Supplement Table 1: Peptide Analyses. Shown are identified candidate peptides identified, with search confidence (probability score), precursor ion charge, and mass of singly protonated M+H + species. Also indicated are UniProt (Swissprot) names, amino acid length, total number of peptides identified (spectral counts) and number of unique peptides, together with protein sequence coverage.

entry	swissprot	protein length	sequence coverage (%)	# unique peptides	total # peptides	peptide sequence	peptide confidence	precursor ion charge	peptide mass (M+H)
1	1433B_MOUSE	246	62.2	11	110	K.TAFDEAIAELDTLNEESYK.D	0.9958	2	2160.2959
						K.DSTLIMQLLR.D	0.9958	1	1190.4436
						K.QTTVSNSQQAYQEAFEISK.K	0.9958	2	2160.3019
						K.YLILNATQAESK.V	0.9958	1,2	1351.5425
						K.EMQPTHPIR.L	0.9958	1	1109.2884
						R.EKIEAELQDICNDVLELLDK.Y	0.9958	2	2388.6405
						R.YLSEVASGENK.Q	0.9958	1	1197.2872
						R.VISSIEQK.T	0.9944	1	904.0513
						R.LGLALNFSVFYYEILNSPEK.A	0.9956	2	2318.6745
						K.AVTEQGHELSNEER.N	0.9958	2	1599.6543
						K.IEAELQDICNDVLELLDK.Y	0.9932	2	2131.3509
2	1433E_MOUSE	255	53.33	10	217	K.AAFDDAIAELDTLSEESYK.D	0.9958	2	2089.2171
						K.AASDIAMTELPPTHPIR.L	0.9958	2	1821.1015
						K.HLIPAANTGESK.V	0.9958	1	1238.3861
						R.DNLTLWTSDMQGDGEEQNK.E	0.9958	2	2182.28
						K.VAGMDVELTVEER.N	0.9944	2	1448.6312
						K.KVAGMDVELTVEER.N	0.9958	2	1576.8053
						R.YLAEFATGNDR.K	0.9958	1	1257.3452
						K.LICCDILDVLDK.H	0.9958	2	1477.6705
						R.IISSIEQK.E	0.9924	1	918.0782
						K.EAAENSLVAYK.A	0.9958	1	1195.3147
3	1433F_MOUSE	246	20.33	3	34	K.QAFDDAIAELDTLNEDSYK.D	0.9958	2	2159.2677
						K.ELETVCNDVLALLDK.F	0.9958	2	1732.9349
						K.EHMQPTHPIR.L	0.9944	2	1246.4295
4	1433G_MOUSE	247	50.61	7	116	K.TAFDDAIAELDTLNEDSYK.D	0.9958	2	2132.2421
						K.NVTELNEPLSNEER.N	0.9958	2	1644.7355
						K.ELEAVCQDVLSLLDNYLIK.N	0.9958	2	2236.5335
						K.AYSEAHEISK.E	0.9958	1,2	1135.2187
						R.LGLALNYSVFYYEIQNAPEQACHLAK.T	0.9958	3	3014.3735
						R.EQLVQK.A	0.9944	1	744.8662
						R.DNLTLWTSDQQDDDGGEGNN.-	0.9958	2	2195.1309
5	1433T_MOUSE	245	31.84	5	21	K.TAFDEAIAELDTLNEDSYK.D	0.9958	2	2146.269

						K.VESELRSICTTVLELLDK.Y	0.9944	3	2106.3875
						R.SICTTVLELLDK.Y	0.9958	2	1392.5989
						K.QTIENSQGAYQEAFDISK.K	0.9958	2	2030.1553
						K.YLIANATNPESKVFYLK.M	0.9944	2	1972.2915
6	1433Z_MOUSE	245	48.98	9	106	K.GIVDQSQQAYQEAFEISK.K	0.9958	2	2042.2096
						K.KGIVDQSQQAYQEAFEISK.K	0.9921	2	2170.3837
						K.TAFDEAIAELDTLSEESYK.D	0.9958	2	2133.2702
						K.SVTEQGAELSNEER.N	0.9958	2	1549.5914
						R.DICNDVLSLLEK.F	0.9958	2	1419.5811
						R.YLAEVAAGDDK.K	0.9958	1	1152.2463
						K.GIVDQSQQAYQEAFEISKK.E	0.9958	2	2170.3837
						R.DNLTLWTSDTQGDEAEAGEGGEN.-	0.9958	2	2410.3801
						K.FLIPNASQPESK.V	0.9944	1	1331.5113
7	2A5A_MOUSE	486	3.5	1	9	R.SQGSQAELHPLPQLK.D	0.9958	2	1633.8448
8	2A5E_MOUSE	467	3.64	1	6	R.SQGKPIELTPLPLLK.D	0.9929	2	1635
9	2AAA_MOUSE	589	33.11	14	231	K.SALASVIMGLSPILGK.D	0.9958	2	1557.9323
						K.IGPILDNSTLQSEVKPILEK.L	0.9958	2	2195.5615
						K.DNTIEHLLPLFLAQLK.D	0.9944	2	1866.2108
						R.AISHEHSPSDLEAHFVPLVK.R	0.9958	2	2214.4857
						K.SEIIPMFSNLASDEQDSVR.L	0.9958	2	2139.3417
						R.QLSQSLLPAIVELAEDAK.W	0.9958	2	1926.2175
						K.VLAMSGDPNYLHR.M	0.9958	2	1473.6898
						K.KLSTIALALGVER.T	0.9958	2	1371.6634
						R.LNIISNLDCVNEVIGIR.Q	0.9958	2	1943.217
						K.DNTIEHLLPLFLAQLKDECPEVR.L	0.9958	2	2752.1059
						K.LSTIALALGVER.T	0.9958	2	1243.4893
						R.TSACGLFSVCYPR.V	0.9958	2	1518.6417
						R.LNIISNLDCVNEVIGIRQLSQSLLPAIVELAEI	0.9958	3	3850.4113
						R.LAGGDWFTSR.T	0.9944	1	1110.2144
10	2ABA_MOUSE	447	20.36	4	21	R.INLWHLEITDR.S	0.9958	2	1410.6157
						R.GEYNVYSTFQSHEPEFDYLK.S	0.9958	2	2454.6111
						R.VPVFRPMDLMVEASPR.R	0.9944	2	1845.2281
						R.SFNIVDIKPANMEELTEVITAAEFHPNSCNT	0.9958	3	4292.7268
11	3BP1_MOUSE	601	4.66	2	3	R.DNHNQADHSPLTTAAPFSR.V	0.9958	2	2080.1808
						R.DNHNQADHSPLTTAAPFSRVYGVSLR.T	0.9958	3	2855.0989
12	3HIDH_MOUSE	335	73.73	12	297	K.KGSLLIDSSTIDPSVSK.E	0.9958	1,2	1747.9836
						K.HGYPLILYDVFPDVCK.E	0.9958	2	1937.2116

						R.IITMLPSSMNAVEVYSGANGILK.K	0.9958		2	2409.8617
						K.TPVGFIGLGNMGNPMAK.N	0.9954		2	1705.043
						K.TPILLGSLAHQIYR.M	0.9958	2,3		1582.8863
						R.CWSSDTYNPVPGVMHGVPSSNNYQGGFC	0.9958		3	3662.0084
						K.ICNNMLLAISMIGTAEAMNLGIR.S	0.9958		3	2507.9938
						K.DLGLAQDSATSTK.T	0.9958	1,2		1307.4002
						K.EAGEQVASSPAEVAEK.A	0.9944		2	1602.6953
						K.MGAVFMDAPVSGGVGAAR.S	0.9958		2	1693.9764
						K.GSLLIDSSTIDPSVSK.E	0.9958		1	1619.8095
						R.SGNLTFMVGGVEDEFAAAQELLECMGSN\	0.9958		3	4356.7521
13	41_MOUSE	858	14.92	7	9	R.IVITGDADIDHDQVLVQAIK.E	0.9958		2	2164.4637
						R.TLNINGQVPTGDGPPLVK.T	0.9958		2	1821.0837
						R.HSNLMLEDLDK.S	0.9958		2	1315.484
						K.IRPGEQEHYESTIGFK.L	0.9958		2	1892.0782
						R.SMTPAQADLEFLENAK.K	0.9958		2	1765.9758
						R.SPRPTSAPAIAQSQVTEGPGAPIK.K	0.9958		2	2361.6603
						K.HHASISELK.K	0.9958		1	1022.149
14	5HT2B_MOUSE	479	3.97	1	4	R.KFSSTLCFGNSMVENSK.F	0.9944		2	1937.1408
15	5HT5B_MOUSE	370	21.08	2	2	K.RAAMMVGILIGVFVLCWIPFFLTELISPLCAC	0.9958		3	4522.4778
						R.ASALMIAITWALSALIALAPLLFGWGEAYDA	0.9944		3	3775.4901
16	5HT7R_MOUSE	448	3.13	1	3	R.SLLQCQYRNINR.K	0.9946		2	1565.7386
17	5NT1A_MOUSE	365	10.41	2	5	R.YQLEHENEPFSPGPAFPFVK.A	0.9958		2	2334.5927
						R.LINSINHYDLFIER.F	0.9958		2	1747.9915
18	5NT3_MOUSE	331	42.3	10	61	K.DNSNIILLGDSQGDLR.M	0.9958		2	1730.8723
						K.EQYYAIEVDPVLTVEEK.F	0.9958		2	2026.2476
						K.VVSNFMDFDENGVLK.G	0.9958		2	1714.9306
						K.IIEMMPEFQK.S	0.9944		1	1266.5562
						K.EESLEVVNSILQK.T	0.9958		2	1488.6781
						K.SHGLLIEQGIPK.A	0.9958		1	1292.5211
						R.MADGVANVEHILK.I	0.9957		2	1397.6324
						K.GELIHVFNK.H	0.9958		1	1057.2376
						R.KLLQLK.E	0.9958		1	742.9804
						K.RCPTCHNIIDNCK.L	0.9958		2	1688.7792
19	5NTC_MOUSE	560	21.25	6	18	K.DILYIGDHIFGDILK.S	0.9958		2	1733.0172
						R.KPLFFGEGTVLR.Q	0.9958		2	1364.6304
						K.HLDSSSNERPDISSIQR.R	0.9958		2	1942.0525
						K.IGTYTGPLQHGIVYSGGSSDTICDLLGAK.G	0.9958	2,3		2982.2831

						R.TFLVIPELAQELHVWTDK.S	0.9958	2	2140.4869
						R.SMFQDVRDAVDWVHYK.G	0.9958	2	1997.2353
20	5NTD_MOUSE	576	7.12	2	2	R.GVDIVVGGHSNTFLYTGNPPSK.E	0.9958	2	2260.5113
						R.GPLAHQISGLFLPSK.V	0.9958	2	1565.8558
21	68MP_MOUSE	58	17.24	1	13	K.GPAPAHGHH.-	0.9958	1	880.9413
22	6PGD_MOUSE	483	23.4	6	35	R.HEMLPANLIQAQR.D	0.9958	2	1521.7777
						K.LVPLLDTGDIIIDGGNSEYR.D	0.9958	2	2161.4167
						R.NPELQNLLLDDFFK.S	0.9958	2	1706.9359
						K.VVQLEGSK.K	0.9944	1	859.9982
						R.DYFGAHTYELLTKPGEFIHTNWTGHGGSV	0.9958	3	3933.1981
						R.HEEMAQAFEEWNK.T	0.9958	2	1649.7748
23	6PGL_MOUSE	257	72.37	10	232	K.LPIPDSQVLTINPALPVEDAAEDYAR.K	0.9958	2	2809.1455
						R.DLPAAAAPAGPASFAR.W	0.9958	1	1483.6671
						R.VTLTLPVLNAAQSIIFVATGEGK.A	0.9958	2	2343.7691
						R.QALQGDAVPVFDLLILGVGPDGHTCSLFPD	0.9958	3	4027.5353
						R.LVPFDHAESTYGLYR.T	0.9915	2	1768.9665
						R.FALGLSGGSLVSMLAR.D	0.9958	2	1579.8981
						K.IVAPISDSPKPPPQR.V	0.9958	2	1602.8741
						R.LLSVPFEK.H	0.9924	1	933.1357
						R.TGALCWFLDEAAAR.L	0.9958	2	1581.7344
						R.THLLSK.L	0.9924	1	698.8405
24	A0A5D7_MOUSE	238	27.73	4	242	K.RADAAPTVSIFPPSSEQLTSGGASVVCFLN	0.9944	3	3730.1346
						R.QNGVLNSWTDQDSK.D	0.9958	2	1592.6622
						R.ADAAPTVSIFPPSSEQLTSGGASVVCFLNN	0.9958	3	3573.9471
						R.HNSYTCEATHK.T	0.9958	2	1348.3807
25	A0A5E1_MOUSE	281	22.06	3	4	R.GEGEPCGGGAAGGGHCAPGMECVK.S	0.9958	3	2303.3634
						K.VFLSCEVIGIPTPVLIWNK.V	0.9958	2	2186.6086
						K.ITVVDALHEIPLK.K	0.9958	2	1448.7459
26	A0AUM9_MOUSE	365	10.14	2	7	K.YVVDFLMENRSITSIR.S	0.9958	2	1944.2561
						R.LLFMANEADLDEELVIK.G	0.9912	2	1964.2813
27	A0JLW6_MOUSE	497	7.24	2	5	R.HLVVPNVQTGQLEPLLSR.F	0.9915	2	2001.3365
						R.FFHQMAAEQGQAGR.A	0.9958	2	1578.7453
28	A0N274_MOUSE	152	21.71	1	2	K.ATLTSDKSSSTAYMELSSLTSEDSAVYYCA	0.9958	3	3396.6242
29	A0N3V1_MOUSE	117	24.79	1	3	K.LEWIGYIYYSGTITYNPSLTSRTTITR.D	0.9958	3	3171.5768
30	A0PJJ1_MOUSE	855	2.57	1	2	R.SFSLDEPPLFIPDNIATVKK.E	0.993	2	2232.5817
31	A0T1J8_MOUSE	1699	3.59	4	5	K.KEVPLSGAPDR.Y	0.9958	1	1169.3231
						R.QVRYEEMQK.I	0.9924	1	1211.3783

						R.ATGPKPDSSHFISGSASEK.E	0.9958		2	1904.0434
						R.SHSPSMSQSGSQLR.N	0.9932		2	1489.603
32	A16A1_MOUSE	802	5.24	2	8	R.GAVEAAHQAAPGWGAQSPR.A	0.9958		2	1862.0146
						R.VQDQGQTLQVTGLRGPVLR.L	0.993		2	2066.3683
33	A1AG1_MOUSE	207	23.19	3	23	K.YEGGVETFAHLIVLR.K	0.9958		2	1704.9664
						K.AVTHVGMDESEIIFVDWK.K	0.9958		2	2077.3594
						K.RPDITPELR.E	0.9923		2	1097.2596
34	A1AT1_MOUSE	413	47.94	15	2108	K.DQSPASHEIATNLGDFAISLYR.E	0.9958		2	2406.614
						R.IFNNGADLSGITEENAPLK.L	0.9952		2	2004.2041
						K.KLDQDTVFALANYILFK.G	0.9958	2,3		2000.3452
						R.LSISGEYNLK.T	0.9924		1	1124.2792
						K.NHYQAEVFSVNFAESEEAK.K	0.9958		2	2200.3257
						K.MQHLEQTLSK.E	0.9958	1,2		1215.41
						K.SFQHLLQTLNRPDSELQLSTGNGLFVNNDI	0.9958		3	3500.8931
						K.LDQDTVFALANYILFK.G	0.9958		2	1872.1711
						K.TLMSPLGITR.I	0.9944	1,2		1089.3385
						K.KPFDPENTEEAEFHVDESTTVK.V	0.9958		2	2550.6947
						K.NHYQAEVFSVNFAESEEAKK.V	0.9958		2	2328.4998
						R.LAQIHFPR.L	0.9958		2	982.1734
						K.VINDFVEK.G	0.9924		1	964.1063
						K.KVINDFVEK.G	0.9958	1,2		1092.2804
						K.LSQAVHK.A	0.9924		1	782.9181
35	A1AT2_MOUSE	413	23.97	7	148	K.KPFDPENTEEAEFHVDK.S	0.9958		2	2033.1583
						K.ELDQDTVFALANYILFK.G	0.9958		2	2001.2866
						R.LVQIHIPR.L	0.9952		2	976.2101
						K.KPFDPENTEEAEFHVDKSTTVK.V	0.9925	2,3		2549.7533
						R.FDHPFLFIIFEEHTQSPIFVGK.V	0.9958		2	2650.0514
						K.MQHLEQTLNK.E	0.9958		1	1242.4357
						R.LSISGDYNLK.T	0.9958		1	1110.2523
36	A1AT4_MOUSE	413	7.99	2	38	K.DQSPASHEIATNLGDFALR.L	0.9958		2	2043.2004
						R.RSDAQIHIPR.L	0.9958		2	1193.3511
37	A1AT5_MOUSE	413	8.23	2	10	K.KPFDPENTKQAEFHVDESTTVK.V	0.9958		2	2548.7686
						R.LAQIHIPR.L	0.9944		2	948.1563
38	A1IGU4_MOUSE	676	4.73	2	2	K.YPLLLQK.I	0.9958		1	875.099
						R.NNVVDFMGNLEVFLSFRPHER.S	0.9958		3	2521.8559
39	A1L349_MOUSE	642	3.58	1	5	R.MVMIEEFKQGLAITHEILLNK.A	0.9958		3	2458.9801
40	A2A4I3_MOUSE	261	7.66	1	5	K.ELTELFHHYYPIEIDPHR.T	0.9907		2	2310.5737

41	A2A4N9_MOUSE	1175	1.19	1	3	K.RWEGLVHISELR.R	0.9958	1	1495.7244
42	A2A5D6_MOUSE	118	14.41	1	2	R.SRGARPCWLISLQHR.V	0.9958	2	1838.0916
43	A2A5E7_MOUSE	250	11.6	1	3	K.RPSYTLCDVCNIQLNSAAQAQVHCGGR.A	0.991	3	3077.2819
44	A2A642_MOUSE	607	9.23	2	6	R.VSARPYHLLQGPKPDLVIGFNSGFGLK.D	0.9958	3	2912.4074
						R.FPQEAKPAPESEVTQQEASREEGSR.E	0.9944	2	2788.9445
45	A2A654_MOUSE	3036	0.96	2	3	K.WNGSVHGSKVLTISTLR.L	0.993	2	1856.1349
						K.GNINNYFK.L	0.9958	1	970.0727
46	A2A699_MOUSE	822	5.72	1	2	K.LPLYASVSLYLLPERPATLILYEDLVHILLGS	0.9958	3	5123.0086
47	A2A6Q5_MOUSE	825	4.73	2	2	R.ASVLFANEK.Y	0.9944	1	979.121
						K.ITTVTPQIQAFNLQKAAAEGLMSLLR.E	0.9944	3	2816.3318
48	A2A6Q8_MOUSE	192	12.5	1	4	K.KETAKPAAAPAPAASAAPEPLK.D	0.9958	2	2088.4117
49	A2A761_MOUSE	587	4.77	2	4	R.EVMLENYR.N	0.9958	1	1054.206
						K.LENPESSNVILEQKHR.K	0.9915	2	1894.0947
50	A2A781_MOUSE	289	7.27	1	4	K.RPITGGSGGGEGAGLGGGK.Y	0.9958	2	1585.7171
51	A2A784_MOUSE	467	17.13	3	3	R.TSIEVGVK.G	0.9958	1	832.9725
						K.WLEETDSSSGSPTNLDKIAAQGR.K	0.9958	3	2463.6201
						K.LMHHEWLGAGAGHPVGLAHPQWLPTGGC	0.9958	3	4341.8179
52	A2A7I1_MOUSE	336	7.14	1	3	K.CNESSNIIHESSESTPHKTNHR.D	0.9958	3	2565.6415
53	A2A7K5_MOUSE	146	13.01	1	10	K.HHLGAATPENPEIELLR.L	0.9958	2	1898.1289
54	A2A7S7_MOUSE	564	12.23	4	7	K.QVEHPLLSGLLYPGLQALDEEYLK.V	0.9958	2	2727.1296
						K.DFAAEVVHPGDLK.N	0.9958	2	1398.5584
						R.EKFNTPALK.K	0.9958	1	1048.2273
						R.VHLMNPMVPGLTGSK.M	0.9958	2	1581.9318
55	A2A850_MOUSE	661	3.63	1	55	R.AAATFNPELITHILDGSPENTR.R	0.9958	2	2368.6085
56	A2A856_MOUSE	1085	6.36	2	2	K.AEQREELATSFTSLLAYGLSLIR.K	0.9958	3	2569.9176
						R.TQVKSQTLNPVWDETFILEFEDIANASFHLI	0.9944	3	4942.4646
57	A2A8C4_MOUSE	496	2.02	1	2	R.ELFPPLFK.A	0.9944	1	991.2181
58	A2A8L5_MOUSE	1898	1.79	2	38	K.HEKTVDIYGHVTCMR.S	0.9958	2	1847.065
						R.SDLGVGVFTPTVEAR.T	0.9958	2	1548.7361
59	A2A930_MOUSE	1257	0.88	1	2	K.VADPVGVLK.E	0.9958	1	898.0904
60	A2A9C3_MOUSE	3431	1.54	2	2	R.YSTIQCRISHSSLTSLLR.D	0.9932	2	2123.3831
						R.DAACIGSLLTFEYLIQLCQSKEWGPLPPEPI	0.9958	3	3591.0303
61	A2A9H6_MOUSE	3643	1.15	3	5	R.YIERGTFEPLPFLK.Y	0.9958	2	1711.0135
						K.TENYINENTETQSKLK.S	0.9958	1	1913.0483
						K.YNSVQK.N	0.9944	1	738.8186
62	A2AAU3_MOUSE	1616	2.1	2	2	K.QLSGSYMETLIEK.W	0.9937	2	1499.7192
						K.SLSGESLNGMVTKDLTR.L	0.9958	2	1809.0447

63	A2AAX3_MOUSE	604	3.31	1	8	R.YDITNDKWEFVDPYPVNK.Y	0.9958	2	2244.465
64	A2AB75_MOUSE	275	12	1	2	K.VSVSGAHTGNIGQSVQSHGSIIKSSESFSV	0.9944	3	3116.4148
65	A2ACU2_MOUSE	892	5.38	3	13	R.GLLLYGPPGTGK.T	0.9958	1,2	1173.3977
						K.SANICIGRPVLLTSLDGK.Q	0.9958	2	1915.2066
						K.EAALLALEENIK.A	0.9958	1	1314.5217
66	A2ADE7_MOUSE	182	18.13	1	3	K.GSSVHPPPGHAIPSEEELPPPPEEPVTLPE	0.9958	3	3280.6183
67	A2ADI4_MOUSE	785	5.1	1	2	R.SHCSSLVPLVNYPYDTDDENGDDPYGNDN	0.9958	3	4342.3328
68	A2ADM8_MOUSE	1628	4.55	2	2	R.LSLESEGSGSSLLEEGDRPGETASVDSRG	0.9958	3	3677.7851
						R.TQTSQGGEVSTQAPELPYPSVPELRAEDQ	0.9944	3	3712.0245
69	A2AFK4_MOUSE	405	3.7	1	2	K.YELEKFEEGLSER.S	0.9958	2	1629.7637
70	A2AFQ2_MOUSE	271	16.61	3	118	K.GLVAVVTGGASGLGLATAK.R	0.9958	1,2	1642.9365
						K.RLVGQGATAVLLDVPDSEGEAQAK.K	0.9958	2	2425.7013
						R.LVGQGATAVLLDVPDSEGEAQAK.K	0.9958	2	2269.5138
71	A2AG06_MOUSE	965	2.9	2	3	K.QYLHNSSLTPQQK.I	0.9958	2	1544.7074
						R.EQARVVTLLGK.M	0.9958	1	1214.4508
72	A2AGL3_MOUSE	4863	2.41	6	11	K.EGEALVQQRENEK.L	0.9945	2	1530.6347
						R.MPSSFLKVETER.V	0.9944	1	1424.655
						R.MGREEELLMINGLGDIMNNK.V	0.9927	2	2278.662
						K.LPETEKNYNLQMSTETLK.T	0.9958	2	2140.4132
						K.LMMKNEYIIPITSATR.N	0.9958	2	1882.2868
						K.QLVLTVGLLAVVVYLYTVVAFNFFRK.F	0.9944	3	2974.6457
73	A2AGN7_MOUSE	400	19	4	15	K.DSYLILETLPTEYDSR.V	0.9958	2	1916.0918
						R.GATELTHEDYMEGILEVQAK.K	0.9958	2	2235.4706
						K.LLDVDPNDQEEDGANIDLDSQRK.G	0.9958	2	2600.7124
						K.LKPGDLVGVNKDSYLILETLPTEYDSR.V	0.9958	3	3037.4369
74	A2AGT5_MOUSE	2032	2.85	2	2	R.LLPDTINSINLDRILLDIHIFMK.V	0.9915	2	2709.2628
						K.AEAMSGHIDQFLIATFMQLRLIYSTHMADEI	0.9924	3	3570.1336
75	A2AGU5_MOUSE	210	16.19	1	2	K.IGTALAMATLSCFLFLVGGIIPLSFTLPPRSR	0.9958	3	3422.1188
76	A2AGX2_MOUSE	461	8.03	2	2	R.AGHGFPRAELDGTDSPSTSYDEDEEAPGF	0.9944	3	3715.8389
						R.AELDGTDSPSTSYDEDEEAPGPSQQPLR.N	0.9944	3	2993.0344
77	A2AGX3_MOUSE	565	3.01	1	2	R.EGIACANLYILLVNK.I	0.993	2	1691.9745
78	A2AH75_MOUSE	1150	1.3	1	3	R.HSRQEIEALAIVK.M	0.9915	2	1494.7342
79	A2AHC8_MOUSE	147	12.93	1	2	R.MTDLGVTVNQPVFMRGK.E	0.9958	2	1894.2574
80	A2AHD2_MOUSE	324	4.01	1	3	R.FSADDYRELER.L	0.9958	2	1401.4753
81	A2AHT1_MOUSE	821	1.83	1	3	R.QDLEALQRSGLEK.I	0.9958	2	1487.653
82	A2AHY8_MOUSE	747	2.01	1	4	R.EVIGAQGGQGLSR.H	0.9958	1	1272.4037
83	A2AIM7_MOUSE	278	14.75	1	7	R.QNLLQAAGNVGQASGELLQQIGESDTDPH	0.9958	3	4166.6092

84	A2AIR4_MOUSE	1115	2.51	1	2	K.YIFNDEEGQNQLGTQTHQDIPLPPRR.R	0.9917	2	3068.3323
85	A2AIX1_MOUSE	2377	3.53	3	12	K.SHLVGVKPVEADR.A	0.9929	2	1407.6127
						R.HFHQAPGDHCPTGAPHGGSVPFYNPAQL	0.9958	3	4395.7257
						R.GPLELSPAYGPPGSALGFPESSR.S	0.9958	2	2287.534
86	A2AJ15_MOUSE	658	4.1	1	8	K.TFSEWFGLGLTLIDALDTMWILGLK.Q	0.9944	3	2842.3656
87	A2AJ76_MOUSE	5100	3.24	6	6	R.IPFDPSLKEVTIALSGPGPEIEVR.D	0.9926	2	2565.9695
						R.ELRELYVQGGGDCPEMSVGAIK.A	0.9958	3	2409.6827
						R.DPLGRVLQTDEGLNVLLNIPDSAK.V	0.9958	2	2578.9255
						R.LTCNATGTPRPTLIWLK.D	0.9917	2	1943.2628
						R.ALPDGSLWLEHVEAGDAGVYECVAHNHLC	0.9958	3	4228.7203
						R.SVVGLAPGQLILECSVEAEPAPEIEWHR.G	0.9909	2	3088.4535
88	A2AJN7_MOUSE	862	4.29	2	2	R.VALLLKEQTSYPPTHYIR.R	0.9958	3	2130.4948
						R.LVRPQNWGENSCEVR.F	0.9945	2	1844.9909
89	A2AJW9_MOUSE	461	6.07	2	4	K.SRPEDVLTLPYCLLQEVLK.S	0.9958	2	2274.6288
						K.HLSELLKSRPEDVLTLPYCLLQEVLK.S	0.9958	3	3095.6159
90	A2AJX5_MOUSE	1955	4.55	3	4	K.KPSLLSEQQQAASALVETIR.Q	0.9958	2	2170.471
						R.SHSVGGPLQNIDFSQRPFHGVSTVSLPSSI	0.9944	3	4174.5761
						R.FIEECSFVSDKDTGLAFFDDCIEK.L	0.9958	3	2874.0591
91	A2AKI2_MOUSE	79	21.52	1	6	R.NVKVDSRPESFGDTR.E	0.9926	1,2	1707.8405
92	A2AKV6_MOUSE	287	6.62	1	2	R.ITMEPNPHWLPVLWTLK.S	0.9936	2	2076.5072
93	A2AKX2_MOUSE	430	8.6	2	2	R.MLPRTSSCFCGDTLPDCLISAR.L	0.9958	2	2558.8075
						K.DLLLLQESAAK.G	0.9944	1	1201.4057
94	A2ALA6_MOUSE	338	17.16	2	2	R.NEHMQYILTWYGLCAATSYLWFQKFVR.R	0.9958	3	3427.9136
						R.LSSTESGAHVVTPFHCSDLGVTILVNR.G	0.9958	3	2898.2115
95	A2ALK6_MOUSE	899	2	1	3	R.LPFSLEENGGTPFAPK.T	0.9958	1	1704.9201
96	A2ALL9_MOUSE	1173	2.56	2	3	K.KCTNILNSNGELR.G	0.9958	2	1519.6641
						K.QDGAVAMEMQPLK.S	0.9958	1	1418.6661
97	A2ALS2_MOUSE	165	9.09	1	2	R.MDEQRCSFPPPLK.T	0.993	2	1605.8152
98	A2ALS4_MOUSE	729	5.9	2	2	K.HFLGKEHFNYYSLDTALGHLVFSLK.Y	0.9944	3	2938.358
						R.SRSQSMDAMGLSNK.K	0.9944	1	1512.696
99	A2AM52_MOUSE	1532	3.46	2	6	R.SHLENQDLLPKPSEQRFPPMAVPAHK.H	0.9958	3	2968.4033
						K.DGQHSISSAHVTVAPFGYLKIHR.L	0.9944	3	2521.8411
100	A2AM64_MOUSE	516	10.27	2	8	K.GFSGTFQLSFPYYPSPGVLFPK.K	0.9958	2	2437.7998
						K.SGEKPLLGGSLMEYAILSAIAAMNEPK.T	0.9958	2,3	2792.2783
101	A2AM68_MOUSE	554	3.07	1	7	K.ALPLIVGAQLIHADK.L	0.9958	2	1559.8925
102	A2AN43_MOUSE	999	6.51	3	4	R.AQLETHVSQLMESLK.Q	0.9958	2	1714.9745
						K.FLAVSQNPGDVLTPVPTGSQEFGAADQQD	0.9924	3	3374.6452

