLDNAYMEK	pyruvate kinase 3 [Mus musculus]	1197.5767	30.7	1.561208312
6679291	ITLPVDFVTADKFDENAK	phosphoglycerate kinase 1 [Mus musculus]	2023.0459	74.08	1.053945518
34328204	ITPAHDQNDYEVGQR	valyl-tRNA synthetase 2 [Mus musculus]	1742.8101	62.31	0.912619525
31981722	ITPSYVAFTPEGER	heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1566.7797	79.01	0.727055291
9790073	ITQVQWNDPGAQYSLVNK	cadherin 17 [Mus musculus]	2061.0403	50.76	2.395392351
54287684	ITSLEVENQNLR	eukaryotic translation elongation factor 1 delta isoform b [Mus musculus]	1415.7491	38.88	2.511742266
21450277	IVEIPFNSTNK	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1261.6791	37.27	0.935471668
33598964	IVFQEFR	myosin heavy chain 10, non-muscle [Mus musculus]	938.5177	28.83	1.966967828
7305295	IVFQEFR	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	938.5177	28.83	1.966967828
6753010	IVFVDPSLTVR	anterior gradient 2 [Mus musculus]	1245.7255	64.61	0.781197717
51491845	IVLDNSVFSEHR	clathrin, heavy polypeptide (Hc) [Mus musculus]	1415.7201	66.8	0.788445924

6754482	IVLQIDNAR		keratin complex 1, acidic, gene 18 [Mus musculus]	1041.6072	30.35	1.21701258
6680606	IVLQIDNAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1041.6072	30.35	1.21701258
24418919	IVNGWQVEEADDWLR		brain glycogen phosphorylase [Mus musculus]	1829.8887	57.85	1.101058855
6671622	IVQAEGEAEAAK		B-cell receptor-associated protein 37 [Mus musculus]	1215.6267	40.57	1.257921746
18079339	IVYGHLDDPANQEIER		aconitase 2, mitochondrial [Mus musculus]	1868.9192	60.25	1.319423491
8567336	IWALGGVTSDR		chloride channel calcium activated 3 [Mus musculus]	1174.6299	68.93	0.184543222
6678483	IYDDDFFQNLDGVANALDNIDAR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	2614.2122	24.2	1.108271183
33859554	IYELAAGGTAVGTGLNTR		fumarate hydratase 1 [Mus musculus]	1763.9302	89.98	1.424713641
6679299	IYTSIGEDYDER		prohibitin [Mus musculus]	1460.6639	27.86	0
21703998	IYVISLAEPR		aspartyl-tRNA synthetase [Mus musculus]	1160.67	20.27	1.161496348
22164798	IYVVDVGSEPR		selenium binding protein 1 [Mus musculus]	1233.651	38.78	2.033470768
7305295	KATLQAEQLSNELATER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1901.9943	53.79	1.773995932
6671507	KDLYANNVLSGGTTMYPGIADR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2356.1685	120.75	0.825755492
6671507	KDLYANNVLSGGTTMYPGIADR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2357.1497	108.35	3.118719297
6671509	KDLYANTVLSGGTTMYPGIADR		actin, beta, cytoplasmic [Mus musculus]	2343.1587	131.37	1.06426474
29789191	KEDGTFYEFGDDIPEAPER		asparaginyl-tRNA synthetase [Mus musculus]	2214.9851	55.48	0.786024439
30425112	KEEEEEEEEYDEGSNLK		hypothetical protein LOC109154 [Mus musculus]	2085.8726	43.12	1.040491972
30425112	KEEEEEEEEYDEGSNLKR		hypothetical protein LOC109154 [Mus musculus]	2241.9617	91.41	2.973120524
33598964	KFDQLLAEEK		myosin heavy chain 10, non-muscle [Mus musculus]	1220.6432	34.37	0
7305295	KFDQLLAEEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1220.6432	34.37	0
20137006	KFDQLLAEEK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1220.6432	34.37	0
29336026	KFDQLLAEEK		nonmuscle myosin heavy chain [Mus musculus]	1220.6432	34.37	0
6753262	KLEVEANNAFDQYR		capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1696.8232	77.31	0.733264565
31981246	KNPDSQYGELIEK		UMP-CMP kinase [Mus musculus]	1520.7592	45.33	1.216997086
6679184	KPEEVDDEVFYSPR		ornithine transcarbamylase [Mus musculus]	1709.801	43.26	0
6677871	KPELPDGDNDDDVVADISNR		scinderin [Mus musculus]	2184.0034	99.73	0.509455421
31981722	KSDIDEIVLVGGSTR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1588.855	40.46	0.813359692
8393866	KTEQGPPSSEYIFER		ornithine aminotransferase [Mus musculus]	1767.8536	42.94	2.052265523
21704100	LAAAFAVSR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	905.5295	34.47	0
15617203	LAALNPESNTSGLDIFAK		chloride intracellular channel 1 [Mus musculus]	1860.9601	56.88	1.287336322
6678499	LAANAFLAQR		UDP-glucose dehydrogenase [Mus musculus]	1074.6053	40.17	2.286283862
58037267	LAAVDATMNQVLASR		protein disulfide isomerase-associated 6 [Mus musculus]	1559.8306	41.34	0
50355692	LADALQELR		lamin A isoform A [Mus musculus]	1028.5603	28	1.042671244
31982522	LADMALALESAR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1260.6478	37.78	0
13624315	LAELEAALQR		keratin complex 2, basic, gene 8 [Mus musculus]	1113.63	47.63	1.71578959
31560731	LAEMPADSGYPAYLGAR		ATPase, H+ transporting, V1 subunit A, isoform 1 [Mus musculus]	1781.8549	33.5	1.13206189
6753010	LAEQFVLLNLVYETTDK		anterior gradient 2 [Mus musculus]	1996.0641	71.3	1.531584033
6678483	LAGTQPLEVLEAVQR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1623.9102	83.54	0.818996817
33563266	LALFNPDVSWDR		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 [Mus musculus]	1432.7251	58.33	1.185571133
23956396	LALQQDLTSMAPGLVIQAVR		SPFH domain family, member 2 [Mus musculus]	2124.1938	26.38	0.936676906
23956166	LALSQNQQSSGAAGPTGK		cisplatin resistance-associated overexpressed protein [Mus musculus]	1714.8693	63.54	0.963875633
51770896	LAMQEFMILPVGASSFR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1896.9752	42.4	1.154412373
51768219	LAPAVLLSGLTEVPVPTR		PREDICTED: similar to sodium bicarbonate cotransporter 2b [Mus musculus]	1833.0835	25.95	0
46430508	LAPDYDALDVANK		ribosomal protein L23a [Mus musculus]	1404.6904	47.07	1.386991433
31981562	LAPITSDPTEAAAVGAVEASFK		pyruvate kinase 3 [Mus musculus]	2145.1025	110.01	1.059505899
21313640	LAPPLVTLLSGEPEVQYVALR		adaptor-related protein complex 2, beta 1 subunit [Mus musculus]	2265.2725	23.87	1.28749211
6755809	LAQAAQSSVATITR		talin 1 [Mus musculus]	1416.7588	36.82	2.157138298
19527018	LAQDFLDSQNLSAYNTR		dipeptidylpeptidase III [Mus musculus]	1955.9513	44.66	0
18079351	LAQDPFPLYPGELLEK		major vault protein [Mus musculus]	1829.9603	49.5	1.083207484
6753272	LAQEDPDYGLR		catalase [Mus musculus]	1276.6172	22.13	0.999903752
30794206	LAQQQAALLMQQEER		splicing factor 3b, subunit 2 [Mus musculus]	1756.9019	21.53	4.857139346
51770896	LAQSNGWGVMVSHR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1541.7715	40.54	1.53200771
11230802	LASDLLEWIR		actinin alpha 4 [Mus musculus]	1215.6792	57.87	1.173571958
33186863	LATQLTGPVMPIR		ribosomal protein L13 [Mus musculus]	1396.7997	56.63	0.932951995
63650229	LAVNMVPFPR		PREDICTED: similar to TUBULIN BETA CHAIN (T BETA-15) [Mus musculus]	1143.6415	45.92	0.86338516
22165384	LAVNMVPFPR		tubulin, beta, 2 [Mus musculus]	1143.6415	45.92	0.86338516
12963615	LAVNMVPFPR		tubulin, beta 3 [Mus musculus]	1143.6415	45.92	0.86338516
31981939	LAVNMVPFPR		tubulin, beta 4 [Mus musculus]	1143.6415	45.92	0.86338516
7106439	LAVNMVPFPR		tubulin, beta 5 [Mus musculus]	1143.6415	45.92	0.86338516
27754056	LAVNMVPFPR		tubulin, beta 6 [Mus musculus]	1143.6415	45.92	0.86338516

21746161	LAVNMVPFPR		tubulin, beta [Mus musculus]	1143.6415	45.92	0.86338516
7305295	LDAFLVLEQLR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1316.7635	52.61	1.913357737
21312950	LDDLINWAR		NADH dehydrogenase (ubiquinone) Fe-S protein 7 [Mus musculus]	1115.5796	35.49	1.417012007
30794450	LDELYGTWR		ribosomal protein L4 [Mus musculus]	1152.5779	38	1.035548551
21704206	LDFTEEEELLSR		carboxylesterase 2 [Mus musculus]	1480.7168	50.24	1.50441724
31981562	LDIDSAPITAR		pyruvate kinase 3 [Mus musculus]	1171.6318	44.28	1.128284555
6677819	LDILDTAGQEEFGAMR		Harvey rat sarcoma oncogene, subgroup R [Mus musculus]	1765.8459	57.84	2.100540769
13399308	LDILDTAGQEEFGAMR		related RAS viral (r-ras) oncogene homolog 2 [Mus musculus]	1765.8459	57.84	2.100540769
54607112	LDLGSNEFTEVPEVLEQLSGLR		Erbb2 interacting protein isoform 2 [Mus musculus]	2445.24	21.25	0
6678359	LDNLVAIFDINR		transketolase [Mus musculus]	1402.7755	80.31	0.969652456
33598964	LDPHLVLDQLR		myosin heavy chain 10, non-muscle [Mus musculus]	1318.7496	67.55	0
20137006	LDPHLVLDQLR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1318.7496	67.55	0
33859686	LDQETAQWLR		phosphoglucomutase 1 [Mus musculus]	1259.6407	47.85	3.071239435
30023842	LDQLIYIPLPDEK		valosin containing protein [Mus musculus]	1556.8505	44.52	0.836321052
6678483	LDQPMTEIVSR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1288.6648	42.31	0.813146228
6754482	LEAEIATYR		keratin complex 1, acidic, gene 18 [Mus musculus]	1065.5613	40.33	1.068574632
13624315	LEAELGNMQGLVEDFK		keratin complex 2, basic, gene 8 [Mus musculus]	1792.8839	122.03	1.284336683
2506774	LEAELGNMQGLVEDFK		Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)	1792.8839	122.03	1.284336683
63565108	LEAELGNMQGLVEDFK		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1792.8839	122.03	1.284336683
18079339	LEAPDADELPR		aconitase 2, mitochondrial [Mus musculus]	1225.6046	50.59	1.142129953
6755817	LEDKDDLDVTELSNEELLDQLVR		thymopoietin [Mus musculus]	2701.3318	53.39	0.845472686
21312062	LEDLSESIVNDFAYMK		transmembrane trafficking protein [Mus musculus]	1873.8931	47.74	1.526349084
31982275	LEDTENWLYEDGEDQPK		heat shock protein 4 [Mus musculus]	2080.8965	52.28	1.037840132
6679261	LEEGPPVTTVLTR		pyruvate dehydrogenase E1 alpha 1 [Mus musculus]	1411.7776	52.41	1.096762039
6671668	LEEVDDADDYDNR		calpain 1 [Mus musculus]	1568.6348	74.55	0.979779047
20137006	LEGDSTDLSDQIAELQAQIAELK	Deamidation (NQ)	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2488.2271	43.3	0
13624315	LEGLTDEINFLR		keratin complex 2, basic, gene 8 [Mus musculus]	1419.7573	73.64	1.285306547
2506774	LEGLTDEINFLR		Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)	1419.7573	73.64	1.285306547
63565108	LEGLTDEINFLR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1419.7573	73.64	1.285306547
51890205	LEGTNVQEAQNILK		succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	1556.8265	31.22	2.806280008
547749	LENEIQTYR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1165.5751	30.66	0.491802121
6754480	LEQEIATYR		keratin 13 [Mus musculus]	1122.5834	51.63	1.262567273
21592285	LEQEIATYR		keratin 20 [Mus musculus]	1122.5834	51.63	1.262567273
6680606	LEQEIATYR		keratin complex 1, acidic, gene 19 [Mus musculus]	1122.5834	51.63	1.262567273
125081	LEQEIATYR		Keratin, type I cytoskeletal 15 (Cytokeratin 15) (K15) (CK 15)	1122.5834	51.63	1.262567273
63517295	LEQVSSDEGIGTLAENLLEALR		PREDICTED: RIKEN cDNA 1810009A16 [Mus musculus]	2357.2112	36.01	1.130637342
21704156	LEQYTNAIEGTK		caldesmon 1 [Mus musculus]	1366.6768	48.8	2.024113271
29336026	LESQLQEVQGR		nonmuscle myosin heavy chain [Mus musculus]	1286.67	44.9	18.66047315
63565108	LEVDPNIQAVR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1253.6908	55.19	0.954807299
6753262	LEVEANNAFDQYR		capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1568.7374	31.54	0
7305173	LFDQAFGVPR		heat shock protein 1 [Mus musculus]	1149.6116	48.45	2.227362491
55742711	LFELEEQDLFR		EH-domain containing 2 [Mus musculus]	1438.7286	60.18	1.600020005
55742711	LFELEEQDLFR	Deamidation (NQ)	EH-domain containing 2 [Mus musculus]	1439.7314	24.39	0
63650187	LFIGGLNVQTSESGLR		PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A0 [Mus musculus]	1690.9128	22.47	1.241621403
31559916	LFIGGLSFETTDDSLR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1770.8896	47.28	0.790893932
6680836	LFPSGLDQK		calreticulin [Mus musculus]	1004.5355	35.91	0
8567338	LFQSNDPTLR		coatomer protein complex, subunit gamma [Mus musculus]	1190.6177	28.15	2.171817292
23956214	LFVGNLPADITEDEFK		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1807.9087	57.77	1.419457615
31560613	LFVTNDAATILR		chaperonin subunit 8 (theta) [Mus musculus]	1333.7517	43.63	0
38198665	LGAAPEEESAYVAGER		p47 protein [Mus musculus]	1648.7825	54.63	1.192075899
6680163	LGAGYPMGPFELLDYVGLDTTK		L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	2357.1833	35.97	1.859357919
54607098	LGANSLLDLVVFGR		succinate dehydrogenase Fp subunit [Mus musculus]	1473.8423	44.74	0.908864914
31982755	LGDLYEEEMR		vimentin [Mus musculus]	1254.5725	63.56	1.472674051
6679291	LGDVYVNDAFGTAHR		phosphoglycerate kinase 1 [Mus musculus]	1634.7968	93.52	1.593630663
136429	LGEHNIDVLEGNEQFINAAK		Trypsin precursor	2211.1084	121.71	0
6755893	LGEHNINVLEGNEQFVNSAK	Deamidation (NQ)	trypsin 4 [Mus musculus]	2213.0764	26.63	0
6671571	LGEIVTTIPTIGFNVETVEYK		ADP-ribosylation factor 2 [Mus musculus]	2323.2439	96.23	1.164282593
6754208	LGEMWNNTAADDKQPYEK		high mobility group box 1 [Mus musculus]	2109.9548	61.75	0.972219394
33859506	LGEYGFQNAILVR		albumin 1 [Mus musculus]	1479.802	85.86	1.854845055
10946574	LGFSEVELVQMVVDGVK		creatine kinase, brain [Mus musculus]	1848.9823	51.86	2.51298349

6754084	LGLDFPNLPYLIDGSHK	glutathione S-transferase, mu 1 [Mus musculus]	1898.9863	40.77	1.016424652
6680121	LGLDFPNLPYLIDGSHK	glutathione S-transferase, mu 2 [Mus musculus]	1898.9863	40.77	1.016424652
6678097	LGMTDAFGGR	serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	1024.4945	58.94	1.214442
6753036	LGPALATGNVVVMK	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1369.7806	49.94	1.221844425
6678359	LGQSDPAPLQHQVDIYQK	transketolase [Mus musculus]	2037.0414	79.22	0.90990654
25020120	LGSQATGVQGQAGQLLDTTESTLGR	PREDICTED: laminin, alpha 5 [Mus musculus]	2488.26	50.12	0
31560611	LGTDQPLDQATISLQMGTNK	calponin 1 [Mus musculus]	2131.0691	73.58	1.545531272
31542159	LHEFTISGTTYTPEGEVR	ATPase, Ca++ transporting, ubiquitous [Mus musculus]	2036.9844	34.47	0.626248647
6755901	LIGQIVSSITASLR	tubulin, alpha 1 [Mus musculus]	1457.8715	29.55	1.269169458
6678573	LIIQWNGPESNR	villin 1 [Mus musculus]	1426.7566	41.56	1.413016003
22164798	LILPGLISSR	selenium binding protein 1 [Mus musculus]	1068.6881	34.25	2.241288938
63489754	LIQEQHPEEELIK	PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1605.8162	21.6	0
34740335	LISQIVSSITASLR	tubulin, alpha 2 [Mus musculus]	1487.8838	86.88	1.396427913
6678467	LISQIVSSITASLR	tubulin, alpha 4 [Mus musculus]	1487.8838	86.88	1.396427913
6678469	LISQIVSSITASLR	tubulin, alpha 6 [Mus musculus]	1487.8838	86.88	1.396427913
6679937	LISWYDNEYGYSNR	similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1779.8066	73.25	1.006036466
6680748	LKEIVTNFLAGFEP	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1577.8457	34.62	0
547749	LKYENEVALR	Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1234.6809	37.49	0
27370092	LLDAVDTYIPVPTR	Tu translation elongation factor, mitochondrial [Mus musculus]	1572.8672	71.24	1.625036071
6755002	LLDEEEATDNDLR	programmed cell death 6 interacting protein [Mus musculus]	1532.7037	36.93	1.996012597
15809004	LLDFVLGQEIR	cyclin M4 [Mus musculus]	1302.7435	28.78	1.311744125
9790261	LLDSLEPPGEPGPSTSIPENDTVDGR	Trk-fused gene [Mus musculus]	2692.2883	46.26	0.8113052
55742711	LLEALDDMLAQDIAK	EH-domain containing 2 [Mus musculus]	1658.8549	49.4	1.208689523
6754482	LLEDGEDFSLNDALDSSNSMQTVQK	keratin complex 1, acidic, gene 18 [Mus musculus]	2756.2646	21.1	0.926706526
31981828	LLELGPKPEVAQQTR	coatomer protein complex subunit alpha [Mus musculus]	1678.9519	50.96	0.907075302
54607037	LLELQEVDSLLR	integrin beta 4 isoform 2 [Mus musculus]	1427.8203	22.79	1.141649789
16716471	LLENMTEVVR	hypothetical protein LOC94184 [Mus musculus]	1203.6481	23.49	3.802239556
6753066	LLETEEEAAFPLGGATPR	amine oxidase, copper containing 3 [Mus musculus]	1900.9585	73.63	1.382570173
29336026	LLGLGVTDFSR	nonmuscle myosin heavy chain [Mus musculus]	1177.6633	49.63	1.273331133
31982300	LLGNMIVIVLGHHLGK	hemoglobin, beta adult major chain [Mus musculus]	1714.0273	34.41	0
6754256	LLGQFTLIGIPPAPR	heat shock protein 9A [Mus musculus]	1592.9508	21.07	1.029090602
10946574	LLIEMEQR	creatine kinase, brain [Mus musculus]	1031.5581	27.06	1.852869069
27370510	LLIYNPEDPPGSEVLR	paraoxonase 3 [Mus musculus]	1811.926	21.61	0
6671672	LLLNNDNLLR	capping protein (actin filament) muscle Z-line, alpha 2 [Mus musculus]	1197.7069	30.9	1.696714324
28316750	LLLPGELAK	histone 1, H2ba [Mus musculus]	953.6071	59.17	0.77730347
20874851	LLLPGELAK	PREDICTED: similar to histone H2b-616 [Mus musculus]	953.6071	59.17	0.77730347
63556656	LLNPQGAIR	PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	981.5851	41.59	0.250476959
31981690	LLQDFFNGK	heat shock protein 8 [Mus musculus]	1081.5712	51.41	1.139423465
50080209	LLQDFFNGR	heat shock protein 1A [Mus musculus]	1109.588	31.29	1.092102049
24418919	LLSLVDDEAFIR	brain glycogen phosphorylase [Mus musculus]	1390.7628	81.86	1.200234559
63562740	LLTSAAFEDCQTR	PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1454.7007	79.93	1.021630372
31982300	LLVVYPWTQR	hemoglobin, beta adult major chain [Mus musculus]	1274.7296	22.74	1.736049847
28077013	LLYEANLPENFR	stromal membrane-associated protein 1 [Mus musculus]	1478.7648	26.76	1.800241032
51491845	LLYNNVSNFGR	clathrin, heavy polypeptide (Hc) [Mus musculus]	1296.6796	63.41	1.110842353
19923052	LMDEVAGIVAAR	brain acyl-CoA hydrolase [Mus musculus]	1244.6642	36.11	1.188990735
31560689	LMFNDFLSSSSDK	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	1490.7101	46.22	1.16217849
1346343	LNDLEDALQQAK	Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1357.7006	73.89	0.25308302
6755809	LNEAAAGLNQAATELVQASR	talin 1 [Mus musculus]	2027.0554	46.11	2.060406912
21450277	LNIPVNQVNPR	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1263.724	38.71	0.979294365
52317152	LNIQADQAPVIAVLGSGGGLR	phospholipase A2, group IVC (cytosolic, calcium-independent) [Mus musculus]	2049.1536	33.07	0
45387933	LNIQPSETDYAVDIR	UDP-glucose ceramide glucosyltransferase-like 1 [Mus musculus]	1733.8716	60.12	1.092467168
63476037	LNLLDLDYELAEQLDNIAEK	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2332.187	113.45	0.762174101
55742711	LNPFGNTFLNR	EH-domain containing 2 [Mus musculus]	1292.6732	23.73	1.171551326
22164798	LNPNFLVDFGK	selenium binding protein 1 [Mus musculus]	1263.6713	59.97	2.041601203
13384736	LNTQEIFDDWAR	dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1507.7321	41.85	0.868370732
33859811	LPAKPEVSSDEDVQYR	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1832.889	111.33	0.696838963
33859506	LPCVEDYLSAILNR	albumin 1 [Mus musculus]	1605.8308	53.23	1.932565726
31982330	LPDQQDTAQDASVEVNR	Golgi autoantigen, golgin subfamily a, 3 [Mus musculus]	1885.8807	41.03	2.428147005
28916703	LPFPIIDDK	peroxiredoxin 5 related sequence 1 protein [Mus musculus]	1057.5907	45.45	2.441682853
6671549	LPFPIIDDK	peroxiredoxin 6 [Mus musculus]	1057.5907	45.45	2.441682853

56119103	LPGQPPASMGR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1110.5741	39.36	0.752725109
51873060	LPLQDVYK		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	975.5501	45.77	0.844130438
12963765	LPNQTHPDTPVGDESQAR		seryl-aminoacyl-tRNA synthetase 2 [Mus musculus]	1961.9332	39.21	0
63746482	LPQLPITNFSR		PREDICTED: filamin, alpha [Mus musculus]	1285.7231	35.07	1.039097111
31543918	LPQPPEGQTYNN		ubiquitin-conjugating enzyme E2 variant 2 [Mus musculus]	1357.6304	42.02	1.358311708
21450325	LPSEGPQPAHVVVGDVR		biliverdin reductase B (flavin reductase (NADPH)) [Mus musculus]	1756.9364	37.42	1.947303086
63738313	LPSGSGPASPTTGSAVDIR		PREDICTED: similar to AHNAK [Mus musculus]	1769.8965	42.79	1.353176416
41322904	LPVDVAYQR		plectin 1 isoform 1 [Mus musculus]	1060.5828	31.91	1.865692134
31560689	LPWDAVGR		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	913.4964	35.17	1.598094172
7710042	LPYDVTPEQALSHEEVK		IQ motif containing GTPase activating protein 1 [Mus musculus]	1954.9806	26.72	0.717307402
13624315	LQAEIEALK		keratin complex 2, basic, gene 8 [Mus musculus]	1014.5792	35.3	1.711600125
31982755	LQDEIQNMKEEMAR		vimentin [Mus musculus]	1734.8159	36.64	0.939752697
34328286	LQDPFSVYR		succinate dehydrogenase Ip subunit [Mus musculus]	1124.5852	39.11	1.313315552
33563250	LQEEIQLR		desmin [Mus musculus]	1028.5776	37.96	2.229784273
6678573	LQEENQVITPR		villin 1 [Mus musculus]	1326.7067	64.15	1.122268913
50355692	LQEKEDLQELNDR		lamin A isoform A [Mus musculus]	1629.8136	59.92	1.216483641
6677905	LQETEMMDPELDYTLMR		golgi apparatus protein 1 [Mus musculus]	2114.9546	40.03	1.43573059
34594657	LQGPQTSAEVYR		glycerol-3-phosphate dehydrogenase 1-like [Mus musculus]	1348.6932	34.84	0
10946940	LQIWDTAGQESFR		RAB2, member RAS oncogene family [Mus musculus]	1550.7677	70.4	0.874413717
21450625	LQMEAPHIIVGTPGR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1618.8804	63.05	0.908798773
51771446	LQMEAPHIIVGTPGR		PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 [Mus musculus]	1618.8804	63.05	0.908798773
31982091	LQMEQQQQLQQR		translocase of outer mitochondrial membrane 22 homolog [Mus musculus]	1557.783	23.66	2.184215805
7305295	LQNEVESVTGMLNEAEGK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1947.9318	83.38	1.809295967
41322904	LQNVQIALDYLR		plectin 1 isoform 1 [Mus musculus]	1445.8188	25.08	1.415340846
29336026	LQQELDDATVDLGQQK		nonmuscle myosin heavy chain [Mus musculus]	1800.8622	63.64	0.874497191
7305295	LQQELDDLVVDLDNQR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1912.9697	132.02	2.148399271
7305295	LQQELDDLVVDLDNQR	Deamidation (NQ)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1913.9442	21.79	3.808194588
19527026	LQQLPADFGR		hypothetical protein LOC98238 [Mus musculus]	1144.6118	50.15	0.928047227
51829617	LQSGIEDLR	Deamidation (NQ)	PREDICTED: hypothetical protein XP_484257 [Mus musculus]	1031.5376	20.05	0
31980942	LQVSQQEDITK		Inositol (myo)-1(or 4)-monophosphatase 1 [Mus musculus]	1288.6779	45.83	1.090341673
31791057	LSAEDLVLEGAGLR		laminin, gamma 1 [Mus musculus]	1442.7946	52.62	0.789549162
63476037	LSDAGITPLFLTSQEDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1862.9487	64.39	0.731002578
63489759	LSDDNTIGQEEIQQR		PREDICTED: spectrin alpha 2 [Mus musculus]	1745.8319	78.02	1.443509505
6671666	LSDLLAPISEQIQEVITFR		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	2172.1914	112.23	1.210294302
12963539	LSGAQADLHIGEGDSIR		ETHE1 protein [Mus musculus]	1738.879	69.93	1.532704229
27229048	LSGVSVSSDAFFPFR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1615.8165	44.95	1.043333777
6671549	LSILYPATTGR		peroxiredoxin 6 [Mus musculus]	1191.6729	61.09	3.816559717
21450277	LSLDELHR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	982.5351	29.69	2.0983929
6679166	LSLLEELTLAENQLLR		osteoglycin [Mus musculus]	1855.0563	35.92	1.039064276
63641940	LSLQDAVNQGLIDQDMATR		PREDICTED: desmoplakin [Mus musculus]	2088.041	40	0.896352992
6755787	LSPPYSSPQEFAQDVGR		tripartite motif protein 28 [Mus musculus]	1877.9105	44.09	0.943147592
29336026	LSQLEEELEEEQNNSELLK		nonmuscle myosin heavy chain [Mus musculus]	2274.0874	25.54	0.647323197
6755967	LSQNNFALGYK		voltage-dependent anion channel 3 [Mus musculus]	1254.647	45.56	1.365163408
12963539	LSQQSASGAPVLLR		ETHE1 protein [Mus musculus]	1426.8058	23.7	0.857354177
33859506	LSQTFPNADFAEITK		albumin 1 [Mus musculus]	1681.8477	55.32	1.580429038
6754556	LSSEMNTSTVNSAR		lamin B1 [Mus musculus]	1496.7075	29.39	0.786693683
6754556	LSSEMNTSTVNSAR	Oxidation (M)	lamin B1 [Mus musculus]	1512.6971	24.65	0
34996495	LSSGYYDFSVR		ribophorin II [Mus musculus]	1293.6139	23.51	0.940538709
136429	LSSPATLNSR		Trypsin precursor	1045.5665	48.54	0
7305085	LSTDHIPILYR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1327.74	47.6	0.910219488
6680606	LSVEADINGLR		keratin complex 1, acidic, gene 19 [Mus musculus]	1186.6418	34.27	0
22122387	LSVGLEDEQDLLEDLDR		cystathionase [Mus musculus]	1958.9635	73.02	0
6679012	LTDQVMQNPQVLAALQER		nucleosome assembly protein 1-like 4 [Mus musculus]	2054.0635	30.52	0.832410821
31981983	LTEPQLGLGSQR		stromal interaction molecule 1 [Mus musculus]	1298.7091	28.47	1.782475378
29789191	LTESVDVLMPNVGEIVGGSMR		asparaginyl-tRNA synthetase [Mus musculus]	2203.1118	51.79	1.108362696
6755963	LTFDSSFSPNTGK		voltage-dependent anion channel 1 [Mus musculus]	1400.6658	71.53	1.075048056
6755965	LTFDTTFSPNTGK		voltage-dependent anion channel 2 [Mus musculus]	1428.6903	25.89	0
51765915	LTLIDPETLLPR		PREDICTED: TBP-interacting protein [Mus musculus]	1380.8096	51.61	0.937309628
63501125	LTQQAGDLTVPAGGQR		PREDICTED: ADP-ribosylation factor interacting protein 1 [Mus musculus]	1611.842	41.34	0.900352045
7106389	LTVEDPVTVEYITR		proteasome (prosome, macropain) subunit, alpha type 7 [Mus musculus]	1634.8674	34.26	1.161096854

51556274	LVAGEMGQNEPDQGGQR		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	1785.8229	73.33	1.549410146
13385472	LVAIVDVIDQNR		ribosomal protein L14 [Mus musculus]	1354.7694	43.6	1.054063525
19527028	LVGEIMQETGTR		high density lipoprotein binding protein [Mus musculus]	1333.6807	29.14	1.406542405
6678992	LVGILDILDEENR		myosin VI [Mus musculus]	1498.8101	45.76	1.281190491
31981273	LVPDMIPEVVSEQVSSYLSK		CNDP dipeptidase 2 (metallopeptidase M20 family) [Mus musculus]	2220.1084	28.21	1.752646216
63518159	LVPLLDTGDIIIDGGNSEYR		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	2160.1165	94.95	1.393665808
31543942	LVQAAQMLQSDPYSVPAR		vinculin [Mus musculus]	1974.0072	24.6	1.070431445
6754976	LVQAFQFTDK		peroxiredoxin 1 [Mus musculus]	1196.6294	48.36	1.130673842
31981679	LVQDVANNTNEEAGDGTTTATVLAR		heat shock protein 1 (chaperonin) [Mus musculus]	2560.2554	133.13	0.994217848
33859506	LVQEVTDFAK		albumin 1 [Mus musculus]	1149.6145	55.41	1.565183744
14149635	LVSSENFDDYMK		fatty acid binding protein 4, adipocyte [Mus musculus]	1447.6532	40.1	0.98510164
63530525	LVTFESVAVPLQQGAEQQR		PREDICTED: SEC31-like 1 [Mus musculus]	2100.1196	43.9	0.697242621
19527026	LVTLPVSFAQLK		hypothetical protein LOC98238 [Mus musculus]	1315.7906	40.05	0.381162838
24418919	LVTSIGDVVNHDPVVGDR		brain glycogen phosphorylase [Mus musculus]	1891.9851	40.5	0.970682721
6680047	LWDLTTGTTTR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1264.6593	59.62	1.044453326
6754090	LWMAAMQQDPVASSHK		glutathione S-transferase omega 1 [Mus musculus]	1799.8497	21.64	0.972488774
31560517	LWTLVSEQTR		ribosomal protein L27a [Mus musculus]	1232.6688	44.66	0.876457228
6753010	LYAYEPSDTALLYDNMK		anterior gradient 2 [Mus musculus]	2006.943	80.98	0.74517534
6753010	LYAYEPSDTALLYDNMK	Oxidation (M)	anterior gradient 2 [Mus musculus]	2022.9613	33.25	0.461912735
19525729	LYDIEQQQITDALENIR		crystallin, lamda 1 [Mus musculus]	2062.0461	62.24	1.794445841
6755048	LYDPLDGMVSIDGQDIR		ATP-binding cassette, sub-family B (MDR/TAP), member 1A [Mus musculus]	1906.9288	27.61	1.579581989
31560618	LYDVPANSMR		budding uninhibited by benzimidazoles 3 homolog [Mus musculus]	1165.5665	28.52	0
6753304	LYGPSSVSFADDFVR		serine (or cysteine) proteinase inhibitor, clade H, member 1 [Mus musculus]	1659.8029	36.96	1.450809392
31981722	LYGSGGPPPTGEEDTSEKDEL		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	2177.9731	98.52	0.809021466
6753266	LYPIANGNNQSPIDIK		carbonic anhydrase 1 [Mus musculus]	1756.9187	79.19	3.748214709
6753428	LYPPSAEYPDLR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	1420.7155	49.76	2.239612439
31542333	LYQPEYQEVSTEEQR		hypoxia up-regulated 1 [Mus musculus]	1898.8776	83.23	0.893299748
7106389	LYQTDPSGTYHAWK		proteasome (prosome, macropain) subunit, alpha type 7 [Mus musculus]	1666.7904	29.85	1.265003303
16716589	LYTLVTYVPVTTFK		ribosomal protein L31 [Mus musculus]	1644.9172	39.99	1.077266094
30519997	LYTVDYLSNMVGGR		bleomycin hydrolase [Mus musculus]	1587.7814	25.77	0
31981939	MAATFIGNSTAIQELFK	Oxidation (M)	tubulin, beta 4 [Mus musculus]	1857.941	38.16	1.819989721
63530525	MADAIILAIAGGQELLAQTQK		PREDICTED: SEC31-like 1 [Mus musculus]	2155.1797	37.32	0
11230802	MAPYQGPDAAPGALDYK		actinin alpha 4 [Mus musculus]	1764.8274	44.53	1.127079411
7305295	MAQQMLDLEEQLEEEEAAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2263.0254	100.66	1.930927507
6679687	MDATANDVPSPYEVK		glucose regulated protein [Mus musculus]	1636.7549	63.03	0.895023585
22203749	MDDPTVNWSNER		G1 to S phase transition 1 [Mus musculus]	1463.6294	44.21	1.491261874
6678097	MDEEEVEVFLPK		serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	1464.7145	23.47	0.177748887
30023842	MDELQLFR		valosin containing protein [Mus musculus]	1051.5287	35.23	0.95166289
40068507	MDENQFVAVTSTNAAK		collapsin response mediator protein 1 [Mus musculus]	1725.8163	58.82	0.720479325
40254595	MDENQFVAVTSTNAAK		dihydropyrimidinase-like 2 [Mus musculus]	1725.8163	58.82	0.720479325
6681219	MDENQFVAVTSTNAAK		dihydropyrimidinase-like 3 [Mus musculus]	1725.8163	58.82	0.720479325
18700026	MDESEANEAPAGEAAAR		oxidation resistance 1 [Mus musculus]	1718.7202	30.17	0
63738313	MDINAPDMDVQGPDWHLK		PREDICTED: similar to AHNAK [Mus musculus]	2081.9487	28.79	0.72555481
10946972	MFAEYLASENQR		epsilon subunit of coatomer protein complex [Mus musculus]	1458.6854	26.83	2.081462264
47578123	MFTQQQPQELAR		potassium channel tetramerisation domain containing 12 [Mus musculus]	1476.7296	35.03	0
7949037	MFTSGIDLMDMASELMQPSGDDAAR		enoyl coenzyme A hydratase 1, peroxisomal [Mus musculus]	2689.1802	23.55	1.512194657
21450625	MFVLDEADEMLSR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1555.7218	56.77	1.203357555
51771446	MFVLDEADEMLSR		PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 [Mus musculus]	1555.7218	56.77	1.203357555
23956214	MGGGGTMNMGDPYGSGGQK		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1801.7355	49.3	0.955498089
33859811	MGLVDQLVEPLGPGIK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1665.9203	43.8	0.85821085
31980685	MIEQDDFDINTR		glucosamine [Mus musculus]	1496.6738	48.38	1.482728792
21704206	MIPAVVDGEFFPR		carboxylesterase 2 [Mus musculus]	1477.7549	22.07	1.794984212
11230802	MLDAEDIVNTARPDEK		actinin alpha 4 [Mus musculus]	1816.8789	22.34	0
6681157	MLDMGFEPQIR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1336.6545	31.54	1.050833506
40068493	MLDMGFEPQIR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1336.6545	31.54	1.050833506
6753620	MLDMGFEPQIR		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1336.6545	31.54	1.050833506
7305505	MLDQTTNFEER		smoothelin [Mus musculus]	1383.6229	38.01	3.048541905
6679891	MLDYLQGSGETPQTDIR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1923.9072	44.96	0.557266769
10092608	MLLADQGQSWK		glutathione S-transferase, pi 1 [Mus musculus]	1276.6366	38.28	0
6754084	MLLEYTDSSYDEK		glutathione S-transferase, mu 1 [Mus musculus]	1593.703	31.33	1.029781255

31982290	MLYDMENPPADDYFGR		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1933.8114	57.16	1.398526811
31981273	MMEVAAADVQR		CNDP dipeptidase 2 (metallopeptidase M20 family) [Mus musculus]	1220.5759	21.34	1.14371136
6754036	MNLGVGAYR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	980.5053	21.27	1.254712421
63556656	MPDGSMLVHQK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1242.5939	32.67	0
6996911	MPEFYNR		argininosuccinate synthetase [Mus musculus]	956.4396	24.29	0.827311089
6679465	MPPYDEETQAIIDAAQEAR		protein kinase C substrate 80K-H [Mus musculus]	2147.9966	90.4	0.844225307
6678359	MPTPPSYK		transketolase [Mus musculus]	920.4526	35.68	1.15888033
6678726	MQEVYNFNAINNSEIR		leukotriene A4 hydrolase [Mus musculus]	1941.9152	43.05	1.232376282
21704156	MQNDSAENETAEGEEKR	Deamidation (NQ)	caldesmon 1 [Mus musculus]	1938.8004	51.43	0
8394269	MQQFDDLFR		ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltra	1199.5535	36.23	1.118483826
20137006	MQQNIQELEEQLEEEESAR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2333.0564	111	0.946761979
50355692	MQQQLDEYQELLDIK		lamin A isoform A [Mus musculus]	1893.9268	90.27	1.243009713
13385356	MREDYDSVEQDGDEPGPQR		RNA binding motif protein 8a [Mus musculus]	2222.9355	33.07	0.769309644
6679108	MSVQPTVSLGGFEITPPVVLR		nucleophosmin 1 [Mus musculus]	2227.2205	45.32	0.942171972
6679108	MTDQEAIQDLWQWR		nucleophosmin 1 [Mus musculus]	1819.8541	61.63	0.711738702
56119103	MTGSEFDFEEMKR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1606.6969	42.25	1.180587029
6678573	MVDDGSGEVQVWR		villin 1 [Mus musculus]	1477.6771	68.13	1.47344132
33859811	MVGVPAAFDMMLTGR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1595.7811	21.59	1.795352197
6753438	MYDSLLALPQDLQAAR		claudin 3 [Mus musculus]	1804.9321	25.87	1.540400058
8393144	MYDSVLALPGALQATR		claudin 7 [Mus musculus]	1705.9006	59.75	1.541391125
13384828	MYGADLAPVDFLHASEDAR		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	2077.9673	73.43	1.077468967
6677871	MYLETDPSGR		scinderin [Mus musculus]	1168.535	33.92	0.298820411
6753294	NAGNEQDLGIQYK		catenin alpha 1 [Mus musculus]	1449.6974	35.5	0
30023842	NAPAIIFIDELDAIAPK		valosin containing protein [Mus musculus]	1811.0021	113.69	0.98988666
31982275	NAVEEYVYEMR		heat shock protein 4 [Mus musculus]	1402.6425	23.43	0.8361727
6754256	NAVITVPAYFNDSQR		heat shock protein 9A [Mus musculus]	1694.8562	60.98	0.881281985
18079339	NAVTQEFGPVPDTAR		aconitase 2, mitochondrial [Mus musculus]	1601.8002	110.4	1.643002681
31560543	NDFTEEEEAQVR		S-phase kinase-associated protein 1A [Mus musculus]	1466.6458	58.12	0.972107327
9790067	NDISSHPPVEGSYAPR		staphylococcal nuclease domain containing 1 [Mus musculus]	1725.8159	56.65	0.735253364
33667042	NDQDTWDYTNPNLSGQGDPGSNPNKR		heterogeneous nuclear ribonucleoprotein L [Mus musculus]	2890.2673	88.65	0.835795595
9790247	NDVFDSLGISPDLLPDDFVR		ubiquitin-like 1 (sentrin) activating enzyme subunit 1 [Mus musculus]	2234.0999	20.03	1.623104905
9790247	NDVFDSLGISPDLLPDDFVR	Deamidation (NQ)	ubiquitin-like 1 (sentrin) activating enzyme subunit 1 [Mus musculus]	2235.1089	28.99	0
21313536	NDVITVQTPAFAESVTEGDVR		dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]	2248.0999	51.44	1.333584525
31981722	NELESYAYSLK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1316.6385	45.02	0.923922755
24429590	NELTYQMEQDHNLQSVLQER		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	2475.1587	27.45	1.176173436
13384720	NFDFEDVFVNIPR		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Mus musculus]	1611.7881	54.85	1.313888329
7305443	NFGIGQDIQPK		ribosomal protein L7a [Mus musculus]	1216.6298	62.25	0
7949051	NFILDQTNVSAAAQR		heterogenous nuclear ribonucleoprotein U [Mus musculus]	1647.8462	98.21	0.968302573
20137006	NFINNPLAQADWAAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1672.8441	52.51	1.074569756
51556274	NFLASQVPFPSR		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	1362.7238	45.89	1.223286589
33859490	NFLTEDSADLDSIEAVANEVLK		laminin B1 subunit 1 [Mus musculus]	2393.1604	42.58	1.081994901
7305295	NFMNSPMAQADWVAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1709.7795	80.01	2.08550662
22203747	NFVINVVNR		procollagen, type VI, alpha 2 [Mus musculus]	1074.6012	31.05	0
6681157	NFYQEHPDLAR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1389.6592	34.98	0.99112462
34328108	NGDRGETGPAGPAGPIGPAGAR		procollagen, type I, alpha 1 [Mus musculus]	1974.9812	50.05	0.523636068
51771420	NGEDLGVAFR		PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1077.5327	23.26	0
7304993	NGPALQEAYVR		drebrin-like [Mus musculus]	1217.6311	33.03	0.905302796
46358078	NGQEETVGVSSTQLIR		response to metastatic cancers 1 [Mus musculus]	1717.8794	32.45	0.973815503
18875368	NGQLLENPR	Deamidation (NQ)	myotubularin related protein 4 [Mus musculus]	1041.5499	21.24	0
31981327	NGYELSPTAAANFTR		proteasome (prosome, macropain) subunit, beta type 2 [Mus musculus]	1611.7808	36.45	0
20806532	NGYGFINR	Deamidation (NQ)	cold shock domain protein A short isoform [Mus musculus]	941.4564	21.28	0
6756033	NGYGFINR	Deamidation (NQ)	nuclease sensitive element binding protein 1 [Mus musculus]	941.4564	21.28	0
63562136	NGYGFINR	Deamidation (NQ)	PREDICTED: hypothetical protein LOC78552 [Mus musculus]	941.4564	21.28	0
8567336	NHNQEAPNDQNQR		chloride channel calcium activated 3 [Mus musculus]	1564.6915	29.21	0
58037546	NILGGTVFR		isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	976.563	46.95	1.293046268
27370516	NILGGTVFR		isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	976.563	46.95	1.293046268
31542333	NINADEAAAMGAVYQAAALSK		hypoxia up-regulated 1 [Mus musculus]	2079.0024	46.29	5.298119773
31543605	NIQVDSPYDISR		ribophorin I [Mus musculus]	1406.6935	62.73	0.918575998
33563250	NISEAEEWYK		desmin [Mus musculus]	1268.5824	60.94	1.755138375
34996495	NIVEEIEDLVAR		ribophorin II [Mus musculus]	1399.7488	49.23	0.853217155

23956222	NIVLSGGSTMFR		ARP3 actin-related protein 3 homolog [Mus musculus]	1281.6639	39.03	1.152660318
6755901	NLDIERPTYTNLNR		tubulin, alpha 1 [Mus musculus]	1718.8898	42.15	1.002729228
34740335	NLDIERPTYTNLNR		tubulin, alpha 2 [Mus musculus]	1718.8898	42.15	1.002729228
6678467	NLDIERPTYTNLNR		tubulin, alpha 4 [Mus musculus]	1718.8898	42.15	1.002729228
6678469	NLDIERPTYTNLNR		tubulin, alpha 6 [Mus musculus]	1718.8898	42.15	1.002729228
482387	NLDLDSIIAEVK		keratin, 67K type II epidermal - human	1329.7258	51.2	0
1346345	NLDLDSIIAEVK		Keratin, type II cytoskeletal 6B (Cytokeratin 6B) (CK 6B) (K6b keratin)	1329.7258	51.2	0
28173550	NLEGYVGFANLPNQVYR		cell division cycle 10 homolog [Mus musculus]	1953.9785	37.41	1.324509325
58037267	NLEPEWAAAATEVK		protein disulfide isomerase-associated 6 [Mus musculus]	1528.7703	66.29	0
22203747	NLEWIAGGTWTPSALK		procollagen, type VI, alpha 2 [Mus musculus]	1743.8939	55.13	0
6678499	NLFFSTNIDDAIR		UDP-glucose dehydrogenase [Mus musculus]	1525.771	37.34	1.408655159
40254595	NLHQSGFSLSGAQIDDNIPR		dihydropyrimidinase-like 2 [Mus musculus]	2169.074	24.45	3.912902145
9790067	NLPGLVQEGEPFSEEATLFTK		staphylococcal nuclease domain containing 1 [Mus musculus]	2306.1594	36	1.326000852
20137006	NLPIYSEEIVEMYK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1727.8513	38.48	0.815394532
31982755	NLQEAEEWYK		vimentin [Mus musculus]	1309.6063	46.02	1.233167217
6678365	NLQYYDISAK		RAN, member RAS oncogene family [Mus musculus]	1214.6083	48.16	1.473588803
6678359	NMAEQIIQEIYSQVQSK		transketolase [Mus musculus]	2009.005	70.67	1.055783401
20137006	NMDPLNDNIATLLHQSSDK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2126.0166	57.53	0.834024339
29336026	NMDPLNDNVAALLHQSTDR		nonmuscle myosin heavy chain [Mus musculus]	2124.02	27.96	1.138510315
7305295	NMDPLNDNVTSLLNASSDK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2047.9565	86.17	1.503993881
7949053	NMGGPYGGGNYGPGGSGGSGGYGGR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2189.9084	181.5	0.964300098
7949053	NMGGPYGGGNYGPGGSGGSGGYGGR	Deamidation (NQ)	heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2190.8992	80.1	1.282256674
7949053	NMGGPYGGGNYGPGGSGGSGGYGGR	Oxidation (M)	heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2205.8945	55.82	1.021237534
1346343	NMQDMVEDYR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1300.5502	28.03	0
7242197	NMQNVEHVPLTLDR		proteasome (prosome, macropain) subunit, beta type 1 [Mus musculus]	1665.8335	43.58	1.303401168
21450277	NMVPQQALVIR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1268.7175	46.68	1.12993734
6754556	NMYEEEINETR		lamin B1 [Mus musculus]	1427.6154	44.11	0.403886079
6678145	NNEDVSIIPPLFTVSVDHR		signal sequence receptor, delta [Mus musculus]	2152.0994	33.13	1.029705766
31980868	NNFLEDEPSAQHR		kallikrein 6 [Mus musculus]	1556.7217	33.94	0.604717043
51491845	NNLAGAEELFAR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1304.6672	54.75	1.35089711
6679583	NNLSFIETSALDSTNVEEAFK		RAB11B, member RAS oncogene family [Mus musculus]	2329.104	34.76	0
6679515	NNQFQALLQYADPVSAQHAK		polypyrimidine tract binding protein 1 [Mus musculus]	2243.0845	32.69	0
22203747	NNYATMRPDSTEIDQDTINR		procollagen, type VI, alpha 2 [Mus musculus]	2354.0771	59.83	0.552043425
22203747	NNYATMRPDSTEIDQDTINR	Deamidation (NQ)	procollagen, type VI, alpha 2 [Mus musculus]	2355.0569	53	0
63530525	NPAVLSAASFDGR		PREDICTED: SEC31-like 1 [Mus musculus]	1304.6649	26.86	0
6754254	NPDDITNEEYGEFYK		heat shock protein 1, alpha [Mus musculus]	1833.7855	104.09	1.171946927
40556608	NPDDITQEEYGEFYK		heat shock protein 1, beta [Mus musculus]	1847.7974	107.07	0.939350043
51827543	NPEILAIAPVLLDALTDPSR		PREDICTED: GCN1 general control of amino-acid synthesis 1-like 1 [Mus musculus]	2118.1721	23.14	0
63518159	NPELQNLLLDDFFK		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1705.8817	77.09	1.112586487
63556656	NPNDDLTAVGGKPEGWK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1797.8743	114.63	0.230105826
8567402	NPPGFAFVEFEDPR		splicing factor, arginine/serine-rich 3 (SRp20) [Mus musculus]	1621.7673	51.72	1.086317948
18875324	NQAPGQPGASQWGSR		DAZ associated protein 1 [Mus musculus]	1540.7301	43.92	0
13384622	NQEAGHEAAGEEAAEASGPPEK		Ly1 antibody reactive clone [Mus musculus]	2178.9595	66.88	0
6754220	NQGGYGGSSSSSSYGSGR		heterogeneous nuclear ribonucleoprotein A1 [Mus musculus]	1694.7068	25.27	1.143608551
33563270	NQGYYDYVKPR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1402.6774	46.28	1.698857961
547749	NQILNLTTDNANILLQIDNAR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	2367.2588	61.35	0.223318695
31981722	NQLTSNPENTVFDAK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1677.8081	96.01	0.958159011
6754482	NQNINLENSLGDVEAR		keratin complex 1, acidic, gene 18 [Mus musculus]	1785.8735	122.05	0
31981690	NQVAMNPTNTVFDAK		heat shock protein 8 [Mus musculus]	1649.7847	73.31	0.944736643
33563282	NQYDNDVTVWSPQGR		proteasome (prosome, macropain) subunit, alpha type 1 [Mus musculus]	1778.814	36.47	0.931841038
31981647	NSEPEEVIPSR		tyrosyl-tRNA synthetase [Mus musculus]	1256.6145	31.97	1.464587219
46849705	NSFMNGSWGAEER		lectin, galactose binding, soluble 4 [Mus musculus]	1484.6276	99.13	1.255850986
63621835	NSGSPYGGGYGSGGGSGGYGSR	Deamidation (NQ)	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3 [Mus musculus]	1938.7904	28.87	1.125866977
31981690	NSLESYAFNMK		heat shock protein 8 [Mus musculus]	1303.6042	55.93	0
7305295	NSLQDQLDEEMEAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1649.7383	73.31	2.367817169
33598964	NSLQEQQEEEEEAR		myosin heavy chain 10, non-muscle [Mus musculus]	1718.7445	33.25	0
54020742	NSNILEDLETLR		archain 1 [Mus musculus]	1416.7375	59.57	1.045114976
50355692	NSNLVGAAHEELQQSR		lamin A isoform A [Mus musculus]	1752.8674	84.17	1.016324903
22165384	NSSYFVEWIPNNVK		tubulin, beta, 2 [Mus musculus]	1696.8168	32.4	0.855148188
12963615	NSSYFVEWIPNNVK		tubulin, beta 3 [Mus musculus]	1696.8168	32.4	0.855148188

31981939	NSSYFVEWIPNNVK		tubulin, beta 4 [Mus musculus]	1696.8168	32.4	0.855148188
7106439	NSSYFVEWIPNNVK		tubulin, beta 5 [Mus musculus]	1696.8168	32.4	0.855148188
27754056	NSSYFVEWIPNNVK		tubulin, beta 6 [Mus musculus]	1696.8168	32.4	0.855148188
21746161	NSSYFVEWIPNNVK		tubulin, beta [Mus musculus]	1696.8168	32.4	0.855148188
6996917	NSYVAGQYDDAASYK		glucose-6-phosphate dehydrogenase X-linked [Mus musculus]	1651.7192	75.03	1.454058157
31981562	NTGIICTIGPASR		pyruvate kinase 3 [Mus musculus]	1302.6726	20.13	0.865701901
22164798	NTGTEAPDYLATVDVDPK		selenium binding protein 1 [Mus musculus]	1905.9156	65.68	4.000396306
46195798	NTLLIAGLQAR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1169.704	34.49	0
33563270	NTNAGAPPGTAYQSPLSLSR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	2001.9951	54.9	1.220850933
33859560	NTNDANSCQIIIPQNQVNR		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	2142.0359	77.68	1.074650291
56119103	NTNDANSCQIIIPQNQVNR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	2142.0359	77.68	1.074650291
6754556	NTSEQDQPMGGWEMIR		lamin B1 [Mus musculus]	1878.8158	74.32	0.587126951
8567336	NVAILIPESWK		chloride channel calcium activated 3 [Mus musculus]	1269.7231	49.38	0.194573528
6680678	NVDEAINFINDR		aldehyde dehydrogenase family 3, subfamily A2 [Mus musculus]	1419.6921	60.52	1.484174044
31981570	NVDLQVLAPEPELLYK		polymeric immunoglobulin receptor [Mus musculus]	1840.9922	30.52	1.478440418
27552760	NVDLSTFYQNR		translocase of outer mitochondrial membrane 70 homolog A [Mus musculus]	1356.6589	21.07	1.047401023
6753364	NVFDEAILAALEPPEPK		cell division cycle 42 homolog [Mus musculus]	1852.9633	65.32	1.145543053
6753364	NVFDEAILAALEPPEPK	Deamidation (NQ)	cell division cycle 42 homolog [Mus musculus]	1853.9373	25.82	0
26986563	NVPVYKPQTLDTQR		choline dehydrogenase [Mus musculus]	1658.8907	30.09	1.05370276
13994195	NVQLTENEIR		protein phosphatase 1, catalytic subunit, alpha [Mus musculus]	1215.6284	22.33	0.446071928
13385168	NVVSQFVSSMSASADVLAMSK		ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Mus musculus]	2158.0479	64.04	1.392727789
31543113	NWMNSLGVNPR		lymphocyte cytosolic protein 1 [Mus musculus]	1287.6343	30.13	6.262900611
21450323	NYILDQTNVYGSAQR		EIB-55kDa associated protein 5 [Mus musculus]	1741.8455	33.17	1.543250264
6756033	NYQQNYQNSESGEKNEGSESAPEGQAQQR		nuclease sensitive element binding protein 1 [Mus musculus]	3257.3867	119.59	0.972539538
7949053	NYYEQWGK		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1087.4935	43.79	0.943813005
51771420	NYYGYQGYR		PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1183.5162	38.73	1.231417633
58037109	PDSWDKDVYPEPPSR		NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 [Mus musculus]	1787.828	34.28	1.654588446
6753618	PFVELETNLPASR		D-dopachrome tautomerase [Mus musculus]	1472.7689	32.67	0
6671549	PGGLLLGDEAPNFEANTTIGR		peroxiredoxin 6 [Mus musculus]	2142.0872	91.37	3.259932386
10092608	PPYTIVYFPVR		glutathione S-transferase, pi 1 [Mus musculus]	1351.7468	29.34	1.917064476
6680842	QAALQVADGFISR		gelsolin-like capping protein [Mus musculus]	1375.7418	32.42	1.10713282
7305295	QADLEKEELAEELASSLSGR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2175.0813	132.76	1.65270755
7305295	QADLEKEELAEELASSLSGR	Deamidation (NQ)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2176.0911	65.99	1.369702094
6754482	QAQEYEALLNIK		keratin complex 1, acidic, gene 18 [Mus musculus]	1419.7476	78.34	0
6754256	QAVTNPNNTFYATK		heat shock protein 9A [Mus musculus]	1568.7604	23.25	1.616723417
6996913	QDIAFAYQR		annexin A2 [Mus musculus]	1111.5583	66.67	1.250634769
31791057	QDIAVISDSYFPR		laminin, gamma 1 [Mus musculus]	1510.7485	23.36	0
6753294	QDLLAYLQR		catenin alpha 1 [Mus musculus]	1119.6156	23.92	0
6753296	QDLLAYLQR		catenin alpha 2 isoform 2 [Mus musculus]	1119.6156	23.92	0
31982275	QDLPALEEKPR		heat shock protein 4 [Mus musculus]	1295.6959	38.67	0
6671571	QDLPNAMNAAEITDK		ADP-ribosylation factor 2 [Mus musculus]	1630.7749	34.01	4.49614766
63489754	QEAFLLNEDLGDSLDSVEALLK		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	2419.2166	61.1	0.948283179
63574590	QEAGAQQPTR		PREDICTED: RIKEN cDNA 4930565N07 [Mus musculus]	1085.5157	22.22	0
55742711	QEELESVEAGVQGGAFEGTR		EH-domain containing 2 [Mus musculus]	2092.9856	35.84	1.392970539
30794206	QEEMNSQQEEEEMETDTR		splicing factor 3b, subunit 2 [Mus musculus]	2242.8799	84.15	1.285887476
41322904	QEEVYSELQAR		plectin 1 isoform 1 [Mus musculus]	1351.6481	23.83	1.699011658
6679599	QETEVELYNEFPEPIK		RAB7, member RAS oncogene family [Mus musculus]	1964.9478	44.81	0.879125109
7304993	QEWESAGQQAPHPR		drebrin-like [Mus musculus]	1620.7592	55.47	2.103977155
6671507	QEYDEAGPSIVHR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1500.7147	100.53	1.149045186
6671509	QEYDESGPSIVHR		actin, beta, cytoplasmic [Mus musculus]	1516.7108	72.08	1.016697257
33859482	QFAEMYVAK		eukaryotic translation elongation factor 2 [Mus musculus]	1086.5331	21.2	1.231888111
63476037	QFGVAPLTIAR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1172.6857	45.67	0.785022987
21450625	QFYINVER		eukaryotic translation initiation factor 4A1 [Mus musculus]	1068.552	31.66	0.828750771
51771446	QFYINVER		PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 [Mus musculus]	1068.552	31.66	0.828750771
22164798	QFYPDLIR		selenium binding protein 1 [Mus musculus]	1051.5673	31.66	2.391996458
6753086	QGFGELLQAVPLADSFR		apurinic/apyrimidinic endonuclease 1 [Mus musculus]	1847.9674	38.51	1.03206314
6680748	QGQYSPMAIEEQVAVIYAGVR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2309.1584	40.96	1.256287279
9845299	QGTFHSQQALEYGTK		succinate-CoA ligase, GDP-forming, alpha subunit [Mus musculus]	1694.8107	92.09	1.041915792
453155	QGVDADINGLR		keratin 9 [Homo sapiens]	1157.5957	57.57	1.440835877
6753294	QIIVDPLSFSEER		catenin alpha 1 [Mus musculus]	1532.8011	30.45	1.189783168

18250296	QINWTVLYR		ribosomal protein L24 [Mus musculus]	1192.6578	23.36	0.884967588
16716471	QIPVVGSVLNWFSPVQASQK		hypothetical protein LOC94184 [Mus musculus]	2184.1477	37.98	1.185701921
31982526	QIQEEITGNTEALSGR		parvin, alpha [Mus musculus]	1745.8682	67.91	1.371561425
1346343	QISNLQQSISDAEQR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1716.8481	113.88	0.049606533
6754976	QITINDLPVGR		peroxiredoxin 1 [Mus musculus]	1225.6998	61.78	0.955521852
21704156	QKEFDPTITDGSLSGPSR		caldesmon 1 [Mus musculus]	1934.9435	56.61	1.638957073
41322904	QLAEEDLAQQR		plectin 1 isoform 1 [Mus musculus]	1300.6498	25.13	0
21312570	QLDMILDEQR		lectin, mannose-binding, 1 [Mus musculus]	1260.6284	21.81	0.692956403
6755354	QLDSGLLLVTGPLVINR		ribosomal protein L6 [Mus musculus]	1808.0663	51.7	0.928703397
6755901	QLFHPEQLITGK		tubulin, alpha 1 [Mus musculus]	1410.7695	61.8	0
34740335	QLFHPEQLITGK		tubulin, alpha 2 [Mus musculus]	1410.7695	61.8	0
6678467	QLFHPEQLITGK		tubulin, alpha 4 [Mus musculus]	1410.7695	61.8	0
6678469	QLFHPEQLITGK		tubulin, alpha 6 [Mus musculus]	1410.7695	61.8	0
7305295	QLHEYETELEDER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1690.7576	92.33	1.942546152
7305295	QLHEYETELEDERK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1818.8501	73.97	1.881253033
7305295	QLLQANPILEAFGNAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1726.9503	115.46	1.579149628
20137006	QLLQANPILEAFGNAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1726.9503	115.46	1.579149628
29336026	QLLQANPILEAFGNAK		nonmuscle myosin heavy chain [Mus musculus]	1726.9503	115.46	1.579149628
7305295	QLLQANPILEAFGNAK	2 Deamidation (NQ)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1728.8949	21.49	0
20137006	QLLQANPILEAFGNAK	2 Deamidation (NQ)	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1728.8949	21.49	0
29336026	QLLQANPILEAFGNAK	2 Deamidation (NQ)	nonmuscle myosin heavy chain [Mus musculus]	1728.8949	21.49	0
6678571	QLLTLSNELSQAR		villin 2 [Mus musculus]	1472.8094	44.27	0.909334076
22122569	QLSQNFLLDLR	3 Deamidation (NQ)	transcription factor B1, mitochondrial [Mus musculus]	1349.7091	30.52	0.932990864
56605979	QLTEMLPSILNQLGADSLTSLR		basic transcription factor 3 [Mus musculus]	2400.2598	35.15	0.987713292
30519911	QMEQISQFLQAAER		transgelin 2 [Mus musculus]	1678.8307	39.32	1.206033368
6755714	QMEQVAQFLK		transgelin [Mus musculus]	1221.6259	31.2	0.963348341
50355692	QNGDDPLMTYR		lamin A isoform A [Mus musculus]	1309.5895	30.12	1.716960493
29789245	QNQLLLER	Deamidation (NQ)	centrosomal colon cancer autoantigen [Mus musculus]	1014.5604	29.86	0
30794450	QPYAVSELAGHQTSAESWGTGR		ribosomal protein L4 [Mus musculus]	2332.0999	99.35	0.761389468
13507628	QQEQTAQGTAPDAVDQQR		LPS-responsive beige-like anchor [Mus musculus]	1970.9191	103.66	1.399189521
29789189	QQKQQMLEMR	3 Deamidation (NQ); Oxidation (M)	minichromosome maintenance protein 10 [Mus musculus]	1338.6207	22.55	0
14861854	QQLETLQLDGGR		keratin complex 2, basic, gene 7 [Mus musculus]	1357.712	51.33	0
6755763	QQLSAEELDAQLDAYNAR		THO complex 4 [Mus musculus]	2034.9965	52.47	1.284145144
7106421	QQMLENQMEVR		spectrin beta 2 isoform 2 [Mus musculus]	1405.6567	30.12	2.440397001
41322904	QQNLASYDYVR		plectin 1 isoform 1 [Mus musculus]	1356.6637	27.76	2.694420898
31981828	QQPLFVSGGDDYK		coatomer protein complex subunit alpha [Mus musculus]	1453.6722	32.28	0
22550094	QQPPDLVDFAVEYFTR		protein kinase, cAMP dependent regulatory, type II alpha [Mus musculus]	1924.954	25.78	0.918563561
13385878	QQQFENLDQQLR		sorting nexin 2 [Mus musculus]	1546.7609	29.35	0
21312968	QQSEEDLLLQDFSR		signal sequence receptor, gamma [Mus musculus]	1707.8229	104.78	0.746255689
63476037	QQSLETAMSFVAR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1467.7311	33.66	0.813152855
13507696	QRMQHILTPNQDARGQAETR	Deamidation (NQ); Oxidation (M)	vomeronasal 1 receptor, D14 [Mus musculus]	2367.1948	24.78	0
41322904	QSAEEQAQAQAQAQAAAEK		plectin 1 isoform 1 [Mus musculus]	1957.9249	102.31	1.325119668
6754508	QSFTMVADTPENLR		LIM and SH3 protein 1 [Mus musculus]	1608.7708	48.58	0.966913382
8567336	QSGAIIHTVALGPAAAK		chloride channel calcium activated 3 [Mus musculus]	1604.9021	99.45	0
547749	QSLEASLAETEGR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1390.6871	101.25	0
30794412	QSSYGQQSYNNQGQQNTESSGGQGGR		TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Mus musculus]	2747.1611	110.36	1.013031714
6753072	QSVANGVEISVPVPSDADSPR		adaptor protein complex AP-1, mu 2 subunit [Mus musculus]	2124.0486	78.43	1.349742823
6754480	QSVEADINGLR		keratin 13 [Mus musculus]	1201.6205	61.11	0
547749	QSVEADINGLR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1201.6205	61.11	0
41322904	QTNLENLDQAFSVAER		plectin 1 isoform 1 [Mus musculus]	1834.8892	43.48	1.187666146
30023842	QTNPSAMEVEEDDPVPEIR		valosin containing protein [Mus musculus]	2155.9856	63.84	0.927237936
7305291	QTPAAPETEEEPYR		metaxin 1 [Mus musculus]	1617.7418	61.33	1.210093371
50080209	QTQTFTTYSDNQPGVLIQVYEGER		heat shock protein 1A [Mus musculus]	2774.3257	67.27	1.060091338
31981690	QTQTFTTYSDNQPGVLIQVYEGER		heat shock protein 8 [Mus musculus]	2774.3257	67.27	1.060091338
6680606	QTSAMSSFGGTGGGSVR		keratin complex 1, acidic, gene 19 [Mus musculus]	1586.73	123.82	1.171361731
8567336	QTTPMTAQPPAPTFSLLQIGQR		chloride channel calcium activated 3 [Mus musculus]	2383.2493	79.39	0.245852313
8567336	QTTPMTAQPPAPTFSLLQIGQR	Oxidation (M)	chloride channel calcium activated 3 [Mus musculus]	2399.2378	55.36	0.283255407
13507656	QTWTDEGSVSER		type 1 tumor necrosis factor receptor shedding aminopeptidase regulator [Mus musculus]	1394.6223	48.57	1.105966863
22267442	QVAEQFLNMR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1235.625	26.1	1.111121196

6677935	QVDENWYEGR		sorbin and SH3 domain containing 1 [Mus musculus]	1295.571	24.21	0
28316750	QVHPDTGISSK		histone 1, H2ba [Mus musculus]	1168.5974	64.74	0.560447384
20874851	QVHPDTGISSK		PREDICTED: similar to histone H2b-616 [Mus musculus]	1168.5974	64.74	0.560447384
22122789	QVLLSEPQEAAALYR		acylpeptide hydrolase [Mus musculus]	1687.9027	36.16	1.025919744
31981555	QVVEAVQAPVQERPEAEEER		ladinin [Mus musculus]	2293.146	31.97	1.537363337
63562723	QVVNIPSFIVR		PREDICTED: similar to 40S ribosomal protein S9 [Mus musculus]	1271.7545	44.17	0.963287771
6678573	QVVVEGQEPANFWMALGGK		villin 1 [Mus musculus]	2059.998	21.35	1.254731377
21313162	QWLQEIDR		RAB1B, member RAS oncogene family [Mus musculus]	1087.5631	24.94	1.382551637
6679587	QWLQEIDR		RAB1, member RAS oncogene family [Mus musculus]	1087.5631	24.94	1.382551637
21592285	QWYETNAPSTIR		keratin 20 [Mus musculus]	1465.7106	41.94	1.20951653
6753620	QYPISLVLAPTR		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1357.7897	24.79	0.881442891
29789080	QYPLVTPNEER		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1345.6648	21.25	0.444565358
6678005	QYQGPTGDSSATFEK		solute carrier family 1 (neutral amino acid transporter), member 5 [Mus musculus]	1615.7311	42.52	0.299830357
6996913	RAEDGSVIDYELIDQDAR		annexin A2 [Mus musculus]	2064.9824	67.49	0.857658077
42475990	RAVSGNTPVQPQRR	3 Deamidation (NQ)	TPX2, microtubule-associated protein homolog [Mus musculus]	1568.8044	20.15	0
51889716	REAIQANKPK	2 Deamidation (NQ)	UTP14, U3 small nucleolar ribonucleoprotein, homolog A [Mus musculus]	1156.6359	20.88	0
31981690	RFDDAVVQSDMK		heat shock protein 8 [Mus musculus]	1410.6711	48.31	1.289244535
63664182	RFDDAVVQSDMK		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1410.6711	48.31	1.289244535
63674587	RGFTVIVDMR		PREDICTED: triple functional domain (PTPRF interacting) [Mus musculus]	1193.6267	20.45	0
22203755	RLDEEEEDNEGGEWER		eukaryotic translation initiation factor 3, subunit 8 [Mus musculus]	1991.844	21.04	0.32247455
29336026	RLDGESSELQEQMVEQK		nonmuscle myosin heavy chain [Mus musculus]	2005.9541	36.71	0.970541401
13385582	RLISGHR		hypothetical protein LOC67304 [Mus musculus]	838.4847	25.79	0
13384620	RPAEDMEEEQAFK		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1579.7061	51.94	1.120947136
31542159	SAAEMVLSDDNFASIVAAVEEGR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	2381.1223	33.37	0
63489754	SADESGQALLAASHYASDEVR		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	2177.0129	79.85	1.39160237
6754524	SADTLWGIQK		lactate dehydrogenase 1, A chain [Mus musculus]	1118.5795	39.75	1.007839
34328108	SAGVSVPGPMGPSGPR		procollagen, type I, alpha 1 [Mus musculus]	1452.7344	27.61	0.632164661
63476037	SALLDSIQNLQVALTSK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1800.9897	44.14	0
30348966	SALPAQSAATLPAR		spectrin beta 2 isoform 1 [Mus musculus]	1353.749	33.88	1.156531187
6754206	SANLVAATLGAILNR		hexokinase 1 [Mus musculus]	1483.8661	24.05	1.179223009
31982290	SAQPSPHYMAGPSSGQIYGPGPR		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	2342.103	30.47	1.616318628
29293809	SAYDSTMETMNYAQIR		ATP citrate lyase [Mus musculus]	1880.8241	58.56	1.559862039
136429	SCAAAGTECLISGWGNTK		Trypsin precursor	1768.7963	26.99	0.106745022
54020676	SDAAPTPVPQSAPR		hypothetical protein LOC229317 [Mus musculus]	1393.7087	65.11	1.140414536
33667042	SDALETLGFLNHYQMK		heterogeneous nuclear ribonucleoprotein L [Mus musculus]	1866.9169	47.6	0
13928670	SDDPDQQYLILNTAR		vacuolar protein sorting 35 [Mus musculus]	1748.8469	24.61	1.637659151
31543051	SDFDMVDYLNELR		karyopherin (importin) beta 1 [Mus musculus]	1616.7418	38.53	1.22603879
18079339	SDFDPGQDTYQHPPK		aconitase 2, mitochondrial [Mus musculus]	1731.7627	60.94	1.113997114
31981722	SDIDEIVLVGGSTR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1460.7616	61.2	0
6754256	SDIGEVILVGGMTR		heat shock protein 9A [Mus musculus]	1446.7689	35.43	1.248043461
58037546	SDYLNTFEFMDK		isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	1509.6655	55.75	1.61301877
9845257	SEAAPAAPAAAPPAEK		histone 1, H1c [Mus musculus]	1448.7385	37.14	1.006992944
63738313	SEDGVEGDLGETQSR		PREDICTED: similar to AHNAK [Mus musculus]	1578.6918	59.16	1.923077797
31543605	SEDVLDYGPFK		ribophorin I [Mus musculus]	1269.6206	24.83	0.714771324
6753498	SEDYAFPTYADR		cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	1434.6255	60.69	1.176839126
31982856	SEEQLKEEGIEFK		dihydrolipoamide dehydrogenase [Mus musculus]	1565.7402	26.24	0.868865535
31982290	SEGDTAYGQQVQPNTWK		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1908.882	45.35	1.375645349
9910308	SEGQLNGETNPPIEGNQAGDTAASAR		Son cell proliferation protein truncated isoform [Mus musculus]	2584.1619	75.58	0.940814901
6753060	SEIDLFNIR		annexin A5 [Mus musculus]	1106.5916	38.15	1.025794349
13385340	SELVAMLEEEELR		ADP-ribosylation factor-like 1 [Mus musculus]	1547.7704	20.45	1.095129054
6755817	SELVANNVTLPAGEQR		thymopoietin [Mus musculus]	1697.8857	90.59	1.201911776
6755963	SENGLEFTSSGSANTETTK		voltage-dependent anion channel 1 [Mus musculus]	1959.8765	124.37	1.365056984
6679687	SEPIPESNEGPVK		glucose regulated protein [Mus musculus]	1382.6761	61.49	0.538139733
6755566	SEQAEPPAAADTHEAGDQNEAEK		solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1 [Mus musculus]	2395.0332	71.25	1.285460517
22203755	SEQDQAENEGEDSAVLMER		eukaryotic translation initiation factor 3, subunit 8 [Mus musculus]	2136.895	130.79	1.086925145
13430890	SETAPAAPAAPAPAEK		histone 1, H1e [Mus musculus]	1478.7479	63.95	2.23846585
34328365	SETAPAAPAAPAPVEK		histone 1, H1d [Mus musculus]	1506.7789	59.85	1.790494513
21426893	SETAPAETAAPAPVEK		histone 1, H1b [Mus musculus]	1568.7749	55.57	0
6671690	SETITEEELVGLMNK		carbonyl reductase 1 [Mus musculus]	1692.8267	35.19	0
51830180	SETITEEELVGLMNK		PREDICTED: similar to Carbonyl reductase 1 [Mus musculus]	1692.8267	35.19	0

7304889	SETSGSFEDALLAIVK		annexin A4 [Mus musculus]	1666.8459	27.64	1.137805456
28487651	SEVDEVEAALSSLEVTLEGGK		PREDICTED: RIKEN cDNA 5830467P10 gene [Mus musculus]	2162.0728	40.86	1.283119713
45598381	SFEDTIAQGITFVK		thioredoxin domain containing 5 [Mus musculus]	1555.7804	25.02	0.980125723
21314832	SFENSLGINVPR		UDP-glucose pyrophosphorylase 2 [Mus musculus]	1332.6942	53.25	0
18079351	SFFLQPGER		major vault protein [Mus musculus]	1080.5546	20.8	1.72018456
63624633	SFITTDVNPYYDSFVR		PREDICTED: similar to neurexin III [Mus musculus]	1923.9159	46.83	0.99279489
6679567	SFTPDHVVYAR		polymerase I and transcript release factor [Mus musculus]	1291.6394	27.44	1.297760762
31981690	SFYPEEVSSMVLTK		heat shock protein 8 [Mus musculus]	1616.7899	63.2	1.265867781
31980726	SGEHDFGAAFDGDGDR		phosphoglucomutase 2 [Mus musculus]	1652.6666	44.96	1.121810256
51770896	SGETEDTFIADLVVGLCTGQIK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	2296.137	68.29	1.385022509
29293809	SGGMSNELNNIISR		ATP citrate lyase [Mus musculus]	1491.7328	31.17	1.549634845
6680970	SGLGSQVGLMPGSVGPVGPR	Oxidation (M)	procollagen, type V, alpha 2 [Mus musculus]	1867.9741	46.89	0.330775105
40254244	SGSMDSPMSTENNSQLR		loss of heterozygosity, 11, chromosomal region 2, gene A homolog [Mus musculus]	1840.7793	64.46	1.408230028
38090154	SGVLDEPTIATILR		PREDICTED: oxidative-stress responsive 1 [Mus musculus]	1484.8292	24.69	1.407645701
6755863	SILFVPTSAPR		tumor rejection antigen gp96 [Mus musculus]	1187.6832	48.8	0.914346657
31981690	SINPDEAVAYGAAVQAAILSGDK		heat shock protein 8 [Mus musculus]	2260.1462	131.13	0.928760528
13384736	SIPLDEGEDEAQR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1458.6697	52.48	1.187913222
31982030	SIQEIQELDKDDESLR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1917.9398	74.36	0.935429492
34740335	SIQFVDWCPTGFK		tubulin, alpha 2 [Mus musculus]	1527.7302	28.33	1.85949222
6678467	SIQFVDWCPTGFK		tubulin, alpha 4 [Mus musculus]	1527.7302	28.33	1.85949222
6753074	SISFIPPDGEFELMR		adaptor protein complex AP-2, mu1 [Mus musculus]	1737.8457	43.08	1.10915104
38090003	SISTSLPVLDLIDAIAPNAVR		PREDICTED: expressed sequence AI427122 [Mus musculus]	2165.2246	84.99	1.434949061
31981657	SIVNNGHSFNVEFDDSQDNAVLK		carbonic anhydrase 2 [Mus musculus]	2549.2043	87.5	2.114205115
63556656	SLAAYTAACQAAGAAVKPWR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	2006.0283	37.23	0.723866092
54287684	SLAGSSGPGASSGPGGDHSELIVR		eukaryotic translation elongation factor 1 delta isoform b [Mus musculus]	2195.0774	27.14	1.63041171
29789317	SLDLDSIIAEVK		keratinocyte associated protein 1 [Mus musculus]	1302.7111	71.32	0
1346343	SLDLDSIIAEVK		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1302.7111	71.32	0
13624315	SLDMDGIIAEVR		keratin complex 2, basic, gene 8 [Mus musculus]	1318.6747	86.09	1.396761319
63565108	SLDMDGIIAEVR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1318.6747	86.09	1.396761319
7305295	SLEADLMQLQEDLAAAER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2002.98	99.74	2.043365211
51717092	SLEEIYLFSLPIK		PREDICTED: similar to 40S ribosomal protein S2 [Mus musculus]	1551.8629	37.8	1.080710788
18087805	SLEEIYLFSLPIK		ribosomal protein S2 [Mus musculus]	1551.8629	37.8	1.080710788
6754556	SLETENSALQLQVTER		lamin B1 [Mus musculus]	1817.9224	96.67	0.788511408
46275826	SLFPVVLEQLDDYNAK		laminin, alpha 4 [Mus musculus]	1850.9358	23.96	0
63622083	SLGYAYVNFQQPADAER		PREDICTED: similar to Poly(A) binding protein, cytoplasmic 4, isoform 1 [Mus musculus]	1928.9139	57.52	0.996583935
6680606	SLLEGQEAHYNNLPTPK		keratin complex 1, acidic, gene 19 [Mus musculus]	1910.955	88.56	1.276283149
1346343	SLNNQFASFIDK		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1383.6917	94.51	0
6754524	SLNPELGTDADKEQWK		lactate dehydrogenase 1, A chain [Mus musculus]	1830.8911	81.21	1.389926184
33859811	SLNSEMDNILANLR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1589.7975	68.23	0.96342097
6680572	SLSALGNVISALAEGSTYVPYR		kinesin family member 5B [Mus musculus]	2268.1841	33.01	1.392910656
9789931	SLSLLAKAMDPR		diaphanous homolog 3 [Mus musculus]	1301.7473	31.66	0
21592285	SLSSSSQGPALSMSGSLYR		keratin 20 [Mus musculus]	1914.9175	21.77	1.391418294
40556608	SLTNDWEDHLAVK		heat shock protein 1, beta [Mus musculus]	1527.7424	42.59	0.643214641
6754254	SLTNDWEEHLAVK		heat shock protein 1, alpha [Mus musculus]	1541.7771	27.36	1.375102713
31982755	SLYSSSPGGAYVTR		vimentin [Mus musculus]	1444.7129	62.48	1.275672302
22267442	SMAASGNLGHTPFLDEL		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1759.8376	31.6	0
20137006	SMEAEMIQLQEELAAAER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2048.9634	62.24	1.074516744
63487095	SMGYDDLDYGMMSDYGTAR		PREDICTED: catenin src [Mus musculus]	2147.8484	67.42	1.34116238
22122825	SMLEVNYPMENGIVR		actin-related protein 2 [Mus musculus]	1751.8672	37.64	0
50355692	SNEDQSMGNWQIR		lamin A isoform A [Mus musculus]	1564.6863	87.15	0.887464101
31982275	SNLAYDIVQLPTGLTGIK		heat shock protein 4 [Mus musculus]	1903.0417	73.22	1.099610583
6681291	SNLVDNTNQVEVLQR		Ddx19-like protein [Mus musculus]	1728.8636	44.66	1.935114835
13624315	SNMDNMFESYINNLR		keratin complex 2, basic, gene 8 [Mus musculus]	1847.8066	66.61	1.258641917
2506774	SNMDNMFESYINNLR		Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)	1847.8066	66.61	1.258641917
63565108	SNMDNMFESYINNLR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1847.8066	66.61	1.258641917
21450277	SPDFTNENPLETR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1519.7078	67.3	1.122242063
9790167	SPESQLFSIEDIQEVR		phospholipase C, delta 1 [Mus musculus]	1876.9408	35.22	1.749662253
6679761	SPFETDMLTLTR		fructose bisphosphatase 2 [Mus musculus]	1410.702	58.62	1.112441191
31980969	SPFLQVFNNSPDESSYYR		SEC23B [Mus musculus]	2149.9978	34.98	0.698344049
63746482	SPFSVGVSPSLDLSK		PREDICTED: filamin, alpha [Mus musculus]	1519.7964	82.82	0

22164770	SPYEQFLK		oncoprotein induced transcript 1 [Mus musculus]	1011.5145	28.92	1.159709888
33859560	SPYLYPLYGLGELPQGFAR		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	2141.1118	35.86	0.990327024
56119103	SPYLYPLYGLGELPQGFAR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	2141.1118	35.86	0.990327024
18087805	SPYQEFTDHLVK		ribosomal protein S2 [Mus musculus]	1463.7222	31.77	1.409097137
12746446	SQDVGFWEGEVVR		epithelial protein lost in neoplasm [Mus musculus]	1507.7271	39.39	0
6755354	SQFSLTNGMYPHK		ribosomal protein L6 [Mus musculus]	1509.7153	29.7	1.504305661
18079339	SQFTITPGSEQIR		aconitase 2, mitochondrial [Mus musculus]	1463.7512	68.87	1.377476738
22094115	SQGDMQDLNGNNQSVTR		signal transducer and activator of transcription 3 isoform 3 [Mus musculus]	1863.8507	56.09	0.743870275
31981722	SQIFSTASDNQPTVTIK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1836.934	105.45	0.780269293
31981690	SQIHDIVLVGGSTR		heat shock protein 8 [Mus musculus]	1481.8148	75.37	0.806030116
6677871	SQLIVVEEGSEPSELMK		scinderin [Mus musculus]	1874.9429	55.26	1.139918373
21703972	SQLYDDLMDEFMK		malic enzyme 2, NAD(+)-dependent, mitochondrial [Mus musculus]	1634.7161	32.28	1.712698949
9256555	SQMDGLIPGVEPR		nucleolar protein 5 [Mus musculus]	1398.705	37.88	1.699896098
63487095	SQSSHSYDDSTLPLIDR		PREDICTED: catenin src [Mus musculus]	1920.8972	50.75	1.034610994
6754558	SQTNWGPGESFR		lamin B2 [Mus musculus]	1365.6285	30.1	1.341791952
547749	SQYEQLAEQNR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1365.6395	70.69	0
547749	SQYEQLAEQNR	Deamidation (NQ)	Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1366.6293	24.24	0
63738313	SSEVVLSGDDEDYQR		PREDICTED: similar to AHNAK [Mus musculus]	1698.7526	31.39	2.217015226
6755040	SSFFVNGLTLGGQK		profilin 1 [Mus musculus]	1454.7605	82.11	0.994052268
31559916	SSGSPYGGGYGSGGGSGGYGSR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1910.7955	163.5	1.371615841
136429	SSGSSYPSLLQCLK		Trypsin precursor	1469.7402	33.26	0
12083691	SSGTGASVGPPQPSDQDTLVQR		PDZ and LIM domain 5 isoform ENH1 [Mus musculus]	2184.0625	55.93	1.18145108
9790067	SSHYDELLAAEAR		staphylococcal nuclease domain containing 1 [Mus musculus]	1461.6903	27.88	0.334928296
46195798	SSLNPILFR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1046.6093	20.29	1.506397559
63489759	SSLSSAQADFNQLAELDR		PREDICTED: spectrin alpha 2 [Mus musculus]	1951.9434	53.51	3.588668019
8567338	SSPEPVALTESETEYVIR		coatomer protein complex, subunit gamma [Mus musculus]	2006.9999	60.95	0
6755817	SSTPLPTVSSSAENTR		thymopoietin [Mus musculus]	1633.8053	29.88	0.695647729
31981690	STAGDTHLGGEDFDNR		heat shock protein 8 [Mus musculus]	1691.728	117.44	1.04777573
33859482	STAISLFYELSENDLNFIK		eukaryotic translation elongation factor 2 [Mus musculus]	2204.116	61.75	0.86945353
33186863	STESLQANVQR		ribosomal protein L13 [Mus musculus]	1232.621	51.08	0.99367214
34328415	STGSVVGQQPFGGAR		aldehyde dehydrogenase 4 family, member A1 [Mus musculus]	1447.7318	25.7	0
31981549	STLSVIPSGVQWIQDR		sulfide quinone reductase-like [Mus musculus]	1785.9558	46.5	1.554560194
6754256	STNGDTFLGGEDFDQALLR		heat shock protein 9A [Mus musculus]	2055.9656	88.17	0.956910855
6754256	STNGDTFLGGEDFDQALLR	Deamidation (NQ)	heat shock protein 9A [Mus musculus]	2056.9624	89.06	1.525384205
30425112	STPEDQILYQTER		hypothetical protein LOC109154 [Mus musculus]	1579.7635	33.04	0.946673485
8567336	STWEVIQESEDFK		chloride channel calcium activated 3 [Mus musculus]	1597.7355	75.27	0.30953837
51491845	SVDPTLALSVYLR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1433.8025	46	1.131411843
50355692	SVGGSGGGSFGDNLVTR		lamin A isoform A [Mus musculus]	1566.7533	100.35	1.234913594
27370510	SVNDIVVLGPEQFYATR		paraoxonase 3 [Mus musculus]	1907.9807	23.4	2.388115428
51491845	SVNESLNNLFITEEDYQALR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2355.1482	75.59	1.062932062
6678359	SVPMSTVFYPSDGVATEK		transketolase [Mus musculus]	1914.9152	66.85	1.003194836
6753658	SVSTPSEAGSQDSGDGAVGSR		dynein, cytoplasmic, intermediate chain 2 [Mus musculus]	1950.8617	105.52	0.892042813
13385310	SVTNEDVTQEQLGGAK		propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]	1675.8076	46.53	1.714125951
51828444	SVVTEEFNGSDWER		PREDICTED: proline-rich polypeptide 6 [Mus musculus]	1654.7526	31.09	0.809441436
31982233	SWQDELAQQAEEGSAR		LYRIC [Mus musculus]	1804.824	47	1.72711888
6753138	SYEAYVLNIIR		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1340.7256	56.16	1.358791139
6671507	SYELPDGQVITIGNER		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1790.8894	64.47	2.592370216
6671509	SYELPDGQVITIGNER		actin, beta, cytoplasmic [Mus musculus]	1790.8894	64.47	2.592370216
30425250	SYELPDGQVITIGNER		hypothetical protein LOC238880 [Mus musculus]	1790.8894	64.47	2.592370216
6671507	SYELPDGQVITIGNER	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1791.8969	38.56	1.360030419
6671509	SYELPDGQVITIGNER	Deamidation (NQ)	actin, beta, cytoplasmic [Mus musculus]	1791.8969	38.56	1.360030419
30425250	SYELPDGQVITIGNER	Deamidation (NQ)	hypothetical protein LOC238880 [Mus musculus]	1791.8969	38.56	1.360030419
38198665	SYQDPSNAQFLESIR		p47 protein [Mus musculus]	1754.8439	25.55	0.956720858
31981549	TAAAVAAQSGILDR		sulfide quinone reductase-like [Mus musculus]	1343.7321	54.85	0.936392391
6753620	TAAFLLPILSQIYADGPGEALR		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	2316.25	22.47	1.049696378
31543974	TAFDEAIAELDTLNEESYK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Mus muscu	2159.0037	65.31	1.234985613
6756041	TAFDEAIAELDTLSEESYK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	2131.9922	49.8	1.214054595
63489754	TATDEAYKDPSNLQGK		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1737.8331	56.61	1.227578541
6671664	TDAPQPDVKDEEGKEEEK		calnexin [Mus musculus]	2043.9429	59.19	0.925626035
6755963	TDEFQLHTNVNDGTEFGGSIYQK		voltage-dependent anion channel 1 [Mus musculus]	2600.1829	25.68	1.081045293

6754034	TDESQPWVLPVVR	glutamate oxaloacetate transaminase 1, soluble [Mus musculus]	1525.7977	25.67	2.464163833
10946574	TDLNPDNLQGGDDLDPNYVLSSR	creatine kinase, brain [Mus musculus]	2518.1726	57.12	1.276220659
63476037	TDLQTITNDPR	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1273.6385	54.82	0.77462169
46593021	TDLTDYLNR	ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1110.547	29.61	1.726520352
63540743	TDTYVTDNGDGTYR	PREDICTED: filamin C, gamma [Mus musculus]	1577.6899	26.19	0
13384620	TDYNASVSVPDSSGPER	heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1780.806	108.58	1.171759214
25141233	TEEGPTLSYGR	matrin 3 [Mus musculus]	1209.5808	29.22	1.035531948
6755534	TEEPESPESVDQTSPTPGDGNPR	solute carrier family 12, member 7 [Mus musculus]	2426.0544	83.61	0.922287137
6753928	TEGEEEEEEEESPDTGGEYK	X-ray repair complementing defective repair in Chinese hamster cells 6 [Mus musculus]	2272.8826	35.06	0.727934364
20137006	TELEDTLDSTAAQQELR	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1919.9159	115.1	1.055756876
7305295	TELEDTLDSTATQQELR	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1949.9341	129.69	2.084057426
29244560	TELQGLWINDIVPIGR	hypothetical protein LOC331063 [Mus musculus]	1824.0034	81.26	0.320042267
31559959	TELSQSDMFDQR	eukaryotic translation termination factor 1 [Mus musculus]	1456.6591	34.14	1.352096667
13624315	TEMENEFVLIK	keratin complex 2, basic, gene 8 [Mus musculus]	1352.6774	62.62	1.263166478
2506774	TEMENEFVLIK	Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)	1352.6774	62.62	1.263166478
63565108	TEMENEFVLIK	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1352.6774	62.62	1.263166478
6755863	TETVEEPLEEDEAAKEEK	tumor rejection antigen gp96 [Mus musculus]	2075.9438	78.56	0.618073352
31981722	TFAPEEISAMVLTK	heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1536.7955	63.34	0.912673052
33563250	TFGGAPGFSLGSPLSSPVFPR	desmin [Mus musculus]	2078.0769	95.16	2.027353397
13384828	TFHFDSVEDIHSR	serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1589.7471	27.45	0
6679078	TFIAIKPDGVQR	nucleoside-diphosphate kinase 2 [Mus musculus]	1344.7662	54.85	1.222577311
21312260	TFPTVNPTTGEVIGHVAEGDR	aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	2197.0798	63.86	1.018678633
6680067	TFTTQETITNAETAK	glucose phosphate isomerase 1 [Mus musculus]	1655.8086	71.5	1.685224906
21312260	TFVEESIYR	aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1143.5719	51.9	1.11471845
6753036	TFVQENVYDEFVER	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1774.8373	66.6	1.888764581
6755040	TFVSITPAEVGVLVGK	profilin 1 [Mus musculus]	1616.9211	80.61	1.013652608
6680748	TGAIVDVPVGEELLGR	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1624.8956	108.65	1.105003094
58037267	TGEAIVDAALSALR	protein disulfide isomerase-associated 6 [Mus musculus]	1386.7616	87.59	0.94312395
6755004	TGGLEIDSDFGGFR	programmed cell death 8 [Mus musculus]	1470.696	42.02	1.098360256
6753304	TGLYNYYDDEKEK	serine (or cysteine) proteinase inhibitor, clade H, member 1 [Mus musculus]	1637.7407	30.45	0.666399734
6681095	TGQAAGFSYTDANK	cytochrome c, somatic [Mus musculus]	1430.6521	70.56	1.620988088
31981273	TGQEIPVNLR	CNDP dipeptidase 2 (metallopeptidase M20 family) [Mus musculus]	1126.618	25.66	1.815674731
34996495	TGQEVVFVAEPDNK	ribophorin II [Mus musculus]	1532.7577	55.65	0.904823828
63481281	TGQEYKPGNPSAAAVQTVSTK	PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	2134.072	49.24	1.161618446
31560517	TGVAPIIDVVR	ribosomal protein L27a [Mus musculus]	1139.686	51.98	0.840982322
13242328	TGYTLDVTTGQR	NS1-associated protein 1 [Mus musculus]	1311.653	32.62	1.321598304
29293809	TIAIIAEGIPEALTR	ATP citrate lyase [Mus musculus]	1567.9116	58.36	1.586980712
31980648	TIAMDGTEGLVR	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1262.645	48.16	1.498298454
6754976	TIAQDYGVLK	peroxiredoxin 1 [Mus musculus]	1107.6045	60.37	1.334027628
6754854	TIFWTDSQLDR	nidogen 1 [Mus musculus]	1381.6729	28	1.597973693
6755901	TIGGGDDSFNTFFSETGAGK	tubulin, alpha 1 [Mus musculus]	2007.9146	54.75	0.497936003
34740335	TIGGGDDSFNTFFSETGAGK	tubulin, alpha 2 [Mus musculus]	2007.9146	54.75	0.497936003
6678469	TIGGGDDSFNTFFSETGAGK	tubulin, alpha 6 [Mus musculus]	2007.9146	54.75	0.497936003
31981909	TIGVSNFNPLQIER	aldo-keto reductase family 1, member B3 (aldose reductase) [Mus musculus]	1587.8474	23.88	0.888193033
31543605	TILPAAAQDVYYR	ribophorin I [Mus musculus]	1480.7804	57.56	0.852099492
14149647	TILSNQTVDIPENVEITLK	ribosomal protein L9 [Mus musculus]	2127.1589	30.35	1.057538145
11230802	TINEVENQILTR	actinin alpha 4 [Mus musculus]	1429.7709	66.83	0.929743015
33468903	TIPAWATLSASQLAR	heterochromatin protein 1, binding protein 3 [Mus musculus]	1585.8779	28.09	1.449134364
59709449	TIPWLENR	actinin alpha 2 [Mus musculus]	1028.5626	33.36	1.233268656
63638100	TIQFVDWCPTGFK	PREDICTED: similar to tubulin, alpha 1 [Mus musculus]	1541.745	45.7	1.588631702
6755901	TIQFVDWCPTGFK	tubulin, alpha 1 [Mus musculus]	1541.745	45.7	1.588631702
6678469	TIQFVDWCPTGFK	tubulin, alpha 6 [Mus musculus]	1541.745	45.7	1.588631702
9845265	TITLEVEPSDTIENVK	ubiquitin A-52 residue ribosomal protein fusion product 1 [Mus musculus]	1787.9231	87.79	1.24273352
6680067	TLASLSPETSLFIIASK	glucose phosphate isomerase 1 [Mus musculus]	1777.9866	37.57	0
31981828	TLDLPIYVTR	coatomer protein complex subunit alpha [Mus musculus]	1190.6814	39.57	0.932384677
30911099	TLEAVQDLLEQGR	fatty acid synthase [Mus musculus]	1471.7886	50.44	0.706611919
63641940	TLELQGLINDLQR	PREDICTED: desmoplakin [Mus musculus]	1512.839	47.21	1.219885564
22779912	TLESVDPLGGLNTIDILTAIR	dynamin 1-like [Mus musculus]	2211.2227	32.83	1.469206491
27754067	TLEVEIEPGVR	DnaJ (Hsp40) homolog, subfamily B, member 11 [Mus musculus]	1241.6652	38.09	0.740246106
33563236	TLLGDVPVVADPTVPNVTVTR	Rho, GDP dissociation inhibitor (GDI) beta [Mus musculus]	2163.2012	50.98	0.641929004

31981679	TLNDELEIIEGMK		heat shock protein 1 (chaperonin) [Mus musculus]	1504.7493	28.05	0
41322904	TLQEEHVTVAQLR		plectin 1 isoform 1 [Mus musculus]	1523.8207	36.33	0
7305133	TLQISPLDNGDLVR		hemopoietic cell phosphatase [Mus musculus]	1540.8331	31.24	0
6678726	TLTGTAALTVQSQEENLR		leukotriene A4 hydrolase [Mus musculus]	1932.0015	20.66	26.48167318
6679501	TMLELLNQLDGFDSR		protease (prosome, macropain) 26S subunit, ATPase 1 [Mus musculus]	1751.8704	22.43	5.214324897
6755809	TMLESAGGLIQTAR		talin 1 [Mus musculus]	1447.7516	37.69	0
6678643	TNAENEFVTIK		keratin complex 2, basic, gene 1 [Mus musculus]	1265.6338	48.71	0
1346343	TNAENEFVTIK		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1265.6338	48.71	0
31560653	TNVLGHLQQGGAPTPFDR		phosphofructokinase, liver, B-type [Mus musculus]	1907.9811	22.82	2.069659117
29126205	TNVSGGAIALGHPLGGSGSR		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1807.9432	58.37	1.220021441
22094123	TPAQSGAWDPNNPNTPSR		suppressor of Ty 5 homolog [Mus musculus]	1909.8748	43.8	1.02362891
63607160	TPLSEAEFEEIMNR		PREDICTED: cleavage and polyadenylation specific factor 6 [Mus musculus]	1665.7899	21.82	1.551594051
29336026	TPNVGGPGGPQVEWTAR		nonmuscle myosin heavy chain [Mus musculus]	1722.8629	43.8	1.101522962
30023814	TPSPPEPEPAGTAQK		breast carcinoma amplified sequence 1 [Mus musculus]	1506.7504	45.35	0.872985168
6677935	TPVDYIDLPYSSSPSR		sorbin and SH3 domain containing 1 [Mus musculus]	1796.8643	60.13	1.11495301
19527174	TPVEEVPAAIAPFQGR		splicing factor 3b, subunit 3 [Mus musculus]	1681.8943	35.59	1.697370893
13385652	TPVEPEVAIHR		ribosomal protein S20 [Mus musculus]	1247.6759	58.39	0.865536484
19882201	TPVQSQQPSATTPSGADEK		proteasome 26S non-ATPase subunit 2 [Mus musculus]	1928.9191	82.97	1.41770542
18250284	TPYTDVNIVTIR		isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	1391.7548	56.68	1.319055781
31980726	TQAYPDQKPGTSGLR		phosphoglucomutase 2 [Mus musculus]	1618.8123	22.92	1.939674816
31981824	TQDDIETILQLFR		ankyrin repeat domain 25 [Mus musculus]	1591.8438	63.62	1.772607694
6678752	TQDDVDIADVAYYFEK		lymphocyte antigen 74 [Mus musculus]	1891.8734	85.71	1.050942641
55741460	TQGPYDVVVLPGGNLGAQNLSESPMVK		DJ-1 protein [Mus musculus]	2770.4023	21.31	0
33598964	TQLEELEDELQATEDAK		myosin heavy chain 10, non-muscle [Mus musculus]	1961.9218	124.06	1.84238076
20137006	TQLEELEDELQATEDAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1961.9218	124.06	1.84238076
9256555	TQLYEYLQNR		nucleolar protein 5 [Mus musculus]	1327.6688	32.46	1.313737921
6680572	TQMLDQEELLASTR		kinesin family member 5B [Mus musculus]	1634.8176	23.2	0
31980636	TQQTNDIELQQEQR		mannosidase, beta A, lysosomal [Mus musculus]	1730.8275	33.67	1.962381827
31980838	TSAITLGNAQAGQDPGPGEK		RAB25, member RAS oncogene family [Mus musculus]	1911.9313	90.7	0
21704096	TSDLIVLGLPWK		TAR DNA binding protein isoform 1 [Mus musculus]	1341.7716	33.08	1.28296609
33563270	TSFDEMLPGTHFQR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1665.7799	47.77	0.622685626
13430890	TSGPPVSELITK		histone 1, H1e [Mus musculus]	1228.6747	41.68	0.56131907
51491845	TSIDAYDNFDNISLAQR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1942.9193	77.94	1.237765657
6671684	TSMGGTQQQFVEGVR		catenin beta [Mus musculus]	1624.7795	36.09	0
6678359	TSRPENAIIYSNNEDFQVGQAK		transketolase [Mus musculus]	2481.2046	46.11	0.914744641
21313262	TSSAEMPTIPLGSAVEAIR		inner membrane protein, mitochondrial [Mus musculus]	1930.0005	65.33	1.006875573
31982275	TSTVDLPIESQLLWQLDR		heat shock protein 4 [Mus musculus]	2114.1221	28.31	0
6753294	TSVQTEDDQLIAGQSAR		catenin alpha 1 [Mus musculus]	1818.8777	27.01	1.563090596
29293809	TTDGVYEGVAIGGDR		ATP citrate lyase [Mus musculus]	1509.7208	42.4	1.488467153
46519156	TTGFGMIYDSLDYAK		ribosomal protein S24 isoform 1 [Mus musculus]	1681.7903	23.45	1.159702554
31981515	TTHFVEGGDAGNREDQINR		ribosomal protein L7 [Mus musculus]	2115.9839	36.78	1.141486629
6754556	TTIPEEEEEEEEEPIGVAVEEER		lamin B1 [Mus musculus]	2672.1982	128.73	0.66799561
18034769	TTLSTFQSPEFSVTR		sorting nexin 5 [Mus musculus]	1700.8525	21.99	1.011976486
50080209	TTPSYVAFTDTER		heat shock protein 1A [Mus musculus]	1487.7085	85.15	1.059193853
7305163	TTPSYVAFTDTER		heat shock protein 1-like [Mus musculus]	1487.7085	85.15	1.059193853
31981690	TTPSYVAFTDTER		heat shock protein 8 [Mus musculus]	1487.7085	85.15	1.059193853
24429590	TTQVPQYILDDFIQNDR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	2066.021	55.69	0.69925686
29243964	TTRTNTNDIQNSSLR	2 Deamidation (NQ)	hypothetical protein LOC211936 [Mus musculus]	1722.8381	22.41	0
6679237	TVAVYSEQDTGQMHR		pyruvate carboxylase [Mus musculus]	1721.7887	39.76	1.439975653
6679601	TVFDEAIR		RAS-related C3 botulinum substrate 2 [Mus musculus]	950.5001	45.18	1.223239254
8393988	TVGYTVTAPEDTR		phosphomannomutase 2 [Mus musculus]	1409.6906	42.21	1.020148227
31981679	TVIIEQSWGSPK		heat shock protein 1 (chaperonin) [Mus musculus]	1344.7097	57.17	1.057393646
33859811	TVLGVPEVLLGILPGAGGTQR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	2047.196	62.56	1.367374439
31980648	TVLIMELINNVAK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1457.8409	74.36	1.253323865
21729786	TVQQHAGETDPVTTMR		hydroxyacyl glutathione hydrolase [Mus musculus]	1770.8364	53.16	1.764302033
21361209	TVTAMDVVYALK		germinal histone H4 [Mus musculus]	1310.718	57.51	0
8567336	TVTLELLDNGAGADATK		chloride channel calcium activated 3 [Mus musculus]	1688.8672	110.37	0.173575396
31981690	TVTNAVVTVPAYFNDSQR		heat shock protein 8 [Mus musculus]	1982.006	93.91	1.035678311
12963563	TVTQVVPAEGQENGQR		apoptotic chromatin condensation inducer 1 [Mus musculus]	1712.8568	38.75	0.869695338
31981722	TWNDPSVQQDIK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1430.6888	75.62	1.318309727

29789080	TYLPSQVSR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1050.5621	40.2	0.862406466
13384828	TYNFLPEYLASTQK		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1674.8358	54.17	1.068562709
18087805	TYSYLTPDLWK		ribosomal protein S2 [Mus musculus]	1386.7096	29.82	0
13384736	VAAPDVVVPTLDTVR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1551.8846	39.81	1.532587726
21704128	VAAVQPPEEGPSR		eukaryotic translation initiation factor 4B [Mus musculus]	1336.6893	58.37	1.013453797
63471580	VADIGLAAWGR		PREDICTED: similar to S-adenosylhomocysteine hydrolase [Mus musculus]	1128.6274	40.48	1.249709772
31981549	VAELNPDENCIR		sulfide quinone reductase-like [Mus musculus]	1372.6591	20.88	2.051853756
21312260	VAEQTPLSALYLASLIK		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1817.0411	57.45	1.17166399
6753036	VAEQTPLTALYVANLIK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1844.0515	55.11	2.213139494
9910556	VAGQDGSVVQFK		SMT3 (supressor of mif two, 3) homolog 1 [Mus musculus]	1234.6366	48.12	1.075436977
7304993	VAGTGEGGLEELVEELNSGK		drebrin-like [Mus musculus]	1987.9631	31.91	0
63476037	VAIAQFSDDVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1220.6326	40.64	1.023892917
31980648	VALTGLTVAEYFR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1439.7885	78.03	1.130068106
18079339	VAMSHFEPSEYIR		aconitase 2, mitochondrial [Mus musculus]	1565.7422	55.24	1.325697077
31542559	VAPAPAGVFTDIPISNIR		dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) [Mus musculus	1838.0216	28.06	1.389055176
6671507	VAPEEHPTLLTEAPLNPK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1956.0463	105.97	0.848796967
6671509	VAPEEHPVLLTEAPLNPK		actin, beta, cytoplasmic [Mus musculus]	1954.0642	86.09	0.783031326
54607037	VAPGYYTVTAEQDAR		integrin beta 4 isoform 2 [Mus musculus]	1640.7902	33.61	1.786685667
6753138	VAPPGLTQIPQIQK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1489.8694	21.78	0
13385598	VAQLEQVYIR		small nuclear ribonucleoprotein D3 [Mus musculus]	1218.6884	21.2	0.937944068
63746482	VAQPSITDNKDGTVTVR		PREDICTED: filamin, alpha [Mus musculus]	1800.9447	27.74	0
27545181	VAQPTAEQAQAFK		v-raf murine sarcoma 3611 viral oncogene homolog [Mus musculus]	1388.701	33.24	0
33563270	VASSVPVENFTIHGGLSR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1869.9799	33.27	1.418908864
63746482	VATVPQHATSGPGPADVSK		PREDICTED: filamin, alpha [Mus musculus]	1818.9385	83.75	1.630586832
136429	VATVSLPR		Trypsin precursor	842.5146	42.72	0
31982186	VAVLGASGGIGQPLSLLLK		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1793.0912	103.27	1.394439774
33859580	VAVNDAHLLQYNHR		galectin-3 [Mus musculus]	1649.85	53.13	1.774245588
31982030	VAVSADPNVPNVIVTR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1650.9224	56.94	1.488132116
6753484	VAVVQYSGQGQQQPGR		procollagen, type VI, alpha 1 [Mus musculus]	1701.8684	67.34	0.570070544
63476037	VAVVTYNNEVTTEIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1707.8911	72.73	1.153118845
63556656	VAYDLVYYVR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1260.6674	35.94	0.312991044
8567336	VAYLQVPGTAK		chloride channel calcium activated 3 [Mus musculus]	1146.6476	69.62	0.225409662
46849705	VAYNPFGPGQFFDLSIR		lectin, galactose binding, soluble 4 [Mus musculus]	1927.9747	58.1	1.157032265
31541988	VCIGDAEVGSLNAVQK	Deamidation (NQ)	hypothetical protein LOC237465 [Mus musculus]	1603.778	22.46	1.162975878
31981647	VDAQFGGVDQR		tyrosyl-tRNA synthetase [Mus musculus]	1191.5757	47.38	1.099469769
42415475	VDATEESDLAQQYGVR		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1780.8398	105.27	1.109039388
54607098	VDEYDYSKPIQGQQK		succinate dehydrogenase Fp subunit [Mus musculus]	1797.8691	89.41	1.115241713
31982186	VDFPQDQLATLTGR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1560.7938	38.61	0.588904075
6680121	VDILENQAMDTR		glutathione S-transferase, mu 2 [Mus musculus]	1404.6849	39.8	1.949757843
63738313	VDINAPDVDVR		PREDICTED: similar to AHNAK [Mus musculus]	1212.6188	31.25	1.822538272
63556656	VDLPATVLTSVSVR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1456.8435	81.76	0.274825883
20149728	VDNSSLTGESEPQAR		ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Mus musculus]	1589.74	36.57	5.5248045
21450277	VDNSSLTGESEPQTR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1619.7487	81.53	1.064385158
7710042	VDQIQEIVTGNPTVIK		IQ motif containing GTPase activating protein 1 [Mus musculus]	1753.9688	20.94	0
33186863	VDTWFNQPAR		ribosomal protein L13 [Mus musculus]	1233.6039	46.94	0.984958712
63522357	VDVEALENSPGATYIR		PREDICTED: signal recognition particle 72 [Mus musculus]	1733.8698	20.29	0.761803497
63746482	VDVGKDQEFTVK		PREDICTED: filamin, alpha [Mus musculus]	1364.6838	31.08	1.363624522
33859722	VDVTEQTGLSGR		thioredoxin domain containing 1 [Mus musculus]	1261.6295	45.7	1.274508559
7305295	VDYNASAWLTK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1267.6394	66.15	2.121059577
21313536	VEGGTPLFTLR		dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]	1189.6658	32.47	1.136722328
31543315	VEGSEPTTPFNLFIGNLNPNK		nucleolin [Mus musculus]	2288.1389	35.29	0.672706695
7106435	VEGYSGTAGDSMNYHNGR		tenascin C [Mus musculus]	1914.8112	24.6	5.374554416
31981722	VEIIANDQGNR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1228.6322	52.11	1.278492801
50080209	VEIIANDQGNR		heat shock protein 1A [Mus musculus]	1228.6322	52.11	1.278492801
7305163	VEIIANDQGNR		heat shock protein 1-like [Mus musculus]	1228.6322	52.11	1.278492801
31981690	VEIIANDQGNR		heat shock protein 8 [Mus musculus]	1228.6322	52.11	1.278492801
63664182	VEIIANDQGNR		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1228.6322	52.11	1.278492801
33563250	VELQELNDR		desmin [Mus musculus]	1115.5747	48.33	1.803790897
31982755	VELQELNDR		vimentin [Mus musculus]	1115.5747	48.33	1.803790897
63746482	VEPGLGADNSVVR		PREDICTED: filamin, alpha [Mus musculus]	1312.6847	69.25	1.702739666

20373167	VEQLGAEGNVEESQK		LUC7-like 2 [Mus musculus]	1616.7794	87.05	1.343652186
16716471	VEQLSSGLEHDNLEAHSPEQPPR		hypothetical protein LOC94184 [Mus musculus]	2569.2268	66.86	0.877100284
31542333	VESVFETLVEDSPEEESTLTK		hypoxia up-regulated 1 [Mus musculus]	2368.1487	68.77	0.713508464
51873060	VETGVLKPGMVVTFAPVNVTTEVK		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2515.3848	44.65	0.901109702
6753762	VETSDEEIKDLHQR		epoxide hydrolase 1, microsomal [Mus musculus]	1698.8221	34.15	2.342097621
46849705	VFANGQHLFDFSHR	Deamidation (NQ)	lectin, galactose binding, soluble 4 [Mus musculus]	1675.8143	56.01	1.787357951
22203747	VFAVVITDGR		procollagen, type VI, alpha 2 [Mus musculus]	1076.5944	23.5	0
33859482	VFDAIMNFR		eukaryotic translation elongation factor 2 [Mus musculus]	1112.566	37.27	0
21450625	VFDMLNR		eukaryotic translation initiation factor 4A1 [Mus musculus]	894.4486	20.99	0.986433456
51771446	VFDMLNR		PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 [Mus musculus]	894.4486	20.99	0.986433456
6755863	VFITDDFHDMMPK		tumor rejection antigen gp96 [Mus musculus]	1595.75	37.94	0.692391153
21361209	VFLENVIR		germinal histone H4 [Mus musculus]	989.5858	42.54	0.58834535
8567338	VFNETPINPR		coatomer protein complex, subunit gamma [Mus musculus]	1186.611	22.43	1.153855347
6753484	VFSVAITPDHLEPR		procollagen, type VI, alpha 1 [Mus musculus]	1580.8519	39.89	2.5800184
31981549	VGAENVAIVEPSER		sulfide quinone reductase-like [Mus musculus]	1469.7616	69.5	1.234725193
6755809	VGAIPANALDDGQWSQGLISAAR		talin 1 [Mus musculus]	2310.1802	20.24	1.097682392
14149645	VGDTSLDPNDFDFTVTGR		methyl CpG binding protein 2 [Mus musculus]	1955.9183	34.64	1.223329497
51491845	VGEQAQVVIIDMNDPSNPIR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2195.1289	39.86	1.162421082
31560737	VGIGAFPTEQDNEIGELLQTR		adenylosuccinate synthetase, non muscle [Mus musculus]	2287.1477	54.58	1.289091503
63638100	VGINYQPPTVVPGGDLAK		PREDICTED: similar to tubulin, alpha 1 [Mus musculus]	1824.9878	36.44	1.043625447
6755901	VGINYQPPTVVPGGDLAK		tubulin, alpha 1 [Mus musculus]	1824.9878	36.44	1.043625447
34740335	VGINYQPPTVVPGGDLAK		tubulin, alpha 2 [Mus musculus]	1824.9878	36.44	1.043625447
6678467	VGINYQPPTVVPGGDLAK		tubulin, alpha 4 [Mus musculus]	1824.9878	36.44	1.043625447
6678469	VGINYQPPTVVPGGDLAK		tubulin, alpha 6 [Mus musculus]	1824.9878	36.44	1.043625447
18079339	VGLIGSCTNSSYEDMGR		aconitase 2, mitochondrial [Mus musculus]	1788.8033	26.35	0
6680117	VGLLEALLPGQPEAVAR		glutathione synthetase [Mus musculus]	1732.9988	44.92	1.13764494
7657429	VGLSDLYNGQILETIGGK		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	1876.9718	43.38	0
63476037	VGLVQYNSDPTDEFFLR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1999.9766	32.96	0.864686972
63476037	VGLVQYNSDPTDEFFLR	Deamidation (NQ)	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2000.9613	54.39	0
6753620	VGNLGLATSFFNER		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1524.7848	29.17	1.0671415
21312260	VGNPFELDTQQGPQVDKEQFER		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	2561.2249	68.73	1.3817746
6753738	VGQEIEVRPGIVSK		eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked [Mus musculus]	1510.8662	29.23	2.034832187
63746482	VGSAADIPINISETDLSLLTATVVPPSGR		PREDICTED: filamin, alpha [Mus musculus]	2893.5547	55.11	1.262437727
16716467	VGSGDTNNFPYLEK		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1540.7218	34.76	1.330568319
46849705	VGSSGDIALHLNPR		lectin, galactose binding, soluble 4 [Mus musculus]	1435.7684	93.34	1.233957892
31543902	VGVKPVGSDPDFQPELSGAGSR		thioredoxin-like 1 [Mus musculus]	2199.1084	63.12	0.949040022
29126205	VGVPTETGALTLNR		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1427.7917	67.29	1.555025093
63680429	VGVSQQPEDSQQDLPGER		PREDICTED: plexin B2 [Mus musculus]	1968.9312	47.64	1.301196789
30348966	VIESTQDLGNDLAGVMALQR		spectrin beta 2 isoform 1 [Mus musculus]	2130.0908	94.18	1.0062707
7305085	VIFLEDDDVAAVVDGR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1732.8691	62.59	1.29388851
6679937	VIISAPSADAPMFVMGVNHEK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	2213.1147	80.58	0
30023842	VINQILTEMDGMSTK		valosin containing protein [Mus musculus]	1679.8068	27.36	0.898352836
45597447	VISLSGEHSIIGR		superoxide dismutase 1, soluble [Mus musculus]	1367.7671	53.78	1.296114335
6678321	VISTITNNIQQIIEIEDTFETLR		transforming growth factor, beta induced [Mus musculus]	2690.4155	25.09	1.347159421
31982275	VLATAFDTTLGGR		heat shock protein 4 [Mus musculus]	1321.7153	45.4	2.284124865
11230802	VLAVNQENEHLMEDYER		actinin alpha 4 [Mus musculus]	2088.9658	58.92	1.493986053
6678449	VLDASWYSPGTR		thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	1351.6678	44.28	1.498233799
6680606	VLDELTLAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1029.6038	34.35	1.615955516
125081	VLDELTLAR		Keratin, type I cytoskeletal 15 (Cytokeratin 15) (K15) (CK 15)	1029.6038	34.35	1.615955516
51766008	VLDNTWPAAPYR		PREDICTED: myosin IA [Mus musculus]	1402.7097	31.18	1.165589219
15617203	VLDNYLTSPLPEEVDETSAEDEGISQR		chloride intracellular channel 1 [Mus musculus]	3006.3877	21.46	0.976295819
6678359	VLDPFTIKPLDR		transketolase [Mus musculus]	1413.8099	32.23	1.070575848
40068493	VLEEANQAINPK		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1325.7023	48.25	0
13385408	VLEQLTGQTPVFSK		ribosomal protein L11 [Mus musculus]	1546.8452	57.38	1.444425957
63489754	VLETAEDIQER		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1302.6575	23.22	0
19923052	VLEVPPIVYLR		brain acyl-CoA hydrolase [Mus musculus]	1297.7915	37.1	1.057464802
6754854	VLFDTGLVNPR		nidogen 1 [Mus musculus]	1230.6934	46.66	1.327208065
29336026	VLGLLPEEITAMLR		nonmuscle myosin heavy chain [Mus musculus]	1554.8965	55.44	1.595164019
27804325	VLGSQEALSPVHYEEK		monoamine oxidase A [Mus musculus]	1785.8953	67.79	1.511079151
21450625	VLITTDLLAR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1114.6992	21.33	1.137460403

6755004	VLIVSEDPELPYMRPPLSK		programmed cell death 8 [Mus musculus]	2183.168	20.79	1.18688836
49402267	VLLVTASNR	Deamidation (NQ)	hypothetical protein LOC99382 [Mus musculus]	973.5502	20.72	0
6679291	VLNNMEIGTSLYDEEGAK		phosphoglycerate kinase 1 [Mus musculus]	1982.9397	57.5	1.012365463
13385036	VLNSYWVGEDSTYK		ribosomal protein L15 [Mus musculus]	1660.7915	53.41	0.834644376
7948997	VLQDLVNDGPDDRPAGTR		PDZ and LIM domain 3 [Mus musculus]	1937.9675	53.31	1.620471618
31542333	VLQLINDNTATALSYGVFR		hypoxia up-regulated 1 [Mus musculus]	2095.1106	45.77	1.044788656
13384736	VLRPQVTAVAQQNQGEAPEPQDMK		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	2634.3259	26.03	1.271021777
6680748	VLSIGDGIAR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1000.5841	41.09	1.134093101
63556656	VLSPLEYFR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1123.6223	53.55	0.30517962
10946574	VLTPELYAELR		creatine kinase, brain [Mus musculus]	1303.7333	49.31	1.803262486
13569841	VLVLDFVTPTPLGTR		thioredoxin reductase 1 [Mus musculus]	1627.9465	24.81	1.302389905
63655455	VLWLDEIQQAINEANVDENR		PREDICTED: similar to Ras GTPase-activating-like protein IQGAP2 [Mus musculus]	2369.1746	43.19	1.315892058
12963539	VMDNLNLPKPQQIDIAVPANMR		ETHE1 protein [Mus musculus]	2477.3088	39.64	1.214852664
6679078	VMLGETNPADSKPGTIR		nucleoside-diphosphate kinase 2 [Mus musculus]	1785.9192	113.95	0.96746053
34576561	VMQQQQQATQQQLPQK		splicing factor 3a, subunit 1 [Mus musculus]	1911.9736	58.71	1.039212515
34576561	VMQQQQQATQQQLPQK	Oxidation (M)	splicing factor 3a, subunit 1 [Mus musculus]	1927.9623	60.01	0
31543113	VNDDIIVNWVNTTLK		lymphocyte cytosolic protein 1 [Mus musculus]	1743.9142	35.59	1.134789924
63607012	VNEQLALR	2 Deamidation (NQ)	PREDICTED: similar to centrosome protein cep290 [Mus musculus]	944.5101	30.09	0
31560611	VNESTQNWHQLENIGNFIK		calponin 1 [Mus musculus]	2271.1138	72.25	1.27503534
7305085	VNFDDYTVNLGGLK		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1554.7792	63.48	1.292420385
13384736	VNFLPEIITLSK		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1373.8013	24.17	7.378302871
31560689	VNFSPPGDTSNLFPGTWYLER		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	2397.1511	33.51	1.414564371
33859482	VNFTVDQIR		eukaryotic translation elongation factor 2 [Mus musculus]	1091.5846	45.6	0.773054467
6678752	VNGEPLDLDPGQTLIYYVDEK		lymphocyte antigen 74 [Mus musculus]	2378.1638	28.6	1.706038373
63556656	VNGVLMALPVYLAGGR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1629.9205	53.69	0
63556656	VNGVLMALPVYLAGGR	Deamidation (NQ)	PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1630.9091	30.38	0
9790069	VNIAFNYDMPEDSDTYLHR		HLA-B-associated transcript 1A [Mus musculus]	2300.0376	63.67	0.780525858
6755963	VNNSSLIGLGYTQTLKPGIK		voltage-dependent anion channel 1 [Mus musculus]	2103.1853	47.73	2.692952955
6755965	VNNSSLIGVGYTQTLRPGVK		voltage-dependent anion channel 2 [Mus musculus]	2103.1616	69.2	0.897467221
6679439	VNPTVFFDITADDEPLGR		peptidylprolyl isomerase A [Mus musculus]	2005.9824	122.21	0.98638699
63746482	VNQPASFAVSLNGAK		PREDICTED: filamin, alpha [Mus musculus]	1502.7853	43.28	0.782048717
31981824	VPAPEVASGPDPEEEIR		ankyrin repeat domain 25 [Mus musculus]	1791.8793	35.24	1.867447537
41322904	VPAQQLQEAGILSQEELQR		plectin 1 isoform 1 [Mus musculus]	2137.1277	20.62	0.955929617
13385168	VPDFSDYR		ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Mus musculus]	998.4652	55.66	1.382181503
6755714	VPENPPSMVFK		transgelin [Mus musculus]	1244.6301	36.61	2.207170015
18079351	VPHNAAVQVYDYR		major vault protein [Mus musculus]	1531.7692	61.17	0
7305443	VPPAINQFTQALDR		ribosomal protein L7a [Mus musculus]	1569.8373	27.02	1.241384216
56119103	VPSTEAEALASSLMGLFEK		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1980	98.86	0.962368
6679937	VPTPNVSVVDLTCR		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1499.7963	90.18	1.199152474
6754004	VPTTGIIEYPFDLENIIFR		guanine nucleotide binding protein, alpha 11 [Mus musculus]	2237.1792	41.83	1.324309147
37537522	VPVDVAYQR		epiplakin 1 [Mus musculus]	1046.5663	33.66	1.337314376
46849705	VPYVGALQGGLTVR		lectin, galactose binding, soluble 4 [Mus musculus]	1429.8273	108.63	1.159801994
6671700	VQDDEVGDGTTSVTVLAAELLR		chaperonin subunit 2 (beta) [Mus musculus]	2288.1533	31.31	1.254637644
63552538	VQEVEVPEDFGPVR		PREDICTED: echinoderm microtubule associated protein like 2 [Mus musculus]	1599.8044	52.8	1.489191046
33469093	VQIYHNPTANSFR		vasodilator-stimulated phosphoprotein [Mus musculus]	1546.7804	25.56	1.207559879
31982520	VQPIYGGTNEIMK		acetyl-Coenzyme A dehydrogenase, long-chain [Mus musculus]	1449.7393	20.83	9.179180483
6754256	VQQTVQDLFGR		heat shock protein 9A [Mus musculus]	1290.6866	63.49	1.238075841
41322904	VQSGSESVIQEYVDLR		plectin 1 isoform 1 [Mus musculus]	1808.8818	24.3	0.986880959
6754482	VRPASSAASVYAGAGGSGSR		keratin complex 1, acidic, gene 18 [Mus musculus]	1807.9102	62.89	0.801210809
21312216	VSDVVDGNIQGR		gasdermin domain containing 1 [Mus musculus]	1258.6368	26.04	1.632163236
37620153	VSDVYDIEER		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1224.5803	33.04	1.703894438
30348966	VSEEAESQQWDTSK		spectrin beta 2 isoform 1 [Mus musculus]	1623.7155	67.47	1.243276161
7106421	VSEEAESQQWDTSK		spectrin beta 2 isoform 2 [Mus musculus]	1623.7155	67.47	1.243276161
6679439	VSFELFADK		peptidylprolyl isomerase A [Mus musculus]	1055.5443	53.87	1.271588377
31982373	VSISEGDDKIEYR		fibrillarin [Mus musculus]	1510.7417	38	2.16768641
30520375	VSMAPDGNGGLYR		UDP-N-acteylglucosamine pyrophosphorylase 1 homolog [Mus musculus]	1336.6332	20.21	1.404010931
63474408	VSPSIQPQPQSQPTSLSR		PREDICTED: RIKEN cDNA E030037J05 gene [Mus musculus]	1937.0104	36.14	1.487397228
63556656	VSQHGSDVVIETDFGLR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1858.9307	33.4	0.293094091
38142460	VSVISVEEPPQR		electron transferring flavoprotein, beta polypeptide [Mus musculus]	1339.7224	34.68	1.091902185
31982169	VSVVEPGNFIAATSLYSPER		3-hydroxybutyrate dehydrogenase (heart, mitochondrial) [Mus musculus]	2136.1067	62.02	1.841164911

6753086	VSYGIGEEEHDQEGR		apurinic/apyrimidinic endonuclease 1 [Mus musculus]	1704.7501	61.54	1.601124034
31543605	VTAEVVLVHPGGGSTSR		ribophorin I [Mus musculus]	1665.8969	50.84	0.730776634
63746482	VTAQGPGLEPSGNIANK		PREDICTED: filamin, alpha [Mus musculus]	1652.8599	89.3	1.322836959
63660302	VTASGPGLSAYGVPASLPVEFAIDAR		PREDICTED: filamin B, beta [Mus musculus]	2545.3235	48.76	0.882494011
31560353	VTASSENFHVGENDENQER		solute carrier family 6 (neurotransmitter transporter), member 14 [Mus musculus]	2161.9402	89.81	0
18079351	VTGEEWLVR		major vault protein [Mus musculus]	1088.5728	27	1.222270362
31981722	VTHAVVTVPAYFNDAQR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1887.9739	68.79	0.633258337
20799907	VTIAQGGVLPNIQAVLLPK		histone 2, H2aa1 [Mus musculus]	1931.1746	107.15	0.767534229
63556656	VTIPGNYYK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1054.558	34.37	0.228752499
54607098	VTLEYRPVIDK		succinate dehydrogenase Fp subunit [Mus musculus]	1332.7471	33.71	0
8393150	VTPPEGYDVVTVFR		carboxyl terminal LIM domain protein 1 [Mus musculus]	1578.8193	42.52	1.306714917
6755963	VTQSNFAVGYK		voltage-dependent anion channel 1 [Mus musculus]	1213.6206	77.49	1.495331191
7305167	VTVLEGDILDTQYLR		hydroxysteroid dehydrogenase-6, delta<5>-3-beta [Mus musculus]	1734.9382	25.29	1.019480786
63746482	VTYTPMAPGSYLISIK		PREDICTED: filamin, alpha [Mus musculus]	1740.9144	43.99	1.625754287
6754084	VTYVDFLAYDILDQYR		glutathione S-transferase, mu 1 [Mus musculus]	1993.9967	64.34	1.391427316
58037117	VVAEPVELAQEFR		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Mus musculus]	1486.7959	36.89	1.360471484
6671664	VVDDWANDGWGLK		calnexin [Mus musculus]	1474.701	56.82	0
31980648	VVDLLAPYAK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1088.6335	46.84	1.318853326
21450241	VVEEAPSIFLDPETR		propionyl-Coenzyme A carboxylase, alpha polypeptide [Mus musculus]	1701.8857	22.61	0
46593021	VVELLADIVQNSSLEDSQIEK		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	2329.2104	68.28	1.040297435
63476037	VVESLDVGPDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1185.6171	39.56	0.995039348
46849705	VVFNTMQSGQWGK		lectin, galactose binding, soluble 4 [Mus musculus]	1481.7227	71.29	1.297430764
63476037	VVIHFTDGADGDMADLYR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1994.9056	24.3	2.123927134
34538601	VVLPMELPIR		cytochrome c oxidase subunit II [Mus musculus]	1166.7029	28.48	1.659140817
26006861	VVPVADIITPNQFEAELLSGR		pyridoxal (pyridoxine, vitamin B6) kinase [Mus musculus]	2268.2214	24.92	1.196751576
19527092	VVQVSAGDSHTAALTEDGR		chromosome condensation 1 [Mus musculus]	1912.9305	62.28	2.277033732
7305295	VVSSVLQLGNIVFK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1502.8905	93.89	1.889684407
13385624	VVTDTDETELAR		eukaryotic translation initiation factor 2, subunit 1 alpha [Mus musculus]	1348.6606	49.54	0
51556274	VVTIAPGLFATPLLTTLPEK		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	2081.2231	66.71	1.263514647
46849705	VVVNGNSFYEYGHR		lectin, galactose binding, soluble 4 [Mus musculus]	1640.785	77.65	1.109373632
46849705	VVVNGNSFYEYGHR	Deamidation (NQ)	lectin, galactose binding, soluble 4 [Mus musculus]	1641.7743	49.17	1.707443835
6677773	VWLDPNETNEIANANSR		ribosomal protein L19 [Mus musculus]	1942.924	77.06	0.783693689
45387933	VWQLQDLSFQTAAR		UDP-glucose ceramide glucosyltransferase-like 1 [Mus musculus]	1662.8586	32.54	0
6680047	VWQVTIGTR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1059.5962	22.34	1.231721426
31543474	VYAEANSQESADR		phosphoglucomutase 3 [Mus musculus]	1439.6417	44.9	0.98049292
21312950	VYDQMPEPR		NADH dehydrogenase (ubiquinone) Fe-S protein 7 [Mus musculus]	1134.5283	35.63	1.148330149
46593021	VYEEDAVPGLTPCR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1548.7344	41.08	1.180268425
63481281	VYEELLAIPVVR		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1400.8215	43.31	0
41322904	VYHDPSTQEPVTYSQLQQR		plectin 1 isoform 1 [Mus musculus]	2276.1001	60	1.173731658
33859686	VYWDNGAQIISPHDR		phosphoglucomutase 1 [Mus musculus]	1770.8561	20.64	8.170416221
42734399	WAEDQALYAEEAR		desmuslin isoform H [Mus musculus]	1551.7104	40.62	1.765758822
30023842	WALSQSNPSALR		valosin containing protein [Mus musculus]	1329.6927	73.53	1.026793627
6754984	WDDGLDQYR		3'-phosphoadenosine 5'-phosphosulfate synthase 2 [Mus musculus]	1167.5103	69.99	1.799828659
31981892	WDDPYYDIAR		Rho GTPase activating protein 1 [Mus musculus]	1313.5851	40.89	2.24313286
6753498	WDYDKNEWK		cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	1283.5811	30.26	0.885203172
1346343	WELLQQVDTSTR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1475.7559	69.52	0.075052741
63746482	WGDEHIPGSPYR		PREDICTED: filamin, alpha [Mus musculus]	1413.6565	74.58	1.2351998
6679937	WGEAGAEYVVESTGVFTTMEK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	2291.0466	44.07	1.3855473
31559916	WGTLTDCVVMR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1280.6196	27.24	0.994674516
8567336	WGVFNEYNNDEK		chloride channel calcium activated 3 [Mus musculus]	1514.6576	87.85	0
31543942	WIDNPTVDDR		vinculin [Mus musculus]	1230.5782	20.75	1.785460172
41322904	WQAVLAQTDVR		plectin 1 isoform 1 [Mus musculus]	1286.6848	24.77	2.22358841
63517139	WQNNLLPSR		PREDICTED: similar to Rps15a protein [Mus musculus]	1127.6045	36.5	0
13624315	WSLLQQQK		keratin complex 2, basic, gene 8 [Mus musculus]	1030.5742	37.87	1.45196051
2506774	WSLLQQQK		Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)	1030.5742	37.87	1.45196051
63565108	WSLLQQQK		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1030.5742	37.87	1.45196051
27804325	WVDVGGAYVGPTQNR		monoamine oxidase A [Mus musculus]	1618.7986	98.16	1.895944471
21450277	WVNDVEDSYGQQWTYEQR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2303.0015	115.37	1.192877698
21704206	WVQQNIAHFGGNPDR		carboxylesterase 2 [Mus musculus]	1738.8499	29.7	1.489466561
18079339	WVVIGDENYGEGSSR		aconitase 2, mitochondrial [Mus musculus]	1667.7435	47.13	0.323337189

31981549	YADALQEIIR	sulfide quinone reductase-like [Mus musculus]	1191.641	56.51	1.25885772
31981983	YAEEELEQVR	stromal interaction molecule 1 [Mus musculus]	1265.6008	40.72	1.059408046
9790219	YALYDASFETK	destrin [Mus musculus]	1307.6191	77.99	1.194370866
6680924	YALYDATYETK	cofilin 1, non-muscle [Mus musculus]	1337.6271	79.84	1.393131698
29244560	YASASEPTEIYR	hypothetical protein LOC331063 [Mus musculus]	1386.6578	72.76	0.375666686
26190606	YDFGIYDDDPEIITLER	ER-resident protein ERdj5 [Mus musculus]	2073.9753	21.9	0
6753262	YDPPLEDGAMPSAR	capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1518.6934	39	1.390159073
21704066	YDPTIEDSYR	RAS-related protein-1a [Mus musculus]	1258.5646	46.87	1.033356079
37497112	YDSRPGGYGYGYGR	RNA binding motif protein 3 [Mus musculus]	1567.6953	20.48	2.600169957
6754180	YEAFQDETFQER	hephaestin [Mus musculus]	1562.6805	24.72	1.594932694
9790051	YEASYDMSDSGK	phosphofructokinase, platelet [Mus musculus]	1352.5264	44.74	4.385170423
6679545	YEDAVQFIR	protein tyrosine phosphatase 4a2 [Mus musculus]	1140.5726	21.59	1.575736497
21313144	YEDFKDEGSENAVK	GTP-binding protein PTD004 [Mus musculus]	1630.7229	77.86	0.722799836
16716471	YEDFVVDGFNVLYNK	hypothetical protein LOC94184 [Mus musculus]	1821.8647	77.31	1.279155764
22267442	YEDSNNLGTSHLLR	ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1618.7848	44.45	0.821467016
27370092	YEEIDNAPEER	Tu translation elongation factor, mitochondrial [Mus musculus]	1364.5984	50.9	1.247938733
1346343	YEELQITAGR	Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1179.6069	81.98	0
13624315	YEELQTLAGK	keratin complex 2, basic, gene 8 [Mus musculus]	1151.5956	84.85	1.531649154
7305295	YEILAANAIPK	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1202.6779	65.58	2.110706895
13385998	YESSALPAGQLTSLPDYASR	TNF receptor-associated protein 1 [Mus musculus]	2126.0447	39.67	1.431673217
33859482	YEWDVAEAR	eukaryotic translation elongation factor 2 [Mus musculus]	1138.5251	58.86	0.938854267
27370516	YFDLGLPNR	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	1094.5741	40.55	1.363867191
6678055	YFILPDSLPLDTLLVDVEPK	small nuclear ribonucleoprotein D1 [Mus musculus]	2287.2427	46.73	1.243020539
30409988	YFNPIGAHASGR	galactose-4-epimerase, UDP [Mus musculus]	1289.6389	23.17	3.146185381
51764087	YFPTQALNFAFK	PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	1446.7456	64.34	1.455375033
22094075	YFPTQALNFAFK	solute carrier family 25, member 5 [Mus musculus]	1446.7456	64.34	1.455375033
34328204	YGEAGDGPGWGGPHPR	valyl-tRNA synthetase 2 [Mus musculus]	1609.7155	44.09	0.704370431
6680193	YGEYFPGTGDLR	histone deacetylase 1 [Mus musculus]	1374.646	38.2	0.522730312
63746482	YGGDEIPFSPYR	PREDICTED: filamin, alpha [Mus musculus]	1400.6561	38.27	1.112846447
63746482	YGGPYHIGGSPFK	PREDICTED: filamin, alpha [Mus musculus]	1379.6771	36.83	1.728934809
6753240	YGIVDYMIEQSGPPSK	calcium binding protein, intestinal [Mus musculus]	1783.8492	35.17	0
21312260	YGLAAAVFTR	aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1068.5884	40.31	1.428857563
31542159	YGPNELPTEEGK	ATPase, Ca++ transporting, ubiquitous [Mus musculus]	1333.6177	26.86	0
11612505	YGSGSGQQSVTGVEESDDANSYWR	stromal cell-derived factor 2-like 1 [Mus musculus]	2579.0962	57.28	0.72082141
6755817	YGVNPGPIVGTTR	thymopoietin [Mus musculus]	1330.7103	45.46	0.967310178
6680606	YGVQLSQIQSVISGFEAQLSDVR	keratin complex 1, acidic, gene 19 [Mus musculus]	2524.3035	108.94	1.529518033
6679687	YGVSGYPTLK	glucose regulated protein [Mus musculus]	1084.5758	61.8	0.546630241
31981246	YGYTHLSAGELLR	UMP-CMP kinase [Mus musculus]	1479.7627	63.02	0.764118632
40556608	YHTSQSGDEMTSLSEYVSR	heat shock protein 1, beta [Mus musculus]	2176.9509	101.04	1.075471081
34996495	YHVPVVVVPEGSTSDTQEQAILR	ribophorin II [Mus musculus]	2524.3037	87.43	0.759104166
19882199	YIASVQGSAPSPR	RAN binding protein 2 [Mus musculus]	1332.6885	22.84	1.518013986
63746482	YIPVQQGPVGVNVTYGGDHIPK	PREDICTED: filamin, alpha [Mus musculus]	2338.2153	59.02	1.229681423
51770896	YITPDQLADLYK	PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1439.74	64.65	0.982986374
7110683	YLEDQVNTDLPYEIER	phosphoenolpyruvate carboxykinase 1, cytosolic [Mus musculus]	1996.9282	32.72	1.121685393
63530525	YLELLGYR	PREDICTED: SEC31-like 1 [Mus musculus]	1026.5756	30.06	3.559171398
20330802	YLGAEYMQSVGNMR	transferrin [Mus musculus]	1618.744	41.39	1.604987963
6754782	YLGLLENVR	myosin IB [Mus musculus]	1076.6232	24.82	1.33418945
51766008	YLGLLENVR	PREDICTED: myosin IA [Mus musculus]	1076.6232	24.82	1.33418945
6678449	YLGTQPEPDIVGLDSGHIR	thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	2067.0503	72.33	1.476873561
33468931	YLIATSEQPIAALHR	seryl-aminoacyl-tRNA synthetase 1 [Mus musculus]	1682.9238	43.53	0.911554085
31560645	YLLSQSSPAPLTAAEEELR	twinfilin [Mus musculus]	2075.0635	62.98	1.154972672
6753254	YLNQDYETLR	calpain 2 [Mus musculus]	1314.6327	67.02	1.431778679
7305295	YLPIYSEK	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1012.5332	30.48	2.830685024
22165384	YLTVAAVFR	tubulin, beta, 2 [Mus musculus]	1039.6021	34.66	1.081387915
31981939	YLTVAAVFR	tubulin, beta 4 [Mus musculus]	1039.6021	34.66	1.081387915
7106439	YLTVAAVFR	tubulin, beta 5 [Mus musculus]	1039.6021	34.66	1.081387915
33859506	YMCENQATISSK	albumin 1 [Mus musculus]	1374.6031	66.67	1.699179641
63660302	YMIGVTYGGDNIPLSPYR	PREDICTED: filamin B, beta [Mus musculus]	2016.0011	24.68	0.957276891
6679078	YMNSGPVVAMVWEGLNVVK	nucleoside-diphosphate kinase 2 [Mus musculus]	2093.0581	38.49	0
63746482	YNDQHIPGSPFTAR	PREDICTED: filamin, alpha [Mus musculus]	1602.7729	56.7	1.507175439

19072792	YNGDNVIYKPPGR	thioredoxin domain containing 4 [Mus musculus]	1492.7587	47.14	0.526081466
7949051	YNILGTNTIMDK	heterogenous nuclear ribonucleoprotein U [Mus musculus]	1382.6863	37.66	1.051907876
31981522	YNQMDSTEDAQEEFGWK	transmembrane 9 superfamily member 2 [Mus musculus]	2077.8618	45.98	0.93465064
51771420	YNVLGAETVLTQMR	PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1594.8296	32.7	0.871606775
31543918	YPEAPPSVR	ubiquitin-conjugating enzyme E2 variant 2 [Mus musculus]	1015.5249	37.9	1.065457571
6671507	YPIEHGIITNWDDMEK	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1960.9148	47	0.790300088
63471580	YPQLLSGIR	PREDICTED: similar to S-adenosylhomocysteine hydrolase [Mus musculus]	1046.6093	31.24	0.951605262
7549795	YQEEGPVPQPR	tight junction protein 2 [Mus musculus]	1299.6383	31.83	1.061783408
27734998	YQVEYDAYK	hypothetical protein LOC216821 [Mus musculus]	1178.5374	26.91	0
28173568	YQYGGLNSGRPVTPPR	protein phosphatase 1, catalytic subunit, beta [Mus musculus]	1761.9059	36.83	0
31560697	YSDMIVAAIQAEK	H1 histone family, member 0 [Mus musculus]	1438.7262	34.57	1.201458662
31982223	YSEIEPSTEGEVIYR	laminin, beta 2 [Mus musculus]	1771.8391	56.99	0
23956406	YSGGLPLPPSYVPVVMSELSDR	UDP glucuronosyltransferase 2 family, polypeptide B34 [Mus musculus]	2363.1885	20.51	1.450328845
6679291	YSLEPVAAELK	phosphoglycerate kinase 1 [Mus musculus]	1219.6517	20.08	1.246584759
63474405	YSMPDNSPETR	PREDICTED: tensin [Mus musculus]	1296.5532	39	1.169896077
6677871	YSTNTQIQVLPEGGETPIFK	scinderin [Mus musculus]	2222.1206	52.72	0.469569343
14161694	YTFDEFSQR	myosin VIIb [Mus musculus]	1192.5372	31.22	1.205711881
33469063	YTINIPEDLKPR	aconitase 1 [Mus musculus]	1458.7772	29.69	0
6754084	YTMGDAPDFDR	glutathione S-transferase, mu 1 [Mus musculus]	1287.5366	43.37	1.208023098
6671539	YTPSGQSGAAASESLFISNHAY	aldolase 1, A isoform [Mus musculus]	2258.0449	106.7	1.197287754
6754016	YTTPEDATPEPGEDPR	guanine nucleotide binding protein alpha stimulating isoform b [Mus musculus]	1774.7804	57.95	1.203688619
6680854	YVDSEGHLYTVPIR	caveolin, caveolae protein 1 [Mus musculus]	1648.8319	65.6	1.401819714
13386062	YVEEQPGNLQR	hypothetical protein LOC68117 [Mus musculus]	1332.6567	25.46	1.214563157
31541863	YVNWIQQTIAAN	RIKEN cDNA 2210010C04 [Mus musculus]	1420.703	89.61	0
40254244	YVQELPLETDGALR	loss of heterozygosity, 11, chromosomal region 2, gene A homolog [Mus musculus]	1603.8286	49.84	1.037881326
13994221	YVQLPADEVDTQLLQDAAR	snRNP core protein SMX5 [Mus musculus]	2145.0867	55.68	1.459737953
64427157	YVVDSDTVQAHTVR	PREDICTED: synaptopodin 2 [Mus musculus]	1589.788	26.12	0
20270275	YVVVTGITPTPLGEGK	methylenetetrahydrofolate dehydrogenase 1 [Mus musculus]	1630.8894	23.15	0
21704206	YWANFAR	carboxylesterase 2 [Mus musculus]	927.4597	23.8	1.385458778
6678499	YWQQVIDMNDYQR	UDP-glucose dehydrogenase [Mus musculus]	1758.8058	37.33	2.077992724
31982290	YYEPYYAAGPSYGGR	LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1713.761	32.44	1.335544166
23943876	YYIVGLQVR	zymogen granule membrane protein 16 [Mus musculus]	1110.6337	31.57	1.186070016
6755354	YYPTEDVPR	ribosomal protein L6 [Mus musculus]	1139.5404	32.04	1.07524377
51873060	YYVTIIDAPGHR	eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	1404.7299	64.67	0.994191215

Mouse Pair 4

GI #	Sequence	Modifications	Protein Name	M/z	Highest Mascot score	Average Ratio (15N:14N), non-Log-transformed
33859554	AAAEVNQEYGLDPK		fumarate hydratase 1 [Mus musculus]	1504.7249	90.77	0
6678573	AAATTVQEYLK		villin 1 [Mus musculus]	1194.6184	27.09	0
33859506	AADKDTCFSTEGPNLVTR		albumin 1 [Mus musculus]	1924.913	124.84	0.090501587
6756033	AADPPAENSSAPEAEQGGAE		nuclease sensitive element binding protein 1 [Mus musculus]	1897.8046	73.36	0.671077517
51767712	AAELLLPAAAAWR		PREDICTED: hypothetical protein LOC70153 [Mus musculus]	1352.7749	25.96	0
29789080	AAESLADPTEYENLFPGLK		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	2065.0095	75.5	0.249621162
31981925	AAFDDAIAELDTLSEESYK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Mus mu	2087.9705	123.15	0
6753036	AAFQLGSPWR		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1132.5896	33.18	0.426706862
6680606	AALEGTLAETEAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1331.6849	82.59	0.431512714
29126205	AANEAGYFNEEMAPIEVK		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1982.9282	48.57	0
13385006	AANNGALPPDLSYIVR		cytochrome c-1 [Mus musculus]	1670.8848	24.08	0.38819335
13386120	AAPEESEAQAEGCSEER		nucleolar protein family A, member 2 [Mus musculus]	1792.7347	32.82	0.443578897
27754065	AAPFTLEYR		pyrophosphatase [Mus musculus]	1067.5521	37.76	0.402998164
6677995	AAQSPQQHSSGDPTEEESPV		solute carrier family 16, member 1 [Mus musculus]	2080.9053	94.9	0.294853826
8567336	AASATLPPITVTPVVNK		chloride channel calcium activated 3 [Mus musculus]	1678.9681	95.95	0
63474405	AASDGQYENQSPEATSPR		PREDICTED: tensin [Mus musculus]	1907.8414	111.72	0.104363297
63474405	AASDGQYENQSPEATSPR	Deamidation (NQ)	PREDICTED: tensin [Mus musculus]	1908.8392	49.06	0
7304889	AASGFNATEDAQTLR		annexin A4 [Mus musculus]	1551.7415	87.74	0.65974391
22550094	AATIIATSEGSLWGLDR		protein kinase, cAMP dependent regulatory, type II alpha [Mus musculus]	1760.9258	24.44	0.663684161
6678483	AAVASLLQSVQVPEFTPK		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1885.041	86.58	0.546272721
7305027	AAVPSGASTGIYEALELR		enolase 2, gamma neuronal [Mus musculus]	1804.9406	99.7	0.596986431
6679651	AAVPSGASTGIYEALELR		enolase 3, beta muscle [Mus musculus]	1804.9406	99.7	0.596986431
51770896	AAVPSGASTGIYEALELR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1804.9406	99.7	0.596986431
27413160	AAVQQLQAEGLSPR		carbonyl reductase 3 [Mus musculus]	1467.792	36.13	0.396566805
50355692	AAYEAELGDAR		lamin A isoform A [Mus musculus]	1165.553	78.17	0.429918389
22094075	AAYFGIYDTAK		solute carrier family 25, member 5 [Mus musculus]	1219.6	66.45	0.257264148
6680045	ACADATLSQITNNIDPVGR		guanine nucleotide-binding protein, beta-1 subunit [Mus musculus]	1958.9576	36.19	0.300322433
13937391	ACGDSTLTQITAGLDPVGR		guanine nucleotide-binding protein, beta-2 subunit [Mus musculus]	1874.9296	46.26	0
46048407	ACPMLSTLR		I-kappa-B-related protein [Mus musculus]	991.4923	23.61	0.414601849
40538830	ADDDTYVIVDNLR		core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase [Mus musculus]	1508.7258	30.01	0
6671539	ADDGRPFPQVIK		aldolase 1, A isoform [Mus musculus]	1342.7145	38.27	0.513693782
51491845	ADDPSSYMEVVQAANASGNWEELVK		clathrin, heavy polypeptide (Hc) [Mus musculus]	2710.2456	60.85	0.229909319
6679237	ADFAQACQDAGVR		pyruvate carboxylase [Mus musculus]	1351.6101	38.66	0
34328489	ADFDNTVAIHPTSSEELVTLR		glutathione reductase 1 [Mus musculus]	2315.1523	112.88	0.38001418
6753266	ADGLAILGVLMK		carbonic anhydrase 1 [Mus musculus]	1200.7032	54.33	0
6753266	ADGLAILGVLMK	Oxidation (M)	carbonic anhydrase 1 [Mus musculus]	1216.6938	37.03	0.927346937
31981522	ADIELFVNR		transmembrane 9 superfamily member 2 [Mus musculus]	1076.5752	52.44	0.371403717
6754084	ADIVENQVMDTR		glutathione S-transferase, mu 1 [Mus musculus]	1390.6674	66.16	0
23956406	ADIWLIR		UDP glucuronosyltransferase 2 family, polypeptide B34 [Mus musculus]	886.5213	23.46	0.205741287
55742711	ADMVETQQLMR		EH-domain containing 2 [Mus musculus]	1321.6232	31.16	1.73122652
33859811	ADMVIEAVFEDLGVK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1635.8275	77.56	0.70384144
33859811	ADMVIEAVFEDLGVK	Oxidation (M)	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1651.8109	39.67	0.156223434
6680201	ADNEKLEEQPGEQAPR		hepatoma-derived growth factor-related protein 2 [Mus musculus]	1810.8629	24.74	0.422073856
7709986	ADPEAAWEPTEAEAR		ubiquitin-like 1 (sentrin) activating enzyme E1B [Mus musculus]	1642.7499	35.34	0.346359644
6753498	ADWSSLSR		cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	921.4437	35.56	0.223477809
31560731	ADYAQLLEDMQNAFR		ATPase, H+ transporting, V1 subunit A, isoform 1 [Mus musculus]	1784.8369	40.81	0
32189330	AEAAAPYTVLAQSAPR		latent transforming growth factor beta binding protein 4 [Mus musculus]	1615.8412	33.63	2.75795006
63562743	AEACVFWR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	981.4619	40.81	0.202167477
6679237	AEAEAQAEELSFPR		pyruvate carboxylase [Mus musculus]	1547.7375	63.36	0.584811565
13624315	AEAETMYQIK	Oxidation (M)	keratin complex 2, basic, gene 8 [Mus musculus]	1199.5608	53.35	0.337741587
63565108	AEAETMYQIK	Oxidation (M)	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1199.5608	53.35	0.337741587
13399310	AEAGAGSATEFQFR		ribosomal protein S10 [Mus musculus]	1441.675	64.21	0.450987742
27370092	AEAGDNLGALVR		Tu translation elongation factor, mitochondrial [Mus musculus]	1185.6218	46.86	0.449432584
6996913	AEDGSVIDYELIDQDAR		annexin A2 [Mus musculus]	1908.8826	127.56	0.520032481