						R.SLSHLAAPVQSK.L	0.9958		2	1238.4294
103	A2AN49_MOUSE	269	10.41	2	2	R.APAVPPARPGSRGPAPGPPPAGSALGG.-	0.9958		2	2360.681
						R.GPAPGPPPAGSALGG.-	0.9958		1	1203.3403
104	A2ANE1_MOUSE	215	6.98	1	2	R.IFRMNYFLSLEAR.K	0.9958		1	1660.9745
105	A2ANY6_MOUSE	5589	2.4	7	10	K.LYKPEIVINELDVQVGRVR.L	0.9958		2	2241.6389
						K.HLIYQIPQLLVNQENK.Y	0.9945		2	1951.2761
						K.MTENALLFAFVEGTLAQAIKK.G	0.9945		2	2296.7302
						K.KMVAFNNHIDHEVTVEK.K	0.9944		2	2012.2909
						K.GYWIVLDELNLAPTDVLEALNR.L	0.9929		2	2515.8687
						K.LVKVMLDLQSYR.R	0.9958		1	1465.7943
						R.QFLVDSVFQPILK.D	0.9958		1	1534.8388
106	A2AP_MOUSE	491	9.16	3	30	R.WFLLEQPEIQVAHFPFK.N	0.9958		2	2130.4967
						R.NPNPSALPQLQEQR.D	0.9958		2	1592.7519
						K.LPLPALFK.L	0.9958		2	899.1643
107	A2AP24_MOUSE	325	16.31	3	6	R.ALSHILQTPIEILQADAPPIIVGEEYPR.N	0.9931	2,3		3085.5706
						R.HAYGLGEHYNSVTR.L	0.9958		2	1604.722
						R.ALSHILQTPIEILQADAPPIIVGEEYPRNPLVI	0.9958		3	4171.9311
108	A2AP74_MOUSE	216	14.81	2	2	K.QETQSAEPPPPEPPRI.-	0.9958		2	1773.9402
						K.KPSAGEAGGWSDK.D	0.9958		2	1290.3751
109	A2AP83_MOUSE	941	4.57	2	2	R.LKQHTLFK.L	0.9958		1	1015.2437
						R.YETSNGLQELWGPYSPSALFSTYKHHSGH	0.9944		3	3480.7771
110	A2APX6_MOUSE	1998	2.85	2	4	R.QRAMSIASILTNTVEELEESR.Q	0.9958		2	2378.6599
						K.FDPDATQFMEFEKLSQFAAALEPPLNLPQF	0.9958		3	3636.1133
111	A2AQ07_MOUSE	451	13.75	2	3	R.RESESCDCLQGFQIVHSLGGGTGSGMGTL	0.9944		3	3528.8661
						R.LTTPTYGDLNHLVSLTMSGITTSLR.F	0.9958	2,3		2693.0875
112	A2AQ53_MOUSE	2873	3.69	6	39	R.GWGPHCEICPFEGTVAYK.K	0.9958		2	2109.2777
						R.SGNCYLDIRPR.G	0.9901		2	1351.4711
						K.LLVCEDIDECQNGPVCQR.N	0.9958		2	2206.3126
						R.GFMTNGADIDECK.V	0.9958	1,2		1458.5489
						R.IGQGHCVSGMGMGR.G	0.9958		2	1447.6362
						R.EGYCFSEVLQNMCQIGSSNR.N	0.9958		2	2380.5233
113	A2AQ92_MOUSE	1551	9.16	4	4	R.SNGTVLEATAALYNQDLSRLELLPGGLLES	0.9958		3	5126.7753
						R.GHLLETFFRHLFSQVLDINQADAGTLPLDS	0.9958		3	3673.1198
						R.HIGCVAVFYTITGALFLERAYYYAFAAHHSC	0.9958		3	4195.6923
						R.FDGWYNNLMEHRWGSK.G	0.9958		2	2041.2506
114	A2AQA9_MOUSE	6909	1.65	8	12	R.LDAIPIKTAK.A	0.9958		1	1070.3177
						K.SKTIYTAPLDMIQVTQAK.K	0.9958		2	2009.3685

						R.YIPIVGAKHADLVNSELK.Y	0.9958	3	1968.3036
						K.YKEAYEK.A	0.9958	1	931.0331
						K.AYDLQSDAVYK.A	0.9944	1	1273.3849
						K.ERGSCHAVPDTPQILLAK.T	0.9958	1	1993.2365
						K.YQEDFENMK.D	0.9944	1	1204.2965
						R.IDAIPIK.A	0.9944	1	769.9597
115	A2AQE2_MOUSE	1089	5.88	2	2	R.SDPNSESLYFEDEDGFQELSENGNSK.D	0.9929	2	2938.9422
						K.TVPHHMGHSRNPSAASAISFCSVISEPISE\	0.9958	3	3678.0369
116	A2AQJ5_MOUSE	559	8.23	2	2	K.GESVQNALVLAELLSAVK.R	0.9958	2	1842.143
						R.NTTILLKFDGEPCDQSLNITWFLK.S	0.9958	3	2855.2263
117	A2AQN4_MOUSE	714	2.8	1	3	K.IGPIATPDYIQNAPGLPK.T	0.9944	2	1866.1674
118	A2AQP0_MOUSE	1941	2.32	2	8	K.NLTEEMAALDEAVVR.L	0.9929	2	1661.8676
						K.ALEGEKSELQAALEEAEGALELEETK.T	0.9958	3	2789.0197
119	A2AR43_MOUSE	178	11.24	1	14	K.VIIISAEGPVFSSGHDLK.E	0.9926	2	1870.1558
120	A2ARZ2_MOUSE	1025	6.63	4	5	K.EVIFVLSKILGINHFENNVR.N	0.9945	2	2342.7465
						K.LDKEISQMEPSPVSILK.E	0.9944	2	1915.2525
						R.RLNSLVGSLR.S	0.9944	1	1115.3212
						K.THNFLPQGSVLQK.L	0.9937	2	1469.6835
121	A2ARZ3_MOUSE	1737	1.78	2	2	K.KDLPEAEIVSLAIK.F	0.9924	1	1526.8137
						K.EHVSEMPRSSISK.Q	0.9958	1	1487.6709
122	A2AS03_MOUSE	2970	1.41	2	2	K.NNLPR.L	0.9958	1	613.6945
						K.HIPPLLIYGPFGTGKTYTLAMAALEVVQQPH	0.9944	3	3594.2525
123	A2ASI9_MOUSE	494	3.44	1	2	K.LHLTLVHEKLFTFLR.T	0.9944	1	1868.2755
124	A2ASM7_MOUSE	336	14.29	2	2	K.ATPGPEPKGAAEGGGGEGEGPPGEAGAE	0.9944	3	2562.6659
						K.GDPKPGAGGGGGSPCAK.A	0.9958	1	1470.5481
125	A2ASP7_MOUSE	199	22.11	1	2	R.STGTPGQPHFGGPHVAASLFLGTLFISTGL	0.9958	3	4365.0801
126	A2ASP9_MOUSE	1151	3.91	2	2	R.ASCYNSPLGCCSDGKTPSLDSEGSNCPAT	0.9958	3	3222.2645
						R.HACANQEHIFK.K	0.9958	2	1355.4619
127	A2ASQ0_MOUSE	1927	3.27	3	5	R.FLDFDWFPTFFTGAATGTTAAVATARATTV	0.9924	3	3399.7869
						K.EPLYVGGAPDFSK.L	0.9912	1	1380.5401
						R.GHQLLTQEHVLR.A	0.9958	2	1431.6377
128	A2AST1_MOUSE	1451	1.72	1	2	R.LHAALDVSPGLGSQPDTSESHQR.R	0.9958	2	2403.5705
129	A2AT37_MOUSE	1269	1.65	2	8	R.QQEEAAAQLK.E	0.9944	1	1116.2163
						R.FIGELTK.F	0.9944	1	807.9652
130	A2AU04_MOUSE	1091	1.83	1	4	K.LRPIPITASVEIQEPSSR.R	0.9958	2	1994.2987
131	A2AU30_MOUSE	314	2.87	1	2	K.EVIAALR.R	0.9924	1	771.9352
132	A2AUA8_MOUSE	773	7.76	2	2	R.YKGPSGTNIIIGSIAGAVLVAAIVLGGTGWG	0.9958	3	3189.7685

						R.WAIAALLLLPLLPPPGLGALGPR.G	0.9944		3	2320.9132
133	A2AUC9_MOUSE	606	13.53	4	8	K.AGAGEVNGDVGDEDLLPGYLNDIPR.H	0.9958		2	2557.7331
						K.DLQTEASLDSVLCYDPVAAK.W	0.9958		2	2196.3821
						R.LYQSTLLQDGLK.D	0.9958		1	1379.5963
						K.EVALDNVDPAILDLIIK.Y	0.9958		2	1852.1785
134	A2AUE0_MOUSE	160	8.75	1	3	R.SWHDVQVSTAYK.K	0.9958		1	1421.5523
135	A2AUK4_MOUSE	880	6.25	2	2	R.EEHLDAPPGDGTWLELAGAHTENWEPKS	0.9958		3	3543.7441
						K.MIASPEGSETMREEDACLR.G	0.9944		3	2183.3792
136	A2AUM9_MOUSE	1736	2.48	3	3	K.EKQECQDLR.R	0.9958		1	1206.264
						R.ESQQLFQNGKER.E	0.9958		1	1464.5779
						R.SLSAGAAESAGPSCSR.Q	0.9944		1	1508.5511
137	A2AUQ8_MOUSE	332	5.42	1	5	K.KNNIEAVWHDESHLNK.Y	0.9958		2	1935.1063
138	A2AUR7_MOUSE	260	13.85	1	9	R.GFGSLPALEVLDLTYNNLNEHSLPGNFFYL	0.9958		3	3828.3159
139	A2AUY4_MOUSE	2123	2.03	2	2	R.IIHAKK.T	0.9924		1	709.9101
						K.HPLGSVPSATTAQSPVGKTDASLFSSGSG	0.9944		3	3177.418
140	A2AV95_MOUSE	425	3.53	1	3	R.FGCNQQEALLGTR.V	0.993		2	1494.6134
141	A2AVE2_MOUSE	856	1.05	1	3	K.IIDPLAR.G	0.9958		1	797.9731
142	A2AVM0_MOUSE	839	5.01	2	2	K.YSTPEALEHHVQTATHSFPCPHCQKVFPC	0.9958		3	3753.023
						K.KHMQTHK.V	0.9958		1	910.0819
143	A2AWL6_MOUSE	2295	3.79	3	3	K.VEGEVDPEPVYIPTPSVIEPIKPLVLPQPDL	0.9931		3	4071.6978
						R.LTEGEGSEIHSGDFDPVLRGHEASSLSLEK	0.9958		3	3198.4271
						K.TDQGILVTNRDAR.A	0.9924		1	1459.6023
144	A2AWT7_MOUSE	752	1.73	1	2	R.MAGTLLSPAVK.M	0.9944		1	1088.3508
145	A2BE97_MOUSE	113	17.7	1	2	R.YCSMPGQLKPGTGQRAPK.D	0.9958		1	1977.2549
146	A2BH49_MOUSE	253	8.3	1	11	R.LNEQYEHASIHLWDLLEGK.E	0.9958		2	2296.5443
147	A2CFD2_MOUSE	790	6.84	2	3	K.ESEAAHLQHMETDKWNLWGLMLSSGALQ	0.9958		3	3981.536
						K.MENSFQNFTNLLIFQK.L	0.9924		1	1975.2696
148	A2CG35_MOUSE	291	7.56	1	29	R.RPAGGSLGAVSPALSGGQAR.R	0.9958		2	1810.0231
149	A2M_MOUSE	1495	55.72	48	1547	K.APFALQVNTLPLNFDK.A	0.9958		2	1789.0843
						K.IKEEGTGIELTGIGSCEIANALSK.L	0.9958		2	2491.7644
						K.QQNSHGGFSSTQDTVVALQALSK.Y	0.9958		2	2404.5987
						R.KYFPETWIWDLVPLDVSGDGELAVK.V	0.9958		2	2879.2818
						K.RSELLESLNK.D	0.9958		2	1189.3543
						R.IHYLLNEDIMK.N	0.9945		2	1389.6526
						K.AAPLSLCALTAVDQSVLLLKPEAK.L	0.9958	2,3		2509.9556
						R.GSIFNLGSHVLSLEQGNMK.G	0.9958		2	2032.3221
						K.VNTNYRPGLPFSGQVLLVDEK.G	0.9958		2	2347.6763

K.TFHVNSGNR.L	0.9958	1	1032.1038
K.HSLGDNDAHSIFQSVGINIFTNSK.I	0.9958	2,3	2602.8229
K.GSGSGCVYLQTSLK.Y	0.9958	2	1457.5897
K.TVQGAFFGVPVYK.D	0.9958	1	1413.6592
K.LSPQSIYNLLPGK.T	0.9958	2	1430.6873
R.LPDLPGNYVTK.G	0.9949	2	1217.4075
R.TEVNTNHVLIYIEK.L	0.9958	1,2	1673.9066
K.KLQDQPNIQR.T	0.9937	2	1240.4049
K.AINYLISGYQR.Q	0.9958	1,2	1298.4844
K.DAVKEEDSLHWQRPGDVQK.V	0.9958	2	2238.4215
R.NALFCLETAWASISQSQESHVYTK.A	0.9958	3	2772.0094
K.AESPVFVQTDKPIYKPGQIVK.F	0.9958	2	2345.7441
K.THITNAFNWLSMK.Q	0.9958	2	1563.8144
K.MVSGFIPMKPSVK.K	0.9958	1,2	1421.7993
K.VNLSFPSAQSLPASDTHLK.V	0.9958	2	2013.2578
K.AFAQAQSHIFIEK.T	0.9958	2	1490.7019
R.FCQEFQHYPAMGGVAPQALAVAASGPGS	0.9958	2,3	3240.5861
K.EEGTGIELTGIGSCEIANALSK.L	0.9958	2	2250.4309
K.VYDYYETDEFTVEEYSAPFSDGSEQGNA.-	0.9958	3	3214.2459
K.EQTYNTLLCPQDTELQDNWSLELPPNVVE	0.9958	3	3819.0962
R.DLSSSDLSTASK.I	0.9958	1	1211.2683
K.ATVLNYMSHCIQIR.V	0.9958	2	1706.9666
K.TMAFLEEELPITACGVYTYGKPVPGLVTLR.	0.9958	3	3327.8697
K.YFPETWIWDLVPLDVSGDGELAVK.V	0.9958	2	2751.1077
K.LTNQTLGFSFAVEQDIPVK.N	0.9958	2	2108.399
K.DHENCISGEDITHNGIVYTPK.H	0.9958	2	2400.5298
K.LQDQPNIQR.T	0.9958	1	1112.2309
K.LTEVPALVHK.D	0.9958	2	1107.3384
K.GVFSLPIQVEPGMAPEAQLLVYAILPNEEL	0.9958	3	4485.1488
K.TVQGAFFGVPVYKDHENCISGEDITHNGIV	0.9958	3	3795.1658
R.QLNYQHSDGSYSTFGNHGGGNTPGNTWL	0.9958	3	3670.9359
K.KIEHSFEVK.E	0.9904	2	1117.2902
K.YNILPVADGK.A	0.9944	1	1090.2645
R.AMGVPMMGLDYSDEINQVVEVR.E	0.9958	2	2454.8337
R.LLLQEVR.L	0.9958	1	871.0678
R.VDLEISPDFLAVPVGGHENSHCICGNER.K	0.9958	3	3123.3381
R.LLLQEVRLPDLPGNYVTK.G	0.9958	2	2069.4521

						K.EEDSLHWQRPGDVQK.V	0.9958		2	1824.9475
						K.DSFYCSPFTISGSPLPYTFITVEIK.G	0.9958		2	2871.2221
150	A2RS43_MOUSE	1069	3.93	2	2	R.EHQTTYTFRVK.A	0.9958		1	1410.5724
						R.RLGPADSAPYPGGGGNSASGGGSGGSK.I	0.9958		2	2319.4093
151	A2RSX9_MOUSE	341	23.17	4	9	K.HSLPSGLGLSETQITSHGFDSTK.E	0.9958		2	2400.6073
						K.LAQTLSTQLFQMVHTQK.Q	0.9958		2	1975.3135
						K.QLELTLK.Q	0.9958		1	845.0269
						K.NSAAEIPVTSNGEVDDAHEHGYNR.D	0.9958		2	2583.6469
152	A2RT60_MOUSE	483	11.18	2	3	K.IEPDTELPVLLLGR.S	0.9925		2	1565.8504
						K.NSDIDYIQTDAIINHGNSGGPLVNLDGDVIG	0.9944		3	3768.129
153	A2RTH5_MOUSE	332	6.02	1	3	R.FAVSIGYWHDPYIEHLVR.Q	0.9958		2	2203.5077
154	A2RTS7_MOUSE	477	3.98	1	3	K.GGPSSPEVLPTAQEPLK.G	0.9944		2	1707.9213
155	A3KFM7_MOUSE	2711	2.55	4	5	K.SLSAEQGVTDGTSDIPERGNIDK.E	0.9909		2	2390.523
						K.FCEEDIDQILQRR.T	0.9958		2	1722.8615
						K.QETIIEVELTNIQK.K	0.9958		1	1658.8895
						K.LLPKLIAGGHK.V	0.9958		2	1147.4495
156	A3KFU5_MOUSE	631	11.73	6	44	K.VDEAVAVLQAHHAK.K	0.9954		2	1488.6866
						K.AHLTNQYMQR.V	0.9958	1,2		1262.4289
						R.SKVDEAVAVLQAHHAK.K	0.9958		2	1703.9389
						K.GYAFVHFETQEAADK.A	0.9915		2	1713.8437
						K.GFGFVSYEK.H	0.9924		1	1034.1565
						R.IVGSKPLYVALAQR.K	0.9917		2	1515.8393
157	A3KFV3_MOUSE	1058	3.4	1	2	R.GDNSEGEPGCSGSPGLPGPPGMPGQRGI	0.9958		3	3332.5055
158	A3KG33_MOUSE	429	4.2	1	2	K.AQVTSLLGELQESQSR.L	0.9958		2	1746.9151
159	A3KGB4_MOUSE	1114	2.87	2	2	K.FEKSFGLPEQEK.L	0.9958		1	1439.6079
						K.AILQLGLAILDYNLDK.L	0.9924		1	1774.1106
160	A4FU74_MOUSE	430	5.12	1	4	R.EQHVLEELERQAVLVYTPSR.K	0.9958		2	2397.6933
161	A4FUJ6_MOUSE	1337	10.32	5	8	R.VGTETVQAPGSLVISAYAVCPDITATVTPDI	0.9958		3	3752.2226
						R.LNFSTPASTNIVSVCQAAGLR.A	0.9958		2	2207.4577
						R.NPSTVEVFDLAQSNSEHSR.H	0.9924		2	2118.2242
						K.LAHSLFESIMSTQASSNPNNVLK.F	0.9954		2	2489.8059
						R.LGGTALAQCFSQLGEHPPDLDLPENLVR.A	0.9958		3	3049.3765
162	A4UUI3_MOUSE	631	4.44	2	3	K.AASHYSEQMAQR.L	0.9958		2	1379.49
						R.EKIEHDYWQVPR.K	0.9958		2	1600.774
163	A5A9W3_MOUSE	245	9.8	1	2	K.ACPLAVAAAVAAHGASRFSSPR.V	0.9909		2	2168.4295
164	A6H584_MOUSE	1212	2.89	2	5	R.YDVTDAVKVLK.D	0.9958		1	1251.4655
						R.VALAQYSDALHNEFQLGTFK.N	0.9958		2	2253.5193

165	A6H585_MOUSE	1171	3.67	3	4	K.GFPGDPGDPGKDSNIK.G	0.9924	2	1601.7129
						K.DDCRLVELER.G	0.9958	1	1305.3966
						K.KHLLQLLSQIK.Y	0.9958	1	1321.6493
166	A6H588_MOUSE	1162	3.61	2	5	R.NQITHTVSVFSER.T	0.9958	2	1518.6695
						R.MTHIGETTLTGSALTFVSQYFSPDK.G	0.9944	2	2733.065
167	A6H5U8_MOUSE	590	2.03	1	6	R.VLELRELFDK.G	0.9958	1	1262.4918
168	A6H648_MOUSE	997	8.43	3	6	K.EQALGGGLAKGQLEK.E	0.993	2	1499.7074
						K.DAARGALSRPVLEGALGTPR.A	0.9958	2	2008.2882
						R.EQAQELGHLLVQEPGAPGNQGPGLRPEGI	0.9958	3	4565.9819
169	A6H652_MOUSE	845	6.04	3	3	K.TEEAMLNQHSQLQVSSNR.L	0.99	2	2073.2451
						K.LFSNQRK.R	0.9958	1	893.0335
						K.LSNMGTLNSSMQFRSAESVR.S	0.9937	2	2216.492
170	A6H663_MOUSE	577	6.41	1	3	K.AIDVPGQVQVYELQPSNLEAEQPLQEIMGA	0.9958	3	3781.2697
171	A6H6A4_MOUSE	596	2.18	1	2	K.NLEILALDDNK.V	0.9958	1	1258.4142
172	A6H6D4_MOUSE	316	9.81	1	3	K.QLPYCHINILSHSYCLHSDLIQLPCADTR.L	0.9958	3	3526.8721
173	A6H6E2_MOUSE	943	11.45	5	7	R.LGQLWQDVEDQLHAQR.R	0.9952	2	1937.1221
						K.RGVYLFAVSITFGPGPGMGQLVFEGHHR.V	0.9958	3	3031.5077
						K.LQETWDSMDGFELGHPVPEFNEIK.V	0.9929	2	2820.1023
						R.LLHGSFTALLEDALR.H	0.9958	2	1656.9224
						R.TSEHLLQPHIDAFLK.A	0.9958	2	1750.0073
174	A6H6I0_MOUSE	337	4.75	1	2	R.SSGQGVSQMTRGAR.I	0.9944	1,2	1422.559
175	A6PWD2_MOUSE	1420	1.27	1	21	K.EIACDHLIDDLLMAQK.E	0.9952	2	1886.1365
176	A6X935_MOUSE	903	33.22	14	32	K.DLSPQDQFNLIEFSGEANQWK.Q	0.9958	2	2467.6537
						K.SQSEQDTVLNGDFIVR.Y	0.9958	2	1808.9426
						R.MLSLPSVAAQYPADPHLVVTEK.S	0.9958	2	2367.7656
						R.RIYEDSDSALQLQDFYHEVANPLLSSVAFE	0.9958	3	4706.0894
						R.AHGGTNINNAVLLAVELLDR.S	0.9958	2	2091.375
						R.FAHTVVTSR.V	0.9917	1,2	1018.1606
						R.LWALLTIQQQLEQR.I	0.9958	2	1741.0433
						K.VTIGLLSLDDPQR.G	0.9958	2	1427.6408
						K.TLFSVLPGLK.M	0.9944	2	1075.3366
						K.SVSLIILLTDGDPTVGETNPTIIQNNVR.E	0.9958	3	2981.3733
						K.YNFVTPLTHMVVTKPEGQEQFQVAEKPVE	0.9958	3	4091.646
						R.SNQAELLPSKSVSLIILLTDGDPTVGETNPT	0.9958	3	4049.5682
						R.SDSGGSIQIEEGYFVHHFAPENLPTMSK.N	0.9958	2	3079.3674
						R.FKPTLSQQQK.S	0.9932	2	1205.3995
177	A6YR19_MOUSE	780	6.67	2	2	R.QVSSAEVRIGPMR.L	0.9944	1	1430.6653

						R.AWLQVIEANYHSSNAYHNSTHAADVLHAT/	0.9958		3	3886.2773
178	A6ZI44_MOUSE	418	5.26	1	3	K.ESTATGTMPHPYPALTPEQK.K	0.9944		3	2157.4028
179	A6ZI46_MOUSE	419	17.66	3	45	R.VNPCIGGVILFHETLYEK.A	0.9932		2	2090.393
						R.TVPPAVPGVTFLSGGQSEEEASINLNAINK.	0.9958		2	3041.3849
						K.IGKHTPSPLAIMENANVLAR.Y	0.9929		2	2133.5169
180	A6ZI47_MOUSE	364	6.32	1	7	K.YTPSNESGAAASESLFISNHAY.-	0.9958		2	2317.4302
181	A7M7C7_MOUSE	1008	2.58	2	5	K.KEDAGTAAEALGGAGAGSAGAAPK.A	0.9958		2	2029.1711
						K.EDAGTAAEALGGAGAGSAGAAPK.A	0.9952		2	1900.997
182	A7MCT6_MOUSE	385	5.45	2	2	R.YYLEAQK.G	0.9958		1	915.0337
						R.YPARETQVQWLR.Y	0.9958		1	1547.7568
183	A7RDN6_MOUSE	342	21.05	3	6	R.MITASSPHNPR.C	0.9958		2	1211.3813
						K.RNIESSECGPSVVIQTTVPFGVQHLEASEA	0.9958		3	3714.0466
						K.LMIQQLETILPGLPQPVATICHK.W	0.9958	2,3		2602.1169
184	A8C756_MOUSE	1938	2.48	2	2	R.EQPSVTLQQYKNFMSSVCNILFEALFPGSS	0.9958		3	3931.3749
						R.FPELYPFLLK.Q	0.9958		1	1267.5535
185	A8CVP1_MOUSE	362	8.01	2	4	R.CDLCQEVLADIGFVK.N	0.9958		2	1767.949
						K.AMNNSWHPECFR.C	0.9958		2	1549.6697
186	A8DUK2_MOUSE	151	15.89	3	40	K.VNADEVGGEALGR.L	0.9944		1	1287.372
						K.AAVSGLWGK.V	0.9958		1	889.0421
						K.AAVSGLWGKVNADEVGGEALGR.L	0.9958		2	2157.3909
187	A8DUK7_MOUSE	147	10.2	2	431	K.VVAGVAAALAHK.Y	0.9958		2	1107.3414
						K.VVAGVAAALAHKYH.-	0.9958		2	1407.6585
188	A8WIS4_MOUSE	146	10.96	1	2	R.TGFDLMVAFGLVAK.E	0.9958	1,2		1469.7821
189	A8Y5E2_MOUSE	1302	11.06	7	15	K.SEDSIGPEAGCEEEGSSVSGLAK.V	0.9944		2	2296.3265
						R.ERPLCPLQPQNR.D	0.9932		2	1508.6867
						R.FLSHSLVELLNQISPTFK.K	0.9958		2	2074.4277
						K.ASDAFHFFQSGQAK.V	0.9958		2	1541.6628
						K.NRPPGAADNTAWAVMTPQELWK.N	0.9944		2	2454.7655
						R.HKPAFTEEDVLNIFPVVK.H	0.9924		2	2084.4228
						K.GRPNAADLPSVMLLNGDCSENLK.K	0.9947		2	2472.7419
190	A9CR35_MOUSE	2309	8.49	8	9	R.VLYAIVASETSIWDREK.L	0.9924		2	1981.256
						K.GEPGFPGYPGVQGEDGNPGHGGEK.G	0.993		2	2340.4271
						K.GLADRTPCEIVDFVR.G	0.9958		1	1748.9427
						R.MDVDFLQSLGETAIHLSLAKVK.V	0.9936		2	2416.8383
						K.DAVEECLVPVPADLVFLVEDFSSAGQPNF(	0.9958		3	3450.7926
						R.GVQQIAVVIMESPSLDNVSTPASYLR.R	0.9958		3	2776.1773
						R.SRGLSGLLLVSLGGAHK.L	0.9958		2	1665.9767

						R.QGPPGFFGQKGDPGTQGNPGPPGPSGSK	0.9944		2	2651.8546
191	AAAS_MOUSE	546	3.48	1	2	R.GQWINLPVLHLTKDPLK.A	0.9929		2	1973.3689
192	AADAT_MOUSE	425	9.18	2	2	K.AIEREVLLVPGNGFFIDGSAPTSFFR.A	0.9944		3	2841.2389
						R.DSILAAADK.W	0.9924		1	904.008
193	AAK1_MOUSE	959	14.6	7	30	K.FQNPQAEGVNAVEDEIK.K	0.9927		2	1889.0288
						K.AGQTQPNPGILPIQPALTPR.K	0.9958		2	2070.3995
						R.ILSDVTHSAVFGVPASK.S	0.9958		2	1728.986
						R.GHYVLCDFGSATNK.F	0.9958		2	1569.6801
						K.TAVVVPQSQAQPATAPQAAAAQEPGQIQA	0.9958		3	3182.5638
						R.ATVQPLPQAAGPSNQPGLLPSVSQPK.A	0.9958		2	2583.9475
						K.TAVVVPQSQAQPATAPQAAAAQEPGQIQA	0.9958		3	3664.116
194	AAKB1_MOUSE	270	18.89	2	2	R.SQNNFVAILDLPEGEHQYK.F	0.9941		2	2203.4161
						K.FFVDGQWTHDPSEPIVTSQLGTVNNIIQVK.	0.9958		3	3371.7741
195	AAKB2_MOUSE	271	11.81	1	5	K.FFVDGQWVHDPSEPVVTSQLGTINNLIHVK	0.9958		3	3378.8119
196	AAKG1_MOUSE	330	10.91	2	4	K.CYLHETLETIINR.L	0.9907		2	1662.8493
						K.GIVSLSDILQALVLTGGEK.K	0.9958		2	1914.2499
197	AAPK1_MOUSE	548	7.12	2	2	R.NHQDPLAVAYHLIIDNRR.I	0.9944		3	2146.4165
						K.IADFGLSNMMSDGEFLR.T	0.9958		2	1904.1628
198	AAPK2_MOUSE	552	9.6	3	10	K.IGHYVLGDTLGVGTFGK.V	0.9958		2	1734.9927
						R.LFQQILSAVDYCHR.H	0.9958		2	1750.961
						R.SVATLLMHMLQVDPLK.R	0.9943		2	1797.2245
199	AASD1_MOUSE	412	12.86	3	5	R.GAQADHFTESPLSPGSQVQVR.V	0.9958		2	2212.3836
						K.SNLIFLAGNRVLK.W	0.9958		1	1445.7483
						R.SSPAWGGVVTLHR.K	0.9958		2	1367.5503
200	AATC_MOUSE	413	76.51	27	1967	R.TDESQPWVLPVVR.K	0.9958	1,2		1526.7325
						R.FLFPFFDSAYQGFASGDLEK.D	0.9958		2	2287.5329
						R.IVAATLSDPELFK.E	0.9958		1	1404.6464
						K.IANDNSLNHEYLPILGLAEFR.S	0.9958		2	2400.6964
						R.LVLGDNSPAIR.E	0.9958	1,2		1155.3396
						K.NLDYVATSIHEAVTK.I	0.9958		2	1661.8522
						R.VGGVQSLGGTGALR.I	0.9946	1,2		1272.4471
						K.NTPIYVSSPTWENHNAVFSAAGFK.D	0.9958		2	2638.8987
						R.RFLFPFFDSAYQGFASGDLEK.D	0.9956		2	2443.7203
						R.KVNLGVGAYR.T	0.9958		2	1077.2718
						K.HIYLLPSGR.I	0.9958		1	1056.2529
						R.GLDLQGFLNDLENAPEFSIFVLHACAHNPT	0.9958		3	4481.8879
						R.IGADFLGR.W	0.9958		1	848.9774