7242171	AEDNADTLALVFEAPNQEK		proliferating cell nuclear antigen [Mus musculus]	2074.9917	55.11	0
21312266	AEELFLWVPR		hypothetical protein LOC52690 [Mus musculus]	1259.6783	24.69	1.615091191
29336026	AEELLAQLGR		nonmuscle myosin heavy chain [Mus musculus]	1099.6091	43.16	0.377962654
33636693	AEEPGGQAYETPR		pleckstrin homology domain containing, family A member 6 [Mus musculus]	1404.6415	34.86	0.43184522
31982030	AEEYEFLTPMEEAPK		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1783.8405	46.33	0
21703832	AEFGPPGPGPGSR		arginyl aminopeptidase (aminopeptidase B) [Mus musculus]	1225.6012	26.09	0.368140565
31981562	AEGSDVANAVLDGADCIMLSGETAK		pyruvate kinase 3 [Mus musculus]	2437.1323	129.45	0
31981562	AEGSDVANAVLDGADCIMLSGETAK	Oxidation (M)	pyruvate kinase 3 [Mus musculus]	2453.1287	67.58	4.044998903
37537522	AEIINQDLFEQLER		epiplakin 1 [Mus musculus]	1717.879	25.53	0
27229048	AEISNAIDQYVTGTIGEGEDLVK		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	2422.2041	65.81	0.71175134
6678573	AELGNSGDWSQIADEVMSPK		villin 1 [Mus musculus]	2133.99	79.23	0.418867189
6678573	AELGNSGDWSQIADEVMSPK	Oxidation (M)	villin 1 [Mus musculus]	2149.9883	36.45	2.513790029
6755372	AELNEFLTR		ribosomal protein S3 [Mus musculus]	1092.5675	38.97	0.416591315
13386054	AENFFILR		actin related protein 2/3 complex, subunit 4 [Mus musculus]	1009.5514	44.36	0.429379677
6678483	AENYDISPADR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1250.5674	53.08	0.40617905
7305583	AEQLASLEAAQR		tight junction protein 3 [Mus musculus]	1286.6604	27.6	0
20149726	AETAPLPTSVDDTPEVLNR		phosphatidate cytidylyltransferase 2 [Mus musculus]	2025.017	64.28	0.339421302
14149645	AETSESSGSAPAVPEASASPK		methyl CpG binding protein 2 [Mus musculus]	1959.9225	25.39	0
13626040	AEVGQEGEAGQFDGEK		A kinase (PRKA) anchor protein (gravin) 12 [Mus musculus]	1650.7324	78.42	0.284590032
63746482	AEVGVPAEFGIWTR		PREDICTED: filamin, alpha [Mus musculus]	1531.797	76.26	0.220445757
6753322	AFADAMEVIPSTLAENAGLNPISTVTELR		chaperonin subunit 4 (delta) [Mus musculus]	3030.5417	35.76	0.288447299
13385310	AFDNDVDALCNLR		propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]	1465.6837	47.97	0
29293809	AFDSGIIPMEFVNK		ATP citrate lyase [Mus musculus]	1567.776	40.57	0
21312444	AFDVPIEEGPVFR		hypothetical protein LOC69824 [Mus musculus]	1475.754	38.84	0
6755100	AFFSEVER		proliferation-associated 2G4 [Mus musculus]	984.4827	37.5	0.462297906
41054974	AFGAPNVVEDEIDQYLSK		nuclear protein localization 4 [Mus musculus]	1994.9753	39.37	0
63746482	AFGPGLQGGNAGSPAR		PREDICTED: filamin, alpha [Mus musculus]	1456.7373	104.07	0.097448723
63746482	AFGPGLQGGNAGSPAR	Deamidation (NQ)	PREDICTED: filamin, alpha [Mus musculus]	1457.7269	36.61	0
8567402	AFGYYGPLR		splicing factor, arginine/serine-rich 3 (SRp20) [Mus musculus]	1043.5316	33.33	0.49923374
13384888	AFIFPQESSTAYVSLIPK		hypothetical protein LOC66289 [Mus musculus]	1998.0665	101.88	0
7710086	AFLTLAEDILR		RAB10, member RAS oncogene family [Mus musculus]	1261.7179	55.71	0.528607679
51491845	AFMTADLPNELIELLEK	Oxidation (M)	clathrin, heavy polypeptide (Hc) [Mus musculus]	1963.0074	29.84	1.206293668
37674269	AFQEQGQGQEQSEPGMSSTPR		slingshot-like 3 [Mus musculus]	2278.9939	49.67	0
6755781	AFSGLTQNPESIELR		thrombospondin 4 [Mus musculus]	1661.847	35	0
13937355	AFSGYLGPDESK		esterase D/formylglutathione hydrolase [Mus musculus]	1270.5964	52.67	0.87238977
8394252	AFSPTTVNTGR		Sec61 alpha subunit homolog [Mus musculus]	1150.589	34.72	0.493939342
31543847	AFSSPQEEEEAGFTGR		transcription elongation factor B (SIII), polypeptide 3 [Mus musculus]	1741.7927	28.15	0.384417243
31982186	AGAGSATLSMAYAGAR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1454.7079	73.38	0.838100017
28916677	AGAYDFPSPEWDTVTPEAK		calcium/calmodulin-dependent protein kinase II alpha [Mus musculus]	2080.9651	49.72	0
20806532	AGEAPTENPAPATEQSSAE		cold shock domain protein A short isoform [Mus musculus]	1856.8226	41.46	0
6755368	AGELTEDEVER		ribosomal protein S18 [Mus musculus]	1247.5793	35.55	0.567515708
6677935	AGEQDPVPTPAELTSPGR		sorbin and SH3 domain containing 1 [Mus musculus]	1821.8878	29.14	0
31543942	AGEVINQPMMMAAR		vinculin [Mus musculus]	1518.726	23.1	0
6671507	AGFAGDDAPR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	976.4518	64.92	0.173678916
6671509	AGFAGDDAPR		actin, beta, cytoplasmic [Mus musculus]	976.4518	64.92	0.173678916
31982275	AGGIETIANEYSDR		heat shock protein 4 [Mus musculus]	1495.7041	34.43	0.56782
7242197	AGGSASAMLQPLLDNQVGFK		proteasome (prosome, macropain) subunit, beta type 1 [Mus musculus]	2004.0184	28.57	0
33859811	AGLEQGSDAGYLAESQK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1723.8096	123.9	0.244824787
19527018	AGLLALEFYTPEAANWR		dipeptidylpeptidase III [Mus musculus]	1921.9774	39.98	0.340638183
20799907	AGLQFPVGR		histone 2, H2aa1 [Mus musculus]	944.5416	52.66	0.539299017
63562740	AGLSLMWNR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1047.5413	45.16	0
6677775	AGNLGGGVVTIER		ribosomal protein L22 [Mus musculus]	1242.6802	72.98	0.567760792
31982223	AGNSLAASTAEETAGSAQSR		laminin, beta 2 [Mus musculus]	1878.8816	35.36	0.067710591
6677871	AGQQAGLQVWR		scinderin [Mus musculus]	1213.6481	30.06	0
41322904	AGTLSITEFADMLSGNAGGFR		plectin 1 isoform 1 [Mus musculus]	2115.021	84.46	0.336472079
11230802	AGTQIENIDEDFR		actinin alpha 4 [Mus musculus]	1507.7042	65.78	0.320594313
59709449	AGTQIENIEEDFR		actinin alpha 2 [Mus musculus]	1521.7203	46.73	0.280602223
16716499	AGVATPGLTEDQLWR		sideroflexin 3 [Mus musculus]	1613.8311	47.84	0.990891083
41322904	AGVGAPVTQVTLQSTQR		plectin 1 isoform 1 [Mus musculus]	1712.931	69.97	0.63366232
41152517	AGVIFPVGR		H2A histone family, member Y [Mus musculus]	915.5458	22.71	0

51770896	AGYTDQVVIGMDVAASEFYR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	2192.0371	47.36	0.671302239
31980648	AIAELGIYPAVDPLDSTSR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1988.0369	111.67	0.341851367
39652626	AIAGIINQPYYNYQAGPDAALGR		bisphosphate 3'-nucleotidase 1 [Mus musculus]	2436.2502	58.14	3.282558961
30023842	AIANECQANFISIK		valosin containing protein [Mus musculus]	1521.7668	50.66	5.957598942
6755004	AIASATEGGSVPQIR		programmed cell death 8 [Mus musculus]	1456.7758	57.45	0.292979187
6671559	AIEQADLLQEEDESPR		adaptor protein complex AP-1, sigma 1 [Mus musculus]	1842.8741	68.8	0.456962537
6678912	AIFASGSPFDPVTLPDGR		malic enzyme, supernatant [Mus musculus]	1846.9301	31.62	0
31560653	AIGVLTSGGDAQGMNAAVR		phosphofructokinase, liver, B-type [Mus musculus]	1787.9097	76.87	0.480075122
9790051	AIGVLTSGGDAQGMNAAVR		phosphofructokinase, platelet [Mus musculus]	1787.9097	76.87	0.480075122
6755376	AIIIFVPVPQLK		ribosomal protein S7 [Mus musculus]	1337.8523	27.76	0.447194639
33859488	AILVDLEPGTMDSVR		tubulin, beta 2 [Mus musculus]	1615.8352	51.6	0.837520328
12963615	AILVDLEPGTMDSVR		tubulin, beta 3 [Mus musculus]	1615.8352	51.6	0.837520328
7106439	AILVDLEPGTMDSVR		tubulin, beta 5 [Mus musculus]	1615.8352	51.6	0.837520328
21746161	AILVDLEPGTMDSVR		tubulin, beta [Mus musculus]	1615.8352	51.6	0.837520328
6755198	AINQGGLTSVAVR		proteasome (prosome, macropain) subunit, alpha type 6 [Mus musculus]	1285.725	61.24	0.375842612
31543942	AIPDLTAPVAAVQAAVSNLVR		vinculin [Mus musculus]	2076.1812	42.92	0.191681103
6753864	AIVAGDQNVEYK		four and a half LIM domains 1 [Mus musculus]	1306.6611	79.25	0.110912874
31560560	AIVAIENPADVSVISSR		laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1740.949	89.11	0.290489909
63514363	AIVAIENPADVSVISSR		PREDICTED: similar to 67 kda laminin receptor [Mus musculus]	1740.949	89.11	0.290489909
31980762	AIWNVINWENVTER		superoxide dismutase 2, mitochondrial [Mus musculus]	1743.8818	46.08	0.301439837
9845257	ALAAAGYDVEK		histone 1, H1c [Mus musculus]	1107.568	87.29	0.456571884
34328365	ALAAAGYDVEK		histone 1, H1d [Mus musculus]	1107.568	87.29	0.456571884
13430890	ALAAAGYDVEK		histone 1, H1e [Mus musculus]	1107.568	87.29	0.456571884
21426893	ALAAGGYDVEK		histone 1, H1b [Mus musculus]	1093.5502	67.32	0.441691747
13386370	ALAIYESQLGPDNPNVAR		kinesin-like 8 [Mus musculus]	1927.9941	34.81	0
6755809	ALDGDFTEENR		talin 1 [Mus musculus]	1266.5751	50.42	0
7709980	ALDIAENEMPGLMR		S-adenosylhomocysteine hydrolase [Mus musculus]	1559.7595	51.13	0.721211294
58037267	ALDLFSDNAPPPELLEIINEDIAK		protein disulfide isomerase-associated 6 [Mus musculus]	2637.3762	60.34	0.935224543
9789873	ALDQASEEIWNDFR		methionine aminopeptidase 2 [Mus musculus]	1693.7886	25.32	0
31981983	ALDTVLFGPPLLTR		stromal interaction molecule 1 [Mus musculus]	1512.8782	52.18	0.236900646
7305295	ALEEALEAKEELER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1629.8269	22.68	8.212616114
33598964	ALELDPNLYR		myosin heavy chain 10, non-muscle [Mus musculus]	1203.6422	43.45	0.082088408
7305295	ALELDPNLYR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1203.6422	43.45	0.082088408
20137006	ALELDSNLYR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1193.6178	54.46	0.378312483
23956212	ALEPEEGNPQTEAQENGPER		HIV TAT specific factor 1 [Mus musculus]	2194.9922	116.2	0.440530115
6680606	ALEQANGELEVK		keratin complex 1, acidic, gene 19 [Mus musculus]	1300.6714	97.29	0.384053311
6679687	ALEQFLQEYFDGNLK		glucose regulated protein [Mus musculus]	1814.8936	42.74	0.358137217
20137006	ALEQQVEEMK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1204.5828	27.73	0
9790083	ALESSIAPIVIFASNR		RuvB-like protein 1 [Mus musculus]	1687.9352	24.22	0.682754943
7305295	ALETQMEEMK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1209.5492	52.52	0
7305295	ALETQMEEMK	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1225.5471	37.83	0
6678573	ALGMTPAAFSALPR		villin 1 [Mus musculus]	1402.7494	26.07	0.707586009
13385942	ALGVLAQLIWSR		citrate synthase [Mus musculus]	1326.792	32.36	0.335922478
27754099	ALIAAQYSGAQVR		eukaryotic translation elongation factor 1 gamma [Mus musculus]	1347.7416	66.26	0.525238726
63489754	ALINADELANDVAGAEALLDR		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	2154.1057	103.93	0
6671666	ALLATASQCQQPAGNK		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1600.8113	78.67	0
42734399	ALLEGESNPEILIWTENIENVPQEPR		desmuslin isoform H [Mus musculus]	2990.5056	50.59	0
46559834	ALLEGESNPEILIWTENIENVPQEPR		desmuslin isoform M [Mus musculus]	2990.5056	50.59	0
33859482	ALLELQLEPEELYQTFQR		eukaryotic translation elongation factor 2 [Mus musculus]	2220.1587	64.19	0.591405047
40556608	ALLFIPR		heat shock protein 1, beta [Mus musculus]	829.5311	32.93	0.481373761
34328489	ALLTPVAIAAGR		glutathione reductase 1 [Mus musculus]	1152.7051	40.35	0.669485951
8567338	ALNAGYILNGLTVSIPGLEK		coatomer protein complex, subunit gamma [Mus musculus]	2043.1394	48.41	0
63476037	ALNLGYALDYALR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1452.7881	75.02	0.19669916
34328204	ALNPLEDWLR		valyl-tRNA synthetase 2 [Mus musculus]	1226.6549	42.78	0.377337873
63506192	ALPFWNEEIVPQIK		PREDICTED: similar to phosphoglycerate mutase (EC 5.4.2.1) B chain - rat [Mus musculus]	1683.9067	30.62	0.535168594
21704020	ALSEIAGITLPYDTLDQVR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	2075.1016	93.83	0.255161655
33859650	ALTLGALTLPLAR		membrane bound C2 domain containing protein [Mus musculus]	1309.8246	27.02	0
6754750	ALTSELANAR		moesin [Mus musculus]	1045.5646	33.02	0
21703972	ALTTQLTDAELAQGR		malic enzyme 2, NAD(+)-dependent, mitochondrial [Mus musculus]	1587.8334	75.15	0.295530255
22165384	ALTVPELTQQMFDAK		tubulin, beta, 2 [Mus musculus]	1691.8616	66.81	0.767827555

12963615	ALTVPELTQQMFDAK		tubulin, beta 3 [Mus musculus]	1691.8616	66.81	0.767827555
31981939	ALTVPELTQQMFDAK		tubulin, beta 4 [Mus musculus]	1691.8616	66.81	0.767827555
27754056	ALTVPELTQQMFDAK		tubulin, beta 6 [Mus musculus]	1691.8616	66.81	0.767827555
33859488	ALTVPELTQQMFDSK		tubulin, beta 2 [Mus musculus]	1707.8414	43.74	0
21746161	ALTVPELTQQMFDSK		tubulin, beta [Mus musculus]	1707.8414	43.74	0
7106439	ALTVPELTQQVFDAK		tubulin, beta 5 [Mus musculus]	1659.8961	45.06	0.466764416
9903607	ALVDELEWEIAR		transmembrane protein 4 [Mus musculus]	1443.7534	41.92	0.956493942
31980953	ALVVTVDAPVLGNR		hydroxyacid oxidase (glycolate oxidase) 3 [Mus musculus]	1423.8284	45.6	0.210013135
31560656	ALYDTFSAFGNILSCK		poly A binding protein, cytoplasmic 1 [Mus musculus]	1749.8579	48.11	0.521086894
63622083	ALYDTFSAFGNILSCK		PREDICTED: similar to Poly(A) binding protein, cytoplasmic 4, isoform 1 [Mus musculus]	1749.8579	48.11	0.521086894
6754556	ALYETELADAR		lamin B1 [Mus musculus]	1251.626	55.28	0.581493374
19526818	ALYSNILGEENTYLWR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1941.9779	85.39	0.32381474
31981983	AMAEEDNGSIGEETDSSPGR		stromal interaction molecule 1 [Mus musculus]	2051.8535	83.72	0.311504127
21704100	AMDSDWFAQNYMGR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1691.7009	71.83	0
47059123	AMEIAEALGR		UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	1060.551	32.35	0
6679503	AMEVDERPTEQYSDIGGLDK		proteasome (prosome, macropain) 26S subunit, ATPase 3 [Mus musculus]	2253.0432	31.18	0.414671591
20874851	AMGIMNSFVNDIFER		PREDICTED: similar to histone H2b-616 [Mus musculus]	1743.8416	79.37	0
20874851	AMGIMNSFVNDIFER	2 Oxidation (M)	PREDICTED: similar to histone H2b-616 [Mus musculus]	1775.7904	27.54	0
20874851	AMGIMNSFVNDIFER	Deamidation (NQ)	PREDICTED: similar to histone H2b-616 [Mus musculus]	1744.8098	75.77	0
20874851	AMGIMNSFVNDIFER	Oxidation (M)	PREDICTED: similar to histone H2b-616 [Mus musculus]	1759.8182	35.32	0
41054806	AMGNLQIDFADPQR		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1575.7648	36.14	0
63704790	AMSLVSGEGEGEQNEIR		PREDICTED: inositol 1,4,5-triphosphate receptor 3 [Mus musculus]	1805.8424	26.63	0.560075925
8567336	AMYIDGWIEDGEVR		chloride channel calcium activated 3 [Mus musculus]	1653.7693	30.44	0
8567336	AMYIDGWIEDGEVR	Oxidation (M)	chloride channel calcium activated 3 [Mus musculus]	1669.7777	34.07	0
27532959	ANATEFGLASGVFTR		aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	1540.7804	45.17	0.329016443
9910128	ANDTTFGLAAGVFTR		aldehyde dehydrogenase 9, subfamily A1 [Mus musculus]	1540.7798	54.94	0
42734351	ANEFIFLELNSSISQR	Deamidation (NQ)	SUMO1/sentrin specific protease 7 isoform 1 [Mus musculus]	1868.9291	24.43	0
31981549	ANIIFNTALGTIFGVK		sulfide quinone reductase-like [Mus musculus]	1678.928	70.07	0.472060075
38372905	ANINVENAFFTLAR		cell line NK14 derived transforming oncogene [Mus musculus]	1579.8225	59.76	0.820362483
63746482	ANLPQSFQVDTSK		PREDICTED: filamin, alpha [Mus musculus]	1434.7175	79.59	0.116947303
20137006	ANLQIDQINTDLNLER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1869.9603	68.24	0.286354986
21313526	ANTNPVPCGLTAR		hypothetical protein LOC78906 [Mus musculus]	1313.6589	23.09	0
6680618	ANWYFLLAR		acetyl-Coenzyme A dehydrogenase, medium chain [Mus musculus]	1153.6216	35.56	0
6755895	APAQAPEATPTYETGQR		tuberous sclerosis 2 [Mus musculus]	1787.8584	32.57	0.793021419
19745150	APDAWDYSQGFVNEEMIR		diaphorase 1 [Mus musculus]	2127.9465	44.43	0.398334313
6754750	APDFVFYAPR		moesin [Mus musculus]	1182.5963	59.16	0.484733745
6677699	APDFVFYAPR		radixin [Mus musculus]	1182.5963	59.16	0.484733745
6678571	APDFVFYAPR		villin 2 [Mus musculus]	1182.5963	59.16	0.484733745
39204553	APEPPPQQVAQQQ		chromodomain helicase DNA binding protein 4 [Mus musculus]	1417.7104	70.14	0.498102938
63738313	APEVDVQGPEWSLK		PREDICTED: similar to AHNAK [Mus musculus]	1554.7797	28.63	0
21313640	APEVSQYIYQVYDSILK		adaptor-related protein complex 2, beta 1 subunit [Mus musculus]	2016.0332	34.04	1.660042598
6681157	APILIATDVASR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1226.7085	52.47	0.771354945
40068493	APILIATDVASR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1226.7085	52.47	0.771354945
63540743	APLQVAVLGPTGVAEPVEVR		PREDICTED: filamin C, gamma [Mus musculus]	2002.1323	82.49	0.682065414
31560689	APLVLEQGLR		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	1095.6509	52.19	0.321454051
6996911	APNSPDVLEIEFK		argininosuccinate synthetase [Mus musculus]	1458.7468	45.5	0.353058175
33859506	APQVSTPTLVEAAR		albumin 1 [Mus musculus]	1439.7861	93.81	0.083130806
31981826	APSSSSVGISEWLDQK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1690.8301	83.19	0
33563250	APSYGAGELLDFSLADAVNQEFLATR		desmin [Mus musculus]	2755.3621	111.41	0.097192688
7106435	APTAQVESFR		tenascin C [Mus musculus]	1105.5629	40.29	0
13384888	APTNLPDPAR		hypothetical protein LOC66289 [Mus musculus]	1051.5559	45.66	0
6671664	APVPTGEVYFADSFDR		calnexin [Mus musculus]	1770.835	77.98	0.379033428
31981647	APWELLELR		tyrosyl-tRNA synthetase [Mus musculus]	1126.6279	34.85	0.285739088
6679515	AQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLR		polypyrimidine tract binding protein 1 [Mus musculus]	3680.844	24.26	0.371779994
41322904	AQAEAQQPVFNTLR		plectin 1 isoform 1 [Mus musculus]	1572.8121	45.14	0.846552535
41322904	AQAELEAQELQR		plectin 1 isoform 1 [Mus musculus]	1385.7037	49.87	0.694547553
18079351	AQALAIETEAELER		major vault protein [Mus musculus]	1543.7844	35.4	0.294211031
31126968	AQAPASPYNDYEGR		retinoic acid induced 3 [Mus musculus]	1538.6909	62.91	0.399366515
31982724	AQDASLNVPER		MYB binding protein (P160) 1a [Mus musculus]	1199.604	35.66	0
63530525	AQDGSSPLSLQDLIEK		PREDICTED: SEC31-like 1 [Mus musculus]	1700.8538	44.68	0

31982520	AQDTAELFFEDVR		acetyl-Coenzyme A dehydrogenase, long-chain [Mus musculus]	1540.7275	93.82	0.481731256
51828444	AQEAAAEEPPPAVTPAASVSALDLGEQR		PREDICTED: proline-rich polypeptide 6 [Mus musculus]	2775.3792	124.26	0.203277336
9789985	AQEIDQTNDFK		isovaleryl coenzyme A dehydrogenase [Mus musculus]	1308.6012	25.86	0
6754256	AQFEGIVTDLIK		heat shock protein 9A [Mus musculus]	1333.7333	81.96	0
29789289	AQFGQPEILLGTIPGAGGTQR		enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Mus musculus]	2111.1272	81.11	0.287380955
63556652	AQGDPHYTTFDGR		PREDICTED: similar to Fc fragment of IgG binding protein [Mus musculus]	1464.6484	38.9	0
6679583	AQIWDTAGQER		RAB11B, member RAS oncogene family [Mus musculus]	1274.6165	65.39	0.570394158
31560313	AQLFALTGVQPAR		ubiquitin specific protease 14 [Mus musculus]	1371.7755	54.92	0
13385998	AQLLQPTLEINPR		TNF receptor-associated protein 1 [Mus musculus]	1492.8522	37.38	0
37537522	AQNIGLENLLEVITSTVEETEK		epiplakin 1 [Mus musculus]	2430.2593	27.7	0
50355692	AQNTWGCGSSLR		lamin A isoform A [Mus musculus]	1279.5897	57.23	0.319439774
6679809	AQQVAVQEQEIAR		flotillin 1 [Mus musculus]	1469.7727	48.79	0
21536220	AQSELSGAADEAAR		ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit precursor [Mus musculus]	1375.6479	73.22	0.252118764
33468857	AQVAQPGGDTIFGK		histidine triad nucleotide binding protein 1 [Mus musculus]	1388.7113	68.08	0
41322904	AQVEQELTTLR		plectin 1 isoform 1 [Mus musculus]	1287.6873	31.57	0
29244176	AQYEDIANR		hypothetical protein 4732456N10 [Mus musculus]	1079.5144	26.75	0.4259699
13624315	AQYEDIANR		keratin complex 2, basic, gene 8 [Mus musculus]	1079.5144	26.75	0.4259699
29789317	AQYEDIANR		keratinocyte associated protein 1 [Mus musculus]	1079.5144	26.75	0.4259699
63565108	AQYEDIANR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1079.5144	26.75	0.4259699
6754036	ASAELALGENNEVLK		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1557.7871	29.83	6.013045919
6754556	ASAPATPLSPTR		lamin B1 [Mus musculus]	1168.6357	53.54	0.308752991
34328206	ASEDFVDPWTVR		tryptophanyl-tRNA synthetase [Mus musculus]	1421.6697	48.46	0.552704125
39930409	ASELVSDKR		Rab6 interacting protein 1 [Mus musculus]	1004.5176	26.95	0.179616267
63540743	ASGPGLNASGIPASLPVEFTIDAR		PREDICTED: filamin C, gamma [Mus musculus]	2340.2144	22.82	2.815373777
63746482	ASGPGLNTTGVPASLPVEFTIDAK		PREDICTED: filamin, alpha [Mus musculus]	2342.2283	72.14	0
9845257	ASGPPVSELITK		histone 1, H1c [Mus musculus]	1198.6655	83.95	0.330550228
34328365	ASGPPVSELITK		histone 1, H1d [Mus musculus]	1198.6655	83.95	0.330550228
6753076	ASGYLELSNWPEVAPDPSVR		adaptor-related protein complex 3, beta 1 subunit [Mus musculus]	2187.0701	42.81	0
13624315	ASLEAAIADAEQR		keratin complex 2, basic, gene 8 [Mus musculus]	1344.6788	95.67	0.45324242
6679931	ASLGTLNTLADVPDDEVQGR		UDP-N-acetyl-alpha-D-galactosamine: (N-acetylneuraminyl)-galactosyl-N- acetylglucosaminylpolypeptid	2071.0295	53.31	0.190184531
23956084	ASNTSEVYFDGVK		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	1416.666	30.21	0.764141292
21746169	ASQEFLEDGDPDGLFSR		zinc finger CCCH type, antiviral 1 [Mus musculus]	1882.8406	26.08	0
31543605	ASSFVLALEPELESR		ribophorin I [Mus musculus]	1647.8612	68.62	0.486024638
38198665	ASSSILINEAEPTTNIQIR		p47 protein [Mus musculus]	2057.0859	48.9	0.542466639
31982522	ASSTANLIFEDCR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1426.6661	62.89	0.383433736
21313526	ASTPDWPSQDPQPGLQR		hypothetical protein LOC78906 [Mus musculus]	1879.8959	55.88	0.792081792

GI #	Sequence	Modifications	Protien Name	M/z	Highest Mascot score	Average Ratio (15N:14N), non-Log-transformed
13385938	ASVASDPESPPGGNEPAAASGQR		RNA (guanine-7-) methyltransferase [Mus musculus]	2151.9941	32.63	1.016684863
6678499	ASVGFGGSCFQK		UDP-glucose dehydrogenase [Mus musculus]	1187.5546	53.91	0
8567336	ASVTALIESVNGK		chloride channel calcium activated 3 [Mus musculus]	1288.7048	101.82	1.085283839
13384736	ASVVTLPVYLNFTR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1579.8848	39.46	0.313531773
12963591	ASYGVEDPEYAVTQLAQTTMR		stomatin-like protein 2 [Mus musculus]	2330.0959	51.99	0.986585588
6681143	ASYSAVSLYGNPVR		decorin [Mus musculus]	1483.7496	42.14	0
9845283	ASYVAPLTAQPATYR		RNA binding motif protein 14 [Mus musculus]	1608.8392	53.15	0.423010479
50080209	ATAGDTHLGGEDFDNR		heat shock protein 1A [Mus musculus]	1675.7378	90.88	0
7305163	ATAGDTHLGGEDFDNR		heat shock protein 1-like [Mus musculus]	1675.7378	90.88	0
6754976	ATAVMPDGQFK		peroxiredoxin 1 [Mus musculus]	1164.5659	64.93	0
6754976	ATAVMPDGQFK	Oxidation (M)	peroxiredoxin 1 [Mus musculus]	1180.5638	31.3	0
6755114	ATDLLLDDSLVSLFGNR		peroxiredoxin 5 precursor [Mus musculus]	1848.9685	28.59	0.741020194
6679567	ATEMVEVGPEDDEVGAER		polymerase I and transcript release factor [Mus musculus]	1932.8521	101.75	0
6679567	ATEMVEVGPEDDEVGAER	Oxidation (M)	polymerase I and transcript release factor [Mus musculus]	1948.8392	75.04	0.156540369
63602733	ATENDIANFFSPLNPIR		PREDICTED: similar to heterogeneous nuclear ribonucleoprotein H3 isoform a [Mus musculus]	1918.9646	45.82	0.27358102
9845253	ATENDIYNFFSPLNPMR		heterogeneous nuclear ribonucleoprotein H2 [Mus musculus]	2028.9524	48.21	0
19527048	ATENDIYNFFSPLNPVR		heterogeneous nuclear ribonucleoprotein F [Mus musculus]	1996.981	79.63	0.515467471
10946928	ATENDIYNFFSPLNPVR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1996.981	79.63	0.515467471
6677871	ATEVPLSWESFNK		scinderin [Mus musculus]	1507.7402	36.21	0
25020120	ATGDPWLTDGSYLDGSGFAR		PREDICTED: laminin, alpha 5 [Mus musculus]	2085.9561	27.58	0.436226721
55741703	ATGVLLYDLVSR		glutaminyl-tRNA synthetase [Mus musculus]	1306.7371	43.26	0.967302001
7305295	ATLQAEQLSNELATER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1773.9043	90.58	0.118911428

6753492	ATPEPSGTPSSDTVSR		coronin, actin binding protein 1A [Mus musculus]	1588.7482	77.6	1.847325656
21450625	ATQALVLAPTR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1140.6744	32.07	0.418627052
21728376	ATSNVFAMFDQSQIQEFK		myosin regulatory light chain-like [Mus musculus]	2090.9885	50.41	0
63492583	ATSNVFAMFDQSQIQEFK		PREDICTED: myosin regulatory light polypeptide 9 [Mus musculus]	2090.9885	50.41	0
33859650	ATYSTNSPVWEEAFR		membrane bound C2 domain containing protein [Mus musculus]	1757.8159	35.98	0
6755809	AVAEQIPLLVQGVR		talin 1 [Mus musculus]	1492.8833	35.17	0.217363025
6753320	AVAQALEVIPR		chaperonin subunit 3 (gamma) [Mus musculus]	1166.6888	36.19	0
22267442	AVAQGNLSSADVQAAK		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1529.7911	120.83	1.093950936
6755566	AVDPDSPAEASGLR		solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1 [Mus musculus]	1384.6688	24.87	0
6680748	AVDSLVPIGR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1026.5908	61.76	0.321238228
25020120	AVEASNAYSSILQAVQAAEDAAGQALR		PREDICTED: laminin, alpha 5 [Mus musculus]	2704.3462	41.56	0
34610207	AVFDETYPDPVR		alanyl-tRNA synthetase [Mus musculus]	1408.6779	34.02	0.61007611
38090591	AVFPIYLDDVYENAVDAAR		PREDICTED: RIKEN cDNA A230046K03 gene [Mus musculus]	2141.0593	23.52	0
18079351	AVFPQNGLVVSSVDVQSVEPVDQR		major vault protein [Mus musculus]	2569.3279	78.13	0.427824803
21450277	AVFQANQENLPILK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1584.8708	95.47	0.389866782
6678467	AVFVDLEPTVIDEIR		tubulin, alpha 4 [Mus musculus]	1715.9208	105.84	0.505735179
34740335	AVFVDLEPTVIDEVR		tubulin, alpha 2 [Mus musculus]	1701.9098	109	0.489381878
6678469	AVFVDLEPTVIDEVR		tubulin, alpha 6 [Mus musculus]	1701.9098	109	0.489381878
28916673	AVITSLLDQIPEMFADTR		SEC24 related gene family, member C [Mus musculus]	2020.0509	28.38	0
34328204	AVLGEVALYSGAR		valyl-tRNA synthetase 2 [Mus musculus]	1305.7161	27.85	0.91877102
30424996	AVLPVAESFGFADEIR		elongation factor Tu GTP binding domain containing 1 [Mus musculus]	1720.8854	34.8	0
22165384	AVLVDLEPGTMDSVR		tubulin, beta, 2 [Mus musculus]	1601.8167	68.31	0.847210127
31981939	AVLVDLEPGTMDSVR		tubulin, beta 4 [Mus musculus]	1601.8167	68.31	0.847210127
6755354	AVPQLQGYLR		ribosomal protein L6 [Mus musculus]	1144.6487	39.11	0.524149702
16716471	AVPVSNIAPAAVGR		hypothetical protein LOC94184 [Mus musculus]	1321.7535	44.37	0.313321698
7305085	AVQTLQMELQQIMK		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1660.8705	60.18	0
6756037	AVTELNEPLSNEDR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide [Mus muscul	1586.7637	44.76	0.47668472
6756039	AVTEQGAELSNEER		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Mus musc	1532.7205	81.08	0
37537522	AVTGYTDPYTGDQISLFQAMQR		epiplakin 1 [Mus musculus]	2462.1768	36.24	0.156072837
7305173	AVTQSAEITIPVTFEAR		heat shock protein 1 [Mus musculus]	1832.9706	49.5	0
31543605	AVTSEIAVLQSR		ribophorin I [Mus musculus]	1273.7086	71.52	0.341967718
22122387	AVVLPISLATTFK		cystathionase [Mus musculus]	1359.8207	73.95	6.043070293
6680982	AVYQGPGSSPVK		catechol-O-methyltransferase [Mus musculus]	1189.6091	28.08	0.569179838
14149750	AWDDFFPGSDR		ADP-ribosylation factor-like 6 interacting protein 5 [Mus musculus]	1312.5654	41.66	0.336811501
63746482	AWGPGLEGGIVGK		PREDICTED: filamin, alpha [Mus musculus]	1240.6615	75.2	0
7106381	AYAQQLTEWAR		protein kinase C and casein kinase substrate in neurons 2 [Mus musculus]	1336.665	42.45	0.88334529
58037109	AYDLVVDWPVTLVR		NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 [Mus musculus]	1645.8939	25.9	0.332504273
6678419	AYDYLIQNTSFANR		tripeptidyl peptidase II [Mus musculus]	1675.8167	47.67	0
6753138	AYGENIGYSEK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1230.5604	80.23	0.276749972
6753138	AYGENIGYSEKDR		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1501.6952	68.07	0.17847243
63746482	AYGPGIEPTGNMVK		PREDICTED: filamin, alpha [Mus musculus]	1433.7079	44.48	0.367421116
63746482	AYGPGIEPTGNMVK	Oxidation (M)	PREDICTED: filamin, alpha [Mus musculus]	1449.6927	43.77	0
33859482	AYLPVNESFGFTADLR		eukaryotic translation elongation factor 2 [Mus musculus]	1799.8972	94	0.444809226
26024211	CIHQSLEDNNR	2 Deamidation (NQ)	constitutive photomorphogenic protein 1 [Mus musculus]	1330.5828	27.98	0
63489795	CQNELLNEQTQLQEDISK	5 Deamidation (NQ)	PREDICTED: centrosomal protein 1 [Mus musculus]	2137.9163	22.84	0
15042957	DAADQNFDYMFK		RAB3D, member RAS oncogene family [Mus musculus]	1464.6195	50.29	0
6679491	DADSIHQYLLQR		aminopeptidase puromycin sensitive [Mus musculus]	1458.7272	35.54	0
6755478	DAEDAMDAMDGAVLDGR		splicing factor, arginine/serine-rich 2 [Mus musculus]	1751.7332	132.5	0
6753484	DAEEVISQTIDTIVDMIK	Oxidation (M)	procollagen, type VI, alpha 1 [Mus musculus]	2036.0209	25.4	0
6754482	DAETTLTELR		keratin complex 1, acidic, gene 18 [Mus musculus]	1148.5708	58.26	0.211870294
6753066	DAFCVFEQNQGLPLR		amine oxidase, copper containing 3 [Mus musculus]	1736.8453	22.16	0
31982526	DAFDTLFDHAPDK		parvin, alpha [Mus musculus]	1491.6792	30.58	0
21450277	DAFQNAYLELGGLGER		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1752.8579	79.38	0.266927893
46358373	DAFVILVENALR		CDW92 antigen [Mus musculus]	1359.7623	25.73	0.31497699
6754036	DAGMQLQGYR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1138.5309	26.86	0
31981690	DAGTIAGLNVLR		heat shock protein 8 [Mus musculus]	1199.6786	64.58	0.386988909
63664182	DAGTIAGLNVLR		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1199.6786	64.58	0.386988909
31981722	DAGTIAGLNVMR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1217.629	65.28	0.785271696
50080209	DAGVIAGLNVLR		heat shock protein 1A [Mus musculus]	1197.694	35.59	0.25341389
7305163	DAGVIAGLNVLR		heat shock protein 1-like [Mus musculus]	1197.694	35.59	0.25341389

30424898	DALVNAVIDSLSAYR		SEC24 related gene family, member A [Mus musculus]	1606.8446	38.99	1.853674387
31542602	DANLYISGLPR		ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) [Mus musculus]	1218.6337	52.32	0
51827543	DAPNDASYDAVR		PREDICTED: GCN1 general control of amino-acid synthesis 1-like 1 [Mus musculus]	1293.5728	30.19	0.770125274
18079351	DAQSSVLFDVTGQVR		major vault protein [Mus musculus]	1621.8135	100.01	0.76142689
21592285	DAQVQNAQCVLR		keratin 20 [Mus musculus]	1344.6715	37.74	0.502911819
9790019	DAQWVGFITR		N-acylsphingosine amidohydrolase (acid ceramidase) 1 [Mus musculus]	1192.6177	33.52	0.461405825
30348966	DASVAEAWLLGQEPYLSSR		spectrin beta 2 isoform 1 [Mus musculus]	2092.0376	63.97	0.358955462
7106421	DASVAEAWLLGQEPYLSSR		spectrin beta 2 isoform 2 [Mus musculus]	2092.0376	63.97	0.358955462
6679687	DASVVGFFR		glucose regulated protein [Mus musculus]	997.5143	58.63	0.75340922
51770896	DATNVGDEGGFAPNILENK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1960.9247	85.3	0.501165359
6679651	DATNVGDEGGFAPNILENNEALELLK		enolase 3, beta muscle [Mus musculus]	2743.3494	62.5	1.156780855
31982273	DATSLNQAALYR		hydroxysteroid (17-beta) dehydrogenase 4 [Mus musculus]	1322.6747	33.44	3.718866173
31542333	DAVIYPILVEFTR		hypoxia up-regulated 1 [Mus musculus]	1535.8544	76.52	0.429473961
6680716	DAVLLVFANK		ADP-ribosylation factor 1 [Mus musculus]	1089.6287	57.85	0.368687983
6680722	DAVLLVFANK		ADP-ribosylation factor 5 [Mus musculus]	1089.6287	57.85	0.368687983
31981562	DAVLNAWAEDVDLR		pyruvate kinase 3 [Mus musculus]	1586.7831	94.13	0.448997295
6755204	DAYSGGAVNLYHVR		proteasome (prosome, macropain) subunit, beta type 5 [Mus musculus]	1521.744	40.21	0.339537653
7242205	DCPDNAEEYER		cytoplasmic FMR1 interacting protein 1 [Mus musculus]	1340.5117	26.51	0
6679291	DCVGPEVENACANPAAGTVILLENLR		phosphoglycerate kinase 1 [Mus musculus]	2668.3081	54.93	0.294650145
56699423	DDFLGQVDVPLYPLPTENPR		neural precursor cell expressed, developmentally down-regulated gene 4 [Mus musculus]	2285.1455	81.31	0.674658345
6680027	DDGSWEVIEGYR		glutamate dehydrogenase 1 [Mus musculus]	1425.6316	71.8	0.332636745
63738313	DDGVFVQEVMQNSPAAR		PREDICTED: similar to AHNAK [Mus musculus]	1862.8665	30.17	0
31982122	DDLIASILSEVTPTPLEELR		phospholipase C, beta 3 [Mus musculus]	2211.1772	62.1	0.375687554
6754036	DDNGKPYVLPSVR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1459.7515	56.08	0.290207302
33859506	DDNPSLPPFERPEAEAMCTSFK		albumin 1 [Mus musculus]	2481.1072	37.64	0.043802017
51831125	DDPAPLGTASEPTLQK		PREDICTED: similar to extensin-like protein [Mus musculus]	1639.8459	25.64	0
41322904	DDPSGQMLLLLSDAR		plectin 1 isoform 1 [Mus musculus]	1630.8141	37.49	1.108678316
19072792	DDTESLEIFQNEVAR		thioredoxin domain containing 4 [Mus musculus]	1765.8326	31.91	0
6681027	DDTYQSYSSPSPR		deleted in malignant brain tumors 1 [Mus musculus]	1502.6465	53.52	0
63622229	DDVAQEPWLVPGSNDLLLEVGPR		PREDICTED: phosphoribosylformylglycinamidine synthase (FGAR amidotransferase) [Mus musculus]	2519.2722	44.2	1.179737152
6671664	DEEEEEEKLEEK		calnexin [Mus musculus]	1535.6593	48.55	0
63487108	DEGSWQDGDSSQEITR		PREDICTED: similar to mKIAA1741 protein [Mus musculus]	1809.7708	45.12	0.648034132
14149647	DELILEGNDIELVSNSAALIQQATTVK		ribosomal protein L9 [Mus musculus]	2884.5244	39.89	1.00940961
38090710	DENGALIR	Deamidation (NQ)	PREDICTED: protein phosphatase 1, regulatory (inhibitor) subunit 12A [Mus musculus]	888.4576	38.8	0
21389320	DESSDNFGSFFLR		leucine-rich PPR motif-containing protein [Mus musculus]	1520.6755	37.37	0.460793773
31981100	DESSPYAAMLAAQDVAQR		ribosomal protein S14 [Mus musculus]	1922.8953	91.95	0.528327212
6680047	DETNYGIPQR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1192.5723	46.93	0.444869835
7305031	DEVDAAESTPTDRR		erythrocyte protein band 4.1-like 3 [Mus musculus]	1561.7007	42.2	0
22203747	DFDSLAQPSFFDR		procollagen, type VI, alpha 2 [Mus musculus]	1544.7076	43.3	0
8393150	DFEQPLAISR		carboxyl terminal LIM domain protein 1 [Mus musculus]	1175.6018	47.97	0.587323566
7305075	DFFQNFGNVVELR		ras-GTPase-activating protein SH3-domain binding protein [Mus musculus]	1584.7856	29.55	0.429595175
21704100	DFIYVSQDPK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1211.592	60.75	0
22094075	DFLAGGVAAAISK		solute carrier family 25, member 5 [Mus musculus]	1219.6616	101.87	0
27734182	DFLAGLAYR		tryptophan hydroxylase 2 [Mus musculus]	1025.5504	26.66	0
31981282	DFLLQQTMLR		glyoxalase 1 [Mus musculus]	1264.6743	34.87	0
6755142	DFMIQGGDFTR		peptidylprolyl isomerase B [Mus musculus]	1286.5845	70.83	0
24418919	DFNVGDYIEAVLDR		brain glycogen phosphorylase [Mus musculus]	1625.7837	65.06	0.247698896
42475998	DFNVPLSISR		PDZ and LIM domain 7 [Mus musculus]	1147.6118	49.4	0
6753240	DFPEYTFAIADEEDYATEVK		calcium binding protein, intestinal [Mus musculus]	2353.0537	44.93	0.452026098
31981657	DFPIANGDR		carbonic anhydrase 2 [Mus musculus]	1004.4816	35.14	0.232090838
58037117	DFPLTGYVELR		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Mus musculus]	1309.6837	57.73	0
22129770	DFPQYFAVVSR		ankyrin 3, epithelial isoform b [Mus musculus]	1328.6616	31.59	0
20137006	DFSALESQLQDTQELLQEENR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2493.1729	149.94	0.615695915
29126205	DFSATDLTEFAAR		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1443.6796	78.7	0.236114258
6679237	DFTATFGPLDSLNTR		pyruvate carboxylase [Mus musculus]	1654.8116	51.36	0
6755714	DFTDSQLQEGK		transgelin [Mus musculus]	1267.5797	69.43	0.105989467
10181184	DFTPSGIAGAFR		ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 [Mus musculus]	1238.6166	63.48	0.308259273
21450625	DFTVSAMHGDMDQK		eukaryotic translation initiation factor 4A1 [Mus musculus]	1581.6803	51.03	0.636103063
63737068	DFVDYFLIQR		PREDICTED: similar to Cyp2c40 protein [Mus musculus]	1315.6732	29.79	0
24429590	DFVNYLVR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1025.5464	43.27	0.4068558

63476037	DFVTNLVNSLDVGSDNIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1977.9904	43.96	1.388671429
21704020	DFYMTDSISR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	1234.543	41.8	0
6753438	DFYNPLVPEAQK		claudin 3 [Mus musculus]	1420.7023	32.09	0.932616074
6681233	DGAFDFFPVLR		solute carrier family 26 (sulfate transporter), member 2 [Mus musculus]	1283.645	35.02	0.141113301
30911099	DGAWGAFR		fatty acid synthase [Mus musculus]	879.4144	27.51	0.494943142
58037267	DGELPVEDDIDLSDVELDDLEKDEL		protein disulfide isomerase-associated 6 [Mus musculus]	2830.2913	79.66	0.328893461
27151748	DGENYVVLLDTTLPR		nodal modulator 1 [Mus musculus]	1704.8802	24.12	0
33563250	DGEVVSEATQQQHEVL		desmin [Mus musculus]	1768.8365	100.29	0
22164798	DGFNPAHVEAGLYGSR		selenium binding protein 1 [Mus musculus]	1689.7979	105.63	0.231591094
31560611	DGIILCEFINK		calponin 1 [Mus musculus]	1264.6602	78.02	0.054501269
26986607	DGIQLSEYLPEVTDLLR		nucleoporin 133 [Mus musculus]	1961.0199	28.44	0
21450129	DGLTDVYNK		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	1024.483	23.22	0.467526037
55742711	DGMLDDEEFALASHLIEAK		EH-domain containing 2 [Mus musculus]	2104.0012	30.1	0
21450277	DGPNALTPPPTTPEWVK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1819.9253	28.57	0
6680047	DGQAMLWDLNEGK		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1476.6737	58.81	0.800760068
6680047	DGQAMLWDLNEGK	Oxidation (M)	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1492.651	42.22	0.436409347
27229048	DGQVIGIGAGQQSR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1385.7065	74.23	0.394524588
31982755	DGQVINETSQHHDDLE		vimentin [Mus musculus]	1836.7998	64.02	0.32581456
6679891	DGSDYEGWCWPGSASYPDFTNPR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	2607.0581	80.15	0.383542913
45597447	DGVANVSIEDR		superoxide dismutase 1, soluble [Mus musculus]	1174.5734	65.72	0.30666931
27754099	DGWSLWYAEYR		eukaryotic translation elongation factor 1 gamma [Mus musculus]	1445.651	22.73	0.476390485
18079339	DGYAQILR		aconitase 2, mitochondrial [Mus musculus]	935.4954	38.81	0.29442778
34328400	DGYDYDGYR		splicing factor, arginine/serine-rich 1 (ASF/SF2) [Mus musculus]	1123.4363	42.14	0.395391572
6680117	DGYMPSQYNSQNWEAR		glutathione synthetase [Mus musculus]	1945.8208	58.34	0.357186381
6671553	DIANENEAQFQIR		adaptor protein complex AP-1, beta 1 subunit [Mus musculus]	1547.751	25.83	0
22203747	DIANSPHELYR		procollagen, type VI, alpha 2 [Mus musculus]	1314.6411	40.83	0.259819904
6756041	DICNDVLSLLEK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	1361.699	72.79	0.477707817
40018610	DIDAFWLQR		U5 snRNP-specific protein, 200 kDa [Mus musculus]	1163.592	45.31	0.460263201
46575903	DIDIEDLEELDPDFIMAK		eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus musculus]	2121.0017	25.22	1.000715084
51772556	DIFAMDDKSENEPIENEAAR		PREDICTED: similar to Succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	2294.0271	105.47	0.267558514
58037564	DIFPIAFPR		protease, serine, 15 [Mus musculus]	1075.5959	44.93	0.336146701
27370516	DIFQEIFDK		isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	1154.5839	47.52	0.725291947
40254595	DIGAIAQVHAENGDIIAEEQQR		dihydropyrimidinase-like 2 [Mus musculus]	2377.177	91.8	0.202471293
6679058	DIGLPNGLTFDPFSK		nidogen 2 [Mus musculus]	1620.818	35.59	0
58037564	DIIALNPLYR		protease, serine, 15 [Mus musculus]	1187.6813	40.95	1.178575172
6753074	DIILPFR		adaptor protein complex AP-2, mu1 [Mus musculus]	873.5259	24.42	0.307137405
6996913	DIISDTSGDFR		annexin A2 [Mus musculus]	1225.5757	75.88	0.376765496
63556656	DILCQALAAYAAACQAAGIK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1964.991	67.38	0
7305445	DILIQYDR		ribosomal protein S16 [Mus musculus]	1035.5439	44.29	0.74808208
19745150	DILLRPELEELR		diaphorase 1 [Mus musculus]	1495.8467	23.49	0
6671549	DINAYNGETPTEK	Deamidation (NQ)	peroxiredoxin 6 [Mus musculus]	1452.6522	70.91	0
6753374	DINDNAPVFNPSTYQGQVPENEVNAR		cadherin 1 [Mus musculus]	2888.342	132.9	0.311697353
9790073	DINDNRPTFLQSK		cadherin 17 [Mus musculus]	1547.7887	23.71	0
18079339	DINQEVYNFLATAGAK		aconitase 2, mitochondrial [Mus musculus]	1753.8743	125.84	0.230338274
24429590	DINTDFLLVVLR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1417.8059	54.79	0.379365553
31543605	DIPAYSQDTFK		ribophorin I [Mus musculus]	1284.6146	41.91	0
7305447	DISEASVFDAYVLPK		ribosomal protein S26 [Mus musculus]	1653.8351	53.69	0
13385998	DISEFQHEEFYR		TNF receptor-associated protein 1 [Mus musculus]	1599.7101	58.47	0
31981748	DISSAVQANPALTELSLR		ribonuclease/angiogenin inhibitor 1 [Mus musculus]	1885.0054	45.96	0.429273917
6755863	DISTNYYASQK		tumor rejection antigen gp96 [Mus musculus]	1289.5997	76.35	0.419425674
23956222	DITYFIQQLLR		ARP3 actin-related protein 3 homolog [Mus musculus]	1409.7849	77.79	0.591684194
6755787	DIVENYFMR		tripartite motif protein 28 [Mus musculus]	1186.5574	27.79	0.591753064
63476037	DIVFLVDGSSSLGPSNFNAIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2208.1262	87.85	0
36031132	DIVPGDIVEVAVGDKVPADIR		ATPase, Ca++ transporting, fast twitch 1 [Mus musculus]	2177.1799	101.63	0.315715732
27804325	DIWVQEPESK		monoamine oxidase A [Mus musculus]	1230.597	34.3	0.128655099
63664138	DIYFLPFQDQLK		PREDICTED: hypothetical protein LOC219189 [Mus musculus]	1526.7968	27.48	0
38348476	DKEPVFAVTGMPENVDR	Deamidation (NQ); Oxidation (M)	ring finger (C3HC4 type) and KH domain containing 1 [Mus musculus]	1920.9211	30.29	0.535542826
19527026	DKLDGNELDLSLSDLNEVPVK		hypothetical protein LOC98238 [Mus musculus]	2313.1484	37.21	0
6754524	DLADELALVDVMEDK		lactate dehydrogenase 1, A chain [Mus musculus]	1675.8073	90.9	0.717539236
6754524	DLADELALVDVMEDK	Oxidation (M)	lactate dehydrogenase 1, A chain [Mus musculus]	1691.7854	64.94	0.200849073

63746482	DLAEDAPWK		PREDICTED: filamin, alpha [Mus musculus]	1044.4952	47.37	0
63660294	DLAEDAPWK		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	1044.4952	47.37	0
51711855	DLAEDAPWK		PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like prot	1044.4952	47.37	0
6671549	DLAILLGMLDPVEK		peroxiredoxin 6 [Mus musculus]	1526.8492	80.06	0
6671549	DLAILLGMLDPVEK	Oxidation (M)	peroxiredoxin 6 [Mus musculus]	1542.8387	83.26	0.101569758
30725863	DLANGNITWADVEAR		glycyl-tRNA synthetase [Mus musculus]	1644.7921	66.88	0.615816483
18079351	DLAVAGPEMQVK		major vault protein [Mus musculus]	1257.6415	36.71	0
30348966	DLDDFQSWLSR		spectrin beta 2 isoform 1 [Mus musculus]	1381.6445	46.93	0.311780129
7106421	DLDDFQSWLSR		spectrin beta 2 isoform 2 [Mus musculus]	1381.6445	46.93	0.311780129
27370092	DLDKPFLLPVESVYSIPGR		Tu translation elongation factor, mitochondrial [Mus musculus]	2145.1575	82.11	0
6755809	DLDQASLAAVSQQLAPR		talin 1 [Mus musculus]	1782.9359	99.09	0
45598381	DLDSLHSFVLR		thioredoxin domain containing 5 [Mus musculus]	1301.6841	44.71	0
31980726	DLEALMLDR		phosphoglucomutase 2 [Mus musculus]	1075.5502	29.32	0
6753658	DLEDKEGEIQAGAK		dynein, cytoplasmic, intermediate chain 2 [Mus musculus]	1502.7345	80.11	0
6680850	DLEIMQILTR		caspase 7 [Mus musculus]	1231.6758	32.44	0
6753762	DLELLYPFK		epoxide hydrolase 1, microsomal [Mus musculus]	1137.6176	41.08	0
10946574	DLFDPIIEER		creatine kinase, brain [Mus musculus]	1246.6356	65.63	0.150129515
6671762	DLFDPIIQDR		creatine kinase, muscle [Mus musculus]	1231.6349	23.22	0
13242328	DLFEDELVPLFEK		NS1-associated protein 1 [Mus musculus]	1593.802	60.05	0
6679687	DLFSDGHSEFLK		glucose regulated protein [Mus musculus]	1394.6553	57.58	0.284572388
13384652	DLGADYVLTEEELR		nuclear receptor-binding factor 1 [Mus musculus]	1622.7939	31.06	0
25020120	DLGAQGAVAEAELAEAQR		PREDICTED: laminin, alpha 5 [Mus musculus]	1798.8844	45.6	0
19111162	DLGDEYGWK		transmembrane protein 9 superfamily member 3 [Mus musculus]	1082.4988	43.34	0
27532959	DLGEAALNEYLR		aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	1363.6853	73.67	0.523565737
20137006	DLGEELEALKTELEDTLDSTAAQQELR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	3017.4778	33.12	27.25473337
7305295	DLGEELEALKTELEDTLDSTATQQELR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	3047.4854	63.87	0.05412737
56119103	DLGTDSQIFISR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1351.6853	72.95	0.752192953
38198665	DLIHDQDEEEEEEEGQR		p47 protein [Mus musculus]	2099.8689	80.37	0.34459416
6753620	DLLDLLVEAK		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1128.6521	69.45	0
31981400	DLLFQALGR		phenylalanine-tRNA synthetase-like, beta subunit [Mus musculus]	1032.5917	46.65	0.261830691
63664138	DLLGQDVFLIGPPGPLR		PREDICTED: hypothetical protein LOC219189 [Mus musculus]	1807.0154	32.65	0.237370631
26024336	DLLHPSPEEEK		ribosomal protein S27 [Mus musculus]	1293.6274	26.24	0
59709449	DLLLDPAWEK		actinin alpha 2 [Mus musculus]	1199.6302	49.44	0.161782402
11230802	DLLLDPAWEK		actinin alpha 4 [Mus musculus]	1199.6302	49.44	0.161782402
6679687	DLLTAYYDVDYEK		glucose regulated protein [Mus musculus]	1607.7559	98.57	0
7657429	DLLTQPGDWTLFAPTNDAFK		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2250.1101	56.14	0.307406647
21312062	DLLVTGAYEITDQSGGAGGLR		transmembrane trafficking protein [Mus musculus]	2093.0503	48.12	0
9790163	DLLYFDGLR		plakophilin 3 [Mus musculus]	1111.5852	22.51	0
30348966	DLMLWMEDVIR		spectrin beta 2 isoform 1 [Mus musculus]	1420.701	22.7	0
7106421	DLMLWMEDVIR		spectrin beta 2 isoform 2 [Mus musculus]	1420.701	22.7	0
63489759	DLMSWINGIR		PREDICTED: spectrin alpha 2 [Mus musculus]	1204.6215	22.75	0
10946928	DLNYCFSGMSDHR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1544.6344	31.91	0.635889729
9845253	DLNYCFSGMSDHR		heterogeneous nuclear ribonucleoprotein H2 [Mus musculus]	1544.6344	31.91	0.635889729
63506134	DLNYCFSGMSDHR		PREDICTED: similar to Murine homolog of human ftp-3 [Mus musculus]	1544.6344	31.91	0.635889729
6681233	DLPEEAFGFPSELPLETQR		solute carrier family 26 (sulfate transporter), member 2 [Mus musculus]	2175.0632	104.06	0.160706905
31560438	DLPFETLDVDAR		mitochondrial ribosomal protein L39 [Mus musculus]	1390.686	39.55	2.513345378
47578123	DLQLVLPDYFPER		potassium channel tetramerisation domain containing 12 [Mus musculus]	1604.8334	77.65	0.602215068
6671622	DLQMVNISLR		B-cell receptor-associated protein 37 [Mus musculus]	1188.6401	39.53	0
6679299	DLQNVNITLR		prohibitin [Mus musculus]	1185.6533	55.76	0.359096136
6678726	DLSSHQLNEFLAQVLQK		leukotriene A4 hydrolase [Mus musculus]	1970.0215	48.39	0.484020902
18266680	DLTAVSNNAGVDNFGLGLLLR		3-oxoacid CoA transferase 1 [Mus musculus]	2159.1477	86.18	0.157883722
6671507	DLTDYLMK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	998.4867	58.83	0.186638331
6671509	DLTDYLMK		actin, beta, cytoplasmic [Mus musculus]	998.4867	58.83	0.186638331
30425250	DLTDYLMK		hypothetical protein LOC238880 [Mus musculus]	998.4867	58.83	0.186638331
63652452	DLTDYLMK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	998.4867	58.83	0.186638331
6671507	DLTDYLMK	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1014.479	42.02	0.489276281
6671509	DLTDYLMK	Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	1014.479	42.02	0.489276281
30425250	DLTDYLMK	Oxidation (M)	hypothetical protein LOC238880 [Mus musculus]	1014.479	42.02	0.489276281
63652452	DLTDYLMK	Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1014.479	42.02	0.489276281
63489759	DLTGVQNLR		PREDICTED: spectrin alpha 2 [Mus musculus]	1015.5463	35.42	0.508196409

58037465	DLTTAGAVTQCYR		Ribosomal protein L18A [Mus musculus]	1398.6687	108	0.614275524
33859686	DLTTGYDDSQPDKK		phosphoglucomutase 1 [Mus musculus]	1582.7241	26.37	0
34328286	DLVPDLSNFYAQYK		succinate dehydrogenase Ip subunit [Mus musculus]	1672.8071	44.3	0.210817604
29293809	DLVSSLTSGLLTIGDR		ATP citrate lyase [Mus musculus]	1646.901	110.05	0
6671507	DLYANNVLSGGTTMYPGIADR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2228.0745	152.91	0
6671507	DLYANNVLSGGTTMYPGIADR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2229.0715	108.68	0
6671507	DLYANNVLSGGTTMYPGIADR	Deamidation (NQ); Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2245.063	63.13	0
6671507	DLYANNVLSGGTTMYPGIADR	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2244.0632	44.22	0.086651063
6671509	DLYANTVLSGGTTMYPGIADR		actin, beta, cytoplasmic [Mus musculus]	2215.0857	108.07	0.616820626
63652452	DLYANTVLSGGTTMYPGIADR		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2215.0857	108.07	0.616820626
6671509	DLYANTVLSGGTTMYPGIADR	Deamidation (NQ)	actin, beta, cytoplasmic [Mus musculus]	2216.0479	74.86	0
63652452	DLYANTVLSGGTTMYPGIADR	Deamidation (NQ)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2216.0479	74.86	0
6671509	DLYANTVLSGGTTMYPGIADR	Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	2231.0754	68.64	0.756442869
63652452	DLYANTVLSGGTTMYPGIADR	Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2231.0754	68.64	0.756442869
29126205	DMDLIDVNEAFAPQFLSVQK		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	2280.1304	74.43	0
20137006	DMFQETMEAMR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1388.5658	32.15	0.638472024
6680836	DMHGDSEYNIMFGPDICGPGTK		calreticulin [Mus musculus]	2384.0085	107.93	0.373600138
6677799	DMIILPEMVGSMVGVYNGK		ribosomal protein S15 [Mus musculus]	2053.0198	74.48	0
6677799	DMIILPEMVGSMVGVYNGK	2 Oxidation (M)	ribosomal protein S15 [Mus musculus]	2085.0063	26.82	0
31560613	DMLEASILDTYLGK		chaperonin subunit 8 (theta) [Mus musculus]	1568.7792	38.03	0
6755626	DMLYQVLAAEEPSVR		sepiapterin reductase [Mus musculus]	1720.8572	32.46	0.551862017
19527028	DMNQFGEGEQAK		high density lipoprotein binding protein [Mus musculus]	1353.5804	39.37	0.86818138
21450277	DMTSEELDDILR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1436.6598	79.08	0
21450277	DMTSEELDDILR	Oxidation (M)	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1452.6427	47.49	0
8567336	DMVTQASPYLFEATGK		chloride channel calcium activated 3 [Mus musculus]	1757.8508	88.54	0
8567336	DNCVFVPDPHQNEK		chloride channel calcium activated 3 [Mus musculus]	1641.7303	79.63	0
6681219	DNFTAIPEGTNGVEER		dihydropyrimidinase-like 3 [Mus musculus]	1748.8158	70.37	3.842337675
40254595	DNFTLIPEGTNGTEER		dihydropyrimidinase-like 2 [Mus musculus]	1792.8203	55.28	0.18094436
63746482	DNGNGTYSCSYVPR		PREDICTED: filamin, alpha [Mus musculus]	1532.649	76.97	0.171905459
63746482	DNGNGTYSCSYVPR	Deamidation (NQ)	PREDICTED: filamin, alpha [Mus musculus]	1533.6532	60.42	0
31981722	DNHLLGTFDLTGIPPAPR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1934.0098	47.71	0.311290004
21361209	DNIQGITKPAIR		germinal histone H4 [Mus musculus]	1325.7526	87.17	0.224192357
31982755	DNLAEDIMR		vimentin [Mus musculus]	1076.505	46.81	0
30911099	DNLEFFLTNLGK		fatty acid synthase [Mus musculus]	1410.7246	41.72	0.600585422
33563250	DNLIDDLQR		desmin [Mus musculus]	1101.5533	56.14	0.1432097
29789080	DNNQFASASLDR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1337.6113	86.34	0.330017526
6753304	DNQSGSLLFIGR		serine (or cysteine) proteinase inhibitor, clade H, member 1 [Mus musculus]	1306.6736	76.54	0.433963172
23621467	DNTINLIHTFR		PREDICTED: actin related protein 2/3 complex, subunit 2 [Mus musculus]	1343.7034	34.32	2.314265239
34328278	DNVDDPTGNFR		lectin, mannose-binding 2 [Mus musculus]	1249.5461	60.11	0
31791057	DNVEGFNCER		laminin, gamma 1 [Mus musculus]	1182.4924	23.22	0
6679891	DPAEGNGAQPEATPGDGDKPEETQEK		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	2667.1626	52.85	0.65371883
6679891	DPAEGNGAQPEATPGDGDKPEETQEK	Deamidation (NQ)	alpha glucosidase 2 alpha neutral subunit [Mus musculus]	2668.1582	24.07	0
28916693	DPDQTDGPGLGYLSSHIANVER		gelsolin [Mus musculus]	2341.1042	41.9	0.58180148
6680502	DPGDVVPVGQR		integral membrane protein 2B [Mus musculus]	1138.5798	27.92	0
9055370	DPIVNVWYSVNGER		eukaryotic translation initiation factor 3, subunit 2 (beta) [Mus musculus]	1647.8145	27.35	1.334246844
31543942	DPNASPGDAGEQAIR		vinculin [Mus musculus]	1497.6973	76.11	0
31982437	DPQLVPILIDAAR		NAD(P) dependent steroid dehydrogenase-like [Mus musculus]	1420.8087	44.44	0.647469744
31980794	DPTSLLFPESELSIR		solute carrier family 39 (metal ion transporter), member 11 [Mus musculus]	1703.8815	32.22	0
63589703	DPVQLNLLYVQAR		PREDICTED: talin 2 [Mus musculus]	1528.8522	66.69	0
6755809	DPVQLNLLYVQAR		talin 1 [Mus musculus]	1528.8522	66.69	0
31560607	DPVTGIEYWIIK		cathepsin C preproprotein [Mus musculus]	1433.7784	35.95	0.835928145
51768600	DQAPSEAELER		PREDICTED: LIM domain only 7 [Mus musculus]	1244.5776	40.85	0.603205461
63481281	DQDVEPGAPSMGAK		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1401.6324	53.93	1.128639537
63481281	DQDVEPGAPSMGAK	Oxidation (M)	PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1417.6162	33.15	0.288029277
31980648	DQEGQDVLLFIDNIFR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1921.9673	91.75	0.321427718
63474405	DQEPGAFIIR		PREDICTED: tensin [Mus musculus]	1145.5968	36.15	0
31542143	DQFPEVYVPTVFENYVADIEVDGK		ras homolog gene family, member A [Mus musculus]	2773.3411	55.1	0
33620739	DQGTYEDYVEGLR		myosin, light polypeptide 6, alkali, smooth muscle and non-muscle [Mus musculus]	1544.6908	61.44	0.198131753
21450625	DQIYDIFQK		eukaryotic translation initiation factor 4A1 [Mus musculus]	1169.5851	52.14	0.989463265
6754524	DQLIVNLLK		lactate dehydrogenase 1, A chain [Mus musculus]	1055.6418	60.55	0.402026002

8392847	DQLQTFSEEHPVLLTEAPLNPR		ARP1 actin-related protein 1 homolog A [Mus musculus]	2534.2805	53.17	0.276491653
6754556	DQMQQQLSDYEQLLDVK		lamin B1 [Mus musculus]	2080.9978	57.36	0.79599065
6754556	DQMQQQLSDYEQLLDVK	Oxidation (M)	lamin B1 [Mus musculus]	2096.9863	60.7	0
6753824	DQPFTILYR		fibulin 5 [Mus musculus]	1152.6066	34.15	0.267463213
27370516	DQTNDQVTIDSALATQK		isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	1847.8972	81.34	0.290622864
6754254	DQVANSAFVER		heat shock protein 1, alpha [Mus musculus]	1235.6052	78.78	0.832932106
51771441	DQVANSAFVER		PREDICTED: similar to heat shock protein 1, alpha [Mus musculus]	1235.6052	78.78	0.832932106
63481281	DQVDSAVQELLQLK		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1585.8207	24.7	1.321453528
20330802	DQYELLCLDNTR		transferrin [Mus musculus]	1482.6924	26.85	0
31982122	DREDEEEDEEEEETTDPK		phospholipase C, beta 3 [Mus musculus]	2223.8608	44.16	0.799099468
23956222	DREVGIPPEQSLETAK		ARP3 actin-related protein 3 homolog [Mus musculus]	1768.9114	36.01	0
6678331	DSATISLDPEEEIQYPVK		transglutaminase 3, E polypeptide [Mus musculus]	2033.9894	125.71	0
6679058	DSGQFTDEFLPEQR		nidogen 2 [Mus musculus]	1668.7528	26.3	0
33859811	DSIFSNLIGQLDYK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1612.8207	112.7	0.314128587
33859811	DSIFSNLIGQLDYK	Deamidation (NQ)	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1613.8182	41.18	0
6753266	DSISLSPEQLAQLR		carbonic anhydrase 1 [Mus musculus]	1556.8298	77.67	0.898506884
6755040	DSLLQDGEFTMDLR		profilin 1 [Mus musculus]	1639.7432	43.64	0.523614495
6678682	DSNNLCLHFNPR		lectin, galactose binding, soluble 1 [Mus musculus]	1429.6688	63.77	0
28478945	DSPGETDAFGNSEGK		PREDICTED: glutaminase [Mus musculus]	1510.6344	33.04	0.335941634
41322904	DSQDAGGFGPEDR		plectin 1 isoform 1 [Mus musculus]	1350.561	45.87	0
28916693	DSQEEEKTEALTSAK		gelsolin [Mus musculus]	1665.7814	65.69	0.161771411
7305295	DSSITGELEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1078.533	43.02	0
9055338	DSTLIMQLLR		stratifin [Mus musculus]	1189.6642	56.65	0
31543974	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Mus muscu	1189.6642	56.65	0
31981925	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Mus mu	1189.6642	56.65	0
6756037	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide [Mus muscul	1189.6642	56.65	0
6756039	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Mus musc	1189.6642	56.65	0
6756041	DSTLIMQLLR		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	1189.6642	56.65	0
30794518	DSVLTWLLK		kinesin family member 13A [Mus musculus]	1074.6117	34.74	0.213384767
23821040	DSVLTWLLK		kinesin family member 1C [Mus musculus]	1074.6117	34.74	0.213384767
63664018	DSVLTWLLK		PREDICTED: kinesin family member 13B [Mus musculus]	1074.6117	34.74	0.213384767
63492438	DSVLTWLLK		PREDICTED: kinesin family member 16B [Mus musculus]	1074.6117	34.74	0.213384767
63492281	DSVLTWLLK		PREDICTED: similar to mKIAA1300 protein [Mus musculus]	1074.6117	34.74	0.213384767
12331400	DSYIEVLLPLGTDPELR		acyl-Coenzyme A thioesterase 3, mitochondrial [Mus musculus]	1930.0184	40.85	0
6671507	DSYVGDEAQSK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1198.5284	47.02	0.25246971
6671509	DSYVGDEAQSK		actin, beta, cytoplasmic [Mus musculus]	1198.5284	47.02	0.25246971
6753374	DTANWLEINPETGAIFTR		cadherin 1 [Mus musculus]	2048.0083	62.18	0.490244891
9790141	DTDIVDEAIYYFK		actin related protein 2/3 complex, subunit 3 [Mus musculus]	1591.7821	32.88	0.68216552
54261793	DTEGMDEIDLAEMELR		plasma membrane calcium ATPase 4 [Mus musculus]	1866.8384	56.58	0
51491845	DTELAEELLQWFLQEEK		clathrin, heavy polypeptide (Hc) [Mus musculus]	2121.0381	44.9	0.424372474
41322904	DTHDQLSEPSEVR		plectin 1 isoform 1 [Mus musculus]	1512.6941	76.83	0.384725381
9790067	DTNGENIAESLVAEGLATR		staphylococcal nuclease domain containing 1 [Mus musculus]	1959.9622	131.65	0.486885417
6755142	DTNGSQFFITTVK		peptidylprolyl isomerase B [Mus musculus]	1457.7203	78.58	0
6680163	DTPGFIVNR		L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1018.5327	50.94	0
42476274	DTPTQEDWLVSVLPEGSR		X-prolyl aminopeptidase (aminopeptidase P) 1, soluble [Mus musculus]	2028.9929	64.1	0.667584326
33859811	DTTASAVAVGLR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1160.6195	54.37	5.875856277
7305295	DVASLGSQLQDTQELLQEETR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2360.1631	189.53	0.106200249
29150272	DVAWAPSIGLPTSTIASCSQDGR		SEC13 related gene [Mus musculus]	2332.1248	101.08	0.380026602
63556656	DVCGLCGNFNGNPDDDLALK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	2079.9175	107.88	0
30023842	DVDLEFLAK		valosin containing protein [Mus musculus]	1049.549	28.57	0
6678726	DVDPDVAYSSIPYEK		leukotriene A4 hydrolase [Mus musculus]	1697.8	44.57	0.383952607
63489759	DVEDEETWIR		PREDICTED: spectrin alpha 2 [Mus musculus]	1291.5834	70.89	0.073953157
30348966	DVEDEILWVGER		spectrin beta 2 isoform 1 [Mus musculus]	1459.7086	58.1	0
7106421	DVEDEILWVGER		spectrin beta 2 isoform 2 [Mus musculus]	1459.7086	58.1	0
33859506	DVFLGTFLYEYSR		albumin 1 [Mus musculus]	1609.7904	67.69	0.071070408
6679491	DVFSPIGER		aminopeptidase puromycin sensitive [Mus musculus]	1019.5123	37.22	0.360155969
18079339	DVGGIVLANACGPCIGQWDR		aconitase 2, mitochondrial [Mus musculus]	2043.9803	23.97	0.35791874
7305515	DVGGNNGGSGNGGGAAFSQTR		trans-acting transcription factor 1 [Mus musculus]	1879.8364	37.52	0.565842736
7305515	DVGGNNGGSGNGGGAAFSQTR	Deamidation (NQ)	trans-acting transcription factor 1 [Mus musculus]	1880.8301	32.89	0
42734399	DVHDSYALLVAESWR		desmuslin isoform H [Mus musculus]	1760.8715	48.35	0

46559834	DVHDSYALLVAESWR		desmuslin isoform M [Mus musculus]	1760.8715	48.35	0
6681115	DVISFFTTSVER		cytochrome P450, family 3, subfamily a, polypeptide 13 [Mus musculus]	1400.7068	41.02	0
46575916	DVLLLGNDYIVPR		hepatic nuclear factor 4, alpha [Mus musculus]	1486.8169	31.63	0
29789383	DVLLPWYNAYR		isoleucine-tRNA synthetase [Mus musculus]	1409.7279	36.89	0.437135936
6680047	DVLSVAFSSDNR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1309.6367	72.81	0.576501982
27804325	DVPALEITHTFLER		monoamine oxidase A [Mus musculus]	1640.8658	36.3	0.196125842
63664018	DVPTGGIFQLR		PREDICTED: kinesin family member 13B [Mus musculus]	1202.651	22.91	0
38372907	DVQEIFR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 [Mus musculus]	906.4734	31.25	0.429539157
9790069	DVQEIFR		HLA-B-associated transcript 1A [Mus musculus]	906.4734	31.25	0.429539157
7304885	DVQELYAAGENR		annexin A11 [Mus musculus]	1364.6436	59.04	0
63489759	DVTGAEALLER		PREDICTED: spectrin alpha 2 [Mus musculus]	1173.5925	28.31	0
28173550	DVTNNVHYENYR		cell division cycle 10 homolog [Mus musculus]	1523.6906	73.31	0.307305237
21704100	DVVDYIIFGTVIQEVK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1837.9929	67.14	0.554907281
63476037	DVVFLIDGSR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1120.6017	33.2	0
24429590	DVVLAYPEVR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1160.6307	25.59	1.449664093
19526822	DVVVSYYNFYK		sulfotransferase family 1A, phenol-preferring, member 1 [Mus musculus]	1396.6649	47.06	0.642547931
20532346	DVYEDELVPVFETVGR		hypothetical protein LOC245945 [Mus musculus]	1866.9169	90.24	0.550223219
6754632	DVYIVQDLMETDLYK		mitogen activated protein kinase 1 [Mus musculus]	1844.9036	40.38	0
21489933	DVYIVQDLMETDLYK		mitogen activated protein kinase 3 [Mus musculus]	1844.9036	40.38	0
31542159	DWGSGSDTLR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	1093.495	48.63	0
33859560	DWNVDLIPK		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	1099.5737	34.35	0
56119103	DWNVDLIPK		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1099.5737	34.35	0
6681157	DWVLNEFK		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1050.5254	40.32	0
40068493	DWVLNEFR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1078.5364	24.96	0.392682102
51467513	DXSHYFKTIQDLR		PREDICTED: similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18) [Homo sapiens]	1708.8529	34.16	0
7949053	DYFEEYGK		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1050.4406	45.07	0.464433121
6754220	DYFEQYGK		heterogeneous nuclear ribonucleoprotein A1 [Mus musculus]	1049.4625	31.72	0.421342723
63663965	DYFEQYGK		PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Sin	1049.4625	31.72	0.421342723
27369998	DYFLFNPVTDIEEIIR		calcium-binding transporter [Mus musculus]	1984.011	50.92	0.369311759
6680690	DYGVLLESAGIALR		peroxiredoxin 3 [Mus musculus]	1476.8113	61.72	0
7948999	DYGVYLEDSGHTLR		peroxiredoxin 4 [Mus musculus]	1624.7649	47.97	0
13384736	DYIPVDQEELR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1376.6721	51.51	0
13385942	DYIWNTLNSGR		citrate synthase [Mus musculus]	1338.645	58.45	0.550564301
21426889	DYLHYIR		ribosomal protein S11 [Mus musculus]	979.5042	23.16	0
6753262	DYLLCDYNR		capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1174.5258	37.34	0.402197816
7304887	DYPGFSPSVDAEAIR		annexin A3 [Mus musculus]	1623.7621	117.19	0.213207071
7242187	DYTGEDVTPENFLAVLR		legumain [Mus musculus]	1938.9449	22.16	0.490451333
14149756	DYTYEELLNR		eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus]	1315.6191	49.97	0.541182022
9790067	DYVPPTANLDQK		staphylococcal nuclease domain containing 1 [Mus musculus]	1360.6676	29.18	0
6753086	EAAGEGPVLYEDPPDQK		apurinic/apyrimidinic endonuclease 1 [Mus musculus]	1814.8427	31.91	0
31982722	EAAGTTAAAGTGGTTEQPPR		squamous cell carcinoma antigen recognized by T-cells 1 [Mus musculus]	1843.885	54.82	0.489648251
63664073	EAAPDTGAEPSPEDSDPTYSSK		PREDICTED: p30 DBC protein [Mus musculus]	2250.9595	63.98	0.650296489
42415475	EADDIVNWLK		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1202.6029	53.1	0.491535045
31981810	EADIQNFTSFISK		dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase) [Mus musculus]	1499.7333	23.51	0
15426055	EAELLEPLMPAIR		coatomer protein complex, subunit beta 1 [Mus musculus]	1481.7936	28.64	0.348671999
47578123	EAEYFELPELVR		potassium channel tetramerisation domain containing 12 [Mus musculus]	1494.7556	60.83	0
6755911	EAFQEALAAAGDK		thioredoxin 1 [Mus musculus]	1320.6403	65.08	0.407842152
29789080	EAFVVEEWVK		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1235.6293	53.88	0.529612328
34328400	EAGDVCYADVYR		splicing factor, arginine/serine-rich 1 (ASF/SF2) [Mus musculus]	1360.6099	40.7	0.683240545
18152793	EAINQGMDEELER		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1533.6893	30.31	1.860962697
6679599	EAINVEQAFQTIAR		RAB7, member RAS oncogene family [Mus musculus]	1589.8304	56.65	0
21311915	EALGGQAEEFSGR		cytochrome P450, family 2, subfamily s, polypeptide 1 [Mus musculus]	1350.6355	24.7	0
30409988	EALNVFGDDYATEDGTGVR		galactose-4-epimerase, UDP [Mus musculus]	2028.9174	59.85	0.370567334
15808988	EALTYDGALLGDR		Williams-Beuren syndrome chromosome region 1 homolog [Mus musculus]	1393.6914	55.65	0
31980674	EANLCKKLR	Deamidation (NQ)	rhophilin, Rho GTPase binding protein 2 [Mus musculus]	1075.5739	25.05	0
31981515	EANNFLWPFK		ribosomal protein L7 [Mus musculus]	1265.6306	43.35	0.380088822
29336026	EAQAGLAEAQEDLEAER		nonmuscle myosin heavy chain [Mus musculus]	1829.8489	83.03	0.715246585
33468887	EASDPQPEDVDGGLK		capping protein (actin filament) muscle Z-line, alpha 1 [Mus musculus]	1556.6925	35.16	0
33859520	EASIYDLTSYFTGSK		caspase 8 [Mus musculus]	1681.7911	62.03	1.08969834
31980645	EASVTPSNLWGGQGLLGVSIR		golgi reassembly stacking protein 2 [Mus musculus]	2141.1387	28.15	0.40154196