						R.ITWSNPPAQGAR.I	0.9958		1	1298.4441
						R.WYNGTDNK.N	0.9958		1	998.0397
						R.YFVSEGFELFCAQSFSK.N	0.9958		2	2047.2373
						K.VNLGVGAYRTDESQPWVLPVVR.K	0.9958		2	2456.8069
						K.TPGTWSHITEQIGMFSFTGLNPK.Q	0.9958		2	2550.8915
						K.NFGLYNER.V	0.9958		1	1013.0977
						K.NLDYVATSIHEAVTKIQ.-	0.9958		2	1903.1424
						K.QIAAVMQR.R	0.9958		1	917.1143
						K.VNLGVGAYR.T	0.9958		2	949.0977
						K.QVEYLVNEK.H	0.9958		1	1122.2633
						R.INMCGLTTK.N	0.9958		1	1038.2135
						K.HIYLLPSGRINMCGLTTK.N	0.9929		2	2075.4431
						K.IVRITWSNPPAQGAR.I	0.9958		2	1666.9235
						R.IVAATLSDPELFKEWK.G	0.9958		2	1848.1491
201	AATM_MOUSE	430	82.09	29	1025	K.ASAELALGENNEVLK.S	0.9958		1	1558.7288
						K.NLFAFFDMAYQGFASGDGDK.D	0.9958		2	2202.4022
						R.IAATILTSPDLR.K	0.9958		2	1271.4997
						R.FVTVQTISGTGALR.V	0.9956		2	1450.6781
						K.ILIRPLYSNPPLNGAR.I	0.9958		2	1795.138
						K.TCGFDFSGALEDISK.I	0.9958		1	1647.7449
						K.EYLPIGGLAEFCK.A	0.9958	1,2		1497.6972
						K.KMNLGVGAYR.D	0.9958	1,2		1109.3318
						R.ISVAGVTSGNVGYLAHAIHQVTK.-	0.9944		2	2323.6573
						R.DAGMQLQGYR.Y	0.9958		1	1139.2713
						R.HFIEQGINVCLCQSYAK.N	0.9944		2	2068.2691
						K.EGSSHNWQHITDQIGMFCFTGLKPEQVER	0.9958	2,3		3433.7455
						K.MNLGVGAYRDDNGKPYVLPSVR.K	0.9958	2,3		2422.7643
						R.ASSWWTHVEMGPPDPILGVTEAFK.R	0.9958		3	2657.0155
						R.DDNGKPYVLPSVR.K	0.9958	1,2		1460.6298
						K.MNLGVGAYR.D	0.9944		2	981.1577
						R.TQLVSNLK.K	0.9924		1	903.0666
						K.NMGLYGER.V	0.9958		1	940.0618
						R.KAEAQIAAK.N	0.9924		1	930.0922
						R.IAATILTSPDLRK.Q	0.9944		2	1399.6738
						R.VGAFTVVCK.D	0.9958		2	981.1461
						R.DVFLPKPSWGNHTPIFR.D	0.9917		2	2012.3213
						K.NLDKEYLPIGGLAEFCK.A	0.9958		2	1968.2232

						K.RVESQLK.I	0.9958	1	860.0012
						R.KQWLQEVK.G	0.9944	1	1059.2535
						K.IPEQSVLLLHACAHNPTGVDPRPEQWK.E	0.9958	3	3094.4662
						K.NLFAFFDMAYQGFASGDGDKDAWAVR.H	0.9958	2	2901.1817
						K.KNLFAFFDMAYQGFASGDGDK.D	0.9958	2	2330.5763
						K.KEGSSHNWQHITDQIGMFCFTGLKPEQVE	0.9958	3	3561.9196
202	AB1IP_MOUSE	670	4.03	1	2	K.EYLLEESFCGTSIIVPELEGALYLK.E	0.991	2	2875.2514
203	ABCA1_MOUSE	2261	2.96	3	4	K.LEEIIQLGDAEVSALCGLPRK.K	0.9944	3	2312.6349
						R.ILDGGGQNDILEIK.E	0.9944	1	1485.6775
						K.VAVDGLALNFYEGQITSFLGHNGAGK.T	0.9946	2	2679.9921
204	ABCA3_MOUSE	1704	3.23	2	3	K.LLSCLLSNVAMAMGAQLIGK.F	0.991	2	2091.5416
						R.GELTVVTALFNNQAYHSPATALAIVDNLLFI	0.9958	3	3332.8241
205	ABCA4_MOUSE	2310	4.89	5	5	K.LPAIPISGEALVGFLSGLGQMMNVSGGPVT	0.9958	3	3486.0821
						K.QRAYASLFR.E	0.9924	1	1112.2767
						R.LNITFYENQITAFLGHNGAGK.T	0.9958	3	2309.5865
						R.FWAGVVFPGMYPWASSLPPHVKYK.I	0.9958	3	2766.2781
						R.NEEAQDLSGGMQRK.L	0.9944	1	1563.6825
206	ABCA7_MOUSE	2159	3.24	4	5	K.GWHAMVAFVNRANNGLLHALLPSGPVR.H	0.9944	3	2899.3921
						R.VTKGATQGDVLVLR.D	0.9917	2	1457.7135
						K.FWDPGPSADPFMDLR.Y	0.991	2	1751.9538
						K.KLEAIK.D	0.9958	1	701.8845
207	ABCA9_MOUSE	1623	7.58	6	8	K.LPVEDVRPLSEAFFK.L	0.9958	2	1748.0318
						R.GLGFDIYEGQITALLGHSGAGK.T	0.9958	2	2205.4753
						K.LQDHLK.A	0.9924	1	753.8766
						R.KSLMTVLLLFGISFVPQLLEHLVYK.V	0.9958	3	2890.5836
						K.STTISMITGDTIPTAGQVFLK.G	0.9958	2	2182.5372
						R.TTGAMATLQTDEKPVIIASCLR.K	0.993	2	2377.7248
208	ABCAD_MOUSE	5034	1.31	3	3	K.MSSALNILTWMLNKK.R	0.9949	1	1751.1554
						R.ELCSLPGSQVFSLLVMMGQNLNLRNLIYK.T	0.9958	3	3339.9454
						K.QELDNFLTHVYINVFK.D	0.9958	1	1981.2585
209	ABCB6_MOUSE	842	2.85	1	2	R.SHIGVVPQDTVLFNDTIANNIR.Y	0.9945	2	2424.719
210	ABCC9_MOUSE	1546	2.13	2	4	K.STLDYSTERLK.K	0.9924	1	1313.4503
						R.TFLQASYYVTIETGINLR.G	0.9958	2	2090.3837
211	ABCE1_MOUSE	599	14.86	5	16	K.YDDPPDWQEILTYFR.G	0.9958	2	1959.1217
						K.AIIKPQYVDQIPK.A	0.9958	2	1513.8204
						R.LKPDEGGEVPVLNVSYKPQK.I	0.9943	2	2198.5242
						K.NTVANSPQTLLAGMNK.F	0.9927	2	1659.8981

						K.TQAIVCQQLDLTHLK.E	0.9958	2	1769.0172
212	ABCF3_MOUSE	709	7.48	2	6	R.VPAHISLLHVEQEVAGDDTPALQSVLESDT	0.9958	3	3427.793
						R.NFLNAIATDIIHLHSQR.L	0.9958	2	1964.2345
213	ABCG3_MOUSE	650	7.85	2	2	K.FFDSLTLVASGK.V	0.9924	1	1285.4827
						K.NDCIEVQMRAGLLYLLTIFQCITSVSAGELF	0.9958	3	4047.6315
214	ABEC2_MOUSE	224	47.32	5	130	K.AFEPWEDIQENFLYYEEK.L	0.9952	2	2351.5305
						K.GGQAQATQGYLEDEHAGAHAEEAFFNTILI	0.9958	3	3917.2396
						R.IMKPQDFEYIWQNFVEQEEGESK.A	0.9958	2	2876.1665
						K.ELIDLPPFEIVTGVR.L	0.9958	2	1699.0001
						R.LPVNFFK.F	0.9958	1	865.0629
215	ABHD1_MOUSE	412	14.08	2	4	R.AIFQHSVGLPDLGVLTPEDGK.S	0.9958	2	2194.4924
						R.TKVDAIHTPVLCLNAADDPFSPVHAFPLQA	0.9958	3	3574.0399
216	ABHD5_MOUSE	351	23.65	3	3	K.SYVKTIAILGAGHYVYADQPEEFNQK.V	0.9944	3	2943.2854
						R.SCIDGNSGTSIQSLRPK.S	0.9958	2	1820.9635
						K.AMAAEEEVDSADAGGGSGWLTGWLPTWC	0.9958	3	3778.0639
217	ABHD8_MOUSE	439	8.66	2	2	R.SGSGDPPAALEVELAEPAGGDTR.A	0.9924	2	2197.3202
						R.LVVENLGRAPR.A	0.9924	1	1224.4489
218	ABHDA_MOUSE	297	27.95	4	10	K.TPGIIFIPGYLSNMNGIK.A	0.9958	2	1936.3197
						K.VIALIGIATAADGLVTQYHALPVETQK.E	0.9958	3	2794.2639
						K.EAEHHCLLHSPIPVTCPVR.L	0.9958	2	2253.4981
						R.IVSPDVDVILR.K	0.9958	1	1226.4588
219	ABHDB_MOUSE	307	45.28	6	61	R.QFLLTNLVEVGGR.F	0.9958	2	1446.6897
						R.LVVVDISPVGTTPGSHIGAFIAAMK.A	0.9958	2	2481.9562
						R.EPYSGPTLFLLGGNSTYVQPSHHSEIR.R	0.9958	2,3	2988.2859
						R.SSGQENADLRPLPLSYNLLDGDATLPAIVF	0.9958	3	4028.5541
						R.LNLDTLAQHLDK.I	0.9958	2	1381.5718
						K.AVEIPEKVPHSQAR.K	0.9958	2	1561.7813
220	ABHEB_MOUSE	210	17.14	2	4	K.TPALIVYGDQDPMGSSSFQHLK.Q	0.9931	2	2392.6887
						R.FSVLLLHGIR.F	0.9952	2	1155.4288
221	ABI1_MOUSE	481	12.27	3	5	K.TLEPVKPPTVPNDYMTSPAR.L	0.9958	2	2214.5414
						R.VTGLFPGNYVESIMHYTD.-	0.9958	2	2044.2861
						R.KPIDYTVLDDVGHGVK.W	0.9958	2	1756.9964
222	ABL2_MOUSE	1182	3.13	2	2	R.TVSTSSQPEENVDRANDMLPK.K	0.9944	2	2319.5054
						R.DKSPSSLLEDAK.E	0.9958	1	1290.413
223	ABLM1_MOUSE	861	14.05	7	7	R.DIKNGQALLALDK.Q	0.9958	2	1399.6304
						R.DCLCQLCAQPMSSSPKEASCSSNCAGCG	0.9958	3	3280.3412
						K.DGSPYCEKDYQGLFGVK.C	0.9958	2	1964.1047

						K.DLAAIPKVK.A	0.9958	1	955.1857
						R.TSSESIYSRPGSSIPGSPGHTIYAK.V	0.9944	2	2580.8137
						K.VDNEILDYK.D	0.9944	1	1109.2212
						K.LNSGLGQLILK.E	0.9917	2	1156.4111
224	ACACA_MOUSE	2345	2.81	3	8	R.IPVQAVWAGWGHASENPK.L	0.9958	2	1948.1912
						R.GGSWVVIDPTINPRHMEMYADR.E	0.9944	3	2545.8933
						R.IGSFGPQEDLLFLRASELAR.A	0.9958	2	2220.5333
225	ACAD8_MOUSE	413	17.43	4	12	R.SQYLQFQLADMATK.L	0.9958	2	1644.8829
						R.INVASCSLGAAHASVILTQEHLK.V	0.9958	2	2420.7374
						R.AVIFEDCAVPVANR.I	0.9958	2	1561.7442
						R.VHQILEGSNEVMR.M	0.9958	2	1512.724
226	ACAD9_MOUSE	625	15.2	5	52	R.AYICAHPLDR.A	0.9958	2	1216.3483
						K.GVFPFPEVSQHELSEINQFVGPLEK.F	0.9958	2	2829.1815
						R.VPVENVLGEVGGGFK.V	0.9958	2	1501.7227
						K.YFILNGSK.V	0.9958	1	942.1027
						K.LSSGEHIAAFCLTEPASGSDAASIQTR.A	0.9958	2	2777.9709
227	ACADL_MOUSE	430	73.95	29	2429	K.CIGAIAMTEPGAGSDLQGVR.T	0.9958	2	2004.2318
						R.VQPIYGGTNEIMK.E	0.9958	1,2	1450.6929
						R.AFVDSCLQLHETK.R	0.9958	2	1548.7021
						R.IFSSEHDIFR.E	0.9958	2	1251.3843
						K.FFQEEVIPHHTEWEK.A	0.9958	2	1957.1522
						R.SPAHGISLFLVENGMK.G	0.9958	2	1700.9934
						R.RIFSSEHDIFR.E	0.9958	2	1407.5717
						K.TVAHIQTVQHK.L	0.9958	2	1262.4544
						R.SGSDWILNGSK.V	0.9958	1,2	1164.2603
						R.LPANALLGEENK.G	0.9958	1	1269.4405
						K.GFYYLMQELPQER.L	0.9958	1	1674.9116
						K.QGLLGINIAEK.H	0.9956	2	1156.3677
						K.KLTDVGIR.R	0.9946	1,2	902.0818
						K.AQDTAELFFEDVR.L	0.9958	2	1541.6574
						K.FIPQMTAGK.C	0.9958	1	993.2091
						K.RSGSDWILNGSK.V	0.9958	2	1320.4477
						K.RLDSGSASMAK.Y	0.9958	1,2	1123.2695
						R.KFFQEEVIPHHTEWEK.A	0.9958	2	2085.3263
						K.VFITNGWLSDLVIVVAVTNR.E	0.9958	2	2217.6164
						K.AQDTAELFFEDVRLPANALLGEENK.G	0.993	2	2792.0746
						R.LLIAELAISACEFMFEETR.N	0.9958	2	2244.574

						R.LPANALLGEENKGFYYLMQELPQER.L	0.9958	2,3	2925.3289
						K.LTDVGIR.R	0.9958	1	773.9077
						R.VQPIYGGTNEIMKELIAR.Q	0.9958	2	2033.3935
						R.SAPRPPPSARCSHSGAEAR.L	0.9958	2	1992.1277
						K.THICVTR.A	0.9924	1	886.9927
						R.AFVDSCLQLHETKR.L	0.9958	2	1704.8895
						K.FFQEEVIPHHTEWEKAGEVSR.E	0.9944	2	2556.7966
						K.YWASELQNSVAYECVQLHGGWGYMWEYI	0.9958	3	3738.1336
228	ACADM_MOUSE	421	53.44	19	2171	K.AFAGDIANQLATDAVQIFGGYGFNTEYPVE	0.9958	2	3308.6281
						K.AFTGFIVEADTPGIHIGK.K	0.9958	2	1874.1467
						R.TRPTVAAGAVGLAQR.A	0.9958	2	1468.6993
						K.IYQIYEGTAQIQR.L	0.9958	1,2	1583.7844
						K.QEPGLGFSFELTEQQK.E	0.9958	2	1839.0117
						R.EEIIPVAPEYDK.S	0.9958	1	1403.5719
						K.AFTGFIVEADTPGIHIGKK.E	0.9952	2	2002.3207
						K.FAREEIIPVAPEYDK.S	0.9958	2	1778.0147
						K.LLVEHQGVSFLLAEMAMK.V	0.9949	2	2017.4523
						K.ENVLIGEGAGFK.I	0.9958	1	1234.3947
						K.AAHKQEPGLGFSFELTEQQK.E	0.9958	2	2246.4845
						K.SGEYPFPLIK.R	0.9958	1	1151.3477
						R.AAWEVDSGR.R	0.9958	1	991.0483
						K.ELNMGQR.C	0.9944	1	847.9647
						R.NTYYASIAK.A	0.9958	1	1031.1534
						R.RNTYYASIAK.A	0.9907	2	1187.3409
						K.MWITNGGK.A	0.9958	1	907.0753
						K.ANWYFLLAR.S	0.9958	2	1154.3567
						K.KGDEYVINGQK.M	0.9947	1,2	1251.3818
229	ACADS_MOUSE	412	59.47	17	494	R.IGIASQALGIAQASLDCAVK.Y	0.9958	2	1987.2701
						R.LVIAGHLLR.S	0.9958	2	992.2528
						R.EHLFPTAQVK.K	0.9958	1	1170.3537
						R.LHTVYQSVELPETHQMLR.Q	0.9958	2	2182.5023
						K.IGCFALSEPGNGSDAGAASTTAR.E	0.9958	2	2211.316
						K.GISAFLVPMPTPGLTLGK.K	0.9958	1,2	1800.2097
						K.ELVPIAAQLDREHLFPTAQVK.K	0.9958	2	2376.7611
						K.ELVPIAAQLDR.E	0.9924	1	1225.4307
						K.LADMALALESAR.L	0.9944	1	1261.4791
						R.NAFGAPLTK.L	0.9958	1	919.0684

						R.ITEIYEGTSEIQR.L	0.9958		2	1539.6824
						R.ASSTANLIFEDCR.I	0.9958	1,2		1484.5719
						K.QQWITPFTNGDK.I	0.9958		2	1435.5791
						K.IAMQTLDMGR.I	0.9958	1,2		1136.3698
						K.YAENRNAFGAPLTK.L	0.9958		2	1552.73
						K.AWITNSWEASATVVFASTDR.S	0.9958		2	2213.4112
						R.ACASTGVIMSVNNSLYLGPILK.F	0.9944		2	2309.6924
230	ACADV_MOUSE	656	64.02	31	1090	K.ELGAFGLQVPSELGGLGLSNTQYAR.L	0.9958		2	2578.8846
						R.EATQAVLDKPETLSSDASTR.E	0.9958		2	2120.278
						K.GQLTIDQVFPYPSVLSEEQAQFLK.E	0.9958		2	2739.0973
						K.NPFGNVGLLMGEAGK.Q	0.9958		1	1504.7442
						R.ENMASLQSSPQHQELFR.N	0.9958		2	2003.1968
						R.TGIGSGLSLSGIVHPELSR.S	0.9958	2,3		1881.1393
						K.ASNTSEVYFDGVK.V	0.9958		1	1417.5151
						K.IWISNGGLADIFTVFAK.T	0.9958		2	1853.1711
						R.SGELAVQALDQFATVVEAK.L	0.9958		2	1977.2218
						K.YYTLNGSKIWISNGGLADIFTVFAK.T	0.9944		3	2780.1956
						R.SFGGVTHGLPEK.K	0.9958	1,2		1229.3781
						R.SLSEGYPTAQHEK.M	0.9958		1	1447.5443
						R.IRENMASLQSSPQHQELFR.N	0.9958		2	2272.5437
						R.LAEIVGMHDLGVSVTLGAHQSIGFK.G	0.9919		2	2581.005
						K.MLCDSWCIEAATR.I	0.9958		2	1613.7579
						K.AMVENGGLVTGNPLGI.-	0.9958		1	1542.7906
						K.VPSENVLGEVGDGFK.V	0.9958		1	1547.705
						R.VASGQALAAFCLTEPSSGSDVASIR.S	0.9958		2	2495.7149
						K.ITAFVVER.S	0.9958		1	935.1112
						R.LADGAIDLYAMVVVLSR.A	0.9958		2	1807.1584
						K.NDALEKVEDDTLQGLK.E	0.9958		2	1788.9494
						R.FFEEVNDPAKNDALEK.V	0.9944		2	1867.0221
						K.IHNFGVIQEK.L	0.9958		2	1185.3683
						K.KGIVNEQFLLQR.L	0.9958		2	1445.7049
						K.SFAVGMFK.G	0.9958	1,2		887.0845
						R.SFGGVTHGLPEKK.M	0.9958		2	1357.5522
						R.RTGIGSGLSLSGIVHPELSR.S	0.9912		2	2037.3267
						R.FFEEVNDPAK.N	0.9944		1	1196.3019
						R.TQFGDKIHNFGVIQEK.L	0.9941		2	1862.0953
						K.VEDDTLQGLK.E	0.9958		1	1118.2291

						K.GILLYGTK.A	0.9944		1	865.0605
231	ACBD5_MOUSE	508	6.69	2	4	K.SSDLTSDLGNVLTSSNAK.A	0.9958		2	1809.9249
						K.EEAMIAYVEEMK.K	0.9924		1	1443.6699
232	ACBP_MOUSE	87	43.68	3	355	K.TQPTDEEMLFIYSHFK.Q	0.9924		1	1987.2342
						K.QATVGDVNTDRPGLLDLK.G	0.9958		2	1913.1381
						R.LKTQPTDEEMLFIYSHFK.Q	0.9958		2	2228.5677
233	ACD10_MOUSE	1069	9.35	8	126	K.AEGLWNLFLPLETDPEK.K	0.9958		2	1973.2329
						R.KLYEQLVQFIEQK.V	0.9958		2	1666.9579
						R.TAFGKPLVEQGTILADIAR.S	0.9917		2	2001.3335
						K.GGLVISPEGLSPAVR.K	0.9944	1,2		1452.6939
						K.LYEQLVQFIEQK.V	0.9958		2	1538.7838
						R.WSPSPLIEDLK.E	0.9924	1,2		1285.4827
						K.TMAIPQDALEKYLK.G	0.993		2	1621.9324
						K.AEGLWNLFLPLETDPEKK.Y	0.9958		2	2101.4069
234	ACD11_MOUSE	779	2.57	1	11	R.SLEAYLNQHLPGFGSDSR.A	0.9958		2	1992.1552
235	ACDSB_MOUSE	432	22.69	5	91	R.IFDFQGLQHQVAQVATQLEATR.L	0.9958		2	2501.8045
						K.FAQEHVAPLVSSMDENSK.M	0.9958		2	1990.1951
						K.IGTIYEGASNIQLNTIAK.H	0.9958		2	1907.1741
						K.SSQPEALVSLTNNAVAFAPLQTLTDEEIMM	0.9944		2	3350.8239
						K.KFAQEHVAPLVSSMDENSK.M	0.9958		2	2118.3691
236	ACE_MOUSE	1312	9.83	6	50	R.RQEEAALVSQEFAEVWGK.K	0.9958		2	2078.289
						K.ALLEYFQPVSQWLEEQNQR.N	0.9958		2	2379.6341
						R.NGEVLGWPENQWRPPLPDNYPEGIDLETI	0.9958		3	3680.9659
						R.TLGPANLPLAQR.Q	0.9958		2	1251.4715
						K.QVLQAGCSRPWQEVLK.D	0.9958		2	1900.154
						K.EAGHQGPLHQCDIYQSAQAGAK.L	0.9958		2	2367.5059
237	ACET_MOUSE	732	6.15	2	4	R.HGETLGWPEYNWAPNTAR.A	0.9958		2	2100.2572
						R.EGANPGFHEAIGDIMALSVSTPK.H	0.9958		2	2342.6288
238	ACHA4_MOUSE	629	3.82	1	2	R.LFSGYNKWSRPVANISDVVLVR.F	0.9956		2	2521.9248
239	ACINU_MOUSE	1338	1.57	1	6	K.LPEYSQTAEEEEDQETPSR.N	0.9958		2	2239.2677
240	ACK1_MOUSE	1055	6.07	3	15	R.YAVQVAEGMAYLESKR.F	0.993		2	1816.082
						K.MVTELAPLGSLLDRLR.K	0.9945		2	1785.1553
						R.QLQVPTGQLTPSPTPGGDDKPQVPPR.V	0.9958		3	2712.0348
241	ACL6A_MOUSE	429	15.62	3	19	R.STGLILDSGATHTTAIPVHDGYVLQQGIVK.S	0.9958		3	3093.5071
						K.SEASLHPVLMSEAPWNTR.A	0.9958		2	2026.2744
						K.VDFPTAIGVVLER.D	0.9958		2	1416.6604
242	ACLY_MOUSE	1091	8.34	5	13	K.LGLVGVNLSLDGVK.S	0.9929		2	1384.6591

						R.SFDELGEIIQSVYEDLVAK.G	0.9958		2	2156.3942
						K.QHFPATPLLDYALEVEK.I	0.9958		2	1972.2481
						K.GVTIIGPATVGGIKPGCFK.I	0.9958		2	1873.2121
						R.YPGSTFMDHVLR.Y	0.9958		2	1423.6293
243	ACM2_MOUSE	466	9.44	2	2	K.QNIVARK.I	0.9958		1	828.9901
						K.TFEVVFIVLVAGSLSLVTIIGNILVMVSIKVNF	0.9958		3	3546.3765
244	ACMSD_MOUSE	336	20.83	2	2	K.YWLPWLVGMPSETTMAICSMIMGGVFEKF	0.9958		3	3609.3209
						R.CVKALGFPGIQIGSHINTWDLNDPELFPIYA	0.9958		3	3915.4064
245	ACO10_MOUSE	439	11.39	3	4	K.LLHSFLPK.S	0.9952		2	955.1881
						K.RPAFVNPLIPENKEEEELFTQGELNK.S	0.9912		3	3043.4033
						K.HSLSPEQDIK.F	0.9958		2	1154.2651
246	ACO11_MOUSE	594	2.86	1	3	R.SVTLPTHHETPEYQR.G	0.9958		2	1795.9493
247	ACON_MOUSE	780	77.05	48	9236	K.DINQEVYNFLATAGAK.Y	0.9958		2	1754.9371
						R.DVGGIVLANACGPCIGQWDR.K	0.9958		2	2159.3387
						R.WVVIGDENYGEGSSR.E	0.9958	1,2		1668.76
						K.QGLLPLTFADPSDYNK.I	0.9958		2	1779.9873
						K.DLEDLQILIK.V	0.9945		2	1200.4179
						R.NAVTQEFGPVPDTAR.Y	0.9958		1	1602.7441
						K.SQFTITPGSEQIR.A	0.9958	1,2		1464.6182
						K.FNPETDFLTGK.D	0.9958		1	1269.3965
						K.IVYGHLDDPANQEIER.G	0.9958		1	1870.0287
						R.GHLDNISNNLLIGAINIENGK.A	0.9958		2	2220.4905
						R.LQLLEPFDKWDGK.D	0.9958		2	1589.8315
						R.NDANPETHAFVTSPEIVTALAIAGTLK.F	0.9958	2,3		2782.1229
						K.FKLEAPDADELPR.S	0.9958		2	1501.6793
						K.CTTDHISAAGPWLK.F	0.9958		3	1557.7124
						K.VAMSHFEPSEYIR.Y	0.9944		2	1566.7717
						K.DFAPGKPLK.C	0.9958		1	973.1601
						K.KQGLLPLTFADPSDYNK.I	0.9958	1,2		1908.1613
						R.IHETNLK.K	0.9958		1	854.9817
						R.NFTGRNDANPETHAFVTSPEIVTALAIAGTL	0.9958		3	3357.7477
						K.VAVPSTIHCDHLIEAQVGGEK.D	0.9958	2,3		2261.5059
						R.LNRPLTLSEK.I	0.9958		2	1171.3824
						K.HPNGTQETILLNHTFNETQIEWFR.A	0.9958		3	2927.2053
						R.TDIANLAEEFK.D	0.9958		1	1251.3788
						K.LTGSLSGWTSPK.D	0.9958		1	1234.3947
						R.EHAALEPR.H	0.9944		1	923.0165

						R.VAMQDATAQMAMLQFISSGLPK.V	0.9958		2	2339.7885
						K.QALAHGLK.C	0.9958		1	837.9975
						R.VGLIGSCTNSSYEDMGR.S	0.9958	1,2		1846.9728
						R.DGYAQILR.D	0.9958		1	936.0556
						K.LEAPDADELPR.S	0.9958		1	1226.3287
						R.VDVSPTSQR.L	0.994		2	989.0733
						R.SDFDPGQDTYQHPPK.D	0.9944		2	1732.8034
						K.GGTGAIVEYHGPGVDSISCTGMATICNMG/	0.9944		3	4558.9707
						K.GKCTTDHISAAGPWLK.F	0.9958		2	1742.9384
						K.NTIVTSYNR.N	0.9958		1	1068.1747
						R.ATIERDGYAQILR.D	0.9958		2	1506.7019
						R.LQLLEPFDK.W	0.9958		1	1103.3037
						R.DVGGIVLANACGPCIGQWDRK.D	0.9958		2	2287.5127
						K.NINIVR.K	0.9944		1	728.8698
						K.DHLVPDPGCQYDQVIEINLNELKPHINGPF	0.9944		3	5175.7296
						K.ANSVRNAVTQEFGPVPDTAR.Y	0.9958		2	2130.3249
						K.IHPVDK.L	0.9958		1	708.8357
						K.VAGILTVK.G	0.9958		2	801.0171
						R.GHLDNISNNLLIGAINIENGKANSVR.N	0.9958		2	2748.0714
						K.VAVPSTIHCDHLIEAQVGGEKDLR.R	0.9958		2	2645.9415
						R.SDFDPGQDTYQHPPKDSSGQR.V	0.9944	2,3		2363.4185
						R.AKDINQEVYNFLATAGAK.Y	0.9958		2	1954.19
						R.WVVIGDENYGEGSSREHAALEPR.H	0.9958		3	2572.7532
248	ACOT1_MOUSE	419	33.65	9	141	R.HFLAPGVR.R	0.9958		1	897.0677
						R.SCWDEPLSIAVR.G	0.9958		2	1433.5701
						K.GITAAVVINGSVAAVGNTISYK.D	0.9958		2	2106.427
						R.SDTTFLFLVGQDDHNWK.S	0.9958		2	2024.1968
						R.GLAPEQPVTLR.S	0.9958		2	1181.3775
						K.GPGIGLLGISK.G	0.9944		2	1012.2376
						R.ATLFLPPEPGPFPGIIDLFGVGGGLLEYR.A	0.9944		3	3044.5633
						R.LAHAVHER.H	0.9944		1	933.0579
						K.GITAAVVINGSVAAVGNTISYKDETIPPVTIL	0.9958		3	3341.873
249	ACOT2_MOUSE	453	25.83	7	225	K.DGLLDVVEALQSPLVDK.K	0.9958		3	1812.0703
						R.DVQTPFLVELEVLDGHEPDGGQR.L	0.9958		2	2551.7722
						K.SIETMHMEYFEEAVNYLR.S	0.9958		2	2263.5447
						R.AHAVAQVDAWQQLQTFFHK.Q	0.9958		2	2226.5021
						R.APALGGSFSGLEPMGLLWAMEPERPLWR.	0.9958		3	3070.5971

						K.DGLLDVVEALQSPLVDKK.S	0.9958		2	1940.2444
						K.RDVQTPFLVELEVLDGHEPDGGQR.L	0.9958		3	2707.9597
250	ACOT8_MOUSE	320	14.37	2	2	K.VNFMASLDHSMWFHAPFR.A	0.9958		3	2194.536
						R.DGVLAVTCAQEGVIRLKPQVSESK.L	0.9929		2	2585.9268
251	ACOT9_MOUSE	439	11.62	3	18	R.NIIHELFLTTLDPK.T	0.9958		2	1654.9469
						K.GPAFVNPLIPENKEEEELFK.Q	0.9958		2	2301.6012
						K.ISEPLHIHQVR.D	0.9958		2	1329.5448
252	ACOX1_MOUSE	661	26.02	9	39	R.GECYGLHAFVVPIR.E	0.9958		2	1618.8419
						K.TSNHAIVLAQLITR.G	0.9958		2	1537.8026
						R.ILELLTVTRPNAVALVDAFDFK.D	0.9958		2	2446.8925
						R.INESIGQGDLSELPELHALTAGLK.A	0.9958		2	2506.8156
						R.EIENLILNDPDFQHEDYNFLTR.S	0.9958		2	2736.9543
						R.ASEAHCHYVTVK.V	0.9958		2	1402.5157
						R.EIGTHKPLPGITVGDIGPK.F	0.9958		2	1930.2547
						R.YDGNVYENLFEWAK.K	0.9958		2	1748.8889
						K.YAQVKPDGTYVKPLSNK.L	0.9958		3	1909.1925
253	ACOX2_MOUSE	681	10.43	3	4	R.LRPSDPEAKILEYQTQQQK.L	0.9958		3	2273.551
						R.LTNILDGGIPNTELRR.R	0.9958		2	1783.0378
						R.SGVDQYDAWNQTSVIHLQAAKAHCYFLTV	0.9958		3	3480.8303
254	ACOX3_MOUSE	700	6.57	2	2	R.TTAHYDPDTQEFILHSPDFEAAK.F	0.9929		2	2634.8181
						R.EIHALASAGKPLASWTAQR.G	0.9958		2	2008.2877
255	ACPM_MOUSE	156	27.56	5	135	K.LMCPQEIVDYIADKK.D	0.9958		1	1824.1085
						K.LMCPQEIVDYIADK.K	0.9958	1,2		1695.9344
						K.LSVNSHFMK.D	0.9912		2	1063.2597
						K.LYDKIDPEK.L	0.9958		1	1121.2756
						R.VLYVLK.L	0.9944		1	734.9573
256	ACS2L_MOUSE	682	47.36	17	170	R.GQDLGDTTTLEDPSVITEILSAFQK.Y	0.9958		2	2679.9379
						R.AYPGYYFTGDGAHR.T	0.9958		1	1575.6799
						R.TLGSVGEPINHEAWEWLHK.V	0.9958		2	2204.4496
						K.SPETIALIWER.D	0.9958		2	1315.5119
						R.LGTAEIEDAMADHPAVPETAVIGYPHDIK.G	0.9958		3	3062.4211
						K.SCPTVQHVLVAHR.T	0.9958	1,2		1504.6983
						R.DTLVWDTPYHTVWDCDFR.T	0.9958		2	2327.4804
						R.LPGCVPAAAQPGSYPALSAQAAQEPAAFV	0.9958		2	3422.834
						K.GNVLEGGDVSGALCISQAWPGMAR.T	0.9958		2	2446.7064
						K.VPMGSLDIPLEQEMAK.E	0.9958		2	1759.0859
						K.GEAAFAFIVLK.D	0.9958	1,2		1166.4057

						K.SPETIALIWERDEPGTEVR.I	0.9958		2	2199.4252
						R.IGAIHTVVFAGFSAESLAGR.I	0.9958		2	2004.2963
						K.IVDEAVKSCPTVQHVLVAHR.T	0.9958		3	2259.5798
						K.DNISDENMVVNELK.L	0.9958		1	1620.7717
						R.MDDVINISGHR.L	0.9958		1	1257.4069
						K.EAPVCTPESMSSEDMLFMLYTSGSTGTPK	0.9958		2	3155.4968
257	ACSF2_MOUSE	615	24.39	7	27	K.GTLLYGTPTMFVDILNQPDFSSYDFTSIR.G	0.9958		3	3300.7071
						R.FLSCYDPINIQFTSGTTGNPK.G	0.9958		2	2361.5793
						R.GGENIYPAELEDFFLK.H	0.9958		2	1843.0429
						R.GGVIAGSPAPPELIR.A	0.9958		2	1434.6787
						K.GATLSHHNIVNNSMLIGQR.L	0.9958		2	2063.3421
						K.HPQVQEAQVVGVK.D	0.9924	1,2		1419.6237
						R.IMPHTEAQIVNVETGELTNLNVPGELYIR.G	0.9924		2	3252.71
258	ACSF3_MOUSE	583	20.58	6	12	R.VTAVVALQEGHSLSHGDLK.E	0.9958		2	1962.2132
						R.VPGSVGTPLPGVEVR.I	0.9958		2	1464.7049
						R.NQMGKVNK.K	0.9958		1	919.0868
						R.GAMIFYTSGTTGRPKGALSTHR.N	0.9958		2	2310.636
						R.GHSLLPTTPEAHTDGSVPVFIR.A	0.9958		2	2332.6213
						R.HLLAHPSITDVAVIGVPDMTWGQR.V	0.9958		2	2615.0251
259	ACSL1_MOUSE	699	43.06	20	476	K.GIAVHPELFSIDNGLLTPTLK.A	0.9958		3	2236.6164
						R.KPNQPYEWISYK.E	0.9958		2	1553.7575
						K.EAGLKPFEQVK.G	0.9958		1	1246.449
						K.ALKPPCDLSMQSVEIAGTTDGIR.R	0.9958		2	2460.7712
						K.GAMITHQNIINDCSGFIK.A	0.9958		2	2020.277
						R.SQIDELYATIK.I	0.9924		1	1281.4485
						K.RGLQGSFEELCR.N	0.9958		2	1452.5761
						R.SAVLEDDKLLVYYYDDVR.T	0.9958		2	2177.4155
						K.LVDVEEMNYLASK.G	0.9958		2	1511.7302
						K.AILDDLLK.L	0.9958		1	901.0911
						R.LMITGAAPVSATVLTFLR.T	0.9958		2	1862.2811
						R.GIQVSNNGPCLGSR.K	0.9925		2	1459.5682
						K.VLQPTIFPVVPR.L	0.9958		2	1366.6897
						R.VKPKPPEPEDLAIICFTSGTTGNPK.G	0.9958		3	2698.0546
						K.DGWLHTGDIGK.W	0.9958		1	1199.3085
						K.EVAELAECIGSGLIQK.G	0.9958		1	1717.9232
						R.GLQGSFEELCR.N	0.9958		1	1296.3887
						R.TAEALDKDGWLHTGDIGK.W	0.9958	1,2		1928.1088

						K.IIVIMDSYGSDLVER.G	0.9958	2	1710.9831
						K.RWLLDFASK.R	0.9931	2	1136.339
260	ACSL5_MOUSE	683	2.05	1	17	R.KPNQPYKWISYK.Q	0.9958	1,2	1552.8161
261	ACSM2_MOUSE	575	4.87	2	16	K.VLQEHVKSVTAPYK.Y	0.9917	2	1599.8705
						R.KVEFVLDLPK.T	0.9927	1	1188.4527
262	ACSM5_MOUSE	578	3.63	1	2	K.AFIVLSPAYASHDPEALTR.E	0.9958	2	2059.3293
263	ACTA_MOUSE	377	70.29	20	2592	K.DLYANNVLSGGTTMYPGIADR.M	0.9958	2	2229.4693
						K.SYELPDGQVITIGNER.F	0.9958	1,2	1791.9555
						K.EITALAPSTMK.I	0.9958	1	1162.3869
						R.DLTDYLMK.I	0.9958	1	999.167
						K.QEYDEAGPSIVHR.K	0.9958	2	1501.5956
						R.KDLYANNVLSGGTTMYPGIADR.M	0.9917	2	2357.6434
						R.VAPEEHPTLLTEAPLNPK.A	0.9958	2	1957.234
						K.YPIEHGIITNWDDMEK.I	0.9943	2	1962.1841
						R.CPETLFQPSFIGMESAGIHETTYNSIMK.C	0.9958	3	3190.576
						R.TTGIVLDSGDGVTHNVPIYEGYALPHAIMR.	0.9958	2,3	3198.6208
						R.HQGVMVGMGQK.D	0.9958	1	1172.4058
						R.GYSFVTTAER.E	0.9958	1,2	1131.2303
						K.LCYVALDFENEMATAASSSSLEK.S	0.9958	2	2537.764
						R.AVFPSIVGRPR.H	0.9958	2	1199.4416
						K.EKLCYVALDFENEMATAASSSSLEK.S	0.9958	2	2795.0536
						K.CDIDIRK.D	0.9958	1	920.0197
						K.DSYVGDEAQSK.R	0.9958	1	1199.2163
						K.IWHHSFYNELR.V	0.9958	1	1502.675
						R.FRCPETLFQPSFIGMESAGIHETTYNSIMK.	0.9958	3	3493.94
						R.HQGVMVGMGQKDSYVGDEAQSK.R	0.9944	2	2352.5989
264	ACTB_MOUSE	375	40.8	9	680	R.VAPEEHPVLLTEAPLNPK.A	0.9958	1	1955.2615
						K.DLYANTVLSGGTTMYPGIADR.M	0.9958	2	2216.4706
						R.KDLYANTVLSGGTTMYPGIADR.M	0.9958	2	2344.6447
						K.IWHHTFYNELR.V	0.9958	1,2	1516.7019
						K.LCYVALDFEQEMATAASSSSLEK.S	0.9958	2	2551.7909
						R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	0.9958	2	3233.6103
						K.YPIEHGIVTNWDDMEK.I	0.9958	2	1948.1572
						K.QEYDESGPSIVHR.K	0.9958	2	1517.595
						R.GYSFTTTAER.E	0.9958	2	1133.2029
265	ACTBL_MOUSE	376	15.69	3	70	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.	0.9958	2	3185.6221
						K.IWYHTFYNELR.V	0.9958	2	1542.7367

						R.GIHETTFNSIMK.C	0.9958	2	1378.586
266	ACTN1_MOUSE	892	16.82	9	26	R.LSNRPAFMPSEGR.M	0.9958	2	1462.6665
						K.TFTAWCNSHLR.K	0.9958	2	1393.5108
						R.VGWEQLLTTIAR.T	0.9958	2	1387.6219
						K.CQLEINFNTLQTK.L	0.9954	2	1609.7857
						R.AAPFNNWMEGAMEDLQDTFIVHTIEEIQGL	0.9912	3	4364.8477
						R.DLLLDPAWEK.Q	0.9958	1	1200.377
						K.KHEAFESDLAAHQDR.V	0.9958	2	1754.8564
						K.HTNYNMEHIR.V	0.9958	2	1315.4491
						R.VPENTMHAMQQK.L	0.9958	2	1414.6374
267	ACTN2_MOUSE	894	12.53	7	20	R.NVNIQNFHTSWK.D	0.9912	2	1488.6457
						R.ETADTDTAEQVIASFR.I	0.9958	2	1754.848
						R.ILASDKPYILAEELR.R	0.9958	2	1732.03
						R.SSIQITGALEDQMNQLK.Q	0.9958	2	1877.1199
						R.ISSSNPYSTVTMDELR.N	0.9958	2	1800.9782
						K.LLETIDQLHLEFAK.R	0.9958	2	1670.9463
						K.HTNYTMEHIR.V	0.9958	2	1302.4503
268	ACTN4_MOUSE	912	30.26	14	36	K.MLDAEDIVNTARPDEK.A	0.9958	2	1818.0087
						R.SIVDYKPSLDLLEQQHQLIQEALIFDNK.H	0.9958	3	3299.7484
						K.DDPVTNLNNAFEVAEK.Y	0.9958	2	1776.8975
						K.LSGSNPYTTVTPQIINSK.W	0.9958	2	1921.1577
						K.NVNVQNFHISWK.D	0.9958	2	1486.6731
						R.ETTDTDTADQVIASFK.V	0.9958	2	1742.834
						R.HRPELIEYDK.L	0.9957	2	1300.4569
						K.ICDQWDNLGSLTHSR.R	0.9958	2	1802.9073
						R.EAILAIHK.E	0.9924	1	895.0898
						R.AAPFNNWMESAMEDLQDMFIVHTIEEIEGL	0.9958	3	4409.9468
						K.VLAVNQENEHLMEDYER.L	0.9958	2	2090.272
						R.VEQIAAIAQELNELDYYDSHNVNTR.C	0.9958	2	2907.1229
						K.DHGGALGPEEFK.A	0.9958	1	1257.3452
						R.MVSDINNGWQHLEQAEK.G	0.9958	2	2000.1932
269	ACTS_MOUSE	377	6.37	2	32	R.KDLYANNVMSGGTTMYPGIADR.M	0.9946	2	2375.6765
						K.DLYANNVMSGGTTMYPGIADR.M	0.9958	2	2247.5025
270	ACTY_MOUSE	376	11.17	3	10	R.TLFSNIVLSGGSTLFK.G	0.9958	2	1684.9732
						K.YCFPNYVGRPK.H	0.9958	2	1401.5737
						R.YPMEHGVVR.D	0.9958	1	1088.2695
271	ACTZ_MOUSE	376	19.41	3	8	K.AQYYLPDGSTIEIGPSR.F	0.9958	2	1868.0532

						K.DQLQTFSEEHPVLLTEAPLNPR.K	0.9958		2	2535.8162
						R.FRAPELLFRPDLIGEESEGIHEVLVFAIQK.S	0.9958		3	3454.9939
272	ACY1_MOUSE	408	33.09	8	17	R.AGFALDEGLANPTDAFTVFYSER.S	0.9944		2	2492.7039
						R.TIHMTFVPDEEVGGHK.G	0.9958		2	1798.0234
						K.RPEFQALR.A	0.9949		2	1017.1759
						R.VTSTGKPGHASR.F	0.9958		2	1198.3243
						R.MTPTDDSDPWWAAFSGACK.A	0.9958		2	2144.2857
						R.ICTVQPNPDYGGAITFLEER.A	0.9958		2	2281.4932
						R.TPVLLHDHNER.L	0.9958		2	1331.474
						K.EHWHHDPFEAFK.D	0.9958		2	1580.7019
273	ACY2_MOUSE	312	5.77	1	2	K.YPVGIEVGPQPHGVLR.A	0.9958		2	1718.9963
274	ACY3_MOUSE	318	30.19	4	17	R.TADGDLAGTVHPQLQDHDFEPLRPGEPIFI	0.9958		3	3302.6274
						R.SCTLTFLGSTATPDDPYEVK.R	0.9958		2	2203.3735
						R.LFLYEPAGTETFSVESISK.N	0.9958		2	2119.3759
						R.VAVTGGTHGNEMCGVYLAR.Y	0.9958		2	1993.211
275	ACYP1_MOUSE	99	43.43	3	12	K.VIANLDYSDFQIVK.-	0.9958		2	1625.862
						K.KLGLVGWVQNTDR.G	0.9958		2	1486.7141
						R.GTVQGQLQGPVSK.V	0.9958	1,2		1299.4697
276	ACYP2_MOUSE	97	45.36	3	31	K.SVDYEVFGTVQGVCFR.M	0.9958		2	1864.0307
						K.GTVTGQVQGPEEK.V	0.9958		1	1330.4374
						K.LEYSDFSIR.Y	0.9945		2	1130.2426
277	ADA10_MOUSE	749	2.8	1	5	K.SLNTGIITVQNYGSHVPPK.V	0.9958		2	2026.2999
278	ADA22_MOUSE	904	5.09	2	2	K.YIELMIVNDHLMFK.K	0.9947		2	1767.1543
						R.QFEFPLDDLPSEFQRVNITPPQFILKPR.L	0.9958		3	3373.8791
279	ADA28_MOUSE	793	4.29	2	2	K.LDAHVALVGVEIWTDGDK.I	0.9958		2	1939.1754
						K.VCINAECVDMEK.T	0.9944		1	1468.5942
280	ADAS_MOUSE	645	4.03	2	2	R.AASAAGASPAATPAAPESGTIPK.K	0.9958		2	1995.1967
						R.RAASAAGASPAATPAAPESGTIPK.K	0.9958		2	2151.3842
281	ADCK1_MOUSE	525	9.33	2	2	K.VGQHLGALDYLLPEEYTSTLK.V	0.9958		2	2348.658
						K.EIHDLFLSFDDTPLGAASLAQVHK.A	0.9958		3	2625.9408
282	ADCK3_MOUSE	645	26.51	10	680	K.LTQAAVETHLQNLGLGGELLLAAR.A	0.9958	2,3		2489.8778
						R.LANFGGLAVGLGIGALAEVAK.K	0.9952		2	1942.3091
						R.ALQSTAVEQFSMVFGK.V	0.9958		2	1744.0155
						R.DKLEYFEERPFAAASIGQVHLAR.M	0.9958	2,3		2648.9811
						R.GAALKLGQMLSIQDDAFINPHLAK.I	0.9915		2	2552.9946
						K.LGQMLSIQDDAFINPHLAK.I	0.9958		2	2112.4516
						K.AVLDSSPFLSEANAER.I	0.9957		2	1706.8498

						K.TLNSDLGPHWR.D	0.9958	2	1296.4282
						K.IHNLIPVMLK.H	0.9958	1	1178.5218
						K.AMFEEAYSNYCR.M	0.9958	1	1541.6411
283	ADCL1_MOUSE	408	14.71	3	13	R.LVPQVYFPEQIHDVIR.A	0.9931	2	1954.2792
						R.IVQEIPQLLDAAASPLIAEQEVLEALPK.T	0.9958	2	3000.5029
						K.TYILTCEHDVLR.D	0.9958	2	1520.6917
284	ADCY3_MOUSE	1145	4.28	2	2	R.VHISQSTMDCLK.G	0.9924	2	1419.602
						K.EPNGSAHASGSTSEEAEEQEAQADNPSFF	0.9958	3	3498.5309
285	ADCY6_MOUSE	1165	4.81	2	3	K.TIGSTYMAASGLNASTYDQVGRSHITALAD	0.9944	3	3594.996
						R.GAQDALNPEDEVDEFLGR.A	0.9958	2	1976.0636
286	ADCY8_MOUSE	1249	3.2	3	3	K.EEINEMK.E	0.9958	1	892.9996
						K.GILLGFFTGIEVVICALVVVRK.D	0.9924	3	2404.9513
						R.IHISK.A	0.9924	1	597.7355
287	ADCYA_MOUSE	1614	3.22	2	2	K.KLAQLYLQASCFSLLWR.I	0.9944	3	2098.4619
						R.MMMYYPGIVSCDSVTYDGSNLPAYFFKELI	0.9944	3	3626.1571
288	ADDA_MOUSE	735	12.65	5	12	K.EYQPHVIVSTTGPNPFNTLTDR.E	0.9958	2	2487.7313
						K.TAGPQSQVLCGVMMDR.S	0.9958	2	1750.9918
						K.SPPDQSAVPNTPPSTPVK.L	0.9958	2	1820.0092
						K.SPPDQSAVPNTPPSTPVKLEEDLPQEPTSF	0.9958	3	3215.498
						K.CIVHIHTPAGAAVSAMK.C	0.9958	2	1764.0619
289	ADDB_MOUSE	725	6.9	3	4	K.SAGPQSQLLASVIAEK.S	0.9915	2	1599.8247
						R.VNVADEVQRNMGSPRPK.T	0.9958	2	1898.1473
						R.LGEHEFEALMR.M	0.9949	2	1332.5169
290	ADDG_MOUSE	706	7.51	3	3	K.IEDPNQFVPLNTNPTEVLEK.R	0.9958	2	2298.5548
						R.YFDRINESDPEYLR.E	0.9944	2	1817.9524
						R.TEEVLSPDGSPSK.S	0.9958	1	1346.4338
291	ADFP_MOUSE	425	4.94	1	11	K.SQETISQLHSTVHLIEFAR.K	0.9944	2	2197.4557
292	ADH1_MOUSE	375	31.2	6	18	K.AAVLWELHKPFTIEDIEVAPPK.A	0.9952	2,3	2504.9317
						K.VIPLFSPQCGECR.I	0.9937	2	1563.726
						K.VCLIGCGFSTGYGSAVK.V	0.9958	2	1776.9594
						R.SDDHVVSGTLVTPLPAVLGHEGAGIVESVC	0.9958	3	4085.5237
						K.FPLDPLITHVLPFEK.I	0.9958	2	1767.121
						K.KFPLDPLITHVLPFEK.I	0.9924	2	1895.2951
293	ADHX_MOUSE	374	58.56	10	137	K.VDEFVTGNLSFDQINQAFDLMHSGDSIR.T	0.9958	3	3157.4382
						K.AAVAWEAGKPLSIEEIEVAPPK.A	0.9958	2	2306.6641
						K.EFGASECISPQDFSK.S	0.9958	2	1702.7809
						K.VEPGSTCAVFGLGGVGLAVIMGCKVAGAS	0.9944	3	2922.3449

						K.VCLLGCGISTGYGAAVNTAK.V	0.9958		2	2013.2306
						K.ILATAVCHTDAYTLSGADPEGCFPVILGHE(	0.9958		3	4500.9357
						K.VEPGSTCAVFGLGGVGLAVIMGCK.V	0.9958		2	2380.7371
						K.AGDTVIPLYIPQCGECK.F	0.9958		2	1922.1176
						K.FCLNPK.T	0.9958		1	778.8926
						K.SIQEVLVEMTDGGVDYSFECIGNVK.V	0.9958		2	2791.0652
294	ADIPO_MOUSE	247	12.55	2	25	K.IFYNQQNHYDGSTGK.F	0.9958		2	1772.8711
						K.AVLFTYDQYQEK.N	0.9944	1,2		1505.6672
295	ADK_MOUSE	361	61.22	16	135	R.AGHYAASVIIR.R	0.9952		2	1158.3457
						K.YSLKPNDQILAEDK.H	0.9958		2	1634.8266
						K.VEAPQALSENVLFGMGNPLLDISAVVDKDF	0.9958		3	3547.0577
						K.VAQWLIQEPHK.A	0.9958		1	1349.5754
						R.RTGCTFPEKPDFH.-	0.9958		2	1592.7173
						K.ELFDELVK.K	0.9958		1	993.1449
						R.SLVANLAAANCYK.K	0.9958		2	1395.5646
						K.VEAPQALSENVLFGMGNPLLDISAVVDK.D	0.9944		2	2928.3704
						K.EALMDVMPYVDILFGNETEAATFAR.E	0.9921		2	2805.1898
						R.VFTLNLSAPFISQFFK.E	0.9958	1,2		1860.2059
						R.VYYIAGFFLTVSPESVLK.V	0.9958		2	2034.4027
						R.TGCTFPEKPDFH.-	0.9944		2	1436.5298
						K.VEYHAGGSTQNSMK.V	0.9958		2	1509.6336
						K.LKVEAPQALSENVLFGMGNPLLDISAVVDK	0.9958		3	3169.7039
						K.AADAHVDAHYYEQNEQPTGTCAACITGGN	0.9958	2,3		3279.3521
						K.HKELFDELVK.K	0.9924		1	1258.46
296	ADM1B_MOUSE	806	3.47	1	2	K.EEAEEQGAVEEEGAEEANEEAAAEKK.D	0.9958		3	2777.7797
297	ADO_MOUSE	1333	6	3	3	R.NHPEPTLDQLTDALGGNLCR.C	0.9958		2	2222.3856
						K.GEGHPFEYFVFGAACSEVEINCLTGDHKNI	0.9958		3	3555.8171
						K.GVFHPIIISPDRIEELGVISQAR.D	0.9958		2	2547.9603
298	ADPGK_MOUSE	496	4.03	2	2	R.VAVGVNACVDVVISGVK.L	0.9958		2	1686.9555
						R.RVAVGVNACVDVVISGVK.L	0.9958		1	1843.143
299	ADPN_MOUSE	413	9.93	2	2	R.LCTGNLQLLTRALFPSDVK.V	0.9944		3	2147.4888
						R.DGLQESLPDNVHQVISGK.V	0.9958		1	1937.1167
300	ADPRH_MOUSE	362	10.22	2	3	R.GILDGNSAPVFPQPFGVK.E	0.9955		2	1844.1204
						R.IPFNSHEGGCGAAMR.A	0.9958		2	1604.7467
301	ADRM1_MOUSE	407	5.16	1	2	R.TSGTVEDDLIIFPDDCEFK.R	0.9958		2	2202.3424
302	ADT1_MOUSE	298	47.65	13	920	K.LLLQVQHASK.Q	0.9958		2	1137.3677
						K.DFLAGGIAAAVSK.T	0.9958	1,2		1220.4111

						K.GADIMYTGTLDCWR.K	0.9958	1,2		1659.8201
						R.YFAGNLASGGAAGATSLCFVYPLDFAR.T	0.9958		2	2798.0931
						R.YFPTQALNFAFK.D	0.9944		1	1447.6763
						K.IAKDEGANAFFK.G	0.9958		2	1311.4802
						R.KGADIMYTGTLDCWR.K	0.9958		2	1787.9942
						R.GMGGAFVLVLYDEIK.K	0.9958		2	1612.9245
						R.GMGGAFVLVLYDEIKK.Y	0.9958		2	1741.0985
						K.DEGANAFFK.G	0.9958		1	999.0679
						K.LLLQVQHASKQISAEK.Q	0.9954		2	1794.1044
						K.GSSQREFNGLGDCLTK.I	0.9958		2	1769.8749
						K.GADIMYTGTLDCWRK.I	0.9958		2	1787.9942
303	ADT2_MOUSE	298	10.74	2	2	K.DFLAGGVAAAISK.T	0.9958		1	1220.4111
						R.KGTDIMYTGTLDCWR.K	0.9958		2	1818.0205
304	ADX_MOUSE	188	12.23	1	15	K.LDAITDEENDMLDLAFGLTDR.S	0.9958		2	2368.5745
305	ADXL_MOUSE	174	7.47	1	3	R.NFYVDGHIPKPH.-	0.9958		2	1424.6017
306	AEDO_MOUSE	256	14.45	2	5	R.RPPPEQQFEPPLQPLER.E	0.9958		2	2059.3323
						R.AEYTEASGPCVLTPHR.D	0.9958		2	1788.9207
307	AFAM_MOUSE	608	6.09	3	7	R.SQSQVVNHICSK.Q	0.9958		2	1387.5016
						R.FLVNLVK.W	0.9944		1	833.0617
						R.RHPDLSTPELLR.I	0.9958		2	1434.6383
308	AFAP1_MOUSE	731	6.02	2	2	K.KPSTDEQTSSAEEDVPTCGYLNVLSNSR.V	0.9958		3	3086.2159
						R.TASNAEQYKYGK.N	0.9944		1	1360.4661
309	AFF4_MOUSE	1160	5.26	2	2	R.GPFSSGQHSSQSFPPSLMSKSSSMLQKPT	0.9958		3	4742.3071
						R.SHGNDHHSKEHQR.S	0.9958		2	1569.5961
310	AFG31_MOUSE	789	1.52	1	2	K.KTQVLQPSEK.T	0.9924		1	1158.3403
311	AFG32_MOUSE	802	23.19	11	39	K.STYEEFVEGTGSLDEDTSLPEGLQDWNK.E	0.9958		2	3148.2739
						K.TVAYHEAGHAVAGWYLEHADPLLK.V	0.9958		2	2649.9683
						K.LASLTPGFSGADVANVCNEAALIAAR.H	0.9958		2	2589.8743
						K.VTQSAYAQIVQFGMNEK.V	0.9958		2	1915.1712
						R.LEVVNKR.F	0.9958		1	858.0287
						K.KEPQPSGPQPSGGAGGGGGK.R	0.9958		2	1750.8656
						R.MYFLWTALFWGGVMIYFVFKSSGR.E	0.9958		3	2908.4939
						K.NDMVQLLGPRPFTEK.S	0.9958		2	1746.0343
						R.KLASLTPGFSGADVANVCNEAALIAAR.H	0.9958		2	2718.0484
						R.KVTQSAYAQIVQFGMNEK.V	0.9958		2	2043.3453
						R.HLSDAINEK.H	0.9958		1	1027.1222
312	AGGF1_MOUSE	711	2.39	1	2	R.VDLQPYQTSSTKPNR.E	0.99		2	1734.9065

313	AGK_MOUSE	421	9.5	2	2	K.VQHITDATLAIVK.G	0.9923	2	1409.6689
						K.IPIGFIPLGQTSSLSHTLFAESGNK.V	0.9958	2	2615.9891
314	AGM1_MOUSE	542	18.63	4	6	R.DTRPSSEKLSQSVIDGVTVLGGQFHDYGLI	0.9944	3	4771.3247
						R.MGLLAVLR.S	0.9944	1	873.1449
						R.AFVRPSGTEDIVR.V	0.9943	2	1447.6341
						R.TLASIIDLFNQAAGDAISDMLVIEAILALK.G	0.9944	3	3131.6954
315	AGR2_MOUSE	175	11.43	1	2	K.FSVSAILLLVAISGTLAK.D	0.9944	2	1804.2236
316	AHI1_MOUSE	1047	6.11	2	6	K.AVSNDNEDTNGDGVHEITSRDSPVHPK.C	0.9958	3	2891.9817
						K.EGTPEDSQHMEGICSREQDVDATVPENAK	0.9958	3	3681.9331
317	AHSA1_MOUSE	338	23.67	4	61	R.VFTTQELVQAFTHAPAALEADR.G	0.9958	2	2416.6958
						R.ADATNVNNWHWTER.D	0.9952	2	1714.7941
						K.FHMVDGNVTGEFTDLVPEK.H	0.9958	2	2136.3839
						K.SWPEGHFATITLTFIDK.N	0.9958	2	1964.2279
318	AHSA2_MOUSE	331	7.25	1	3	R.GGKFQMFDGNISGEYVELVTNR.K	0.9958	3	2462.7393
319	AHSP_MOUSE	102	58.82	2	12	R.AMTEFQQELSTLGSQFLAK.Y	0.9958	2	2130.4205
						K.EFNVLLDQQVFDDPLISEEDMVIVVHDWVN	0.9958	3	4506.0395
320	AHTF1_MOUSE	2243	1.03	2	2	R.EVSVSSVTEEPK.L	0.9958	2	1291.3978
						K.SISNTSK.L	0.9958	1	736.8003
321	AIBP_MOUSE	282	43.97	7	122	R.EPFHSILSVLSGLTVPIASIDIPSGWDVEK.G	0.9958	3	3208.6788
						K.KYQLNLPSYPDTECVYR.L	0.9958	2,3	2147.3582
						K.SATHFTGR.Y	0.9958	1	876.9474
						R.YHYLGGR.F	0.9958	1	865.967
						K.GNPSGIQPDLLISLTAPK.K	0.9958	2	1822.1118
						K.LFGYQPTIYYPK.R	0.9924	2	1490.7417
						K.SPPTVLVICGPGNNGGDGLVCAR.H	0.9958	2	2311.5323
322	AIFM1_MOUSE	612	38.24	16	204	R.VLIVSEDPELPYMRPPLSK.E	0.9958	2,3	2184.5989
						K.SITVIGGGFLGSELACALGR.K	0.9958	2	1979.25
						R.KVETDHIVTAVGLEPNVELAK.T	0.9958	2	2263.5963
						K.SQASGIEVIQLFPEK.G	0.9958	2	1646.8809
						K.ELWFSDDPNVTK.T	0.9907	2	1451.5755
						K.ILPQYLSNWTMEK.V	0.9958	2	1623.9073
						R.SIYFQPPSFYVSAQDLPNIENGGVAVLTGK	0.9958	2	3213.6141
						R.SNIWVAGDAACFYDIK.L	0.9958	2	1831.0008
						R.AIASATEGGSVPQIR.A	0.9958	1	1457.6267
						R.APSHVPFLLIGGGTAAFAAAR.S	0.9954	2	2025.361
						R.KSQASGIEVIQLFPEK.G	0.9958	2	1775.055
						R.RVEHHDHAVVSGR.L	0.9958	2	1499.6321