31981562	EATESFASDPILYRPVAVALDTK		pyruvate kinase 3 [Mus musculus]	2493.2856	35.93	0.46708163
6679687	EATNPPIIQEEKPK		glucose regulated protein [Mus musculus]	1593.8464	63.4	0.371549558
23956084	EATQAVLDKPETLSSDASTR		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	2119.0613	68.87	0.754061767
63746482	EATTEFSVDAR		PREDICTED: filamin, alpha [Mus musculus]	1225.5706	70.61	0.13859516
12963539	EAVLIDPVLETAHR		ETHE1 protein [Mus musculus]	1562.8486	46.24	0
63594458	EAYFWLR		PREDICTED: source of immunodominant MHC-associated peptides [Mus musculus]	984.4965	35.1	0.380397436
6680748	EAYPGDVFYLHSR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1553.7405	64.57	0.346443328
27532959	ECDVLPDDTVSTLYNR		aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	1839.8547	43.13	0.40163328
63556656	ECGILADPEGPFR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1403.6613	30.7	0.125104535
6677805	ECLPLIIFLR		ribosomal protein S4, X-linked [Mus musculus]	1216.7172	29.6	0.471953985
63562740	EDALMVELDSR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1277.6078	77.05	0
30023842	EDEEESLNEVGYDDIGGCR		valosin containing protein [Mus musculus]	2128.8655	130.62	0.476096149
6756033	EDGNEEDKENQGDETQGQQPPQR		nuclease sensitive element binding protein 1 [Mus musculus]	2628.106	171.74	0.440943411
7710014	EDGSEVGVGGAQVTGSNTR		cullin 3 [Mus musculus]	1819.847	56.82	0.625057289
31982275	EDIYAVEIVGGATR		heat shock protein 4 [Mus musculus]	1492.7675	59.58	0
20330802	EDLIWEILK		transferrin [Mus musculus]	1158.6398	46.16	0
50355692	EDLQELNDR		lamin A isoform A [Mus musculus]	1131.5253	47.75	0
33859482	EDLYLKPIQR		eukaryotic translation elongation factor 2 [Mus musculus]	1274.7098	57.44	0.835872627
20070418	EDNEGVYNGSWGGR		aldehyde dehydrogenase family 7, member A1 [Mus musculus]	1539.6442	33.45	0
15426055	EDQFQLSLLAAMGNTQR		coatomer protein complex, subunit beta 1 [Mus musculus]	1921.9791	37.55	0.625341246
33598964	EDQSILCTGESGAGK		myosin heavy chain 10, non-muscle [Mus musculus]	1494.6821	81.46	0
7305295	EDQSILCTGESGAGK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1494.6821	81.46	0
20137006	EDQSILCTGESGAGK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1494.6821	81.46	0
29336026	EDQSILCTGESGAGK		nonmuscle myosin heavy chain [Mus musculus]	1494.6821	81.46	0
6754254	EDQTEYLEER		heat shock protein 1, alpha [Mus musculus]	1311.5702	77.16	0.62677122
40556608	EDQTEYLEER		heat shock protein 1, beta [Mus musculus]	1311.5702	77.16	0.62677122
34996495	EDQVIQLMNTIFSK		ribophorin II [Mus musculus]	1665.85	46.46	0
29293809	EEADEYVDIGALNGIFVLGR	Deamidation (NQ)	ATP citrate lyase [Mus musculus]	2181.0916	22.21	0
33563250	EEAENNLAAFR		desmin [Mus musculus]	1263.6011	78.51	0.150813444
31982755	EEAESTLQSFR		vimentin [Mus musculus]	1296.6102	65.08	0.297668863
6755863	EEASDYLELDTIK		tumor rejection antigen gp96 [Mus musculus]	1525.7205	30.87	0
6755863	EEEAIQLDGLNASQIR		tumor rejection antigen gp96 [Mus musculus]	1785.9003	32.79	0
30425112	EEEEEEEEYDEGSNLKR		hypothetical protein LOC109154 [Mus musculus]	2113.8647	25.61	0.458016837
31982522	EEGDSWVLNGTK		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1334.6349	34.06	0
63504601	EEGVDREPR		PREDICTED: hypothetical protein XP_487763 [Mus musculus]	1086.5361	22.1	0
22208854	EEGYDSVFSVVR		cytidine monophospho-N-acetylneuraminic acid synthetase [Mus musculus]	1386.6549	74.5	0.313721219
6753036	EEIFGPVMQILK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1403.7583	54.96	0
21312260	EEIFGPVQPLFK		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1403.7581	55.77	0
45544618	EEIQPGDMVIIDQFIDR		methylthioadenosine phosphorylase [Mus musculus]	2017.9872	24.1	0
7710042	EEIQSSISGVTAAYNR		IQ motif containing GTPase activating protein 1 [Mus musculus]	1724.8501	45.88	0
7305295	EELAEELASSLSGR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1490.7324	44.33	0
27777677	EELGDEWLTPDLFR		deoxyribose-phosphate aldolase-like [Mus musculus]	1719.834	33.21	0.624651713
22122535	EELIGIAYNR		pleckstrin homology domain containing, family C (with FERM domain) member 1 [Mus musculus]	1177.6204	25.09	0
19527034	EELSPASSGNAVYDFFIGR		lamin B receptor [Mus musculus]	2058.9797	28.45	0.465025187
36031035	EENAEQQALAAKR	Deamidation (NQ)	chondroitin sulfate proteoglycan 6 [Mus musculus]	1458.7247	22.16	0
31560222	EESGAVAAAASVPAQSTAR		PYD and CARD domain containing [Mus musculus]	1772.8806	80.67	0.438795764
12584968	EESGVPGPNSPPTNR		solute carrier family 29 (nucleoside transporters), member 1 [Mus musculus]	1537.7291	43.66	0.263869151
55741703	EESLLLFEAMR		glutaminyl-tRNA synthetase [Mus musculus]	1337.6827	26.91	0
7710042	EEVQAGVDAANSAAQQYQR		IQ motif containing GTPase activating protein 1 [Mus musculus]	2034.9487	132.99	0.247302983
13385680	EEWDIIEGLIR		2,4-dienoyl CoA reductase 1, mitochondrial [Mus musculus]	1372.7151	45.96	0.444817852
20330802	EEYNGYTGAFR		transferrin [Mus musculus]	1306.5771	42.59	0.473986205
21703832	EEYSGVIEEFLATGEK		arginyl aminopeptidase (aminopeptidase B) [Mus musculus]	1800.8807	29.41	0.425121838
6679587	EFADSLGIPFLETSAK		RAB1, member RAS oncogene family [Mus musculus]	1724.8723	86.14	0.320828264
21313162	EFADSLGVPFLETSAK		RAB1B, member RAS oncogene family [Mus musculus]	1710.8572	48.78	0.695382773
31542159	EFDDLSPEQQR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	1363.6154	58.76	0.427775167
6806903	EFDELSPSAQR		ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	1278.5946	68.45	0.462829046
21704156	EFDPTITDGSLSGPSR		caldesmon 1 [Mus musculus]	1678.798	24.2	0.295004147
51491880	EFEEESKQPGVSEQQR		metastasis-associated protein 2 [Mus musculus]	1906.8823	53.49	0.484945046
6755863	EFEPLLNWMK	Oxidation (M)	tumor rejection antigen gp96 [Mus musculus]	1322.6411	23.81	0.230771545
13385310	EFFNFLPLSSQDPAPIR		propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]	1978.0089	37.24	0.245347798

13242328	EFNEDGALAVLQQFK		NS1-associated protein 1 [Mus musculus]	1708.8545	35.24	0
31980706	EFQEQLESAR		methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) [Mus musculus]	1236.5876	33.19	3.131146161
23956222	EFSIDVGYER		ARP3 actin-related protein 3 homolog [Mus musculus]	1214.5726	23.67	0.629978427
31982275	EFSITDVVPYPISLR		heat shock protein 4 [Mus musculus]	1735.9237	63.26	0.490031747
6806903	EFTLEFSR		ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	1028.5051	49.83	0.448277188
36031132	EFTLEFSR		ATPase, Ca++ transporting, fast twitch 1 [Mus musculus]	1028.5051	49.83	0.448277188
31542159	EFTLEFSR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	1028.5051	49.83	0.448277188
6677991	EGAQYLMQAAGLGR		solute carrier family 12, member 2 [Mus musculus]	1464.7223	34.26	0
21426821	EGDVLTLLESR		ribosomal protein S28 [Mus musculus]	1360.7097	75.92	0.519855004
63594458	EGDYFTQQGEFR		PREDICTED: source of immunodominant MHC-associated peptides [Mus musculus]	1476.6417	68.17	0.417671572
45387933	EGETYYDVVAVVDPVTR		UDP-glucose ceramide glucosyltransferase-like 1 [Mus musculus]	1911.9349	37.56	0
31560539	EGGLGPLNIPLLADVTK		peroxiredoxin 2 [Mus musculus]	1706.9573	29.68	0.373013493
29789191	EGIDPAPYYWYTDQR		asparaginyl-tRNA synthetase [Mus musculus]	1873.8445	53.86	0.494325567
18152793	EGIECEVINLR		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1274.639	26.98	0
6754750	EGILNDDIYCPPETAVLLASYAVQSK		moesin [Mus musculus]	2809.3911	30.1	0.597003605
33859482	EGIPALDNFLDKL		eukaryotic translation elongation factor 2 [Mus musculus]	1444.7697	87.31	0.628791012
59709449	EGLLLWCQR		actinin alpha 2 [Mus musculus]	1117.5885	51.38	0.249466099
11230802	EGLLLWCQR		actinin alpha 4 [Mus musculus]	1117.5885	51.38	0.249466099
6679439	EGMNIVEAMER		peptidylprolyl isomerase A [Mus musculus]	1278.5863	64.03	0
63650244	EGMNIVEAMER		PREDICTED: similar to Peptidyl-prolyl cis-trans isomerase A (PPIase) (Rotamase) (Cyclophilin A) (Cy	1278.5863	64.03	0
31981549	EGNALFTFPNTPVK		sulfide quinone reductase-like [Mus musculus]	1534.7832	53.14	0.333362461
31980648	EGNDLYHEMIESGVINLK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2060.998	103.01	0.759062362
63746482	EGSYSISVLYGEEEVPR		PREDICTED: filamin, alpha [Mus musculus]	1913.9132	109.03	0.100499809
31982186	EGVVECSFVQSK		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1311.6199	48.2	0.280800861
18079339	EGWPLDIR		aconitase 2, mitochondrial [Mus musculus]	985.5128	42.77	0.230195995
31981690	EIAEAYLGK		heat shock protein 8 [Mus musculus]	993.5202	32.35	0
63664182	EIAEAYLGK		PREDICTED: similar to heat shock protein 8 [Mus musculus]	993.5202	32.35	0
14269570	EICPDGENIFPVTSYVETVTGEILVTPR		seminal vesicle antigen-like 1 [Mus musculus]	3078.5374	29.11	0
63578850	EIDDEANSYFQR		PREDICTED: CCR4-NOT transcription complex, subunit 1 [Mus musculus]	1486.6445	28.2	0
13385168	EIDQEAAVEVSQLR		ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Mus musculus]	1586.8035	102.24	0.47013352
51592084	EIEIAEQEMPALMALR		hypothetical protein LOC74340 [Mus musculus]	1843.9299	75.98	0
31980942	EIEIIPLQR		Inositol (myo)-1(or 4)-monophosphatase 1 [Mus musculus]	1110.6537	35.86	0.384304673
41054996	EIEVPDQYGTIR		echinoderm microtubule associated protein like 4 [Mus musculus]	1419.7092	40.42	1.378089381
26986563	EIFAQEALAPFR		choline dehydrogenase [Mus musculus]	1391.7385	53.34	0.406001298
7305085	EIFEQPESVVNTMR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1678.8135	84.65	0.63711797
28173568	EIFLSQPILLELEAPLK		protein phosphatase 1, catalytic subunit, beta [Mus musculus]	1953.1288	90.39	0.329866987
9790051	EIGWADVGGWTGQGGSILGTK		phosphofructokinase, platelet [Mus musculus]	2089.0308	32.06	0
34740335	EIIDLVLDR		tubulin, alpha 2 [Mus musculus]	1085.6201	50.14	0.457965931
6678469	EIIDLVLDR		tubulin, alpha 6 [Mus musculus]	1085.6201	50.14	0.457965931
6678467	EIIDPVLDR		tubulin, alpha 4 [Mus musculus]	1069.5854	32.6	0
6755048	EIIGVVSQEPVLFATTIAENIR		ATP-binding cassette, sub-family B (MDR/TAP), member 1A [Mus musculus]	2399.2976	38.53	0.187659856
6677769	EILGTAQSVGCNVDGR		ribosomal protein L12 [Mus musculus]	1618.7794	43.93	0
9790219	EILVGDVGATITDPFK		destrin [Mus musculus]	1674.8932	119.32	0.21422673
6680924	EILVGDVGQTVDDPYTTFVK		cofilin 1, non-muscle [Mus musculus]	2196.1096	108.51	0
27804325	EIPVDAPWQAR		monoamine oxidase A [Mus musculus]	1281.66	44.79	0.366501484
40254124	EIQEPDPTYEEK		SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 [	1477.6664	23.34	0
51766545	EIQGFFSFPVDNLR		PREDICTED: phosphoribosyl pyrophosphate synthetase-associated protein 1 [Mus musculus]	1668.8342	22.25	0.613547156
6671507	EITALAPSTMK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1161.6162	76.6	0.27459138
6671509	EITALAPSTMK		actin, beta, cytoplasmic [Mus musculus]	1161.6162	76.6	0.27459138
63652452	EITALAPSTMK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1161.6162	76.6	0.27459138
6671507	EITALAPSTMK	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1177.6053	27.87	0
6671509	EITALAPSTMK	Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	1177.6053	27.87	0
63652452	EITALAPSTMK	Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1177.6053	27.87	0
14861854	EITINQSLLAPLSVDIDPTIQQVR		keratin complex 2, basic, gene 7 [Mus musculus]	2663.4583	37.22	0.258116543
13385434	EIVLADVIDNDSWR		phosphoribosylaminoimidazole carboxylase [Mus musculus]	1644.8279	55.54	0
22203747	EKDFDSLAQPSFFDR		procollagen, type VI, alpha 2 [Mus musculus]	1801.8369	39.11	0
28269703	EKEEEEEEEDEDASGGDQDQEER		RAD21 homolog [Mus musculus]	2711.0366	27.17	0.503631151
7949051	EKPYFPIPEDCTFIQNVPLEDR		heterogenous nuclear ribonucleoprotein U [Mus musculus]	2650.2825	68.93	0.411375682
6755372	ELAEDGYSGVEVR		ribosomal protein S3 [Mus musculus]	1423.6707	82.92	0.817939117
51712562	ELAPYDENWFYTR		PREDICTED: similar to ribosomal protein S19 [Mus musculus]	1703.7716	59.17	0.52040303

12963511	ELAPYDENWFYTR		ribosomal protein S19 [Mus musculus]	1703.7716	59.17	0.52040303
6681157	ELAQQVQQVAAEYCR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1735.8478	47.81	0.548954088
63621901	ELAQQVQQVAAEYCR		PREDICTED: similar to ddx5 [Mus musculus]	1735.8478	47.81	0.548954088
24429590	ELDALDANDELTPLGR		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1741.8599	75.5	0.422076336
7305295	ELDEATESNEAMGR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1551.6658	126.51	0
7305295	ELDEATESNEAMGR	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1567.6526	54.08	0.084005839
29336026	ELEDVTESAESMNR		nonmuscle myosin heavy chain [Mus musculus]	1609.7065	50.39	0
31981722	ELEEIVQPIISK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1397.7831	42.31	1.359129854
7949023	ELEEWYAR		clathrin, light polypeptide (Lca) [Mus musculus]	1095.5105	26.48	0
6677813	ELEFYLR		ribosomal protein S8 [Mus musculus]	969.5059	37.9	0.487731641
7305295	ELEGHISDLQEDLDSER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1984.9103	103.32	0.09399438
7106435	ELEPGVEYFIR		tenascin C [Mus musculus]	1351.6941	34.35	0.235661625
20137006	ELETQISELQEDLESER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2047.9701	107.63	0.461688505
6680067	ELFEADPER		glucose phosphate isomerase 1 [Mus musculus]	1105.5167	38.7	0.490789231
29336026	ELFQETLESLR		nonmuscle myosin heavy chain [Mus musculus]	1364.7085	68.93	0.304277131
33563290	ELFSNLQEFAGPSGK		DKFZP586A0522 protein [Mus musculus]	1623.7911	32.31	0
23956084	ELGAFGLQVPSELGGLGLSNTQYAR		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	2577.3281	118.67	0.223179372
6753036	ELGEYGLQAYTEVK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1599.7902	87.1	0.254474201
20147793	ELGQDGEEAEAPGAGDGPPR		RD RNA-binding protein [Mus musculus]	1951.8606	50.99	0.523851656
63476037	ELGTIQQVISER		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1372.7428	65.04	0.17260768
13385878	ELILSSEPSPAVTPVTPTTLIAPR		sorting nexin 2 [Mus musculus]	2489.3977	38.87	0.546249694
13386054	ELLLQPVTISR		actin related protein 2/3 complex, subunit 4 [Mus musculus]	1268.7548	40.84	0.46654625
13385998	ELLQESALIR		TNF receptor-associated protein 1 [Mus musculus]	1171.6682	23.4	0
31982233	ELLSVGLGFLR		LYRIC [Mus musculus]	1203.7139	33.47	0.882258145
56744242	ELLYFLDSCEPEFK		adaptor protein complex AP-1, gamma 1 subunit [Mus musculus]	1732.8279	32.86	0
6679687	ELNDFISYLQR		glucose regulated protein [Mus musculus]	1397.7095	86.95	0.509166585
63476037	ELPNIEER		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	999.511	35.84	0.146551529
11230802	ELPPDQAEYCIAR		actinin alpha 4 [Mus musculus]	1504.7141	43.14	0.618424176
63489759	ELPTAFDYVEFTR		PREDICTED: spectrin alpha 2 [Mus musculus]	1587.7754	50.41	0.415856205
31560737	ELPVNAQNYVR		adenylosuccinate synthetase, non muscle [Mus musculus]	1302.6775	50.07	0
51708271	ELQAEQQNQEVTGR		PREDICTED: cingulin [Mus musculus]	1629.7864	58.45	0.490659898
33563250	ELQAQLQEQQVQVEMDMSKPDLTAALR		desmin [Mus musculus]	3099.5493	50.9	0.119591838
30023842	ELQELVQYPVEHPDK		valosin containing protein [Mus musculus]	1823.9194	60.33	0.507186217
13624315	ELQSQISDTSVVLSMDNSR		keratin complex 2, basic, gene 8 [Mus musculus]	2109.0156	155.58	0.375135134
63565108	ELQSQISDTSVVLSMDNSR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	2109.0156	155.58	0.375135134
13624315	ELQSQISDTSVVLSMDNSR	Oxidation (M)	keratin complex 2, basic, gene 8 [Mus musculus]	2125.0103	23.27	0.517632143
63565108	ELQSQISDTSVVLSMDNSR	Oxidation (M)	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	2125.0103	23.27	0.517632143
31981044	ELSADGAQEATGTQR		ubiquitin specific protease 8 [Mus musculus]	1533.7026	25.15	0
46275826	ELVDEEADEAQELLSQAENWQR		laminin, alpha 4 [Mus musculus]	2602.1909	50.36	0
31982522	ELVPIAAQLDR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1224.6938	28.92	0
28416440	ELVVVDTPGIFDTEVPDADTQR		GTPase, IMAP family member 4 isoform a [Mus musculus]	2416.1912	77.06	1.4668783
13385076	ELWAVLNGWR		sorcin [Mus musculus]	1243.6638	46.95	0.277025057
33469123	ELYLFDVLR		asparagine synthetase [Mus musculus]	1167.6433	23.81	0.864348379
31982755	EMEENFALEAANYQDTIGR		vimentin [Mus musculus]	2201.0022	128.5	0
7305295	EMEGLSQQYEEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1470.6447	77.52	0
7305295	EMEGLSQQYEEK	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1486.6503	24.15	0
6671666	EMNDAAMFYTNR		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	1462.6263	73.5	0.699264015
18079351	EMTEALGPGTIR		major vault protein [Mus musculus]	1274.6405	27.49	0
30023842	EMVELPLR		valosin containing protein [Mus musculus]	986.5326	25.85	0.252224905
22122523	EMVQADVELMR		GDP-mannose 4, 6-dehydratase [Mus musculus]	1320.6216	27.87	0
21313526	EMWYAGINPSDSVNSEVLGATR		hypothetical protein LOC78906 [Mus musculus]	2396.1238	49.52	0.615935335
7305295	ENADLAGELR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1087.5367	65.55	0
31560680	ENDYYTPTGEFR		intergral membrane protein 1 [Mus musculus]	1491.6371	58.56	0.393942109
39204553	ENEFSFEDNAIR		chromodomain helicase DNA binding protein 4 [Mus musculus]	1470.6493	34.93	0.849162165
13384736	ENFIPTIVNFSAEEISDAIR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	2265.1387	73.54	0.203456424
63746482	ENGIYLIDVK		PREDICTED: filamin, alpha [Mus musculus]	1163.6166	32.48	0
21450129	ENGTITAANASTLNDGAAALVLMTAEAAQR		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	2945.459	51.59	0.226306531
13277350	ENIETVVTGSLDDLVK		meiotic recombination protein REC14 [Mus musculus]	1731.8752	52.04	3.152168597
31982522	ENLLGEPGMGFK		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1291.6292	56.36	0
42734399	ENLLLEEELR		desmuslin isoform H [Mus musculus]	1257.6702	31.11	0

46559834	ENLLLEEELR		desmuslin isoform M [Mus musculus]	1257.6702	31.11	0
22267442	ENMAYTVEGIR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1282.6093	32.37	0
6671678	ENQQSPINIVTAR		carbonic anhydrase 4 [Mus musculus]	1469.7681	47.52	0.845000099
18250284	ENTEGEYSGIEHVIVDGVVQSIK		isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	2502.2349	37.57	0.471315309
6753484	ENYAELLDDGFLK		procollagen, type VI, alpha 1 [Mus musculus]	1526.7386	82.83	0.190648915
33859506	ENYGELADCCTK		albumin 1 [Mus musculus]	1345.543	32.78	1.98420131
19526926	EPFTFPVR		hypothetical protein LOC70984 [Mus musculus]	992.5217	23.85	0
33469029	EPGEAAAEGAAEEAR		acyl-Coenzyme A binding domain containing 3 [Mus musculus]	1457.6581	94.69	0.263563442
31982290	EPIMPAPGQEETVR		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1553.7634	61.39	0
31982290	EPIMPAPGQEETVR	Oxidation (M)	LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1569.7513	27.37	0
31981657	EPITVSSEQMSHFR		carbonic anhydrase 2 [Mus musculus]	1647.7786	125.57	0
31981657	EPITVSSEQMSHFR	Oxidation (M)	carbonic anhydrase 2 [Mus musculus]	1663.7682	50.52	0
8567390	EPPEAVWADDVDR		pyruvate kinase liver and red blood cell [Mus musculus]	1498.6891	41.74	1.047744882
51708124	EPPTDVTPTFLTTGVLSTLR		PREDICTED: similar to GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase) (GMP synthe	2145.136	39.76	0
6679891	EPWLLASQYQDAIR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1689.8624	35.32	0
7305295	EQADFAIEALAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1305.6924	63.13	0
20137006	EQADFAIEALAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1305.6924	63.13	0
54607037	EQASGVVSFEQPEYSVSR		integrin beta 4 isoform 2 [Mus musculus]	1998.9419	49.24	0.623996468
6680836	EQFLDGDAWTNR		calreticulin [Mus musculus]	1451.6666	27.65	0.563118054
51764087	EQGFLSFWR		PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	1169.5807	57.1	0.189143782
6755809	EQGVEEHETLLLR		talin 1 [Mus musculus]	1552.7954	68.59	0
22094075	EQGVLSFWR		solute carrier family 25, member 5 [Mus musculus]	1121.5807	60.75	0.351944807
6996911	EQGYDVIAYLANIGQK		argininosuccinate synthetase [Mus musculus]	1781.8956	41.52	0
51772556	EQIDIFEGIK		PREDICTED: similar to Succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	1191.6078	47.51	0
6678499	EQIVVDLSHPGVSADDQVSR		UDP-glucose dehydrogenase [Mus musculus]	2151.0684	79.58	0.228066641
7305565	EQLAIAEFAR		t-complex protein 1 [Mus musculus]	1147.6129	22.09	0
6754782	EQLLQSNPVLEAFGNAK		myosin IB [Mus musculus]	1857.9678	42.28	0.613345219
51766008	EQLLQSNPVLEAFGNAK		PREDICTED: myosin IA [Mus musculus]	1857.9678	42.28	0.613345219
34536813	EQLMEENECLR	Deamidation (NQ)	hypothetical protein LOC75089 [Mus musculus]	1394.62	32.26	0
18252782	EQLQDMGLIDLFSPEK		serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1 [Mus musculus]	1862.9272	64.67	0
21450277	EQPLDEELKDAFQNAYLELGGLGER		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2834.3801	121.84	0.254103306
13384736	EQPWVSVQPR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1225.6315	34.47	0.409112793
18700024	EQTEGEYSSLEHESAK		isocitrate dehydrogenase 3, beta subunit [Mus musculus]	1823.7946	22.14	0.114336174
40556608	EQVANSAFVER		heat shock protein 1, beta [Mus musculus]	1249.6178	68.49	0.643804384
31560653	EQWWLNLR		phosphofructokinase, liver, B-type [Mus musculus]	1144.5936	42.08	0
6677935	ESDGTPGGLASLENER		sorbin and SH3 domain containing 1 [Mus musculus]	1631.752	65.93	0
31560128	ESENEANPEEQGLEESGEEFAR		hypothetical protein LOC68303 [Mus musculus]	2480.0659	43.93	0
6679465	ESLQQLAEVTR		protein kinase C substrate 80K-H [Mus musculus]	1273.6721	24.95	0
63750688	ESNQPPEDSSPPASSESSSTR		PREDICTED: HECT, UBA and WWE domain containing 1 [Mus musculus]	2175.928	26.07	1.111654603
13384736	ESPEVLLTLDILK		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1469.8459	29.06	0
6678752	ESPYDHQSLQTALQEAFTSR		lymphocyte antigen 74 [Mus musculus]	2308.0852	44.87	0.615922648
6754994	ESTGAQVQVAGDMLPNSTER		poly(rC) binding protein 1 [Mus musculus]	2089.9834	119.1	0.3134606
6678185	ESVFALDFLR		surfeit gene 6 [Mus musculus]	1196.6324	26.2	0
42734399	ESVQLYEDEVR		desmuslin isoform H [Mus musculus]	1366.6532	73.43	0
46559834	ESVQLYEDEVR		desmuslin isoform M [Mus musculus]	1366.6532	73.43	0
9910482	ESVQVPDDQDFR		START domain containing 10 [Mus musculus]	1434.6547	35.28	0.401641079
20874851	ESYSVYVYK		PREDICTED: similar to histone H2b-616 [Mus musculus]	1137.5437	44.4	0
22122515	ETFLTSPEELYR		AHA1, activator of heat shock 90kDa protein ATPase homolog 1 [Mus musculus]	1484.7271	32.05	0.517872518
24429590	ETPFELIEALLK		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1402.7764	43.89	0.429612428
7106363	ETPGSQPSEPCSGVSR		microtubule-associated protein 4 [Mus musculus]	1617.7214	41.43	0.287983312
31982223	ETPSWTGPGFVR		laminin, beta 2 [Mus musculus]	1333.652	25.78	0
42734399	ETSFTFQMDLSDTR	Oxidation (M)	desmuslin isoform H [Mus musculus]	1693.7388	22.24	0
63492203	ETSYEEALANQR		PREDICTED: ribosome binding protein 1 [Mus musculus]	1410.6503	94.5	0.522986141
21450291	ETTIQGLDGLSER		aldolase 2, B isoform [Mus musculus]	1418.7141	32.02	0
22122523	ETTPFYPR		GDP-mannose 4, 6-dehydratase [Mus musculus]	1010.4962	23.31	0.43151827
30023842	ETVVEVPQVTWEDIGGLEDVK		valosin containing protein [Mus musculus]	2342.1482	48.88	0
30023842	ETVVEVPQVTWEDIGGLEDVKR		valosin containing protein [Mus musculus]	2498.2834	93.84	0
30023842	ETVVEVPQVTWEDIGGLEDVKR	Deamidation (NQ)	valosin containing protein [Mus musculus]	2499.2708	23	0
51772556	ETYLAILMDR		PREDICTED: similar to Succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	1224.6327	50.58	0
6680748	EVAAFAQFGSDLDAATQQLLSR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2338.1707	127.4	0.356017053

31982169	EVAEVNLWGTVR		3-hydroxybutyrate dehydrogenase (heart, mitochondrial) [Mus musculus]	1372.7205	48.4	0
30425008	EVAEYYAQSGNSAEK		RIKEN cDNA 5730439E10 [Mus musculus]	1645.739	58.94	0.369119581
31560449	EVAGQVGVPLQDLMVR		aspartyl aminopeptidase [Mus musculus]	1710.9218	38.38	0
9055322	EVCGFAPYER		ribosomal protein L36 [Mus musculus]	1170.5291	33.24	0.490299559
30348966	EVDDLEQWIAER		spectrin beta 2 isoform 1 [Mus musculus]	1502.7184	66.65	0.353921296
7106421	EVDDLEQWIAER		spectrin beta 2 isoform 2 [Mus musculus]	1502.7184	66.65	0.353921296
63650229	EVDEQMLNVQNK		PREDICTED: similar to TUBULIN BETA CHAIN (T BETA-15) [Mus musculus]	1446.6868	56.55	0.878324998
22165384	EVDEQMLNVQNK		tubulin, beta, 2 [Mus musculus]	1446.6868	56.55	0.878324998
33859488	EVDEQMLNVQNK		tubulin, beta 2 [Mus musculus]	1446.6868	56.55	0.878324998
7106439	EVDEQMLNVQNK		tubulin, beta 5 [Mus musculus]	1446.6868	56.55	0.878324998
21746161	EVDEQMLNVQNK		tubulin, beta [Mus musculus]	1446.6868	56.55	0.878324998
63650229	EVDEQMLNVQNK	Oxidation (M)	PREDICTED: similar to TUBULIN BETA CHAIN (T BETA-15) [Mus musculus]	1462.6677	53.37	0.230364382
22165384	EVDEQMLNVQNK	Oxidation (M)	tubulin, beta, 2 [Mus musculus]	1462.6677	53.37	0.230364382
33859488	EVDEQMLNVQNK	Oxidation (M)	tubulin, beta 2 [Mus musculus]	1462.6677	53.37	0.230364382
7106439	EVDEQMLNVQNK	Oxidation (M)	tubulin, beta 5 [Mus musculus]	1462.6677	53.37	0.230364382
21746161	EVDEQMLNVQNK	Oxidation (M)	tubulin, beta [Mus musculus]	1462.6677	53.37	0.230364382
30023842	EVDIGIPDATGR		valosin containing protein [Mus musculus]	1242.634	90.92	0.600986767
12963527	EVEERPAPTPWGSK		actin related protein 2/3 complex, subunit 1B [Mus musculus]	1582.7848	27.44	0.354667734
29789052	EVENEQTPVSEPEEEK		erythrocyte protein band 4.1-like 2 [Mus musculus]	1872.8297	28.63	1.047164539
14149756	EVEPEPTEEKDVDADEEDSR		eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus]	2317.9824	83.33	0.427127331
46593021	EVESIGAHLNAYSTR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1646.8127	56.73	0.642012176
31542143	EVFEMATR		ras homolog gene family, member A [Mus musculus]	982.4681	28.07	0
31980685	EVGAFGTPVINLGTR		glucosamine [Mus musculus]	1530.828	71.91	0.531541504
27754103	EVIELPLTNPELFQR		proteasome 26S ATPase subunit 6 [Mus musculus]	1797.9719	33.09	0.253950544
26986563	EVILSGGAINSPQLLMLSGVGNADDLR		choline dehydrogenase [Mus musculus]	2739.4189	23.78	0.466502997
6755809	EVIQEWSLTNIK		talin 1 [Mus musculus]	1459.7665	31.48	0
7305295	EVLLQVEDER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1229.6372	53.14	0
6680572	EVLQALEELAVNYDQK		kinesin family member 5B [Mus musculus]	1861.9424	38.02	0
33468931	EVMQEVAQLSQFDEELYK		seryl-aminoacyl-tRNA synthetase 1 [Mus musculus]	2186.0432	44.98	0.570795411
6680067	EVMQMLVELAK		glucose phosphate isomerase 1 [Mus musculus]	1290.6797	49.74	0
6678573	EVQGNESETFR		villin 1 [Mus musculus]	1295.5902	32.65	0.355035589
33859811	EVQSEFIEVMNEIWANDQIR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	2450.1719	34.04	0
27229048	EVSDGIVAPGYEEEALK		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1805.8779	61.59	1.271974281
6680816	EVSFQATGDSEWR		complement component 1, q subcomponent binding protein [Mus musculus]	1511.6812	31.84	0.372331554
6679737	EVSGNELIQTYTYEGVEAK		fatty acid binding protein 2, intestinal [Mus musculus]	2129.9897	40.1	0
6753240	EVSQPDWTPPPEVTLSLTK		calcium binding protein, intestinal [Mus musculus]	2124.0881	29.38	0
21450129	EVYMGNVIQGGEGQAPTR		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	1905.9183	87.73	0.275406256
21450129	EVYMGNVIQGGEGQAPTR	Oxidation (M)	acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	1921.9106	44.65	0.339856306
31560611	EWIEGVTGR		calponin 1 [Mus musculus]	1046.5332	54.67	0
9790051	EWSGLLEELAR		phosphofructokinase, platelet [Mus musculus]	1302.6753	81.21	0.394670216
19526822	EWWELR		sulfotransferase family 1A, phenol-preferring, member 1 [Mus musculus]	918.4546	28.05	0.147731554
6679759	EYEELCPR		fibrillin 1 [Mus musculus]	1038.454	31.4	0
6754222	EYFGQFGEIEAIELPIDPK		heterogeneous nuclear ribonucleoprotein A/B [Mus musculus]	2195.0933	63.45	1.121519806
9625037	EYIPTVFDNYSAQSAVDGR		ras homolog gene family, member G [Mus musculus]	2131.9983	47.22	0.45731385
33563250	EYQDLLNVK		desmin [Mus musculus]	1121.58	54.86	0
34328368	EYQDLLNVK		internexin neuronal intermediate filament protein, alpha [Mus musculus]	1121.58	54.86	0
39204499	EYQDLLNVK		neurofilament, light polypeptide [Mus musculus]	1121.58	54.86	0
31982755	EYQDLLNVK		vimentin [Mus musculus]	1121.58	54.86	0
29244176	EYQELMNVK		hypothetical protein 4732456N10 [Mus musculus]	1153.5476	39.07	0
33563238	EYQELMNVK		keratin complex 2, basic, gene 16 [Mus musculus]	1153.5476	39.07	0
13624315	EYQELMNVK		keratin complex 2, basic, gene 8 [Mus musculus]	1153.5476	39.07	0
29789317	EYQELMNVK		keratinocyte associated protein 1 [Mus musculus]	1153.5476	39.07	0
1346345	EYQELMNVK		Keratin, type II cytoskeletal 6B (Cytokeratin 6B) (CK 6B) (K6b keratin)	1153.5476	39.07	0
20903595	EYQELMNVK		PREDICTED: RIKEN cDNA 2310001L23 [Mus musculus]	1153.5476	39.07	0
41054806	EYQLNDSAAYYLNDLER		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	2076.9558	112.15	0.40796285
13384736	EYQTQLIQR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1178.6185	43.01	1.087081876
63635087	EYSSELNAPSQESDSHPR		PREDICTED: RNA binding motif protein 25 [Mus musculus]	2032.8887	41.05	0.42436805
31560560	FAAATGATPIAGR		laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1203.6533	60.35	0.42912239
6680067	FAAYFQQGDMESNGK		glucose phosphate isomerase 1 [Mus musculus]	1692.7467	71.65	0
6753254	FADDELIIDFDNFVR		calpain 2 [Mus musculus]	1828.8795	97.83	0.277144217

31982755	FADLSEAANR		vimentin [Mus musculus]	1093.5308	62.27	0.459405408
22726197	FADQDDIGNVSFDR		sporulation-induced transcript 4-associated protein [Mus musculus]	1598.7305	35.05	0.337990843
31560613	FAEAFEAIPR		chaperonin subunit 8 (theta) [Mus musculus]	1150.5876	37.53	0.447066012
30425112	FAEVYFAQSQQK		hypothetical protein LOC109154 [Mus musculus]	1445.7032	51.87	0.20806398
6755863	FAFQAEVNR		tumor rejection antigen gp96 [Mus musculus]	1081.5455	39.33	0.527526335
7305445	FAGVDIR		ribosomal protein S16 [Mus musculus]	777.4224	40.91	0.3946452
59709449	FAIQDISVEETSAK		actinin alpha 2 [Mus musculus]	1537.7716	79.7	0.394672219
11230802	FAIQDISVEETSAK		actinin alpha 4 [Mus musculus]	1537.7716	79.7	0.394672219
31543315	FAISELFAK		nucleolin [Mus musculus]	1025.5657	41.95	0.597884425
7710042	FALGISAINEAVDSGDVGR		IQ motif containing GTPase activating protein 1 [Mus musculus]	1890.9564	91.34	0.382544853
19482160	FALITWIGEDVSGLQR		coactosin-like 1 [Mus musculus]	1804.964	64.42	0.693579481
6754984	FALMYEGR		3'-phosphoadenosine 5'-phosphosulfate synthase 2 [Mus musculus]	986.4827	32.42	1.392155209
6753240	FAMEPEEFDSDTLR		calcium binding protein, intestinal [Mus musculus]	1686.7366	74.29	0.925547489
6753240	FAMEPEEFDSDTLR	Oxidation (M)	calcium binding protein, intestinal [Mus musculus]	1702.7118	51.19	0.256990729
31982720	FANILTEACSLQR		SA rat hypertension-associated homolog [Mus musculus]	1465.7527	26.49	0
30348966	FANSLVGVQQQLQAFNTYR		spectrin beta 2 isoform 1 [Mus musculus]	2184.113	23.8	0
7106421	FANSLVGVQQQLQAFNTYR		spectrin beta 2 isoform 2 [Mus musculus]	2184.113	23.8	0
63563013	FAPGYDVCVK		PREDICTED: mucin 2 [Mus musculus]	1098.5251	33.38	1.754371437
21704206	FAPPEAPEPWSGVR		carboxylesterase 2 [Mus musculus]	1539.7638	43.25	0.39826915
27370126	FAPPEAPEPWSGVR		carboxylesterase 5 [Mus musculus]	1539.7638	43.25	0.39826915
19527178	FAPPEDPEPWSGVR		carboxylesterase 6 [Mus musculus]	1583.7501	32.7	0
51772153	FAQPGSFEYEYAMR		PREDICTED: similar to Non-POU-domain-containing, octamer binding protein [Mus musculus]	1695.7533	37.8	0.794129762
33563250	FASEANGYQDNIAR		desmin [Mus musculus]	1555.7183	70.18	0.109621619
33563250	FASEANGYQDNIAR	Deamidation (NQ)	desmin [Mus musculus]	1556.7051	113.3	0.256049945
63476037	FASEIVDTVYEDGDSIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1915.894	100.72	0.091531889
29244176	FASFIDK		hypothetical protein 4732456N10 [Mus musculus]	827.4299	45.28	0.572450355
482387	FASFIDK		keratin, 67K type II epidermal - human	827.4299	45.28	0.572450355
33563238	FASFIDK		keratin complex 2, basic, gene 16 [Mus musculus]	827.4299	45.28	0.572450355
6678643	FASFIDK		keratin complex 2, basic, gene 1 [Mus musculus]	827.4299	45.28	0.572450355
47523977	FASFIDK		keratin complex 2, basic, gene 35 [Mus musculus]	827.4299	45.28	0.572450355
51092293	FASFIDK		keratin complex 2, basic, gene 39 [Mus musculus]	827.4299	45.28	0.572450355
14861854	FASFIDK		keratin complex 2, basic, gene 7 [Mus musculus]	827.4299	45.28	0.572450355
13624315	FASFIDK		keratin complex 2, basic, gene 8 [Mus musculus]	827.4299	45.28	0.572450355
29789317	FASFIDK		keratinocyte associated protein 1 [Mus musculus]	827.4299	45.28	0.572450355
125098	FASFIDK		Keratin, type II cytoskeletal 3 (Cytokeratin 3) (K3) (CK3) (65 kDa cytokeratin)	827.4299	45.28	0.572450355
1346345	FASFIDK		Keratin, type II cytoskeletal 6B (Cytokeratin 6B) (CK 6B) (K6b keratin)	827.4299	45.28	0.572450355
20903595	FASFIDK		PREDICTED: RIKEN cDNA 2310001L23 [Mus musculus]	827.4299	45.28	0.572450355
63565108	FASFIDK		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	827.4299	45.28	0.572450355
31560611	FASQQGMTAYGTR		calponin 1 [Mus musculus]	1417.6719	107.7	0
31560611	FASQQGMTAYGTR	Oxidation (M)	calponin 1 [Mus musculus]	1433.6447	23.74	0.131641873
13937355	FAVYLPPQAESGK		esterase D/formylglutathione hydrolase [Mus musculus]	1406.7236	36.6	0
22203747	FAYNQLIK		procollagen, type VI, alpha 2 [Mus musculus]	996.547	47.69	0.291427949
10946574	FCTGLTQIETLFK		creatine kinase, brain [Mus musculus]	1500.7745	48.44	0.125725428
6679299	FDAGELITQR		prohibitin [Mus musculus]	1149.5928	44.99	0
31981690	FDDAVVQSDMK		heat shock protein 8 [Mus musculus]	1254.5654	32.23	0
63664182	FDDAVVQSDMK		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1254.5654	32.23	0
31981690	FDDAVVQSDMK	Oxidation (M)	heat shock protein 8 [Mus musculus]	1270.5712	24.34	1.231684155
63664182	FDDAVVQSDMK	Oxidation (M)	PREDICTED: similar to heat shock protein 8 [Mus musculus]	1270.5712	24.34	1.231684155
31560653	FDEAIQLR		phosphofructokinase, liver, B-type [Mus musculus]	991.5245	24.52	0
20330802	FDEFFSQGCAPGYEK		transferrin [Mus musculus]	1724.7355	52.16	0.341818089
63650172	FDETEQALANER		PREDICTED: DEAD box polypeptide 46 [Mus musculus]	1422.6573	65.75	0.452626951
34740335	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 2 [Mus musculus]	2409.217	95.46	0.372046734
6678467	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 4 [Mus musculus]	2409.217	95.46	0.372046734
6678469	FDGALNVDLTEFQTNLVPYPR		tubulin, alpha 6 [Mus musculus]	2409.217	95.46	0.372046734
7657067	FDGILTEGEGPR		ERO1-like [Mus musculus]	1290.6136	27.46	0
56119103	FDLGQDVIDFTGHSLALYR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	2167.0752	25.67	0.716424835
63562017	FDLGQDVIDFTGHSLALYR		PREDICTED: similar to GDP dissociation inhibitor 2 [Mus musculus]	2167.0752	25.67	0.716424835
51767507	FDLMYAK		PREDICTED: similar to tubulin, alpha-like 3 [Mus musculus]	887.4374	41.25	0.31984234
34740335	FDLMYAK		tubulin, alpha 2 [Mus musculus]	887.4374	41.25	0.31984234
6678467	FDLMYAK		tubulin, alpha 4 [Mus musculus]	887.4374	41.25	0.31984234

6678469	FDLMYAK		tubulin, alpha 6 [Mus musculus]	887.4374	41.25	0.31984234
13385280	FDQLFDDESDPFEVLK		PAI-1 mRNA-binding protein [Mus musculus]	1943.906	49.9	0.379690841
33598964	FDQLLAEEK		myosin heavy chain 10, non-muscle [Mus musculus]	1092.5571	35.61	0
7305295	FDQLLAEEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1092.5571	35.61	0
20137006	FDQLLAEEK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1092.5571	35.61	0
29336026	FDQLLAEEK		nonmuscle myosin heavy chain [Mus musculus]	1092.5571	35.61	0
6677805	FDTGNLCMVTGGANLGR		ribosomal protein S4, X-linked [Mus musculus]	1725.8033	119.43	0.452714195
21704020	FEAPLFNAR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	1064.5553	33.88	1.290582343
63635087	FEDEDSDDVPR		PREDICTED: RNA binding motif protein 25 [Mus musculus]	1323.554	47.61	0
6679439	FEDENFILK		peptidylprolyl isomerase A [Mus musculus]	1154.5703	59.24	0.432742813
10092608	FEDGDLTLYQSNAILR		glutathione S-transferase, pi 1 [Mus musculus]	1854.918	86.88	0.293759279
28173550	FEDYLNAESR		cell division cycle 10 homolog [Mus musculus]	1243.563	37.86	2.367712779
63655551	FEEEGNPYYSSAR		PREDICTED: methylcrotonoyl-Coenzyme A carboxylase 2 (beta) [Mus musculus]	1548.6661	38.71	0
33563270	FEEFLQR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	968.4835	30.6	0.338137169
50080209	FEELCSDLFR		heat shock protein 1A [Mus musculus]	1258.5859	37.37	0
31981690	FEELNADLFR		heat shock protein 8 [Mus musculus]	1253.6108	50.61	0.55939141
31981722	FEELNMDLFR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1313.6243	56.75	0
31981722	FEELNMDLFR	Oxidation (M)	heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1329.6117	26.22	0.54408869
22203755	FEELTNLIR		eukaryotic translation initiation factor 3, subunit 8 [Mus musculus]	1134.6122	40.77	0
23510263	FEENAPAQSTGVR		microtubule associated monoxygenase, calponin and LIM domain containing 3 [Mus musculus]	1405.6707	26.59	0
6678355	FEEPAPLSYDSR		tight junction protein 1 [Mus musculus]	1410.6615	25.25	0.212876521
9790073	FEEQVYNIPIR		cadherin 17 [Mus musculus]	1407.73	56.63	0.42205566
38090154	FEFTPGR		PREDICTED: oxidative-stress responsive 1 [Mus musculus]	853.4218	31.93	0.449304295
8394347	FEFTPGR		serine/threonine kinase 39, STE20/SPS1 homolog [Mus musculus]	853.4218	31.93	0.449304295
6678331	FEIFPTR		transglutaminase 3, E polypeptide [Mus musculus]	909.4838	29.48	0
6671557	FEIPYFTTSGIQVR		adaptor-related protein complex AP-1, mu subunit 1 [Mus musculus]	1657.8605	28.77	0
6753072	FEIPYFTVSGIQVR		adaptor protein complex AP-1, mu 2 subunit [Mus musculus]	1655.8796	52.06	0.432161607
58037117	FEIVYNLLSLR		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Mus musculus]	1366.777	35.58	0.397017509
13385374	FEIWDTAGQER		RAB5A, member RAS oncogene family [Mus musculus]	1351.6384	58.85	0.382765567
29789257	FEIWDTAGQER		RAB5C, member RAS oncogene family [Mus musculus]	1351.6384	58.85	0.382765567
34996495	FELDTSER		ribophorin II [Mus musculus]	996.4647	39.33	0
31981690	FELTGIPPAPR		heat shock protein 8 [Mus musculus]	1197.6539	28.79	0.479945422
27151748	FEQAFYTYDTSSPSILTLTAIR		nodal modulator 1 [Mus musculus]	2524.2419	26.8	0
57634518	FESDPATHNEPGVR		septin 11 [Mus musculus]	1555.7164	45.23	0
30348966	FESLEPEMNNQASR		spectrin beta 2 isoform 1 [Mus musculus]	1651.7433	77.09	0
7106421	FESLEPEMNNQASR		spectrin beta 2 isoform 2 [Mus musculus]	1651.7433	77.09	0
21313308	FESPEVAER		heterogeneous nuclear ribonucleoprotein M [Mus musculus]	1063.5061	29.71	0.417252998
9790069	FEVNISELPDEIDISSYIEQTR		HLA-B-associated transcript 1A [Mus musculus]	2597.2585	78.28	0.356578359
38372907	FEVNVAELPEEIDISTYIEQSR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 [Mus musculus]	2581.2646	22.1	0.552453744
33859650	FEWDLPLDGTLR		membrane bound C2 domain containing protein [Mus musculus]	1461.74	45.05	0.514682041
7305155	FFADLLDYIK		hypoxanthine guanine phosphoribosyl transferase 1 [Mus musculus]	1244.6554	50.51	0.329136461
6678145	FFDEESYSLLR		signal sequence receptor, delta [Mus musculus]	1405.6659	83.05	0.435944152
63641940	FFDQYR		PREDICTED: desmoplakin [Mus musculus]	875.4084	29.2	0.519784826
13385998	FFEDYGLFMR		TNF receptor-associated protein 1 [Mus musculus]	1324.6083	32.23	0.492183557
30409988	FFIEEMIR		galactose-4-epimerase, UDP [Mus musculus]	1084.5554	32.1	0.42148206
6677699	FFPEDVSEELIQEITQR		radixin [Mus musculus]	2080.0254	36.66	0
16716471	FFQELPASDSAFK		hypothetical protein LOC94184 [Mus musculus]	1486.7181	72.37	0
8567336	FFTAFDANGR		chloride channel calcium activated 3 [Mus musculus]	1145.5393	55.96	0.088084133
8567336	FFTAFDANGR	Deamidation (NQ)	chloride channel calcium activated 3 [Mus musculus]	1146.5293	53.62	0
31559883	FFTEEVDSR		very-long-chain acyl-CoA dehydrogenase VLCAD homolog [Mus musculus]	1129.5209	35.64	0
63589703	FFYSDQNVDSR		PREDICTED: talin 2 [Mus musculus]	1377.6133	68.82	0.214674257
6755809	FFYSDQNVDSR		talin 1 [Mus musculus]	1377.6133	68.82	0.214674257
7305305	FGDMQEIIQNFVR		N-myc downstream regulated gene 2 [Mus musculus]	1596.7904	29.06	0
19526818	FGFYEVFK		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1036.511	45.71	0.291698591
63746482	FGGEHVPNSPFQVTALAGDQPTVQTPLR		PREDICTED: filamin, alpha [Mus musculus]	2963.4897	22.27	0
21704096	FGGNPGGFGNQGGFGNSR		TAR DNA binding protein isoform 1 [Mus musculus]	1726.7734	97.02	0.466318447
33563270	FGLEGCEVLIPALK		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1488.8125	38.28	0
13384736	FGNPLLVQDVESYDPVLNPVLNR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	2598.3552	72.18	0.245951521
23956214	FGQGGAGPVGGQGPR		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1341.6707	94.12	0.504233417
7710084	FGQVPDQLGGLR		prolactin regulatory element binding protein [Mus musculus]	1286.6917	34.38	0.473390789

31981562	FGVEQDVDMVFASFIR		pyruvate kinase 3 [Mus musculus]	1859.9033	97.18	0
31981562	FGVEQDVDMVFASFIR	Oxidation (M)	pyruvate kinase 3 [Mus musculus]	1875.8918	40.41	0
31543315	FGYVDFESAEDLEK		nucleolin [Mus musculus]	1648.7633	82.89	0.250632979
6671690	FHQLDIDNPQSIR		carbonyl reductase 1 [Mus musculus]	1582.7915	27.55	1.425225164
52317152	FIEGPVTYSEAPR		phospholipase A2, group IVC (cytosolic, calcium-independent) [Mus musculus]	1465.7341	35.08	0
6678097	FIEWTR		serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	851.4461	35.87	0.453879184
6679237	FIGPSPEVVR		pyruvate carboxylase [Mus musculus]	1100.6053	32.97	0.306109474
31981327	FILNLPTFSVR		proteasome (prosome, macropain) subunit, beta type 2 [Mus musculus]	1306.754	28.52	0.347045853
6755002	FIQQTYPSGGEEQAQYCR		programmed cell death 6 interacting protein [Mus musculus]	2104.9453	59.76	0.345978379
6679687	FISDKDASVVGFFR		glucose regulated protein [Mus musculus]	1587.8214	37.76	0
6753138	FIWNSEK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	923.4601	30.09	0
18079339	FKLEAPDADELPR		aconitase 2, mitochondrial [Mus musculus]	1500.7678	31.81	0
31560680	FLAEEGFYK		intergral membrane protein 1 [Mus musculus]	1103.5552	30.46	0.355751137
6677903	FLDASQYSAAGGSSVR		SEC8 [Mus musculus]	1615.7836	37.77	1.621053521
14149647	FLDGIYVSEK		ribosomal protein L9 [Mus musculus]	1170.5908	35.46	0.524296142
33563270	FLDTAFDLDAFK		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1402.6901	75.9	0
6753598	FLEEYLSSTPQR		defender against cell death 1 [Mus musculus]	1469.7291	49.9	0.956391793
31982275	FLEMCDDLLAR		heat shock protein 4 [Mus musculus]	1325.6284	38.36	0
33563250	FLEQQNAALAAEVNR		desmin [Mus musculus]	1673.8611	104.67	0.1144656
33563250	FLEQQNAALAAEVNR	2 Deamidation (NQ)	desmin [Mus musculus]	1675.8461	47.38	0
33563250	FLEQQNAALAAEVNR	Deamidation (NQ)	desmin [Mus musculus]	1674.8372	46.8	2.391974263
482387	FLEQQNQVLQTK		keratin, 67K type II epidermal - human	1475.7791	72.23	0.350535478
51092293	FLEQQNQVLQTK		keratin complex 2, basic, gene 39 [Mus musculus]	1475.7791	72.23	0.350535478
1346343	FLEQQNQVLQTK		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1475.7791	72.23	0.350535478
41322904	FLEVQYLTGGLIEPDTPGR		plectin 1 isoform 1 [Mus musculus]	2105.0903	64.14	0.525808572
45387933	FLFVDADQIVR		UDP-glucose ceramide glucosyltransferase-like 1 [Mus musculus]	1322.7119	41.48	0.472995512
22164798	FLHDPSATQGFVGCALSSNIQR		selenium binding protein 1 [Mus musculus]	2348.1445	53.89	0.161239133
31981246	FLIDGFPR		UMP-CMP kinase [Mus musculus]	964.5255	43.12	0.430012383
31981892	FLLDHQGELFPSTDAQGV		Rho GTPase activating protein 1 [Mus musculus]	1973.9708	30.02	0
6680309	FLPLFDR		heat shock protein 1 (chaperonin 10) [Mus musculus]	907.5062	24.38	0.412044622
63618296	FLQDSSPSEELAR		PREDICTED: similar to E330039G21Rik protein [Mus musculus]	1478.7111	29.07	1.241068139
31980648	FLSQPFQVAEVFTGHMGK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2023.0038	54.77	0
7106429	FLSQPQVVTR		synaptogyrin 2 [Mus musculus]	1174.6556	33.38	0
29789191	FLSWILNR		asparaginyl-tRNA synthetase [Mus musculus]	1048.6013	35.49	0.561796766
6755002	FLTALAQDGVINEEALSVTELDR		programmed cell death 6 interacting protein [Mus musculus]	2504.2822	32.57	0.361304042
6753618	FLTEELSLDQDR		D-dopachrome tautomerase [Mus musculus]	1465.7194	60.55	0
29336026	FLTNGPSSSPGQER		nonmuscle myosin heavy chain [Mus musculus]	1476.7094	70.22	0.473727634
29336026	FLTNGPSSSPGQER	Deamidation (NQ)	nonmuscle myosin heavy chain [Mus musculus]	1477.7043	50.54	0
46849812	FLTTTPNSLLVSWQAPR		fibronectin 1 [Mus musculus]	1931.0349	22.42	0
19527256	FLVLDEADGLLSQGYSDFINR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 [Mus musculus]	2372.1792	80.2	0.488175229
50838806	FMLQDVIDLR		eukaryotic translation initiation factor 4 gamma, 3 [Mus musculus]	1249.6637	37.97	0
9790069	FMQDPMEIFVDDETK		HLA-B-associated transcript 1A [Mus musculus]	1844.8203	49.21	0.884060411
13384828	FMTEDTTDAPFR		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1430.6266	71.4	0
13384828	FMTEDTTDAPFR	Oxidation (M)	serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1446.6068	38.88	0.341429402
16418339	FNADEFEDMVAEK		ribosomal protein 10 [Mus musculus]	1544.6703	26.77	1.237486172
6671622	FNASQLITQR		B-cell receptor-associated protein 37 [Mus musculus]	1177.6309	41.74	0.353301297
63540743	FNDEHIPDSPFVVPVASLSDDAR		PREDICTED: filamin C, gamma [Mus musculus]	2527.2075	64.89	0
63660302	FNDEHIPDSPYLVPVIAPSDDAR		PREDICTED: filamin B, beta [Mus musculus]	2567.2388	53.29	0.442231429
63746482	FNEEHIPDSPFVVPVASPSGDAR		PREDICTED: filamin, alpha [Mus musculus]	2467.1816	83.34	0.133466273
47578123	FNFLEQAFDK	Deamidation (NQ)	potassium channel tetramerisation domain containing 12 [Mus musculus]	1259.5968	43.3	0.776684565
18079339	FNPETDFLTGK		aconitase 2, mitochondrial [Mus musculus]	1268.6138	66.79	0.195605444
51769759	FNPFVTSDR		PREDICTED: similar to 60S ribosomal protein L26-like 1 [Mus musculus]	1082.5271	47.23	0.51161011
31542151	FNQDPEAEDEGR		arginine-tRNA-protein transferase 1 [Mus musculus]	1406.5839	43.42	0.329745588
27228985	FNVSATPEQYVPYSTTR		13kDa differentiation-associated protein [Mus musculus]	1959.9489	45.93	0
6678365	FNVWDTAGQEK		RAN, member RAS oncogene family [Mus musculus]	1294.6135	70.27	0.414052863
6680724	FNVWDVGGQDK		ADP-ribosylation factor 6 [Mus musculus]	1264.5975	40.04	0.671747792
13384736	FNYGFEYLGVQDK		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1579.7469	37.22	0.92409848
19527018	FPEDGPELEEVLIQLAAADAR		dipeptidylpeptidase III [Mus musculus]	2283.1563	23.71	0.465254971
30911099	FPQLDDTSFANSR		fatty acid synthase [Mus musculus]	1497.6987	97.55	0.632906849
8567336	FPSPVTVYASIR		chloride channel calcium activated 3 [Mus musculus]	1336.7278	73.45	0.120249456

31981828	FPVFNMSYNPAENAVLLCTR		coatomer protein complex subunit alpha [Mus musculus]	2286.1145	25.32	0
51491880	FQAEIPDR		metastasis-associated protein 2 [Mus musculus]	975.4892	27.18	0
40254595	FQLTDSQIYEVLSVIR		dihydropyrimidinase-like 2 [Mus musculus]	1911.026	100.06	0.296966883
40254595	FQMPDQGMTSADDFFQGTK		dihydropyrimidinase-like 2 [Mus musculus]	2150.9292	100.16	0
6679599	FQSLGVAFYR		RAB7, member RAS oncogene family [Mus musculus]	1187.623	46.82	0.470624653
21746142	FSADEYFIPR		zinc finger and BTB domain containing 8 opposite strand [Mus musculus]	1244.5878	27.01	0.443223593
6753282	FSFEQPEFR		caspase 1 [Mus musculus]	1186.5583	26.93	0.431027025
23943876	FSHSGNQLDGPITAFR		zymogen granule membrane protein 16 [Mus musculus]	1746.8584	46.48	0.413224824
6678499	FSLQDPPNK		UDP-glucose dehydrogenase [Mus musculus]	1045.5305	42.26	0.502689336
31541909	FSMVLPEVEAALAEIPGVR		isochorismatase domain containing 1 [Mus musculus]	2028.0856	29.64	1.409292452
6671539	FSNEEIAMATVTALR		aldolase 1, A isoform [Mus musculus]	1652.8346	125.37	0.709639172
13386146	FSNQETSVEIGESVR		phosphoribosyl pyrophosphate synthetase 2 [Mus musculus]	1681.7994	36.12	0.405310998
16716471	FSPLMTAEGLGTR		hypothetical protein LOC94184 [Mus musculus]	1379.6958	54.92	1.297058708
28893559	FSPPEETGPSR		melanoma inhibitory activity 3 [Mus musculus]	1203.567	44.21	0.439559012
21450241	FSSQEAASSFGDDR		propionyl-Coenzyme A carboxylase, alpha polypeptide [Mus musculus]	1503.6364	119.52	0.181374709
54020742	FSTETTFLVDKYEIL		archain 1 [Mus musculus]	1805.9117	22.18	0
19527018	FSTIASSYEECR		dipeptidylpeptidase III [Mus musculus]	1392.6182	30.07	2.080341402
31981570	FSVLITGLR		polymeric immunoglobulin receptor [Mus musculus]	1005.6133	27.67	0.416368487
33859482	FSVSPVVR		eukaryotic translation elongation factor 2 [Mus musculus]	890.5081	31.91	0.461141913
9790073	FTFALGR		cadherin 17 [Mus musculus]	811.4487	27.11	0.449683293
31560560	FTPGTFTNQIQAAFR		laminin receptor 1 (ribosomal protein SA) [Mus musculus]	1698.8674	66.16	1.168669888
31980648	FTQAGSEVSALLGR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1435.7542	108.46	0.353768008
7106435	FTTDLDSPR		tenascin C [Mus musculus]	1051.5151	24.44	0.46282645
6755100	FTVLLMPNGPMR		proliferation-associated 2G4 [Mus musculus]	1375.7222	26.65	0.697406698
7305295	FVADLWK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	878.4724	34.05	0
9790067	FVDGEWYR		staphylococcal nuclease domain containing 1 [Mus musculus]	1071.4971	39.93	0.534140195
33469063	FVEFFGPGVAQLSIADR		aconitase 1 [Mus musculus]	1852.9615	59.14	0.379421408
31982178	FVEGLPINDFSR		malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1393.7174	68.53	0.400052038
7949029	FVGQDVEGER		CTP synthase [Mus musculus]	1135.5399	40.38	0.663826753
21704144	FVIGGPQGDAGLTGR		methionine adenosyltransferase II, alpha [Mus musculus]	1444.7568	64	2.50561517
6679687	FVMQEEFSR		glucose regulated protein [Mus musculus]	1172.5435	41.8	0
6679753	FVNVVPTFGK		Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) [Mus musc	1107.6139	55.03	0.426009429
7305395	FVSILMESIPLPDR		purine-nucleoside phosphorylase [Mus musculus]	1616.8751	45.81	1.154199334
6680606	FVTSSSGSYGGVR		keratin complex 1, acidic, gene 19 [Mus musculus]	1303.6283	123.29	0.433683637
6754036	FVTVQTISGTGALR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1449.8041	59.1	0.258797093
58037465	FWYFVSQLK		Ribosomal protein L18A [Mus musculus]	1217.6372	68.06	0.458547727
33859482	FYAFGR		eukaryotic translation elongation factor 2 [Mus musculus]	760.3804	24.58	0.504861023
40556608	FYEAFSK		heat shock protein 1, beta [Mus musculus]	891.4227	33.37	0.475906512
6754254	FYEQFSK		heat shock protein 1, alpha [Mus musculus]	948.4596	28.73	0.224902896
51771441	FYEQFSK		PREDICTED: similar to heat shock protein 1, alpha [Mus musculus]	948.4596	28.73	0.224902896
54287684	FYEQMNGPVTSGSR		eukaryotic translation elongation factor 1 delta isoform b [Mus musculus]	1572.7123	51.43	0
13384736	FYFVGDEDLLEIIGNSK		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1958.9653	22.98	0
6755002	FYNELTEILVR		programmed cell death 6 interacting protein [Mus musculus]	1396.749	45.27	0
6678571	FYPEDVAEELIQDITQK		villin 2 [Mus musculus]	2038.0028	84.04	0.509094655
6754750	FYPEDVSEELIQDITQR		moesin [Mus musculus]	2082.0068	84.73	0.521138122
22122523	FYQASTSELYGK		GDP-mannose 4, 6-dehydratase [Mus musculus]	1393.6599	87.53	0.44027731
33859594	FYSQAIELNPGNAIYYGNR		protein phosphatase 5, catalytic subunit [Mus musculus]	2190.0715	42.19	0.867119213
33563266	FYSVNVDYSK		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 [Mus musculus]	1221.5742	43.5	1.503918177
21450351	GAAFLGLGTDSVR		cysteine sulfinic acid decarboxylase [Mus musculus]	1263.6674	29.09	0
10946940	GAAGALLVYDITR		RAB2, member RAS oncogene family [Mus musculus]	1319.7321	30.99	0
63561841	GAAQNIIPASTGAAK		PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]	1369.7408	104.12	0.465961011
6679937	GAAQNIIPASTGAAK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1369.7408	104.12	0.465961011
33239431	GAAWEEPSSGNGTAR		RCC1-like [Mus musculus]	1489.677	29.85	0
33239431	GAAWEEPSSGNGTAR	Deamidation (NQ)	RCC1-like [Mus musculus]	1490.6567	32.57	2.88741055
40549395	GADVNAPPVPSSR		ankyrin repeat domain protein 17 isoform b [Mus musculus]	1266.6458	26.14	0.611201703
20806532	GAEAANVTGPDGVPVEGSR		cold shock domain protein A short isoform [Mus musculus]	1782.8556	54.44	0.340505247
6756033	GAEAANVTGPGGVPVQGSK		nuclease sensitive element binding protein 1 [Mus musculus]	1695.8643	88.19	0.434625165
55741460	GAEEMETVIPVDVMR		DJ-1 protein [Mus musculus]	1675.7979	58.43	0
7304887	GAGTDEFTLNR		annexin A3 [Mus musculus]	1180.5695	23.2	0
63746482	GAGTGGLGLAVEGPSEAK		PREDICTED: filamin, alpha [Mus musculus]	1570.8033	110.81	0

47059123	GAGVTLNVLEMTADDLENALK		UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	2174.1074	77.02	0
47059123	GAGVTLNVLEMTADDLENALK	Oxidation (M)	UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	2190.1357	32.78	0
29293809	GAIVPAQEVPPPTVPMDYSWAR		ATP citrate lyase [Mus musculus]	2381.197	40.49	0.225194914
7305085	GALTVGITNTVGSSISR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1632.8855	27.64	0.267431981
10946678	GANIQLLDLPGIIEGAAQGR		developmentally regulated GTP binding protein 2 [Mus musculus]	2006.1	39.45	0.472735853
7242197	GAVYSFDPVGSYQR		proteasome (prosome, macropain) subunit, beta type 1 [Mus musculus]	1545.7319	57.81	0.44160875
31542882	GAWDWSMLWK		UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7 [Mus musculus]	1279.5946	34.65	0
51764087	GAWSNVLR		PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	902.4882	25.48	0.1624527
22094075	GAWSNVLR		solute carrier family 25, member 5 [Mus musculus]	902.4882	25.48	0.1624527
9845253	GAYGGGYGGYDDYGGYNDGYGFGSDR		heterogeneous nuclear ribonucleoprotein H2 [Mus musculus]	2660.0359	57.48	0.406422024
10946928	GAYGGGYGGYDDYNGYNDGYGFGSDR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	2717.0459	56.39	0.422949488
31982186	GCDVVVIPAGVPR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1281.7	43.76	0.367190755
6679715	GDATVSYEDPPTAK		Ewing sarcoma breakpoint region 1 [Mus musculus]	1450.6709	54.75	0.31351139
21644581	GDDDVFVNPTNLLEFLSDR		UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 [Mus musculus]	2166.0339	108.83	0.182355082
6753484	GDEGEVGDPGEDNNDISPR		procollagen, type VI, alpha 1 [Mus musculus]	1971.8273	83.84	0
6753484	GDEGPPGPEGLR		procollagen, type VI, alpha 1 [Mus musculus]	1180.5601	47.52	0
6679078	GDFCIQVGR		nucleoside-diphosphate kinase 2 [Mus musculus]	994.4821	29.53	0.266811036
6754206	GDFIALDLGGSSFR		hexokinase 1 [Mus musculus]	1454.7297	81.07	0.282895162
7305143	GDFLALDLGGTNFR		hexokinase 2 [Mus musculus]	1495.757	59.19	0.558632365
45597447	GDGPVQGTIHFEQK		superoxide dismutase 1, soluble [Mus musculus]	1512.7463	61.09	0
21313554	GDLLFLTNFR		Sec11-like 3 [Mus musculus]	1195.6473	31.8	0.499619666
6755714	GDPNWFMK		transgelin [Mus musculus]	994.4456	27.5	0
30348966	GDQVSQNGLPAEQGSPR		spectrin beta 2 isoform 1 [Mus musculus]	1739.8356	76.76	0.377275135
7106421	GDQVSQNGLPAEQGSPR		spectrin beta 2 isoform 2 [Mus musculus]	1739.8356	76.76	0.377275135
30348966	GDQVSQNGLPAEQGSPR	Deamidation (NQ)	spectrin beta 2 isoform 1 [Mus musculus]	1740.8302	69.49	0
7106421	GDQVSQNGLPAEQGSPR	Deamidation (NQ)	spectrin beta 2 isoform 2 [Mus musculus]	1740.8302	69.49	0
25141233	GDTDQASNILASFGLSAR		matrin 3 [Mus musculus]	1822.8967	49.5	1.552977115
63650187	GDVAEGDLIEHFSQFGAVEK		PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A0 [Mus musculus]	2148.0298	39.34	1.120746764
31981562	GDYPLEAVR		pyruvate kinase 3 [Mus musculus]	1019.5142	29.41	0.507126123
63660302	GEAGIPAEFSIWTR		PREDICTED: filamin B, beta [Mus musculus]	1533.7738	59.03	0.68671042
31980685	GEDEAAMVESVGLALVK		glucosamine [Mus musculus]	1717.8752	47.46	0
6678986	GEELLSPLNLEQAAYAR		myosin IC [Mus musculus]	1873.9669	59.36	0.164669465
27370092	GEETPVIVGSALCALEQR		Tu translation elongation factor, mitochondrial [Mus musculus]	1871.9537	84.54	1.357773791
45504394	GEFFNELVGQQR		integrin beta 1 (fibronectin receptor beta) [Mus musculus]	1423.6991	69.49	0.188345763
31982178	GEFITTVQQR		malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1178.6202	49.96	0.316148457
19526814	GEFYNEASNLQVAIR		NADH dehydrogenase (ubiquinone) flavoprotein 1 [Mus musculus]	1710.8433	28.46	0
54607098	GEGGILINSQGER		succinate dehydrogenase Fp subunit [Mus musculus]	1329.6757	35.62	0.294611021
31542956	GEIAGPPDTPYEGGR		huntingtin interacting protein 2 [Mus musculus]	1515.7095	34.88	0
18700024	GELASYDMQLR		isocitrate dehydrogenase 3, beta subunit [Mus musculus]	1282.6143	46.26	0
29336026	GELEDTLDSTNAQQELR		nonmuscle myosin heavy chain [Mus musculus]	1918.9042	34.8	0
51592084	GESEDDFWWCIDR		hypothetical protein LOC74340 [Mus musculus]	1657.666	75.5	0.412788903
63738313	GEYDVTVPR		PREDICTED: similar to AHNAK [Mus musculus]	1035.5094	27.73	0.357358448
8393544	GFAFVQYVNER		heterogeneous nuclear ribonucleoprotein C [Mus musculus]	1329.6615	33.38	0.458866731
31559916	GFAFVTFDDHDTVDK		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1713.7742	70.66	0.327003494
6755296	GFAFVTFESPADAK		RNA binding motif protein, X-linked [Mus musculus]	1486.7189	52.58	0.561378321
6753820	GFAYVQFEDVR		FUS interacting protein (serine-arginine rich) 1 [Mus musculus]	1330.6493	35.52	0.392510262
6679082	GFDVFNALDLMENK		N-myristoyltransferase 1 [Mus musculus]	1612.7834	44.79	0
6679082	GFDVFNALDLMENK	Oxidation (M)	N-myristoyltransferase 1 [Mus musculus]	1628.7626	46.12	0
7549795	GFEVIEEFDGR		tight junction protein 2 [Mus musculus]	1297.6208	26.69	0
21592285	GFEVQVTELR		keratin 20 [Mus musculus]	1177.6196	41.6	0.463471642
40556608	GFEVVYMTEPIDEYCVQQLK		heat shock protein 1, beta [Mus musculus]	2391.1301	85.47	0
40556608	GFEVVYMTEPIDEYCVQQLK	Oxidation (M)	heat shock protein 1, beta [Mus musculus]	2407.1277	31.66	0
63641940	GFFDPNTEENLTYLQLK		PREDICTED: desmoplakin [Mus musculus]	2028.9921	56.47	0
41322904	GFFDPNTEENLTYLQLMER		plectin 1 isoform 1 [Mus musculus]	2317.0723	68.81	0.293726309
37537522	GFFDPNTHENLTYLQLLER		epiplakin 1 [Mus musculus]	2307.1362	31.28	0
41322904	GFFDPNTHENLTYLQLLER		plectin 1 isoform 1 [Mus musculus]	2307.1362	31.28	0
31560449	GFFELFPSVSR		aspartyl aminopeptidase [Mus musculus]	1285.6626	34.77	0.334802494
7304881	GFFVQPTVFSNVTDEMR		aldehyde dehydrogenase family 1, subfamily A1 [Mus musculus]	1973.9468	47.33	0
7949053	GFGDGYNGYGGGPGGGNFGGSPGYGGGR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2495.0405	184.46	0.422906682
7949053	GFGDGYNGYGGGPGGGNFGGSPGYGGGR	Deamidation (NQ)	heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2496.0254	80.61	0.407117776