						R.RAIASATEGGSVPQIR.A	0.9958	2	1613.8142
						K.KVVHLDVR.G	0.9924	1	966.1716
						R.VMGLGLSPEEK.Q	0.9958	1	1160.371
						R.VEHHDHAVVSGR.L	0.9915	2	1343.4446
323	AK1A1_MOUSE	325	37.85	8	51	R.HPDEPVLLEEPVVLALAEK.H	0.9958	2	2099.432
						R.ILQNIQVFDFTFSPEEMK.Q	0.9958	2	2187.5152
						R.GLEVTAYSPLGSSDR.A	0.9958	2	1552.6812
						K.HALSAGYR.H	0.9944	1	874.9749
						R.HIDCASVYGNETEIGEALK.E	0.9958	2	2107.2476
						R.EELFVTSK.L	0.9944	1	953.0801
						K.MPLIGLGTWK.S	0.9958	1	1116.407
						R.DAGHPLYPFNDPY.-	0.9958	1	1506.614
324	AK1CD_MOUSE	323	6.5	2	61	R.ILNKPGLK.Y	0.9958	1	883.1221
						K.RSPALIALR.Y	0.9958	1	997.229
325	AK1E1_MOUSE	301	25.91	4	14	K.NLGVSNFNHEQLER.L	0.9958	2	1657.7831
						R.NVSVTAYRPLGGSGGGFHLMDDTVIR.K	0.9958	3	2721.063
						R.NLIVIPK.S	0.9924	1	797.0287
						K.VIPSHTSFLDTWEAMEDLVFEGLVK.N	0.9958	2	2865.2703
326	AKA12_MOUSE	1684	23.75	17	45	R.DVLEPTQALAAGAVPILAK.A	0.9958	2	1878.2193
						R.SPSWISASMTEPLEHAEGVATPPVGEVTEI	0.9958	3	3138.4731
						K.TLVHTVSVAVIDGTR.A	0.9958	2	1568.8137
						K.VELPLEDQVGDLEALSEK.C	0.9958	2	1985.1956
						K.QRSDEDNKPDAGPDAAGK.E	0.9958	2	1871.9151
						R.GKALGSLEGSPSLPDQDK.A	0.9937	2	1799.9756
						K.VQGSPLK.K	0.9944	1	728.8668
						K.IVQSVIQTAVDQFAR.T	0.9958	2	1675.9255
						K.ELEVPVHTGPNSQK.T	0.9958	2	1535.697
						K.DVVPEGPVQEAETEHLAQGSETVQATPES	0.9958	3	4418.6795
						K.KDEGEGAEASVGAGDHQEPGVETVGESA	0.9958	2,3	2928.994
						K.VKEDSQVPATQTLQR.A	0.9958	2	1700.8894
						K.EPTKPLESPTSPVSNETTSSFK.K	0.9958	2	2364.5683
						K.LSETGGYGTLQHGEDTVPQGPESQAESIP	0.9958	3	4857.2989
						K.TEQASEEHEQETAAPEHEGTHPKPVLTAD	0.9923	3	3908.1181
						R.AEDSGAEQLASEIEPSREESWVSIK.K	0.9944	3	2748.9171
						R.EKEPTKPLESPTSPVSNETTSSFK.K	0.9958	2	2621.8578
327	AKAP1_MOUSE	857	16.1	8	34	K.QVETLK.V	0.9924	1	717.8406
						R.SVDKPSTEPLALPR.T	0.9958	2	1510.7306

						K.LPSSFVEPVHSEPVKDEDALEPQVK.G	0.9958		3	2778.0881
						K.TVAQVHPISATQPK.G	0.9958		2	1477.7037
						K.SEFPILAPGGGEGEEVSHGPPQVAELLKK.I	0.9944		3	2974.3403
						K.SEFPILAPGGGEGEEVSHGPPQVAELLK.K	0.9958		2	2846.1663
						R.RLSEEACPGVLSVAPTVTQPPGR.E	0.9944		2	2422.7099
						K.KVDLIIWEIEVPK.H	0.9958		2	1582.9237
328	AKAP3_MOUSE	864	2.89	2	2	K.DLEKSTAGFQDSR.F	0.9924		1	1454.5364
						R.YMSTLKIK.E	0.9944		1	984.2421
329	AKIB1_MOUSE	1085	1.94	1	3	K.AFVENNPAIKWCPTAGCER.A	0.9958		2	2221.4095
330	AKNA_MOUSE	1404	3.42	2	2	R.TQQHFSSLSSPGRGAQSCHLEETSVAK.I	0.9958		3	2931.1143
						R.DVPRLYLSSESESPAPR.L	0.9924		1	1904.0868
331	AKT1_MOUSE	480	3.13	1	134	R.FFANIVWQDVYEK.K	0.9958		2	1659.8816
332	AL1A1_MOUSE	501	30.94	13	89	K.KYVLGNPLTPGINQGPQIDK.E	0.9958		2	2153.4863
						K.RVTLELGGK.S	0.9958		2	973.1606
						K.FPVLNPATEEVICHVEEGDKADVDK.A	0.9958		3	2813.0565
						R.ANNTTYGLAAGLFTK.D	0.9958		2	1542.7319
						K.IHGQTIPSDGDIFTYTR.R	0.9958		2	1922.1045
						K.GFFVQPTVFSNVTDEMR.I	0.9958		2	1975.2262
						K.YVLGNPLTPGINQGPQIDK.E	0.9958		2	2025.3122
						K.VFANAYLSDLGGCIK.A	0.9958		2	1628.8316
						K.RANNTTYGLAAGLFTK.D	0.9958		2	1698.9193
						R.ELGEHGLYEYTELK.T	0.9958		2	1681.8395
						K.YVLGNPLTPGINQGPQIDKEQHDK.I	0.9944		3	2662.9621
						K.FPVLNPATEEVICHVEEGDK.A	0.9958		2	2284.4938
						K.KFPVLNPATEEVICHVEEGDK.A	0.9958		2	2412.6679
333	AL1A7_MOUSE	501	3.79	1	7	K.IHGQTIPSDGNIFTYTR.R	0.9945		2	1921.1197
334	AL1B1_MOUSE	519	14.07	5	11	R.GFFIKPTVFGDVQDGMR.I	0.9958		2	1915.217
						K.TFPTVNPTTGEVIGHVAEGDR.A	0.9958		2	2198.3971
						K.KTFPTVNPTTGEVIGHVAEGDR.A	0.9958		2	2326.5712
						K.LFINNEWHDAVSK.K	0.9924	1,2		1573.7483
						K.VAFTGSTEVGHLIQK.A	0.9958		2	1587.8161
335	AL2CL_MOUSE	952	6.72	4	4	K.HLQEMAQEEVKQHAR.E	0.9958		3	1835.0477
						R.EKLEVLEK.T	0.9958		1	988.1693
						K.VTQAVCQALCGK.K	0.9924		1	1335.4755
						K.GKVTFPNGFTLDGSFSSGTDK.G	0.9911		3	2163.3483
336	AL2SC_MOUSE	584	10.27	2	2	R.GGGGGGNNGGNGGASGPSGGGGSGGPI	0.9958		2	2013.9516
						K.VNFIPKSGSAFCLVSILKPLLPTPDLTLK.G	0.9958		3	3170.8127

337	AL4A1_MOUSE	562	56.41	15	258	K.STGSVVGQQPFGGAR.A	0.9958	2	1448.5785
						K.VGDPAEDFGTFFSAVIDAK.A	0.9958	2	1987.173
						K.NFHFVHSSADVDSVVSGTLR.S	0.9958	2	2175.3653
						R.ASGTNDKPGGPHYILR.W	0.9958	2	1683.8643
						R.EAGLPPNIIQFVPADGPTFGDTVTSSEHLC	0.9958	3	4420.8855
						K.VANEPILAFSQGSPER.D	0.9958 1,2		1715.9035
						K.LVDSTTSYGLTGAVFAQDK.A	0.9958	2	1974.1748
						K.EEIFGPVLTVYVYPDDK.Y	0.9958	2	1985.2409
						K.FAVELEGEQPISVPPSTNHTVYR.G	0.9944	2	2571.8492
						K.GQTEAIPCVVGDEEVWTSDIQYQLSPFNH	0.9958	3	3657.941
						K.TVIQAEIDAAAELIDFFR.F	0.9958	3	2023.2933
						K.ETHKPLGDWR.Y	0.9958	1	1239.3763
						R.SSPSLSILAGGQCNESVGYYVEPCIIESK.D	0.9958	2	3146.4073
						R.ETLKLVDSTTSYGLTGAVFAQDK.A	0.9958	2	2445.7289
						R.KEWDLKPMADR.A	0.9958	2	1389.6122
338	ALAT1_MOUSE	496	40.73	11	55	R.DGGIPADPNNIFLSTGASDAIVTMLK.L	0.9958	2	2618.9617
						K.LTEQVFNEAPGIR.C	0.9958	2	1474.6567
						R.CNPVQGAMYSFPQIQLPLK.A	0.9944	2	2192.547
						K.VLTEMGPPYATQQELASFHSVSK.G	0.9958	2	2521.8475
						K.KVLTEMGPPYATQQELASFHSVSK.G	0.9958	3	2650.0216
						R.ILQACGGHSLGAYSISSGIQPIR.E	0.9958	2	2386.6794
						R.VLCVINPGNPTGQVQTR.E	0.9958	2	1854.0825
						R.ILQACGGHSLGAYSISSGIQPIREDVAQYIE	0.9958	3	3490.8639
						R.QVLALCVYPNLLSSPDFPEDAK.R	0.9958	2	2477.7828
						K.KPFTEVIR.A	0.9958	1	990.1906
						R.LCPPVPGQALMGMVVSPPTPSEPSFK.Q	0.9944	2	2725.1996
339	ALBU_MOUSE	608	85.86	49	6840	R.LPCVEDYLSAILNR.V	0.9958	2	1663.8774
						K.DVFLGTFLYEYSR.R	0.9958	2	1610.8065
						R.LSQTFPNADFAEITK.L	0.9958	1	1682.8706
						K.DDNPSLPPFERPEAEAMCTSFK.E	0.9958	2	2539.742
						K.LVQEVTDFAK.T	0.9944	1	1150.3171
						K.LGEYGFQNAILVR.Y	0.9958 1,2		1480.7068
						K.DTCFSTEGPNLVTR.C	0.9958	2	1597.688
						R.YNDLGEQHFK.G	0.9958	1	1251.3409
						K.AETFTFHSDICTLPEK.E	0.9958	2	1897.0577
						K.AADKDTCFSTEGPNLVTR.C	0.9958	2	1983.1083
						K.APQVSTPTLVEAAR.N	0.9958	1	1440.6396

K.KYEATLEK.C	0.9958	1	982.1216
R.LSQTFPNADFAEITKLATDLTK.V	0.9958	2	2425.7411
K.AHCLSEVEHDTMPADLPAIAADFVEDQEVC	0.9958	2,3	3499.7599
K.AETFTFHSDICTLPEKEK.Q	0.9958	2	2154.3472
K.LQTCCDKPLLK.K	0.9958	1,2	1376.5684
K.TPVSEHVTK.C	0.9958	2	998.124
K.GLVLIAFSQYLQK.C	0.9958	2	1480.7905
K.KQTALAELVK.H	0.9931	2	1101.3317
K.AHCLSEVEHDTMPADLPAIAADFVEDQEVC	0.9958	3	4176.4868
R.HPDYSVSLLLR.L	0.9958	1,2	1300.5003
K.SLHTLFGDK.L	0.9958	1,2	1018.1576
R.RPCFSALTVDETYVPK.E	0.9958	2	1884.1053
K.ENPTTFMGHYLHEVAR.R	0.9958	2	1903.1223
K.TPVSEHVTKCCSGSLVER.R	0.9958	2	2047.2049
K.KAHCLSEVEHDTMPADLPAIAADFVEDQEV	0.9958	3	3627.9339
K.TVMDDFAQFLDTCCK.A	0.9958	1	1851.9981
K.YMCENQATISSK.L	0.9958	1,2	1432.5544
R.YTQKAPQVSTPTLVEAAR.N	0.9958	2	1961.2254
R.VCLLHEK.T	0.9944	1	899.0441
R.RHPDYSVSLLLR.L	0.9958	2	1456.6878
R.NECFLQHK.D	0.9958	1	1076.1632
K.APQVSTPTLVEAARNLGR.V	0.9958	2	1881.1423
K.GLVLIAFSQYLQKCSYDEHAK.L	0.9958	3	2471.7815
K.SLHTLFGDKLCAIPNLR.E	0.9958	2	1956.2615
R.VGTKCCTLPEDQR.L	0.993	2	1564.6679
K.CCAEANPPACYGTVLAEFQPLVEEPK.N	0.9958	2	2952.1856
K.QEPERNECFLQHK.D	0.9958	2	1715.8291
K.AWAVARLSQTFPNADFAEITK.L	0.9958	2	2337.6402
K.CCTLPEDQR.L	0.9958	1,2	1179.2043
K.ECCHGDLLECADDR.A	0.9958	2	1750.7145
K.CCSGSLVER.R	0.9958	2	1068.1041
K.ECCHGDLLECADDRAELAK.Y	0.9958	2	2263.3211
R.HPYFYAPELLYYAEQYNEILTQCCAEADK.E	0.9958	3	3601.8795
K.LCAIPNLR.E	0.9924	1	957.1271
K.TCVADESAANCDK.S	0.9958	2	1441.4237
R.ENYGELADCCTK.Q	0.9958	1	1460.4695
K.CCAEANPPACYGTVLAEFQPLVEEPKNLVH	0.9958	3	3406.7555

						R.HPYFYAPELLYYAEQYNEILTQCCAEADKE	0.9958		3	4417.7673
340	ALD1_MOUSE	316	3.8	1	2	K.MPLVGLGTWK.S	0.9958		1	1102.3801
341	ALD2_MOUSE	316	18.04	3	38	K.ALGVSNFNHFQIER.L	0.9958		2	1632.8191
						K.LDYLDLYLIHWPQGLQPGK.E	0.9958		2	2270.636
						K.HKPVTNQVECHPYLTQEK.L	0.9958		2	2209.4326
342	ALDH2_MOUSE	519	52.22	16	302	K.VAFTGSTEVGHLIQVAAGSSNLK.R	0.9958		2	2287.5779
						R.TFVQENVYDEFVER.S	0.9958		2	1775.9121
						K.VAEQTPLTALYVANLIK.E	0.9924		2	1845.1894
						K.EAGFPPGVVNIVPGFGPTAGAAIASHEGVD	0.9907	2,3		2963.3195
						K.TFPTVNPSTGEVICQVAEGNKEDVDK.A	0.9958		2	2836.0479
						R.GYFIQPTVFGDVK.D	0.9958		1	1471.6959
						K.ANYLSQALQAGTVWINCYDVFGAQSPFGG	0.9958		2	3427.7632
						K.KILGYIK.S	0.9958		1	835.0776
						R.ELGEYGLQAYTEVK.T	0.9958	1,2		1600.7655
						K.EEIFGPVMQILK.F	0.9958		1	1404.7076
						K.LGPALATGNVVVMK.V	0.9958		2	1370.6935
						R.TEQGPQVDETQFK.K	0.9958		2	1507.5969
						R.AAFQLGSPWR.R	0.9958		2	1133.295
						K.TIPIDGDFFSYTR.H	0.9958		1	1532.6928
						R.KTFPTVNPSTGEVICQVAEGNK.E	0.9958		2	2377.6227
						R.YYAGWADKYHGK.T	0.9958		2	1459.6036
343	ALDOA_MOUSE	364	81.04	24	2292	K.YTPSGQSGAAASESLFISNHAY.-	0.9944		2	2259.3935
						K.GVVPLAGTNGETTTQGLDGLSER.C	0.9958		2	2273.4619
						R.TVPPAVTGVTFLSGGQSEEEASINLNAINK.	0.9944		2	3045.3733
						K.FSNEEIAMATVTALR.R	0.9958		2	1653.8908
						R.LQSIGTENTEENR.R	0.9958		1	1491.5547
						R.YASICQQNGIVPIVEPEILPDGDHDLK.R	0.9958		3	3022.3478
						R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	0.9958	2,3		3178.5353
						K.IGEHTPSALAIMENANVLAR.Y	0.9943		2	2108.4204
						K.ADDGRPFPQVIK.S	0.9958		1	1343.5253
						K.RLQSIGTENTEENR.R	0.9958		2	1647.7422
						K.KELSDIAHR.I	0.9952		2	1069.2058
						R.VNPCIGGVILFHETLYQK.A	0.9952		2	2089.4082
						K.GILAADESTGSIAK.R	0.9944		1	1333.4814
						K.ELSDIAHR.I	0.9958		1	941.0317
						R.ALANSLACQGK.Y	0.9958		1	1133.2561
						K.RCQYVTEK.V	0.9958		1	1084.1834

						R.RTVPPAVTGVTFLSGGQSEEEASINLNAINI	0.9958		3	3201.5608
						K.RALANSLACQGK.Y	0.9958		2	1289.4435
						R.ALQASALK.A	0.9944		1	801.9615
						R.QLLLTADDR.V	0.9958		1	1045.1808
						K.VLAAVYK.A	0.9958		1	763.9554
						R.IVAPGK.G	0.9924		1	584.7367
						K.ALSDHHVYLEGTLLKPNMVTPGHACTQK.F	0.9958		2	3119.5317
						R.LQSIGTENTEENRR.F	0.9943		2	1647.7422
344	ALDOC_MOUSE	363	19.56	4	100	K.YSPEEIAMATVTALR.R	0.9958		2	1652.9031
						K.GVVPLAGTDGETTTQGLDGLLER.C	0.993		2	2300.5279
						K.RLSQIGVENTEENR.R	0.9952		2	1645.7697
						R.QVLFSADDRVK.K	0.9958		2	1278.4508
345	ALDR_MOUSE	316	58.23	13	555	K.TIGVSNFNPLQIER.I	0.9958	1,2		1588.8039
						K.EVGVALQEK.L	0.9924		1	973.1143
						R.NLVVIPK.S	0.9958		1	783.0018
						K.SPPGQVTEAVK.V	0.9906		1	1113.256
						R.HIDCAQVYQNEK.E	0.9958		2	1505.5933
						K.GIVVTAYSPLGSPDRPWAKPEDPSLLEDPF	0.9958	2,3		3264.6623
						K.YKPAVNQIECHPYLTQEK.L	0.9958		2	2219.4681
						K.HKDYPFHAEV.-	0.9958		1	1243.3641
						K.VFDFEVSSEDMATLLSYNR.N	0.9958		2	2224.4468
						K.RQDLFIVSK.L	0.9947		2	1106.3103
						K.MPTLGLGTWK.S	0.9958	1,2		1104.3526
						K.LWCTFHDK.S	0.9944		1	1107.2201
						K.TTAQVLIR.F	0.9947		2	902.0818
346	ALKB7_MOUSE	221	15.84	2	4	R.AAAFGPDQSLLSPVHVLDLEPR.G	0.9958		2	2333.6494
						R.GYIKPHVDSVK.F	0.9958		2	1243.4484
347	ALMS1_MOUSE	3251	3.11	4	5	K.ESSTTDVCTQRESFVEEVPHIEYVQK.D	0.9944		3	3099.3008
						K.MKVTNHLLGR.K	0.9924		1	1169.4307
						K.AWLQAHPDRPGSAFSLPPPTPPPPPPPLSI	0.9944		3	3279.7715
						K.VPRISGSTEQTNVTTGSSSSYSVGEK.S	0.9958		3	2659.8235
348	ALPK1_MOUSE	1231	5.12	3	3	R.SSFASLAGQTSQEILEARTLQPDDLEK.L	0.9944		3	2936.2023
						K.SPAFSRSSSDGESSWSLLNSSR.S	0.9958		3	2345.4441
						K.LLQVAKGLHK.L	0.9924		1	1107.3848
349	ALPK2_MOUSE	1921	1.82	2	5	R.IQAEMAPEHSGNIK.L	0.9958		1	1525.7197
						K.EQSAESTANVDCHQVTR.E	0.9945		2	1932.9647
350	ALS_MOUSE	603	6.14	2	2	R.VAGLLEDTFPGLLGLHVLR.L	0.9958		2	2021.4105

						R.NLTQLPDGIPVSTR.A	0.9904	2	1511.7184
351	ALS2_MOUSE	1651	2.79	2	3	K.YLIKACDTPLHPLGR.L	0.9944	2	1755.0361
						R.AISQAVDQALRGTSDFPLYGGGSSVQR.Q	0.9944	3	2782.0421
352	AMACR_MOUSE	381	29.4	6	8	R.EYGFSQEEILQLHSDR.I	0.9958	2	1952.0874
						R.TPAVPSAK.R	0.9958	1	770.9041
						K.QPRGQNILDGGAPFYTTYK.T	0.9944	3	2127.3641
						K.VAGHDINYLALSGVLSK.I	0.9958	2	1758.0275
						K.RDPSVGEHTVEVLR.E	0.9952	2	1594.7678
						K.AEWCQIFDGTDACVTPVLTFEEALHHQHNI	0.9958	3	3583.8305
353	AMBP_MOUSE	349	4.87	1	4	R.TIAACNLPIVQGPCR.A	0.9958	2	1670.8817
354	AMD_MOUSE	979	3.78	2	2	K.AGIEVPEIKEAEAVVEPK.V	0.9946	2	1909.187
						R.LPVDEEAFVIDFKPR.A	0.9958	2	1776.0422
355	AMFR_MOUSE	643	4.82	2	4	R.TYTGLSGLALLGTIVSAYR.A	0.9958	3	1957.2774
						K.FWNFIFYK.F	0.9958	1	1165.3794
356	AMHR2_MOUSE	568	7.22	1	2	R.CSDLRPDHRPPPFQLAYEAELGSNPSACE	0.9944	3	4511.927
357	AMNLS_MOUSE	458	10.04	2	6	R.VALGPGPNPVHVR.S	0.9909	2	1313.5454
						R.NPDRFSWLDPHLWSSGTQAPGLFSVDAEI	0.9958	3	3287.5749
358	AMP1D_MOUSE	335	6.57	1	4	R.DISHSVVSPAAVSPAHPVPK.R	0.9958	2	1996.2737
359	AMPB_MOUSE	650	6.62	2	29	K.DTFAATASQLHSNVVNYVQQILAPK.D	0.9958	2	2717.0538
						K.KPFVYTQGQAVLNR.A	0.9958	2	1621.8796
360	AMPD1_MOUSE	745	3.62	1	2	K.TDNYINGEYFATIIKEVGADLVEAK.Y	0.9958	3	2775.0845
361	AMPD2_MOUSE	798	5.39	2	2	K.VKSHWLGPNYTK.E	0.9958	1	1430.6493
						R.NPLPEYLSRGLMVSLSTDDPLQFHFTK.E	0.9944	3	3107.5512
362	AMPL_MOUSE	519	46.24	13	351	K.LNLPINIIGLAPLCENMPSGK.A	0.9958	2	2265.6826
						R.HLMESPANEMTPTR.F	0.9958	2	1614.8317
						R.TFYGLHQDFPSVVVVGLGK.R	0.9958	2	2064.3916
						K.DKDDDLPQFTSAGESFNK.L	0.9958	2	2015.0973
						K.GSEEPPVFLEIHYMGSPNATEAPLVFVGK.(	0.9958	2	3117.5433
						R.LILADALCYAHTFNPK.V	0.9958	2	1848.1181
						R.QVQDLELPSVEVDPCGDAQAAAEGAVLGL	0.9958	3	3880.1739
						K.SWIEEQEMGSFLSVAK.G	0.9958	2	1842.0735
						K.WAHLDIAGVMTNKDEIPYLR.K	0.9958	2	2343.7057
						K.GITFDSGGISIK.A	0.9958	2	1195.358
						K.GVLFASGQNLAR.H	0.9958	2	1233.4129
						K.WAHLDIAGVMTNK.D	0.9958	2	1456.7026
						R.MPLFEHYTR.Q	0.9958	2	1194.3935
363	AMPM1_MOUSE	386	14.51	3	7	K.LFHTAPNVPHYAK.N	0.9958	1	1495.7239

						R.RPLQEGDIVNVDITLYR.N	0.9958	2	2002.2779
						R.SAQFEHTLLVTDTGCEILTR.R	0.9958	2	2292.517
364	AMPN_MOUSE	966	24.22	13	43	R.RFSSEFELQQLEQFK.A	0.9958	2	1917.1283
						K.KLQNQLQTDLSVIPVINR.A	0.9958	2	2080.4355
						R.FSSEFELQQLEQFK.A	0.9958	2	1760.9409
						K.LFENYGGGSFSFANLIQGVTR.R	0.9958	2	2278.5291
						R.VMAVDALASSHPLSSPADEIK.T	0.9958	2	2139.4284
						K.TPDQIMELFDSITYSK.G	0.9917	2	1889.1273
						R.WILQMGFPVITVNTNTGEISQK.H	0.9958	2	2477.8811
						R.TNNWVNRPPTLMEQYNEINAISTACSSGLK	0.9958	3	3410.7492
						R.QYEMDSQFQGELADDLAGFYR.S	0.9958	2	2484.6557
						K.LQNQLQTDLSVIPVINR.A	0.9958	2	1952.2614
						K.KVVATTQMQAADAR.K	0.9958	2	1490.7179
						R.AQIIHDSFNLASAK.M	0.9958	2	1515.7092
						R.KQDTTSTIISIASNVAGHPLVWDFVR.S	0.9958	2	2857.2389
365	AMRA1_MOUSE	1300	8.31	3	3	R.GFPDEGILAVYSLAPHNLGEMLYTKR.F	0.9958	3	2893.3301
						R.SSGIQVGEQSTVQDSATPSPPPPPPQPSTI	0.9958	3	4105.4673
						R.GQPGLATHSSVNRVLAGAVIGDGQSAVAS	0.9958	3	3655.0219
366	AMRP_MOUSE	360	16.39	5	9	K.HVESIGDPEHISR.N	0.9924	2	1476.5889
						K.VSHQGYGSTTEFEEPR.V	0.9958	2	1824.9011
						K.LIHNLNVILAR.Y	0.9958	1	1276.568
						R.MEKLNQLWEK.A	0.9958	1	1319.5615
						R.KVSHQGYGSTTEFEEPR.V	0.9958	2	1953.0752
367	AN32A_MOUSE	247	39.68	6	35	K.SLDLFNCEVTNLNAYR.E	0.9958	2	1930.0906
						K.DLSTIEPLK.K	0.9944	1	1016.1797
						K.HLNLSGNK.I	0.9958	1	882.9951
						K.IEGLTDEFEELEFLSTINVGLTSISNLPK.L	0.9958	3	3210.6025
						K.LLPQVMYLDGYDRDNK.E	0.9958	2	1941.2091
						K.KLELSENR.I	0.9958	1	989.1167
368	AN32B_MOUSE	272	19.49	2	20	R.LAEELPSLTHLNLSGNNLK.D	0.9958	2	2064.3464
						R.EDQEAPDSDVEVDSVEEAPDSDGEVDGVI	0.9958	3	3178.1219
369	AN32E_MOUSE	260	11.15	2	4	R.LPSLNK.L	0.9944	1	671.8149
						R.KLELSDNIISGGLEVLAEK.C	0.9958	2	2029.3385
370	AN34B_MOUSE	508	2.95	1	2	K.ELVEPAPPGPLSR.R	0.9958	1	1362.5687
371	ANC2_MOUSE	837	9.08	4	6	K.WIERVVGWLGK.V	0.9936	1	1343.6145
						R.QALEQFNQLSQVLHR.L	0.9924	2	1812.0384
						K.VFLQDNPTRPTSPEAGNTLRR.W	0.9952	2	2370.6303

						R.MFVMTGPALAEIDLQELQGYLQK.K	0.9958	3	2597.0596
372	ANC5_MOUSE	740	1.89	1	2	K.QMEKEELDVSVR.E	0.9924	1	1463.6459
373	ANF_MOUSE	152	44.74	3	17	K.MPVEDEVMPPQALSEQTEEAGAALSSLPE	0.9958	3	4501.0365
						R.IGAQSGLGCNSFR.Y	0.9915	2	1367.4705
						K.NLLDHLEEK.M	0.9958	2	1111.2401
374	ANFY1_MOUSE	1169	3.42	2	4	K.GNPPLWLALASNLEDIASTLVR.H	0.9958	2	2351.708
						R.NLLLAGAKVNELTK.H	0.9958	2	1484.7795
375	ANGE2_MOUSE	544	8.09	2	2	K.ENTAQGPGAEVALVGGLKLLAR.L	0.9944	2	2165.4978
						R.AASPSICIANTHLLYNPR.R	0.9958	2	1999.2432
376	ANGL1_MOUSE	490	6.12	2	3	R.MDLENLKDVLSR.Q	0.9924	1	1433.6629
						R.VTQLYMQLLHEIIR.K	0.9958	2	1758.1321
377	ANGL2_MOUSE	493	6.49	2	3	R.ILNQTADMLQLASK.Y	0.9958	2	1546.8224
						K.QELELLNNELLKQK.R	0.9958	2	1712.9841
378	ANGL6_MOUSE	457	2.41	1	2	K.AVMLTRLVR.L	0.9958	1	1059.3586
379	ANK1_MOUSE	1862	33.62	29	96	R.TAAVLLQNDPNPDVLSK.T	0.9958	2	1796.0306
						K.FLLENGANQNVATEDGFTPLAVALQQGHE	0.9958	3	4395.8754
						R.GGSPHSPAWNGYTPLHIAAK.Q	0.9958	2	2062.295
						K.LLGNQATFSPIVTVEPR.R	0.9958	2	1843.1332
						R.ITTIQGPEPGALQEYEQVLVSTR.E	0.9958	2	2530.8376
						R.ISEILLDHGAPIQAK.T	0.9958	2	1605.8748
						R.MSYPETVDEILDVSEDEGDELVGSK.A	0.9958	3	2757.9338
						K.GFTPLYMAAQENHLEVVK.F	0.9958	2	2048.3643
						K.FLLQHQADVNAK.T	0.9958	2	1384.5779
						K.LLLENGASPNLATTAGHTPLHTAAR.E	0.9958	2,3	2527.8429
						R.SENGSVWKEHK.S	0.9943	2	1301.4013
						R.NGVDINTCNQNGLNGLHLASKEGHVK.M	0.9944	3	2791.019
						K.GNTALHIAALAGQDEVVR.E	0.9958	2	1836.058
						R.SLLQYGGSANAESVQGVTPLHLAAQEGHT	0.9958	3	3922.4455
						K.SGLTPLHLVSQEGHVPVADVLIK.H	0.9958	2	2410.8192
						R.DIEVLEGMPLFAELSGNLVPVK.K	0.9958	2	2371.7944
						R.LAELLLEHDAHPNAAGK.N	0.9958	2	1800.0244
						R.TAEAVHFATLLYK.E	0.9958	2	1464.7044
						K.LVPLVQATFPENAVTK.K	0.9958	2	1728.0416
						K.NGLTPLHVAVHHNNLDIVK.L	0.9958	2	2092.4086
						K.LEGAHSEDTQGPELGSQDLVEDDTVDSDA	0.9958	3	4613.7278
						K.HGVTVDATTR.M	0.9958	1	1057.1515
						R.EHLGLSWAELAR.E	0.9958	1	1382.562

						K.AKDDQTPLHCAAR.I	0.9958	2	1483.5902
						R.TKDELTPLHCAAR.N	0.9958	2	1512.6721
						K.TKNGLSPIHMAAQGDHLDCVR.L	0.9958	2	2321.5823
						K.KGNTALHIAALAGQDEVVR.E	0.9958	2	1964.2321
						R.YGESYLDQILNGMDEELGSLEELEK.K	0.9958	2	2876.1152
						K.LGYSPLHQAAQQGHTDIVTLLLK.N	0.9958	2	2504.8919
380	ANKS1_MOUSE	1150	7.39	3	7	R.DVVEVLLRNDALTNVADSK.G	0.9958	2	2072.3232
						K.RLSSGFGGGGGGSGSGGGSGGGGLGSS	0.9958	3	3466.7264
						R.TLEQSVGEWLESIGLQQYESK.L	0.9931	2	2425.6544
381	ANKS6_MOUSE	883	5.32	2	2	R.GLAANQPLPFSDEPELALDSTMRAPPQDR	0.9958	3	3138.4791
						K.YLLNQGADVALRAK.N	0.9958	1	1532.7831
382	ANKZ1_MOUSE	748	2.67	2	4	R.QREQQQR.K	0.9944	1	973.0365
						R.RPTFGELQR.V	0.9958	2	1104.2541
383	ANM1_MOUSE	371	8.36	2	2	R.TGFSTSPESPYTHWK.Q	0.9958	2	1725.8547
						K.WLAPDGLIFPDR.A	0.991	2	1400.6201
384	ANM3_MOUSE	532	7.14	2	28	R.LNKLEDTIVLIK.G	0.9958	2	1399.7141
						K.TAMCTAVAGYFDIYFEKNCHNR.V	0.9958	2	2669.9033
385	ANM5_MOUSE	637	7.38	2	2	K.DDGVSIPGEYTSFLAPISSSK.L	0.9958	2	2171.3655
						K.KVWYEWAVTAPVCSSIHNPTGR.S	0.9924	3	2559.8529
386	ANPRA_MOUSE	1057	1.8	1	2	K.IITYKEPDNPEYLEFLK.Q	0.9924	2	2113.4149
387	ANPRC_MOUSE	536	4.29	1	4	R.GAKPDLILGPVCEYAAAPVAR.L	0.9958	2	2169.4949
388	ANR17_MOUSE	2603	1.73	3	4	R.GMVRVCDLLLK.K	0.9944	1	1304.6001
						R.GIKGDITPLMAAANGGHVK.I	0.9958	2	1851.1742
						K.AFADPEVLR.R	0.9958	1	1018.1576
389	ANR23_MOUSE	306	4.9	1	2	K.YLADGGDPNAHDK.L	0.9958	1	1373.4215
390	ANR26_MOUSE	1581	1.33	2	4	R.YLEDIKIANEK.N	0.9958	1	1336.5279
						K.YKGLQK.E	0.9958	1	736.8894
391	ANR53_MOUSE	497	6.04	1	3	K.GAAINSQTYNGSTPLHLASCNGLLGCIK.L	0.9958	3	2919.1963
392	ANT3_MOUSE	465	40.43	9	63	K.EQLQDMGLIDLFSPEK.S	0.9958	2	1864.1206
						R.FATNFYQHLADSK.N	0.9958	2	1542.6909
						R.VAEGTQVLELPFKGDDITMVLILPKPEK.S	0.9958	3	3082.6661
						K.TSDQIHFFFAK.L	0.9958	2	1341.5089
						K.DVIPQGAINELTALVLVNTIYFK.G	0.9958	2	2532.983
						K.NDNDNIFLSPLSISTAFAMTK.L	0.9958	2	2300.5885
						K.SQLPGIVAGGR.D	0.9958	1	1055.2223
						K.VEQELTPELLQEWLDELSETMLVVHMPR.F	0.9958	3	3366.8691
						K.AFLEVNEEGSEAAASTSVVITGR.S	0.993	2	2338.5334