6681069	GFGFGQGAGALVHSE		cysteine and glycine-rich protein 1 [Mus musculus]	1433.6792	94.64	0.113871778
6754222	GFGFILFK		heterogeneous nuclear ribonucleoprotein A/B [Mus musculus]	928.5286	42	0
6677919	GFGFVEFEDPR		splicing factor, arginine/serine-rich 5 (SRp40, HRS) [Mus musculus]	1299.6052	26.1	0.583361407
31560656	GFGFVSFER		poly A binding protein, cytoplasmic 1 [Mus musculus]	1045.5179	38.51	0.453049413
21312912	GFGFVSFER		polyA binding protein, cytoplasmic homolog [Mus musculus]	1045.5179	38.51	0.453049413
7949053	GFGFVTFDDHDPVDK		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1695.7706	68.25	0.896634046
63602815	GFGFVTFDDHDPVDK		PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A2/B1 isoform 2 [Mus musculus]	1695.7706	68.25	0.896634046
7304885	GFGTDEQAIIDCLGSR		annexin A11 [Mus musculus]	1681.7942	85.93	0.416846902
6680027	GFIGPGIDVPAPDMSTGER		glutamate dehydrogenase 1 [Mus musculus]	1915.924	24.77	0.320375803
6679687	GFPTIYFSPANK		glucose regulated protein [Mus musculus]	1341.6843	35.67	0.401453662
27229277	GFQEVVTPNIFNSR		threonyl-tRNA synthetase [Mus musculus]	1607.812	27.78	0.343268649
31981111	GFSAEQIAR		implantation-associated protein [Mus musculus]	978.5016	31.45	0.440303427
31560691	GFSEGLWEIENNPTVK		hepatoma-derived growth factor [Mus musculus]	1819.8817	46.77	0
33186863	GFSLEELR		ribosomal protein L13 [Mus musculus]	950.499	41.2	0.512835613
6754508	GFSVVADTPELQR		LIM and SH3 protein 1 [Mus musculus]	1418.7299	63.37	0.710699676
15617203	GFTIPEAFR		chloride intracellular channel 1 [Mus musculus]	1037.543	33.85	0.519927608
31982520	GFYYLMQELPQER		acetyl-Coenzyme A dehydrogenase, long-chain [Mus musculus]	1673.806	27.14	0.607639123
6681209	GGAPAEGEGTETPPEASR		DNA methyltransferase 3A isoform 1 [Mus musculus]	1712.7843	26.11	0.236312559
41322904	GGELVYTDTEAR		plectin 1 isoform 1 [Mus musculus]	1310.6282	57.93	0
24418933	GGENIYPAELEDFFLK		hypothetical protein LOC264895 [Mus musculus]	1841.8966	94.63	0.332510528
6755252	GGGGGGGGPGGEQETQELASK		purine rich element binding protein B [Mus musculus]	1829.8317	99.63	0.473775512
1346343	GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	2383.9531	122.86	0
7949053	GGGGNFGPGPGSNFR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1377.6312	97.32	0.417320537
6680572	GGGSFVQNNQPVGLR		kinesin family member 5B [Mus musculus]	1529.7871	38.33	1.048213249
63476037	GGPGQPGFEGEQGTR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1473.6761	68.3	0.093796569
34328400	GGPPFAFVEFEDPR		splicing factor, arginine/serine-rich 1 (ASF/SF2) [Mus musculus]	1564.7441	37.79	0.318726051
6680606	GGSFSGTLAVSDGLLSGNEK		keratin complex 1, acidic, gene 19 [Mus musculus]	1895.9319	116.58	3.331518074
22164798	GGSVQVLEDQELTCQPEPLVVK		selenium binding protein 1 [Mus musculus]	2368.2163	74.48	0.371028817
24418933	GGVIAGSPAPPELIR		hypothetical protein LOC264895 [Mus musculus]	1433.8132	40.78	0.393185072
29789343	GHPSAGAEEEGGSDGSAAEAEPR		eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]	2167.9128	24.99	0.675318939
22165384	GHYTEGAELVDSVLDVVR		tubulin, beta, 2 [Mus musculus]	1958.9835	31.83	0.493562495
33859488	GHYTEGAELVDSVLDVVR		tubulin, beta 2 [Mus musculus]	1958.9835	31.83	0.493562495
12963615	GHYTEGAELVDSVLDVVR		tubulin, beta 3 [Mus musculus]	1958.9835	31.83	0.493562495
7106439	GHYTEGAELVDSVLDVVR		tubulin, beta 5 [Mus musculus]	1958.9835	31.83	0.493562495
27754056	GHYTEGAELVDSVLDVVR		tubulin, beta 6 [Mus musculus]	1958.9835	31.83	0.493562495
21746161	GHYTEGAELVDSVLDVVR		tubulin, beta [Mus musculus]	1958.9835	31.83	0.493562495
21313520	GIADVPEWFR		acetoacetyl-CoA synthetase [Mus musculus]	1189.6052	32.29	0.538833761
24418919	GIAGLGDVAEVR		brain glycogen phosphorylase [Mus musculus]	1156.6359	34.95	0
19526818	GIFNGFSITLK		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1196.6652	65.31	0.390903622
19526818	GIFNGFSITLK	Deamidation (NQ)	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1197.6436	59.61	0
21450291	GILAADESVGTMGNR		aldolase 2, B isoform [Mus musculus]	1490.7284	25.6	0
63518159	GILFVGSGVSGGEEGAR		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1591.8101	100.49	0.50052745
30023842	GILLYGPPGTGK		valosin containing protein [Mus musculus]	1172.6632	43.45	0
31543942	GILSGTSDLLLTFDEAEVR		vinculin [Mus musculus]	2036.064	24.99	0
6679457	GINQGQVWIGGR		proteoglycan 2, bone marrow [Mus musculus]	1284.6844	46.9	0
18079351	GIQDVYVLSEQQGLLLK		major vault protein [Mus musculus]	1903.048	60.31	1.039417564
51766008	GIQEIGEMMGLNSTELER		PREDICTED: myosin IA [Mus musculus]	2006.9626	61.22	0.457705216
27754065	GISCMNTTVSESPFK		pyrophosphatase [Mus musculus]	1600.7295	22.71	0
11230802	GISQEQMQEFR		actinin alpha 4 [Mus musculus]	1352.6295	46.56	0.744781517
6756041	GIVDQSQQAYQEAFEISK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	2040.9861	60.84	0.514850729
23956084	GIVNEQFLLQR		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	1316.7323	38.2	0.304422806
20149756	GIYAYGFEKPSAIQQR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Mus musculus]	1827.941	22.92	0.476532325
21450625	GIYAYGFEKPSAIQQR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1827.941	22.92	0.476532325
6755809	GLAGAVSELLR		talin 1 [Mus musculus]	1085.6321	35.72	0.279581357
13386034	GLAPDLPEDLYHLIK		ribosomal protein S13 [Mus musculus]	1693.9039	27.16	0.80202375
6671561	GLAVFISDIR		adaptor protein complex AP-2, alpha 1 subunit [Mus musculus]	1090.6238	52.78	0
40254646	GLAVFISDIR		adaptor protein complex AP-2, alpha 2 subunit [Mus musculus]	1090.6238	52.78	0
6755372	GLCAIAQAESLR		ribosomal protein S3 [Mus musculus]	1231.6498	28.54	0
36031080	GLDGFQGPSGPR		procollagen, type IV, alpha 2 [Mus musculus]	1187.5833	57.38	0.234191274
20149756	GLDVPQVSLIINYDLPNNR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Mus musculus]	2140.1448	38.4	0.574862947

6681069	GLESTTLADKDGEIYCK		cysteine and glycine-rich protein 1 [Mus musculus]	1842.8702	81.84	0
10946870	GLEVTAYSPLGSSDR		aldo-keto reductase family 1, member A4 (aldehyde reductase) [Mus musculus]	1551.7827	62	0
6755863	GLFDEYGSK		tumor rejection antigen gp96 [Mus musculus]	1015.4725	44.12	0.454327238
6680690	GLFIIDPNGVVK		peroxiredoxin 3 [Mus musculus]	1271.7327	39.81	1.393229908
12746448	GLFLPEDENLR		aspartyl beta-hydroxylase [Mus musculus]	1302.6641	55.26	0
7304889	GLGTDEDAIIGILAYR		annexin A4 [Mus musculus]	1676.8853	76.61	0.311874783
6753060	GLGTDEDSILNLLTSR		annexin A5 [Mus musculus]	1703.881	83.43	0.232893546
6996913	GLGTDEDSLIEIICSR		annexin A2 [Mus musculus]	1720.8494	110.62	0.385891264
6754570	GLGTDEDTLIEILTTR		annexin A1 [Mus musculus]	1746.9108	106.13	0.376688895
31982159	GLGTEVPGNFQGPDPYR		hypothetical protein LOC235043 [Mus musculus]	1803.8654	46.67	0.509165231
40018610	GLIEIISNAAEYENIPIR		U5 snRNP-specific protein, 200 kDa [Mus musculus]	2015.0819	59.56	0.374388437
7948997	GLIPGSLQNEPTASVPPQSDVYR		PDZ and LIM domain 3 [Mus musculus]	2425.2334	76.53	0
6678329	GLLIEPAANSYLLAER		transglutaminase 2, C polypeptide [Mus musculus]	1729.9473	46.87	0.411648667
31981826	GLLPEELTPLILETQK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1794.0265	53.61	0.305474149
21704020	GLLTYTSWEDALSR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	1611.8041	48.67	0.287824969
31981549	GLPEGFAYPK		sulfide quinone reductase-like [Mus musculus]	1078.5491	25.52	0
10946928	GLPWSCSADEVQR		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1447.6809	29.02	0
27754118	GLTSLYALILNNNK		asporin [Mus musculus]	1533.8549	24.86	0
63746482	GLVEPVDVVDNADGTQTVNYVPSR		PREDICTED: filamin, alpha [Mus musculus]	2544.2512	162.57	0.089303838
13386272	GLVYETSVLDPDEGIR		citrate synthase-like protein [Mus musculus]	1762.8922	50.59	0.492254024
13385942	GLVYETSVLDPDEGIR		citrate synthase [Mus musculus]	1762.8922	50.59	0.492254024
6680748	GMSLNLEPDNVGVVVFGNDK		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2104.0422	99.82	0.440635699
6680748	GMSLNLEPDNVGVVVFGNDK	Oxidation (M)	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2120.0342	86.78	1.059663274
31560611	GMTVYGLPR		calponin 1 [Mus musculus]	993.5214	44.73	0.15241458
31560611	GMTVYGLPR	Oxidation (M)	calponin 1 [Mus musculus]	1009.5106	23.35	0
30911099	GNAGQTNYGFANSTMER		fatty acid synthase [Mus musculus]	1817.7927	62.32	0.46104134
21728376	GNFNYIEFTR		myosin regulatory light chain-like [Mus musculus]	1260.6057	23.02	0.282265715
7949051	GNFTLPEVAECFDEITYVELQK		heterogenous nuclear ribonucleoprotein U [Mus musculus]	2545.2307	46.07	0.616511876
6754854	GNLYWTDWNR		nidogen 1 [Mus musculus]	1324.6146	59.54	0.273812149
6679058	GNLYWTDWNR		nidogen 2 [Mus musculus]	1324.6146	59.54	0.273812149
7305027	GNPTVEVDLYTAK		enolase 2, gamma neuronal [Mus musculus]	1406.7141	70.29	0.42269624
51770896	GNPTVEVDLYTAK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1406.7141	70.29	0.42269624
13385994	GNSIIMLEALER		small nuclear ribonucleoprotein polypeptide G [Mus musculus]	1345.7169	25.7	1.954408543
21704206	GNWGYLDQAAALR		carboxylesterase 2 [Mus musculus]	1434.7128	69.53	0
27370126	GNWGYLDQVAALR		carboxylesterase 5 [Mus musculus]	1462.7469	74.84	0.422407402
19527178	GNWGYLDQVAALR		carboxylesterase 6 [Mus musculus]	1462.7469	74.84	0.422407402
37202121	GNYLVDVDGNR		4-aminobutyrate aminotransferase [Mus musculus]	1221.5859	44.23	1.259886468
31560611	GPAYGLSAEVK		calponin 1 [Mus musculus]	1091.5709	94.91	0.064833071
30023842	GPELLTMWFGESEANVR	Oxidation (M)	valosin containing protein [Mus musculus]	1951.9247	40.07	0.487582683
6679573	GPGLGSTQGQTIALPAQGLIEFR		purine rich element binding protein A [Mus musculus]	2311.2434	92.57	0.353870368
6755204	GPGLYYVDSEGNR		proteasome (prosome, macropain) subunit, beta type 5 [Mus musculus]	1426.6652	58.9	0.848509086
7305445	GPLQSVQVFGR		ribosomal protein S16 [Mus musculus]	1187.6532	31.05	0.559893964
13626040	GPSEAPQEAEAEEGATSDGEK		A kinase (PRKA) anchor protein (gravin) 12 [Mus musculus]	2088.8884	54.47	0.323787297
6680980	GPSGPQGIRGDKGEPGDK	Deamidation (NQ)	procollagen, type I, alpha 2 [Mus musculus]	1752.826	23.49	0
30911099	GPSIALDTACSSSLLALQNAYQAIR		fatty acid synthase [Mus musculus]	2563.3105	33.11	0.766214404
33859600	GPTEQLVSPEPEVYEIVR		protein phosphatase 1B, magnesium dependent, beta isoform [Mus musculus]	2042.0388	44.7	0.158681917
51766545	GQDIFIIQTIPR		PREDICTED: phosphoribosyl pyrophosphate synthetase-associated protein 1 [Mus musculus]	1400.788	22.71	0
27754099	GQELAFPLSPDWQVDYESYTWR		eukaryotic translation elongation factor 1 gamma [Mus musculus]	2687.2366	45.26	0.387143952
29293809	GQELIYAGMPITEVFK		ATP citrate lyase [Mus musculus]	1795.9257	22.4	0
58037546	GQETSTNPIASIFAWSR		isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	1864.9222	112.16	0.458632237
51491845	GQFSTDELVAEVEKR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1707.8628	24.69	0
13386370	GQGAAAAQQGGYEIPAR		kinesin-like 8 [Mus musculus]	1644.812	39.27	0.430576181
6677871	GQIIYTWQGANATR		scinderin [Mus musculus]	1578.8018	57.06	0.6499798
23956084	GQLTIDQVFPYPSVLSEEQAQFLK		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	2737.4031	37.82	0
6755698	GQNDLMGTAEDFADQFLR		surfeit gene 4 [Mus musculus]	2027.9152	99.06	0.409797405
6755698	GQNDLMGTAEDFADQFLR	Oxidation (M)	surfeit gene 4 [Mus musculus]	2043.9093	35.59	0.444398951
21489933	GQPFDVGPR		mitogen activated protein kinase 3 [Mus musculus]	972.4838	30.47	0.497444442
6678331	GQPWEIILVCNR		transglutaminase 3, E polypeptide [Mus musculus]	1427.7527	37.05	0
21536248	GQQYTDSFAQVNPLR		glutathione S-transferase, theta 3 [Mus musculus]	1723.8438	36.82	0.374490946
6754632	GQVFDVGPR		mitogen activated protein kinase 1 [Mus musculus]	974.5047	24.16	0.328658017

6754090	GSAPPGPVPEGQIR		glutathione S-transferase omega 1 [Mus musculus]	1361.7197	50.27	0.383968372
27532959	GSASSALELTEEELATAEAVR		aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	2134.0522	84.16	0.267056698
16716467	GSDHSASLEPGELAELVR		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1866.9166	69.05	0.157146006
23346461	GSGIQWDLR		NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Mus musculus]	1031.5289	26.78	0.321311464
6678143	GSIFAVFDSIQSAK		autoantigen La [Mus musculus]	1469.7599	55.36	0.73900571
6678573	GSLNITTPGIQIWR		villin 1 [Mus musculus]	1555.8611	68.16	0.548192652
6678449	GSVNMPFMDFLTK		thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	1486.7076	40.06	0
7657429	GSYTYFAPSNEAWENLDSDIR		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2435.0898	113.85	0
22094075	GTDIMYTGTLDCWR		solute carrier family 25, member 5 [Mus musculus]	1631.7251	96.25	0.571722512
22094075	GTDIMYTGTLDCWR	Oxidation (M)	solute carrier family 25, member 5 [Mus musculus]	1647.7166	22.41	0
6754570	GTDVNVFTTILTSR		annexin A1 [Mus musculus]	1523.8048	44.07	1.169436789
31982666	GTEDFIVESLDASFR		signal sequence receptor, alpha [Mus musculus]	1685.8088	54.9	0
6680850	GTELDDGIQADSGPINDIDANPR		caspase 7 [Mus musculus]	2383.1038	70.58	0.354541344
37202121	GTFCSFDTPDEAIR		4-aminobutyrate aminotransferase [Mus musculus]	1558.6908	50.49	0.302669891
6679761	GTGELTQLLNSMLTAIK		fructose bisphosphatase 2 [Mus musculus]	1789.9739	49.93	0
6753428	GTGGVDTAATGSVFDISNLDR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	2052.9827	135.39	0.239486674
10946574	GTGGVDTAAVGGVFDVSNADR		creatine kinase, brain [Mus musculus]	1964.9304	103.03	0.115007934
13385340	GTGLDEAMEWLVETLK		ADP-ribosylation factor-like 1 [Mus musculus]	1791.8856	46.61	0.951560187
7304887	GTGTDEDALIEILTTR		annexin A3 [Mus musculus]	1704.8695	96.29	0.190997359
13385274	GTLYIVEQIPTYVEYSDQTNVLR		hypothetical protein LOC66857 [Mus musculus]	2701.3613	22.16	0
31560449	GTPEPGPLGATDER		aspartyl aminopeptidase [Mus musculus]	1396.6664	55.09	0.418932188
6679237	GTPLDTEVPLER		pyruvate carboxylase [Mus musculus]	1326.6921	26.03	0
6677935	GTPSSSPVSPQESPK		sorbin and SH3 domain containing 1 [Mus musculus]	1484.7245	43.62	0.425162696
29789343	GTQGVVTNFEIFR		eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]	1467.7622	30.79	1.451485188
31981826	GTSFEAAATSGGSASSEK		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1644.7375	57.99	1.461447022
6678097	GTTASQMAQALALDK		serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	1505.7557	84.73	0.932623095
31981302	GTVCAANDFNPDADAK		annexin A6 [Mus musculus]	1608.693	24.27	0
40254595	GTVVYGEPITASLGTDGSHYWSK		dihydropyrimidinase-like 2 [Mus musculus]	2425.167	62.8	0
22164798	GTWEKPGDAAPMGYDFWYQPR		selenium binding protein 1 [Mus musculus]	2472.1147	60.12	0.192568274
20149742	GTYFPTWEGLFWEK		pre-mRNA processing factor 8 [Mus musculus]	1760.8353	39.26	0
63540743	GVAGVPAEFSIWTR		PREDICTED: filamin C, gamma [Mus musculus]	1489.7814	28.59	0.25097204
19526818	GVAPLWMR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	929.5046	31.09	0.305005612
23956222	GVDDLDFFIGDEAIEKPTYATK		ARP3 actin-related protein 3 homolog [Mus musculus]	2444.2024	67.95	0
6754570	GVDEATIIDILTK		annexin A1 [Mus musculus]	1387.7614	55.48	0
6996913	GVDEVTIVNILTNR		annexin A2 [Mus musculus]	1542.8519	88.82	0.572600491
29789257	GVDLQESNPASR		RAB5C, member RAS oncogene family [Mus musculus]	1272.6223	56.97	0.405528958
13385374	GVDLTEPAQPAR		RAB5A, member RAS oncogene family [Mus musculus]	1253.6522	32.55	0
40018610	GVESVFDIMEMEDEER		U5 snRNP-specific protein, 200 kDa [Mus musculus]	1914.8334	34.17	0
21450277	GVGIISEGNETVEDIAAR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1829.9196	89.72	0.227673424
31981147	GVLFASGQNLAR		leucine aminopeptidase 3 [Mus musculus]	1232.6761	28.9	0.428189099
7710042	GVLLEIEDLQANQFK		IQ motif containing GTPase activating protein 1 [Mus musculus]	1716.916	44.69	0
33859482	GVQYLNEIK		eukaryotic translation elongation factor 2 [Mus musculus]	1063.5763	40.13	0.342357143
6753514	GVTLPELYQDPAYQR		carnitine palmitoyltransferase 2 [Mus musculus]	1749.8835	60.45	0
6755863	GVVDSDDLPLNVSR		tumor rejection antigen gp96 [Mus musculus]	1485.7561	86.74	0.600579892
6754254	GVVDSEDLPLNISR		heat shock protein 1, alpha [Mus musculus]	1513.7885	64.59	0.593479522
40556608	GVVDSEDLPLNISR		heat shock protein 1, beta [Mus musculus]	1513.7885	64.59	0.593479522
27532959	GVVNILPGSGSLVGQR		aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	1552.8821	35.29	0.286297999
6671539	GVVPLAGTNGETTTQGLDGLSER		aldolase 1, A isoform [Mus musculus]	2272.1467	133.7	0.414039683
6671539	GVVPLAGTNGETTTQGLDGLSER	Deamidation (NQ)	aldolase 1, A isoform [Mus musculus]	2273.1262	102.27	0.337045658
12963691	GVVSDNCYPFSGR		tubulointerstitial nephritis antigen-like [Mus musculus]	1400.6412	26.11	0.244608587
6753428	GWEFMWNER		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	1254.5438	52.26	0
38259206	GWEFMWNER		creatine kinase, mitochondrial 2 [Mus musculus]	1254.5438	52.26	0
6753010	GWGDQLIWTQTYEEALYR		anterior gradient 2 [Mus musculus]	2229.0659	87.94	0.301550046
12746446	GWSESEQSEEFGGGIATMER		epithelial protein lost in neoplasm [Mus musculus]	2186.9409	28.48	1.131408671
22267440	GYADIVQLLLAK		SH3 domain protein 3 [Mus musculus]	1303.7605	80.01	1.524648179
22122825	GYAFNHSADFETVR		actin-related protein 2 [Mus musculus]	1613.7327	53.54	0.696391747
7305085	GYDFESETDTETIAK		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1705.7437	99.02	0.280326457
55742711	GYDFPAVLR		EH-domain containing 2 [Mus musculus]	1037.5422	42.13	0
7305085	GYDVDFPR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	968.4494	38.29	0.296819159
21450625	GYDVIAQAQSGTGK		eukaryotic translation initiation factor 4A1 [Mus musculus]	1394.6879	69.19	0.546649214

59709449	GYEEWLLNEIR		actinin alpha 2 [Mus musculus]	1421.7102	63.85	0.332511855
11230802	GYEEWLLNEIR		actinin alpha 4 [Mus musculus]	1421.7102	63.85	0.332511855
63487095	GYELLFQPEVVR		PREDICTED: catenin src [Mus musculus]	1449.7744	38.98	0.425324893
6755863	GYEVIYLTEPVDEYCIQALPEFDGK		tumor rejection antigen gp96 [Mus musculus]	2891.385	68.4	0
37537522	GYFDEDMNSILADPGDDTK		epiplakin 1 [Mus musculus]	2102.9204	40.93	0
41322904	GYFDEEMNR		plectin 1 isoform 1 [Mus musculus]	1160.4698	25.18	0
7949051	GYFEYIEENK		heterogenous nuclear ribonucleoprotein U [Mus musculus]	1291.5863	55.18	0.428892333
6753036	GYFIQPTVFGDVK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1470.7612	61.94	0
6681069	GYGYGQGAGTLSTDK		cysteine and glycine-rich protein 1 [Mus musculus]	1474.6802	88.06	0.247669719
6681069	GYGYGQGAGTLSTDKGESLGIK		cysteine and glycine-rich protein 1 [Mus musculus]	2159.0642	143.16	0.15801096
31981679	GYISPYFINTSK		heat shock protein 1 (chaperonin) [Mus musculus]	1389.6869	27.97	0
27754065	GYIWNYGAIPQTWEDPGHSDK		pyrophosphatase [Mus musculus]	2434.1194	32.79	0
16716467	GYPPEDIFNLAGK		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1420.7089	41.48	0.337861445
45598381	GYPTLLLFR		thioredoxin domain containing 5 [Mus musculus]	1079.6288	27.51	0.327285871
45598381	GYPTLLWFR		thioredoxin domain containing 5 [Mus musculus]	1152.6222	31.42	0.333459731
6671509	GYSFTTTAER		actin, beta, cytoplasmic [Mus musculus]	1132.5491	67.31	0.916380457
63652452	GYSFTTTAER		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	1132.5491	67.31	0.916380457
30911099	GYTVLGVEGR		fatty acid synthase [Mus musculus]	1050.5568	22.69	1.252635624
46849705	GYVLPTAR		lectin, galactose binding, soluble 4 [Mus musculus]	876.4974	32.73	0.465158661
31981549	GYWGGPAFLR		sulfide quinone reductase-like [Mus musculus]	1123.5721	31.42	0.640641004
41322904	GYYSPYSVSGSGSTAGSR		plectin 1 isoform 1 [Mus musculus]	1782.7958	42.74	0
9790219	HEYQANGPEDLNR	Deamidation (NQ)	destrin [Mus musculus]	1543.6824	69.18	0
6753010	HLSPDGQYVPR		anterior gradient 2 [Mus musculus]	1268.6393	39.19	0.290073929
6680047	HLYTLDGGDIINALCFSPNR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	2219.0811	26.65	0.6605258
7305295	HTQAVEELTEQLEQFK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1929.957	72.35	0
63487095	HYEDGYPGGSDNYGSLSR		PREDICTED: catenin src [Mus musculus]	1973.8262	115.46	0.409723532
21450129	IAAFADAAVDPIDFPLAPAYAVPK		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	2443.2986	68.12	0
6754036	IAATILTSPDLR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	1270.735	49.48	0.068544704
21450291	IADQCPSSLAIQENANALAR		aldolase 2, B isoform [Mus musculus]	2085.0479	104.92	0.358665267
18250284	IAEFAFEYAR		isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	1216.6055	57.74	0.224922258
63476037	IAEGVPQLLIVLTAEPSGDDVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2292.2449	92.56	0.083473692
29788770	IAELQQR	Deamidation (NQ)	nuclear mitotic apparatus protein 1 [Mus musculus]	858.4652	24.05	0
6753294	IAEQVASFQEEK		catenin alpha 1 [Mus musculus]	1378.666	47.55	0
6671561	IAGDYVSEEVWYR		adaptor protein complex AP-2, alpha 1 subunit [Mus musculus]	1586.7513	26.59	0
40254646	IAGDYVSEEVWYR		adaptor protein complex AP-2, alpha 2 subunit [Mus musculus]	1586.7513	26.59	0
6679515	IAIPGLAGAGNSVLLVSNLNPER		polypyrimidine tract binding protein 1 [Mus musculus]	2275.282	55.44	0.506502719
13399310	IAIYELLFK		ribosomal protein S10 [Mus musculus]	1109.6595	42.2	0.370091382
31981515	IALTDNSLIAR		ribosomal protein L7 [Mus musculus]	1186.6803	35.72	1.422390619
31982522	IAMQTLDMGR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1135.5614	64.46	0
55742877	IANLNGLK	Deamidation (NQ)	hypothetical protein LOC105000 [Mus musculus]	843.4777	28.14	0
63746482	IANLQTDLSDGLR		PREDICTED: filamin, alpha [Mus musculus]	1415.7531	87.72	0
33942112	IAPAEGPDVSER		IGF-II mRNA-binding protein 2 [Mus musculus]	1240.6343	23.85	0
27369581	IAPLAEGALPYNLAELQR		solute carrier family 25 (mitochondrial carrier, Aralar), member 12 [Mus musculus]	1939.0664	30.18	0
22122797	IAQFLSGIPETVPLSTVNR		3-ketoacyl-CoA thiolase B [Mus musculus]	2042.1251	33.25	0.249703231
7305295	IAQLEEELEEEQGNMEAMSDR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2451.0747	108.12	0.084039532
7305295	IAQLEEELEEEQGNMEAMSDR	2 Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2483.0701	40.65	0
7305295	IAQLEEQVEQEAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1542.7794	81.36	0.078606581
41054806	IAQSDYIPTQQDVLR		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1746.9034	68.91	0.641840264
13385010	IASGLGLAWIIGR		microsomal glutathione S-transferase 3 [Mus musculus]	1326.7933	49.56	0.392833576
36031080	IAVQPGTLGPQGR		procollagen, type IV, alpha 2 [Mus musculus]	1293.7325	49.87	0.272883251
21450241	IAWDDEETR		propionyl-Coenzyme A carboxylase, alpha polypeptide [Mus musculus]	1134.5179	27.48	0
6678331	IAYSQYER		transglutaminase 3, E polypeptide [Mus musculus]	1029.5015	54.76	0.069900121
51772556	IDATQVEVNPFGETPEGQVVCFDAK		PREDICTED: similar to Succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	2693.2925	58.25	0.475724652
13384620	IDEPLEGSEDR		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1259.5769	54.64	0.458955722
23346461	IDEVEEMLTNNR		NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Mus musculus]	1462.6917	66.6	0.782509328
6680854	IDFEDVIAEPEGTHSFDGIWK		caveolin, caveolae protein 1 [Mus musculus]	2405.1377	64.15	0
33469063	IDFEKEPLGVNAQGR		aconitase 1 [Mus musculus]	1672.8689	56.42	2.950062211
38090003	IDIDNSGYVSDYELQDLFK		PREDICTED: expressed sequence AI427122 [Mus musculus]	2234.0669	69.72	0.777895762
37202121	IDIPSFDWPIAPFPR		4-aminobutyrate aminotransferase [Mus musculus]	1770.9336	28.39	0
22507339	IDKMEEEMHK	Oxidation (M)	forkhead box N4 [Mus musculus]	1305.5981	23.26	0

31982030	IDKTDYMVGSYGPR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1601.7635	37.23	0
31982030	IDKTDYMVGSYGPR	Oxidation (M)	Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1617.7426	24.69	0
31980969	IDMNLTDLLGELQR		SEC23B [Mus musculus]	1630.8457	77.26	0
31543902	IDQYQGADAVGLEEK		thioredoxin-like 1 [Mus musculus]	1635.7871	86.44	0.831177246
50355692	IDSLSAQLSQLQK		lamin A isoform A [Mus musculus]	1430.7794	73.62	0
9790073	IDSVTGEIFSAAPLDR		cadherin 17 [Mus musculus]	1690.8698	125.91	0.493611122
7949053	IDTIEIITDR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1188.6526	68.67	0.76747986
63602815	IDTIEIITDR		PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A2/B1 isoform 2 [Mus musculus]	1188.6526	68.67	0.76747986
63562723	IEDFLER		PREDICTED: similar to 40S ribosomal protein S9 [Mus musculus]	921.465	30.07	0.396383067
63476037	IEDNVQQFLVLLVAGR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1814.0184	91.8	0.602395809
31981100	IEDVTPIPSDSTR		ribosomal protein S14 [Mus musculus]	1429.7203	68.29	0.56473153
9845263	IEEFQSTPGDIVITTYPK		dopa/tyrosine sulfotransferase [Mus musculus]	2038.0394	52.03	0.314515119
63476037	IEEGVPQFLVLISSGK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1715.9567	52.56	0.147489896
6680606	IEELNTQVAVHSEQIQISK		keratin complex 1, acidic, gene 19 [Mus musculus]	2166.1411	97.38	0.336481981
30794450	IEEVPELPLVVEDK		ribosomal protein L4 [Mus musculus]	1608.8712	72.84	0.628588119
19527334	IEFDDFEECLLR		NADH dehydrogenase (ubiquinone) Fe-S protein 5 [Mus musculus]	1528.7101	54.8	0
37620153	IEGYPDPEVVWFK		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1578.7828	53.41	0
31981722	IEIESFFEGEDFSETLTR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	2149.0012	59.43	0.361636675
31982720	IEIPEYFNFAK		SA rat hypertension-associated homolog [Mus musculus]	1370.698	37.62	0
482387	IEISELNR		keratin, 67K type II epidermal - human	973.5314	35.55	0
1346343	IEISELNR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	973.5314	35.55	0
13569841	IEQIEAGTPGR		thioredoxin reductase 1 [Mus musculus]	1170.6143	33.12	0.580948315
33563270	IEQLSPFPFDLLLK		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1659.932	28.45	0.553251455
33563250	IESLNEEIAFLK		desmin [Mus musculus]	1405.7512	73.33	0.058864442
31559916	IETIEVMEDR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1234.598	55.63	0
21703972	IETQDIQALR		malic enzyme 2, NAD(+)-dependent, mitochondrial [Mus musculus]	1186.6437	41.04	0
6754220	IEVIEIMTDR		heterogeneous nuclear ribonucleoprotein A1 [Mus musculus]	1218.636	31.67	1.295287771
63663965	IEVIEIMTDR		PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Sin	1218.636	31.67	1.295287771
23956396	IEVVNFLVPNAVYDIVK		SPFH domain family, member 2 [Mus musculus]	1932.0757	33.89	0.598942925
31981722	IEWLESHQDADIEDFK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1974.9059	72.19	0.555677698
30520301	IFAWATLR		putative lysophosphatidic acid acyltransferase [Mus musculus]	977.5609	25.7	0
14861854	IFEAQIAGLR		keratin complex 2, basic, gene 7 [Mus musculus]	1117.6337	41.38	0.46831308
31982186	IFGVTTLDIVR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1233.7249	65.74	0.367272351
27804325	IFSVTNGGQER		monoamine oxidase A [Mus musculus]	1207.6061	59.91	0
27804325	IFSVTNGGQER	Deamidation (NQ)	monoamine oxidase A [Mus musculus]	1208.5913	51.81	0
19526814	IFTNLYGR		NADH dehydrogenase (ubiquinone) flavoprotein 1 [Mus musculus]	983.5263	30.15	0.333952262
31559916	IFVGGIKEDTEEYNLR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1882.955	95.48	0
6754222	IFVGGLNPEATEEK		heterogeneous nuclear ribonucleoprotein A/B [Mus musculus]	1503.7583	61.17	0.358216775
6671602	IFVGGLSPDTPEEK		heterogeneous nuclear ribonucleoprotein D [Mus musculus]	1488.75	72.8	0.528629014
22164798	IFVWDWQR		selenium binding protein 1 [Mus musculus]	1149.5883	40.15	0.18131427
9790219	IFYDMK		destrin [Mus musculus]	816.3946	31.39	0.19235342
31560689	IGAFSYGSGLAASFFSFR		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	1884.9349	23.28	0.37140039
31982522	IGCFALSEPGNGSDAGAASTTAR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	2152.9963	133.16	0.347860875
31560438	IGDFIDVSEGPLIPR		mitochondrial ribosomal protein L39 [Mus musculus]	1627.876	35.25	0
63476037	IGDLQSQIVSLLK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1413.8289	71.49	0.274346783
31559995	IGDQEFDSLPALLEFYK		v-crk sarcoma virus CT10 oncogene homolog [Mus musculus]	1984.9905	61.64	0
24418919	IGEGFLTDLSQLK		brain glycogen phosphorylase [Mus musculus]	1420.7668	70.17	0
6754750	IGFPWSEIR		moesin [Mus musculus]	1104.5895	40.51	0.395154876
6677699	IGFPWSEIR		radixin [Mus musculus]	1104.5895	40.51	0.395154876
6678571	IGFPWSEIR		villin 2 [Mus musculus]	1104.5895	40.51	0.395154876
51873060	IGGIGTVPVGR		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	1025.6173	64.59	0.556464374
63660294	IGNLQTDLSDGLR		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	1401.735	44.81	0
51492007	IGQQPQQPGAPPQQDYTK		KH-type splicing regulatory protein [Mus musculus]	1980.978	38.87	0.524162261
63476037	IGVVQFSNDVFPEFYLK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2002.0332	75.84	0
51873060	IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	3567.7246	51.29	0.527853051
6754976	IGYPAPNFK		peroxiredoxin 1 [Mus musculus]	1006.533	39.44	0
6680027	IIAEGANGPTTPEADK		glutamate dehydrogenase 1 [Mus musculus]	1583.7889	95.52	0.352795047
6680027	IIAEGANGPTTPEADKIFLER		glutamate dehydrogenase 1 [Mus musculus]	2242.1699	36.6	0.579862723
6671507	IIAPPER		actin, alpha 2, smooth muscle, aorta [Mus musculus]	795.4727	23.99	0.187926997
6671509	IIAPPER		actin, beta, cytoplasmic [Mus musculus]	795.4727	23.99	0.187926997

30425250	IIAPPER		hypothetical protein LOC238880 [Mus musculus]	795.4727	23.99	0.187926997
63652452	IIAPPER		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	795.4727	23.99	0.187926997
37620153	IIDEDFELTER		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1379.6698	68.83	0
30425168	IIDFGLAR		myosin light chain kinase [Mus musculus]	904.5275	23.86	0.11527906
6677813	IIDVVYNASNNELVR		ribosomal protein S8 [Mus musculus]	1718.9094	102.22	0.515344348
34734056	IIEDNEYTAR		hemopoietic cell kinase isoform p59Hck [Mus musculus]	1223.5917	30.51	0
63476037	IIEELDVKPDGTR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1484.798	61.22	0.271011688
31560680	IIFDDFR		intergral membrane protein 1 [Mus musculus]	925.4765	32.1	0.386499978
6679567	IIGAVDQIQLTQAQLEER		polymerase I and transcript release factor [Mus musculus]	2025.1014	106.14	0.149203784
20137006	IIGLDQVAGMSETALPGAFK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2018.0651	89.26	0.480197258
20137006	IIGLDQVAGMSETALPGAFK	Oxidation (M)	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2034.0417	68.75	0.522035114
7710042	IIGNLLYYR		IQ motif containing GTPase activating protein 1 [Mus musculus]	1124.6506	31.6	0
41054806	IIHEDGYSEEECR		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1579.6825	38.04	0.325307808
7709980	IILLAEGR		S-adenosylhomocysteine hydrolase [Mus musculus]	884.5583	31.34	0.336701707
6679891	IILTAQPFR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1058.6368	35.97	0.513954006
51492007	IINDLLQSLR		KH-type splicing regulatory protein [Mus musculus]	1184.7023	43.98	0.467137943
29789343	IINDYYPEEDGK		eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]	1455.6632	35.51	4.740345036
31981722	IINEPTAAAIAYGLDK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1659.9037	79.37	0.413659127
7305163	IINEPTAAAIAYGLDK		heat shock protein 1-like [Mus musculus]	1659.9037	79.37	0.413659127
31981690	IINEPTAAAIAYGLDK		heat shock protein 8 [Mus musculus]	1659.9037	79.37	0.413659127
63664182	IINEPTAAAIAYGLDK		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1659.9037	79.37	0.413659127
50080209	IINEPTAAAIAYGLDR		heat shock protein 1A [Mus musculus]	1687.9075	69.38	2.170381236
6679439	IIPGFMCQGGDFTR		peptidylprolyl isomerase A [Mus musculus]	1541.7255	81.34	0.558461081
41322904	IISLETYNLFR		plectin 1 isoform 1 [Mus musculus]	1368.7562	56.8	0.418394283
136429	IITHPNFNGNTLDNDIMLIK		Trypsin precursor	2283.1848	149.12	0
136429	IITHPNFNGNTLDNDIMLIK	Deamidation (NQ)	Trypsin precursor	2284.1658	36.71	0
136429	IITHPNFNGNTLDNDIMLIK	Oxidation (M)	Trypsin precursor	2299.175	92.32	0.035607057
13384620	IITITGTQDQIQNAQYLLQNSVK		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	2589.3875	85.15	0
13384620	IITITGTQDQIQNAQYLLQNSVK	2 Deamidation (NQ)	heterogeneous nuclear ribonucleoprotein K [Mus musculus]	2591.3313	26.4	0
13507656	ILAATQFEPTAAR		type 1 tumor necrosis factor receptor shedding aminopeptidase regulator [Mus musculus]	1388.7545	58.56	0.876661952
6678359	ILATPPQEDAPSVDIANIR		transketolase [Mus musculus]	2020.0657	88.19	0.470971164
42415475	ILEFFGLK		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	966.5648	48.49	0.458778634
19526822	ILEFLGR		sulfotransferase family 1A, phenol-preferring, member 1 [Mus musculus]	847.5081	34.42	0.225895866
13937395	ILEQEEEEEQAGK		arsenate resistance protein 2 [Mus musculus]	1531.6892	37.25	1.728345305
45387933	ILETTTFFQR		UDP-glucose ceramide glucosyltransferase-like 1 [Mus musculus]	1255.6672	25.87	0.394362877
30794394	ILEVVNQVQDEER		hypothetical protein LOC71946 [Mus musculus]	1570.8063	29.19	0
42415475	ILFIFIDSDHTDNQR		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1833.9083	45.95	0.952362651
29336026	ILFQEFR		nonmuscle myosin heavy chain [Mus musculus]	952.5278	30.74	0.473433373
6680748	ILGADTSVDLEETGR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1575.7852	107.77	0.316054094
24762230	ILGFFF		ribosomal protein S15a [Mus musculus]	743.4057	24.97	0.891065916
31982755	ILLAELEQLK		vimentin [Mus musculus]	1169.7139	67.59	0.349270096
6680067	ILLANFLAQTEALMK		glucose phosphate isomerase 1 [Mus musculus]	1675.9435	57.75	1.153365091
6680067	ILLANFLAQTEALMK	Oxidation (M)	glucose phosphate isomerase 1 [Mus musculus]	1691.9249	50.57	0.345665589
31559883	ILLIFEGTNEILR		very-long-chain acyl-CoA dehydrogenase VLCAD homolog [Mus musculus]	1530.8878	24.97	0.470533705
46195430	ILMWTELIR		NADH dehydrogenase (ubiquinone) Fe-S protein 8 [Mus musculus]	1174.6703	41.42	0
6755076	ILQAVEFPFLVR		protein kinase, cAMP dependent, catalytic, beta [Mus musculus]	1431.8417	29.43	0.237640398
10946870	ILQNIQVFDFTFSPEEMK		aldo-keto reductase family 1, member A4 (aldehyde reductase) [Mus musculus]	2186.0684	46.03	0
31981679	ILQSSSEVGYDAMLGDFVNMVEK		heat shock protein 1 (chaperonin) [Mus musculus]	2532.2007	74.76	0.434327107
31981679	ILQSSSEVGYDAMLGDFVNMVEK	Oxidation (M)	heat shock protein 1 (chaperonin) [Mus musculus]	2548.1953	46.09	0
16716471	ILSDTTLWLR		hypothetical protein LOC94184 [Mus musculus]	1217.6904	62.7	0.242957574
13384620	ILSISADIETIGEILK		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1714.9832	45.44	0.578131042
6677771	ILTFDQLALESPK		ribosomal protein L18 [Mus musculus]	1474.8065	72.1	0
42734449	ILYLFYEDMK		sulfotransferase family 1D, member 1 [Mus musculus]	1334.6644	40.57	0
34538601	ILYMMDEINNPVLTVK		cytochrome c oxidase subunit II [Mus musculus]	1892.9849	39.95	0
31980648	IMDPNIVGNEHYDVAR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1842.8832	66.72	0.338660538
31980648	IMDPNIVGNEHYDVAR	Oxidation (M)	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1858.8738	30.74	0.553648814
18152793	IMEGPAFNFLDAPAVR		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1747.8889	82.27	0
18152793	IMEGPAFNFLDAPAVR	Oxidation (M)	pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1763.8773	23.46	0
20137006	IMGIPEDEQMGLLR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1601.8058	61.64	0.938729202
33859482	IMGPNYTPGK		eukaryotic translation elongation factor 2 [Mus musculus]	1077.537	42.36	1.242985901

6755372	IMLPWDPSGK		ribosomal protein S3 [Mus musculus]	1143.5681	22.85	0.409142846
30425202	IMNHSSILR	Deamidation (NQ)	nicotinamide nucleotide adenylyltransferase 2 [Mus musculus]	1071.579	23.76	0
22165384	IMNTFSVVPSPK		tubulin, beta, 2 [Mus musculus]	1319.6998	67.43	0
12963615	IMNTFSVVPSPK		tubulin, beta 3 [Mus musculus]	1319.6998	67.43	0
31981939	IMNTFSVVPSPK		tubulin, beta 4 [Mus musculus]	1319.6998	67.43	0
7106439	IMNTFSVVPSPK		tubulin, beta 5 [Mus musculus]	1319.6998	67.43	0
22165384	IMNTFSVVPSPK	Oxidation (M)	tubulin, beta, 2 [Mus musculus]	1335.6882	36.54	0.731535649
12963615	IMNTFSVVPSPK	Oxidation (M)	tubulin, beta 3 [Mus musculus]	1335.6882	36.54	0.731535649
31981939	IMNTFSVVPSPK	Oxidation (M)	tubulin, beta 4 [Mus musculus]	1335.6882	36.54	0.731535649
7106439	IMNTFSVVPSPK	Oxidation (M)	tubulin, beta 5 [Mus musculus]	1335.6882	36.54	0.731535649
31980648	IMNVIGEPIDER		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1385.7112	68.78	0.54107535
31981549	IMYLSEAYFR		sulfide quinone reductase-like [Mus musculus]	1292.637	35.17	0
29244556	INAGMYILSPAVLQR		GDP-mannose pyrophosphorylase B [Mus musculus]	1645.8782	25.76	0
6678499	INAWNSPTLPIYEPGLK		UDP-glucose dehydrogenase [Mus musculus]	1913.0159	65.17	2.061730949
6724311	INEAFDLLR		alcohol dehydrogenase 1 (class I) [Mus musculus]	1090.5908	63.61	0.266479541
31542111	INESDPEYLR		adducin 3 (gamma) [Mus musculus]	1235.5946	37.34	0
13384736	INEWLTLVEK		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1244.6729	26.68	0
51772556	INFDDNAEFR		PREDICTED: similar to Succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	1240.5569	59.9	0.281041308
46849708	INFDSNSAYR		succinate-Coenzyme A ligase, ADP-forming, beta subunit [Mus musculus]	1186.563	47.79	0.378083614
33598964	INFDVTGYIVGANIETYLLEK		myosin heavy chain 10, non-muscle [Mus musculus]	2372.2383	46.77	0
7305295	INFDVTGYIVGANIETYLLEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2372.2383	46.77	0
33563250	INLPIQTFSALNFR		desmin [Mus musculus]	1633.9103	71.43	0.073690736
33563250	INLPIQTFSALNFR	Deamidation (NQ)	desmin [Mus musculus]	1634.8793	27.83	0
31560666	INQDPLGIQGR		N-acetyl galactosaminidase, alpha [Mus musculus]	1210.6554	31.6	0.472493708
18034773	INQFYGAPTAVR		acetyl-CoA synthetase 2-like [Mus musculus]	1336.6973	24.55	0.386469986
19526986	INVLPLGSGAIAGNPLGVDR		argininosuccinate lyase [Mus musculus]	1933.0846	43.49	0
27804325	INVLVLEAR		monoamine oxidase A [Mus musculus]	1026.6289	39.69	0.188313323
33859753	INVNEIFYDLVR		RAS related protein 1b [Mus musculus]	1494.7963	64.45	0.374096157
33859488	INVYYNEAAGNK		tubulin, beta 2 [Mus musculus]	1355.6626	61.05	0.509154531
22165384	INVYYNEATGGK		tubulin, beta, 2 [Mus musculus]	1328.6465	81.45	0.34237541
21313144	IPAFLNVVDIAGLVK		GTP-binding protein PTD004 [Mus musculus]	1568.9402	36.28	0
16716467	IPAGTTLTLDMLTVK		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1573.8822	63	0.703647136
30911099	IPALLNTQPMLQLEYTATDR		fatty acid synthase [Mus musculus]	2288.1975	32.67	0.695526315
22094989	IPDEFDSDPILVQQLR		translocase of inner mitochondrial membrane 50 homolog [Mus musculus]	1884.9661	56.59	0.333494923
21312062	IPDQLVILDMK		transmembrane trafficking protein [Mus musculus]	1284.7155	45.57	0
6755368	IPDWFLNR		ribosomal protein S18 [Mus musculus]	1060.5604	38.32	0.417050369
31560444	IPEGPIDQGTATGR		fucosyltransferase 8 [Mus musculus]	1411.7158	63.94	0.332446511
22164798	IPGGPQMIQLSLDGK		selenium binding protein 1 [Mus musculus]	1553.8225	53.81	1.134101215
21313526	IPLDAYQPYLGPGTPK		hypothetical protein LOC78906 [Mus musculus]	1729.9083	35.75	0
31980648	IPSAVGYQPTLATDMGTMQER		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2266.0906	108.66	0.387132457
31980648	IPSAVGYQPTLATDMGTMQER	Oxidation (M)	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	2282.0835	23.96	0.303151937
31980648	IPVGPETLGR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1038.5938	57.83	0.43647942
6671622	IPWFQYPIIYDIR		B-cell receptor-associated protein 37 [Mus musculus]	1723.9232	52.09	0
63660294	IPYLPITNFNQNWQDGK		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	2048.0186	38.56	0.611106279
9790077	IQAAASPPANATAASDTNAGDR		glycogen synthase kinase 3 beta [Mus musculus]	2069.9895	42.08	0.776438957
20137008	IQAIELEDLLR		biglycan [Mus musculus]	1312.7467	37.31	0.216802265
21313620	IQDALSTVLQYAEDVLSGK		eukaryotic translation initiation factor 3, subunit 5 (epsilon) [Mus musculus]	2050.0486	35.41	0
13385310	IQEGVESLAGYADIFLR		propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]	1880.9762	25.45	0.500622591
10946940	IQEGVFDINNEANGIK		RAB2, member RAS oncogene family [Mus musculus]	1760.8787	83.67	0.77745232
46593021	IQEVDAQMLR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1202.6177	65.14	0
6678790	IQFGTLSDYFDALEK		mannosidase 2, alpha 1 [Mus musculus]	1746.868	44.4	0
6753498	IQFNESFAEMNR		cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	1485.6807	50.83	0.789488172
58037546	IQGGSVVEMQGDEMTR		isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	1736.8014	37.09	0
7657429	IQIEGDPDFR		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	1189.5852	41.79	0
31559981	IQIWDTAGQER		RAB15, member RAS oncogene family [Mus musculus]	1316.6602	72.13	0.507092936
31560030	IQLVEEELDR		tropomyosin 1, alpha [Mus musculus]	1243.6563	57.68	0.453250964
11875203	IQLVEEELDR		tropomyosin 2, beta [Mus musculus]	1243.6563	57.68	0.453250964
40254525	IQLVEEELDR		tropomyosin 3, gamma [Mus musculus]	1243.6563	57.68	0.453250964
33859600	IQNAGGSVMIQR		protein phosphatase 1B, magnesium dependent, beta isoform [Mus musculus]	1273.6667	29.31	0
19527388	IQQEIAVQNPLVSER		OTU domain, ubiquitin aldehyde binding 1 [Mus musculus]	1723.9301	36.02	0.354006474

27477057	IQQLNEEVGR		translocated promoter region protein [Mus musculus]	1185.6273	23.86	0
19526818	IQTQPGYANTLR		solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3 [Mus musculus]	1361.7238	60.03	0.396176111
31981246	IQTYLESTKPIIDLYEEMGK		UMP-CMP kinase [Mus musculus]	2371.2017	41.53	0.56669038
51762762	IQVLEEQLR	2 Deamidation (NQ)	PREDICTED: similar to pleckstrin homology-like domain, family B, member 3 [Mus musculus]	1129.6134	28.26	0
63476037	ISCSGNQLPTVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1274.6476	41.21	0
23956396	ISEIEDAAFLAR		SPFH domain family, member 2 [Mus musculus]	1334.6946	35.15	0.565515147
22165384	ISEQFTAMFR		tubulin, beta, 2 [Mus musculus]	1229.6023	53.98	0
33859488	ISEQFTAMFR		tubulin, beta 2 [Mus musculus]	1229.6023	53.98	0
12963615	ISEQFTAMFR		tubulin, beta 3 [Mus musculus]	1229.6023	53.98	0
31981939	ISEQFTAMFR		tubulin, beta 4 [Mus musculus]	1229.6023	53.98	0
7106439	ISEQFTAMFR		tubulin, beta 5 [Mus musculus]	1229.6023	53.98	0
21746161	ISEQFTAMFR		tubulin, beta [Mus musculus]	1229.6023	53.98	0
22122523	ISFDLAEYTADVDGVGTLR		GDP-mannose 4, 6-dehydratase [Mus musculus]	2041.9827	35.31	0.442993626
34328206	ISFPAVQAAPSFSNSFPK		tryptophanyl-tRNA synthetase [Mus musculus]	1894.9569	55.02	0.31716545
51491845	ISGETIFVTAPHEATAGIIGVNR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2353.2551	72.63	0
21361209	ISGLIYEETR		germinal histone H4 [Mus musculus]	1180.6277	73.53	0
12963603	ISLLQSEFPQAVYIDSYSSR		nuclear protein E3-3 [Mus musculus]	2303.1602	29.59	0
31982755	ISLPLPTFSSLNLR		vimentin [Mus musculus]	1557.9039	72.41	0.367179076
63476037	ISLSPEYVYSVSTFR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1747.8969	72.96	0.734585474
45387933	ISMINNPSQEISDSSTPIFR		UDP-glucose ceramide glucosyltransferase-like 1 [Mus musculus]	2236.0979	98.75	1.389320617
6678499	ISSINSISALCEATGADVEEVATAIGMDQR		UDP-glucose dehydrogenase [Mus musculus]	3051.4648	75.3	0.286301761
6677813	ISSLLEEQFQQGK		ribosomal protein S8 [Mus musculus]	1506.7769	81.14	0.457253676
6753320	ISTPVDVNNR		chaperonin subunit 3 (gamma) [Mus musculus]	1114.5905	37.21	0.424252824
7106439	ISVYYNEATGGK		tubulin, beta 5 [Mus musculus]	1301.6379	86.34	2.504689991
31542095	ITEEYYVHLIADNLPVATR		transmembrane 9 superfamily protein member 4 [Mus musculus]	2217.1392	33.74	0
31982522	ITEIYEGTSEIQR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1538.7722	62.07	0.392093027
9789937	ITFTGEADQAPGVEPGDIVLLLQEK		DnaJ (Hsp40) homolog, subfamily A, member 2 [Mus musculus]	2640.3777	64.63	0.611351984
12963691	ITGWGEETLPDGR		tubulointerstitial nephritis antigen-like [Mus musculus]	1430.692	57.82	0.31237551
31981562	ITLDNAYMEK		pyruvate kinase 3 [Mus musculus]	1197.5768	43.39	0.306148732
6679291	ITLPVDFVTADKFDENAK		phosphoglycerate kinase 1 [Mus musculus]	2023.042	64.82	0.441999565
6754480	ITMQNLNDR		keratin 13 [Mus musculus]	1104.5494	47.09	0
6680606	ITMQNLNDR		keratin complex 1, acidic, gene 19 [Mus musculus]	1104.5494	47.09	0
6016411	ITMQNLNDR		Keratin, type I cytoskeletal 13 (Cytokeratin 13) (K13) (CK 13)	1104.5494	47.09	0
125081	ITMQNLNDR		Keratin, type I cytoskeletal 15 (Cytokeratin 15) (K15) (CK 15)	1104.5494	47.09	0
6754480	ITMQNLNDR	Oxidation (M)	keratin 13 [Mus musculus]	1120.5341	29.52	0
6680606	ITMQNLNDR	Oxidation (M)	keratin complex 1, acidic, gene 19 [Mus musculus]	1120.5341	29.52	0
6016411	ITMQNLNDR	Oxidation (M)	Keratin, type I cytoskeletal 13 (Cytokeratin 13) (K13) (CK 13)	1120.5341	29.52	0
125081	ITMQNLNDR	Oxidation (M)	Keratin, type I cytoskeletal 15 (Cytokeratin 15) (K15) (CK 15)	1120.5341	29.52	0
34328204	ITPAHDQNDYEVGQR		valyl-tRNA synthetase 2 [Mus musculus]	1742.8121	42.18	0.452154019
31981722	ITPSYVAFTPEGER		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1566.7823	88.29	0.495442077
9790073	ITQVQWNDPGAQYSLVNK		cadherin 17 [Mus musculus]	2061.0413	43.99	1.003125737
54287684	ITSLEVENQNLR		eukaryotic translation elongation factor 1 delta isoform b [Mus musculus]	1415.7518	49.35	2.405552592
63680429	ITVAGQNCAFEPR		PREDICTED: plexin B2 [Mus musculus]	1405.6901	32.03	0
6678331	ITWIYNNR		transglutaminase 3, E polypeptide [Mus musculus]	1079.5665	37.77	0
6680960	ITYQPSTGEGNEQTITVGGR		procollagen, type XII, alpha 1 [Mus musculus]	2108.0264	93.75	0.264588662
7106435	ITYVPMTGGAPSMVTVDGTDTETR		tenascin C [Mus musculus]	2499.1765	59.24	0.218194485
23956096	IVAFENAFER		vesicle docking protein [Mus musculus]	1195.6073	26.98	0.836265862
21450277	IVEIPFNSTNK		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1261.6704	49.68	0.383054817
63476037	IVEYLDIGFDTTR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1541.7839	73.23	0
8393866	IVFADGNFWGR		ornithine aminotransferase [Mus musculus]	1281.6375	24.92	0.344358074
33598964	IVFQEFR		myosin heavy chain 10, non-muscle [Mus musculus]	938.5141	35.97	0.099904665
7305295	IVFQEFR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	938.5141	35.97	0.099904665
6753010	IVFVDPSLTVR		anterior gradient 2 [Mus musculus]	1245.7294	82.76	0.381242828
19527028	IVGELEQMVSEDVPLDHR		high density lipoprotein binding protein [Mus musculus]	2066.0151	34.39	1.57858863
7305619	IVILPDYLEIAR		ubiquitin specific protease 5 (isopeptidase T) [Mus musculus]	1414.8302	61.61	0.376106559
33859580	IVLDFR		galectin-3 [Mus musculus]	762.454	39.45	0.582360789
51491845	IVLDNSVFSEHR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1415.7133	40.6	0
40254595	IVLEDGTLHVTEGSGR		dihydropyrimidinase-like 2 [Mus musculus]	1682.864	30.71	0
6754482	IVLQIDNAR		keratin complex 1, acidic, gene 18 [Mus musculus]	1041.6018	32.43	0.339846214
6680606	IVLQIDNAR		keratin complex 1, acidic, gene 19 [Mus musculus]	1041.6018	32.43	0.339846214

125083	IVLQIDNAR		Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18)	1041.6018	32.43	0.339846214
417200	IVLQIDNAR		Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1041.6018	32.43	0.339846214
24418919	IVNGWQVEEADDWLR		brain glycogen phosphorylase [Mus musculus]	1829.8843	55.47	0.239212958
24418919	IVNGWQVEEADDWLR	Deamidation (NQ)	brain glycogen phosphorylase [Mus musculus]	1830.8817	46.46	0
31981246	IVPVEITISLLK		UMP-CMP kinase [Mus musculus]	1324.8423	60.23	0.335640299
31560353	IVQAEGNILQR		solute carrier family 6 (neurotransmitter transporter), member 14 [Mus musculus]	1240.7012	22.24	0.836552994
28173568	IVQMTEAEVR		protein phosphatase 1, catalytic subunit, beta [Mus musculus]	1175.6105	24.93	0
63630002	IVSNASCTTNCLAPLAK		PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]	1705.8571	119.69	0.606923974
6679937	IVSNASCTTNCLAPLAK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1705.8571	119.69	0.606923974
63746482	IVSPSGAAVPCK		PREDICTED: filamin, alpha [Mus musculus]	1128.6072	63.2	0
30023842	IVSQLLTLMDGLK		valosin containing protein [Mus musculus]	1430.8217	62.92	0
30023842	IVSQLLTLMDGLK	Oxidation (M)	valosin containing protein [Mus musculus]	1446.804	57.39	0.286451895
18079339	IVYGHLDDPANQEIER		aconitase 2, mitochondrial [Mus musculus]	1868.9152	74.85	0.27105032
8567336	IWALGGVTSDR		chloride channel calcium activated 3 [Mus musculus]	1174.6254	67.4	0
33859482	IWCFGPDGTGPNILTDITK		eukaryotic translation elongation factor 2 [Mus musculus]	2048.0154	75.3	0.559913132
6678483	IYDDDFFQNLDGVANALDNIDAR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	2614.2048	47.09	0.492079195
29568084	IYDYNSVIR		sorting nexin 9 [Mus musculus]	1142.585	23.52	6.252945713
33859554	IYELAAGGTAVGTGLNTR		fumarate hydratase 1 [Mus musculus]	1763.9303	132.89	0.214519356
31980685	IYGDGNAVPR		glucosamine [Mus musculus]	1061.5391	27.7	0
8567390	IYIDDGLISLVVR		pyruvate kinase liver and red blood cell [Mus musculus]	1475.8486	48.67	0
51491845	IYIDSNNNPER		clathrin, heavy polypeptide (Hc) [Mus musculus]	1334.6384	53.44	0.44269614
22122523	IYLGQLECFSLGNLDAK		GDP-mannose 4, 6-dehydratase [Mus musculus]	1883.9576	112.67	0
6671622	IYLTADNLVLNLQDESFTR		B-cell receptor-associated protein 37 [Mus musculus]	2225.1401	77.41	0.258463754
19705578	IYPEEMIQTGISAIDGMNSIAR		ATPase, H+ transporting, V1 subunit B, isoform 2 [Mus musculus]	2409.1843	22.24	0.318686755
6680618	IYQIYEGTAQIQR		acetyl-Coenzyme A dehydrogenase, medium chain [Mus musculus]	1582.8241	33.73	0.672501144
6679299	IYTSIGEDYDER		prohibitin [Mus musculus]	1460.6586	44.34	0.207636124
21703998	IYVISLAEPR		aspartyl-tRNA synthetase [Mus musculus]	1160.6559	30.44	0.399879405
22164798	IYVVDVGSEPR		selenium binding protein 1 [Mus musculus]	1233.6477	57.17	0.194538864
6754982	IYWNDGLDQYR		3'-phosphoadenosine 5'-phosphosulfate synthase 1 [Mus musculus]	1442.6719	33.17	0
7304901	KCYEAGMTLGARK	Oxidation (M)	androgen receptor [Mus musculus]	1443.7002	22.39	0
6671507	KDLYANNVLSGGTTMYPGIADR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2356.1628	135.84	0
6671507	KDLYANNVLSGGTTMYPGIADR	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2357.1531	122.97	0
6671507	KDLYANNVLSGGTTMYPGIADR	Oxidation (M)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2372.1538	49.43	0
6671509	KDLYANTVLSGGTTMYPGIADR		actin, beta, cytoplasmic [Mus musculus]	2343.1619	82.12	0.411461786
29789191	KEDGTFYEFGDDIPEAPER		asparaginyl-tRNA synthetase [Mus musculus]	2215.0022	51.23	0.52679447
7305295	KLEDDILVMDDQNSK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1762.8458	31.88	0
6753262	KLEVEANNAFDQYR		capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1696.8252	49.42	0.334791859
27370092	KYEEIDNAPEER		Tu translation elongation factor, mitochondrial [Mus musculus]	1492.6949	45.95	0
21704100	LAAAFAVSR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	905.5204	27.6	0
31982099	LAAIQESGVER		proteasome (prosome, macropain) subunit, beta type 6 [Mus musculus]	1172.6205	24.72	0.165995246
15617203	LAALNPESNTSGLDIFAK		chloride intracellular channel 1 [Mus musculus]	1860.9626	82.73	0
6678499	LAANAFLAQR		UDP-glucose dehydrogenase [Mus musculus]	1074.6006	44.19	0.376704249
50355692	LADALQELR		lamin A isoform A [Mus musculus]	1028.5742	31.72	0.316702839
31982522	LADMALALESAR		acyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1260.6395	44.4	0
41322904	LAEDEAFQR		plectin 1 isoform 1 [Mus musculus]	1078.5195	37.58	0.53516106
13624315	LAELEAALQR		keratin complex 2, basic, gene 8 [Mus musculus]	1113.6301	62.7	0.333335481
31560731	LAEMPADSGYPAYLGAR		ATPase, H+ transporting, V1 subunit A, isoform 1 [Mus musculus]	1781.8562	32.49	0
6753010	LAEQFVLLNLVYETTDK		anterior gradient 2 [Mus musculus]	1996.066	87.74	0
51093840	LAGFLDLTEQEFR		eukaryotic translation initiation factor 3 subunit 6 interacting protein [Mus musculus]	1538.7872	55.24	0
22164798	LAGQIFLGGSIVR		selenium binding protein 1 [Mus musculus]	1330.7859	46.79	0.199686292
6678483	LAGTQPLEVLEAVQR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1623.9092	64.87	0.271295626
13624315	LALDIEITTYR		keratin complex 2, basic, gene 8 [Mus musculus]	1307.7236	54.49	0
33563266	LALFNPDVSWDR		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 [Mus musculus]	1432.7262	42.59	0.442770094
23956396	LALQQDLTSMAPGLVIQAVR		SPFH domain family, member 2 [Mus musculus]	2124.188	39.78	0.672248068
23956166	LALSQNQQSSGAAGPTGK		cisplatin resistance-associated overexpressed protein [Mus musculus]	1714.8724	84.13	0.473940464
51770896	LAMQEFMILPVGASSFR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1896.9758	73.58	0
51770896	LAMQEFMILPVGASSFR	Oxidation (M)	PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1912.9664	29.31	0
6678103	LANSAFAVDLFK		serine (or cysteine) proteinase inhibitor, clade B, member 5 [Mus musculus]	1295.6937	44.82	0
51768219	LAPAVLLSGLTEVPVPTR		PREDICTED: similar to sodium bicarbonate cotransporter 2b [Mus musculus]	1833.0834	31.48	0
46430508	LAPDYDALDVANK		ribosomal protein L23a [Mus musculus]	1404.6958	62.98	0.557712683

6679687	LAPEYEAAATR		glucose regulated protein [Mus musculus]	1191.6022	36.07	0.659002613
31981562	LAPITSDPTEAAAVGAVEASFK		pyruvate kinase 3 [Mus musculus]	2145.1101	130.59	0.532897577
6755809	LAQAAQSSVATITR		talin 1 [Mus musculus]	1416.7867	60.54	0
29336026	LAQAEEQLEQESR		nonmuscle myosin heavy chain [Mus musculus]	1530.743	69.83	0.403494476
19527018	LAQDFLDSQNLSAYNTR		dipeptidylpeptidase III [Mus musculus]	1955.9493	96.33	0
18079351	LAQDPFPLYPGELLEK		major vault protein [Mus musculus]	1829.9663	38.42	0.732493648
30794206	LAQQQAALLMQQEER		splicing factor 3b, subunit 2 [Mus musculus]	1756.9	36.07	7.071716886
6679651	LAQSNGWGVMVSHR		enolase 3, beta muscle [Mus musculus]	1541.7599	52.91	0.459402849
51770896	LAQSNGWGVMVSHR		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1541.7599	52.91	0.459402849
6679651	LAQSNGWGVMVSHR	Deamidation (NQ)	enolase 3, beta muscle [Mus musculus]	1542.7531	25.04	0
51770896	LAQSNGWGVMVSHR	Deamidation (NQ)	PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1542.7531	25.04	0
11230802	LASDLLEWIR		actinin alpha 4 [Mus musculus]	1215.676	65.99	0.279758278
6755995	LATGSDDNCAAFFEGPPFK		WD repeat domain 1 [Mus musculus]	1986.8969	64.27	0
33186863	LATQLTGPVMPIR		ribosomal protein L13 [Mus musculus]	1396.7985	47.74	0.687436337
10946574	LAVEALSSLDGDLSGR		creatine kinase, brain [Mus musculus]	1602.8336	47.08	0
63650229	LAVNMVPFPR		PREDICTED: similar to TUBULIN BETA CHAIN (T BETA-15) [Mus musculus]	1143.6393	39.3	0
63488040	LAVNMVPFPR		PREDICTED: similar to tubulin Mbeta 1 [Mus musculus]	1143.6393	39.3	0
22165384	LAVNMVPFPR		tubulin, beta, 2 [Mus musculus]	1143.6393	39.3	0
33859488	LAVNMVPFPR		tubulin, beta 2 [Mus musculus]	1143.6393	39.3	0
12963615	LAVNMVPFPR		tubulin, beta 3 [Mus musculus]	1143.6393	39.3	0
31981939	LAVNMVPFPR		tubulin, beta 4 [Mus musculus]	1143.6393	39.3	0
7106439	LAVNMVPFPR		tubulin, beta 5 [Mus musculus]	1143.6393	39.3	0
27754056	LAVNMVPFPR		tubulin, beta 6 [Mus musculus]	1143.6393	39.3	0
21746161	LAVNMVPFPR		tubulin, beta [Mus musculus]	1143.6393	39.3	0
50355692	LAVYIDR		lamin A isoform A [Mus musculus]	849.485	36.29	0.289893306
33859506	LCAIPNLR		albumin 1 [Mus musculus]	899.5171	30.17	0.057109864
6671507	LCYVALDFENEMATAASSSSLEK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	2479.165	29.41	0
6671507	LCYVALDFENEMATAASSSSLEK	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	2480.1611	26.72	0
6671509	LCYVALDFEQEMATAASSSSLEK		actin, beta, cytoplasmic [Mus musculus]	2493.1577	64.63	0
63652452	LCYVALDFEQEMATAASSSSLEK		PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2493.1577	64.63	0
6671509	LCYVALDFEQEMATAASSSSLEK	Deamidation (NQ)	actin, beta, cytoplasmic [Mus musculus]	2494.1533	60.53	0.359185516
63652452	LCYVALDFEQEMATAASSSSLEK	Deamidation (NQ)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2494.1533	60.53	0.359185516
6671509	LCYVALDFEQEMATAASSSSLEK	Deamidation (NQ); Oxidation (M)	actin, beta, cytoplasmic [Mus musculus]	2510.1558	32.04	0
63652452	LCYVALDFEQEMATAASSSSLEK	Deamidation (NQ); Oxidation (M)	PREDICTED: similar to cytoplasmic beta-actin [Mus musculus]	2510.1558	32.04	0
7305295	LDAFLVLEQLR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1316.7628	74.05	0.0943286
21312950	LDDLINWAR		NADH dehydrogenase (ubiquinone) Fe-S protein 7 [Mus musculus]	1115.5759	50.23	0.21387914
6678143	LDEGWVPLETMIK		autoantigen La [Mus musculus]	1530.7837	26.08	0
30794450	LDELYGTWR		ribosomal protein L4 [Mus musculus]	1152.5802	31.53	0.557298099
21704206	LDFTEEEELLSR		carboxylesterase 2 [Mus musculus]	1480.718	78.5	0.415269961
12963691	LDGAWWFLR		tubulointerstitial nephritis antigen-like [Mus musculus]	1163.6025	28.8	0.232621849
20270275	LDIDPETITWQR		methylenetetrahydrofolate dehydrogenase 1 [Mus musculus]	1486.7546	53.2	0.605523465
31981562	LDIDSAPITAR		pyruvate kinase 3 [Mus musculus]	1171.6271	64.51	0.523468495
6677819	LDILDTAGQEEFGAMR		Harvey rat sarcoma oncogene, subgroup R [Mus musculus]	1765.8511	71.49	0
54607112	LDLGSNEFTEVPEVLEQLSGLR		Erbb2 interacting protein isoform 2 [Mus musculus]	2445.239	22.94	0
6753658	LDLWNLNNDTEVPTASISVEGNPALNR		dynein, cytoplasmic, intermediate chain 2 [Mus musculus]	2952.4575	93.08	0.434172485
6678359	LDNLVAIFDINR		transketolase [Mus musculus]	1402.7684	83.16	0.471650171
58037546	LDNNTELSFFAK		isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	1398.6777	42.72	0
33598964	LDPHLVLDQLR		myosin heavy chain 10, non-muscle [Mus musculus]	1318.7468	41	0
20137006	LDPHLVLDQLR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1318.7468	41	0
33859686	LDQETAQWLR		phosphoglucomutase 1 [Mus musculus]	1259.6404	46.82	1.022577777
30023842	LDQLIYIPLPDEK		valosin containing protein [Mus musculus]	1556.8521	63.52	0
6678483	LDQPMTEIVSR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1288.6573	48.59	0
33859650	LDQVLQWNR		membrane bound C2 domain containing protein [Mus musculus]	1171.6206	24.59	0.358513082
31981522	LDSVESVLPYEYTAFDFCQASEGK		transmembrane 9 superfamily member 2 [Mus musculus]	2698.2395	71.26	0.688990552
42734399	LDTQDTASSLQSDSTTETIAESIVTTILK		desmuslin isoform H [Mus musculus]	3068.5437	56.02	0
46559834	LDTQDTASSLQSDSTTETIAESIVTTILK		desmuslin isoform M [Mus musculus]	3068.5437	56.02	0
55741829	LDVATDNFFQNPELYIR		testis derived transcript 3 [Mus musculus]	2055.0088	30.78	19.4070105
6677813	LDVGNFSWGSECCTR		ribosomal protein S8 [Mus musculus]	1673.7021	43.74	0.432363409
13507628	LDVSSVASDTER		LPS-responsive beige-like anchor [Mus musculus]	1278.6256	23.39	0.219259103

6754482	LEAEIATYR		keratin complex 1, acidic, gene 18 [Mus musculus]	1065.5527	28.39	0.729715861
125083	LEAEIATYR		Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18)	1065.5527	28.39	0.729715861
13624315	LEAELGNMQGLVEDFK		keratin complex 2, basic, gene 8 [Mus musculus]	1792.8784	120.85	0.683646221
63565108	LEAELGNMQGLVEDFK		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1792.8784	120.85	0.683646221
13624315	LEAELGNMQGLVEDFK	Oxidation (M)	keratin complex 2, basic, gene 8 [Mus musculus]	1808.8723	53.2	0
63565108	LEAELGNMQGLVEDFK	Oxidation (M)	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1808.8723	53.2	0
18079339	LEAPDADELPR		aconitase 2, mitochondrial [Mus musculus]	1225.6013	68.24	0.248209806
6755817	LEDKDDLDVTELSNEELLDQLVR		thymopoietin [Mus musculus]	2701.343	112.59	0.302100312
21312062	LEDLSESIVNDFAYMK	Oxidation (M)	transmembrane trafficking protein [Mus musculus]	1889.8776	57.75	0.327944103
33468903	LEDVLPLAFTR		heterochromatin protein 1, binding protein 3 [Mus musculus]	1273.7155	32.74	0.300207074
6679261	LEEGPPVTTVLTR		pyruvate dehydrogenase E1 alpha 1 [Mus musculus]	1411.7778	59.7	0
63592948	LEELQELEFGR		PREDICTED: hypothetical protein LOC68553 [Mus musculus]	1362.6907	52.05	0
21704020	LEEVSPNLVR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	1155.6362	24.08	0
7305295	LEGDASDFHEQIADLQAQIAELK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2541.2522	60.04	0
20137006	LEGDSTDLSDQIAELQAQIAELK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2487.2461	35.03	0
13624315	LEGLTDEINFLR		keratin complex 2, basic, gene 8 [Mus musculus]	1419.7612	96.38	0.519751533
63565108	LEGLTDEINFLR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1419.7612	96.38	0.519751533
19527018	LEGSEVQLVEYEASAAGLIR		dipeptidylpeptidase III [Mus musculus]	2134.1028	37.35	0.69110544
63688576	LEGWELFPTPK		PREDICTED: similar to NADH-ubiquinone oxidoreductase subunit B14.7 (Complex I-B14.7) (CI-B14.7) [Mu	1316.6924	30.07	0
63618109	LEIPAQLATLLER		PREDICTED: similar to mKIAA1783 protein [Mus musculus]	1466.8608	29.4	0
55742711	LEISDEFSEAIGALR		EH-domain containing 2 [Mus musculus]	1649.8439	84.98	0.222422787
6680748	LELAQYR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	892.4902	29.31	0.348118287
13569841	LELTPVAIQAGR		thioredoxin reductase 1 [Mus musculus]	1267.7411	32.61	0
51711855	LENVSVALEFLER		PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like prot	1518.8192	47.77	0.10096376
6754480	LEQEIATYR		keratin 13 [Mus musculus]	1122.582	42.93	0.541154091
12803709	LEQEIATYR		Keratin 14 [Homo sapiens]	1122.582	42.93	0.541154091
47679095	LEQEIATYR		keratin 17n [Mus musculus]	1122.582	42.93	0.541154091
21592285	LEQEIATYR		keratin 20 [Mus musculus]	1122.582	42.93	0.541154091
6680602	LEQEIATYR		keratin complex 1, acidic, gene 15 [Mus musculus]	1122.582	42.93	0.541154091
6680606	LEQEIATYR		keratin complex 1, acidic, gene 19 [Mus musculus]	1122.582	42.93	0.541154091
6016411	LEQEIATYR		Keratin, type I cytoskeletal 13 (Cytokeratin 13) (K13) (CK 13)	1122.582	42.93	0.541154091
125081	LEQEIATYR		Keratin, type I cytoskeletal 15 (Cytokeratin 15) (K15) (CK 15)	1122.582	42.93	0.541154091
547751	LEQEIATYR		Keratin, type I cytoskeletal 17 (Cytokeratin 17) (K17) (CK 17) (39.1)	1122.582	42.93	0.541154091
417200	LEQEIATYR		Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1122.582	42.93	0.541154091
6753620	LEQELFSGGNTGINFEK		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1882.9139	69.76	0
63517295	LEQVSSDEGIGTLAENLLEALR		PREDICTED: RIKEN cDNA 1810009A16 [Mus musculus]	2357.2087	40.18	0.593641397
21704156	LEQYTNAIEGTK		caldesmon 1 [Mus musculus]	1366.6804	78.02	0
29336026	LESQLQEVQGR		nonmuscle myosin heavy chain [Mus musculus]	1286.6659	48.35	19.82810968
29789080	LESTLNYGMER		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1312.6184	42.67	0
31982236	LETTSNQDNLAPITAK		integrin alpha 6 [Mus musculus]	1715.8721	28.75	0
63565108	LEVDPNIQAVR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1253.7015	68.42	0.670288845
6753262	LEVEANNAFDQYR		capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1568.733	43.94	0
7305295	LEVNMQALK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1045.5616	40.51	0
7305295	LEVQLQDLQSK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1300.698	56.47	0
9790073	LEVVTDPTTNAGYVK		cadherin 17 [Mus musculus]	1606.8322	86.14	0
13928670	LFDIFSQQVATVIQSR		vacuolar protein sorting 35 [Mus musculus]	1851.9932	24.8	0.496808164
7305173	LFDQAFGVPR		heat shock protein 1 [Mus musculus]	1149.6058	58.67	0.155991041
31981147	LFEASVETGDR		leucine aminopeptidase 3 [Mus musculus]	1223.5894	29.95	0.57094675
63664040	LFEEPEDPSNR		PREDICTED: alpha isoform of regulatory subunit B55, protein phosphatase 2 [Mus musculus]	1332.6272	23.6	0.295944511
19882225	LFEFAGYDVLR		arginyl-tRNA synthetase [Mus musculus]	1329.6858	36.62	0
55742711	LFELEEQDLFR		EH-domain containing 2 [Mus musculus]	1438.7273	60.86	0.250830463
21313668	LFENQLSGPESIVNIGDVLFTGTADGR		RIKEN cDNA 2310001A20 [Mus musculus]	2849.4255	31.88	0.358287408
13384720	LFGLSPFEPWTTK		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Mus musculus]	1522.7869	23.85	0.334328025
21703832	LFGPYVWGR		arginyl aminopeptidase (aminopeptidase B) [Mus musculus]	1094.5833	30.7	0.517809924
63650187	LFIGGLNVQTSESGLR		PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A0 [Mus musculus]	1690.9116	45.41	0.356681475
31559916	LFIGGLSFETTDDSLR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1770.8914	116.76	0
6754220	LFIGGLSFETTDESLR		heterogeneous nuclear ribonucleoprotein A1 [Mus musculus]	1784.9036	34.1	0
7949053	LFIGGLSFETTEESLR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	1798.922	104.51	0.445855163
19526826	LFLAGYDPTPTMR		vacuolar protein sorting 26 [Mus musculus]	1481.7511	22.9	0.700267441
6680836	LFPSGLDQK		calreticulin [Mus musculus]	1004.5358	27.24	0

8567338	LFQSNDPTLR		coatomer protein complex, subunit gamma [Mus musculus]	1190.6189	27.98	0.723584144
8567340	LFQSNDQTLR		coatomer protein complex, subunit gamma 2 [Mus musculus]	1221.6179	47.1	0
18079351	LFSVPDFVGDACK		major vault protein [Mus musculus]	1397.6774	50.65	0.533569271
18875324	LFVGGLDWSTTQETLR		DAZ associated protein 1 [Mus musculus]	1822.936	43.04	0.895307702
23956214	LFVGNLPADITEDEFK		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1807.9139	37.37	0.569688555
23956214	LFVGNLPADITEDEFKR		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1964.0115	50.3	0
31560613	LFVTNDAATILR		chaperonin subunit 8 (theta) [Mus musculus]	1333.7458	42.26	0.362881237
6996917	LFYLALPPTVYEAVTK		glucose-6-phosphate dehydrogenase X-linked [Mus musculus]	1825.0024	22.16	2.8655802
38198665	LGAAPEEESAYVAGER		p47 protein [Mus musculus]	1648.7839	80.32	0.491523031
6680163	LGAGYPMGPFELLDYVGLDTTK		L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	2357.1807	72.61	0.303893572
54607098	LGANSLLDLVVFGR		succinate dehydrogenase Fp subunit [Mus musculus]	1473.8428	96.71	0
19527174	LGAVFNQVAFPLQYTPR		splicing factor 3b, subunit 3 [Mus musculus]	1921.0325	36.97	0.519571448
30725863	LGDAVEQGVINNSVLGYFIGR		glycyl-tRNA synthetase [Mus musculus]	2221.1589	53.4	0.521906777
31982755	LGDLYEEEMR		vimentin [Mus musculus]	1254.5706	71.73	0
6679291	LGDVYVNDAFGTAHR		phosphoglycerate kinase 1 [Mus musculus]	1634.7985	64.79	0
13654249	LGDVYVNDAFGTAHR		phosphoglycerate kinase 2 [Mus musculus]	1634.7985	64.79	0
136429	LGEHNIDVLEGNEQFINAAK		Trypsin precursor	2211.1062	136.66	0
27369816	LGEIQVVDASSLLAPLPR		RIKEN cDNA D230014K01 [Mus musculus]	1878.068	55.53	2.029226949
6680716	LGEIVTTIPTIGFNVETVEYK		ADP-ribosylation factor 1 [Mus musculus]	2323.2529	81.84	0.491146538
6680722	LGEIVTTIPTIGFNVETVEYK		ADP-ribosylation factor 5 [Mus musculus]	2323.2529	81.84	0.491146538
10181184	LGELPSWIMMR		ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 [Mus musculus]	1332.6835	34.92	0
6680960	LGELVLGPYDNTVVLEELR		procollagen, type XII, alpha 1 [Mus musculus]	2129.1553	34.33	0
26449160	LGEVQSESAGIQR		phosphoinositol 3-phosphate-binding protein-2 [Mus musculus]	1373.705	44.38	0.27278365
33859506	LGEYGFQNAILVR		albumin 1 [Mus musculus]	1479.7986	72.4	0.030773417
6755714	LGFQVWLK		transgelin [Mus musculus]	990.5749	37.35	0.081589685
10946574	LGFSEVELVQMVVDGVK		creatine kinase, brain [Mus musculus]	1848.9742	67	0
10946574	LGFSEVELVQMVVDGVK	Oxidation (M)	creatine kinase, brain [Mus musculus]	1864.9568	22.7	0
33859514	LGGNYGPTVAVQR		branched chain aminotransferase 2, mitochondrial [Mus musculus]	1331.7086	45.8	0.325462176
6754084	LGLDFPNLPYLIDGSHK		glutathione S-transferase, mu 1 [Mus musculus]	1899.0031	55.37	0.314549203
6680121	LGLDFPNLPYLIDGSHK		glutathione S-transferase, mu 2 [Mus musculus]	1899.0031	55.37	0.314549203
13385274	LGLDYSYDLAPR		hypothetical protein LOC66857 [Mus musculus]	1382.6917	40.97	0
6754254	LGLGIDEDDPTVDDTSAAVTEEMPPLEGDDDTSR		heat shock protein 1, alpha [Mus musculus]	3575.5786	119.56	0.286572293
40556608	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR		heat shock protein 1, beta [Mus musculus]	3535.6443	108.87	0.547280316
6679491	LGLQNDLFSLAR		aminopeptidase puromycin sensitive [Mus musculus]	1346.7396	24.76	0
6678097	LGMTDAFGGR		serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	1024.4899	46.07	0
6753036	LGPALATGNVVVMK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1369.7806	71.12	0
6678359	LGQSDPAPLQHQVDIYQK		transketolase [Mus musculus]	2037.0394	67.52	0.409635525
25020120	LGSQATGVQGQAGQLLDTTESTLGR		PREDICTED: laminin, alpha 5 [Mus musculus]	2488.2639	137.1	0.517244579
31560611	LGTDQPLDQATISLQMGTNK		calponin 1 [Mus musculus]	2131.0725	103.02	0
31560611	LGTDQPLDQATISLQMGTNK	Oxidation (M)	calponin 1 [Mus musculus]	2147.0642	96.51	0
7242205	LGTPQQIAIAR		cytoplasmic FMR1 interacting protein 1 [Mus musculus]	1167.689	23.09	0
40254582	LGVPDYIPSQQDILLAR		guanine nucleotide binding protein, alpha 13 [Mus musculus]	1898.0349	39.32	0.468559778
23956222	LGYAGNTEPQFIIPSCIAIK		ARP3 actin-related protein 3 homolog [Mus musculus]	2135.1226	34.35	0.568130808
6753428	LGYILTCPSNLGTGLR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	1677.9008	73.42	0.221769721
38259206	LGYILTCPSNLGTGLR		creatine kinase, mitochondrial 2 [Mus musculus]	1677.9008	73.42	0.221769721
63746482	LIALLEVLSQK		PREDICTED: filamin, alpha [Mus musculus]	1226.7695	70.35	0.10969998
63660294	LIALLEVLSQK		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	1226.7695	70.35	0.10969998
51711855	LIALLEVLSQK		PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like prot	1226.7695	70.35	0.10969998
31982236	LIATFPDTLTYSAYR		integrin alpha 6 [Mus musculus]	1731.8873	52.31	0.451297828
10946676	LIDAVGFSPLR		solute carrier family 26, member 3 [Mus musculus]	1187.6812	43.77	0
16716381	LIFYDLR		lysyl-tRNA synthetase [Mus musculus]	939.5353	22.32	0.462445786
40018610	LIGLSATLPNYEDVATFLR		U5 snRNP-specific protein, 200 kDa [Mus musculus]	2093.1316	22.8	0.539612637
33238874	LIIGQNGILSTPAVSCIIR		phosphoglucomutase 5 [Mus musculus]	1968.13	29.51	0
6678573	LIIQWNGPESNR		villin 1 [Mus musculus]	1426.7484	54.4	0.419275264
20149728	LIIVEGCQR		ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Mus musculus]	1030.5695	40.9	0
21450277	LIIVEGCQR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1030.5695	40.9	0
63479997	LIIVEGCQR		PREDICTED: similar to Sodium/potassium-transporting ATPase alpha-4 chain (Sodium pump 4) (Na+/K+ AT	1030.5695	40.9	0
22164798	LILPGLISSR		selenium binding protein 1 [Mus musculus]	1068.681	38.48	0.209167408
31542333	LIPEMDQVFTEVEMTTLEK		hypoxia up-regulated 1 [Mus musculus]	2253.1101	33.35	0
34740335	LISQIVSSITASLR		tubulin, alpha 2 [Mus musculus]	1487.8778	93.38	0.538307485

6678467	LISQIVSSITASLR		tubulin, alpha 4 [Mus musculus]	1487.8778	93.38	0.538307485
6678469	LISQIVSSITASLR		tubulin, alpha 6 [Mus musculus]	1487.8778	93.38	0.538307485
63561841	LISWYDNEYGYSNR		PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]	1779.8027	91.5	0.52325999
6679937	LISWYDNEYGYSNR		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1779.8027	91.5	0.52325999
31543689	LIVENLSSR		arginine/serine-rich splicing factor 6 [Mus musculus]	1030.5858	24.51	0
6677919	LIVENLSSR		splicing factor, arginine/serine-rich 5 (SRp40, HRS) [Mus musculus]	1030.5858	24.51	0
6680748	LKEIVTNFLAGFEP		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1577.8569	103.44	0.30361788
6755082	LLAEALNQVTQR		protein kinase C, delta [Mus musculus]	1355.765	35.93	0.368202845
31982122	LLAQLTQECQEQR		phospholipase C, beta 3 [Mus musculus]	1559.7841	29.27	0
27370092	LLDAVDTYIPVPTR		Tu translation elongation factor, mitochondrial [Mus musculus]	1572.8624	69.6	0.614506423
6755002	LLDEEEATDNDLR		programmed cell death 6 interacting protein [Mus musculus]	1532.7098	46.19	0.746402321
6677801	LLDFGSLSNLQVTQPTVGMNFK		ribosomal protein S17 [Mus musculus]	2409.2498	59.86	0.712989141
15809004	LLDFVLGQEIR		cyclin M4 [Mus musculus]	1302.7448	57.1	0.19617142
55742711	LLEALDDMLAQDIAK		EH-domain containing 2 [Mus musculus]	1658.8632	82.09	1.8247012
55742711	LLEALDDMLAQDIAK	Oxidation (M)	EH-domain containing 2 [Mus musculus]	1674.8409	40.08	0
21313234	LLEENEAMSVPTPSPAPVR		BAI1-associated protein 2-like 1 [Mus musculus]	2037.032	28.56	0.541436638
54607037	LLELQEVDSLLR		integrin beta 4 isoform 2 [Mus musculus]	1427.8105	34.86	0.531505932
16716471	LLENMTEVVR		hypothetical protein LOC94184 [Mus musculus]	1203.6398	37.94	2.550621417
6753066	LLETEEEAAFPLGGATPR		amine oxidase, copper containing 3 [Mus musculus]	1900.9635	84.26	0
29336026	LLGLGVTDFSR		nonmuscle myosin heavy chain [Mus musculus]	1177.6593	47.22	0.311452222
6754256	LLGQFTLIGIPPAPR		heat shock protein 9A [Mus musculus]	1592.9521	22.65	0.40983036
63746482	LLGWIQNK		PREDICTED: filamin, alpha [Mus musculus]	971.5653	48.31	0.151044795
63660294	LLGWIQNK		PREDICTED: similar to Filamin B (FLN-B) (Beta-filamin) (Actin-binding like protein) (ABP-280-like p	971.5653	48.31	0.151044795
51711855	LLGWIQNK		PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like prot	971.5653	48.31	0.151044795
10946574	LLIEMEQR		creatine kinase, brain [Mus musculus]	1031.5552	25.5	0
6754524	LLIVSNPVDILTYVAWK		lactate dehydrogenase 1, A chain [Mus musculus]	1944.1057	50.83	0
27370510	LLIYNPEDPPGSEVLR		paraoxonase 3 [Mus musculus]	1811.9476	27.61	0
51828444	LLLDTFEYQGLVK		PREDICTED: proline-rich polypeptide 6 [Mus musculus]	1538.8397	28.45	0
33468887	LLLNNDNLLR		capping protein (actin filament) muscle Z-line, alpha 1 [Mus musculus]	1197.6963	41.36	0.693889074
30911099	LLLPEDPLISGLLNSQALK		fatty acid synthase [Mus musculus]	2034.1871	45.98	0.821891819
28316750	LLLPGELAK		histone 1, H2ba [Mus musculus]	953.6012	64.58	0.463228413
20874851	LLLPGELAK		PREDICTED: similar to histone H2b-616 [Mus musculus]	953.6012	64.58	0.463228413
51491845	LLLPWLEAR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1110.6698	43.01	0.351691306
12025542	LLNFPTIVER		arsA (bacterial) arsenite transporter, ATP-binding, homolog 1 [Mus musculus]	1201.6903	28.7	0.390957802
63556656	LLNPQGAIR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	981.5861	39.13	0.107027789
6680960	LLPETPSDPFAIWQITDR		procollagen, type XII, alpha 1 [Mus musculus]	2099.0815	55.72	0
31981690	LLQDFFNGK		heat shock protein 8 [Mus musculus]	1081.5635	56.38	0.504988134
31981690	LLQDFFNGK	Deamidation (NQ)	heat shock protein 8 [Mus musculus]	1082.5516	30.65	0
50080209	LLQDFFNGR		heat shock protein 1A [Mus musculus]	1109.5787	45.37	0.216816506
31982755	LLQDSVDFSLADAINTEFK		vimentin [Mus musculus]	2126.0642	69.7	0
6678986	LLQFYAETCPAPER		myosin IC [Mus musculus]	1637.7972	22.66	2.712007869
24418919	LLSLVDDEAFIR		brain glycogen phosphorylase [Mus musculus]	1390.7607	84.15	0.305506841
63562740	LLTSAAFEDCQTR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	1454.6998	83.25	0.252489305
33859650	LLVPLVPDLQDVAQLR		membrane bound C2 domain containing protein [Mus musculus]	1789.0621	45.46	0.291748776
6755566	LLVVDPETDER		solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1 [Mus musculus]	1285.6494	33.13	0.33861598
31981826	LLYDLADQLHAAVGASR		electron transferring flavoprotein, alpha polypeptide [Mus musculus]	1812.9546	23.19	0
28077013	LLYEANLPENFR		stromal membrane-associated protein 1 [Mus musculus]	1478.7661	41.88	1.43496168
51491845	LLYNNVSNFGR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1296.6725	65.42	0.33540301
7657429	LLYPADIPVGNDQLLELLNK		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2238.239	36.36	0.346246925
29336026	LMATLSNTNPSFVR		nonmuscle myosin heavy chain [Mus musculus]	1550.8025	22.97	0
19923052	LMDEVAGIVAAR		brain acyl-CoA hydrolase [Mus musculus]	1244.6575	43.71	0
31560689	LMFNDFLSSSSDK		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	1490.7034	40.89	0
30794402	LMILFNK	Oxidation (M)	hypothetical protein LOC70950 [Mus musculus]	894.5214	33.14	0.250017584
59709449	LMLLLEVISGER		actinin alpha 2 [Mus musculus]	1372.7905	37.62	0
11230802	LMLLLEVISGER		actinin alpha 4 [Mus musculus]	1372.7905	37.62	0
6680986	LNDFASAVR		cytochrome c oxidase, subunit Va [Mus musculus]	992.5175	38.44	0.491141291
63641940	LNDSILQATEQR		PREDICTED: desmoplakin [Mus musculus]	1387.7166	34.67	0
19882225	LNDYIFSFDK		arginyl-tRNA synthetase [Mus musculus]	1261.614	39.02	0
6755809	LNEAAAGLNQAATELVQASR		talin 1 [Mus musculus]	2027.052	90.15	0.38332862
6755809	LNEAAAGLNQAATELVQASR	2 Deamidation (NQ)	talin 1 [Mus musculus]	2029.0574	38.7	0

6679687	LNFAVASR		glucose regulated protein [Mus musculus]	877.4917	50.29	0.300813822
21704100	LNFLSPELPAVAEFSTNETMGHSADR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	2833.3403	32.58	0.207415908
21450277	LNIPVNQVNPR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1263.7222	42.74	0.487077721
45387933	LNIQPSETDYAVDIR		UDP-glucose ceramide glucosyltransferase-like 1 [Mus musculus]	1733.8674	60.57	0.346733602
63476037	LNLLDLDYELAEQLDNIAEK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2332.1926	85.79	0.160625191
55742711	LNPFGNTFLNR		EH-domain containing 2 [Mus musculus]	1292.6715	32.48	0
22164798	LNPNFLVDFGK		selenium binding protein 1 [Mus musculus]	1263.6692	53.61	0.123805361
15638942	LNSLVSEK	Deamidation (NQ)	carnitine deficiency-associated gene expressed in ventricle 1 [Mus musculus]	890.4778	25.38	0
13384736	LNTQEIFDDWAR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1507.7318	41.87	0.570937668
6677819	LNVDEAFEQLVR		Harvey rat sarcoma oncogene, subgroup R [Mus musculus]	1432.7421	39.86	0
33563270	LNVLANVIR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1011.6401	33.46	1.257496306
9790017	LNWLSVDFNNWK		telomerase binding protein, p23 [Mus musculus]	1535.7654	62.81	0.429834491
33859811	LPAKPEVSSDEDVQYR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1832.8816	41.25	0
33859506	LPCVEDYLSAILNR		albumin 1 [Mus musculus]	1605.8344	106.72	0.092958467
46195798	LPDVYGVFQFK		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1312.6896	66.46	0.445431036
29789080	LPEAAFLAR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	987.5592	25.91	0.394292785
28916703	LPFPIIDDK		peroxiredoxin 5 related sequence 1 protein [Mus musculus]	1057.5953	67	0
6671549	LPFPIIDDK		peroxiredoxin 6 [Mus musculus]	1057.5953	67	0
51873060	LPLQDVYK		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	975.5473	54.49	0.533096999
7305075	LPNFGFVVFDDSEPVQK		ras-GTPase-activating protein SH3-domain binding protein [Mus musculus]	1937.9619	48.63	0
19527174	LPPNTNDEVDEDPTGNK		splicing factor 3b, subunit 3 [Mus musculus]	1854.8469	55.65	0.572579442
63746482	LPQLPITNFSR		PREDICTED: filamin, alpha [Mus musculus]	1285.7277	69.73	0
42741690	LPQPPEGQCYSN		ubiquitin-conjugating enzyme E2 variant 1 [Mus musculus]	1332.5979	25.79	0
8393866	LPSDVVTSVR		ornithine aminotransferase [Mus musculus]	1072.5964	25.52	0
63738313	LPSGSGPASPTTGSAVDIR		PREDICTED: similar to AHNAK [Mus musculus]	1769.9034	107.8	0.260535214
41322904	LPVDVAYQR		plectin 1 isoform 1 [Mus musculus]	1060.578	47.03	1.267543798
27370126	LPYTEEEEQLSR		carboxylesterase 5 [Mus musculus]	1493.7148	75.94	0.365122611
13624315	LQAEIEALK		keratin complex 2, basic, gene 8 [Mus musculus]	1014.5787	48.55	0
27532959	LQAGTVFVNTYNK		aldehyde dehydrogenase 1 family, member L1 [Mus musculus]	1454.7526	38.06	0
31982755	LQDEIQNMKEEMAR		vimentin [Mus musculus]	1734.8143	40.03	0
7305295	LQDFASTIEVMEEGK	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1712.7963	23.18	0
34328286	LQDPFSVYR		succinate dehydrogenase Ip subunit [Mus musculus]	1124.574	32.81	0.324225405
10946972	LQEAYYIFQELADK		epsilon subunit of coatomer protein complex [Mus musculus]	1730.8584	44.23	0
33147082	LQEDPNYSPQR		HLA-B-associated transcript 3 [Mus musculus]	1346.6392	41.85	0.504104811
33563250	LQEEIQLR		desmin [Mus musculus]	1028.5725	55.15	0
31982755	LQEEMLQR		vimentin [Mus musculus]	1046.532	38.61	0
6678573	LQEENQVITPR		villin 1 [Mus musculus]	1326.7019	69.27	0.42554184
50355692	LQEKEDLQELNDR		lamin A isoform A [Mus musculus]	1629.8069	71.99	0.769334249
31791057	LQELESLIANLGTGDDMVTDQAFEDR		laminin, gamma 1 [Mus musculus]	2880.373	22.09	0
8393988	LQEQLGNDVVEK		phosphomannomutase 2 [Mus musculus]	1371.71	66.7	0
34594657	LQGPQTSAEVYR		glycerol-3-phosphate dehydrogenase 1-like [Mus musculus]	1348.6876	40.56	0
39930335	LQGQLEQGDDTAAEK		ATP-binding cassette, sub-family F (GCN20), member 1 [Mus musculus]	1602.7659	85.34	0
10946940	LQIWDTAGQESFR		RAB2, member RAS oncogene family [Mus musculus]	1550.7699	86.13	0
20137006	LQLQEQLQAETELCAEAEELR	Deamidation (NQ)	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2445.1978	22.46	0
63664138	LQLTDEQLQNR		PREDICTED: hypothetical protein LOC219189 [Mus musculus]	1357.7072	25.72	0
41322904	LQMEAGLCEEQLNQADALLQSDIR		plectin 1 isoform 1 [Mus musculus]	2688.291	80.89	0
21450625	LQMEAPHIIVGTPGR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1618.8701	23.13	0
7305295	LQNEVESVTGMLNEAEGK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1947.9365	119.79	0
7305295	LQNEVESVTGMLNEAEGK	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1963.9344	72.7	0.384481708
12963569	LQNLDALTNLTVLSVQSNR		protein phosphatase-1 regulatory subunit 7 [Mus musculus]	2099.1421	52.44	0.844401125
38089265	LQNTGVADGYPVR		PREDICTED: palladin [Mus musculus]	1389.7137	52.82	0
41322904	LQNVQIALDYLR		plectin 1 isoform 1 [Mus musculus]	1445.818	50.29	0.479214045
20137006	LQQELDDLLVDLDHQR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1949.9948	74.7	0.551832237
7305295	LQQELDDLVVDLDNQR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1912.9713	129.96	0.109469724
19527026	LQQLPADFGR		hypothetical protein LOC98238 [Mus musculus]	1144.6115	51.37	0.664409155
13195624	LQSWLYASR		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 [Mus musculus]	1123.5862	25.71	0.296042706
10048462	LQTQPPSLSGQPPMYSGTLDCFR		carnitine/acylcarnitine translocase [Mus musculus]	2523.2146	33.07	0.280043285
63746482	LQVEPAVDTSGVQCYGPGIEGQGVFR		PREDICTED: filamin, alpha [Mus musculus]	2706.3206	132.26	0.069288679
31980942	LQVSQQEDITK		Inositol (myo)-1(or 4)-monophosphatase 1 [Mus musculus]	1288.6729	68.35	0.411791118
19525729	LQYAVISEAWR		crystallin, lamda 1 [Mus musculus]	1335.7106	27.34	1.10465967

41322904	LRAETEQGEQQR		plectin 1 isoform 1 [Mus musculus]	1444.7418	26.06	0
31791057	LSAEDLVLEGAGLR		laminin, gamma 1 [Mus musculus]	1442.7872	95.5	0.155076703
63476037	LSDAGITPLFLTSQEDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1862.9489	74.62	0
63489759	LSDDNTIGQEEIQQR		PREDICTED: spectrin alpha 2 [Mus musculus]	1745.8324	83.76	0.259979127
6754206	LSDEILIDILTR		hexokinase 1 [Mus musculus]	1400.8037	51.43	0
6755156	LSDFNIIDTLGVGGFGR		protein kinase, cGMP-dependent, type I beta isoform [Mus musculus]	1780.9241	27.65	0
6671666	LSDLLAPISEQIQEVITFR		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	2172.1902	90.11	0.831420037
34368584	LSEASGGLAENGER		erythropoietin 4 immediate early response [Mus musculus]	1389.6635	23.09	1.130436397
31981828	LSFLYLITGNLEK		coatomer protein complex subunit alpha [Mus musculus]	1510.851	58.12	0.327142704
21450291	LSFSYGR		aldolase 2, B isoform [Mus musculus]	829.4251	28.3	0.302649393
23956150	LSFYETGEIPR		nucleolar protein 5A [Mus musculus]	1311.6487	23.36	0
12963539	LSGAQADLHIGEGDSIR		ETHE1 protein [Mus musculus]	1738.8726	101.51	0
7948997	LSGGIDFNQPLVITR		PDZ and LIM domain 3 [Mus musculus]	1629.8937	63.68	0.384526578
11230802	LSGSNPYTTVTPQIINSK		actinin alpha 4 [Mus musculus]	1919.9758	45.78	0.380629525
27229048	LSGVSVSSDAFFPFR		5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase [Mus musculus]	1615.8167	99.55	0.499380333
6671549	LSILYPATTGR		peroxiredoxin 6 [Mus musculus]	1191.6743	52.3	0.438559876
6679166	LSLLEELTLAENQLLR		osteoglycin [Mus musculus]	1855.0582	56.49	0.175294964
13384736	LSLSNAISTVLPLTQLR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1826.0759	30.66	0.260545418
13507622	LSNTSPEFQEMSLLER		SAC1 (supressor of actin mutations 1, homolog)-like [Mus musculus]	1880.897	55.21	0
6755787	LSPPYSSPQEFAQDVGR		tripartite motif protein 28 [Mus musculus]	1877.9048	52.32	0.647120887
29336026	LSQLEEELEEEQNNSELLK		nonmuscle myosin heavy chain [Mus musculus]	2274.0879	42.74	0
6755967	LSQNNFALGYK		voltage-dependent anion channel 3 [Mus musculus]	1254.6442	61.83	0.386013798
12963539	LSQQSASGAPVLLR		ETHE1 protein [Mus musculus]	1426.8011	29.45	0.920239512
33859506	LSQTFPNADFAEITK		albumin 1 [Mus musculus]	1681.842	75.88	0
6754556	LSSEMNTSTVNSAR		lamin B1 [Mus musculus]	1496.7036	43.91	0
6754556	LSSEMNTSTVNSAR	Oxidation (M)	lamin B1 [Mus musculus]	1512.6891	33.42	0.579315888
34996495	LSSGYYDFSVR		ribophorin II [Mus musculus]	1293.6151	58.22	1.269029665
37620153	LSSMAMISGLSGR		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1309.6631	24.49	0
136429	LSSPATLNSR		Trypsin precursor	1045.5673	45.38	0
7305085	LSTDHIPILYR		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1327.7366	30.75	0.714453471
6680606	LSVEADINGLR		keratin complex 1, acidic, gene 19 [Mus musculus]	1186.6409	33.72	0
547751	LSVEADINGLR		Keratin, type I cytoskeletal 17 (Cytokeratin 17) (K17) (CK 17) (39.1)	1186.6409	33.72	0
6755078	LSVEIWDWDR		protein kinase C, alpha [Mus musculus]	1318.6488	22.15	0
22122387	LSVGLEDEQDLLEDLDR		cystathionase [Mus musculus]	1958.9606	80.7	0
7305007	LSYQNDPSFGSYAVPIR		desmocollin 2 [Mus musculus]	1913.9448	35.56	0
51491845	LTDQLPLIIVCDR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1498.829	63.96	0.435803413
6679012	LTDQVMQNPQVLAALQER		nucleosome assembly protein 1-like 4 [Mus musculus]	2054.0696	57.64	0
20137006	LTEMETMQSQLMAEK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1769.8131	48.98	0
31981983	LTEPQLGLGSQR		stromal interaction molecule 1 [Mus musculus]	1298.7043	51.45	0
6755863	LTESPCALVASQYGWSGNMER		tumor rejection antigen gp96 [Mus musculus]	2299.0498	46.27	0.37457224
29789191	LTESVDVLMPNVGEIVGGSMR		asparaginyl-tRNA synthetase [Mus musculus]	2203.1147	37.94	0.662105731
7304887	LTFDEYR		annexin A3 [Mus musculus]	943.4609	47.73	0.207268257
6755963	LTFDSSFSPNTGK		voltage-dependent anion channel 1 [Mus musculus]	1400.6637	82.03	0.335269597
6755965	LTFDTTFSPNTGK		voltage-dependent anion channel 2 [Mus musculus]	1428.6953	80.23	0.415563129
18079339	LTGSLSGWTSPK		aconitase 2, mitochondrial [Mus musculus]	1233.6399	58.35	0.224732977
50053824	LTLAQEDLISNR		early endosome antigen 1 [Mus musculus]	1372.7373	25.52	0.188985832
6755967	LTLDTIFVPNTGK		voltage-dependent anion channel 3 [Mus musculus]	1418.7845	30.06	0
63476037	LTLLGGPTPNTGAALEFVLR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2040.1478	74.11	0.107530271
6677813	LTPEEEEILNK		ribosomal protein S8 [Mus musculus]	1314.675	28.66	0
31981722	LTPEEIER		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	986.5164	26.55	0.379339651
63501125	LTQQAGDLTVPAGGQR		PREDICTED: ADP-ribosylation factor interacting protein 1 [Mus musculus]	1611.851	52.11	0.56638683
46575903	LTSLVPFVDAFQLER		eukaryotic translation initiation factor 3, subunit 10 (theta) [Mus musculus]	1734.9476	54.28	0.357749428
22165384	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta, 2 [Mus musculus]	2651.3181	31.54	0.325871318
33859488	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta 2 [Mus musculus]	2651.3181	31.54	0.325871318
31981939	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta 4 [Mus musculus]	2651.3181	31.54	0.325871318
7106439	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta 5 [Mus musculus]	2651.3181	31.54	0.325871318
21746161	LTTPTYGDLNHLVSATMSGVTTCLR		tubulin, beta [Mus musculus]	2651.3181	31.54	0.325871318
38083795	LTVEDPVTVEYITR		PREDICTED: proteasome (prosome, macropain) subunit, alpha type, 8 [Mus musculus]	1634.8639	37.2	0.368268895
51556274	LVAGEMGQNEPDQGGQR		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	1785.8218	70.59	0.591199993
13385472	LVAIVDVIDQNR		ribosomal protein L14 [Mus musculus]	1354.7679	56.61	0.614348995

7305395	LVFGLLNGR		purine-nucleoside phosphorylase [Mus musculus]	988.5979	34.56	0.505701177
6678992	LVGILDILDEENR		myosin VI [Mus musculus]	1498.8121	48.1	0.549177452
6754524	LVIITAGAR		lactate dehydrogenase 1, A chain [Mus musculus]	913.5837	50.79	0.565730333
6677783	LVILANNCPALR		ribosomal protein L30 [Mus musculus]	1296.7393	26.78	0
31980648	LVLEVAQHLGESTVR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1650.9081	47.36	0
29336026	LVLQVESLTTELSAER		nonmuscle myosin heavy chain [Mus musculus]	1787.9775	47.38	0.470291851
13384828	LVLVNAIYFK		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1179.7051	24.64	1.628736352
21704020	LVNQEVLADPLVPPQLTIK		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	2087.2141	29.18	0
31981273	LVPDMIPEVVSEQVSSYLSK		CNDP dipeptidase 2 (metallopeptidase M20 family) [Mus musculus]	2220.1362	32.76	0
63518159	LVPLLDTGDIIIDGGNSEYR		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	2160.1155	81.54	0.508985277
31543942	LVQAAQMLQSDPYSVPAR		vinculin [Mus musculus]	1974.0105	28.58	0.22539387
6754976	LVQAFQFTDK		peroxiredoxin 1 [Mus musculus]	1196.6292	60.36	0.757256528
31981679	LVQDVANNTNEEAGDGTTTATVLAR		heat shock protein 1 (chaperonin) [Mus musculus]	2560.25	137.24	0.453983194
33859506	LVQEVTDFAK		albumin 1 [Mus musculus]	1149.6116	70.26	0.036899417
31981769	LVSEFPYIEAEVK		glycerol-3-phosphate dehydrogenase 2 [Mus musculus]	1523.7692	34.36	13.85050601
63660302	LVSPGSANETSSILVESVTR		PREDICTED: filamin B, beta [Mus musculus]	2046.0719	85.32	0.382157537
14149635	LVSSENFDDYMK		fatty acid binding protein 4, adipocyte [Mus musculus]	1447.6406	39.35	0
40556608	LVSSPCCIVTSTYGWTANMER		heat shock protein 1, beta [Mus musculus]	2318.0659	39.51	0.50902482
63530525	LVTFESVAVPLQQGAEQQR		PREDICTED: SEC31-like 1 [Mus musculus]	2100.1167	86.4	0.314880702
6679158	LVTLEEFLASTQR		nucleobindin 1 [Mus musculus]	1506.8191	44.24	0
6679599	LVTMQIWDTAGQER		RAB7, member RAS oncogene family [Mus musculus]	1647.8065	44.35	0
24418919	LVTSIGDVVNHDPVVGDR		brain glycogen phosphorylase [Mus musculus]	1891.9812	49.51	0.341994175
37059806	LVYQNIFTAMQAMIRAMDTLK	2 Deamidation (NQ); 2 Oxidation (M)	guanine nucleotide binding protein, alpha q polypeptide [Mus musculus]	2492.208	25.06	0
31542895	LVYQNIFTAMQAMIRAMDTLR	2 Deamidation (NQ)	guanine nucleotide binding protein, alpha 14 [Mus musculus]	2488.1917	30.94	0
28077103	LWAPDSPNR		phospholipase A2, activating protein [Mus musculus]	1055.5347	25.08	1.581433449
6680047	LWDLTTGTTTR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1264.6523	58.92	0.498608017
31560517	LWTLVSEQTR		ribosomal protein L27a [Mus musculus]	1232.6639	57.63	0.468732867
22164798	LYATTSLYSAWDK		selenium binding protein 1 [Mus musculus]	1518.7419	81.41	0.271077565
6753010	LYAYEPSDTALLYDNMK		anterior gradient 2 [Mus musculus]	2006.9282	44.55	0
6753010	LYAYEPSDTALLYDNMK	Oxidation (M)	anterior gradient 2 [Mus musculus]	2022.9121	53.64	0
6680748	LYCIYVAIGQK		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1270.6908	44.9	0.697825414
19525729	LYDIEQQQITDALENIR		crystallin, lamda 1 [Mus musculus]	2062.0371	79.63	0.224890999
30519947	LYDNLLEQNLIR		proteasome 26S non-ATPase subunit 11 [Mus musculus]	1503.813	27.21	0
6755048	LYDPLDGMVSIDGQDIR		ATP-binding cassette, sub-family B (MDR/TAP), member 1A [Mus musculus]	1906.9211	31.77	0
31560618	LYDVPANSMR		budding uninhibited by benzimidazoles 3 homolog [Mus musculus]	1165.5669	29.53	0
9789985	LYEIGAGTSEVR		isovaleryl coenzyme A dehydrogenase [Mus musculus]	1294.6615	44.83	0
6753304	LYGPSSVSFADDFVR		serine (or cysteine) proteinase inhibitor, clade H, member 1 [Mus musculus]	1659.7974	60	0.523078502
31981722	LYGSGGPPPTGEEDTSEKDEL		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	2177.9753	86.64	0.417133523
6755202	LYIGLAGLATDVQTVAQR		proteasome beta 3 subunit [Mus musculus]	1889.0355	47.58	0.356155691
34328510	LYMNLQPVLR	Deamidation (NQ)	RIKEN cDNA 4930488L10 [Mus musculus]	1247.6617	23.42	0
6753266	LYPIANGNNQSPIDIK		carbonic anhydrase 1 [Mus musculus]	1756.9242	65.55	1.607378049
6753428	LYPPSAEYPDLR		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	1420.7136	70.42	0.223541982
31542333	LYQPEYQEVSTEEQR		hypoxia up-regulated 1 [Mus musculus]	1898.8779	64.27	0.466078608
6754256	LYSPSQIGAFVLMK		heat shock protein 9A [Mus musculus]	1553.8105	27.4	1.014564331
9256572	LYTLVLTDPDAPSR		phosphatidylethanolamine binding protein [Mus musculus]	1560.8214	24.66	0
16716589	LYTLVTYVPVTTFK		ribosomal protein L31 [Mus musculus]	1644.916	56.69	0.505308751
63594549	MAAAEEEEPPPPSQGQIASGAGR	2 Deamidation (NQ)	PREDICTED: similar to ring finger protein 5 [Mus musculus]	2282.0313	23.73	0
51772556	MAENLGFLGSLK		PREDICTED: similar to Succinate-Coenzyme A ligase, GDP-forming, beta subunit [Mus musculus]	1279.6719	45.57	0
28478945	MAGNEYVGFSNATFQSER		PREDICTED: glutaminase [Mus musculus]	2007.8915	27.29	0
30348966	MAGTMETSEMVNGAAEQR		spectrin beta 2 isoform 1 [Mus musculus]	1912.8365	27.23	0
33563250	MALDVEIATYR		desmin [Mus musculus]	1281.6549	59.17	0
7305295	MAQQMLDLEEQLEEEEAAR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2263.0239	127.41	0
7305295	MAQQMLDLEEQLEEEEAAR	2 Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2295.0134	53.35	0
7305295	MAQQMLDLEEQLEEEEAAR	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2279.0168	81.36	0
27754056	MASTFIGNSTAIQELFK		tubulin, beta 6 [Mus musculus]	1857.9441	96.08	0
27754056	MASTFIGNSTAIQELFK	Oxidation (M)	tubulin, beta 6 [Mus musculus]	1873.9321	96.96	0
18079351	MAVFGFEMSEDAGPDGALLPR		major vault protein [Mus musculus]	2210.0339	38.5	0
6679687	MDATANDVPSPYEVK		glucose regulated protein [Mus musculus]	1636.7534	60.43	0.876863503
6679687	MDATANDVPSPYEVK	Oxidation (M)	glucose regulated protein [Mus musculus]	1652.729	31.87	0.196529615
22203749	MDDPTVNWSNER		G1 to S phase transition 1 [Mus musculus]	1463.6262	87.47	1.014242049

30023842	MDELQLFR		valosin containing protein [Mus musculus]	1051.528	44.74	0.571649445
40068507	MDENQFVAVTSTNAAK		collapsin response mediator protein 1 [Mus musculus]	1725.8097	93.03	0
40254595	MDENQFVAVTSTNAAK		dihydropyrimidinase-like 2 [Mus musculus]	1725.8097	93.03	0
6681219	MDENQFVAVTSTNAAK		dihydropyrimidinase-like 3 [Mus musculus]	1725.8097	93.03	0
42415475	MDSTANEVEAVK	Oxidation (M)	prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1309.595	35.93	0.596109037
33859686	MEFGTAGLR		phosphoglucomutase 1 [Mus musculus]	981.4965	26.04	0.785977678
63506278	MELRSGSVGTGQRMDR	Oxidation (M)	PREDICTED: hypothetical protein XP_487709 [Mus musculus]	1795.826	22.52	0
7305505	MEPDPAEPPSTTVEAANGAEQAR		smoothelin [Mus musculus]	2368.0745	82.29	0.106296432
64427157	MEQFTAQNEEEK		PREDICTED: synaptopodin 2 [Mus musculus]	1483.6381	53.49	0.346531307
64427157	MEQFTAQNEEEK	Oxidation (M)	PREDICTED: synaptopodin 2 [Mus musculus]	1499.6301	50.09	0.130094834
10946972	MFAEYLASENQR		epsilon subunit of coatomer protein complex [Mus musculus]	1458.6741	39.24	6.458401992
6671602	MFIGGLSWDTTK		heterogeneous nuclear ribonucleoprotein D [Mus musculus]	1355.6614	77.54	1.459814188
47578123	MFTQQQPQELAR		potassium channel tetramerisation domain containing 12 [Mus musculus]	1476.7236	36.48	0
21450625	MFVLDEADEMLSR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1555.7192	80.62	0.814438218
23956214	MGGGGTMNMGDPYGSGGQK		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1801.7329	65.62	0
33859811	MGLVDQLVEPLGPGIK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1665.9149	26.07	0.466399743
6754508	MGPSGGEGVEPER		LIM and SH3 protein 1 [Mus musculus]	1301.5853	27.83	0.961257619
13384720	MGSQVIIPYR		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Mus musculus]	1163.6162	25.69	0
31982186	MIAEAIPELK		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1114.5984	22.1	0.435773254
31980685	MIEQDDFDINTR		glucosamine [Mus musculus]	1496.6688	50.06	0.671835499
21704206	MIPAVVDGEFFPR		carboxylesterase 2 [Mus musculus]	1477.7544	38.48	0.513351597
29336026	MIQALELDPNLYR		nonmuscle myosin heavy chain [Mus musculus]	1575.8179	37.27	0.506221475
6754206	MISGMYLGEIVR		hexokinase 1 [Mus musculus]	1368.7029	48.43	0
7305143	MISGMYLGEIVR		hexokinase 2 [Mus musculus]	1368.7029	48.43	0
6680716	MLAEDELR		ADP-ribosylation factor 1 [Mus musculus]	976.4776	48.96	0.389661265
6681157	MLDMGFEPQIR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1336.6411	58.11	0
40068493	MLDMGFEPQIR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1336.6411	58.11	0
6753620	MLDMGFEPQIR		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1336.6411	58.11	0
63621901	MLDMGFEPQIR		PREDICTED: similar to ddx5 [Mus musculus]	1336.6411	58.11	0
7305505	MLDQTTNFEER		smoothelin [Mus musculus]	1383.6222	63.94	0.792921294
6679891	MLDYLQGSGETPQTDIR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1923.9127	78.1	0.450500628
6679891	MLDYLQGSGETPQTDIR	Oxidation (M)	alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1939.9077	34.05	0
38372907	MLEQLDMR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 [Mus musculus]	1035.5018	31.23	3.061514143
9790069	MLEQLDMR		HLA-B-associated transcript 1A [Mus musculus]	1035.5018	31.23	3.061514143
10092608	MLLADQGQSWK		glutathione S-transferase, pi 1 [Mus musculus]	1276.6263	47.84	0
6754084	MLLEYTDSSYDEK		glutathione S-transferase, mu 1 [Mus musculus]	1593.7045	62.13	0
56119103	MLLFTEVTR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1109.6022	29.17	0
63562017	MLLFTEVTR		PREDICTED: similar to GDP dissociation inhibitor 2 [Mus musculus]	1109.6022	29.17	0
6678483	MLQTSSVLVSGLR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1390.7725	40.6	0.963761205
9910550	MLSLDFLDDVR		Sec11-like 1 [Mus musculus]	1323.667	29.88	0
30348966	MLTAQDMSYDEAR		spectrin beta 2 isoform 1 [Mus musculus]	1530.6624	38.18	0.972232227
7106421	MLTAQDMSYDEAR		spectrin beta 2 isoform 2 [Mus musculus]	1530.6624	38.18	0.972232227
31982290	MLYDMENPPADDYFGR		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1933.8171	57.58	0
31982290	MLYDMENPPADDYFGR	Oxidation (M)	LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1949.8098	43.35	0
31981273	MMEVAAADVQR		CNDP dipeptidase 2 (metallopeptidase M20 family) [Mus musculus]	1220.5781	44.86	0
6754036	MNLGVGAYR		glutamate oxaloacetate transaminase 2, mitochondrial [Mus musculus]	980.5021	39.34	0
19923070	MPIIPFLL		glycoprotein, synaptic 2 [Mus musculus]	943.5571	24.93	0.539390083
29244560	MPLSALYGSLSFLQQLR		hypothetical protein LOC331063 [Mus musculus]	1924.0336	39.08	0
6679465	MPPYDEETQAIIDAAQEAR		protein kinase C substrate 80K-H [Mus musculus]	2147.9941	111.88	0.322751284
6678359	MPTPPSYK		transketolase [Mus musculus]	920.455	44.06	0.394438986
6678359	MPTPPSYK	Oxidation (M)	transketolase [Mus musculus]	936.4473	35.76	0.366308988
7549795	MQELQEAQNAR		tight junction protein 2 [Mus musculus]	1317.6223	41.52	1.569241448
6678726	MQEVYNFNAINNSEIR		leukotriene A4 hydrolase [Mus musculus]	1941.9187	53.81	0.378762238
6754084	MQLIMLCYNPDFEK		glutathione S-transferase, mu 1 [Mus musculus]	1744.8232	31.78	0
33859811	MQLLEIITTDK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1304.7051	53.53	0
21312550	MQLQGELQAPGTYQR		hypothetical protein LOC71998 [Mus musculus]	1719.8551	24.35	0
8394269	MQQFDDLFR		ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltra	1199.552	64.87	0
20137006	MQQNIQELEEQLEEEESAR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2333.051	87.01	0.485562628
50355692	MQQQLDEYQELLDIK		lamin A isoform A [Mus musculus]	1893.9235	84.17	0
6678093	MQQVEASLQPETLR		serine (or cysteine) proteinase inhibitor, clade A, member 3N [Mus musculus]	1629.8198	33.43	0

33469043	MQQYDLQGQPYGTR		nicalin homolog [Mus musculus]	1684.7816	30.77	0
64427157	MQSSVSESSFQMGR		PREDICTED: synaptopodin 2 [Mus musculus]	1560.6895	54.01	0
6680231	MSAYAFFVQTCR	Oxidation (M)	high mobility group box 3 [Mus musculus]	1439.6538	29.17	0.480451256
21450277	MSINAEDVVVGDLVEVK	Deamidation (NQ); Oxidation (M)	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1833.8983	23.82	0
6679108	MSVQPTVSLGGFEITPPVVLR		nucleophosmin 1 [Mus musculus]	2227.2188	56.37	0.468734211
63601668	MSVQPTVSLGGFEITPPVVLR		PREDICTED: similar to Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numatrin) (Nucleolar prot	2227.2188	56.37	0.468734211
6679108	MTDQEAIQDLWQWR		nucleophosmin 1 [Mus musculus]	1819.8556	56.83	0
63746404	MTDQEAIQDLWQWR		PREDICTED: similar to checkpoint suppressor 1 [Mus musculus]	1819.8556	56.83	0
56119103	MTGSEFDFEEMKR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1606.6919	31.12	0.739051355
51827543	MTTETASEDDNFGTAQSNK		PREDICTED: GCN1 general control of amino-acid synthesis 1-like 1 [Mus musculus]	2046.8582	32.04	0
6678097	MTYIGEIFTK		serine (or cysteine) proteinase inhibitor, clade B, member 6a [Mus musculus]	1202.6064	62.98	0.423716474
6678573	MVDDGSGEVQVWR		villin 1 [Mus musculus]	1477.6744	73.76	0.922647872
6680027	MVEGFFDR		glutamate dehydrogenase 1 [Mus musculus]	1000.465	22.46	0
33859811	MVGVPAAFDMMLTGR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1595.7754	41.88	0
6754342	MYAPAWVAPEALQK		integrin linked kinase [Mus musculus]	1574.8064	28.02	0
6753438	MYDSLLALPQDLQAAR		claudin 3 [Mus musculus]	1804.928	35.35	0
8393144	MYDSVLALPGALQATR		claudin 7 [Mus musculus]	1705.8932	69.98	1.143938882
13384828	MYGADLAPVDFLHASEDAR		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	2077.9624	88.16	0.354905383
13384828	MYGADLAPVDFLHASEDAR	Oxidation (M)	serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	2093.968	41.24	1.021305117
6677871	MYLETDPSGR		scinderin [Mus musculus]	1168.5328	40.8	0
13937355	MYSYVTEELPQLINANFPVDPQR		esterase D/formylglutathione hydrolase [Mus musculus]	2724.3328	28.36	0.25975215
13937355	MYSYVTEELPQLINANFPVDPQR	Oxidation (M)	esterase D/formylglutathione hydrolase [Mus musculus]	2740.3279	24.76	0.169173386
31982724	NAASQQDAVTEGAMPAATGK		MYB binding protein (P160) 1a [Mus musculus]	1917.8727	30.75	0
19526814	NACGSDYDFDVFVVR		NADH dehydrogenase (ubiquinone) flavoprotein 1 [Mus musculus]	1706.756	37.23	0
6756013	NADPETTLLVYLR		xanthine dehydrogenase [Mus musculus]	1504.8007	48.01	0.67097624
8567336	NADVLVSTTSPLGNDEPYTEHIGACGEK		chloride channel calcium activated 3 [Mus musculus]	2917.3572	116.95	0.046233107
13507628	NAGLAFIELVNEGR		LPS-responsive beige-like anchor [Mus musculus]	1502.7985	42.63	0
6753294	NAGNEQDLGIQYK		catenin alpha 1 [Mus musculus]	1449.6949	48.78	0
63476037	NAGPEFQYIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1194.5875	55.04	0.114801931
6753324	NAIDDGCVVPGAGAVEVALAEALIK		chaperonin subunit 6a (zeta) [Mus musculus]	2395.2217	54.36	0
22267442	NALANPLYCPDYR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1509.717	44.59	0.309147799
63476037	NANPSELEQIVLSPAFILAAESLPK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2651.4287	51.83	0
30023842	NAPAIIFIDELDAIAPK		valosin containing protein [Mus musculus]	1810.9937	90.81	0.404419572
6681087	NASTFEEVVQVPSAYQK		cortactin [Mus musculus]	1896.9086	32.68	0
7305169	NAVEECVYEFR		heat shock protein 105 [Mus musculus]	1358.6067	22.9	0
40254361	NAVEEYVYDFR		heat shock 70kDa protein 4 like [Mus musculus]	1404.6487	30.47	0.345464896
31982275	NAVEEYVYEMR		heat shock protein 4 [Mus musculus]	1402.63	28.25	0
6754256	NAVITVPAYFNDSQR		heat shock protein 9A [Mus musculus]	1694.851	87.96	0.418681902
18079339	NAVTQEFGPVPDTAR		aconitase 2, mitochondrial [Mus musculus]	1601.7996	107.95	0.269363608
6677813	NCIVLIDSTPYR		ribosomal protein S8 [Mus musculus]	1393.7161	47.61	0.696903444
31712036	NDFQLIGIQDGYLSLLQDSGEVR		eukaryotic translation initiation factor 5A [Mus musculus]	2580.2998	22.57	0.419944304
31560543	NDFTEEEEAQVR		S-phase kinase-associated protein 1A [Mus musculus]	1466.641	22.73	0.39463757
9790067	NDISSHPPVEGSYAPR		staphylococcal nuclease domain containing 1 [Mus musculus]	1725.821	37.46	0.706191388
33667082	NDNDSWDYTKPYLGR		heterogeneous nuclear ribonucleoprotein L-like [Mus musculus]	1843.8397	28.85	0.367194749
33667042	NDQDTWDYTNPNLSGQGDPGSNPNKR		heterogeneous nuclear ribonucleoprotein L [Mus musculus]	2890.2573	73.45	0.320180586
9790247	NDVFDSLGISPDLLPDDFVR		ubiquitin-like 1 (sentrin) activating enzyme subunit 1 [Mus musculus]	2234.093	81.1	0.471634603
21313536	NDVITVQTPAFAESVTEGDVR		dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]	2248.0916	104.59	0.294705629
36031035	NDVMNLLESAGFSR		chondroitin sulfate proteoglycan 6 [Mus musculus]	1552.7614	23.68	0
51768458	NDVQIANPAFIQDSVR		PREDICTED: similar to mKIAA0177 protein [Mus musculus]	1786.9025	27.59	0
6678483	NEEDATELVGLAQAVNAR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1899.9303	132.46	0.410754244
28395018	NEGTATYAAAVLFR		junction plakoglobin [Mus musculus]	1483.7383	26.08	0.471035413
6671684	NEGVATYAAAVLFR		catenin beta [Mus musculus]	1481.7764	69.25	0.392102216
27229277	NELSGALTGLTR		threonyl-tRNA synthetase [Mus musculus]	1231.6637	27.06	7.42533792
19527174	NENQLIIFADDTYPR		splicing factor 3b, subunit 3 [Mus musculus]	1808.8905	38.47	0
21314832	NENTFLDLTVQQIEHLNK		UDP-glucose pyrophosphorylase 2 [Mus musculus]	2156.085	24.99	4.155788531
31560653	NEWGSLLEELVK		phosphofructokinase, liver, B-type [Mus musculus]	1416.7474	55.29	0.182640483
19526824	NFAFLEFR		U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2 [Mus musculus]	1043.5397	28.52	0.422302974
13384720	NFDFEDVFVNIPR		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Mus musculus]	1611.7828	84.74	0.361260364
34996495	NFESLSEAFSVASAAAALSQNR		ribophorin II [Mus musculus]	2270.1082	64.91	0.335020888
7305443	NFGIGQDIQPK		ribosomal protein L7a [Mus musculus]	1216.6267	60.63	0

58037465	NFGIWLR		Ribosomal protein L18A [Mus musculus]	905.5065	31.56	0.43257955
7949051	NFILDQTNVSAAAQR		heterogenous nuclear ribonucleoprotein U [Mus musculus]	1647.8485	99.3	0.417831407
20137006	NFINNPLAQADWAAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1672.8438	76.38	0.323435181
19705578	NFITQGPYENR		ATPase, H+ transporting, V1 subunit B, isoform 2 [Mus musculus]	1338.6489	47.85	0
51556274	NFLASQVPFPSR		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	1362.7174	27.3	0.294904614
18034769	NFLINYYNR		sorting nexin 5 [Mus musculus]	1216.6143	24.42	0.460896711
13195638	NFLSTPQFLYR		Der1-like domain family, member 1 [Mus musculus]	1385.7294	22.48	0.365502423
33859490	NFLTEDSADLDSIEAVANEVLK		laminin B1 subunit 1 [Mus musculus]	2393.1763	50.33	0
7305295	NFMNSPMAQADWVAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1709.7754	71.7	0
7305295	NFMNSPMAQADWVAK	2 Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1741.7609	31.22	0
7305295	NFMNSPMAQADWVAK	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1725.7698	66.96	0
46849705	NFVINFK		lectin, galactose binding, soluble 4 [Mus musculus]	881.4863	41.44	0.294318346
22203747	NFVINVVNR		procollagen, type VI, alpha 2 [Mus musculus]	1074.604	46.13	0
6681157	NFYQEHPDLAR		DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1389.6544	32.82	0.52577936
63621901	NFYQEHPDLAR		PREDICTED: similar to ddx5 [Mus musculus]	1389.6544	32.82	0.52577936
51771420	NGEDLGVAFR		PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1077.5387	35.96	0
30794140	NGEQQAVPALR		protein disulfide isomerase-associated 5 [Mus musculus]	1182.621	38.24	0.850425398
30794140	NGEQQAVPALR	Deamidation (NQ)	protein disulfide isomerase-associated 5 [Mus musculus]	1183.6162	34.09	0
63487095	NGNGGPGPYVGQAGTATLPR	Deamidation (NQ)	PREDICTED: catenin src [Mus musculus]	1884.9288	93.44	0.542951192
46358078	NGQEETVGVSSTQLIR		response to metastatic cancers 1 [Mus musculus]	1717.8704	65.84	0.835989758
31981327	NGYELSPTAAANFTR		proteasome (prosome, macropain) subunit, beta type 2 [Mus musculus]	1611.7813	36.81	0
20806532	NGYGFINR		cold shock domain protein A short isoform [Mus musculus]	940.4684	40.86	1.156344124
6756033	NGYGFINR		nuclease sensitive element binding protein 1 [Mus musculus]	940.4684	40.86	1.156344124
63562136	NGYGFINR		PREDICTED: hypothetical protein LOC78552 [Mus musculus]	940.4684	40.86	1.156344124
20806532	NGYGFINR	Deamidation (NQ)	cold shock domain protein A short isoform [Mus musculus]	941.4547	40.25	0
6756033	NGYGFINR	Deamidation (NQ)	nuclease sensitive element binding protein 1 [Mus musculus]	941.4547	40.25	0
63562136	NGYGFINR	Deamidation (NQ)	PREDICTED: hypothetical protein LOC78552 [Mus musculus]	941.4547	40.25	0
31543689	NGYGFVEFEDSR		arginine/serine-rich splicing factor 6 [Mus musculus]	1419.6261	27.54	0.884945055
18700024	NIANPTAMLLSATNMLR		isocitrate dehydrogenase 3, beta subunit [Mus musculus]	1830.9662	36.25	0.88946275
6680722	NICFTVWDVGGQDK		ADP-ribosylation factor 5 [Mus musculus]	1581.7448	55.84	0
33238874	NIFDFNAIK		phosphoglucomutase 5 [Mus musculus]	1081.5673	37.69	0.389672876
6753556	NIFSFYLNR		cathepsin D [Mus musculus]	1173.6107	34.02	0.345528925
31560611	NIIGLQMGTNK	Oxidation (M)	calponin 1 [Mus musculus]	1204.6263	34.43	0.296865714
58037546	NILGGTVFR		isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	976.5551	29.06	0.356665008
27370516	NILGGTVFR		isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	976.5551	29.06	0.356665008
15147224	NILLTNEQLENAR		sideroflexin 1 [Mus musculus]	1527.816	45.53	0
31542333	NINADEAAAMGAVYQAAALSK		hypoxia up-regulated 1 [Mus musculus]	2079.01	58.66	0
31543605	NIQVDSPYDISR		ribophorin I [Mus musculus]	1406.6926	70.89	0.432436777
33563250	NISEAEEWYK		desmin [Mus musculus]	1268.574	64.69	0.075262996
34996495	NIVEEIEDLVAR		ribophorin II [Mus musculus]	1399.7443	55.41	0.492781059
23956222	NIVLSGGSTMFR		ARP3 actin-related protein 3 homolog [Mus musculus]	1281.6616	55.92	0.678435277
21704100	NIVVVEGVR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	984.5839	46.45	0.338340994
63664138	NLADQGIINYPYSTR		PREDICTED: hypothetical protein LOC219189 [Mus musculus]	1724.8617	37.62	0
45598381	NLAPTWEELSK		thioredoxin domain containing 5 [Mus musculus]	1287.6488	28.74	0
6755002	NLATAYDNFVELVANLK		programmed cell death 6 interacting protein [Mus musculus]	1894.9833	26.15	0.366242884
34740335	NLDIERPTYTNLNR		tubulin, alpha 2 [Mus musculus]	1718.8879	48.49	0.494986193
6678467	NLDIERPTYTNLNR		tubulin, alpha 4 [Mus musculus]	1718.8879	48.49	0.494986193
6678469	NLDIERPTYTNLNR		tubulin, alpha 6 [Mus musculus]	1718.8879	48.49	0.494986193
22550094	NLDQEQLSQVLDAMFEK		protein kinase, cAMP dependent regulatory, type II alpha [Mus musculus]	2007.9764	56.91	0
22550094	NLDQEQLSQVLDAMFEK	Oxidation (M)	protein kinase, cAMP dependent regulatory, type II alpha [Mus musculus]	2023.969	32.02	0
28173550	NLEGYVGFANLPNQVYR		cell division cycle 10 homolog [Mus musculus]	1953.9766	46.49	0.35947287
58037267	NLEPEWAAAATEVK		protein disulfide isomerase-associated 6 [Mus musculus]	1528.7635	48.35	0.526566865
51770961	NLETLQQELGIEGENR		PREDICTED: AFG3(ATPase family gene 3)-like 2 [Mus musculus]	1842.9054	53.09	0
22203747	NLEWIAGGTWTPSALK		procollagen, type VI, alpha 2 [Mus musculus]	1743.9069	72.8	0
6678499	NLFFSTNIDDAIR		UDP-glucose dehydrogenase [Mus musculus]	1525.7672	80.8	0.298726503
40254595	NLHQSGFSLSGAQIDDNIPR		dihydropyrimidinase-like 2 [Mus musculus]	2169.0605	37.83	3.516542914
21313308	NLPFDFTWK		heterogeneous nuclear ribonucleoprotein M [Mus musculus]	1167.5846	35.93	0
9790067	NLPGLVQEGEPFSEEATLFTK		staphylococcal nuclease domain containing 1 [Mus musculus]	2306.1594	79.34	0.634604327
20137006	NLPIYSEEIVEMYK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1727.8519	41.86	0.429057869
13384620	NLPLPPPPPPR		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1194.6945	26.41	0

7305413	NLQEAEEWYK		peripherin 1 [Mus musculus]	1309.6051	69.92	0.310484673
31982755	NLQEAEEWYK		vimentin [Mus musculus]	1309.6051	69.92	0.310484673
51491845	NLQNLLILTAIK		clathrin, heavy polypeptide (Hc) [Mus musculus]	1353.8469	78.81	0.519812089
6678365	NLQYYDISAK		RAN, member RAS oncogene family [Mus musculus]	1214.6027	52.28	0
21313290	NLSIYDGPEQR		electron transferring flavoprotein, dehydrogenase [Mus musculus]	1291.626	22.4	0.276524287
23956214	NLSPYVSNELLEEAFSQFGPIER		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	2639.2996	45.99	0.558078335
6678331	NLSVDVYYDAMGNPLEK		transglutaminase 3, E polypeptide [Mus musculus]	1927.9149	85.75	0
6678331	NLSVDVYYDAMGNPLEK	Oxidation (M)	transglutaminase 3, E polypeptide [Mus musculus]	1943.9108	47.87	0
51708441	NLTCLDLSSNR	Deamidation (NQ)	PREDICTED: similar to FLJ44691 protein [Mus musculus]	1236.5939	25.9	0
6678359	NMAEQIIQEIYSQVQSK		transketolase [Mus musculus]	2008.9976	78.64	0.552208556
37693505	NMAPSQQSPVRTASVNQRNR	4 Deamidation (NQ); Oxidation (M)	abl-interactor 2 [Mus musculus]	2261.0632	22.14	0
7305295	NMDPLNDNVTSLLNASSDK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2047.9611	114.22	0
7305295	NMDPLNDNVTSLLNASSDK	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2063.9553	133.84	0.297463563
7949053	NMGGPYGGGNYGPGGSGGSGGYGGR		heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2189.9148	171.53	0.424659807
7949053	NMGGPYGGGNYGPGGSGGSGGYGGR	Oxidation (M)	heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1 [Mus musculus]	2205.9031	120.26	0.359492819
21450277	NMVPQQALVIR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1268.7153	51.17	0.716552387
6678145	NNEDVSIIPPLFTVSVDHR		signal sequence receptor, delta [Mus musculus]	2152.1021	26.92	0.985877433
31980868	NNFLEDEPSAQHR		kallikrein 6 [Mus musculus]	1556.7205	26.11	0.194442035
51491845	NNLAGAEELFAR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1304.6586	68.53	0.452709773
6679583	NNLSFIETSALDSTNVEEAFK		RAB11B, member RAS oncogene family [Mus musculus]	2329.1223	90.2	0
22203747	NNYATMRPDSTEIDQDTINR		procollagen, type VI, alpha 2 [Mus musculus]	2354.0676	61.4	0.095299487
22203747	NNYATMRPDSTEIDQDTINR	Deamidation (NQ)	procollagen, type VI, alpha 2 [Mus musculus]	2355.0623	75.48	0.086053057
6754856	NPAETLLLSEPLNGDLLGQYSQLAR		nitrilase 1 [Mus musculus]	2712.4009	24.64	0
63530525	NPAVLSAASFDGR		PREDICTED: SEC31-like 1 [Mus musculus]	1304.6598	41.56	0
6754254	NPDDITNEEYGEFYK		heat shock protein 1, alpha [Mus musculus]	1833.7792	108.11	0.552744112
40556608	NPDDITQEEYGEFYK		heat shock protein 1, beta [Mus musculus]	1847.8004	102.46	0.599709389
51827543	NPEILAIAPVLLDALTDPSR		PREDICTED: GCN1 general control of amino-acid synthesis 1-like 1 [Mus musculus]	2118.1697	30.77	0
63518159	NPELQNLLLDDFFK		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1705.8781	92.51	0.70052655
6679891	NPEPELLVR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1066.5875	40.95	0
34996495	NPILWNVADVVIK		ribophorin II [Mus musculus]	1480.8429	40.63	0
6678329	NPLSDPLYDCIFTVEGAGLTK		transglutaminase 2, C polypeptide [Mus musculus]	2253.1067	100.07	0.569854117
63556656	NPNDDLTAVGGKPEGWK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1797.8718	91.71	0
8567402	NPPGFAFVEFEDPR		splicing factor, arginine/serine-rich 3 (SRp20) [Mus musculus]	1621.7687	71.19	0.52970837
22122585	NPPGFAFVEFEDPR		splicing factor, arginine/serine-rich 7 [Mus musculus]	1621.7687	71.19	0.52970837
42734399	NQALELEQLR		desmuslin isoform H [Mus musculus]	1213.655	60.46	0.07869974
46559834	NQALELEQLR		desmuslin isoform M [Mus musculus]	1213.655	60.46	0.07869974
18875324	NQAPGQPGASQWGSR		DAZ associated protein 1 [Mus musculus]	1540.7323	53.72	0.494654393
42734449	NQFTVAQYEK		sulfotransferase family 1D, member 1 [Mus musculus]	1227.6133	26.65	0
33563270	NQGYYDYVKPR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1402.6725	29.94	1.624422586
31981722	NQLTSNPENTVFDAK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1677.806	105.72	0.367814029
6754482	NQNINLENSLGDVEAR		keratin complex 1, acidic, gene 18 [Mus musculus]	1785.8761	93.09	0.369222948
20149720	NQNLQEALQR	3 Deamidation (NQ)	oxidized low density lipoprotein (lectin-like) receptor 1 [Mus musculus]	1216.5837	26.27	0
19526884	NQQDGQLEESPGSWPGAGTIR		GDP-mannose pyrophosphorylase A [Mus musculus]	2227.0371	114.33	0.367723706
20330802	NQQEGVCPEGSIDNSPVK		transferrin [Mus musculus]	1900.8706	111.5	0.240458931
50080209	NQVALNPQNTVFDAK		heat shock protein 1A [Mus musculus]	1658.8546	39.4	0
31981690	NQVAMNPTNTVFDAK		heat shock protein 8 [Mus musculus]	1649.793	85.59	0
31981690	NQVAMNPTNTVFDAK	2 Deamidation (NQ); Oxidation (M)	heat shock protein 8 [Mus musculus]	1667.7611	30.51	0
31981690	NQVAMNPTNTVFDAK	Oxidation (M)	heat shock protein 8 [Mus musculus]	1665.7839	63.96	0
33563282	NQYDNDVTVWSPQGR		proteasome (prosome, macropain) subunit, alpha type 1 [Mus musculus]	1778.8177	53.04	0.593511361
46849705	NSFMNGSWGAEER		lectin, galactose binding, soluble 4 [Mus musculus]	1484.6322	94.94	0.762166645
46849705	NSFMNGSWGAEER	Deamidation (NQ)	lectin, galactose binding, soluble 4 [Mus musculus]	1485.6158	51.26	0
46849705	NSFMNGSWGAEER	Deamidation (NQ); Oxidation (M)	lectin, galactose binding, soluble 4 [Mus musculus]	1501.6227	35.52	0
46849705	NSFMNGSWGAEER	Oxidation (M)	lectin, galactose binding, soluble 4 [Mus musculus]	1500.6217	25.05	0
31981690	NSLESYAFNMK		heat shock protein 8 [Mus musculus]	1303.5958	73.23	0
31981690	NSLESYAFNMK	Oxidation (M)	heat shock protein 8 [Mus musculus]	1319.5975	42.44	0.557008728
12746444	NSLPLQEEENR		melanoma cell adhesion molecule [Mus musculus]	1328.649	22.35	0
7305295	NSLQDQLDEEMEAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1649.7349	90.66	2.337137289
54020742	NSNILEDLETLR		archain 1 [Mus musculus]	1416.7368	86.8	0.410366747
50355692	NSNLVGAAHEELQQSR		lamin A isoform A [Mus musculus]	1752.8618	72.62	0.18138311

27312018	NSRDQLLAAIR	2 Deamidation (NQ)	leiomodin 1 (smooth muscle) [Mus musculus]	1258.675	26.32	0
22165384	NSSYFVEWIPNNVK		tubulin, beta, 2 [Mus musculus]	1696.8239	46.97	0.374662483
33859488	NSSYFVEWIPNNVK		tubulin, beta 2 [Mus musculus]	1696.8239	46.97	0.374662483
12963615	NSSYFVEWIPNNVK		tubulin, beta 3 [Mus musculus]	1696.8239	46.97	0.374662483
31981939	NSSYFVEWIPNNVK		tubulin, beta 4 [Mus musculus]	1696.8239	46.97	0.374662483
7106439	NSSYFVEWIPNNVK		tubulin, beta 5 [Mus musculus]	1696.8239	46.97	0.374662483
27754056	NSSYFVEWIPNNVK		tubulin, beta 6 [Mus musculus]	1696.8239	46.97	0.374662483
21746161	NSSYFVEWIPNNVK		tubulin, beta [Mus musculus]	1696.8239	46.97	0.374662483
6678359	NSTFSELFK		transketolase [Mus musculus]	1072.5436	41.58	0.439064263
31982236	NSYPDLAVGSLSDSVTIFR		integrin alpha 6 [Mus musculus]	2041.0161	47.31	0
6996917	NSYVAGQYDDAASYK		glucose-6-phosphate dehydrogenase X-linked [Mus musculus]	1651.7247	98.72	0.718177518
31981983	NTGASSGATSEESTEAEFCR		stromal interaction molecule 1 [Mus musculus]	2033.8451	39.66	0.305875646
31981562	NTGIICTIGPASR		pyruvate kinase 3 [Mus musculus]	1302.6785	47.04	0.564651522
22164798	NTGTEAPDYLATVDVDPK		selenium binding protein 1 [Mus musculus]	1905.9116	91.12	0
31791057	NTIEETGILAER		laminin, gamma 1 [Mus musculus]	1345.6923	22.58	0
6680572	NTIQWLENELNR		kinesin family member 5B [Mus musculus]	1529.7739	32.95	0
32567788	NTLFNLSNFLDK		phosphatidylinositol-binding clathrin assembly protein [Mus musculus]	1425.7487	40.31	0.466015206
46195798	NTLLIAGLQAR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1169.6993	43.23	0
33563270	NTNAGAPPGTAYQSPLSLSR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	2002.0038	87.68	0.227818213
33859560	NTNDANSCQIIIPQNQVNR		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	2142.0374	80.63	0.285742426
56119103	NTNDANSCQIIIPQNQVNR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	2142.0374	80.63	0.285742426
6754556	NTSEQDQPMGGWEMIR		lamin B1 [Mus musculus]	1878.8158	51.43	0.401712416
54607098	NTVIATGGYGR		succinate dehydrogenase Fp subunit [Mus musculus]	1108.5797	32.07	0.391014719
8567336	NVAILIPESWK		chloride channel calcium activated 3 [Mus musculus]	1269.7168	51.88	0
8567336	NVAILIPESWK	Deamidation (NQ)	chloride channel calcium activated 3 [Mus musculus]	1270.7207	40.76	0
6680678	NVDEAINFINDR		aldehyde dehydrogenase family 3, subfamily A2 [Mus musculus]	1419.6906	67.84	0
31981570	NVDLQVLAPEPELLYK		polymeric immunoglobulin receptor [Mus musculus]	1841.0033	22.8	0
6679012	NVDMLSELVQEYDEPILK		nucleosome assembly protein 1-like 4 [Mus musculus]	2135.0649	24.54	0
21313536	NVETMNYADIER	Oxidation (M)	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]	1470.6514	23.79	0.178933712
6753364	NVFDEAILAALEPPEPK		cell division cycle 42 homolog [Mus musculus]	1852.9637	77.03	0.49411963
6678986	NVLDTSWPTPPPALR		myosin IC [Mus musculus]	1663.8807	28.68	0
29788753	NVLITDFFGSVR		phosphatidylinositol glycan, class K [Mus musculus]	1367.735	34.31	0
9790261	NVMSAFGLTDDQVSGPPSAPTEDR		Trk-fused gene [Mus musculus]	2491.1365	83.24	0.549595937
11968166	NVNGVNYASVTR		cathepsin Z preproprotein [Mus musculus]	1293.6611	42.99	0.758374599
21450341	NVNTALNTTQIPSSIEDIFNDDR		amyloid beta precursor protein binding protein 1 [Mus musculus]	2577.2529	42.46	0.47460931
6680748	NVQAEEMVEFSSGLK		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1667.7917	41.38	0
31560607	NVQGVNYVSPVR		cathepsin C preproprotein [Mus musculus]	1331.7078	26.18	0.566306476
34536819	NVSINTVTYEWAPPVQNQALAR		testis derived transcript [Mus musculus]	2471.2686	46.05	0.226080605
10946676	NYAEVYEPEGVK		solute carrier family 26, member 3 [Mus musculus]	1397.6571	46.87	0
51768458	NYDPLSPAPAAPPAER		PREDICTED: similar to mKIAA0177 protein [Mus musculus]	1665.83	34.95	0
21450323	NYILDQTNVYGSAQR		EIB-55kDa associated protein 5 [Mus musculus]	1741.8488	65.02	0.846704844
33859520	NYIPDEADFLLGMATVK		caspase 8 [Mus musculus]	1896.922	27.46	0
6680934	NYLNYGEEGDQGR		chromogranin B [Mus musculus]	1514.6564	48.48	0
13384736	NYMSNPSYNYEIVNR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1863.8304	80.39	0
21703842	NYNDELQFLDK		hypothetical protein LOC28088 [Mus musculus]	1398.6638	35.54	0
6756033	NYQQNYQNSESGEKNEGSESAPEGQAQQR		nuclease sensitive element binding protein 1 [Mus musculus]	3257.3828	50.67	0.517183872
51771420	NYYGYQGYR		PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1183.5197	41.33	0.485180404
6753618	PFVELETNLPASR		D-dopachrome tautomerase [Mus musculus]	1472.7698	48.27	0
6671549	PGGLLLGDEAPNFEANTTIGR		peroxiredoxin 6 [Mus musculus]	2142.0837	134.56	0.112396793
16716467	PLELELCPGR		N-acetylneuraminic acid synthase (sialic acid synthase) [Mus musculus]	1126.5928	45.46	0.231761973
51766008	PLLEGPVGVEDLILLEPLDEESLIK		PREDICTED: myosin IA [Mus musculus]	2730.5015	64.98	0
6754084	PMILGYWNVR		glutathione S-transferase, mu 1 [Mus musculus]	1248.6598	42.48	0
10092608	PPYTIVYFPVR		glutathione S-transferase, pi 1 [Mus musculus]	1351.7416	35.09	0.598568424
6680842	QAALQVADGFISR		gelsolin-like capping protein [Mus musculus]	1375.7324	27.54	1.371875271
31981111	QADEEFQILANSWR		implantation-associated protein [Mus musculus]	1706.8231	53.57	0.484793954
7305295	QADLEKEELAEELASSLSGR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2175.0742	144.67	0
7305295	QADLEKEELAEELASSLSGR	Deamidation (NQ)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2176.0898	113.6	0.243642061
7304881	QAFQIGSPWR		aldehyde dehydrogenase family 1, subfamily A1 [Mus musculus]	1189.6112	22.72	0.670270974
18079351	QAIPLDQNEGIYVQDVK		major vault protein [Mus musculus]	1929.9961	38.9	0
6754482	QAQEYEALLNIK		keratin complex 1, acidic, gene 18 [Mus musculus]	1419.7416	73.94	0.890650716