393	ANX10_MOUSE	324	3.09	1	3	K.EQLSSHFK.E	0.9958	1	976.077
394	ANX11_MOUSE	503	15.71	5	14	R.AHLVAVFNEYQR.M	0.9958	2	1447.6365
						K.GFGTDEQAIIDCLGSR.S	0.9958	2	1739.8456
						K.TPVLFDVYEIK.E	0.9958	2	1324.5597
						K.GAGTDEACLIEIFASR.S	0.9958	2	1710.8475
						R.IMVSRSELDLLDIR.A	0.9944	1	1660.9696
395	ANXA1_MOUSE	346	45.38	9	84	K.GLGTDEDTLIEILTTR.S	0.9958	2	1747.9402
						K.GGPGSAVSPYPSFNVSSDVAALHK.A	0.9958	2	2345.5737
						R.KGTDVNVFTTILTSR.S	0.9958	2	1652.8882
						K.ALTGHLEEVVLAMLK.T	0.9958	2	1624.9794
						K.KYGISLCQAILDETK.G	0.9958	2	1739.9727
						R.FLENQEQEYVQAVK.S	0.9958	2	1725.8956
						K.AAYLQENGKPLDEVLR.K	0.9958	2	1817.0519
						K.GDIEKCLTTIVK.C	0.9958	1	1377.5872
						K.GVDEATIIDILTK.R	0.9958	2	1388.6012
396	ANXA2_MOUSE	339	40.71	8	278	K.SALSGHLETVILGLLK.T	0.9958	2,3	1651.9872
						R.AEDGSVIDYELIDQDAR.E	0.9958	2	1910.0013
						R.RAEDGSVIDYELIDQDAR.E	0.9958	2	2066.1888
						K.LSLEGDHSTPPSAYGSVKPYTNFDAER.D	0.9958	2	2940.1522
						K.ALLYLCGGDD.-	0.9958	1	1097.1761
						K.GDLENAFLNLVQCIQNKPLYFADR.L	0.9958	2	2840.1743
						K.GLGTDEDSLIEIICSR.T	0.9958	2	1778.9202
						K.GVDEVTIVNILTNR.S	0.9958	2	1543.7605
397	ANXA3_MOUSE	323	30.34	6	18	K.GTGTDEDALIEILTTR.S	0.9958	2	1705.8596
						K.DYPGFSPSVDAEAIR.K	0.9958	2	1624.7472
						K.GELSGHFEDLLLAIVHCAR.N	0.9958	2	2138.3972
						K.SLGDDISSETSGDFR.K	0.9958	2	1586.6091
						K.DAQILYNAGENK.W	0.9958	2	1336.4441
						K.TLINILTER.S	0.9958	1	1073.2779
398	ANXA4_MOUSE	319	28.53	5	11	R.NHLLHVFDEYK.R	0.9958	2	1415.5913
						K.SELSSNFEQVILGLMTPTVLYDVQELR.R	0.9958	2	3083.5238
						K.SETSGSFEDALLAIVK.C	0.9958	2	1667.8535
						K.QDAQELYEAGEK.R	0.9924	1	1381.4387
						K.AASGFNATEDAQTLR.K	0.9925	2	1552.6408
399	ANXA5_MOUSE	319	54.23	11	129	K.GLGTDEDSILNLLTSR.S	0.9958	2	1704.8748
						R.ETSGNLEQLLLAVVK.S	0.9958	2	1614.8797
						K.QVYEEEYGSNLEDDVVGDTSGYYQR.M	0.9958	2	2916.9819

						R.GTVTDFPGFDGR.A	0.9958	1,2	1269.3562
						R.SIPAYLAETLYYAMK.G	0.9944	2	1735.0479
						R.DPDTAIDDAQVELDAQALFQAGELK.W	0.9958	2,3	2674.878
						K.ALLLLCGGEDD.-	0.9958	1	1176.2751
						R.SEIDLFNIR.K	0.9909	2	1107.2517
						R.DLVDDLK.S	0.9917	1	817.9145
						R.LYDAYELK.H	0.9958	1	1015.151
						K.VLTEIIASR.T	0.9958	1	1002.1991
400	ANXA6_MOUSE	673	57.21	26	310	R.ENDDVVSEDLVQQDVQDLYEAGELK.W	0.9958	2	2851.9917
						K.SLHQAIEGDTSGDFMK.A	0.9958	2	1736.8939
						R.GSVHDFPEFDANQDAEALYTAMK.G	0.9958	2	2557.7504
						R.TNEQMHQLVAAYK.D	0.9958	1,2	1533.7423
						K.KTNYDIEHVIK.K	0.9958	1,2	1360.5529
						R.DQAQEDAQVAAEILEIADTPSGDK.T	0.9958	2	2515.6471
						K.SLEDALSSDTSGHFR.R	0.9958	2	1622.6885
						K.GIGTDEATIIDIVTHR.S	0.9958	2	1711.9127
						K.TTGKPIEASIR.G	0.9958	2	1173.3549
						K.ALLALCGGED.-	0.9958	1	1019.1059
						R.SEIDLLNIR.R	0.9958	1	1073.2346
						R.DLESDIIGDTSGHFQK.M	0.9958	2	1762.8706
						K.GFGSDKESILELITSR.S	0.9958	2	1752.9622
						R.LILGLMMPPAHYDAK.Q	0.9958	2	1671.0687
						R.LIVNLMRPLAYCDAK.E	0.9958	2	1778.1291
						K.GTVCAANDFNPDADAK.A	0.9958	2	1666.7076
						K.DAISGIGTDEK.C	0.9944	1	1106.1748
						K.TLIEILATR.T	0.9924	1	1030.2529
						K.WGTDEAQFIYILGNR.S	0.9958	2	1783.9811
						K.ESILELITSR.S	0.9907	1,2	1161.3409
						K.NKPLFFADK.L	0.9924	1	1080.2719
						K.DLIEDLKYELTGK.F	0.9958	2	1537.7503
						K.MLVVLLQGTR.E	0.9917	2	1130.4344
						K.DAFVAIVQSVK.N	0.9958	1	1177.3861
						R.ILISLATGNR.E	0.9958	2	1058.2663
						R.AINEAYKEDYHK.S	0.9958	2	1481.6048
401	AOC3_MOUSE	765	7.71	3	8	R.THPSQSQPFADLSPEELTAVMSFLTK.H	0.9944	2	2863.2116
						R.YHLAVTQR.K	0.9924	1	988.1343
						R.KLLETEEEAAFPLGGATPR.Y	0.9958	2	2030.2853

402	AOFB_MOUSE	520	26.54	8	47	K.VLNSQEALQPVHYEEK.N	0.9958	2	1885.0837
						K.IPEDEIWQPEPESLDVPARPITSTFLER.H	0.9958	3	3266.6318
						R.GPFPPVWNPITYLDNNNLWR.T	0.9958	2	2414.7282
						K.LERPVIHIDQTGENVIVK.T	0.9958	2	2061.3891
						K.LLHDCGLSVVVLEAR.D	0.9909	2	1681.939
						R.LAKELGLETYK.V	0.9924	1	1265.4924
						R.NQLISRVPLGSVIK.C	0.9937	2	1524.8472
						R.VKLERPVIHIDQTGENVIVK.T	0.9958	2	2288.6957
403	AP180_MOUSE	901	3	1	2	K.GLGSDLDSSLASLVGNLGISGTTSK.K	0.9958	2	2350.5853
404	AP1G2_MOUSE	791	1.01	1	5	K.MPLVER.G	0.9958	1	744.9274
405	AP1M2_MOUSE	423	4.96	1	2	R.VHFLWIKHSNLYLVATTLK.N	0.9958	3	2284.7526
406	AP2A1_MOUSE	977	11.26	5	8	K.FFQPTEMAAQDFFQR.W	0.9958	2	1864.0851
						R.ACNQLGQFLQHR.E	0.9958	2	1472.6127
						K.LLGFGSALLDNVDPNPENFVGAGIIQTK.A	0.9958	2	2901.289
						R.GLAVFISDIR.N	0.993	2	1091.2957
						R.MYLFYGNKTSVQFQNFLPTVVHPGDLQTQ	0.9958	3	4015.619
407	AP2A2_MOUSE	938	9.91	5	10	K.QLSNPQQEVQNIFK.A	0.9958	2	1673.8662
						K.ILVAGDTMDSVKQSAALCLLR.L	0.9958	2	2262.6362
						K.TSVSLAVSR.L	0.9958	1	920.0537
						R.VVHLLNDQHLGVVTAATSLITTLAQK.N	0.9958	2	2744.2071
						R.SSPLIQFNLLHSK.F	0.9958	2	1484.7385
408	AP2B1_MOUSE	937	11.95	6	13	R.APEVSQYIYQVYDSILK.N	0.9958	2	2017.286
						K.ALQHMTDFAIQFNK.N	0.9958	2	1664.9195
						K.RNVEGQDMLYQSLK.L	0.9958	2	1681.9042
						R.LSHANSAVVLSAVK.V	0.9915	2	1396.6298
						K.LHDINAQMVEDQGFLDSLR.D	0.9958	2	2202.4467
						K.KLAPPLVTLLSGEPEVQYVALR.N	0.9958	2	2394.8601
409	AP2E_MOUSE	442	4.98	1	2	K.DSLVGGISNPSEVFCSVPGR.L	0.9911	3	2078.2525
410	AP2M1_MOUSE	435	5.06	1	30	K.WARPPISMNFEVPFAPSGLK.V	0.9925	2,3	2245.6471
411	AP3B1_MOUSE	1105	3.26	2	4	K.VVNVANLGAVPSSQDNVHR.F	0.9936	2	1977.1875
						R.FQLGTLSHTLNIK.A	0.9958	2	1472.7275
412	AP3B2_MOUSE	1082	2.77	2	2	K.KLFLAPKPAPILESSFK.D	0.9958	2	1887.3159
						K.DQLIEVIEK.L	0.9958	1	1087.2585
413	AP4A_MOUSE	147	25.17	2	5	R.LSQEHQAYR.W	0.9958	2	1132.2211
						K.MDNSTIEFLLLQASDGIHHWTPPK.G	0.9958	2	2752.1169
414	AP4E1_MOUSE	1122	7.4	2	2	K.TPSAPTAPCSALSLGSDVAGGDEDGLSAVI	0.9958	3	4166.3784
						K.YLGLKALTYVIQQDPSLALQHQITIIGCLDHF	0.9944	3	4187.8786

415	APBA2_MOUSE	750	2.53	1	4	R.SDLNGPTDNNNIPETKK.V	0.9958	1,2	1857.9719
416	APBB3_MOUSE	486	12.35	2	2	R.SQPHDGTWGEGQNMLMILK.K	0.9958	2	2143.4401
						R.KTWVPAMLSVSDSLMTAHAIQAEAGAEEE	0.9944	3	4111.6431
417	APC_MOUSE	2845	1.3	3	81	K.EKDWYYAQLQNLTK.R	0.9958	1	1801.0086
						K.DWYYAQLQNLTK.R	0.9944	1	1543.7191
						K.YKDANIMSPGSSLPSLHVR.K	0.9943	2	2073.3746
418	APEH_MOUSE	732	34.15	12	89	R.QVLLSEPQEAAALYR.G	0.9929	2	1688.9212
						R.GSTGFGQDSILSLPGNVGHQDVK.D	0.9958	2	2314.5168
						K.DVQFAVQQVLQEEHFDAR.R	0.9958	2	2160.3507
						R.QYLVFHDGDSVVFAGPAGNSVETPGELLS	0.9958	3	3163.4705
						R.QPSLSAACLGPEVTTQYGGLYR.T	0.9958	2	2369.6025
						R.QDLFAVDTQTGSVTSLTAGGSAGSWK.L	0.9958	2	2585.7869
						R.DLMVAQFSTPNLPPSLK.V	0.9958	2	1859.1908
						K.EQSVSWVSLEEAEPIPDIHWGIR.V	0.9958	2	2678.961
						K.GDQFVFYEDWGETMVSK.S	0.9958	2	2039.2233
						K.STHALSEVEVESDSFMNTVLWLHTHLGS.-	0.9958	3	3128.4401
						R.DLMVAQFSTPNLPPSLKVGFLPPAGK.E	0.9958	2	2726.2494
						K.KPDQAIK.G	0.9958	1	799.9456
419	APEX1_MOUSE	317	13.56	2	3	R.QGFGELLQAVPLADSFR.H	0.9958	2	1849.0965
						K.LPAELQELPGLTHQYWSAPSDK.E	0.9912	2	2481.7673
420	APEX2_MOUSE	516	12.79	3	11	R.DVLTEPLAIVEGYNSYFSFSRSR.S	0.9943	2	2651.9353
						R.KSQGGPK.R	0.9958	1	701.8008
						K.WMDGLLSNPGDEAGPHIGLFMDSYRYLHF	0.9958	3	3418.869
421	API5_MOUSE	504	13.49	3	4	K.LFDKLLEYMPLPPEEAENGENAGNEEPK.L	0.9909	3	3175.4909
						R.NYGILADATEQVGQHK.D	0.9958	2	1744.9017
						K.GTLGGLFSQILQGEDIVR.E	0.9958	2	1904.1735
422	APIP_MOUSE	241	39	6	47	K.AAVMATLLFPGQEFK.I	0.9944	2	1623.9507
						R.HGVYVWGETWEK.A	0.9947	2	1491.6457
						R.MAHAMNEYPDSCAVLVR.R	0.9958	2	1965.2154
						K.HGNEIYIAPSGVQK.E	0.9958	2	1513.6933
						K.QFYHLGWVTGTGGGISLK.H	0.9958	2	1922.1937
						R.GAGAVIHTHSK.A	0.9958	1	1078.2162
423	APLF_MOUSE	499	3.41	1	4	K.QKDGILIEELGEVSK.H	0.9944	2	1658.8895
424	APMAP_MOUSE	415	7.71	1	4	R.RSLHDPDGQVVTYVSEAHEHDGYLYLGSF	0.9958	3	3449.7203
425	APOA1_MOUSE	264	59.47	12	607	R.DYVSQFESSSLGQQLNLNLLENWDTLGST	0.9958	3	4101.4296
						K.DFANVYVDAVK.D	0.9958	1	1241.3861
						R.LSPVAEEFR.D	0.9944	1	1048.1839

						K.SNPTLNEYHTR.A	0.9958	1,2		1332.4154
						R.THVDSLR.T	0.9958		1	827.9157
						R.TQLAPHSEQMR.E	0.9958	1,2		1298.4595
						R.HSLMPMLETLK.T	0.9958		2	1300.6173
						K.VQPYLDEFQK.K	0.9958		1	1267.424
						R.DFWDNLEK.E	0.9944		1	1067.143
						K.VAPLGAELQESAR.Q	0.9958	1,2		1341.507
						K.WKEDVELYR.Q	0.9958	1,2		1238.3855
						K.VKDFANVYVDAVK.D	0.9958		2	1468.6928
426	APOA2_MOUSE	102	47.06	3	216	R.QADGPDMQSLFTQYFQSMTEYGK.D	0.9958		2	2673.9283
						K.THEQLTPLVR.S	0.9958		2	1194.3763
						K.TSEIQSQVK.A	0.9926		2	1020.1277
427	APOA4_MOUSE	395	56.71	13	192	K.ENVDNLHTSMMPLATNLK.D	0.9958		2	2029.3338
						R.QQLGPNSGEVESHLSFLEK.S	0.9958	2,3		2100.2927
						K.KGSPDQPQALPLPEQAQEQAQEQAQEQV	0.9958		3	3854.1791
						K.LVPFVVQLSGHLAKETER.V	0.9958		2	2024.3708
						K.TDVTQQLSTLFQDK.L	0.9958	1,2		1624.7881
						K.ALVQQLEQFR.Q	0.991		2	1232.4251
						K.LGDASTYADGVHNK.L	0.9958		2	1448.5321
						K.LQEHLKPYAVDLQDQINTQTQEMK.L	0.9958	2,3		2872.2225
						K.LNHQMEGLAFQMK.K	0.9958	1,2		1547.8304
						K.VTQTFGENMQK.L	0.9958		1	1283.4418
						R.SLAPLTVGVQEK.L	0.9958		1	1242.4582
						K.NLAPLVEDVQSK.V	0.9958		1	1313.4936
						R.TVEPMGEMFNK.A	0.9944		1	1283.5
428	APOC1_MOUSE	88	27.27	2	2	R.AWFSEAFGK.V	0.9958		1	1043.1668
						K.LKEFGNTLEDK.A	0.9958		1	1294.4472
429	APOC2_MOUSE	97	23.71	1	6	K.SSAAMSTYAGIFTDQLLTLLR.G	0.9958		2	2260.6105
430	APOC3_MOUSE	99	49.49	3	28	K.TVQDALSSVQESDIAVVAR.G	0.9958		2	1989.19
						K.FTGFWDSNPEDQPTPAIES.-	0.9958		2	2139.239
						R.GWMDNHFR.F	0.9929		2	1063.1785
431	APOE_MOUSE	311	16.08	2	3	K.GWFEPIVEDMHR.Q	0.9958		2	1516.7143
						R.WVQTLSDQVQEELQSSQVTQELTALMEDT	0.9958		3	3927.3413
432	APOH_MOUSE	345	41.16	10	74	R.ICPKPDDLPFATVVPLK.T	0.9958		1	1911.258
						R.FTCPLTGMWPINTLR.C	0.9958		2	1808.1145
						R.ITCPPPPVPK.F	0.9958		2	1106.3166
						R.VCPFAGILENGIVR.Y	0.9958		2	1545.7881

						K.EHSSLAFWK.T	0.9958	1	1105.2383
						K.TSYDPGEQIVYSCKPGYVSR.G	0.9958	2	2307.4877
						K.IQEQFKNGMMHGDK.I	0.9958	2	1663.9068
						K.IHFYCK.N	0.9958	1	867.9891
						K.CPFPPRPENGYVNYPAKPVLLYK.D	0.9958	3	2721.1401
						R.ICPKPDDLPFATVVPLKTSYDPGEQIVYSCI	0.9958	3	4199.7225
433	APOOL_MOUSE	265	47.55	9	47	K.AYATSQQIFQAIK.S	0.9958	2	1469.6805
						K.IAYPLGLATLGATVCYPAQSVIIAK.I	0.9958	2	2592.0601
						K.MGVITASGLAGLLSAR.K	0.9958	2	1517.8272
						K.LMDHGQSHPDDK.D	0.9958	1,2	1380.4748
						K.HSVSLPK.E	0.9958	1	767.9035
						K.QLVRPDQLPIYTAPPLHSK.Y	0.9958	2	2174.551
						K.LMDHGQSHPDDKDMYSTR.S	0.9944	2	2134.3027
						K.SESTSGTTQFIPDPK.L	0.9958	1	1595.7032
						K.KAYATSQQIFQAIK.S	0.9958	2	1597.8546
434	APT_MOUSE	180	12.22	1	13	R.GFLFGPSLAQELGVGCVLIR.K	0.9958	2	2134.4925
435	AQP1_MOUSE	269	21.19	2	5	K.VWTSGQVEEYDLDADDINSR.V	0.9958	2	2313.396
						K.LFWRAVVAEFLAMTLFVFISIGSALGFNYPL	0.9958	3	3780.5085
436	AQR_MOUSE	1481	6.41	6	10	R.KFWNLIK.K	0.9958	1	949.1839
						R.FIELMIDLEALLPTR.R	0.9958	1,2	1775.1566
						R.NTIQFTHTQIEAIRAGMQPGLTMVVGPPGT	0.9944	3	3352.8945
						K.RNTIQFTHTQIEAIR.A	0.9958	2	1829.0689
						R.KNGERPPHEVQVIK.N	0.9958	1	1631.8753
						K.GRSYEEDMEIAEGCFR.H	0.9944	1	1950.0529
437	AR13B_MOUSE	427	14.05	2	2	K.GLYWLLHIIAKDFDALSER.I	0.9944	2	2261.6286
						R.EQTELDGTSGLAEIDSGPVLANPFQPIAAVI	0.9944	3	3896.3404
438	ARAF_MOUSE	604	3.15	1	2	R.DQEHFSFPAPANPPLQR.I	0.9958	2	1952.1362
439	ARC1A_MOUSE	370	15.41	3	23	R.TQIALSPNNHEVHIYK.K	0.9956	2	1865.0989
						K.DGIWKPTLVILR.I	0.9926	2	1411.7306
						R.STVLSLDWHPNNVLLAAGSCDFK.C	0.9958	2	2545.8206
440	ARF1_MOUSE	181	40.88	3	73	R.HYFQNTQGLIFVVDSNDR.E	0.9958	2	2154.3464
						R.NWYIQATCATSGDGLYEGLDWLSNQLR.N	0.9958	2	3133.3667
						K.LKLGEIVTTIPTIGFNVETVEYK.N	0.9958	2	2566.0099
441	ARFG1_MOUSE	414	11.35	2	2	K.EWSLESSPAQNWTPPQPK.T	0.9952	2	2083.2646
						R.EDDFLNNAMSSLYSGWSSFTTGASK.F	0.9958	2	2716.8922
442	ARHG1_MOUSE	920	8.04	2	2	R.FIQEVVQSQQAAVSRQLEDFR.S	0.9924	2	2479.755
						R.EPGVDTPQEPGDTPPQGPTSLEPLAPPES	0.9931	3	5011.1121

443	ARHGC_MOUSE	1543	3.5	3	3	R.ITSPVLVGEENNVVHNQK.V	0.9958	2	1978.2126
						R.FHTFVQDAESNPLCR.R	0.9924	1	1821.9531
						K.SAAEHLFVTATQFAK.E	0.9958	2	1621.8333
444	ARHGG_MOUSE	713	7.85	2	3	R.HKAQVCVEDISDILEDHAQHHFHPYIAYCSI	0.9958	3	4539.8561
						K.SPARHQSFGAAVLSK.E	0.993	2	1556.7647
445	ARHGH_MOUSE	2057	5.01	4	8	K.LQHAASVTCILYLNNK.V	0.9958	2	1846.1027
						R.AATSEEPSGFSVDSNLLGSLNSK.T	0.9912	2	2311.4644
						R.GSLEDLLSVDPEAYQSSVWLGTEDGCVHV	0.9944	3	4372.6252
						K.DDDLWSSRSSVGWGVYR.S	0.9958	3	1986.1075
446	ARHL1_MOUSE	353	50.14	9	115	R.ENSVLGSIQEELQK.T	0.9958	1,2	1574.7282
						R.LEDLGAALHR.L	0.9944	1	1095.2437
						K.GRLEDLGAALHR.L	0.9958	2	1308.4831
						R.GHDAPMIAYDALLASGSNWTELCQR.A	0.9955	2	2778.0345
						R.HMAEYQEHWFYFEAK.W	0.9958	2	2017.225
						R.YVETVETLSEHRPDPSTIEGCSQLKPDNYL	0.9958	3	4677.1035
						K.AAMLLGSVGDALGYGNICR.E	0.9958	2	1939.2031
						K.TGGLDSLVLSPGR.W	0.9944	1	1272.4441
						R.WPVSDNTIMHMATAEALTTDYWCLDDLYR	0.9958	3	3490.8497
447	ARI1_MOUSE	555	5.95	2	5	R.VLLQHVHEGYEK.D	0.9958	2	1452.653
						K.KCDDDSETSNWIAANTK.E	0.9944	1	1955.9959
448	ARI4B_MOUSE	1314	3.58	3	5	R.NGDKDPDLK.E	0.9924	1	1002.0691
						K.EDNSSEEEEEIEPFPEER.E	0.9907	2	2195.1682
						K.VEHSTHSRNELISK.E	0.9958	2	1637.7929
449	ARI5B_MOUSE	1188	4.04	2	2	K.EAEEMGDKGLAPLLPSPPLPPEK.D	0.9956	2	2416.7919
						K.NQTVLSPLMQPLAFHSLVMQR.G	0.9944	2	2411.886
450	ARIP4_MOUSE	1466	4.91	3	4	K.KPCHIYRLVADYTLEK.K	0.9958	2	2007.3062
						K.SSRDEVIELSSGEEDTLHIVDSSESVSEEDE	0.9944	3	3925.9686
						K.GGTHVNDALNQHDALGR.V	0.9958	1	1775.8783
451	ARK72_MOUSE	367	27.79	6	80	R.VDLFYLHAPDHSTPVEETLR.A	0.9958	2,3	2340.5975
						R.AASGAPLRPATVLGTMEMGR.R	0.9958	2	1987.3429
						R.FFGNNWAETYR.N	0.9958	2	1405.5119
						R.FYAYNPLAGGLLTGK.Y	0.9958	2	1585.8431
						R.WMYHHSQLQGTR.G	0.9958	2	1544.7307
						K.EHHFEAIALVEK.A	0.9958	2	1423.6115
452	ARL10_MOUSE	243	7.41	1	6	K.NFEVDLLEIGDSQNLR.F	0.9958	2	1863.0343
453	ARL3_MOUSE	182	24.73	2	2	K.QLASEDISHITPTQGFNIK.S	0.9952	2	2100.336
						K.QDLLTAAPASEIAEGLNLHTIR.D	0.9958	2	2334.6347

454	ARL8A_MOUSE	186	13.44	1	21	K.NELHNLLDKPQLQGIPVLVLGNK.R	0.994	2	2554.0079
455	ARMC1_MOUSE	282	22.7	3	27	R.VGSHPEGGASWLSTAANFLSR.S	0.9958	2	2145.339
						K.AQFFLGTTNK.R	0.9958	1	1127.2853
						K.LLASEIYDILQSSNLADGDSFNEMNSR.R	0.9958	3	3004.2519
456	ARMC5_MOUSE	926	3.13	1	18	R.GCSRACAEQLSLGGALGPLVSLASHPK.R	0.9958	2	2738.0485
457	ARMET_MOUSE	179	16.2	2	3	K.IINEVSKPLAHHIPVEK.I	0.9958	2	1925.2816
						R.KINELMPK.Y	0.9958	1	973.2188
458	ARP10_MOUSE	417	13.67	3	3	R.YLVEKPKYK.K	0.9958	1	1168.4215
						R.KQLAENLVIIGGTSMLPGFLHR.L	0.9937	2	2395.8687
						K.GQSLPSVMGSVPEGVLEDIK.V	0.9958	2	2043.3399
459	ARP19_MOUSE	112	43.75	3	6	R.KPSLVASK.L	0.9958	1	830.0153
						K.QLPAAAPDKTEVTGDHIPTPQDLPQR.K	0.9958	3	2797.0971
						K.EMEDKVTSPEK.A	0.9958	1	1293.4315
460	ARP2_MOUSE	394	16.5	4	11	K.HIVLSGGSTMYPGLPSR.L	0.9958	2	1773.06
						K.HMVFLGGAVLADIMK.D	0.9958	2	1602.9935
						R.GYAFNHSADFETVR.M	0.9958	2	1614.7141
						K.HLWDYTFGPEK.L	0.9958	2	1393.5413
461	ARP3_MOUSE	418	15.79	3	12	K.NIVLSGGSTMFR.D	0.9958	2	1282.5004
						R.FLGPEIFFHPEFANPDFTQPISEVVDEVIQN	0.9958	3	4318.7951
						R.DITYFIQQLLR.D	0.9958	2	1410.6561
462	ARP5L_MOUSE	153	39.87	4	8	K.ALAVGGLGSIIR.V	0.9958	2	1127.3726
						K.GFEKPTENSSAVLLQWHEK.A	0.9958	2	2201.4435
						K.SSEIEQAVQSLDR.N	0.9958	2	1462.5565
						R.RVDIDEFDENK.F	0.9958	2	1380.4539
463	ARPC2_MOUSE	300	7	2	3	R.DNTINLIHTFR.D	0.9944	2	1344.5131
						R.DYLHYHIK.C	0.9958	1	1089.2389
464	ARSA_MOUSE	506	7.91	1	5	R.LTAHEPPLLYDLSQDPGENYNVLESIEGVS	0.9958	3	4152.6013
465	ARSA1_MOUSE	348	11.78	2	10	K.YLDQMEDLYEDFHIVK.L	0.9958	2	2059.2978
						K.IDTHNIIVNQLVFPDPEKPCK.M	0.9958	2	2478.8169
466	ARSG_MOUSE	525	10.48	2	2	K.QTTWEGGHRVPALAYWPGR.V	0.9929	2	2183.4367
						K.ACDGSVGPEQHHVAPLIFNLEDAADEGMP	0.9958	3	3447.767
467	AS3MT_MOUSE	376	5.85	1	7	R.FAPDFLFTPVDASLPAPQGR.S	0.9958	2	2147.4381
468	ASAH1_MOUSE	394	22.34	5	28	K.NLSFATIYDVLSTKPVLNK.L	0.9958	2	2124.4851
						K.LPGMIGSLPDPFGEEMR.G	0.9958	2	1847.1543
						R.ILVNSITSLVNTFVPSGK.L	0.9958	2	1890.2303
						R.KESLDVYELDPK.H	0.9944	2	1436.6018
						K.IMAPVYFILGGK.K	0.9919	2	1309.6526