125083	QAQEYEALLNIK		Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18)	1419.7416	73.94	0.890650716
6754256	QAVTNPNNTFYATK		heat shock protein 9A [Mus musculus]	1568.7687	48.85	0.622237261
7304889	QDAQELYEAGEK		annexin A4 [Mus musculus]	1380.6357	50.8	0.312768755
63489754	QDEVNAAWQR		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1216.5745	33.81	0
6996913	QDIAFAYQR		annexin A2 [Mus musculus]	1111.5656	42.3	0.591451842
31791057	QDIAVISDSYFPR		laminin, gamma 1 [Mus musculus]	1510.7521	43.53	0
6754854	QDLGSPEGIALDHLGR		nidogen 1 [Mus musculus]	1677.8512	35.8	0
6753294	QDLLAYLQR		catenin alpha 1 [Mus musculus]	1119.6207	30.63	0
6680716	QDLPNAMNAAEITDK		ADP-ribosylation factor 1 [Mus musculus]	1630.7739	52.61	2.256326712
6680716	QDLPNAMNAAEITDK	Oxidation (M)	ADP-ribosylation factor 1 [Mus musculus]	1646.7572	29.97	0
63487095	QDVYGPQPQVR		PREDICTED: catenin src [Mus musculus]	1286.6547	35.01	0.554148939
20838286	QEANGKGNR	2 Deamidation (NQ)	PREDICTED: similar to fatty acid desaturase 2 [Mus musculus]	975.4631	33.81	0
31559995	QEAVALLQGQR		v-crk sarcoma virus CT10 oncogene homolog [Mus musculus]	1212.6639	37.64	0.464411268
55742711	QEELESVEAGVQGGAFEGTR		EH-domain containing 2 [Mus musculus]	2092.9841	150.91	0
30794206	QEEMNSQQEEEEMETDTR		splicing factor 3b, subunit 2 [Mus musculus]	2242.8694	48.07	0.435172557
41322904	QEEVYSELQAR		plectin 1 isoform 1 [Mus musculus]	1351.6509	33.25	0
21450129	QEQDTYALSSYTR		acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	1561.7179	67.95	0.442734026
6671507	QEYDEAGPSIVHR		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1500.7241	81.13	0
6671509	QEYDESGPSIVHR		actin, beta, cytoplasmic [Mus musculus]	1516.7228	73.92	0.683335372
6678331	QEYVEEDSGIIYVGSTNR		transglutaminase 3, E polypeptide [Mus musculus]	2058.9631	121.33	0.09579279
33859482	QFAEMYVAK		eukaryotic translation elongation factor 2 [Mus musculus]	1086.5276	52.11	0.561276121
20149756	QFFVAVER		DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Mus musculus]	995.5349	28.72	0.430434275
63476037	QFGVAPLTIAR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1172.6776	41.02	0
13385878	QFLESSELPR		sorting nexin 2 [Mus musculus]	1205.6044	23.16	0
42415475	QFLLAAEAIDDIPFGITSNSGVFSK		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	2640.3474	83.69	0.661697104
18266680	QFLSGELEVELTPQGTLAER		3-oxoacid CoA transferase 1 [Mus musculus]	2217.1001	29.52	0
42734399	QFTQSPGAEEEATSFPDTK		desmuslin isoform H [Mus musculus]	2069.9358	61.3	0.104711753
46559834	QFTQSPGAEEEATSFPDTK		desmuslin isoform M [Mus musculus]	2069.9358	61.3	0.104711753
21450625	QFYINVER		eukaryotic translation initiation factor 4A1 [Mus musculus]	1068.5491	35.3	0.392269013
22164798	QFYPDLIR		selenium binding protein 1 [Mus musculus]	1051.5603	42.8	0.211473237
6753086	QGFGELLQAVPLADSFR		apurinic/apyrimidinic endonuclease 1 [Mus musculus]	1847.9657	42.11	0.47525779
6754976	QGGLGPMNIPLISDPK		peroxiredoxin 1 [Mus musculus]	1636.8665	55.71	1.494116804
15147224	QGIVPAGLTENELWR		sideroflexin 1 [Mus musculus]	1682.8859	46.78	0.408893728
18079339	QGLLPLTFADPSDYNK		aconitase 2, mitochondrial [Mus musculus]	1778.8651	45.72	0
6680748	QGQYSPMAIEEQVAVIYAGVR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2309.1633	124.82	0.269625879
6680748	QGQYSPMAIEEQVAVIYAGVR	Oxidation (M)	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	2325.1536	33.73	0.247800668
9845299	QGTFHSQQALEYGTK		succinate-CoA ligase, GDP-forming, alpha subunit [Mus musculus]	1694.8092	38.67	0
33695134	QGTQYTFSSIER		structure specific recognition protein 1 [Mus musculus]	1416.676	29.22	1.536581371
453155	QGVDADINGLR		keratin 9 [Homo sapiens]	1157.5894	42.86	0
6680117	QIEINTISASFGGLASR		glutathione synthetase [Mus musculus]	1763.9169	36.28	0
6753820	QIEIQFAQGDR		FUS interacting protein (serine-arginine rich) 1 [Mus musculus]	1304.6567	24.17	0.37816203
7549752	QIGLDQIWDDLR		cullin 1 [Mus musculus]	1471.759	27.2	0
6753294	QIIVDPLSFSEER		catenin alpha 1 [Mus musculus]	1532.7998	36.13	0
18250296	QINWTVLYR		ribosomal protein L24 [Mus musculus]	1192.6503	52.95	0.489554128
16716471	QIPVVGSVLNWFSPVQASQK		hypothetical protein LOC94184 [Mus musculus]	2184.1787	78.31	0.954290835
31982526	QIQEEITGNTEALSGR		parvin, alpha [Mus musculus]	1745.8643	99.14	0
37620153	QISEGVEYIHK		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1302.6556	29.91	0
1346343	QISNLQQSISDAEQR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1716.8513	94.01	0.346559325
6754976	QITINDLPVGR		peroxiredoxin 1 [Mus musculus]	1225.6949	64.04	0.344903507
8394024	QITQVYGFYDECLR		protein phosphatase 2a, catalytic subunit, beta isoform [Mus musculus]	1734.8224	23.35	0.321617552
9790175	QITQVYGFYDECLR		protein phosphatase 4, catalytic subunit [Mus musculus]	1734.8224	23.35	0.321617552
34610207	QIWQNLGLDEAR		alanyl-tRNA synthetase [Mus musculus]	1442.7286	24.63	0
21704156	QKEFDPTITDGSLSGPSR		caldesmon 1 [Mus musculus]	1934.947	90.06	0.158694961
42415475	QLAPIWDK		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	970.5438	39.08	0.114199873
6755354	QLDSGLLLVTGPLVINR		ribosomal protein L6 [Mus musculus]	1808.0681	119.05	0.504214046
11875203	QLEEEQQALQK		tropomyosin 2, beta [Mus musculus]	1343.6787	37.93	1.615732041
6754750	QLFDQVVK		moesin [Mus musculus]	976.5435	42.56	0.404878157
6677699	QLFDQVVK		radixin [Mus musculus]	976.5435	42.56	0.404878157
6678571	QLFDQVVK		villin 2 [Mus musculus]	976.5435	42.56	0.404878157
34740335	QLFHPEQLITGK		tubulin, alpha 2 [Mus musculus]	1410.7701	43.96	0

6678467	QLFHPEQLITGK		tubulin, alpha 4 [Mus musculus]	1410.7701	43.96	0
6678469	QLFHPEQLITGK		tubulin, alpha 6 [Mus musculus]	1410.7701	43.96	0
7305295	QLHEYETELEDER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1690.7578	62.12	0.061269913
7305295	QLLQANPILEAFGNAK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1726.9481	100.55	0
20137006	QLLQANPILEAFGNAK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1726.9481	100.55	0
29336026	QLLQANPILEAFGNAK		nonmuscle myosin heavy chain [Mus musculus]	1726.9481	100.55	0
6678571	QLLTLSNELSQAR		villin 2 [Mus musculus]	1472.8022	48.93	0.345892406
6755608	QLMGMINQLTSLR	2 Deamidation (NQ)	SRY (sex determining region Y)-box 5 [Mus musculus]	1506.7772	23.98	0.194999069
50355692	QLQDEMLR	Oxidation (M)	lamin A isoform A [Mus musculus]	1048.514	22.48	0.366502279
63641940	QLQNIIQATSR		PREDICTED: desmoplakin [Mus musculus]	1271.7021	22.68	4.433971763
22122569	QLSQNFLLDLR	3 Deamidation (NQ)	transcription factor B1, mitochondrial [Mus musculus]	1349.7084	42.34	0
56605979	QLTEMLPSILNQLGADSLTSLR		basic transcription factor 3 [Mus musculus]	2400.2769	44.86	0.575700919
7304993	QLTQPETSYGR		drebrin-like [Mus musculus]	1279.6301	35.96	0.854744463
13385718	QLVEQVEQIQK		transmembrane emp24 protein transport domain containing 9 [Mus musculus]	1341.7312	54.09	0
31542427	QLYQTLTDYDIR		casein kinase II, alpha 1 polypeptide [Mus musculus]	1528.7603	52.85	0
30519911	QMEQISQFLQAAER		transgelin 2 [Mus musculus]	1678.8286	37.78	0
6755714	QMEQVAQFLK		transgelin [Mus musculus]	1221.6283	42.06	0
63746482	QMQLENVSVALEFLDR		PREDICTED: filamin, alpha [Mus musculus]	1891.9574	78.65	0
50355692	QNGDDPLMTYR		lamin A isoform A [Mus musculus]	1309.5854	43.11	0.661437651
51712333	QNGVLNSWTDQDSK		PREDICTED: similar to anti-PRSV coat protein monoclonal antibody PRSV-L 3-8 immunoglobulin light ch	1591.7341	69.98	0
29789245	QNQLLLER	Deamidation (NQ)	centrosomal colon cancer autoantigen [Mus musculus]	1014.553	33.08	0
6678483	QNSLDEDLIR		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1202.5983	28.2	0.205915178
6753914	QNYSTEVEAAVNR		ferritin light chain 1 [Mus musculus]	1480.7015	56.08	0
22122789	QPSLSAACLGPEVTTQYGGLYR		acylpeptide hydrolase [Mus musculus]	2311.1338	25.35	0.439890878
30794450	QPYAVSELAGHQTSAESWGTGR		ribosomal protein L4 [Mus musculus]	2332.092	40.47	0.565328441
28892785	QPYFGAVVGR		aldose 1-epimerase [Mus musculus]	1093.5787	29.19	0
29789080	QQALTVSTDPEHR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1481.7396	50.03	0.326412741
13507628	QQEQTAQGTAPDAVDQQR		LPS-responsive beige-like anchor [Mus musculus]	1970.9199	86.23	0.424312997
6671702	QQISLATQMVR		chaperonin subunit 5 (epsilon) [Mus musculus]	1274.6903	29.36	0
29789189	QQKQQMLEMR	3 Deamidation (NQ); Oxidation (M)	minichromosome maintenance protein 10 [Mus musculus]	1338.6144	24.54	0
42734399	QQLDELNWSTALAEGER		desmuslin isoform H [Mus musculus]	1959.9419	96.51	0
46559834	QQLDELNWSTALAEGER		desmuslin isoform M [Mus musculus]	1959.9419	96.51	0
14861854	QQLETLQLDGGR		keratin complex 2, basic, gene 7 [Mus musculus]	1357.7028	48.2	0
14861854	QQLETLQLDGGR	2 Deamidation (NQ)	keratin complex 2, basic, gene 7 [Mus musculus]	1359.6967	44.92	0
41322904	QQNLASYDYVR		plectin 1 isoform 1 [Mus musculus]	1356.658	56.33	0
31981828	QQPLFVSGGDDYK		coatomer protein complex subunit alpha [Mus musculus]	1453.6868	39.19	0
22550094	QQPPDLVDFAVEYFTR		protein kinase, cAMP dependent regulatory, type II alpha [Mus musculus]	1924.9468	57.05	0.207507914
13385878	QQQFENLDQQLR		sorting nexin 2 [Mus musculus]	1546.7616	30.72	0
21312968	QQSEEDLLLQDFSR		signal sequence receptor, gamma [Mus musculus]	1707.823	84.16	0.392162191
63476037	QQSLETAMSFVAR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1467.7255	39.65	0.487787433
63660302	QQYNVTYVVK		PREDICTED: filamin B, beta [Mus musculus]	1241.6426	53.14	0
41322904	QSAEEQAQAQAQAQAAAEK		plectin 1 isoform 1 [Mus musculus]	1957.9255	103.06	0.655475046
6754508	QSFTMVADTPENLR		LIM and SH3 protein 1 [Mus musculus]	1608.7766	66.66	0
30794412	QSSYGQQSYNNQGQQNTESSGGQGGR		TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor [Mus musculus]	2747.1614	102.11	0.333623326
41322904	QTNLENLDQAFSVAER		plectin 1 isoform 1 [Mus musculus]	1834.8993	59.93	0.499154077
30023842	QTNPSAMEVEEDDPVPEIR		valosin containing protein [Mus musculus]	2155.9861	46.97	0.471260162
7305291	QTPAAPETEEEPYR		metaxin 1 [Mus musculus]	1617.7443	46.52	0.276469737
50080209	QTQTFTTYSDNQPGVLIQVYEGER		heat shock protein 1A [Mus musculus]	2774.3301	116.83	0.358451541
31981690	QTQTFTTYSDNQPGVLIQVYEGER		heat shock protein 8 [Mus musculus]	2774.3301	116.83	0.358451541
6680606	QTSAMSSFGGTGGGSVR		keratin complex 1, acidic, gene 19 [Mus musculus]	1586.7299	137.33	0
6680606	QTSAMSSFGGTGGGSVR	Oxidation (M)	keratin complex 1, acidic, gene 19 [Mus musculus]	1602.719	44.08	0.716398306
8567336	QTTPMTAQPPAPTFSLLQIGQR		chloride channel calcium activated 3 [Mus musculus]	2383.2568	88.42	0.049863646
8567336	QTTPMTAQPPAPTFSLLQIGQR	Oxidation (M)	chloride channel calcium activated 3 [Mus musculus]	2399.2441	80.78	0
6679503	QTYFLPVIGLVDAEK		proteasome (prosome, macropain) 26S subunit, ATPase 3 [Mus musculus]	1692.9163	67.03	0
22267442	QVAEQFLNMR		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1235.6217	38.39	0.472144687
31542143	QVELALWDTAGQEDYDR		ras homolog gene family, member A [Mus musculus]	2008.9106	60.79	0.339199723
33859753	QVEVDAQQCMLEILDTAGTEQFTAMR		RAS related protein 1b [Mus musculus]	2927.3286	31.38	0.342582965
28316750	QVHPDTGISSK		histone 1, H2ba [Mus musculus]	1168.5958	25.35	0
20874851	QVHPDTGISSK		PREDICTED: similar to histone H2b-616 [Mus musculus]	1168.5958	25.35	0
6753864	QVIGTGSFFPK		four and a half LIM domains 1 [Mus musculus]	1180.6323	47.24	0

27754099	QVLEPSFR		eukaryotic translation elongation factor 1 gamma [Mus musculus]	975.5236	37.79	0.691441859
22122789	QVLLSEPQEAAALYR		acylpeptide hydrolase [Mus musculus]	1687.9015	41.03	0.240073075
63680681	QVSVGQVPGR	2 Deamidation (NQ)	PREDICTED: similar to Zinc finger protein 132 [Mus musculus]	1028.5203	32.92	0
6754524	QVVDSAYEVIK		lactate dehydrogenase 1, A chain [Mus musculus]	1250.6572	69.02	0
63562723	QVVNIPSFIVR		PREDICTED: similar to 40S ribosomal protein S9 [Mus musculus]	1271.7471	36.09	0.591871708
6678573	QVVVEGQEPANFWMALGGK		villin 1 [Mus musculus]	2060.0234	33.28	1.235159793
50355690	QWGWTQGR		ribosomal protein L17 [Mus musculus]	1018.4883	39.63	0.546940631
21313162	QWLQEIDR		RAB1B, member RAS oncogene family [Mus musculus]	1087.5511	30.92	0.417513588
6679587	QWLQEIDR		RAB1, member RAS oncogene family [Mus musculus]	1087.5511	30.92	0.417513588
21592285	QWYETNAPSTIR		keratin 20 [Mus musculus]	1465.7083	66.03	0.49573228
11528504	QYDYDSSTIR		niban protein [Mus musculus]	1247.5568	25.44	0
6753620	QYPISLVLAPTR		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1357.788	25.02	0.928057291
13385558	QYPYNNLYLER		NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 [Mus musculus]	1472.7188	27.01	0
33563250	RIESLNEEIAFLK		desmin [Mus musculus]	1561.8551	31.49	0.368019064
31542159	SAAEMVLSDDNFASIVAAVEEGR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	2381.1423	61.22	0
6754524	SADTLWGIQK		lactate dehydrogenase 1, A chain [Mus musculus]	1118.58	74.44	0.381413808
63476037	SALLDSIQNLQVALTSK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1801.0035	70.36	0
30348966	SALPAQSAATLPAR		spectrin beta 2 isoform 1 [Mus musculus]	1353.7511	34.01	0.844658969
6754206	SANLVAATLGAILNR		hexokinase 1 [Mus musculus]	1483.8619	36.53	0
6678992	SAPSLEYCAELLGLDQDDLR		myosin VI [Mus musculus]	2208.05	56.46	0.706761987
63518159	SAVDNCQDSWR		PREDICTED: phosphogluconate dehydrogenase [Mus musculus]	1280.5377	42.91	0.826470911
6754342	SAVVEMLIMR		integrin linked kinase [Mus musculus]	1148.6144	44.94	0
31981013	SAVYPTSAVQMEAALR		methionine sulfoxide reductase A [Mus musculus]	1693.8472	32.56	1.528902036
29293809	SAYDSTMETMNYAQIR		ATP citrate lyase [Mus musculus]	1880.8199	77.02	0
29293809	SAYDSTMETMNYAQIR	Oxidation (M)	ATP citrate lyase [Mus musculus]	1896.8148	24	0
136429	SCAAAGTECLISGWGNTK		Trypsin precursor	1768.8016	124.68	0
6755965	SCSGVEFSTSGSSNTDTGK		voltage-dependent anion channel 2 [Mus musculus]	1850.7749	117.53	0.440041878
54020676	SDAAPTPVPQSAPR		hypothetical protein LOC229317 [Mus musculus]	1393.7128	60.18	0.444944957
15809004	SDAILDFNTMSEIMESGYTR		cyclin M4 [Mus musculus]	2280.0261	29.76	0
31543051	SDFDMVDYLNELR		karyopherin (importin) beta 1 [Mus musculus]	1616.7434	33.12	0
18079339	SDFDPGQDTYQHPPK		aconitase 2, mitochondrial [Mus musculus]	1731.7627	65.17	0.102009696
31981722	SDIDEIVLVGGSTR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1460.7596	88.23	0
6754256	SDIGEVILVGGMTR		heat shock protein 9A [Mus musculus]	1446.7639	57.28	1.039691279
25141330	SDPFLEFFR		copine I [Mus musculus]	1157.5713	31.1	0.523050802
6679567	SDQVNGVLVLSLLDK		polymerase I and transcript release factor [Mus musculus]	1599.892	86.79	0
58037546	SDYLNTFEFMDK		isocitrate dehydrogenase 1 (NADP+), soluble [Mus musculus]	1509.6593	73.57	0
9845257	SEAAPAAPAAAPPAEK		histone 1, H1c [Mus musculus]	1448.7404	61.24	0.618906531
31982236	SEDEVGSLIEYEFR		integrin alpha 6 [Mus musculus]	1672.7723	27.39	0
63738313	SEDGVEGDLGETQSR		PREDICTED: similar to AHNAK [Mus musculus]	1578.6923	57.96	0.273749239
6753498	SEDYAFPTYADR		cytochrome c oxidase subunit IV isoform 1 [Mus musculus]	1434.6207	68.13	0.410892641
31982275	SEESEEPMETDQNAKEEEK	Oxidation (M)	heat shock protein 4 [Mus musculus]	2254.9272	33.53	0
31982290	SEGDTAYGQQVQPNTWK		LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1908.8748	107.91	0.233263967
6753060	SEIDLFNIR		annexin A5 [Mus musculus]	1106.5818	40.58	0
15809004	SEILDESDMYTDNR		cyclin M4 [Mus musculus]	1687.7157	35.43	0
13385340	SELVAMLEEEELR		ADP-ribosylation factor-like 1 [Mus musculus]	1547.7649	39.79	0.435273078
6755817	SELVANNVTLPAGEQR		thymopoietin [Mus musculus]	1697.8843	85.37	0.293737199
6755963	SENGLEFTSSGSANTETTK		voltage-dependent anion channel 1 [Mus musculus]	1959.8789	132.44	0.282118267
6679687	SEPIPESNEGPVK		glucose regulated protein [Mus musculus]	1382.6735	78.46	0.311324989
6755566	SEQAEPPAAADTHEAGDQNEAEK		solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1 [Mus musculus]	2395.0352	61.54	0.293287913
51768458	SEQPVDILQIFR		PREDICTED: similar to mKIAA0177 protein [Mus musculus]	1444.7791	23.49	0.753054201
13430890	SETAPAAPAAPAPAEK		histone 1, H1e [Mus musculus]	1478.7467	59.45	0
34328365	SETAPAAPAAPAPVEK		histone 1, H1d [Mus musculus]	1506.7817	58.29	3.742245112
21426893	SETAPAETAAPAPVEK		histone 1, H1b [Mus musculus]	1568.778	38.42	0
6671690	SETITEEELVGLMNK		carbonyl reductase 1 [Mus musculus]	1692.8429	37.36	0
7304889	SETSGSFEDALLAIVK		annexin A4 [Mus musculus]	1666.8507	53.25	0.352361187
31982122	SFDPFTEVIVDGIVANALR		phospholipase C, beta 3 [Mus musculus]	2063.0798	30.03	0.292087293
45598381	SFEDTIAQGITFVK		thioredoxin domain containing 5 [Mus musculus]	1555.7906	59.19	0.498779949
21314832	SFENSLGINVPR		UDP-glucose pyrophosphorylase 2 [Mus musculus]	1332.6888	69.88	0.407480161
13384736	SFEWLSQMR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1183.5625	34.92	0.454722776
50080209	SFFPEEISSMVLTK		heat shock protein 1A [Mus musculus]	1614.8057	43.52	0

63664040	SFFSEIISSISDVK		PREDICTED: alpha isoform of regulatory subunit B55, protein phosphatase 2 [Mus musculus]	1558.7942	45.25	0.530806817
51767507	SFGGGTGSGFTSLLMER		PREDICTED: similar to tubulin, alpha-like 3 [Mus musculus]	1703.8086	40.84	0
63723778	SFITTDVNPYYDSFVR		PREDICTED: leucyl-tRNA synthetase [Mus musculus]	1923.9183	56.67	0.581662428
6753620	SFLLDLLNATGK		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1291.7205	70.28	0.39924443
7110713	SFQNYIR	Deamidation (NQ)	RAS p21 protein activator 3 [Mus musculus]	928.4548	25.33	0
51770896	SFVQNYPVVSIEDPFDQDDWGAWQK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	2970.376	79.73	0.318958395
31981690	SFYPEEVSSMVLTK		heat shock protein 8 [Mus musculus]	1616.7872	67.24	0
28916693	SGALNSNDAFVLK		gelsolin [Mus musculus]	1335.6862	40.53	0.503490634
19527048	SGAYSAGYGGYEEYSGLSDGYGFTTDLFGR		heterogeneous nuclear ribonucleoprotein F [Mus musculus]	3147.3894	76.53	0.307905859
51873060	SGDAAIVDMVPGKPMCVESFSDYPPLGR		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2938.3813	31.78	0.406578109
7304879	SGDNDFPVNEQGK		aldo-keto reductase family 1, member C13 [Mus musculus]	1406.6202	22.98	0.697303938
47058964	SGDSEVYQMGDVSQK		single-stranded DNA binding protein 1 isoform 2 [Mus musculus]	1629.7156	40.37	0.758524184
6755787	SGEGEVSGLLR		tripartite motif protein 28 [Mus musculus]	1103.5664	23.25	0
31980726	SGEHDFGAAFDGDGDR		phosphoglucomutase 2 [Mus musculus]	1652.665	93.22	0.243678955
23956084	SGELAVQALDQFATVVEAK		acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	1976.0018	60.57	0.427468186
7305027	SGETEDTFIADLVVGLCTGQIK		enolase 2, gamma neuronal [Mus musculus]	2296.1382	103.18	0.586420629
6679651	SGETEDTFIADLVVGLCTGQIK		enolase 3, beta muscle [Mus musculus]	2296.1382	103.18	0.586420629
51770896	SGETEDTFIADLVVGLCTGQIK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	2296.1382	103.18	0.586420629
6680618	SGEYPFPLIK		acetyl-Coenzyme A dehydrogenase, medium chain [Mus musculus]	1150.6221	25.73	0
29293809	SGGMSNELNNIISR		ATP citrate lyase [Mus musculus]	1491.7247	40.56	0
6679793	SGIGTGDEPGPQGLNGEAGPEDPSR		protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform [Mus musculus]	2394.0928	78.43	0.282781547
6680970	SGLGSQVGLMPGSVGPVGPR	Oxidation (M)	procollagen, type V, alpha 2 [Mus musculus]	1867.9666	30.23	0
40254244	SGSMDSPMSTENNSQLR		loss of heterozygosity, 11, chromosomal region 2, gene A homolog [Mus musculus]	1840.7834	26.4	0
19526822	SGTTWMSEIMDMIYQGGK		sulfotransferase family 1A, phenol-preferring, member 1 [Mus musculus]	2034.9255	28.89	0
41152517	SIAFPSIGSGR		H2A histone family, member Y [Mus musculus]	1091.5839	24.09	0.423553268
29244556	SIGESVPEPR		GDP-mannose pyrophosphorylase B [Mus musculus]	1070.5514	32.93	0.286484048
19527294	SIGVSNFNFR		aldo-keto reductase family 1, member C14 [Mus musculus]	1140.5817	25.47	0.242609072
63645619	SIGVSNFNSR		PREDICTED: hypothetical protein XP_621309 [Mus musculus]	1080.5439	24.54	0.67914524
41322904	SIITYVSSLYDAMPR		plectin 1 isoform 1 [Mus musculus]	1715.8718	29.48	1.014764
6755863	SILFVPTSAPR		tumor rejection antigen gp96 [Mus musculus]	1187.6813	54.32	0.485288719
31981828	SILLSVPLLVVDNK		coatomer protein complex subunit alpha [Mus musculus]	1509.9242	51.14	1.15470513
31981690	SINPDEAVAYGAAVQAAILSGDK		heat shock protein 8 [Mus musculus]	2260.1479	140.96	0.485278737
6754206	SIPDGTEHGDFLALDLGGTNFR		hexokinase 1 [Mus musculus]	2332.1084	37.55	0
31982030	SIQEIQELDKDDESLR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1917.9414	68.49	0.397474557
34740335	SIQFVDWCPTGFK		tubulin, alpha 2 [Mus musculus]	1527.7308	67.26	0.404049443
6678467	SIQFVDWCPTGFK		tubulin, alpha 4 [Mus musculus]	1527.7308	67.26	0.404049443
38090003	SISTSLPVLDLIDAIAPNAVR		PREDICTED: expressed sequence AI427122 [Mus musculus]	2165.217	64.63	0.560192094
31981657	SIVNNGHSFNVEFDDSQDNAVLK		carbonic anhydrase 2 [Mus musculus]	2549.2043	115.71	0.145589774
40556608	SIYYITGESK		heat shock protein 1, beta [Mus musculus]	1160.5781	34.92	0
64427157	SLASVPQQNGFSGVSETAGAQR		PREDICTED: synaptopodin 2 [Mus musculus]	2191.0781	90.09	0
63476037	SLDEVSQPAQELKR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1599.8325	25.82	0
13624315	SLDMDGIIAEVR		keratin complex 2, basic, gene 8 [Mus musculus]	1318.6627	55.94	0
63565108	SLDMDGIIAEVR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1318.6627	55.94	0
63487095	SLDNNYSTLNER		PREDICTED: catenin src [Mus musculus]	1425.6648	29.2	0.715849508
7305295	SLEADLMQLQEDLAAAER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2002.9786	101.15	0
7305295	SLEADLMQLQEDLAAAER	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2018.9642	69.25	0.119111771
31981302	SLEDALSSDTSGHFR		annexin A6 [Mus musculus]	1621.7476	68.19	0
51717092	SLEEIYLFSLPIK		PREDICTED: similar to 40S ribosomal protein S2 [Mus musculus]	1551.8691	62.97	0.508185267
20373163	SLEELLLDANQLR		PDZ-domain protein scribble [Mus musculus]	1513.8252	39.45	0
6678331	SLESGEDLNFIVSTGPQPSESAR		transglutaminase 3, E polypeptide [Mus musculus]	2420.158	147.52	0.075910711
6754556	SLETENSALQLQVTER		lamin B1 [Mus musculus]	1817.924	92.48	0
46275826	SLFPVVLEQLDDYNAK		laminin, alpha 4 [Mus musculus]	1850.947	24.57	0
7304887	SLGDDISSETSGDFR		annexin A3 [Mus musculus]	1585.7102	62.51	0
31560656	SLGYAYVNFQQPADAER		poly A binding protein, cytoplasmic 1 [Mus musculus]	1928.9188	88.35	0.441616853
63622083	SLGYAYVNFQQPADAER		PREDICTED: similar to Poly(A) binding protein, cytoplasmic 4, isoform 1 [Mus musculus]	1928.9188	88.35	0.441616853
41322904	SLLAWQSLSR		plectin 1 isoform 1 [Mus musculus]	1160.6405	32.93	0
7304879	SLLDTVDFCDTWER		aldo-keto reductase family 1, member C13 [Mus musculus]	1699.7772	50.25	0.339128782
6680606	SLLEGQEAHYNNLPTPK		keratin complex 1, acidic, gene 19 [Mus musculus]	1910.9608	82.15	0.378926132
7106407	SLLNEIESIYDER		transcriptional regulator, SIN3A [Mus musculus]	1580.7811	31.89	0
12963539	SLLPGCQSVISR		ETHE1 protein [Mus musculus]	1259.6809	33.21	0

29244176	SLNLDSIIAEVK	Deamidation (NQ)	hypothetical protein 4732456N10 [Mus musculus]	1302.7126	85.98	0
47086911	SLNNQFASFIDK		keratin Kb40 [Mus musculus]	1383.6934	50.04	0
1346343	SLNNQFASFIDK		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1383.6934	50.04	0
6754524	SLNPELGTDADKEQWK		lactate dehydrogenase 1, A chain [Mus musculus]	1830.8873	87.31	0.403399769
33859811	SLNSEMDNILANLR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1589.7992	91.74	0
33859811	SLNSEMDNILANLR	Oxidation (M)	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1605.7866	35.14	0.699984131
51709154	SLPADILYEDQQCLVFR		PREDICTED: histidine triad nucleotide binding protein 2 [Mus musculus]	2010.0029	22.71	0
51706331	SLQGLAGEIVGEVR		PREDICTED: hypothetical protein LOC67809 [Mus musculus]	1427.7896	37.18	0
6680572	SLSALGNVISALAEGSTYVPYR		kinesin family member 5B [Mus musculus]	2268.1831	50.36	0.615219782
28395023	SLSDALISLQMVYPR		NCK-associated protein 1 [Mus musculus]	1692.8992	22.97	0.81298834
21592285	SLSSSSQGPALSMSGSLYR		keratin 20 [Mus musculus]	1914.9247	32.61	0
27754118	SLYSAISLFNNPMK	Oxidation (M)	asporin [Mus musculus]	1600.8055	42.08	0
31982755	SLYSSSPGGAYVTR		vimentin [Mus musculus]	1444.7086	81.41	0.353631982
6996913	SLYYYIQQDTK		annexin A2 [Mus musculus]	1421.693	34.39	1.074531508
22267442	SMAASGNLGHTPFLDEL		ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1759.8433	24.83	0
20137006	SMEAEMIQLQEELAAAER		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	2048.9653	76.55	0.495438299
63487095	SMGYDDLDYGMMSDYGTAR		PREDICTED: catenin src [Mus musculus]	2147.8552	84.4	0
22122825	SMLEVNYPMENGIVR		actin-related protein 2 [Mus musculus]	1751.8578	27.77	0
9790051	SNCNVAVINVGAPAAGMNAAVR		phosphofructokinase, platelet [Mus musculus]	2099.0518	64.73	1.020559445
50355692	SNEDQSMGNWQIR		lamin A isoform A [Mus musculus]	1564.6853	90.04	0
31560653	SNFSLAILNVGAPAAGMNAAVR		phosphofructokinase, liver, B-type [Mus musculus]	2144.1299	63.23	0
31982275	SNLAYDIVQLPTGLTGIK		heat shock protein 4 [Mus musculus]	1903.0509	68.85	0.260737861
6681291	SNLVDNTNQVEVLQR		Ddx19-like protein [Mus musculus]	1728.8889	71.15	0
33469063	SNLVGMGVIPLEYLPGETADSLGLTGR		aconitase 1 [Mus musculus]	2759.4199	54.98	0.203927728
13624315	SNMDNMFESYINNLR		keratin complex 2, basic, gene 8 [Mus musculus]	1847.8153	86.48	0
63565108	SNMDNMFESYINNLR		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1847.8153	86.48	0
13624315	SNMDNMFESYINNLR	2 Oxidation (M)	keratin complex 2, basic, gene 8 [Mus musculus]	1879.79	36.64	0.558914903
63565108	SNMDNMFESYINNLR	2 Oxidation (M)	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1879.79	36.64	0.558914903
13624315	SNMDNMFESYINNLR	Deamidation (NQ)	keratin complex 2, basic, gene 8 [Mus musculus]	1848.7959	39.58	0
63565108	SNMDNMFESYINNLR	Deamidation (NQ)	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1848.7959	39.58	0
13624315	SNMDNMFESYINNLR	Oxidation (M)	keratin complex 2, basic, gene 8 [Mus musculus]	1863.8035	50.24	0
63565108	SNMDNMFESYINNLR	Oxidation (M)	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1863.8035	50.24	0
10946928	SNNVEMDWVLK		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1334.6482	55.21	0
6679505	SNPENNVGLITLANDCEVLTTLTPDTGR		proteasome 26S non-ATPase subunit 4 [Mus musculus]	2957.4534	24.88	0.64898384
21450277	SPDFTNENPLETR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1519.7064	97.74	0.327063883
8394024	SPDTNYLFMGDYVDR		protein phosphatase 2a, catalytic subunit, beta isoform [Mus musculus]	1792.7953	34.94	0
7710042	SPDVGLYGVIPECGETYQSDLAEAK		IQ motif containing GTPase activating protein 1 [Mus musculus]	2641.241	30.98	0
9790167	SPESQLFSIEDIQEVR		phospholipase C, delta 1 [Mus musculus]	1876.9362	46.55	0.883513547
6679761	SPFETDMLTLTR		fructose bisphosphatase 2 [Mus musculus]	1410.6935	69.63	0
31980969	SPFLQVFNNSPDESSYYR		SEC23B [Mus musculus]	2149.9878	56.65	0.345594876
63746482	SPFSVGVSPSLDLSK		PREDICTED: filamin, alpha [Mus musculus]	1519.7955	105.75	0
28916673	SPLDSTAEPPAVR		SEC24 related gene family, member C [Mus musculus]	1339.6858	29.46	0.582471074
31981555	SPPSSAEQSTPAPPTK		ladinin [Mus musculus]	1581.7815	52.27	0.570625404
51766377	SPQSFFDTTPSGR		PREDICTED: ATP-binding cassette, sub-family C (CFTR/MRP), member 3 [Mus musculus]	1426.6635	29.25	0
37620153	SPSENGGNSAEVLNVK	Deamidation (NQ)	myosin, light polypeptide kinase telokin isoform [Mus musculus]	1602.759	25.48	0
31541815	SPTGLTLGSLVDEIQR		L-specific multifunctional beta-oxdiation protein [Mus musculus]	1685.8984	36.47	0
33859560	SPYLYPLYGLGELPQGFAR		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	2141.1089	54.37	0.366184729
56119103	SPYLYPLYGLGELPQGFAR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	2141.1089	54.37	0.366184729
63746482	SPYTVTVGQACNPAACR		PREDICTED: filamin, alpha [Mus musculus]	1737.817	28.42	0
31982472	SQDAEVGDGTTSVTLLAAEFLK		chaperonin subunit 7 (eta) [Mus musculus]	2252.1301	73.46	0
12746446	SQDVGFWEGEVVR		epithelial protein lost in neoplasm [Mus musculus]	1507.7174	82.21	0
31791057	SQECYFDPELYR		laminin, gamma 1 [Mus musculus]	1549.6638	28.83	0
7305169	SQFEELCAELLQK		heat shock protein 105 [Mus musculus]	1537.7531	34.44	0.782132414
51768600	SQFFEQGSSDSVAPDLPVPTLSAPSR		PREDICTED: LIM domain only 7 [Mus musculus]	2719.3403	37.25	0.578202781
18079339	SQFTITPGSEQIR		aconitase 2, mitochondrial [Mus musculus]	1463.7506	61.31	0.325616577
22094115	SQGDMQDLNGNNQSVTR		signal transducer and activator of transcription 3 isoform 3 [Mus musculus]	1863.8499	26.4	0.387102362
22094115	SQGDMQDLNGNNQSVTR	Oxidation (M)	signal transducer and activator of transcription 3 isoform 3 [Mus musculus]	1879.826	38.28	0.568158952
6678331	SQGVFQCGPASVNAIK		transglutaminase 3, E polypeptide [Mus musculus]	1605.8002	79.27	0
31981722	SQIFSTASDNQPTVTIK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1836.9283	89.33	0.516119174
31981690	SQIHDIVLVGGSTR		heat shock protein 8 [Mus musculus]	1481.809	63.82	0

6677871	SQLIVVEEGSEPSELMK		scinderin [Mus musculus]	1874.9402	67.85	0
21703972	SQLYDDLMDEFMK		malic enzyme 2, NAD(+)-dependent, mitochondrial [Mus musculus]	1634.7275	47.61	0
47059123	SQQEGGILPLLDSPAK		UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	1652.8821	58.62	1.572173902
19882199	SQSNESAGSQVGTEFK		RAN binding protein 2 [Mus musculus]	1655.7454	24.98	0.317112886
63487095	SQSSHSYDDSTLPLIDR		PREDICTED: catenin src [Mus musculus]	1920.8914	26.36	0.338355402
63476037	SQSSVLEAIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1089.5852	44.09	0
6754558	SQTNWGPGESFR		lamin B2 [Mus musculus]	1365.6226	27.22	0
41322904	SQVEEELFSVR		plectin 1 isoform 1 [Mus musculus]	1322.6599	31.38	0
54607037	SQVSPQGLQVR		integrin beta 4 isoform 2 [Mus musculus]	1198.6317	28.08	0.489394173
547749	SQYEQLAEQNR		Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)	1365.6462	47.86	0
30424882	SRFIQLVR		hypothetical protein LOC76608 [Mus musculus]	1018.5965	22.9	0
26986563	SSDPTAVVDAQTK		choline dehydrogenase [Mus musculus]	1318.6411	46.25	2.974044137
6671666	SSEMNVLIPTEGGDFNEFPVPEQFK		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	2811.3416	68.31	0.351876957
63738313	SSEVVLSGDDEDYQR		PREDICTED: similar to AHNAK [Mus musculus]	1698.7493	96.94	0.448573153
6755040	SSFFVNGLTLGGQK		profilin 1 [Mus musculus]	1454.7578	79.14	0.392306719
58037465	SSGEIVYCGQVFEK		Ribosomal protein L18A [Mus musculus]	1545.7222	24.72	0
31559916	SSGSPYGGGYGSGGGSGGYGSR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1910.799	161.41	0.552479208
8394258	SSGSQGVPGPPAPAR		semaF cytoplasmic domain associated protein 2 [Mus musculus]	1364.6976	23.12	0
136429	SSGSSYPSLLQCLK		Trypsin precursor	1469.7264	87.18	0
12083691	SSGTGASVGPPQPSDQDTLVQR		PDZ and LIM domain 5 isoform ENH1 [Mus musculus]	2184.0562	79.96	0.328336012
6755354	SSITPGTVLIILTGR		ribosomal protein L6 [Mus musculus]	1527.9081	44.94	0.509097453
22779912	SSLLDDLLTESEDMAQR		dynamin 1-like [Mus musculus]	1922.9061	45.84	0
46195798	SSLNPILFR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1046.5996	32.94	0
63489759	SSLSSAQADFNQLAELDR		PREDICTED: spectrin alpha 2 [Mus musculus]	1951.9333	54.14	0.331133591
15147224	SSMSVTSLEDELQASIQR		sideroflexin 1 [Mus musculus]	1980.9586	41.89	0
8567338	SSPEPVALTESETEYVIR		coatomer protein complex, subunit gamma [Mus musculus]	2007.0005	73.05	0
46849812	SSPVIIDASTAIDAPSNLR		fibronectin 1 [Mus musculus]	1927.0095	23.3	0
40068493	SSQSSSQQFSGIGR		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1455.6885	26.01	0
63481281	SSSNTVESTSLYNK		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1516.7046	22.33	1.282418738
31559891	SSTFWLR		mitochondrial Rho 1 [Mus musculus]	896.4514	28.71	0.307066128
6755817	SSTPLPTVSSSAENTR		thymopoietin [Mus musculus]	1633.806	57.05	0
31981690	STAGDTHLGGEDFDNR		heat shock protein 8 [Mus musculus]	1691.7345	106.4	0.502442607
33859482	STAISLFYELSENDLNFIK		eukaryotic translation elongation factor 2 [Mus musculus]	2204.1094	120.95	0.363847817
30841021	STELDSNWSWFQLR		ADP-ribosylation factor GTPase activating protein 3 [Mus musculus]	1768.8352	30.32	0.375140462
33186863	STESLQANVQR		ribosomal protein L13 [Mus musculus]	1232.6285	27.11	0.371696119
42734399	STETMIGEMINLGLK		desmuslin isoform H [Mus musculus]	1636.8292	43.24	1.244533822
46559834	STETMIGEMINLGLK		desmuslin isoform M [Mus musculus]	1636.8292	43.24	1.244533822
10946928	STGEAFVQFASQEIAEK		heterogeneous nuclear ribonucleoprotein H1 [Mus musculus]	1841.8896	67.67	0
9845253	STGEAFVQFASQEIAEK		heterogeneous nuclear ribonucleoprotein H2 [Mus musculus]	1841.8896	67.67	0
6679583	STIGVEFATR		RAB11B, member RAS oncogene family [Mus musculus]	1080.5702	25.68	0.520624216
6754816	STLINSLFLTDLYPER		septin 2 [Mus musculus]	1881.9922	38.72	0.238896432
31981549	STLSVIPSGVQWIQDR		sulfide quinone reductase-like [Mus musculus]	1785.9574	54.42	0.48168957
6754256	STNGDTFLGGEDFDQALLR		heat shock protein 9A [Mus musculus]	2055.9673	126.1	0.457183878
6754256	STNGDTFLGGEDFDQALLR	Deamidation (NQ)	heat shock protein 9A [Mus musculus]	2056.9612	120.51	0.415288512
30425112	STPEDQILYQTER		hypothetical protein LOC109154 [Mus musculus]	1579.7622	55.74	0.415318959
8567336	STWEVIQESEDFK		chloride channel calcium activated 3 [Mus musculus]	1597.7357	72.94	0.107384373
31980953	SVAEISPDLIQFSR		hydroxyacid oxidase (glycolate oxidase) 3 [Mus musculus]	1561.818	36.08	0.201838052
51491845	SVDPTLALSVYLR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1433.798	63.2	0.35444315
6678573	SVEDLPEGVDPSR		villin 1 [Mus musculus]	1399.6445	37.63	0.231471861
63641940	SVEEVASEIQPFLR		PREDICTED: desmoplakin [Mus musculus]	1603.8312	54.21	0.574736332
19705424	SVFPEQANNNEWAR		proteasome 26S non-ATPase subunit 3 [Mus musculus]	1661.7733	56.53	0.413974643
50355692	SVGGSGGGSFGDNLVTR		lamin A isoform A [Mus musculus]	1566.7505	124.07	0.314912894
19745150	SVGMIAGGTGITPMLQVIR		diaphorase 1 [Mus musculus]	1901.0355	50.93	0
63664018	SVLAVENLLTLDR		PREDICTED: kinesin family member 13B [Mus musculus]	1442.8221	35.48	0
6677935	SVLEGGDIPLQGLSGLK		sorbin and SH3 domain containing 1 [Mus musculus]	1682.9253	34.29	0
18875408	SVLVTSVLNLEPLDEDLYR		peroxisomal acyl-CoA thioesterase 1 [Mus musculus]	2175.1421	26.66	0
27370510	SVNDIVVLGPEQFYATR		paraoxonase 3 [Mus musculus]	1907.9863	43.79	0.555234472
51491845	SVNESLNNLFITEEDYQALR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2355.1477	154.25	0.44540299
6753824	SVPADIFQMQATTR		fibulin 5 [Mus musculus]	1564.7743	22.81	0
6678609	SVPATVDDDDDDNDPENR		alpha thalassemia/mental retardation syndrome X-linked homolog [Mus musculus]	1988.8146	23.66	0.551146383

6678359	SVPMSTVFYPSDGVATEK		transketolase [Mus musculus]	1914.9163	47.05	0
6678359	SVPMSTVFYPSDGVATEK	Oxidation (M)	transketolase [Mus musculus]	1930.9005	22.62	0
63641940	SVQNDSQALAEVLNQLK		PREDICTED: desmoplakin [Mus musculus]	1856.9701	52.8	0
6753658	SVSTPSEAGSQDSGDGAVGSR		dynein, cytoplasmic, intermediate chain 2 [Mus musculus]	1950.8772	32.77	0.45307922
11037800	SVTLPCTYNTYVSDR		glycoprotein A33 (transmembrane) [Mus musculus]	1718.8066	42.1	0.329071437
13385310	SVTNEDVTQEQLGGAK		propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]	1675.816	88.29	0.180645842
34328204	SVTQQPGSEVIAPQK		valyl-tRNA synthetase 2 [Mus musculus]	1568.8235	25.98	0.317886571
51828444	SVVTEEFNGSDWER		PREDICTED: proline-rich polypeptide 6 [Mus musculus]	1654.7394	59.52	0.412510165
6754482	SVWGGSVGSAGLAGMGGIQTEK		keratin complex 1, acidic, gene 18 [Mus musculus]	2049.0166	93.24	0
33563270	SWDIFFR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	970.4803	23.1	0.236103362
31982233	SWQDELAQQAEEGSAR		LYRIC [Mus musculus]	1804.8184	97.67	0.40838352
6753138	SYEAYVLNIIR		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1340.7271	47.79	0.264160525
6671507	SYELPDGQVITIGNER		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1790.8876	83.1	0.478557643
6671509	SYELPDGQVITIGNER		actin, beta, cytoplasmic [Mus musculus]	1790.8876	83.1	0.478557643
30425250	SYELPDGQVITIGNER		hypothetical protein LOC238880 [Mus musculus]	1790.8876	83.1	0.478557643
6671507	SYELPDGQVITIGNER	Deamidation (NQ)	actin, alpha 2, smooth muscle, aorta [Mus musculus]	1791.8907	39.74	0.317325341
6671509	SYELPDGQVITIGNER	Deamidation (NQ)	actin, beta, cytoplasmic [Mus musculus]	1791.8907	39.74	0.317325341
30425250	SYELPDGQVITIGNER	Deamidation (NQ)	hypothetical protein LOC238880 [Mus musculus]	1791.8907	39.74	0.317325341
57634518	SYELQESNVR		septin 11 [Mus musculus]	1224.5892	36.79	0.343533749
29568084	SYIEYQLTPTNTNR		sorting nexin 9 [Mus musculus]	1699.8257	44.88	0
38090710	SYLTPVRDEESESQR		PREDICTED: protein phosphatase 1, regulatory (inhibitor) subunit 12A [Mus musculus]	1795.8451	36.31	2.661628676
38198665	SYQDPSNAQFLESIR		p47 protein [Mus musculus]	1754.8373	33.29	0.405209613
6996913	SYSPYDMLESIK		annexin A2 [Mus musculus]	1432.6665	51.15	0
31791057	SYYYAISDFAVGGR		laminin, gamma 1 [Mus musculus]	1568.7561	24.51	0
31981549	TAAAVAAQSGILDR		sulfide quinone reductase-like [Mus musculus]	1343.729	62.85	0.243563488
6753620	TAAFLLPILSQIYADGPGEALR		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	2316.2634	35.26	0
6753484	TAEYDVAFGER		procollagen, type VI, alpha 1 [Mus musculus]	1257.5782	58.93	0.159333128
31543974	TAFDEAIAELDTLNEESYK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Mus muscu	2159.0061	99.39	0.196934653
6756041	TAFDEAIAELDTLSEESYK		tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide [Mus muscu	2132	136.99	0.356662457
50355692	TALINSTGEEVAMR	Oxidation (M)	lamin A isoform A [Mus musculus]	1507.7319	34.23	0.264083812
63489754	TALLELWELR		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1243.7074	40.42	0.263004919
6806903	TASEMVLADDNFSTIVAAVEEGR		ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	2425.1624	57.85	0.390068647
36031132	TASEMVLADDNFSTIVAAVEEGR		ATPase, Ca++ transporting, fast twitch 1 [Mus musculus]	2425.1624	57.85	0.390068647
10946940	TASNVEEAFINTAK		RAB2, member RAS oncogene family [Mus musculus]	1494.7495	22.36	0
63489754	TATDEAYKDPSNLQGK		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1737.8328	37.33	0.294854075
6677771	TAVVVGTVTDDVR		ribosomal protein L18 [Mus musculus]	1331.7159	31.89	0.688883807
6671664	TDAPQPDVKDEEGKEEEK		calnexin [Mus musculus]	2043.9476	27.88	0
6755863	TDDEVVQREEEAIQLDGLNASQIR		tumor rejection antigen gp96 [Mus musculus]	2728.3481	32.51	0.879936867
56119103	TDDYLDQPCCETINR		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1785.7461	53.87	0.329983981
33859560	TDDYLDQPCLETINR		guanosine diphosphate (GDP) dissociation inhibitor 1 [Mus musculus]	1795.8173	58.89	0.31587775
22550094	TDEHVIDQGDDGDNFYVIER		protein kinase, cAMP dependent regulatory, type II alpha [Mus musculus]	2337.0283	45.15	0
6754034	TDESQPWVLPVVR		glutamate oxaloacetate transaminase 1, soluble [Mus musculus]	1525.7961	37.57	0
6677805	TDITYPAGFMDVISIDK		ribosomal protein S4, X-linked [Mus musculus]	1885.9224	75.43	1.06616154
6677805	TDITYPAGFMDVISIDK	Oxidation (M)	ribosomal protein S4, X-linked [Mus musculus]	1901.9044	26.04	0.401506868
63501125	TDLEELNLGPR		PREDICTED: ADP-ribosylation factor interacting protein 1 [Mus musculus]	1256.6592	25.18	0
6680606	TDLEMQIESLKEELAYLK		keratin complex 1, acidic, gene 19 [Mus musculus]	2153.0984	35.42	0
6678331	TDLGPTYNGWQVLDATPQER		transglutaminase 3, E polypeptide [Mus musculus]	2261.0837	106.73	0.060437676
6678331	TDLGPTYNGWQVLDATPQER	Deamidation (NQ)	transglutaminase 3, E polypeptide [Mus musculus]	2262.0659	62.77	0
10946574	TDLNPDNLQGGDDLDPNYVLSSR		creatine kinase, brain [Mus musculus]	2518.1687	87.5	0
63476037	TDLQTITNDPR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1273.64	52.67	0
46593021	TDLTDYLNR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1110.5394	43.05	0.605280592
6755714	TDMFQTVDLYEGK		transgelin [Mus musculus]	1546.7131	61.76	0.636494731
6754982	TDSCDVNDCVQQVVELLQER		3'-phosphoadenosine 5'-phosphosulfate synthase 1 [Mus musculus]	2293.0735	23.13	0
63540743	TDTYVTDNGDGTYR		PREDICTED: filamin C, gamma [Mus musculus]	1577.6821	51.29	0
13384620	TDYNASVSVPDSSGPER		heterogeneous nuclear ribonucleoprotein K [Mus musculus]	1780.802	116.57	0.395134274
63540743	TEAAEIVEGEDSAYSVR		PREDICTED: filamin C, gamma [Mus musculus]	1825.8462	84.36	0
6755534	TEEPESPESVDQTSPTPGDGNPR		solute carrier family 12, member 7 [Mus musculus]	2426.0623	49.15	0.336109507
6753928	TEGEEEEEEEESPDTGGEYK		X-ray repair complementing defective repair in Chinese hamster cells 6 [Mus musculus]	2272.8875	63.08	0
6753138	TEISFRPNDPK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1303.6666	24.35	1.921030114
20137006	TELEDTLDSTAAQQELR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1919.9185	128.83	0.601408647

7305295	TELEDTLDSTATQQELR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1949.9281	124.32	0.101480193
29244560	TELQGLWINDIVPIGR		hypothetical protein LOC331063 [Mus musculus]	1824.0027	90.19	0.10519198
31559959	TELSQSDMFDQR		eukaryotic translation termination factor 1 [Mus musculus]	1456.6486	37.57	0.837387296
13624315	TEMENEFVLIK		keratin complex 2, basic, gene 8 [Mus musculus]	1352.6724	70.7	0
63565108	TEMENEFVLIK		PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1352.6724	70.7	0
13624315	TEMENEFVLIK	Oxidation (M)	keratin complex 2, basic, gene 8 [Mus musculus]	1368.6658	53.28	0.300048603
63565108	TEMENEFVLIK	Oxidation (M)	PREDICTED: similar to cytokeratin EndoA - mouse [Mus musculus]	1368.6658	53.28	0.300048603
6755690	TEQDLALGTDAEGQR		syntaxin binding protein 3 [Mus musculus]	1603.7565	45.29	0
6753036	TEQGPQVDETQFK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1506.7128	63.91	0.334161441
31981769	TEQLTDSTEISLLPSDIDR		glycerol-3-phosphate dehydrogenase 2 [Mus musculus]	2133.0518	65.93	0.349703012
46559834	TEQVTFGGPTAQVVEMDLSDTR		desmuslin isoform M [Mus musculus]	2381.1499	36.19	0
13195624	TEVLNYTTIPVYLPEITIGAHQGSR		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 [Mus musculus]	2772.4204	26.87	0.347582326
31981722	TFAPEEISAMVLTK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1536.792	58.35	1.174163031
31981722	TFAPEEISAMVLTK	Oxidation (M)	heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1552.7819	48.07	0
33859482	TFCQLILDPIFK		eukaryotic translation elongation factor 2 [Mus musculus]	1437.7836	41.47	0.611238278
63660302	TFEMSDFIVDTR		PREDICTED: filamin B, beta [Mus musculus]	1460.6761	57.91	1.064042564
6680163	TFESLVDFCK		L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain [Mus musculus]	1188.5697	39.33	0.261088551
29789080	TFEVCDLPVR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1178.5895	39.21	0.983253637
30725863	TFFSFPAVVAPFK		glycyl-tRNA synthetase [Mus musculus]	1457.7834	44.33	0.178967174
33563250	TFGGAPGFSLGSPLSSPVFPR		desmin [Mus musculus]	2078.0776	115.7	0.136029437
6679078	TFIAIKPDGVQR		nucleoside-diphosphate kinase 2 [Mus musculus]	1344.7637	36.87	0.435889293
34328206	TFIFSDLEYMGQSPGFYR		tryptophanyl-tRNA synthetase [Mus musculus]	2157.9961	48.75	0
6755152	TFPLDVGSVVGYSGR		prolyl endopeptidase [Mus musculus]	1553.7915	31.41	0
21312260	TFPTVNPTTGEVIGHVAEGDR		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	2197.0801	46.47	0
63746482	TFSVWYVPEVTGTHK		PREDICTED: filamin, alpha [Mus musculus]	1750.8885	52.81	0
6680067	TFTTQETITNAETAK		glucose phosphate isomerase 1 [Mus musculus]	1655.809	96.08	0.889165018
21312260	TFVEESIYR		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1143.5682	54.01	0.201326455
6753036	TFVQENVYDEFVER		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1774.8336	92.77	0.34924423
6755040	TFVSITPAEVGVLVGK		profilin 1 [Mus musculus]	1616.9209	84.18	0.495860095
46849812	TFYQIGDSWEK		fibronectin 1 [Mus musculus]	1373.6506	32.16	0
6680748	TGAIVDVPVGEELLGR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1624.8953	73.39	0.336694083
12331398	TGASFQQAQEEFSQGIFSSR		secretory carrier membrane protein 2 [Mus musculus]	2205.0266	39.56	1.355840161
31560790	TGDAISVMSEVAQTLLTQDVR		1-acylglycerol-3-phosphate O-acyltransferase 1 [Mus musculus]	2234.1284	28.23	0.499742993
28077103	TGDLGDINAEQLPGR		phospholipase A2, activating protein [Mus musculus]	1555.7694	38.69	0
58037267	TGEAIVDAALSALR		protein disulfide isomerase-associated 6 [Mus musculus]	1386.7612	105.65	0.835308833
6755004	TGGLEIDSDFGGFR		programmed cell death 8 [Mus musculus]	1470.6863	87.24	0.346160284
64427157	TGGMAGGGPDALQTDGLR		PREDICTED: synaptopodin 2 [Mus musculus]	1673.7806	24.12	0
42415475	TGPAATTLSDTAAAESLVDSSEVTVIGFFK		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	2985.5022	128.84	0.325343412
6681095	TGQAAGFSYTDANK		cytochrome c, somatic [Mus musculus]	1430.652	84.2	0.315970764
31981273	TGQEIPVNLR		CNDP dipeptidase 2 (metallopeptidase M20 family) [Mus musculus]	1126.6241	61.33	1.44417284
34996495	TGQEVVFVAEPDNK		ribophorin II [Mus musculus]	1532.7555	64.68	0
6680748	TGTAEMSSILEER		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1423.673	69.43	0.476705021
6806903	TGTLTTNQMSVCR		ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	1411.6685	37.08	1.006896401
31542159	TGTLTTNQMSVCR		ATPase, Ca++ transporting, ubiquitous [Mus musculus]	1411.6685	37.08	1.006896401
51767879	TGVAPIIDVVR		PREDICTED: similar to ribosomal protein L27A [Mus musculus]	1139.6781	62.84	0.379127639
31560517	TGVAPIIDVVR		ribosomal protein L27a [Mus musculus]	1139.6781	62.84	0.379127639
63746482	TGVAVNKPAEFTVDAK		PREDICTED: filamin, alpha [Mus musculus]	1646.8739	62.87	0
7305295	TGVLAHLEEER		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1253.6534	47.84	0
6754576	TGVPSQTPNPYANQR		lymphocyte antigen 64 [Mus musculus]	1629.8011	43.85	0.362426071
33859724	TGYTLDVTTGQR		heterogeneous nuclear ribonucleoprotein R [Mus musculus]	1311.6588	69.74	0.474100598
13242328	TGYTLDVTTGQR		NS1-associated protein 1 [Mus musculus]	1311.6588	69.74	0.474100598
29293809	TIAIIAEGIPEALTR		ATP citrate lyase [Mus musculus]	1567.9125	76.66	0.331821612
31980648	TIAMDGTEGLVR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1262.6421	84.83	0
6754976	TIAQDYGVLK		peroxiredoxin 1 [Mus musculus]	1107.5985	53.85	0.577243176
33859811	TIEYLEEVAVNFAK		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	1625.8329	62.83	0.89087703
6754854	TIFWTDSQLDR		nidogen 1 [Mus musculus]	1381.6639	30.96	0
34740335	TIGGGDDSFNTFFSETGAGK		tubulin, alpha 2 [Mus musculus]	2007.9021	69.06	0.316651826
6678469	TIGGGDDSFNTFFSETGAGK		tubulin, alpha 6 [Mus musculus]	2007.9021	69.06	0.316651826
6678467	TIGGGDDSFTTFFCETGAGK		tubulin, alpha 4 [Mus musculus]	2010.8928	53.01	0.524387767
31981909	TIGVSNFNPLQIER		aldo-keto reductase family 1, member B3 (aldose reductase) [Mus musculus]	1587.8464	40.81	0.394575053

6754816	TIISYIDEQFER		septin 2 [Mus musculus]	1513.7556	67.81	0.294709184
31543605	TILPAAAQDVYYR		ribophorin I [Mus musculus]	1480.7822	49.65	0
14149647	TILSNQTVDIPENVEITLK		ribosomal protein L9 [Mus musculus]	2127.1582	65.51	0.604901069
11230802	TINEVENQILTR		actinin alpha 4 [Mus musculus]	1429.7673	70.96	0.30465498
33468903	TIPAWATLSASQLAR		heterochromatin protein 1, binding protein 3 [Mus musculus]	1585.8699	28.7	1.127892831
33667082	TIPGTALVEMGDEYAVER		heterogeneous nuclear ribonucleoprotein L-like [Mus musculus]	1950.9542	45.41	0
11230802	TIPWLEDR		actinin alpha 4 [Mus musculus]	1029.5378	34.71	0.337515177
59709449	TIPWLENR		actinin alpha 2 [Mus musculus]	1028.5552	28.77	0.132955876
6678469	TIQFVDWCPTGFK		tubulin, alpha 6 [Mus musculus]	1541.7457	58.59	0.464347386
6753072	TISFIPPDGDFELMSYR		adaptor protein complex AP-1, mu 2 subunit [Mus musculus]	1987.9612	33.54	0.919501408
9845265	TITLEVEPSDTIENVK		ubiquitin A-52 residue ribosomal protein fusion product 1 [Mus musculus]	1787.9265	89.79	0.409676428
6755809	TLAESALQLLYTAK		talin 1 [Mus musculus]	1521.8496	68.6	0.29749901
6680067	TLASLSPETSLFIIASK		glucose phosphate isomerase 1 [Mus musculus]	1777.9937	65.64	0
6753190	TLATSLYNLLAR		galactosidase, beta 1 [Mus musculus]	1335.7704	25.13	0.193917253
21314832	TLDGGLNVIQLETAVGAAIK		UDP-glucose pyrophosphorylase 2 [Mus musculus]	1983.0974	40.1	0.655729693
31981828	TLDLPIYVTR		coatomer protein complex subunit alpha [Mus musculus]	1190.6775	50.23	0.304738102
30911099	TLEAVQDLLEQGR		fatty acid synthase [Mus musculus]	1471.7728	61.32	0
50355692	TLEGELHDLR		lamin A isoform A [Mus musculus]	1182.6102	31.56	1.913977568
63641940	TLELQGLINDLQR		PREDICTED: desmoplakin [Mus musculus]	1512.8407	47.73	1.027849089
22129770	TLEQQENFEEVAR		ankyrin 3, epithelial isoform b [Mus musculus]	1592.7548	50.82	0.339271169
22779912	TLESVDPLGGLNTIDILTAIR		dynamin 1-like [Mus musculus]	2211.2246	25.31	0.312693987
27754067	TLEVEIEPGVR		DnaJ (Hsp40) homolog, subfamily B, member 11 [Mus musculus]	1241.6671	34.6	0
30520375	TLFQIQAER		UDP-N-acteylglucosamine pyrophosphorylase 1 homolog [Mus musculus]	1105.5973	26.77	6.431210376
8392847	TLFSNIVLSGGSTLFK		ARP1 actin-related protein 1 homolog A [Mus musculus]	1683.9315	68.09	0
22122615	TLFSNIVLSGGSTLFK		ARP1 actin-related protein 1 homolog B [Mus musculus]	1683.9315	68.09	0
30725863	TLHVEEVVPSVIEPSFGLGR		glycyl-tRNA synthetase [Mus musculus]	2165.1592	22.93	0.486851732
21389320	TLLELIPELR		leucine-rich PPR motif-containing protein [Mus musculus]	1196.7305	31.07	0.368898751
33563236	TLLGDVPVVADPTVPNVTVTR		Rho, GDP dissociation inhibitor (GDI) beta [Mus musculus]	2163.2031	55.68	2.177407404
7305295	TLLQEQLQAETELYAESEEMR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2511.1882	38.6	0.088591423
37202121	TLLTGLLDLQAQYPQFISR		4-aminobutyrate aminotransferase [Mus musculus]	2177.198	32	0.239610039
31981679	TLNDELEIIEGMK		heat shock protein 1 (chaperonin) [Mus musculus]	1504.7555	40.4	0.522739143
54607098	TLNEADCATVPPAIR		succinate dehydrogenase Fp subunit [Mus musculus]	1570.7902	73.22	0.511487072
31981657	TLNFNEEGDAEEAMVDNWRPAQPLK		carbonic anhydrase 2 [Mus musculus]	2874.3276	71.5	0.190232039
31981657	TLNFNEEGDAEEAMVDNWRPAQPLK	Oxidation (M)	carbonic anhydrase 2 [Mus musculus]	2890.3401	54.9	0.943914489
31541791	TLPELYELVNR		fucosidase, alpha-L- 2, plasma [Mus musculus]	1346.7333	23.11	0.384367447
6754480	TLQGLEIELQSQLSMK		keratin 13 [Mus musculus]	1817.9668	37.45	3.71303892
6680602	TLQGLEIELQSQLSMK		keratin complex 1, acidic, gene 15 [Mus musculus]	1817.9668	37.45	3.71303892
6680606	TLQGLEIELQSQLSMK		keratin complex 1, acidic, gene 19 [Mus musculus]	1817.9668	37.45	3.71303892
6016411	TLQGLEIELQSQLSMK		Keratin, type I cytoskeletal 13 (Cytokeratin 13) (K13) (CK 13)	1817.9668	37.45	3.71303892
417200	TLQGLEIELQSQLSMK		Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)	1817.9668	37.45	3.71303892
15426055	TLQLALDLVSSR		coatomer protein complex, subunit beta 1 [Mus musculus]	1315.7653	30	0
6755376	TLTAVHDAILEDLVFPSEIVGK		ribosomal protein S7 [Mus musculus]	2367.2537	26.74	1.588007855
6678726	TLTGTAALTVQSQEENLR		leukotriene A4 hydrolase [Mus musculus]	1932.0051	65.54	0.37852453
6754254	TLTIVDTGIGMTK		heat shock protein 1, alpha [Mus musculus]	1349.7233	68.28	0
46195798	TLVLLDNLNVR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1269.7554	52.65	1.079192166
31543315	TLVLSNLSYSATK		nucleolin [Mus musculus]	1396.7727	22.97	0
22122535	TMADSSYNLEVQNILSFLK		pleckstrin homology domain containing, family C (with FERM domain) member 1 [Mus musculus]	2173.0769	48.01	0
7110703	TMLELLNQLDGFEATK		protease (prosome, macropain) 26S subunit, ATPase 5 [Mus musculus]	1822.9205	45.59	0.782736588
6679503	TMLELLNQLDGFQPNTQVK		proteasome (prosome, macropain) 26S subunit, ATPase 3 [Mus musculus]	2189.1216	33.51	0
6755809	TMLESAGGLIQTAR		talin 1 [Mus musculus]	1447.7579	38.41	0
33563250	TNEKVELQELNDR		desmin [Mus musculus]	1587.7975	42.87	0
31982755	TNEKVELQELNDR		vimentin [Mus musculus]	1587.7975	42.87	0
63589808	TNYNDRYDEIR		PREDICTED: similar to 60S ribosomal protein L7a (Surfeit locus protein 3) [Mus musculus]	1458.6682	27.77	0.362698392
7305443	TNYNDRYDEIR		ribosomal protein L7a [Mus musculus]	1458.6682	27.77	0.362698392
22094123	TPAQSGAWDPNNPNTPSR		suppressor of Ty 5 homolog [Mus musculus]	1909.8748	34.48	0.676852048
6996913	TPAQYDASELK		annexin A2 [Mus musculus]	1222.5885	74.39	0
51592084	TPELTWER		hypothetical protein LOC74340 [Mus musculus]	1031.5148	40.56	0.359207449
8394269	TPETVFIFWGPPNK		ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltra	1632.8468	33.69	1.456911198
6753364	TPFLLVGTQIDLR		cell division cycle 42 homolog [Mus musculus]	1472.8455	71.11	0.420671326
9790061	TPLFDQIIDMLR		pyrroline-5-carboxylate synthetase [Mus musculus]	1461.7803	22.66	0.968643471

63607160	TPLSEAEFEEIMNR	PREDICTED: cleavage and polyadenylation specific factor 6 [Mus musculus]	1665.7853	44.47	0.956567737
29336026	TPNVGGPGGPQVEWTAR	nonmuscle myosin heavy chain [Mus musculus]	1722.8617	63.28	0.357232837
6677935	TPVDYIDLPYSSSPSR	sorbin and SH3 domain containing 1 [Mus musculus]	1796.8687	74.34	0
19527174	TPVEEVPAAIAPFQGR	splicing factor 3b, subunit 3 [Mus musculus]	1681.8899	61.4	0.45010778
13385652	TPVEPEVAIHR	ribosomal protein S20 [Mus musculus]	1247.6748	64.74	0.830224614
7304885	TPVLFDVYEIK	annexin A11 [Mus musculus]	1323.7102	61.82	0
19882201	TPVQSQQPSATTPSGADEK	proteasome 26S non-ATPase subunit 2 [Mus musculus]	1928.9176	71.17	0.74874817
18250284	TPYTDVNIVTIR	isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	1391.7501	68.11	0.313226305
31980726	TQAYPDQKPGTSGLR	phosphoglucomutase 2 [Mus musculus]	1618.8202	24.41	0.268602712
31981824	TQDDIETILQLFR	ankyrin repeat domain 25 [Mus musculus]	1591.8271	57.53	0.502659545
6678752	TQDDVDIADVAYYFEK	lymphocyte antigen 74 [Mus musculus]	1891.8701	102	0.246882151
6754750	TQEQLASEMAELTAR	moesin [Mus musculus]	1677.8113	59.76	0
33598964	TQLEELEDELQATEDAK	myosin heavy chain 10, non-muscle [Mus musculus]	1961.9242	121.86	0.112207593
20137006	TQLEELEDELQATEDAK	myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1961.9242	121.86	0.112207593
9256555	TQLYEYLQNR	nucleolar protein 5 [Mus musculus]	1327.6649	47.47	0.685734863
6680572	TQMLDQEELLASTR	kinesin family member 5B [Mus musculus]	1634.8157	35.54	0
31980636	TQQTNDIELQQEQR	mannosidase, beta A, lysosomal [Mus musculus]	1730.8342	69.41	0.220436202
56090231	TQSDDSEER	WD repeat domain 22 [Mus musculus]	1066.4479	22.83	0.350356597
29336026	TQVTELEDELTAAEDAK	nonmuscle myosin heavy chain [Mus musculus]	1862.8879	41.6	0
21704144	TQVTVQYMQDR	methionine adenosyltransferase II, alpha [Mus musculus]	1368.6586	31.76	1.334887868
22267442	TSAAPGGVPLQPQDLEFTK	ubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1955.9996	36.72	0
21450277	TSATWFALSR	Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1139.5784	48.52	0.262384885
21704096	TSDLIVLGLPWK	TAR DNA binding protein isoform 1 [Mus musculus]	1341.7791	60.34	0.377573141
55742711	TSFIQYLLEQEVPGSR	EH-domain containing 2 [Mus musculus]	1866.9583	57.97	0.14317476
13384736	TSFLDDAFR	dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1071.5203	26.12	0
26986539	TSFSQEQSCDSAGEGSER	Rho GTPase activating protein 12 [Mus musculus]	1904.7689	39.53	0
13430890	TSGPPVSELITK	histone 1, H1e [Mus musculus]	1228.6716	57.94	0.132367854
6680748	TSIAIDTIINQK	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1316.7314	56.38	0
51491845	TSIDAYDNFDNISLAQR	clathrin, heavy polypeptide (Hc) [Mus musculus]	1942.9154	65.83	0.351499523
27501448	TSIEDQDELSSLLQVPLVAGTVNR	integrin beta 4 binding protein [Mus musculus]	2584.3503	84.18	0.400019298
9506945	TSLALDESLFR	poly(A) binding protein, nuclear 1 [Mus musculus]	1251.6606	34.14	0
6671684	TSMGGTQQQFVEGVR	catenin beta [Mus musculus]	1624.7783	43.44	0
51765817	TSPNEGLSGNPADLER	PREDICTED: plasma membrane calcium ATPase 1 [Mus musculus]	1656.7875	22.36	0
6678359	TSRPENAIIYSNNEDFQVGQAK	transketolase [Mus musculus]	2481.2031	53.52	0.302636081
21313262	TSSAEMPTIPLGSAVEAIR	inner membrane protein, mitochondrial [Mus musculus]	1929.9966	84.04	0
31982275	TSTVDLPIESQLLWQLDR	heat shock protein 4 [Mus musculus]	2114.1133	66.63	0.408906351
6753294	TSVQTEDDQLIAGQSAR	catenin alpha 1 [Mus musculus]	1818.8843	73.3	0.710837781
31980953	TSWDFIEGEADDGITYNDNLAAFR	hydroxyacid oxidase (glycolate oxidase) 3 [Mus musculus]	2720.2192	90.24	0.132813207
29293809	TTDGVYEGVAIGGDR	ATP citrate lyase [Mus musculus]	1509.7218	69.42	0.209495325
6679761	TTEDEPSEKDALQPGR	fructose bisphosphatase 2 [Mus musculus]	1772.8348	44.56	0
63530525	TTFEDLIQR	PREDICTED: SEC31-like 1 [Mus musculus]	1122.5812	32.49	0.531423529
6679791	TTFLEAWEGMEELVDQGLVK	aldo-keto reductase family 1, member B8 [Mus musculus]	2295.1128	71.95	0.733844863
46519156	TTGFGMIYDSLDYAK	ribosomal protein S24 isoform 1 [Mus musculus]	1681.7916	54.15	0.872844528
6671507	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	actin, alpha 2, smooth muscle, aorta [Mus musculus]	3196.6025	62.57	0
6671509	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	actin, beta, cytoplasmic [Mus musculus]	3183.624	57.93	0.285357373
30425250	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	hypothetical protein LOC238880 [Mus musculus]	3183.624	57.93	0.285357373
6754556	TTIPEEEEEEEEEPIGVAVEEER	lamin B1 [Mus musculus]	2672.1917	124.94	0.28486302
8393800	TTITTTTSSSTTVGSAR	myeloid-associated differentiation marker [Mus musculus]	1671.8419	27.87	0.211198811
18034769	TTLSTFQSPEFSVTR	sorting nexin 5 [Mus musculus]	1700.8508	23.41	0.713601352
46519156	TTPDVIFVFGFR	ribosomal protein S24 isoform 1 [Mus musculus]	1398.7451	67.74	0.55307112
6754256	TTPSVVAFTADGER	heat shock protein 9A [Mus musculus]	1450.7212	51.25	0
50080209	TTPSYVAFTDTER	heat shock protein 1A [Mus musculus]	1487.7096	94.63	0.499461123
7305163	TTPSYVAFTDTER	heat shock protein 1-like [Mus musculus]	1487.7096	94.63	0.499461123
31981690	TTPSYVAFTDTER	heat shock protein 8 [Mus musculus]	1487.7096	94.63	0.499461123
6753428	TTPTGWTLDQCIQTGVDNPGHPFIK	creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	2726.3181	66.82	0.220918939
24429590	TTQVPQYILDDFIQNDR	DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	2066.0212	83.84	0.376498836
6681157	TTYLVLDEADR	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Mus musculus]	1295.6493	24.43	4.60343951
63621901	TTYLVLDEADR	PREDICTED: similar to ddx5 [Mus musculus]	1295.6493	24.43	4.60343951
6679237	TVAVYSEQDTGQMHR	pyruvate carboxylase [Mus musculus]	1721.7998	30.98	0
6755142	TVDNFVALATGEK	peptidylprolyl isomerase B [Mus musculus]	1364.6993	83.68	0.919614403

31982233	TVEVPEDEVVR		LYRIC [Mus musculus]	1271.6462	29.34	0
18875380	TVFDEAIR		RAS-related C3 botulinum substrate 3 [Mus musculus]	950.4941	34.31	0.426449638
31981273	TVFGVEPDLTR		CNDP dipeptidase 2 (metallopeptidase M20 family) [Mus musculus]	1233.644	33.55	0
23956104	TVGIDDLTGEPLIQR		adenylate kinase 3 [Mus musculus]	1626.8604	35.33	0.6243784
6753428	TVGMVAGDEETYEVFAELFDPVIQER		creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	2944.394	90.2	0.234201448
6753428	TVGMVAGDEETYEVFAELFDPVIQER	Oxidation (M)	creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	2960.3918	69.9	0
8393988	TVGYTVTAPEDTR		phosphomannomutase 2 [Mus musculus]	1409.6947	26.85	0.345370456
31981679	TVIIEQSWGSPK		heat shock protein 1 (chaperonin) [Mus musculus]	1344.7076	75.6	0.348036871
33859811	TVLGVPEVLLGILPGAGGTQR		hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (tri	2047.1946	85.03	0.317244291
31980648	TVLIMELINNVAK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1457.8507	71.09	0.349826797
31980648	TVLIMELINNVAK	Oxidation (M)	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1473.8207	39.1	0.124359355
33859506	TVMDDFAQFLDTCCK		albumin 1 [Mus musculus]	1736.7303	90.55	0.314438219
33859506	TVMDDFAQFLDTCCK	Oxidation (M)	albumin 1 [Mus musculus]	1752.7194	89.69	0
63479927	TVNQQSVAAPTVK		PREDICTED: BAT2 domain containing 1 [Mus musculus]	1342.7344	23.25	0
7657011	TVPLYESPR		damage specific DNA binding protein 1 [Mus musculus]	1061.5608	27	0.196674674
6678449	TVSVLNGGFR		thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	1049.5693	28.07	0.143345664
21361209	TVTAMDVVYALK		germinal histone H4 [Mus musculus]	1310.7178	58.02	0
21361209	TVTAMDVVYALK	Oxidation (M)	germinal histone H4 [Mus musculus]	1326.709	54.67	0
8567336	TVTLELLDNGAGADATK		chloride channel calcium activated 3 [Mus musculus]	1688.8685	116.7	0
31981690	TVTNAVVTVPAYFNDSQR		heat shock protein 8 [Mus musculus]	1982.0048	96.91	0.509518889
12963563	TVTQVVPAEGQENGQR		apoptotic chromatin condensation inducer 1 [Mus musculus]	1712.8577	22.78	0.388710202
46909602	TWEPEDVCSFLENR		SAM domain- and HD domain-containing protein 1 [Mus musculus]	1724.7744	29.57	1.589473484
31981722	TWNDPSVQQDIK		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1430.692	89.15	1.005330614
6755578	TYAFSENPLPTVEIAIR		SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 [	1920.9998	24.8	0.529003323
47059123	TYAVSHTQEDLNR		UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	1533.7111	38.85	0
63589703	TYGVSFFLVK		PREDICTED: talin 2 [Mus musculus]	1160.6235	28.19	0.902795849
6755809	TYGVSFFLVK		talin 1 [Mus musculus]	1160.6235	28.19	0.902795849
29789080	TYLPSQVSR		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1050.5604	34.34	0.385309231
23346461	TYLQALPYFDR		NADH dehydrogenase (ubiquinone) Fe-S protein 2 [Mus musculus]	1386.7047	38.96	0.287441341
13384828	TYNFLPEYLASTQK		serine (or cysteine) proteinase inhibitor, clade B, member 1a [Mus musculus]	1674.8337	46.77	0.532889933
30409988	TYNLGTGTGYSVLQMVQAMEK		galactose-4-epimerase, UDP [Mus musculus]	2291.1104	44.37	0
18152793	TYYMSAGLQPVPIVFR		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1841.9673	53.87	0
13384736	VAAPDVVVPTLDTVR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1551.8744	73.34	0.317198403
21704128	VAAVQPPEEGPSR		eukaryotic translation initiation factor 4B [Mus musculus]	1336.6909	37.56	0.479635799
7709980	VADIGLAAWGR		S-adenosylhomocysteine hydrolase [Mus musculus]	1128.6163	62.65	0.385928391
37059806	VADPSYLPTQQDVLR		guanine nucleotide binding protein, alpha q polypeptide [Mus musculus]	1701.8802	23.89	0.501695643
6755594	VADPVVTFCETVVETSSLK		U5 small nuclear ribonucleoprotein [Mus musculus]	2024.0044	35.54	1.464010565
20137006	VAEFTTNLMEEEEK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1669.7595	45.5	1.391905973
21313080	VAEGIFETEAPGGYK		hypothetical protein LOC67201 [Mus musculus]	1567.7534	33.53	0
31981549	VAELNPDENCIR		sulfide quinone reductase-like [Mus musculus]	1372.6548	56.66	0.732017166
33563250	VAELYEEEMR		desmin [Mus musculus]	1268.5874	52.52	0
33563250	VAELYEEEMR	Oxidation (M)	desmin [Mus musculus]	1284.5715	23.82	0.087747057
21312260	VAEQTPLSALYLASLIK		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1817.0403	91.24	0.194549283
6753036	VAEQTPLTALYVANLIK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1844.0513	51.36	0.231042228
6753914	VAGPQPAQTGAPQGSLGEYLFER		ferritin light chain 1 [Mus musculus]	2373.1685	69.43	0.082199723
9910556	VAGQDGSVVQFK		SMT3 (supressor of mif two, 3) homolog 1 [Mus musculus]	1234.632	54.55	1.343042806
63476037	VAIAQFSDDVR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1220.6268	64.57	0
22128627	VAIEPGVPR		sorbitol dehydrogenase 1 [Mus musculus]	937.5453	22.43	0
13937395	VALSEPQPER		arsenate resistance protein 2 [Mus musculus]	1125.5906	25.51	0.436242103
31980648	VALTGLTVAEYFR		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1439.7948	106.05	0.345180142
63476037	VALVQYSDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1050.5577	41.23	0.604457416
18079339	VAMSHFEPSEYIR		aconitase 2, mitochondrial [Mus musculus]	1565.7427	38.11	0
63746482	VANPSGNLTDTYVQDCGDGTYK		PREDICTED: filamin, alpha [Mus musculus]	2318.0276	129.45	0.546806661
31542559	VAPAPAGVFTDIPISNIR		dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) [Mus musculus	1838.017	79.43	0.344354908
6671507	VAPEEHPTLLTEAPLNPK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1956.0472	100.43	0.091509051
6671509	VAPEEHPVLLTEAPLNPK		actin, beta, cytoplasmic [Mus musculus]	1954.0635	101.43	0.238791303
54607037	VAPGYYTVTAEQDAR		integrin beta 4 isoform 2 [Mus musculus]	1640.7904	59.85	0.482301978
6753138	VAPPGLTQIPQIQK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1489.8727	27.16	0.522569579
13385598	VAQLEQVYIR		small nuclear ribonucleoprotein D3 [Mus musculus]	1218.6826	24.34	0.515661162
63746482	VAQPSITDNKDGTVTVR		PREDICTED: filamin, alpha [Mus musculus]	1800.9465	71.24	0.176395412

27545181	VAQPTAEQAQAFK		v-raf murine sarcoma 3611 viral oncogene homolog [Mus musculus]	1388.7025	45.32	0
33563270	VASSVPVENFTIHGGLSR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	1869.9803	46.17	0.790197894
15426055	VASTENGIIFGNIVYDVSGAASDR		coatomer protein complex, subunit beta 1 [Mus musculus]	2455.2102	61.6	0
6753324	VATAQDDITGDGTTSNVLIIGELLK		chaperonin subunit 6a (zeta) [Mus musculus]	2544.3374	89.53	0.65160744
63746482	VATVPQHATSGPGPADVSK		PREDICTED: filamin, alpha [Mus musculus]	1818.9336	103.07	0.15707
136429	VATVSLPR		Trypsin precursor	842.5126	44.19	0
63540743	VAVGQEQAFSVNTR		PREDICTED: filamin C, gamma [Mus musculus]	1505.7715	53.29	0.075427179
63476037	VAVIQFSEDSK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1222.6244	32.5	0
31982186	VAVLGASGGIGQPLSLLLK		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1793.0856	88.71	0.328350929
31982030	VAVSADPNVPNVIVTR		Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	1650.918	49.83	0.655568515
21704020	VAVTPPGLAR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	980.5914	39.74	0.219191061
6753484	VAVVQYSGQGQQQPGR		procollagen, type VI, alpha 1 [Mus musculus]	1701.8722	89.09	0.169001073
63476037	VAVVTYNNEVTTEIR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1707.892	93.77	0
63556656	VAYDLVYYVR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1260.6626	43.32	0.089520965
8567336	VAYLQVPGTAK		chloride channel calcium activated 3 [Mus musculus]	1146.646	64.77	0.110364368
46849705	VAYNPFGPGQFFDLSIR		lectin, galactose binding, soluble 4 [Mus musculus]	1927.9777	79.13	0.396141166
31981824	VAYTTVLQEWLR		ankyrin repeat domain 25 [Mus musculus]	1478.8029	24.19	0
6724311	VCLIGCGFSTGYGSAVK		alcohol dehydrogenase 1 (class I) [Mus musculus]	1661.7991	32.11	0
42415475	VDATEESDLAQQYGVR		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1780.8389	109.13	0.457387178
45598381	VDCTADSDVCSAQGVR		thioredoxin domain containing 5 [Mus musculus]	1625.6925	90.51	1.285893671
6755817	VDDEILGFISEATPR		thymopoietin [Mus musculus]	1661.8358	43.51	0
8394258	VDDLLELYMGIR		semaF cytoplasmic domain associated protein 2 [Mus musculus]	1436.7469	25.1	0
54607098	VDEYDYSKPIQGQQK		succinate dehydrogenase Fp subunit [Mus musculus]	1797.8669	86.15	0.179911045
31982186	VDFPQDQLATLTGR		malate dehydrogenase 2, NAD (mitochondrial) [Mus musculus]	1560.7931	57.51	0.235057576
9789893	VDFPTAIGVVLER		BRG1/brm-associated factor 53A [Mus musculus]	1415.7888	44.07	0
63738313	VDIDVPDVNIEGPDAK		PREDICTED: similar to AHNAK [Mus musculus]	1695.842	99.2	0.473369567
63738313	VDIEAPDVSIEGPEGK		PREDICTED: similar to AHNAK [Mus musculus]	1654.8134	60.47	0
63738313	VDIETPNLEGTLTGPK		PREDICTED: similar to AHNAK [Mus musculus]	1683.8772	74.88	0.975914707
63476037	VDIILNR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	842.5109	33.55	0.075138628
6679503	VDILDPALLR		proteasome (prosome, macropain) 26S subunit, ATPase 3 [Mus musculus]	1124.6648	47.82	0.940231159
63738313	VDINAPDVDVR		PREDICTED: similar to AHNAK [Mus musculus]	1212.6234	29.99	0.753211244
63556656	VDLPATVLTSVSVR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1456.8381	87.15	0
7106435	VDLQDHGESAYAVYDR		tenascin C [Mus musculus]	1837.8357	73.72	0.277287633
20149728	VDNSSLTGESEPQAR		ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Mus musculus]	1589.7415	46.44	0.067928863
21450277	VDNSSLTGESEPQTR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	1619.7555	108.18	0.337594612
51827543	VDPLFTELLNGIR		PREDICTED: GCN1 general control of amino-acid synthesis 1-like 1 [Mus musculus]	1486.8269	37.54	0
7710042	VDQIQEIVTGNPTVIK		IQ motif containing GTPase activating protein 1 [Mus musculus]	1753.9642	36.79	0
6681087	VDQSAVGFEYQGK		cortactin [Mus musculus]	1427.6787	88.16	0
6806903	VDQSILTGESVSVIK		ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 [Mus musculus]	1574.8521	28.12	0
36031132	VDQSILTGESVSVIK		ATPase, Ca++ transporting, fast twitch 1 [Mus musculus]	1574.8521	28.12	0
63655455	VDQVQDIVTGNPTVIK	2 Deamidation (NQ)	PREDICTED: similar to Ras GTPase-activating-like protein IQGAP2 [Mus musculus]	1727.8738	30.76	0
21704020	VDSDNLCTEEIFPTEGAGTDLR		NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	2382.0925	69.39	0.280195592
33186863	VDTWFNQPAR		ribosomal protein L13 [Mus musculus]	1233.6014	42.63	0.528069548
63522357	VDVEALENSPGATYIR		PREDICTED: signal recognition particle 72 [Mus musculus]	1733.8706	49.75	0.389878567
6678573	VDVFTANTSLSSGPLPTFPLEQLVNK		villin 1 [Mus musculus]	2774.4475	33.23	0.339553452
63746482	VDVGKDQEFTVK		PREDICTED: filamin, alpha [Mus musculus]	1364.6991	45.96	0.256764431
33859722	VDVTEQTGLSGR		thioredoxin domain containing 1 [Mus musculus]	1261.6433	55.71	0.731245009
7305295	VDYNASAWLTK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1267.6267	79.18	0.134824649
28077103	VEAYQWSVSDGR		phospholipase A2, activating protein [Mus musculus]	1396.65	43.83	0
7305295	VEDMAELTCLNEASVLHNLR		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2257.0974	72.45	0.074124533
7305295	VEDMAELTCLNEASVLHNLR	Oxidation (M)	myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	2273.0942	23.43	0
6755204	VEEAYDLAR		proteasome (prosome, macropain) subunit, beta type 5 [Mus musculus]	1065.5216	35.96	0.443351742
21313356	VEEFSLPDALNEGQVQVR		zinc binding alcohol dehydrogenase, domain containing 1 [Mus musculus]	2030.0054	77.09	0.617948737
31542333	VEFEELCADLFDR		hypoxia up-regulated 1 [Mus musculus]	1585.7289	86.72	0.401507838
21313536	VEGGTPLFTLR		dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]	1189.6581	37.72	0.353172253
31543315	VEGSEPTTPFNLFIGNLNPNK		nucleolin [Mus musculus]	2288.1575	83.89	0.536552784
19526884	VEGTPNDPNPNDPR		GDP-mannose pyrophosphorylase A [Mus musculus]	1521.697	58.11	0.266309734
31981722	VEIIANDQGNR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1228.6307	52.09	0.43015888
50080209	VEIIANDQGNR		heat shock protein 1A [Mus musculus]	1228.6307	52.09	0.43015888
7305163	VEIIANDQGNR		heat shock protein 1-like [Mus musculus]	1228.6307	52.09	0.43015888

31981690	VEIIANDQGNR		heat shock protein 8 [Mus musculus]	1228.6307	52.09	0.43015888
63664182	VEIIANDQGNR		PREDICTED: similar to heat shock protein 8 [Mus musculus]	1228.6307	52.09	0.43015888
51772153	VELDNMPLR		PREDICTED: similar to Non-POU-domain-containing, octamer binding protein [Mus musculus]	1086.5577	34.17	0
6754558	VELEQTYQAK		lamin B2 [Mus musculus]	1208.6078	28.95	0.59104388
33563250	VELQELNDR		desmin [Mus musculus]	1115.5704	44.36	0.189474523
31982755	VELQELNDR		vimentin [Mus musculus]	1115.5704	44.36	0.189474523
7305143	VEMENQIYAIPEDIMR		hexokinase 2 [Mus musculus]	1950.9355	42.92	1.014973238
6671666	VENQENVSNLVIDDTELK		CAP, adenylate cyclase-associated protein 1 [Mus musculus]	2059.0166	113.32	0.378940693
63746482	VEPGLGADNSVVR		PREDICTED: filamin, alpha [Mus musculus]	1312.6884	65.31	0.154345604
11230802	VEQIAAIAQELNELDYYDSHNVNTR		actinin alpha 4 [Mus musculus]	2905.3943	40.7	0.310974115
20373167	VEQLGAEGNVEESQK		LUC7-like 2 [Mus musculus]	1616.776	80.59	0
31542333	VESVFETLVEDSPEEESTLTK		hypoxia up-regulated 1 [Mus musculus]	2368.1436	105.15	0.477709632
6755376	VETFSGVYK		ribosomal protein S7 [Mus musculus]	1029.5261	43.53	0
51873060	VETGVLKPGMVVTFAPVNVTTEVK		eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2515.3845	79.66	0.304857664
51873060	VETGVLKPGMVVTFAPVNVTTEVK	Oxidation (M)	eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	2531.3921	32.99	0.690403905
33859490	VETLSQVEVILQQSAADIAR		laminin B1 subunit 1 [Mus musculus]	2170.1682	45.14	0.330032782
31560653	VFANAPDSACVIGLR		phosphofructokinase, liver, B-type [Mus musculus]	1532.7889	52.58	0.648563479
6755995	VFASLPQVER		WD repeat domain 1 [Mus musculus]	1145.6244	27.88	0.700867575
22203747	VFAVVITDGR		procollagen, type VI, alpha 2 [Mus musculus]	1076.6105	60.3	0
33859482	VFDAIMNFR		eukaryotic translation elongation factor 2 [Mus musculus]	1112.5614	46.62	0
56699432	VFDWIDANLNEQQIASNTLVR		eukaryotic translation initiation factor 4, gamma 1 isoform a [Mus musculus]	2446.238	31.62	0.45224111
31980669	VFEVSLADLQNDEVAFR		ribosomal protein S3a [Mus musculus]	1951.9717	37.06	0.40440863
6754254	VFIMDNCEELIPEYLNFIR		heat shock protein 1, alpha [Mus musculus]	2358.1484	42.3	0.488940649
40556608	VFIMDSCDELIPEYLNFIR		heat shock protein 1, beta [Mus musculus]	2317.126	90.02	0.606828361
40556608	VFIMDSCDELIPEYLNFIR	Oxidation (M)	heat shock protein 1, beta [Mus musculus]	2333.1204	23.37	0.651782199
6755152	VFLDPNTLSDDGTVALR		prolyl endopeptidase [Mus musculus]	1832.9412	47.19	0
21361209	VFLENVIR		germinal histone H4 [Mus musculus]	989.5836	45.15	0.411951746
18152793	VFLLGEEVAQYDGAYK		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1801.9003	61	0
40254582	VFLQYLPAIR		guanine nucleotide binding protein, alpha 13 [Mus musculus]	1219.7225	22.98	0
29789080	VFNYNTLER		coatomer protein complex, subunit beta 2 (beta prime) [Mus musculus]	1155.5822	29.48	0.457923577
6755787	VFPGSTTEDYNLIVIER		tripartite motif protein 28 [Mus musculus]	1952.9785	22.91	0.265567565
6680572	VFQSSTSQEQVYNDCAK		kinesin family member 5B [Mus musculus]	1933.8616	73.4	0.313668803
51093840	VFSDEVQQQAQLSTIR		eukaryotic translation initiation factor 3 subunit 6 interacting protein [Mus musculus]	1848.9467	62.93	0.423383792
6753484	VFSVAITPDHLEPR		procollagen, type VI, alpha 1 [Mus musculus]	1580.8427	36.51	0.702437603
31981549	VGAENVAIVEPSER		sulfide quinone reductase-like [Mus musculus]	1469.7583	75.78	0.514993703
6755809	VGAIPANALDDGQWSQGLISAAR		talin 1 [Mus musculus]	2310.1797	59.04	0.189810659
6755478	VGDVYIPR		splicing factor, arginine/serine-rich 2 [Mus musculus]	918.5043	62.19	0.551427813
51491880	VGDYVYFENSSSNPYLVR		metastasis-associated protein 2 [Mus musculus]	2109.0061	49.25	0.318957521
51491845	VGEQAQVVIIDMNDPSNPIR		clathrin, heavy polypeptide (Hc) [Mus musculus]	2195.1194	58.4	0.424962607
6996917	VGFQYEGTYK		glucose-6-phosphate dehydrogenase X-linked [Mus musculus]	1191.5659	24.93	0
31560737	VGIGAFPTEQDNEIGELLQTR		adenylosuccinate synthetase, non muscle [Mus musculus]	2287.1563	89.24	0.602267599
34740335	VGINYQPPTVVPGGDLAK		tubulin, alpha 2 [Mus musculus]	1824.9833	52.51	0.348395161
6678467	VGINYQPPTVVPGGDLAK		tubulin, alpha 4 [Mus musculus]	1824.9833	52.51	0.348395161
6678469	VGINYQPPTVVPGGDLAK		tubulin, alpha 6 [Mus musculus]	1824.9833	52.51	0.348395161
18079339	VGLIGSCTNSSYEDMGR		aconitase 2, mitochondrial [Mus musculus]	1788.7936	89.64	0
6680117	VGLLEALLPGQPEAVAR		glutathione synthetase [Mus musculus]	1732.9965	51.72	0.310680351
7657429	VGLSDLYNGQILETIGGK		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	1876.993	73.37	0
23956082	VGLTNYAAAYCTGLLLAR		ribosomal protein L5 [Mus musculus]	1869.9895	26.96	0.388044837
63476037	VGLVQYNSDPTDEFFLR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1999.98	59.03	0.364993441
63476037	VGLVQYNSDPTDEFFLR	Deamidation (NQ)	PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	2000.9583	73.85	0
6753620	VGNLGLATSFFNER		DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked [Mus musculus]	1524.7847	63.79	0.780240167
21312260	VGNPFELDTQQGPQVDKEQFER		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	2561.2285	114.55	0.153212372
38090710	VGQTAFDVADEDILGYLEELQK		PREDICTED: protein phosphatase 1, regulatory (inhibitor) subunit 12A [Mus musculus]	2453.2021	72.32	0
63746482	VGSAADIPINISETDLSLLTATVVPPSGR		PREDICTED: filamin, alpha [Mus musculus]	2893.5562	114.62	0.069277461
46849705	VGSSGDIALHLNPR		lectin, galactose binding, soluble 4 [Mus musculus]	1435.7681	97.32	0.325924552
29126205	VGVPTETGALTLNR		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	1427.788	52.37	0.266156125
63680429	VGVSQQPEDSQQDLPGER		PREDICTED: plexin B2 [Mus musculus]	1968.929	48.57	0.361559128
22203747	VGVVQYSHEGTFEAIR		procollagen, type VI, alpha 2 [Mus musculus]	1791.8976	25.35	0
11230802	VGWEQLLTTIAR		actinin alpha 4 [Mus musculus]	1386.7788	42.39	0.49295177
51491845	VGYTPDWIFLLR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1479.8032	37.97	5.276915946

27754065	VIAINVDDPDAANYKDISDVER		pyrophosphatase [Mus musculus]	2432.1997	69.18	0.875259011
6753322	VIDPATATSVDLR		chaperonin subunit 4 (delta) [Mus musculus]	1357.7266	30.22	0
42734399	VIDSLEDEKEALTLAMADR		desmuslin isoform H [Mus musculus]	2119.0632	56.51	0
46559834	VIDSLEDEKEALTLAMADR		desmuslin isoform M [Mus musculus]	2119.0632	56.51	0
30348966	VIESTQDLGNDLAGVMALQR		spectrin beta 2 isoform 1 [Mus musculus]	2130.0806	86.86	0.394707916
6754524	VIGSGCNLDSAR		lactate dehydrogenase 1, A chain [Mus musculus]	1191.5831	65	0.429405622
51767637	VIISAPSADAPMFVMGVNHEK		PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]	2213.1152	52.47	0
6679937	VIISAPSADAPMFVMGVNHEK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	2213.1152	52.47	0
33469063	VILQDFTGVPAVVDFAAMR		aconitase 1 [Mus musculus]	2049.0898	25.85	0.315511704
30023842	VINQILTEMDGMSTK		valosin containing protein [Mus musculus]	1679.8284	34.06	1.343808764
6724311	VIPLFSPQCGECR		alcohol dehydrogenase 1 (class I) [Mus musculus]	1448.71	43.49	0.271257892
51491845	VIQCFAETGQVQK		clathrin, heavy polypeptide (Hc) [Mus musculus]	1450.7301	54.62	0
7305085	VIQQLEGAFALVFK		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1562.8918	68.49	0.227773065
31981013	VISAEEALPGR		methionine sulfoxide reductase A [Mus musculus]	1141.6083	25.95	0
20137006	VISGVLQLGNIAFK		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	1458.8632	94.42	0
45597447	VISLSGEHSIIGR		superoxide dismutase 1, soluble [Mus musculus]	1367.766	49.55	0
6678321	VISTITNNIQQIIEIEDTFETLR		transforming growth factor, beta induced [Mus musculus]	2690.427	56.52	0.379785754
31982178	VIVVGNPANTNCLTASK		malate dehydrogenase 1, NAD (soluble) [Mus musculus]	1700.9004	95.56	0
41322904	VLALPEPSPAAPTLR		plectin 1 isoform 1 [Mus musculus]	1531.887	44.29	0.488163475
31982275	VLATAFDTTLGGR		heat shock protein 4 [Mus musculus]	1321.7087	66.36	0.70822829
11230802	VLAVNQENEHLMEDYER		actinin alpha 4 [Mus musculus]	2088.967	71.87	0.387641066
11230802	VLAVNQENEHLMEDYER	Oxidation (M)	actinin alpha 4 [Mus musculus]	2104.9663	22.08	0.815686558
6678449	VLDASWYSPGTR		thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	1351.6665	51.12	0.443045652
51766008	VLDNTWPAAPYR		PREDICTED: myosin IA [Mus musculus]	1402.7131	29.91	0
15617203	VLDNYLTSPLPEEVDETSAEDEGISQR		chloride intracellular channel 1 [Mus musculus]	3006.3977	77.54	0.454264339
63481281	VLEDIQLNLFTR		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1460.8108	62.76	0.619954321
40068493	VLEEANQAINPK		DEAD box polypeptide 17 isoform 1 [Mus musculus]	1325.7035	59.42	0.906487612
13385408	VLEQLTGQTPVFSK		ribosomal protein L11 [Mus musculus]	1546.8499	87.88	0
22128625	VLEQPIVVQSVGTDGR		mitochondrial ribosomal protein L37 [Mus musculus]	1696.9263	46.74	0.37327017
63489754	VLETAEDIQER		PREDICTED: similar to Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain) (Alpha-II s	1302.6565	25.4	0
19923052	VLEVPPIVYLR		brain acyl-CoA hydrolase [Mus musculus]	1297.7906	35.72	0.386701227
6754854	VLFDTGLVNPR		nidogen 1 [Mus musculus]	1230.6842	44.2	0.225582644
60218877	VLGELWPLFGGR		ATP-binding cassette, sub-family D, member 3 [Mus musculus]	1343.7557	32.94	0.663546903
27754065	VLGILAMIDEGETDWK		pyrophosphatase [Mus musculus]	1789.9047	93.09	0.793652611
27754065	VLGILAMIDEGETDWK	Oxidation (M)	pyrophosphatase [Mus musculus]	1805.8979	29.9	0
29336026	VLGLLPEEITAMLR		nonmuscle myosin heavy chain [Mus musculus]	1554.8945	37.52	1.055499612
27804325	VLGSQEALSPVHYEEK		monoamine oxidase A [Mus musculus]	1785.9037	59.01	0.12863479
31982526	VLIDWINDVLVGER		parvin, alpha [Mus musculus]	1640.9027	40.72	0
21450625	VLITTDLLAR		eukaryotic translation initiation factor 4A1 [Mus musculus]	1114.6862	24.23	0.486844532
6753484	VLLFSDGNSQGATAEAIEK		procollagen, type VI, alpha 1 [Mus musculus]	1949.978	100.38	0.094691343
63664073	VLLLSSPGLEEFYR		PREDICTED: p30 DBC protein [Mus musculus]	1622.8732	26.02	0.666990811
6679291	VLNNMEIGTSLYDEEGAK		phosphoglycerate kinase 1 [Mus musculus]	1982.9509	81.81	0
38080000	VLNSYWVGEDSTYK		PREDICTED: similar to ribosomal protein L15 [Mus musculus]	1660.783	77.9	0
9790067	VLPAQATEYAFAFIQVPQDEDAR		staphylococcal nuclease domain containing 1 [Mus musculus]	2579.2751	72.92	0.407971951
31560790	VLPPVSTEGLTPDDVPALADSVR		1-acylglycerol-3-phosphate O-acyltransferase 1 [Mus musculus]	2348.2104	52.29	0.573697524
15426055	VLQDLVMDILR		coatomer protein complex, subunit beta 1 [Mus musculus]	1314.7498	37.18	0
31542333	VLQLINDNTATALSYGVFR		hypoxia up-regulated 1 [Mus musculus]	2095.1196	100.34	0.453723478
33186923	VLQQLLVLQPEQQLNIYR		CDP-diacylglycerol synthase 1 [Mus musculus]	2195.2344	32.66	0
15426055	VLSECSPLMNDIFNK		coatomer protein complex, subunit beta 1 [Mus musculus]	1709.8401	30.53	0
6680748	VLSIGDGIAR		ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	1000.578	57.43	0.275278911
6754984	VLSMAPGLTSVEIIPFR		3'-phosphoadenosine 5'-phosphosulfate synthase 2 [Mus musculus]	1830.0208	42.25	0
63556656	VLSPLEYFR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1123.6205	38.38	0.109100462
6755626	VLSYAPGPLDNDMQQLAR		sepiapterin reductase [Mus musculus]	1987.9901	37.16	0.569920613
10946574	VLTPELYAELR		creatine kinase, brain [Mus musculus]	1303.7291	46.51	0.140160688
7657429	VLTQIGTSIQDFLEAEDDLSSFR		osteoblast specific factor 2 (fasciclin I-like) [Mus musculus]	2584.2749	47.37	0.186634008
6857793	VLTVTAVQENLMSALAEAR		phosphoribosylglycinamide formyltransferase [Mus musculus]	2016.0792	23.58	0.354352047
6671702	VLVDINNPEPLIQTAK		chaperonin subunit 5 (epsilon) [Mus musculus]	1763.984	38.39	0.446115646
31542602	VLVDQTTGLSR		ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) [Mus musculus]	1188.6592	44.87	0.339425307
42415475	VLVGANFEEVAFDEK		prolyl 4-hydroxylase, beta polypeptide [Mus musculus]	1666.8298	73.63	0.452002346
13569841	VLVLDFVTPTPLGTR		thioredoxin reductase 1 [Mus musculus]	1627.9421	50.56	0.318020383

63655455	VLWLDEIQQAINEANVDENR		PREDICTED: similar to Ras GTPase-activating-like protein IQGAP2 [Mus musculus]	2369.1687	62.17	0.401519248
13385010	VLYAYGYYTGDPSK		microsomal glutathione S-transferase 3 [Mus musculus]	1596.755	85.23	0.450025871
18079351	VMAGDEWLFEGPGTYIPQK		major vault protein [Mus musculus]	2138.0281	25.9	0.794905214
6680193	VMEMFQPSAVVLQCGSDSLSGDR		histone deacetylase 1 [Mus musculus]	2456.1401	26.56	0
6679567	VMIYQDEVK		polymerase I and transcript release factor [Mus musculus]	1124.5625	26.36	0
6679078	VMLGETNPADSKPGTIR		nucleoside-diphosphate kinase 2 [Mus musculus]	1785.9192	58.29	0
6755004	VMPNAIVQSVGVSGGR		programmed cell death 8 [Mus musculus]	1570.8369	30.71	0
34576561	VMQQQQQATQQQLPQK		splicing factor 3a, subunit 1 [Mus musculus]	1911.973	62.25	0.578760032
34576561	VMQQQQQATQQQLPQK	Oxidation (M)	splicing factor 3a, subunit 1 [Mus musculus]	1927.96	29.2	0
6754994	VMTIPYQPMPASSPVICAGGQDR		poly(rC) binding protein 1 [Mus musculus]	2418.1614	31.68	0
21313262	VNCSDNEFTQALTAAIPPESLTR		inner membrane protein, mitochondrial [Mus musculus]	2477.2107	23.26	0
45592932	VNDSTMLGASGDYADFQYLK		proteasome beta 4 subunit [Mus musculus]	2195.0186	85.74	0
63607012	VNEQLALR	2 Deamidation (NQ)	PREDICTED: similar to centrosome protein cep290 [Mus musculus]	944.5052	28.38	0
31560611	VNESTQNWHQLENIGNFIK		calponin 1 [Mus musculus]	2271.1221	78.85	0
7305085	VNFDDYTVNLGGLK		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	1554.7754	50.47	0
31560689	VNFSPPGDTSNLFPGTWYLER		3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	2397.1528	87.97	0.347319947
33859482	VNFTVDQIR		eukaryotic translation elongation factor 2 [Mus musculus]	1091.5862	46.72	0.513539468
6678752	VNGEPLDLDPGQTLIYYVDEK		lymphocyte antigen 74 [Mus musculus]	2378.1702	74.88	0.470107456
63556656	VNGVLMALPVYLAGGR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1629.9209	79.67	0
63556656	VNGVLMALPVYLAGGR	Oxidation (M)	PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1645.9111	38.65	0.121828106
9790069	VNIAFNYDMPEDSDTYLHR		HLA-B-associated transcript 1A [Mus musculus]	2300.0342	81.41	0.365886444
33859751	VNLAIWDTAGQER		RAB21, member RAS oncogene family [Mus musculus]	1472.7534	52.58	0
42741690	VNMSGVSSSNGVVDPR		ubiquitin-conjugating enzyme E2 variant 1 [Mus musculus]	1604.769	24.97	0
6755965	VNNSSLIGVGYTQTLRPGVK		voltage-dependent anion channel 2 [Mus musculus]	2103.1536	23.95	0.371640384
6679439	VNPTVFFDITADDEPLGR		peptidylprolyl isomerase A [Mus musculus]	2005.9928	96.59	0.495715452
6679651	VNQIGSVTESIQACK		enolase 3, beta muscle [Mus musculus]	1576.8003	95.55	0
63660302	VNQPASFAIR		PREDICTED: filamin B, beta [Mus musculus]	1102.6013	32.86	1.610446145
63540743	VNQPASFAVQLNGAR		PREDICTED: filamin C, gamma [Mus musculus]	1571.8296	61.05	0
63746482	VNQPASFAVSLNGAK		PREDICTED: filamin, alpha [Mus musculus]	1502.7872	60.43	0
27229277	VNTPTTTVYR		threonyl-tRNA synthetase [Mus musculus]	1151.6058	35.19	0.379377248
31981824	VPAPEVASGPDPEEEIR		ankyrin repeat domain 25 [Mus musculus]	1791.8781	71.16	0
13385168	VPDFSDYR		ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 [Mus musculus]	998.4579	56.29	0.40326828
31542559	VPEANSSWMDTVIR		dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) [Mus musculus	1604.7876	46.86	0
6755714	VPENPPSMVFK		transgelin [Mus musculus]	1244.6315	36.63	1.056017061
6753484	VPNYQALLR		procollagen, type VI, alpha 1 [Mus musculus]	1073.6093	38.52	0
29126205	VPPETIDSVIVGNVMQSSSDAAYLAR		acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Mus musculus]	2719.365	58.3	0.166382681
9790073	VPSDGLFLIGEYEGK		cadherin 17 [Mus musculus]	1623.826	59.19	0.810420348
56119103	VPSTEAEALASSLMGLFEK		guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1979.9932	88.72	0
56119103	VPSTEAEALASSLMGLFEK	Oxidation (M)	guanosine diphosphate (GDP) dissociation inhibitor 3 [Mus musculus]	1995.9863	49.01	0.564030618
51767637	VPTPNVSVMDLTCR	Oxidation (M)	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]	1547.7654	53.24	0
63655497	VPTPNVSVVDLTCR		PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]	1499.7877	111.37	0.609284022
6679937	VPTPNVSVVDLTCR		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1499.7877	111.37	0.609284022
6754004	VPTTGIIEYPFDLENIIFR		guanine nucleotide binding protein, alpha 11 [Mus musculus]	2237.1868	54.09	0.461177834
31542895	VPTTGIIEYPFDLENIIFR		guanine nucleotide binding protein, alpha 14 [Mus musculus]	2237.1868	54.09	0.461177834
37537522	VPVDVAYQR		epiplakin 1 [Mus musculus]	1046.5587	57.34	0.344256958
63562740	VPVESYVR		PREDICTED: similar to secreted gel-forming mucin [Mus musculus]	948.5182	49.8	0.233921621
46849705	VPYVGALQGGLTVR		lectin, galactose binding, soluble 4 [Mus musculus]	1429.8312	115.8	0.586615717
6671700	VQDDEVGDGTTSVTVLAAELLR		chaperonin subunit 2 (beta) [Mus musculus]	2288.1584	120.93	0
63552538	VQEVEVPEDFGPVR		PREDICTED: echinoderm microtubule associated protein like 2 [Mus musculus]	1599.801	66.8	0.413355432
16716471	VQGTGVTPPPTPLGTR		hypothetical protein LOC94184 [Mus musculus]	1577.8618	46.69	0.188611434
20532338	VQIFEYNENTR		sec13-like protein [Mus musculus]	1412.6838	23.33	0.358654987
31982520	VQPIYGGTNEIMK		acetyl-Coenzyme A dehydrogenase, long-chain [Mus musculus]	1449.739	23.65	4.366407262
6754256	VQQTVQDLFGR		heat shock protein 9A [Mus musculus]	1290.6808	67.48	0.614916041
41322904	VQSGSESVIQEYVDLR		plectin 1 isoform 1 [Mus musculus]	1808.8977	60.33	0.474226786
63746482	VQVQDNEGCSVEATVK		PREDICTED: filamin, alpha [Mus musculus]	1705.8025	38.28	0
23956292	VSAQGITLTDNQR		C1 domain-containing phosphatase and tensin-like protein [Mus musculus]	1402.7161	40.78	0
63615219	VSAQGITLTDNQR		PREDICTED: tensin-like SH2 domain containing 1 [Mus musculus]	1402.7161	40.78	0
63474405	VSAQGITLTDNQR		PREDICTED: tensin [Mus musculus]	1402.7161	40.78	0
6680045	VSCLGVTDDGMAVATGSWDSFLK		guanine nucleotide-binding protein, beta-1 subunit [Mus musculus]	2359.0977	99.05	2.266142312
13937391	VSCLGVTDDGMAVATGSWDSFLK		guanine nucleotide-binding protein, beta-2 subunit [Mus musculus]	2359.0977	99.05	2.266142312

21312216	VSDVVDGNIQGR		gasdermin domain containing 1 [Mus musculus]	1258.6432	47.64	0
37620153	VSDVYDIEER		myosin, light polypeptide kinase telokin isoform [Mus musculus]	1224.5742	57.46	0.116627546
30348966	VSEEAESQQWDTSK		spectrin beta 2 isoform 1 [Mus musculus]	1623.7142	63.91	0.236192232
7106421	VSEEAESQQWDTSK		spectrin beta 2 isoform 2 [Mus musculus]	1623.7142	63.91	0.236192232
51770961	VSEEIFFGR		PREDICTED: AFG3(ATPase family gene 3)-like 2 [Mus musculus]	1083.5493	39.27	0.362861941
63481281	VSETVAFTDVNSILR		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1650.8634	38.65	0.39912834
6679439	VSFELFADK		peptidylprolyl isomerase A [Mus musculus]	1055.5405	53.55	0.432540504
31982373	VSISEGDDKIEYR		fibrillarin [Mus musculus]	1510.7408	38.96	1.123681545
28916693	VSNGAGSMSVSLVADENPFAQGALR		gelsolin [Mus musculus]	2477.2153	54.37	0
28916693	VSNGAGSMSVSLVADENPFAQGALR	Deamidation (NQ)	gelsolin [Mus musculus]	2478.1965	115.63	0
13384736	VSPDMAIFITMNPGYAGR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1939.9424	44.98	0
63474408	VSPSIQPQPQSQPTSLSR		PREDICTED: RIKEN cDNA E030037J05 gene [Mus musculus]	1937.0116	27.77	0.16770044
63556656	VSQHGSDVVIETDFGLR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1858.9303	42.01	0.142681668
51491845	VSQPIEGHAASFAQFK		clathrin, heavy polypeptide (Hc) [Mus musculus]	1716.8573	25.44	0
31980636	VSSQEDWAYNSR		mannosidase, beta A, lysosomal [Mus musculus]	1441.6411	25.33	0
38142460	VSVISVEEPPQR		electron transferring flavoprotein, beta polypeptide [Mus musculus]	1339.7247	42.82	0
63476037	VSVMANTPSGPVEAFDFAEYQPELFEK		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	3002.4497	51.95	0
31982169	VSVVEPGNFIAATSLYSPER		3-hydroxybutyrate dehydrogenase (heart, mitochondrial) [Mus musculus]	2136.0996	98	0.228073771
20149728	VSWETDDINDLEDSYGQEWTR		ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Mus musculus]	2558.1057	92.24	0
63660302	VSYFPTVPGVYIVSTK		PREDICTED: filamin B, beta [Mus musculus]	1756.9486	24.28	0.50885927
6753086	VSYGIGEEEHDQEGR		apurinic/apyrimidinic endonuclease 1 [Mus musculus]	1704.7493	65.6	0.324176206
31543605	VTAEVVLVHPGGGSTSR		ribophorin I [Mus musculus]	1665.8942	63.73	0
51317392	VTAPCTPLR		pleckstrin and Sec7 domain containing homolog [Mus musculus]	957.5346	28.52	0
63746482	VTAQGPGLEPSGNIANK		PREDICTED: filamin, alpha [Mus musculus]	1652.8605	108.25	0
13569841	VTAQSTNSEETIEGEFNTVLLAVGR		thioredoxin reductase 1 [Mus musculus]	2665.3315	37.66	0.431317167
63660302	VTASGPGLSAYGVPASLPVEFAIDAR		PREDICTED: filamin B, beta [Mus musculus]	2545.3274	54.97	0.562308409
31560353	VTASSENFHVGENDENQER		solute carrier family 6 (neurotransmitter transporter), member 14 [Mus musculus]	2161.9392	98.51	0
13384736	VTFVNFTVTR		dynein, cytoplasmic, heavy chain 1 [Mus musculus]	1183.6475	29.51	0
18079351	VTGEEWLVR		major vault protein [Mus musculus]	1088.5681	32.98	0.563792691
31981722	VTHAVVTVPAYFNDAQR		heat shock 70kD protein 5 (glucose-regulated protein) [Mus musculus]	1887.9746	71.64	0.433875513
20799907	VTIAQGGVLPNIQAVLLPK		histone 2, H2aa1 [Mus musculus]	1931.1724	109.07	0.495542507
34328142	VTIASLPR		lymphoid-restricted membrane protein [Mus musculus]	856.5231	25.51	0
63556656	VTIPGNYYK		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1054.5554	38.69	0
54607098	VTLEYRPVIDK		succinate dehydrogenase Fp subunit [Mus musculus]	1332.7504	22.83	0
13385082	VTLPDGHQLTFPNR		lectin, galactose-binding, soluble 2 [Mus musculus]	1594.8333	37.21	0.829743059
6754524	VTLTPEEEAR		lactate dehydrogenase 1, A chain [Mus musculus]	1144.5883	26.58	0.313554753
6678413	VTNGAFTGEISPGMIK		triosephosphate isomerase 1 [Mus musculus]	1621.821	23.88	0.777756115
8393150	VTPPEGYDVVTVFR		carboxyl terminal LIM domain protein 1 [Mus musculus]	1578.8175	53.9	0.34894546
8393150	VTPPEGYDVVTVFRE		carboxyl terminal LIM domain protein 1 [Mus musculus]	1707.859	35.82	0.385763959
6755963	VTQSNFAVGYK		voltage-dependent anion channel 1 [Mus musculus]	1213.6198	76.55	0.331234056
31657132	VTTYPQTTIR		premature ovarian failure 1B [Mus musculus]	1179.6399	25.53	17.19210538
7305167	VTVLEGDILDTQYLR		hydroxysteroid dehydrogenase-6, delta<5>-3-beta [Mus musculus]	1734.92	26.71	0.271432528
6678499	VTVVDVNEAR		UDP-glucose dehydrogenase [Mus musculus]	1101.5883	39.67	0.341956948
31542413	VTWDSSFCAVNPR		coronin, actin binding protein 1C [Mus musculus]	1481.686	63.89	0.366723892
37537522	VTYQELQDR		epiplakin 1 [Mus musculus]	1151.5696	28.27	0.337985407
63746482	VTYTPMAPGSYLISIK		PREDICTED: filamin, alpha [Mus musculus]	1740.9086	70.35	0.364394432
63746482	VTYTPMAPGSYLISIK	Oxidation (M)	PREDICTED: filamin, alpha [Mus musculus]	1756.905	48.95	0
6754084	VTYVDFLAYDILDQYR		glutathione S-transferase, mu 1 [Mus musculus]	1993.9916	66.42	0.302909559
58037117	VVAEPVELAQEFR		NADH dehydrogenase (ubiquinone) Fe-S protein 3 [Mus musculus]	1486.7893	38.38	0.407551571
6755809	VVAPTISSPVCQEQLVEAGR		talin 1 [Mus musculus]	2083.0852	58.94	0.187597464
6671664	VVDDWANDGWGLK		calnexin [Mus musculus]	1474.6996	57.68	0.545116577
31980648	VVDLLAPYAK		ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit [Mus musculus]	1088.6262	42.26	0.369688936
63561841	VVDLMAYMASK		PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]	1227.6107	49.84	0.419006819
6679937	VVDLMAYMASK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	1227.6107	49.84	0.419006819
46593021	VVELLADIVQNSSLEDSQIEK		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	2329.2085	97.36	0.347416794
63476037	VVESLDVGPDR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1185.6125	46.4	0.19150241
6671549	VVFIFGPDK		peroxiredoxin 6 [Mus musculus]	1021.5681	40.13	0.119904108
46849705	VVFNTMQSGQWGK		lectin, galactose binding, soluble 4 [Mus musculus]	1481.7239	72.87	0
46849705	VVFNTMQSGQWGK	Oxidation (M)	lectin, galactose binding, soluble 4 [Mus musculus]	1497.7025	41.86	0
20137006	VVFQEFR		myosin, heavy polypeptide 9, non-muscle [Mus musculus]	924.4946	27.61	0.530119075

6753036	VVGNPFDSR		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	990.5032	49.37	0.315112
6679237	VVHSYEELEENYTR		pyruvate carboxylase [Mus musculus]	1767.8229	41.36	0
63476037	VVIHFTDGADGDMADLYR		PREDICTED: procollagen, type VI, alpha 3 [Mus musculus]	1994.9203	49.83	0
6678413	VVLAYEPVWAIGTGK		triosephosphate isomerase 1 [Mus musculus]	1602.8831	56.16	0
6680309	VVLDDKDYFLFR		heat shock protein 1 (chaperonin 10) [Mus musculus]	1529.7999	40.62	0
42475998	VVLEGPAPWGFR		PDZ and LIM domain 7 [Mus musculus]	1327.7191	44.38	0
34538601	VVLPMELPIR		cytochrome c oxidase subunit II [Mus musculus]	1166.7045	27.07	0
7305169	VVNVELPVEANLVWQLGR		heat shock protein 105 [Mus musculus]	2035.1311	22.36	0.548669942
16716371	VVPSDLYPLVLR		nucleolar and coiled-body phosphoprotein 1 [Mus musculus]	1370.801	25.82	0
26006861	VVPVADIITPNQFEAELLSGR		pyridoxal (pyridoxine, vitamin B6) kinase [Mus musculus]	2268.2241	36.96	0
19527092	VVQVSAGDSHTAALTEDGR		chromosome condensation 1 [Mus musculus]	1912.9436	73.26	0
6678329	VVSAMVNCNDDQGVLLGR		transglutaminase 2, C polypeptide [Mus musculus]	1889.9187	46.06	0
18152793	VVSPWNSEDAK		pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	1231.5886	42.47	0
7305295	VVSSVLQLGNIVFK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1502.8959	96.31	0.123878112
51556274	VVTIAPGLFATPLLTTLPEK		hydroxyacyl-Coenzyme A dehydrogenase type II [Mus musculus]	2081.219	61.37	0.403994344
51766008	VVTVLNVTQAQYAR		PREDICTED: myosin IA [Mus musculus]	1561.8693	46.34	0.257121498
46849705	VVVNGNSFYEYGHR		lectin, galactose binding, soluble 4 [Mus musculus]	1640.7854	69.17	0.326456045
46849705	VVVNGNSFYEYGHR	Deamidation (NQ)	lectin, galactose binding, soluble 4 [Mus musculus]	1641.7668	22.29	0.463450728
63556656	VVVTVAGQVVGLAR		PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1367.8402	35.48	0
6754854	VVYWTDISEPSIGR		nidogen 1 [Mus musculus]	1621.8135	37.46	0.161820559
7305363	VWDYETGDFER		platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit [Mus musculus]	1416.6184	45.36	0.495796682
6677773	VWLDPNETNEIANANSR		ribosomal protein L19 [Mus musculus]	1942.9275	78.93	0.393088059
6680047	VWQVTIGTR		guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1 [Mus musculus]	1059.5941	53.91	0.49961978
31543474	VYAEANSQESADR		phosphoglucomutase 3 [Mus musculus]	1439.6409	32.57	0.359251138
46593021	VYEEDAVPGLTPCR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	1548.7328	67.21	0.437511667
63481281	VYEELLAIPVVR		PREDICTED: glutamyl-prolyl-tRNA synthetase [Mus musculus]	1400.8169	53.74	0.405380083
6755142	VYFDLQIGDESVGR		peptidylprolyl isomerase B [Mus musculus]	1597.783	79.99	0.463811943
41322904	VYHDPSTQEPVTYSQLQQR		plectin 1 isoform 1 [Mus musculus]	2276.0935	33.72	0.536242866
33563270	VYYDLTR		oxoglutarate dehydrogenase (lipoamide) [Mus musculus]	929.4731	29.58	0.30756078
42734399	WAEDQALYAEEAR		desmuslin isoform H [Mus musculus]	1551.7118	65.86	0
46559834	WAEDQALYAEEAR		desmuslin isoform M [Mus musculus]	1551.7118	65.86	0
30023842	WALSQSNPSALR		valosin containing protein [Mus musculus]	1329.6912	72.23	0.699440387
21313526	WAVIQSQAVR		hypothetical protein LOC78906 [Mus musculus]	1157.644	33.23	1.093880358
6754984	WDDGLDQYR		3'-phosphoadenosine 5'-phosphosulfate synthase 2 [Mus musculus]	1167.5139	42.49	0.553972309
31981892	WDDPYYDIAR		Rho GTPase activating protein 1 [Mus musculus]	1313.5829	34.45	0.660467821
6680960	WDPAPGPVQQYR		procollagen, type XII, alpha 1 [Mus musculus]	1413.6843	34.72	0.570056019
14042921	WDQTADQTPGATPK		splicing factor 3b, subunit 1 [Mus musculus]	1515.7103	58.55	3.425096032
9910482	WDSNVIETFDIAR		START domain containing 10 [Mus musculus]	1565.7592	28.15	0
1346343	WELLQQVDTSTR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1475.7361	64.55	0.203863038
63746482	WGDEHIPGSPYR		PREDICTED: filamin, alpha [Mus musculus]	1413.6572	73.95	0.201890735
63540743	WGDESVPGSPFK		PREDICTED: filamin C, gamma [Mus musculus]	1305.6034	25.22	0
29293809	WGDIEFPPPFGR		ATP citrate lyase [Mus musculus]	1417.6918	61	0.339473546
63561841	WGEAGAEYVVESTGVFTTMEK		PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]	2291.0608	53.6	0.663318078
6679937	WGEAGAEYVVESTGVFTTMEK		similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	2291.0608	53.6	0.663318078
63561841	WGEAGAEYVVESTGVFTTMEK	Oxidation (M)	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]	2307.0747	32.8	1.008667935
6679937	WGEAGAEYVVESTGVFTTMEK	Oxidation (M)	similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	2307.0747	32.8	1.008667935
31981302	WGTDEAQFIYILGNR		annexin A6 [Mus musculus]	1782.881	44.91	0
31559916	WGTLTDCVVMR		heterogeneous nuclear ribonucleoprotein A3 isoform b [Mus musculus]	1280.613	58.01	0
8567336	WGVFNEYNNDEK		chloride channel calcium activated 3 [Mus musculus]	1514.6566	81.49	0
31543942	WIDNPTVDDR		vinculin [Mus musculus]	1230.5811	39.42	0
6996913	WISIMTER		annexin A2 [Mus musculus]	1035.5297	35.11	0.500973457
9790109	WLAPDGLIFPDR		heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 [Mus musculus]	1399.743	33.03	0.818927308
51491845	WLLLTGISAQQNR		clathrin, heavy polypeptide (Hc) [Mus musculus]	1499.8398	38.97	0
7709980	WLNENAVEK		S-adenosylhomocysteine hydrolase [Mus musculus]	1102.5538	42.78	0
6754136	WMEQEGPEYWER		histocompatibility 2, Q region locus 2 [Mus musculus]	1639.6908	30.89	0.962102183
6755965	WNTDNTLGTEIAIEDQICQGLK		voltage-dependent anion channel 2 [Mus musculus]	2462.1936	42.88	0
6755963	WNTDNTLGTEITVEDQLAR		voltage-dependent anion channel 1 [Mus musculus]	2176.051	143.79	0.3400114
41322904	WQAVLAQTDVR		plectin 1 isoform 1 [Mus musculus]	1286.6841	38.76	0
39204553	WQDIQNDPR		chromodomain helicase DNA binding protein 4 [Mus musculus]	1171.5519	22.72	0.868034022
24762230	WQNNLLPSR		ribosomal protein S15a [Mus musculus]	1127.5978	24.27	0

25020120	WQSQLGGLQGQDLSQVER		PREDICTED: laminin, alpha 5 [Mus musculus]	2029.0122	60.59	0.895231667
58000405	WRVGDDPYKLYAFNQR	2 Deamidation (NQ)	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 [Mus musculus]	2029.9559	24.81	0
34328278	WSELAGCTADFR		lectin, mannose-binding 2 [Mus musculus]	1355.6105	27.15	0.335738341
31982720	WSFEELGLLSR		SA rat hypertension-associated homolog [Mus musculus]	1336.6954	26.07	0.26712835
13385384	WSTLVEDYGVELR		proteasome 26S non-ATPase subunit 12 [Mus musculus]	1566.7813	32.7	0.395109954
6755963	WTEYGLTFTEK		voltage-dependent anion channel 1 [Mus musculus]	1374.6545	75.76	0.660037492
27804325	WVDVGGAYVGPTQNR		monoamine oxidase A [Mus musculus]	1618.7976	100.75	0.231728158
7657031	WVEQNLGPEFVER		5',3'-nucleotidase, cytosolic [Mus musculus]	1602.7917	29.89	0
6671702	WVGGPEIELIAIATGGR		chaperonin subunit 5 (epsilon) [Mus musculus]	1738.9469	36.12	0
21450277	WVNDVEDSYGQQWTYEQR		Na+/K+ -ATPase alpha 1 subunit [Mus musculus]	2302.9949	105.68	0.287395161
46195798	WVPFDGDDIQLEFVR		dolichyl-di-phosphooligosaccharide-protein glycotransferase [Mus musculus]	1835.895	34.09	0.360733288
18079339	WVVIGDENYGEGSSR		aconitase 2, mitochondrial [Mus musculus]	1667.7651	115.67	0
31981549	YADALQEIIR		sulfide quinone reductase-like [Mus musculus]	1191.6393	52.76	0.404970271
63506192	YADLTEDQLPSCESLKDTIAR		PREDICTED: similar to phosphoglycerate mutase (EC 5.4.2.1) B chain - rat [Mus musculus]	2368.1143	53.14	0.247007202
31981983	YAEEELEQVR		stromal interaction molecule 1 [Mus musculus]	1265.6018	44.98	0
6754854	YALSNSIGPVR		nidogen 1 [Mus musculus]	1176.6294	27.1	0
9790219	YALYDASFETK		destrin [Mus musculus]	1307.6118	78.37	0.240531415
6680924	YALYDATYETK		cofilin 1, non-muscle [Mus musculus]	1337.6245	67.78	0.605214334
6671746	YALYDATYETK		cofilin 2, muscle [Mus musculus]	1337.6245	67.78	0.605214334
13195624	YAPGYNAEVGDK		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 [Mus musculus]	1283.5928	49.25	0
23510269	YAQGADSVEPMFR		eukaryotic translation initiation factor 2C, 1 [Mus musculus]	1470.6689	24.78	0
34147260	YASASEPTEIYR		hypothetical protein LOC270328 [Mus musculus]	1386.6571	68.07	0.115928724
29244560	YASASEPTEIYR		hypothetical protein LOC331063 [Mus musculus]	1386.6571	68.07	0.115928724
31560449	YASNAVSESMIR		aspartyl aminopeptidase [Mus musculus]	1327.6362	23.09	0
7657518	YDDPPDWQEILTYFR		ATP-binding cassette, subfamily E, member 1 [Mus musculus]	1957.902	46.83	0.407576954
41054806	YDEAASYIQSK		guanine nucleotide binding protein, alpha inhibiting 2 [Mus musculus]	1274.6094	44.98	0.279449065
26190606	YDFGIYDDDPEIITLER		ER-resident protein ERdj5 [Mus musculus]	2073.9658	30.75	0.396162722
6678483	YDGQVAVFGSDFQEK		ubiquitin-activating enzyme E1, Chr X [Mus musculus]	1689.7747	79.57	0
31981549	YDGYTSCPLVTGYNR		sulfide quinone reductase-like [Mus musculus]	1708.7634	37.38	0.538252214
6753262	YDPPLEDGAMPSAR		capping protein (actin filament) muscle Z-line, beta [Mus musculus]	1518.6898	23.1	1.061981168
13386338	YDPTIEDFYR		RAP2B, member of RAS oncogene family [Mus musculus]	1318.6088	41.59	0.55295346
33859753	YDPTIEDSYR		RAS related protein 1b [Mus musculus]	1258.559	57.79	0.29309223
21312564	YDQQAEEDLR		calponin 3, acidic [Mus musculus]	1266.5649	49.84	1.710274396
6755594	YDWDLLAAR		U5 small nuclear ribonucleoprotein [Mus musculus]	1122.564	23.47	1.032012856
6754180	YEAFQDETFQER		hephaestin [Mus musculus]	1562.7008	23.74	2.029674585
6679545	YEDAVQFIR		protein tyrosine phosphatase 4a2 [Mus musculus]	1140.5715	43.63	0.874322055
21313144	YEDFKDEGSENAVK		GTP-binding protein PTD004 [Mus musculus]	1630.7241	85.82	0.619603074
16716471	YEDFVVDGFNVLYNK		hypothetical protein LOC94184 [Mus musculus]	1821.8733	74.47	0.295767168
27370092	YEEIDNAPEER		Tu translation elongation factor, mitochondrial [Mus musculus]	1364.5984	68.58	0.318938884
1346343	YEELQITAGR		Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alpha protei	1179.599	33.55	0
13624315	YEELQTLAGK		keratin complex 2, basic, gene 8 [Mus musculus]	1151.593	85.14	0.704210112
7657583	YEGFFGLYR		solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13 [Mus m	1151.5594	25.28	0.301010601
27369581	YEGFFGLYR		solute carrier family 25 (mitochondrial carrier, Aralar), member 12 [Mus musculus]	1151.5594	25.28	0.301010601
16716471	YEHANDDDTSLKSDPEGEK		hypothetical protein LOC94184 [Mus musculus]	2149.9087	24.82	0.64414225
7305295	YEILAANAIPK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1202.6736	68.55	0
21313640	YESIIATLCENLDSLDEPDAR		adaptor-related protein complex 2, beta 1 subunit [Mus musculus]	2367.1187	23.99	0
13385998	YESSALPAGQLTSLPDYASR		TNF receptor-associated protein 1 [Mus musculus]	2126.0381	67.71	0.607085433
33859482	YEWDVAEAR		eukaryotic translation elongation factor 2 [Mus musculus]	1138.5194	69	0.550196417
51764087	YFAGNLASGGAAGATSLCFVYPLDFAR		PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	2739.3206	54.39	0.235259513
22094075	YFAGNLASGGAAGATSLCFVYPLDFAR		solute carrier family 25, member 5 [Mus musculus]	2739.3206	54.39	0.235259513
6679761	YFDAATAEYVQK		fructose bisphosphatase 2 [Mus musculus]	1405.6631	53.01	0.501060446
27370516	YFDLGLPNR		isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	1094.5676	41.45	0.270279965
31541909	YFGDIISVGQR		isochorismatase domain containing 1 [Mus musculus]	1254.6538	34.66	0.342826242
6678055	YFILPDSLPLDTLLVDVEPK		small nuclear ribonucleoprotein D1 [Mus musculus]	2287.2468	56.39	0.420015704
51764087	YFPTQALNFAFK		PREDICTED: solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), membe	1446.7426	69.73	0.394134352
22094075	YFPTQALNFAFK		solute carrier family 25, member 5 [Mus musculus]	1446.7426	69.73	0.394134352
23621467	YFQFQEEGKEGENR		PREDICTED: actin related protein 2/3 complex, subunit 2 [Mus musculus]	1760.788	55	0
47059123	YFSLPSVVFSR		UDP glucuronosyltransferase 1 family, polypeptide A10 [Mus musculus]	1301.6919	51.47	0.445679282
6679891	YFTWDPTR		alpha glucosidase 2 alpha neutral subunit [Mus musculus]	1085.5071	28.38	0.434925018
46593021	YFYDQCPAVAGYGPIEQLPDYNR		ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	2679.2266	103.77	0.286375389

18266680	YGDLANWMIPGK		3-oxoacid CoA transferase 1 [Mus musculus]	1364.6621	26.74	0
54261793	YGDLLPADGILIQGNDLK		plasma membrane calcium ATPase 4 [Mus musculus]	1915.0106	42.47	0
51765817	YGDLLPADGILIQGNDLK		PREDICTED: plasma membrane calcium ATPase 1 [Mus musculus]	1915.0106	42.47	0
23956214	YGEPGEVFINK		splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Mus muscu	1252.6193	49.49	0
6680193	YGEYFPGTGDLR		histone deacetylase 1 [Mus musculus]	1374.6385	62.77	0.385625296
63746482	YGGDEIPFSPYR		PREDICTED: filamin, alpha [Mus musculus]	1400.6559	47.55	0.185323028
22203747	YGGLHFSDQVEVFSPPGSDR		procollagen, type VI, alpha 2 [Mus musculus]	2194.0383	23.29	0
63746482	YGGQPVPNFPSK		PREDICTED: filamin, alpha [Mus musculus]	1290.6501	55.93	0.256371091
6753240	YGIVDYMIEQSGPPSK		calcium binding protein, intestinal [Mus musculus]	1783.8557	64.7	0
6753036	YGLAAAVFTK		aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	1040.5708	53.21	0.464971049
21312260	YGLAAAVFTR		aldehyde dehydrogenase 1 family, member B1 [Mus musculus]	1068.584	50.55	0.265633442
13195624	YGLLAAILGDK		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 [Mus musculus]	1133.6587	47.99	0.242107075
6753820	YGPIVDVYVPLDFYTR		FUS interacting protein (serine-arginine rich) 1 [Mus musculus]	1916.9777	32.28	0.390910013
37674216	YGPLSGVNVVYDQR		RIKEN cDNA G430041M01 [Mus musculus]	1566.7699	25.09	0
11612505	YGSGSGQQSVTGVEESDDANSYWR		stromal cell-derived factor 2-like 1 [Mus musculus]	2579.0996	85.49	0.341748444
20149728	YGTNIIQGLSSIR		ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Mus musculus]	1421.7706	35.68	0.183600692
6755817	YGVNPGPIVGTTR		thymopoietin [Mus musculus]	1330.7111	47.64	0.420084886
6680606	YGVQLSQIQSVISGFEAQLSDVR		keratin complex 1, acidic, gene 19 [Mus musculus]	2524.3037	112.52	0.366718098
6679687	YGVSGYPTLK		glucose regulated protein [Mus musculus]	1084.5624	58.59	0.326270363
40556608	YHTSQSGDEMTSLSEYVSR		heat shock protein 1, beta [Mus musculus]	2176.9451	111.31	0.453227354
34996495	YIANTVELR		ribophorin II [Mus musculus]	1078.5896	57.66	0.399405622
19882199	YIASVQGSAPSPR		RAN binding protein 2 [Mus musculus]	1332.6954	36.93	0.626817237
6754084	YIATPIFSK		glutathione S-transferase, mu 1 [Mus musculus]	1039.573	34.78	0
51491845	YIEIYVQK		clathrin, heavy polypeptide (Hc) [Mus musculus]	1055.5701	27.88	0
6753514	YILSDSSPVPEFPLAYLTSENR		carnitine palmitoyltransferase 2 [Mus musculus]	2498.2275	38.52	0.221967391
63746482	YIPVQQGPVGVNVTYGGDHIPK		PREDICTED: filamin, alpha [Mus musculus]	2338.2224	80.08	0
38080000	YIQELWR		PREDICTED: similar to ribosomal protein L15 [Mus musculus]	1007.5347	37.2	0
51770896	YITPDQLADLYK		PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE)	1439.7374	67.95	0.489684315
6753072	YITQSGDYQLR		adaptor protein complex AP-1, mu 2 subunit [Mus musculus]	1343.6614	33.2	0
24418933	YIVFVEGYPLTISGK		hypothetical protein LOC264895 [Mus musculus]	1685.8937	35.53	127.4431519
16716381	YLDLILNDFVR		lysyl-tRNA synthetase [Mus musculus]	1380.7563	49.61	0.377555234
18875380	YLECSALTQR		RAS-related C3 botulinum substrate 3 [Mus musculus]	1183.5774	52.08	0.374491631
7110683	YLEDQVNTDLPYEIER		phosphoenolpyruvate carboxykinase 1, cytosolic [Mus musculus]	1996.9459	41.73	0
63530525	YLELLGYR		PREDICTED: SEC31-like 1 [Mus musculus]	1026.5613	43.53	0.926868622
45592930	YLFLGDYVDR		protein phosphatase 3, catalytic subunit, beta isoform [Mus musculus]	1260.6393	26.71	0.130748336
20330802	YLGAEYMQSVGNMR		transferrin [Mus musculus]	1618.7416	69.33	0
37537522	YLGGSSCIAGVLVPVQGEPGR		epiplakin 1 [Mus musculus]	2059.0647	75.34	0.283601383
6754782	YLGLLENVR		myosin IB [Mus musculus]	1076.6144	58.36	0.326517169
51766008	YLGLLENVR		PREDICTED: myosin IA [Mus musculus]	1076.6144	58.36	0.326517169
34328286	YLGPAVLMQAYR		succinate dehydrogenase Ip subunit [Mus musculus]	1381.7286	24.77	0.650298514
6671668	YLGQDYETLR		calpain 1 [Mus musculus]	1257.6133	27.93	0.481594934
31981592	YLLEQDFPGMR		EH domain containing protein MPAST2 [Mus musculus]	1368.6643	39.09	0.439223827
29244048	YLLQRHEKIHSR		zinc finger protein 281 [Mus musculus]	1579.8593	22.54	0
31560645	YLLSQSSPAPLTAAEEELR		twinfilin [Mus musculus]	2075.0652	92.29	0.58115801
6753254	YLNQDYETLR		calpain 2 [Mus musculus]	1314.635	63.1	0.322619215
6680982	YLPDTLLLEECGLLR		catechol-O-methyltransferase [Mus musculus]	1747.9315	28.75	0
7305295	YLPIYSEK		myosin, heavy polypeptide 11, smooth muscle [Mus musculus]	1012.5283	37.6	0
41322904	YLQDLLAWVEENQR		plectin 1 isoform 1 [Mus musculus]	1776.8937	49.43	0.586079702
33859488	YLTVAAIFR		tubulin, beta 2 [Mus musculus]	1053.6121	46.6	0.240155759
21746161	YLTVAAIFR		tubulin, beta [Mus musculus]	1053.6121	46.6	0.240155759
22165384	YLTVAAVFR		tubulin, beta, 2 [Mus musculus]	1039.5952	49.93	0.563390236
31981939	YLTVAAVFR		tubulin, beta 4 [Mus musculus]	1039.5952	49.93	0.563390236
7106439	YLTVAAVFR		tubulin, beta 5 [Mus musculus]	1039.5952	49.93	0.563390236
41322904	YLYGTGAVAGVYLPGSR		plectin 1 isoform 1 [Mus musculus]	1743.9133	35.36	0
33859506	YMCENQATISSK		albumin 1 [Mus musculus]	1374.6041	105.87	0
33859506	YMCENQATISSK	Oxidation (M)	albumin 1 [Mus musculus]	1390.5948	78.38	0
63660302	YMIGVTYGGDNIPLSPYR		PREDICTED: filamin B, beta [Mus musculus]	2015.9984	54.25	0.523265191
6679078	YMNSGPVVAMVWEGLNVVK		nucleoside-diphosphate kinase 2 [Mus musculus]	2093.0471	43.7	0.358428805
6679078	YMNSGPVVAMVWEGLNVVK	Oxidation (M)	nucleoside-diphosphate kinase 2 [Mus musculus]	2109.0393	22.3	0
7305085	YMYDNWESQDVSFTTLVER		glutamine fructose-6-phosphate transaminase 1 [Mus musculus]	2383.0581	86.36	0.303996872

6678573	YNDEPVQIR		villin 1 [Mus musculus]	1133.5576	34	0.758947171
6755863	YNDTFWK		tumor rejection antigen gp96 [Mus musculus]	973.4421	35.63	0.427178208
7949051	YNILGTNTIMDK		heterogeneous nuclear ribonucleoprotein U [Mus musculus]	1382.6838	54.86	0
13654268	YNLDFWR		tissue specific transplantation antigen P35B [Mus musculus]	1013.4899	37.52	0.28076963
6753138	YNPNVLPVQCTGK		Na+/K+ -ATPase beta 1 subunit [Mus musculus]	1432.7218	51.53	0.326953519
19526930	YNPPVDATPDTR		WD repeat domain 23 [Mus musculus]	1345.6469	33.92	0
31981522	YNQMDSTEDAQEEFGWK		transmembrane 9 superfamily member 2 [Mus musculus]	2077.8499	91.17	0.422079743
51771420	YNVLGAETVLTQMR		PREDICTED: hypothetical protein LOC68693 [Mus musculus]	1594.826	64.46	0
9790237	YPDANPNPNEQ		SMC1 structural maintenance of chromosomes 1-like 1 [Mus musculus]	1258.5358	25.82	0
42741690	YPEAPPSVR		ubiquitin-conjugating enzyme E2 variant 1 [Mus musculus]	1015.5251	42.4	0.332493892
31543918	YPEAPPSVR		ubiquitin-conjugating enzyme E2 variant 2 [Mus musculus]	1015.5251	42.4	0.332493892
28173568	YPENFFLLR		protein phosphatase 1, catalytic subunit, beta [Mus musculus]	1198.6284	35.33	0.32064097
6671507	YPIEHGIITNWDDMEK		actin, alpha 2, smooth muscle, aorta [Mus musculus]	1960.9116	48.43	0
7709980	YPQLLSGIR		S-adenosylhomocysteine hydrolase [Mus musculus]	1046.5964	45.6	0.281131355
24429590	YPSPFFVFGEK		DEAH (Asp-Glu-Ala-His) box polypeptide 9 [Mus musculus]	1317.6548	63.37	0.633958803
8567336	YPTDGSEIVLLTDGEDNTISSCFDLVK		chloride channel calcium activated 3 [Mus musculus]	2931.4041	99.91	0
7549795	YQEEGPVPQPR		tight junction protein 2 [Mus musculus]	1299.6348	30.49	0.444252844
31560656	YQGVNLYVK		poly A binding protein, cytoplasmic 1 [Mus musculus]	1083.5789	43.62	0
63492638	YQGVNLYVK		PREDICTED: similar to MGC89376 protein [Mus musculus]	1083.5789	43.62	0
6755965	YQLDPTASISAK		voltage-dependent anion channel 2 [Mus musculus]	1293.6622	29.65	0
6755963	YQVDPDACFSAK		voltage-dependent anion channel 1 [Mus musculus]	1343.5957	59.1	0.362943016
33859490	YSDIEPSTEGEVIFR		laminin B1 subunit 1 [Mus musculus]	1741.8392	32.35	0.14442126
31560697	YSDMIVAAIQAEK		H1 histone family, member 0 [Mus musculus]	1438.722	57.71	0
31560697	YSDMIVAAIQAEK	Oxidation (M)	H1 histone family, member 0 [Mus musculus]	1454.7032	45.14	0
31982223	YSEIEPSTEGEVIYR		laminin, beta 2 [Mus musculus]	1771.8424	53.23	0
41322904	YSELTTLTSQYIK		plectin 1 isoform 1 [Mus musculus]	1546.7905	34.58	5.962648677
23956406	YSGGLPLPPSYVPVVMSELSDR		UDP glucuronosyltransferase 2 family, polypeptide B34 [Mus musculus]	2363.1948	27.39	0.206529451
8567336	YSIQASSQTLTLTVTSR		chloride channel calcium activated 3 [Mus musculus]	1855.9734	46.5	0.136082608
6679291	YSLEPVAAELK		phosphoglycerate kinase 1 [Mus musculus]	1219.6458	59.01	0
6679237	YSLEYYMGLAEELVR		pyruvate carboxylase [Mus musculus]	1835.9016	48.76	0
6679237	YSLEYYMGLAEELVR	Oxidation (M)	pyruvate carboxylase [Mus musculus]	1851.8834	22.77	0
34328130	YSNDLYELQASR		host cell factor C1 [Mus musculus]	1458.6863	23.92	0.630193589
34328130	YSNDLYELQASR	Deamidation (NQ)	host cell factor C1 [Mus musculus]	1459.6915	34.58	1.659353021
63746482	YSPSEAGLHEMDIR		PREDICTED: filamin, alpha [Mus musculus]	1604.7434	49.61	0
6755863	YSQFINFPIYVWSSK		tumor rejection antigen gp96 [Mus musculus]	1878.942	93.13	0.407776058
6677871	YSTNTQIQVLPEGGETPIFK		scinderin [Mus musculus]	2222.1328	80.96	0.307644078
42734399	YSWQDEIAQGTWR		desmuslin isoform H [Mus musculus]	1639.7542	51.4	0
46559834	YSWQDEIAQGTWR		desmuslin isoform M [Mus musculus]	1639.7542	51.4	0
6681179	YTAAVPYR		7-dehydrocholesterol reductase [Mus musculus]	940.4871	32.99	0.567126788
14161694	YTFDEFSQR		myosin VIIb [Mus musculus]	1192.5339	42.05	0.531467897
6754084	YTMGDAPDFDR		glutathione S-transferase, mu 1 [Mus musculus]	1287.5327	38.62	0
6754084	YTMGDAPDFDR	Oxidation (M)	glutathione S-transferase, mu 1 [Mus musculus]	1303.5215	27.56	0.214273158
6671539	YTPSGQSGAAASESLFISNHAY		aldolase 1, A isoform [Mus musculus]	2258.0354	106.73	0.388870845
6754016	YTTPEDATPEPGEDPR		guanine nucleotide binding protein alpha stimulating isoform b [Mus musculus]	1774.7828	54.26	0.277528656
27754065	YVANLFPYK		pyrophosphatase [Mus musculus]	1114.5874	25.31	0
27370154	YVDLGGSYVGPTQNR		amine oxidase (flavin-containing) [Mus musculus]	1625.7968	86.53	0
6680854	YVDSEGHLYTVPIR		caveolin, caveolae protein 1 [Mus musculus]	1648.8351	64.97	0.105303763
13386062	YVEEQPGNLQR		hypothetical protein LOC68117 [Mus musculus]	1332.6559	42.2	0.293157009
33859482	YVEPIEDVPCGNIVGLVGVDQFLVK		eukaryotic translation elongation factor 2 [Mus musculus]	2702.4253	81.16	0.548238296
28076981	YVEQLLTLFNR		cullin 5 [Mus musculus]	1395.7609	40.23	0
31541863	YVNWIQQTIAAN		RIKEN cDNA 2210010C04 [Mus musculus]	1420.7173	89.43	0
40254244	YVQELPLETDGALR		loss of heterozygosity, 11, chromosomal region 2, gene A homolog [Mus musculus]	1603.8347	42.58	0
13994221	YVQLPADEVDTQLLQDAAR		snRNP core protein SMX5 [Mus musculus]	2145.0811	58.93	0.612916867
21312570	YVSSLTEEISR		lectin, mannose-binding, 1 [Mus musculus]	1283.6384	32.14	0.31071533
10092608	YVTLIYTNYENGK		glutathione S-transferase, pi 1 [Mus musculus]	1577.7791	68.87	0.643070479
64427157	YVVDSDTVQAHTVR		PREDICTED: synaptopodin 2 [Mus musculus]	1589.7854	67.34	0
21704206	YWANFAR		carboxylesterase 2 [Mus musculus]	927.4471	22.96	0.269131663
27370126	YWANFAR		carboxylesterase 5 [Mus musculus]	927.4471	22.96	0.269131663
19527178	YWANFAR		carboxylesterase 6 [Mus musculus]	927.4471	22.96	0.269131663
6681143	YWEIFPNTFR		decorin [Mus musculus]	1372.6715	28.35	0.183874762

27754118	YWEIQPATFR	asporin [Mus musculus]	1310.6573	34.04	0.160772679
6678499	YWQQVIDMNDYQR	UDP-glucose dehydrogenase [Mus musculus]	1758.8151	35.11	0.469037055
6753036	YYAGWADK	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	973.4493	48.19	0.268256059
31982290	YYEPYYAAGPSYGGR	LIM domain containing preferred translocation partner in lipoma [Mus musculus]	1713.7583	62.61	0.19105974
23943876	YYIVGLQVR	zymogen granule membrane protein 16 [Mus musculus]	1110.6322	44.43	0.272189193
6755354	YYPTEDVPR	ribosomal protein L6 [Mus musculus]	1139.5399	47.65	0.402672182
22122523	YYRPTEVDFLQGDCSK	GDP-mannose 4, 6-dehydratase [Mus musculus]	1920.887	23.63	0.358301898
31981327	YYTPTISR	proteasome (prosome, macropain) subunit, beta type 2 [Mus musculus]	1000.5108	22.94	0.369392434
63556656	YYVLGATFYPGPECER	PREDICTED: RIKEN cDNA A430096B05 gene [Mus musculus]	1864.8815	40.8	0.135432641
51873060	YYVTIIDAPGHR	eukaryotic translation elongation factor 1 alpha 1 [Mus musculus]	1404.7281	57.02	0.598357872