469	ASAHL_MOUSE	362	8.84	2	2	R.VPQWVLGMVGEIVSK.V	0.9958		2	1642.9971
						R.VETNYDHWKPAPK.V	0.9958		2	1585.7593
470	ASB18_MOUSE	467	15.2	2	157	R.ELLEHGATVQLEGGPGRDTPLHVAAQR.G	0.9958		3	2853.1673
						R.GALHEACLGNHTACARLLLQHGADPDLLN	0.9944		3	4373.817
471	ASC_MOUSE	193	31.61	3	3	R.GALLQMDAIDLTDK.L	0.9958		2	1504.7387
						K.EESGAVAAAASVPAQSTARTGHFVDQHR.	0.9958		3	2852.0525
						K.LFSFVPSWNLTCK.D	0.9957		2	1599.8359
472	ASGL1_MOUSE	326	43.56	8	24	R.VGDSPCIGAGGYADNNLGAVSTTGHGESI	0.9912		3	3019.2177
						R.LALFHVEQGK.T	0.9958		2	1142.3433
						K.TVEEAAQLALDYMK.S	0.9958		2	1582.809
						K.FAEDMGIPQVPVEK.L	0.9958		2	1560.8053
						R.ASIDVSLVVVVHGGGASNISANR.K	0.9915		2	2223.4941
						R.GNLAYATSTGGIVNK.M	0.9958		2	1466.6341
						K.GLGGLILVNK.T	0.9944		1	984.2272
						K.TPHCFLTGHGAEK.F	0.9958		1	1455.5792
473	ASHP2_MOUSE	343	15.45	2	2	K.HDVELLERNFQAILCEFETLYK.A	0.9958		3	2769.0925
						R.YLSSQPSIQKPEVFFLPDLPTTPYFSR.D	0.9931		3	3159.6086
474	ASM3A_MOUSE	445	23.15	4	7	K.VYSAVADLWKPWLGEEAISTLK.K	0.9958		2	2477.8627
						K.NSGQEASFMIWTGDSPPHVPVPELSTGTV	0.9958		3	3283.6801
						R.APAVGQFWHVTDLHLDPTYHITDDR.T	0.9958		3	2906.1863
						R.YSSVIAGQFYGHTHR.D	0.9958		2	1723.8882
475	ASPC1_MOUSE	550	4.18	1	3	R.AALQNTTLQSLGLTGGSATIR.F	0.9958		2	2074.3421
476	ASPH_MOUSE	741	5.26	2	2	K.LGVYDADGDGDFDVDDAK.V	0.9929		2	1887.9079
						R.LIFIVDVWHPELTPQQR.R	0.9958		2	2092.4484
477	ASPM_MOUSE	3122	1.7	2	4	R.RARPDPEAGDPSPPVLLLSHFCGVPFLCF	0.9958		3	3681.1206
						K.MCKAALVIQSFYCAYR.A	0.9958		2	1982.2802
478	ASPN_MOUSE	373	5.09	1	6	R.LYLSHNQLSEIPLNLPK.S	0.9924		2	1980.3146
479	ASTL_MOUSE	435	11.95	2	6	R.SGGMQVVSLAPTCLRK.G	0.9958		1	1704.9917
						K.DIPAINQGLISEETPESSFLVEGDIIRPSPFR	0.9958		3	3528.9409
480	ASXL3_MOUSE	2259	2.48	2	2	K.SEPLSFEESLSSSCELGMK.Q	0.9911		3	2118.2833
						R.IPSASSSSCRLSSVEANNPLVTQLLQGNLP	0.9958		3	3511.9207
481	AT12A_MOUSE	1035	5.02	3	27	K.FQLSIHETEDPNDK.R	0.9943		2	1673.7765
						K.VIMVTGDHPITAK.A	0.9958	1,2		1382.6611
						R.QDAVVAVTGDGVNDSPALK.K	0.9958		2	1857.0275
482	AT131_MOUSE	1200	2	2	2	R.DLEEESTPIVK.L	0.9958		2	1260.3837
						R.LHVIFGGTK.V	0.9924		1	972.1753
483	AT134_MOUSE	1193	10.65	5	5	K.ILINGTIFARMSPGQK.S	0.9958		2	1747.1088

						K.ALDVITIAVPPALPAALTTGIIYAQRR.L	0.9958		3	2806.3647
						R.MTVIVQEMGGGR.L	0.9924		1	1278.5274
						K.GAPERVASFCQPDTVPTSFISELQIYTTQGI	0.9958		3	3604.9642
						R.SNSTFASFENTTIWFLGTINCIFVALVFSK.G	0.9958		3	3416.8641
484	AT1A1_MOUSE	1023	36.56	26	334	K.DAFQNAYLELGGLGER.V	0.9958		2	1753.909
						K.VDNSSLTGESEPQTR.S	0.9958		2	1620.6702
						R.QGAIVAVTGDGVNDSPALK.K	0.9958		2	1813.0177
						K.DMTSEELDDILR.Y	0.9958		1	1437.5616
						K.NLEAVETLGSTSTICSDK.T	0.9958		2	1926.0509
						K.GVGIISEGNETVEDIAAR.L	0.9958	1,2		1830.9897
						K.QAADMILLDDNFASIVTGVEEGR.L	0.9958		2	2465.7375
						K.KADIGVAMGIVGSDVSK.Q	0.9958		2	1647.9275
						R.LNIPVNQVNPR.D	0.9958	1,2		1264.4703
						K.RAVAGDASESALLK.C	0.9958		2	1388.5638
						K.MSINAEDVVVGDLVEVK.G	0.9917		2	1818.0925
						R.NSVFQQGMK.N	0.9958		1	1039.1944
						R.SPDFTNENPLETR.N	0.9958		2	1520.5957
						R.AVFQANQENLPILK.R	0.9958	1,2		1585.8436
						K.EQPLDEELKDAFQNAYLELGGLGER.V	0.9958		2	2836.0844
						R.MTVAHMWFDNQIHEADTTENQSGVSFDK.	0.9958	2,3		3240.5025
						K.YQLSIHK.N	0.9958		1	889.0421
						K.NMVPQQALVIR.N	0.9944		2	1269.548
						K.NMVPQQALVIRNGEK.M	0.9958		2	1697.9933
						K.IVEIPFNSTNK.Y	0.9924		1	1262.4484
						R.DKYEPAAVSEHGDK.K	0.9924		1	1546.6335
						K.ACVVHGSDLK.D	0.9946		2	1086.1993
						K.QAADMILLDDNFASIVTGVEEGRLIFDNLK.I	0.9958		3	3309.7589
						R.YHTEIVFAR.T	0.9924		1	1136.2957
						R.CSSILLHGK.E	0.9944		2	1015.1638
						R.NIAFFSTNCVEGTAR.G	0.9958		2	1687.8157
485	AT1A2_MOUSE	1020	2.94	2	2	R.VLGFCQLNLPSGK.F	0.9958		2	1433.6568
						R.SPEFTHENPLETR.N	0.9958		2	1557.6598
486	AT1A3_MOUSE	1013	2.57	2	4	R.DLDDLK.K	0.9958		1	718.782
						R.VLGFCHYYLPEEQFPK.G	0.991		2	2028.2806
487	AT1A4_MOUSE	1032	3.49	2	12	K.NMVPQQALVIRDGEK.M	0.9927		2	1698.9781
						K.KADIGIAMGITGSDVSK.Q	0.9958		2	1663.9269
488	AT1B1_MOUSE	304	10.2	2	14	K.YNPNVLPVQCTGK.R	0.9944		1	1490.6654

						R.VAPPGLTQIPQIQK.T	0.9958		2	1490.7862
489	AT1B3_MOUSE	278	16.19	2	2	R.IIDLIPDGYPQISCLPK.E	0.9958		2	1943.2568
						R.ACQFPVSLLEECSGVTDANFGYSK.G	0.9944		2	2680.8599
490	AT2A1_MOUSE	994	9.76	7	212	R.VDQSILTGESVSVIK.H	0.9931		2	1575.7997
						K.NMLFSGTNIAAGK.A	0.9958		1	1324.5377
						K.KNMLFSGTNIAAGK.A	0.9958		1	1452.7118
						R.SLPSVETLGCTSVICSDK.T	0.9944		1	1954.114
						K.TASEMVLADDNFSTIVAAVEEGR.A	0.9958		2	2426.6575
						K.EFTLEFSR.D	0.9924		1	1029.1375
						K.HTDPVPDPR.A	0.9944		2	1034.1167
491	AT2A2_MOUSE	1044	31.99	27	2080	K.DIVPGDIVEIAVGDK.V	0.9958		1	1540.7539
						K.KSEIGIAMGSGTAVAK.T	0.9958		2	1520.7845
						K.TVEEVLGHFGVNESTGLSLEQVK.K	0.9909		2	2473.7423
						K.IVEFLQSFDEITAMTGDGVNDAPALK.K	0.9943		2	2783.1225
						K.AKDIVPGDIVEIAVGDK.V	0.9958	1,2		1740.0068
						R.CLALATHDNPLK.R	0.9958	1,2		1353.5273
						K.VGEATETALTCLVEK.M	0.9958		1	1621.7913
						K.VEGDTCSLNEFSITGSTYAPIGEVQK.D	0.9958		2	2804.0027
						K.YETNLTFVGCVGMLDPPR.I	0.9958		2	2070.3339
						R.IGIFGQDEDVTSK.A	0.9958	1,2		1409.5358
						R.RIGIFGQDEDVTSK.A	0.9958	1,2		1565.7233
						R.CLALATHDNPLKR.E	0.9958		2	1509.7148
						R.EFDELSPSAQR.D	0.9944	1,2		1279.3489
						R.MFILDKVEGDTCSLNEFSITGSTYAPIGEVQ	0.9958		3	3551.9534
						K.SMSVYCTPNKPSR.T	0.9958		2	1527.7015
						K.VPMTPGVK.Q	0.9958		1	829.0453
						K.MNVFDTELK.G	0.9958		1	1097.2714
						K.SEIGIAMGSGTAVAK.T	0.9958	1,2		1392.6104
						K.IVEFLQSFDEITAMTGDGVNDAPALKK.S	0.9958		2	2911.2965
						K.DIVPGDIVEIAVGDKVPADIR.L	0.9958		2	2192.5175
						K.TVEEVLGHFGVNESTGLSLEQVKK.L	0.9958		2	2601.9164
						K.CHQYDGLVELATICALCNDSALDYNEAK.G	0.9958		2	3245.422
						K.AMGVVVATGVNTEIGK.I	0.9958		1	1546.8224
						K.TGTLTTNQMSVCR.M	0.9958		1	1469.6191
						R.VSFYQLSHFLQCK.E	0.99		2	1657.8755
						K.AFTGREFDELSPSAQR.D	0.9924		2	1811.9487
						K.REEMHLEDSANFIK.Y	0.9944		2	1719.9097

492	AT5F1_MOUSE	256	40.63	9	50	R.LGLIPEEFFQFLYPK.T	0.9958	2	1842.1877
						R.HYLFDVQR.N	0.9958	1,2	1078.2156
						R.NNIALALEVTYR.E	0.9958	2	1377.5834
						R.LDYHISVQNMMR.R	0.9958	1	1507.7657
						K.RHYLFDVQR.N	0.9958	2	1234.4031
						K.KAQAQPIM.-	0.9958	1	887.085
						K.SISVQQEK.E	0.9952	2	919.0226
						K.YGASFGEFIDKLNEEK.I	0.9931	2	1848.0191
						R.KEEEHMIDWVEK.H	0.9958	2	1573.7607
493	AT8B5_MOUSE	1183	3.55	2	16	R.FNSLFEYPDNSIKTSK.Y	0.9925	2	1891.0875
						K.VEGELVYQAQSPDEGALVTATR.N	0.9958	2	2334.545
494	ATAD1_MOUSE	361	38.23	6	55	R.HVDLLEVAQETDGFSGSDLK.E	0.9958	2	2161.33
						R.FHINQPALK.Q	0.9937	2	1068.2639
						R.FINLQPSTLTDKWYGESQK.L	0.9958	2	2256.5199
						R.EYVNSTSEESHDEDEIRPVQQQDLHR.A	0.9958	3	3142.2359
						K.LQPSIIFIDEIDSFLR.N	0.9958	2	1907.2169
						K.AQFMSLWDGLDTDHSCQVIVMGATNRPQI	0.9958	3	4081.5485
495	ATAD3_MOUSE	591	21.32	7	38	R.LVSRPQDALEGVILSPSLEAR.V	0.9958	2	2251.5883
						K.EALSLAQMQEQTLQLEQQSK.L	0.9958	2	2304.5775
						K.GEGTGPPLPLPPAQPGAEGGGDR.G	0.9958	2	2128.3061
						K.EYEAAVEQLK.S	0.9924	1	1180.3
						K.VERPDSQTNKPPHPSLLSC.-	0.9958	2	2163.3611
						K.DKWSNFDPTGLER.A	0.9958	2	1565.6824
						R.HKNEMLR.V	0.9958	1	928.0972
496	ATAD5_MOUSE	1826	2.35	2	2	R.DFLMSGLPDLLK.R	0.9944	1	1349.6282
						R.WAPQSAGELKATAEALSFTECSSTISK.A	0.9958	3	2872.1243
497	ATF6B_MOUSE	699	1.72	1	10	K.KEYLQGLEAR.L	0.9958	1	1207.372
498	ATG3_MOUSE	314	9.87	2	7	K.QFLVTKNVPCYK.R	0.9958	2	1497.7436
						K.AKADAGGEDAILQTR.T	0.9958	2	1516.6512
499	ATG7_MOUSE	698	3.3	1	2	K.LQFAPFNSALDVGFWHELTQK.K	0.9958	2	2449.771
500	ATG9B_MOUSE	922	8.13	3	3	R.CVDYNVLFNNQPK.N	0.9924	1	1611.7607
						R.SPPTPGVLSDCTSPLPEAFLANLLVNPRPP	0.9958	3	3442.9061
						R.WGDLGPSSVPLLHMALPLPASPCR.G	0.9932	2	2572.9941
501	ATIF1_MOUSE	106	29.25	4	7	K.KIQQLK.N	0.9944	1	757.9517
						K.HHEDEIDHHSK.E	0.9958	2	1384.4074
						R.KHHEDEIDHHSK.E	0.9915	2	1512.5815
						K.TKEQLAALR.K	0.9958	2	1030.2125

502	ATL2_MOUSE	957	5.96	2	3	K.RLVLCMELANGKPQIR.S	0.991	2	1899.2714
						K.CEPIGCDGVLFSTHTLDKCGVCQGDGSSC	0.9958	3	4147.2884
503	ATM_MOUSE	3066	1.7	2	2	K.VDPTGEYENLVTIKSFK.T	0.9946	2	1941.1883
						K.EVIIELIQLQIYIHHPQGARAPEEGAYESMK.	0.9911	3	3565.0814
504	ATOX1_MOUSE	68	50	3	109	K.KVCIDSEHSSDTLLATLNK.T	0.9958	2	2132.3417
						K.VCIDSEHSSDTLLATLNK.T	0.9958	2	2004.1676
						K.LGGVEFNIDLPNK.K	0.9958	1	1416.617
505	ATP4A_MOUSE	1033	5.32	3	5	K.NLEAVETLGSTSVICSDK.T	0.9958	2	1924.0784
						K.AGGGGGK.K	0.9924	1	503.5357
						K.AIAASVGIISEGSETVEDIAARLR.M	0.9958	2	2429.7331
506	ATP5H_MOUSE	161	82.61	12	1267	R.LASLSEKPPAIDWAYYR.A	0.9958	2	1981.2585
						R.ANVAKPGLVDDFEK.K	0.9958	1	1503.6952
						R.NIIPFDQMTIDDLNEIFPETK.L	0.9924	2	2494.8189
						K.TIDWVSFVEVMPQNQK.A	0.9958	2,3	1922.2061
						K.YTALVDQEEKEDVK.S	0.9944	2	1667.8101
						K.SCAEFVSGSQLR.I	0.9958	1,2	1341.4296
						K.YTALVDQEEK.E	0.9944	1	1196.2994
						K.IPVPEDKYTALVDQEEK.E	0.9958	2	1975.2029
						K.YPYWPHQPIENL.-	0.9958	1	1557.7484
						K.SWNETFHAR.L	0.9958	1,2	1148.2229
						R.ANVAKPGLVDDFEKK.Y	0.9958	2,3	1631.8693
						K.KYPYWPHQPIENL.-	0.9958	1,2	1685.9225
507	ATP5I_MOUSE	71	69.01	5	33	R.YSALIIGMAYGAK.R	0.9926	2	1358.6385
						-.MVPPVQVSPLIK.F	0.9958	1	1308.6654
						R.YSYLKPR.A	0.9924	1	927.091
						R.ELAEAQDDSILK.-	0.9958	1	1332.4503
						K.RYSYLKPR.A	0.9958	2	1083.2785
508	ATP5J_MOUSE	108	47.22	6	177	K.RQASGGPVDIGPEYQQDLDR.E	0.9958	2	2202.3451
						R.QASGGPVDIGPEYQQDLDR.E	0.9958	2	2046.1577
						K.FDDPKFEVIDKPQS.-	0.9958	1,2	1665.8401
						K.GEMDTFPTFK.F	0.9958	1,2	1173.3258
						R.QASGGPVDIGPEYQQDLDRELYK.L	0.9958	2	2579.7826
						K.FEVIDKPQS.-	0.9924	1	1063.1955
509	ATP5L_MOUSE	103	36.89	2	38	K.VELVPPTPAEIPTAIQSVK.K	0.9958	1	1990.3477
						K.APSMVAAAVTYSKPR.L	0.9958	2	1549.8285
510	ATP8_MOUSE	67	28.36	2	14	K.IYLPHSLPQQ.-	0.9958	1	1196.3916
						K.TPWELK.W	0.9944	1	773.9072

511	ATPA_MOUSE	553	74.5	30	3956	R.EVAAFAQFGSDLDAATQQLLSR.G	0.9924		2	2339.5669
						K.GMSLNLEPDNVGVVVFGNDK.L	0.9958		2	2105.3704
						K.RTGAIVDVPVGEELLGR.V	0.9957		2	1782.0501
						K.FENAFLSHVISQHQSLLGNIR.S	0.9944		3	2411.7257
						R.ILGADTSVDLEETGR.V	0.9958		1	1576.7007
						R.TGAIVDVPVGEELLGR.V	0.9958	1,2		1625.8626
						K.TGTAEMSSILEER.I	0.9958		1	1424.5659
						K.QGQYSPMAIEEQVAVIYAGVR.G	0.9958		2	2310.63
						R.EAYPGDVFYLHSR.L	0.9958		2	1554.7019
						K.HALIIYDDLSK.Q	0.9958		2	1288.4863
						K.APGIIPR.I	0.9958		1	723.8937
						K.GIRPAINVGLSVSR.V	0.9958		2	1439.7012
						K.AVDSLVPIGR.G	0.9958	1,2		1027.2089
						R.NVQAEEMVEFSSGLK.G	0.9958		2	1668.8591
						K.TSIAIDTIINQK.R	0.9958	1,2		1317.5254
						R.VVDALGNAIDGK.G	0.9958		2	1172.3238
						K.EIVTNFLAGFEP.-	0.9958	1,2		1337.5151
						R.VLSIGDGIAR.V	0.9923		2	1001.171
						K.GMSLNLEPDNVGVVVFGNDKLIK.E	0.9958		2	2459.8633
						R.VVDALGNAIDGKGPIGSK.T	0.9958		2	1711.956
						R.GYLDKLEPSK.I	0.9958	1,2		1150.3171
						K.LYCIYVAIGQK.R	0.9958		2	1328.5603
						R.ISVREPMQTGIK.A	0.9958		2	1359.6269
						K.YTIVVSATASDAAPLQYLAPYSGCSMGEYF	0.9958		3	3390.7549
						K.MNDSFGGGSLTALPVIETQAGDVSAYIPTN	0.9944		3	5125.753
						R.VHGLRNVQAEEMVEFSSGLK.G	0.9958		2	2231.5316
						R.VGLKAPGIIPR.I	0.9958	1,2		1121.4117
						K.LKEIVTNFLAGFEP.-	0.9958		2	1578.8486
						K.RLTDADAMK.Y	0.9958		2	1021.1767
						K.TSIAIDTIINQKR.F	0.9958		2	1473.7129
512	ATPB_MOUSE	529	82.61	30	13575	R.DQEGQDVLLFIDNIFR.F	0.993	2,3		1923.1326
						R.IMDPNIVGNEHYDVAR.G	0.9944	1,2		1844.0521
						R.IPSAVGYQPTLATDMGTMQER.I	0.9958		2	2267.577
						R.LVLEVAQHLGESTVR.T	0.9958		2	1651.9035
						K.AHGGYSVFAGVGER.T	0.9958		2	1407.5284
						K.KGSITSVQAIYVPADDLTDPAPATTFAHLDA	0.9958		3	3845.2982
						R.FTQAGSEVSALLGR.I	0.9944		2	1436.6078

						R.AIAELGIYPAVDPLDSTSR.I	0.9958		1	1989.2328
						R.VALTGLTVAEYFR.D	0.9958		2	1440.6824
						R.EGNDLYHEMIESGVINLK.D	0.9958		2	2062.302
						K.SLQDIIAILGMDELSEEDKLTVSR.A	0.9958		2	2677.0393
						R.FLSQPFQVAEVFTGHMGK.L	0.9958		2	2024.3447
						K.GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	0.9958		2	3352.7859
						K.IPVGPETLGR.I	0.9958		1	1039.2199
						K.TVLIMELINNVAK.A	0.9931		2	1458.7998
						K.SLQDIIAILGMDELSEEDK.L	0.9958		2	2120.3766
						R.IMNVIGEPIDER.G	0.9958		1	1386.6061
						R.TIAMDGTEGLVR.G	0.9958		1	1263.4516
						K.VLDSGAPIK.I	0.9958		1	900.0629
						K.VVDLLAPYAK.G	0.9958		1	1089.3201
						K.VALVYGQMNEPPGAR.A	0.9958		2	1602.8486
						K.IGLFGGAGVGK.T	0.9958	1,2		976.1637
						R.IMNVIGEPIDERGPIK.T	0.9958		2	1782.1083
						R.IVAVIGAVVDVQFDEGLPPILNALEVQGR.D	0.9958	2,3		3033.5382
						K.VLDSGAPIKIPVGPETLGR.I	0.9958		2	1920.2596
						K.GSITSVQAIYVPADDLTDPAPATTFAHLDAT	0.9958		3	3717.1241
						R.TREGNDLYHEMIESGVINLK.D	0.9958		2	2319.5945
						R.FTQAGSEVSALLGRIPSAVGYQPTLATDMC	0.9958		3	3685.1616
						K.QFAPIHAEAPEFIEMSVEQEILVTGIK.V	0.9958		3	3028.4902
						K.ILQDYK.S	0.9944		1	779.9115
513	ATPD_MOUSE	168	61.9	4	908	K.AQSELSGAADEAAR.A	0.9958	1,2		1376.4227
						R.IEANEALVK.A	0.9958		2	987.1411
						K.YFVSSGSVTVNADSSVQLLAEEAVTLDMLD	0.9958		2	3631.0461
						K.QVDVPTLTGAFGILASHVPTLQVLRPGLVV	0.9958		3	4169.8113
514	ATPF2_MOUSE	289	20.07	3	4	K.NEWDPVIEWAEK.R	0.9958		1	1516.6501
						K.FYTMHLTTLCNTSLDNPTQR.S	0.9958		2	2414.6613
						K.RYGMEIGSSTSIMGPSIPTQTR.E	0.9958		2	2370.7009
515	ATPG_MOUSE	298	43.96	9	462	K.GILYRTHSDQFLVSFK.D	0.9958		2	1912.1985
						R.GLCGAIHSSVAK.Q	0.9958		2	1200.3465
						K.HLIIGVSSDR.G	0.9947		2	1097.2596
						R.THSDQFLVSFK.D	0.9958	1,2		1309.4643
						R.VYGTGSLALYEK.A	0.9924		1	1301.4821
						K.NASDMIDKLTLTFNR.T	0.9943		2	1739.9843
						R.KPPTFGDASVIALELLNSGYEFDEGSIIFNQ	0.9958		2	3649.0912

						K.NEVAALTAAGK.E	0.9958		1	1045.1808
						K.EVMIVGVGEK.I	0.9958		1	1061.2818
516	ATPK_MOUSE	88	28.41	2	9	R.DFTPSGIAGAFR.R	0.9924		1	1239.3733
						K.LGELPSWIMMR.D	0.9958	1,2		1333.6496
517	ATPO_MOUSE	213	68.54	11	825	R.GEVPCTVTTASPLDDAVLSELK.T	0.9958		2	2303.5348
						K.FSPLTANLMNLLAENGR.L	0.9958	1,2		1862.1541
						K.LVRPPVQVYGIEGR.Y	0.9958		2	1583.8741
						R.LGNTQGIISAFSTIMSVHR.G	0.9944		2	2033.3532
						K.TDPSIMGGMIVR.I	0.9958		2	1277.5397
						R.YATALYSAASK.E	0.9958		1	1146.2853
						K.VSLAVLNPYIK.R	0.9924		2	1217.4942
						K.SFLSPNQILK.L	0.9952	1,2		1147.3598
						R.EKFSPLTANLMNLLAENGR.L	0.9958		2	2119.4436
						K.YVDMSAK.S	0.9944		1	813.944
						R.VGQLLKDPK.V	0.9958		1	998.2107
518	ATR_MOUSE	2635	4.97	6	33	R.ICDALMYMQVKSSFK.D	0.9955		2	1822.1538
						R.LLRIAATPSCHMLHK.K	0.9958		2	1749.0936
						K.DVTLFLPEWEDGHFYLAKYYDK.L	0.9944		3	2751.0668
						R.EPLMSVLKTFLHDPLVEGSKPVK.G	0.9958		2	2566.0741
						R.AEQIVPLSAASFER.G	0.9958		1	1518.7099
						K.SSPLMFVNVNGSQGQNEAKDSCIEFSHWI	0.9944		3	3654.0143
519	ATRIP_MOUSE	785	3.06	2	3	R.EDAHDQDQHPLLK.M	0.9958		1	1546.6365
						K.GSSVVLK.S	0.9924		1	689.8302
520	ATRX_MOUSE	2476	2.87	2	2	K.LYQYYLDHLTGVGNSTEGGRGK.A	0.9958		3	2429.6512
						R.RLQQQYTQQQQQQLTYQQATLSHLMMPK	0.9958		3	5450.2454
521	ATS10_MOUSE	1104	2.36	1	2	K.SNRCITNSIPAAEGTLCQTHTIDK.G	0.9958		3	2688.8866
522	ATS19_MOUSE	1210	7.6	3	3	R.ESLNATGLSGGSSDPGSGR.S	0.9958		3	1749.7887
						K.LDPPMDGTDCDPGKWCK.A	0.9944		2	1993.1275
						R.GSSGDTALSSGTPASWQPPLPPQRPSSPF	0.9958		3	5176.7087
523	ATS20_MOUSE	1906	2.99	3	9	K.CKEAGIK.H	0.9944		1	805.9158
						R.NSFARSHKPCEVSENQMEK.T	0.9944		3	2279.4553
						K.SEDNFSEIYGLRLQNPYECPFNGSR.R	0.9944		3	2994.1694
524	ATS4_MOUSE	833	8.28	3	3	K.HSPWADGTPCGSSQACMGGRCLHVDQLK	0.9944		3	3114.3175
						R.LVILGSGQEGPQVGPSAAQTLR.S	0.9958		2	2179.4813
						K.FDKCMVCGGDGSR.C	0.9924		1	1489.5752
525	ATX2_MOUSE	1285	4.36	3	3	K.QIDDLKK.F	0.9958		1	859.9982
						K.RGPEVTSQGVQTSSPACK.Q	0.9958		2	1890.0264

						R.GSMSSGLEFVSHNPPSEAAAPPVAR.T	0.9958		2	2496.757
526	ATX2L_MOUSE	1049	4	2	3	R.GPHHLDNSSPGPGSEAR.G	0.9958		2	1715.7794
						R.REDIVDTMVFKPSDVLLVHFR.N	0.9958		2	2517.9488
527	AUHM_MOUSE	314	40.45	8	97	K.AVGLISHVLEQNQEGDAAYR.K	0.9958		2	2171.3745
						R.SVINDIANLPVPTIAAIDGLALGGGLELALAC	0.9958		3	3518.0545
						R.GIVVLGINR.A	0.9958		1	941.1618
						K.MHSSEVGPFVSK.I	0.9958		1	1305.4913
						K.LAIIPGGGGTQR.L	0.9941		2	1140.328
						K.AVGLISHVLEQNQEGDAAYRK.A	0.9958		2	2299.5485
						R.SEVPGIFCAGADLK.E	0.9958		1	1464.6245
						K.DRLEGLLAFK.E	0.9958		2	1162.3745
528	AURKB_MOUSE	345	13.62	2	2	K.EPATTSALALVNRSNSQSTAAPGQK.L	0.9958		2	2500.7281
						K.QPFTIDNFEIGRPLGKGK.F	0.99		2	2018.3231
529	AVEN_MOUSE	342	11.4	2	4	R.WEPGGRGGGASTR.V	0.9958		1	1288.3652
						R.LNVASELIQTTIPLELPQVKPR.R	0.9958	2,3		2460.92
530	AVIL_MOUSE	819	1.1	1	2	R.LLHVKGK.R	0.9924		1	795.0158
531	AXUD1_MOUSE	583	2.57	1	2	R.LFSLAEFTQEQVR.A	0.9958		2	1568.7697
532	AZI2_MOUSE	405	12.1	2	2	R.NLNPPSSSWEVEK.L	0.9924		2	1487.6091
						R.DVIRPSLSREEHVPHQGLHHSDNMQHAYV	0.9944		3	3848.2499
533	B2L13_MOUSE	434	29.72	5	50	K.EVSEAFTSTGFDCHTSPVFSPANPESSIED	0.9958		3	4183.3767
						K.QQGPSPPGVQLDVAPQSLNPEVLLK.L	0.9958		2	2612.986
						K.TSPTPSVFVELGEEELEAVTARPEAVER.A	0.9958		2	3044.3422
						K.YVVLSYLGLLSQEK.Q	0.9958		2	1612.9066
						K.ALQTILSQPVTYEAYR.E	0.9958		2	1854.1131
534	B2MG_MOUSE	119	21.01	1	5	K.DWSFYILAHTEFTPTETDTYACR.V	0.9958		2	2826.0137
535	B3AT_MOUSE	929	30.79	14	227	K.GSGFHLDLLLVVGMGGVAALFGMPWLSAT	0.9944		3	3274.9099
						R.SGGASEPLLPHQPSLETQLYCGQAEGGSE	0.9958		3	3830.0766
						R.NQELQWVEAAHWIGLEENLR.E	0.9958		2	2436.6891
						R.SHAEDLGNLEGVKPAVLTR.S	0.9958		2	2007.2541
						R.ANFLEKPVLGFVR.L	0.9958		2	1490.7886
						K.EAVPLEDLVLPEPVGFLLVLLGPEAPHVDY	0.9958		3	3798.4143
						R.YLPSPAKPDPNLYNTLDLNGGK.G	0.9958		2	2388.6824
						R.SVTHANALTVMGK.A	0.9958		2	1329.5572
						K.IPPDSETTLVLVGRANFLEKPVLGFVR.L	0.9944		3	2969.4973
						K.IPPDSETTLVLVGR.A	0.9958		2	1497.7319
						K.GTFLLGLAETSLAGVANHLLDCFIYEDQIRP	0.9958		3	3835.2745
						K.RSHAEDLGNLEGVKPAVLTR.S	0.9958		2	2163.4416

						R.SLESFLDCSLVLPPTDAPSEK.A	0.9958		2	2306.5379
						K.ALLNLVPVQK.E	0.9958	1,2		1095.3708
536	B3GL1_MOUSE	331	6.34	1	6	R.QDFLDTYNNLTLKTIMAFR.W	0.9943		2	2305.6538
537	BACH_MOUSE	381	16.01	3	28	R.IMRPDDANVAGNVHGGTILK.M	0.9952		2	2079.3819
						K.TNIVTASVDAINFHDK.I	0.9958		2	1745.9298
						K.HSVEVQVHVMSENILTGTK.K	0.9958		2	2109.4051
538	BACH1_MOUSE	739	2.03	1	58	K.FLDSTSEQQECAR.K	0.9958		2	1571.6068
539	BAD_MOUSE	204	26.96	2	5	R.GLGPSLTEDQPGPYLAPGLLGSNIHQQGR	0.9958		3	2974.303
						R.HSSYPAGTEEDEGMEEELSPFR.G	0.9958		2	2498.5935
540	BAF_MOUSE	89	44.94	2	16	R.DFVAEPMGEKPVGSLAGIGDVLSK.R	0.9958		2	2417.7797
						K.AYVVLGQFLVLK.K	0.9958		2	1350.6873
541	BAG2_MOUSE	210	9.05	1	8	K.EILLEMIHSIQNSQDMR.Q	0.9958		2	2058.3753
542	BAG3_MOUSE	577	33.8	11	92	K.IDPQTGWPFFVDHNSR.T	0.9958		2	1917.0904
						R.SSLGSHQLPR.G	0.9924	1,2		1082.2046
						K.VSSAPIPCPSPSPAPSAVPSPPK.N	0.9958		2	2228.5164
						K.THYPAQQGEYQPQQPVYHK.I	0.9958		2	2300.4948
						K.AIDVPGQVQVYELQPSNLEAEQPLPEIMGA	0.9958		3	3750.2556
						K.VQGLEQAVDSFEGK.K	0.9958	1,2		1507.6403
						R.SQSPAASDCSSSSSSASLPSSGR.S	0.9915		2	2201.1883
						R.FRTEAAAATPQR.S	0.9958		2	1319.463
						K.KYLMIEEYLTK.E	0.9958		2	1431.7302
						K.AIDVPGQVQVYELQPSNLEAEQPLPEIMGA	0.9958		3	3993.5183
						R.SGTPVHCPSPIR.V	0.9915		2	1308.446
543	BAI1_MOUSE	1582	1.2	1	8	R.YPGGPLPDFPNHSLTLK.K	0.9912		2	1854.1155
544	BAIP2_MOUSE	535	6.73	2	2	K.YSDKELQYIDAISNK.Q	0.994		2	1787.9641
						K.AIFSHAAGDNSTLLSFK.E	0.9931		2	1779.9903
545	BANK1_MOUSE	783	1.53	1	3	K.EEEAGAEARR.S	0.995		1	1118.1484
546	BASI_MOUSE	389	12.6	3	46	R.SGEYSCIFLPEPVGR.S	0.9958	1,2		1711.878
						K.SDASYPPITDWFWFK.T	0.9958		1	1861.0631
						K.VLQEDTLPDLHTK.Y	0.9958	1,2		1509.6995
547	BASP_MOUSE	226	13.27	2	2	K.EEAPKAEPEK.S	0.9958		1	1128.2243
						K.ESTEEKPKDAADGEAK.A	0.9958		1	1705.7729
548	BAT2_MOUSE	2158	1.9	3	3	K.EEPPQLSGPEAGRKPAR.G	0.9944		2	1820.0152
						K.EPLKEK.L	0.9958		1	743.8785
						R.YPTPDGPSRFPR.V	0.9958		2	1390.5412
549	BAT3_MOUSE	1154	8.84	5	9	R.LLGNTFVALSDLR.C	0.9957		2	1419.664
						K.RLQEDPNYSPQR.F	0.9954		2	1503.6145

						K.TMQGEGPQLLLSEAVSR.A	0.9926		2	1817.0673
						R.APPQTQLPSGASSGTGSASATHGGAPLPG	0.9944		3	2818.0323
						R.SFFHQHYLGGQEPTPSNIR.M	0.993		2	2216.4203
550	BAZ1A_MOUSE	1555	3.54	4	4	K.EKELLDK.I	0.9958		1	875.0098
						K.ETLLQEKSR.I	0.9944		1	1104.2486
						R.YELLSEESK.E	0.9924		1	1098.195
						R.SSRQLIPLNTAESLSLQHSESK.R	0.993		2	2426.6891
551	BAZ1B_MOUSE	1479	2.03	2	3	R.RQSLELQK.C	0.9958		1	1002.1588
						K.LQNEDKIISNVPADSLIR.T	0.9957		2	2026.2975
552	BCAS3_MOUSE	928	2.05	1	3	R.FQKSAGLEEIEQELTSK.Q	0.9958		2	1938.1418
553	BCAT2_MOUSE	393	32.82	8	158	K.LGGNYGPTVAVQR.E	0.9958		2	1332.5021
						K.KPAPSQALLFGK.T	0.9958		1	1257.5186
						R.EVFGSGTACQVCPVHQILYEGK.Q	0.9958		2	2480.712
						R.LCLPDFDKQELLECIR.Q	0.9958		2	2050.2917
						K.AIQYGASAHDWMFR.V	0.9958		2	1653.8553
						K.TFTDHMLMVEWNNK.A	0.9958		2	1767.0272
						K.QLHIPTMENGPELILR.F	0.9958	2,3		1862.1974
						R.LFRPWLNMDR.M	0.9958		2	1348.6085
554	BCCIP_MOUSE	316	11.39	2	2	R.FINVPPQIALPMHQQLQK.E	0.9958		2	2103.5334
						K.LLNDTSKPVGLLLSER.F	0.9958		2	1756.0525
555	BCKD_MOUSE	412	16.75	4	14	K.TVTSFYNQSAIDVAAEKPSVR.L	0.9958		2	2284.5309
						R.FPFIPMPLDYILPELLK.N	0.9958		2	2047.5464
						R.SQDGSHLLK.S	0.9915		2	985.0849
						R.STSATDTHHVELAR.E	0.9958		2	1525.6182
556	BCL9L_MOUSE	1494	2.81	2	2	R.FPGNQMQR.V	0.9958		1	978.1137
						R.QMDPAMFPGQMTGGDGLAGTPMGIEFGG	0.9937		2	2985.3921
557	BCLF1_MOUSE	919	3.81	2	3	K.GRADGDWDDQEVLDYFSDK.E	0.9958		2	2232.2811
						R.SSSPYSKSPVSK.R	0.9958		2	1254.3825
558	BDH_MOUSE	343	47.23	10	96	K.VSVVEPGNFIAATSLYSPER.I	0.9958		2	2137.3971
						R.MQIMTHFPGAISDK.I	0.9958		2	1576.8689
						R.VVNISSMLGR.M	0.9958		1	1076.2994
						K.KMWDDLPEVVR.K	0.9944	1,2		1388.6245
						K.METYCNSGSTDTSSVINAVTHALTAATPYT	0.9958		3	3321.563
						K.AILITGCDSGFGFSLAK.H	0.9958		2	1757.9904
						R.YEMHPLGVK.V	0.9958		1	1074.283
						R.YHPMDYYWWLR.M	0.9958		2	1630.8633
						K.GFLVFAGCLMK.D	0.9958		2	1243.5159

						R.TIQLNVCNSEEVEK.A	0.9958		1	1663.7882
559	BEST2_MOUSE	508	13.78	2	2	K.LVIYCDQYASLIPVSFVLGFYVTLVVHR.W	0.9958		3	3273.8518
						K.NSCVSEASTAASCGCAGAADGGGVECGC	0.9944		3	3787.8144
560	BEST3_MOUSE	669	4.78	2	2	K.YWVPFIWFGNLATKAR.N	0.9958		2	1970.3268
						K.FEEDLEDDRFPK.R	0.9958		1	1540.6263
561	BIEA_MOUSE	295	19.66	4	20	K.DPHSSAFLNLIGYVSR.R	0.9958		2	1776.9896
						R.ILHCLELASDIQR.L	0.9944		2	1568.7796
						K.FGFPAFSGISR.L	0.9958		2	1186.3555
						K.FGVVVVGVGR.A	0.9944		1	989.2058
562	BIN1_MOUSE	588	5.44	2	2	K.IAKPVSLLEK.A	0.9944		1	1098.3714
						K.VQAQHDYTATDTDELQLK.A	0.9958		2	2077.2121
563	BIRC4_MOUSE	496	5.04	1	3	K.DNTEDESSQTSLQKDISTEEQLR.R	0.9944		2	2654.7149
564	BLM_MOUSE	1416	1.77	2	3	R.SASCASQATSSASRK.L	0.9958		2	1499.5438
						K.YYVLPK.K	0.9958		1	782.9579
565	BLMH_MOUSE	455	39.34	10	27	K.GEISSTQDAMMEEIFR.V	0.9958		2	1845.0492
						K.EHVKPLFNMEDK.I	0.9957		2	1487.7137
						K.LYTVDYLSNMVGGR.K	0.9958		2	1588.8187
						K.LGLSDMNVYDHELVFGVSLK.N	0.9944		2	2237.5757
						K.LNSDPQFVLAQNVGTTHDLLDICLR.R	0.9958	2,3		2841.1596
						R.NLVHSGATK.G	0.9958		1	927.0482
						R.LAFGESLMTHAMTFTAVSEK.D	0.9958		2	2172.519
						R.KTLYNNQPIDFLK.K	0.9958		2	1594.851
						R.ATVQGAQHVFQHVVPQEGKPVTNQK.S	0.9958	2,3		2729.0708
						K.ICFVNDPRPQHK.Y	0.9944		2	1511.6897
566	BLVRB_MOUSE	206	62.62	6	101	R.LPSEGPQPAHVVVGDVR.Q	0.9958		2	1757.9871
						R.CLTTNEYDGHTTYPSHQYD.-	0.9958		2	2303.3259
						K.YVAVMPPHIGDQPLTGAYTVTLDGR.G	0.9958		2	2673.0588
						R.TGLTTLAQAVQAGYEVTVLVR.D	0.9958		2	2191.5327
						K.TVAGQEAVIVLLGTGNDLSPTTVMSEGTR.I	0.9944		3	2918.2891
						K.HDLGHFMLR.C	0.9958		1	1126.3214
567	BMCC1_MOUSE	1139	1.93	1	4	R.NKPLNSLALEEVAGLSSQSR.N	0.9958		2	2114.3635
568	BMP10_MOUSE	421	6.18	2	3	R.LYTLVQR.D	0.9924		1	893.0739
						R.GVCNYPLAEHLTPTK.H	0.9958		2	1700.8981
569	BMP8A_MOUSE	399	4.26	1	4	R.EILAVLGLPGRPRPR.A	0.9958		2	1645.0041
570	BNIPL_MOUSE	328	21.95	2	2	R.FLDSLGELAQLISLEQVHIPEVVRQLDR.D	0.9958		3	3219.7086
						K.VLSHGGYHGDGLNAVILFASCYLPRSSIPN	0.9958		3	4571.1787
571	BOLA1_MOUSE	137	58.39	5	105	R.LVHEALSEELAGPVHALAIQAK.T	0.9958	2,3		2297.6597

						R.AKLEQALSPEVLELR.N	0.9958		2	1696.9847
						R.NESGGHAVPAGSETHFR.V	0.9958		2	1753.8283
						K.LEQALSPEVLELR.N	0.9958		1	1497.7319
						K.TPAQWRENPQLDISPPCLGGSK.K	0.9958		2	2452.6953
572	BOLA2_MOUSE	86	24.42	1	19	R.LVNECLAEELPHIHAFEQK.T	0.9958		2	2278.5359
573	BOLA3_MOUSE	110	45.45	4	57	R.TVQQHQMVNQALK.E	0.9958		1	1525.7661
						R.ATAIQVTDISGGCGAMYEIK.I	0.9958		2	2086.3308
						R.TVQQHQMVNQALKEEIK.G	0.9958		2	2025.3306
						R.IFTSVPK.C	0.9944		1	791.9658
574	BPA1_MOUSE	7389	1.53	6	8	R.IKLLQGYHPNDIEK.E	0.9958		2	1668.9334
						R.LAGALAGLIAKQELLETLLAWLQWAETTLTI	0.9958		3	3497.1125
						R.YTALVTLMTQYIK.F	0.9958		1	1545.8774
						R.LQNVQIALDYLK.R	0.9958		1	1418.6763
						R.DLEDPGIDPSVVK.Q	0.9944		1	1384.5261
						K.ESGDELSQADRALIEQK.L	0.9952		2	1890.0141
575	BPL1_MOUSE	722	6.09	2	2	K.QHGAGLKPLRADCLIAR.A	0.9926		2	1877.1661
						R.GPNAWLSPVGCALSTLLVFIPLR.S	0.9958		2	2482.9378
576	BPNT1_MOUSE	308	22.73	4	34	R.SHSNQLVTDCISAMNPDTVLR.V	0.9958		2	2359.5824
						K.HMNSAGVLAALR.N	0.9958		2	1240.4661
						K.KWDTCAPEVILHAVGGK.L	0.9958	2,3		1882.1357
						R.NYEYYASHVPESVK.N	0.9958		2	1686.8181
577	BR44_MOUSE	127	10.24	1	3	R.LMDKVELLLPK.K	0.9958		2	1299.655
578	BR44L_MOUSE	109	25.69	1	25	R.DYLMSTHFWGPVANWGLPIAAINDMK.K	0.9958		2	2949.4145
579	BRCA1_MOUSE	1812	2.21	2	3	K.SQGPVNPSPQR.T	0.9924		1	1167.2669
						K.FQLQHLEGPTSGDDESGMGRPSPFK.S	0.9958		3	2718.9574
580	BRCA2_MOUSE	3329	5.14	7	7	K.EWKDTDLHLPVDPSVGQTDHSK.Q	0.9958		2	2505.7032
						K.KVFEDHFPIVTVSQLPAQQHPEYEIESTK.E	0.9958		3	3398.7967
						K.LFSDIENSEEPSAK.V	0.9924		1	1566.6617
						K.EFNISFQTASGKNTR.V	0.9943		2	1700.8485
						R.WSQSNLSGLNETQTGKITLPHISSHSQNISI	0.9958		3	4145.5469
						R.KFIYSVSDDASLQGK.K	0.9944		1	1658.8486
						R.NLHPQTINEYCVQKLETNTSPHANK.D	0.9958		3	2938.1925
581	BRCC3_MOUSE	291	12.37	2	2	K.NLCSQMSAVSGPLLQWLEDR.L	0.9958		2	2305.5769
						R.IHSLTHLDSVTK.I	0.9958		2	1351.5455
582	BRE1B_MOUSE	1001	3.6	2	3	K.VLEMETTVEDLQWDIEKLR.K	0.9958		2	2348.6734
						R.EEKTTTTLIEPIR.L	0.9958		1	1531.7465
583	BRWD1_MOUSE	2304	2.47	3	4	R.YIEHNARTFNEPESVIAR.S	0.9957		2	2147.3549

						R.AAQVLVQELEQYQLLPKR.L	0.9958		2	2127.4917
						R.NNIYELNPHKEPWGK.M	0.9946		2	1840.0483
584	BRWD3_MOUSE	1799	1.78	2	4	R.KLLSASEEDESMGGEEK.E	0.9952		2	1839.9661
						K.IYSSSEDENLK.L	0.9958		1	1285.3501
585	BSDC1_MOUSE	427	16.39	3	3	K.GLSDFLGVISDTFAPSPDK.T	0.9958		2	1967.1828
						K.VHQLEQEQARR.D	0.9958		1	1394.5332
						K.LFEASLEEQSLAEDEGETGPPPPPPSKPLT	0.9958		3	3545.8817
586	BST1_MOUSE	311	18.65	3	12	R.GEGTTPHLQSIFLGR.C	0.9958		2	1613.8137
						R.LEALGFQHSCINDYRPVK.F	0.9924		2	2148.3923
						K.SLFWENNHLLVMSYGENTR.R	0.9958		2	2311.5768
587	BTBD3_MOUSE	532	3.01	1	3	R.CWEVIDAQAELALK.S	0.9958		1	1646.8469
588	BTF3_MOUSE	204	35.29	3	25	K.VQASLAANTFTITGHAETK.Q	0.9958		2	1961.1821
						K.QLTEMLPSILNQLGADSLTSLR.R	0.9958		2	2401.7809
						K.KLGVNNISGIEEVNMFTNQGTVIHFNNPK.V	0.9958		3	3216.6391
589	BUD13_MOUSE	637	4.4	2	2	K.RPKPGGAGGKGMR.I	0.9924		1	1269.5107
						R.EGDPMANFIKK.N	0.9944		1	1250.4553
590	BZW2_MOUSE	419	5.01	1	2	R.DTLVQGLNEAGDDLEAVAK.F	0.9958		2	1959.1174
591	C10_MOUSE	126	23.02	2	8	R.DNACNDMGKMLQFVLPVATQIQQEVIK.A	0.9944		3	3092.5618
						K.MLQFVLPVATQIQQEVIK.A	0.9958		2	2086.5408
592	C19L1_MOUSE	537	6.89	2	2	K.QIAQPGAAYFYVELDTGEK.L	0.9958		3	2101.3202
						R.NHVVLQESAQHATR.F	0.9958		2	1590.7391
593	C19L2_MOUSE	887	2.48	2	2	R.KNQDSSGNLR.S	0.9958		1	1119.1795
						K.EAEKIAYK.K	0.9958		1	952.0953
594	C1QBP_MOUSE	278	65.83	10	363	K.AFVEFLTDEIKEEK.K	0.9958		3	1698.9103
						R.GVDNTFADELVELSTALEHQEYITFLEDLK.	0.9958	2,3		3441.7699
						K.TLVLDCHYPEDEIGHEDEAESDIFSIK.E	0.9958		2	3163.3412
						K.EVSFQATGDSEWRDTNYTLNTDSLDWALY	0.9958		3	4613.9258
						K.MSGDWELEVNGTEAK.L	0.9944		1	1666.7999
						R.SGLLQPPVPCACGCGALHTEGDKAFVEFL	0.9958		3	3719.0811
						K.ITVTFNINNSIPPTFDGEEEPSQGQK.A	0.9907		2	2864.0948
						R.DTNYTLNTDSLDWALYDHLMDFLADR.G	0.9958		2	3120.3735
						K.EVSFQATGDSEWR.D	0.9948		2	1512.5755
						K.KTLVLDCHYPEDEIGHEDEAESDIFSIK.E	0.9924		2	3291.5153
595	C1QR1_MOUSE	644	4.04	2	3	R.LLDDLVTCASR.N	0.9958		2	1263.3997
						R.HVQQALTQLLK.T	0.9958		2	1279.5253
596	C1QT3_MOUSE	246	7.72	1	3	R.FGAPVSGVYFFTFSMMK.H	0.9924		2	1917.2905
597	C1QT4_MOUSE	326	5.21	1	2	K.VYVNIGGDFDAATGR.F	0.9917		2	1555.6873

598	C1TC_MOUSE	935	14.97	8	25	K.STTTIGLVQALGAHLR.Q	0.9958	2	1638.9077
						K.YVVVTGITPTPLGEGK.S	0.9958	2	1631.9097
						R.ASQAPSSFQLLYDLK.L	0.9958	2	1668.8871
						K.CTHWAEGGQGALALAQAVQR.A	0.9958	2	2125.3177
						K.THLSLSHNPEQK.G	0.9958	2	1391.5265
						K.MHGGGPTVTAGLPLPK.A	0.9958	2	1533.8291
						R.IFHELTQTDK.A	0.9958	1	1232.3788
						K.IVGAPMHDLLLWNNATVTTCHSK.T	0.9958	2	2579.9428
599	C2CD3_MOUSE	2323	2.97	2	2	K.DHLYFAENSDAVKGSLCGLQQHLNQGTNV	0.9958	3	3931.2769
						R.TSTTLCVPDPVFNSEHHHSLLLPTDVPVQR	0.9958	3	3398.7662
600	C2D2A_MOUSE	1633	3.92	3	4	K.TVFITRYLKPLNPPQELLHVYPNNPQATAEI	0.9958	3	3905.5351
						R.AYDIPVRKPVVSK.F	0.9958	2	1472.7709
						K.KTEEEELLNGK.D	0.9958	1	1290.413
601	C560_MOUSE	169	10.65	1	10	K.NTSSNRPLSPHLTIYK.W	0.9958	2	1829.0659
602	C8AP2_MOUSE	1962	2.24	3	5	R.NCLDLYEEILTEEGTAK.E	0.9937	2	1999.1451
						K.EIQTQNLNLK.N	0.9958	1	1201.3653
						K.DLENTDKNIDK.S	0.9958	1	1305.3843
603	CA009_MOUSE	1250	5.2	2	2	R.GLQRTATDFYAELQNSTDLGYGNGNLVHG	0.9958	3	3570.8137
						K.ESSSASTSYYSQDDNCAIGSEDTQFQKK.N	0.9924	3	3135.1579
604	CA050_MOUSE	199	9.05	1	4	K.LTVIAEQIQHLQEQAR.K	0.9958	2	1878.1386
605	CA057_MOUSE	190	23.16	2	2	R.VGQYVVNLDSFEQLALPVLRNAGSSCGPK	0.9958	3	3120.4986
						K.GKPLALVEEIR.K	0.9958	2	1225.474
606	CA066_MOUSE	475	7.37	2	4	R.FMSLGLGLMVK.S	0.9958	1	1196.5519
						K.LSDLTGCTQVVDVGSGQGHLSRFMSLGLG	0.9958	3	3464.9863
607	CA069_MOUSE	358	33.8	7	18	K.LEGPLPASGVSPGAIVTVTATGQAAGK.F	0.9958	2	2450.7948
						K.VTVEPSPELHVWAVLPCVPQTSETAPLEEF	0.9958	3	3372.7657
						R.GPDAAPFLLGLSTNELPLSGPPTGAAQPSA	0.9958	2	3004.3696
						R.AAYAHFLNVQGR.T	0.9958	2	1347.5192
						R.GPDAAPFLLGLSTNELPLSGPPTGAAQPSA	0.9944	3	4332.8656
						R.KVTVEPSPELHVWAVLPCVPQTSETAPLEE	0.9958	3	3500.9397
						R.AGQGHVGLALLR.S	0.9958	2	1192.4067
608	CA085_MOUSE	404	12.62	2	27	R.LLHTADVCQLEVALVGASPR.G	0.9945	2	2150.4491
						R.LLEFDSTNASEGAQPPGKPYPPYSLAK.F	0.9947	2	2879.1956
609	CA092_MOUSE	558	3.05	1	10	K.CLPSLSQLQAINLWK.V	0.9958	2	1772.0637
610	CA093_MOUSE	201	41.29	4	7	K.AVGIQGNLSGDLLQSGGLLVVSK.G	0.9952	2	2226.5785
						K.VLLHFIQK.S	0.9929	2	998.2565
						K.SPGDYVPQENILQALGISAEVCSSKPPQCD	0.9958	3	3992.2406

						K.HAVTGEAVELR.S	0.9958	2	1182.3219
611	CA103_MOUSE	755	2.38	2	2	K.SLSNSQLASMANLR.A	0.9932	2	1492.6904
						K.TKSLSNSQLASMANLR.A	0.9958	2	1721.9695
612	CA112_MOUSE	903	2.99	1	2	R.NILQAMVQVIGGFTGCVRHVCATQK.S	0.9958	2	2789.2007
613	CA123_MOUSE	160	23.13	2	26	K.ATLENVTNLRPVGEDFR.W	0.9958	2	1932.1435
						K.AQESVGIFEVTHQFVK.C	0.9958	2	1820.055
614	CA141_MOUSE	446	3.14	1	3	R.YNLSQTFSSLSK.K	0.9958	1	1375.5211
615	CA163_MOUSE	231	32.9	4	12	K.DPEGCYRLVDYLEGIQK.N	0.9958	2	2056.2458
						K.NFDEAAKVLK.F	0.9944	1	1135.3055
						K.SVESCHNVGLLAHDGQVNEDGQPDLGK.A	0.9958	3	2877.0197
						K.SFLENMEVECHYQCYR.E	0.9958	2	2166.3016
616	CA165_MOUSE	421	7.6	2	3	R.KPSEAAHK.S	0.9924	1	867.9804
						K.YILDNGKVHLGSGIWVDEEK.W	0.9958	2	2273.5505
617	CA166_MOUSE	352	6.82	1	2	K.FHPSVQSFTDAIGHYISGERPK.G	0.9958	2	2474.7379
618	CA170_MOUSE	840	37.5	11	97	K.HSGSLDSAATQMSSPQLTRPK.E	0.9958	2	2200.4314
						K.AEFASACTPGLHVDLSAAGSEIKPEVSSSM	0.9958	3	3872.3052
						R.EESGLDLSTPILITEQDQIR.K	0.9958	2	2258.4876
						R.ADTVAPVPPEGLVPISIPEVYEHFFTEEGFC	0.9958	3	3639.0582
						R.FSMAIPSHEDSGSGEPTGSPFLTPEQPPVF	0.9958	2,3	3253.5671
						R.SQCEPVLALEASHQVAGTSTQSEAPLFPSI	0.9958	3	5058.4654
						K.APHSPESPGHSDNPQSSPDSLEASPR.N	0.9958	2	2684.752
						R.LLQGPAPSSPSK.A	0.9958	2	1182.3623
						K.AQQDKPQPDSTSPEQMAR.E	0.9958	2	2015.162
						R.AVLHVVSKPVQEVHPDVPMASPNVSTR.A	0.9958	3	2895.3495
						R.EGGLEASTKPVSPTAEHLSLTVR.K	0.9958	2	2380.6604
619	CA175_MOUSE	1279	2.74	1	2	K.AEVIQILYYQTLDSLQKLLNALFIEDPTPTGL	0.9958	3	3750.3673
620	CA190_MOUSE	239	13.81	1	2	R.GECELGTSGDVLLPGAPSTGHGLGDKIMA	0.9958	3	3110.4755
621	CA2D1_MOUSE	1103	9.34	5	6	R.VFTFSVGQHNYDR.G	0.9929	2	1570.7043
						K.LMNTNLVFIMVESKGTCPCDTR.L	0.9929	2	2587.9413
						R.DEDPTLLWQVFGSATGLAR.Y	0.9958	2	2077.3012
						K.SQEPVTLDFLDAELENEIK.V	0.9958	2	2191.3966
						R.INTQEYLDVLGRPMVLAGDK.A	0.9958	2	2233.5878
622	CA2D4_MOUSE	1116	4.03	2	2	K.QLVDELMVK.G	0.9958	1	1075.3087
						K.QGSLCNQAIMLITDGAVEDYEPVFETYNWF	0.9958	3	3734.0511
623	CAB39_MOUSE	341	8.21	2	3	R.NIQFEAFHVFK.V	0.9958	2	1380.5889
						K.LLSAEFLEQHYDR.F	0.9958	2	1621.7899
624	CABL1_MOUSE	568	7.57	2	2	R.KLCAGACVLLAAK.V	0.9947	2	1375.627

						K.LAQEDCGFEEPTVAMAFVYFEKLALR.G	0.9958		3	3036.4353
625	CAC1A_MOUSE	2368	2.11	2	2	R.LLRMDLPVADDNTVHFNSTLMALIR.T	0.9958		3	2857.3588
						K.IGNSTNPGPALATNPQNAASR.R	0.9958		2	2052.2113
626	CAC1B_MOUSE	2327	2.45	2	2	K.TTRDQTHQAPGGLSQMGPVSLFHPLK.A	0.9958		3	2805.1839
						K.NVLNILIVYMLFMFIFAVIAVQLFKGK.F	0.9958		3	3146.9924
627	CAC1C_MOUSE	2139	1.5	2	4	K.EQGLVGKPSQR.N	0.9958		1	1199.3524
						R.AGGLFGNHVTYYQSDSR.G	0.9944		2	1872.9915
628	CAC1D_MOUSE	2179	0.6	1	2	R.RLLPPTPPSHR.R	0.9944		1	1271.5081
629	CAC1H_MOUSE	2365	3.3	2	2	R.WNQLDLAIVLLSIMGIALEEIEMNAALPINPT	0.9958		3	4291.2148
						R.AEHLTVPNFAFEPLDMGGPGGDCFLDSDQ	0.9944		3	3905.2069
630	CACP_MOUSE	626	38.34	15	319	R.LPVPPLQQSLDYYLK.A	0.9958		2	1775.0978
						K.ALQPIVSEEEWAHTK.Q	0.9958	1,2		1738.9377
						K.AHQDALPRLPVPPLQQSLDYYLK.A	0.9944		3	2664.0794
						R.SPMVPLPMPK.K	0.9958		1	1097.4193
						K.TLQFIVAEDGSCGMVYEHAAAEGPPIVALV	0.9958		3	4150.6737
						K.QLVDEFQTSGGVGER.L	0.9958		2	1622.7319
						K.QDFVDLQGQLR.F	0.9937		2	1319.46
						R.NHVAGQMLHGGGSK.F	0.9958	1,2		1393.5633
						R.TLLQNHPR.A	0.9909		2	979.127
						K.KMENWLSEWWLK.T	0.9958		2	1650.9354
						R.MAHYLEK.A	0.9944		1	892.0606
						R.VSDDVYRNHVAGQMLHGGGSK.F	0.9958		2	2228.4472
						K.IWNSSLQSNKEPVGILTSNHR.N	0.9958		2	2381.6536
						K.KPELVR.S	0.9924		1	741.9089
						K.LQAIEDLVSMPDIFMDTSYAIAMHFNLSTSQ	0.9958		3	3886.485
631	CAD13_MOUSE	714	25.21	10	188	K.TLEGPVPLEVIVIDQNDNRPIFR.E	0.9958		2	2636.0232
						R.SIVVSPILIPENQR.Q	0.9958		1	1565.8534
						R.INENTGSVSVTR.T	0.9958		2	1277.3769
						K.LHYEVSSPHFK.V	0.9958		2	1344.5125
						K.DLHPNTDPFKFEIHK.Q	0.9943		2	1839.0605
						K.GDIVTVVSPALLDR.E	0.9958		2	1455.6946
						K.DIQGSLQDIFK.F	0.9958		2	1264.4209
						R.ETIATYQLYVETTDASGK.T	0.9958		2	1991.159
						K.DLHPNTDPFK.F	0.9958		1	1184.2939
						R.AAYTIINGNPGQSFEIHTNPQTNEGMLSVVI	0.9958		3	5074.7602
632	CAD23_MOUSE	3354	1.76	2	2	R.VIVYVEDVNDEAPVFTQQQYNR.L	0.9932		2	2627.87
						R.DSGPNGQVEYSVVDGDPLGEFVISPVEGV	0.9958		3	3487.848

633	CADH2_MOUSE	906	16.56	6	25	R.YSVTGPGADQPPTGIFIINPISGQLSVTKPLI	0.9958		3	3440.9213
						K.DQPHTPAWNAAYRISGGDPTGR.F	0.9958		3	2368.5302
						R.SAAPHPGDIGDFINEGLK.A	0.9958		2	1839.0147
						R.IAGGRGTLLPLLAALLQASVEASGEIALCK.T	0.9947		3	2994.5114
						R.RLDERPIHAEPQYPVR.S	0.9944		2	1977.2333
						K.FLEAGIYEVPIIITDSGNPPK.S	0.9958		2	2274.6189
634	CADH4_MOUSE	913	6.79	2	2	R.YSITGVGADQPPMEVFNIDSMSGRMYVTR	0.9958		3	3723.2461
						R.EACKAGFSEEGYTALISPNVLEGEK.L	0.9958		3	2700.9251
635	CADH7_MOUSE	785	2.17	1	2	R.YFNIDANSGVITTAK.S	0.9958		2	1614.7954
636	CADM1_MOUSE	456	16.67	3	3	R.LLLLLLLSAAALIPTGDGQNLFTK.D	0.9958		2	2383.8773
						R.FQLLNFSSSELK.V	0.9924		1	1413.6134
						R.AGEEGTIGAVDHAVIGGVVAVVVFAMLCLL	0.9944		3	3522.1933
637	CAH1_MOUSE	261	55.17	8	153	K.TSEANHDSSLKPLSISYNPATAK.E	0.9944	2,3		2432.6494
						R.YSGELHLVHWNSAK.Y	0.9958	1,2		1641.8265
						K.EIVNVGHSFHVIFDDSSNQSVLK.G	0.9944		2	2572.8369
						K.DSISLSPEQLAQLR.G	0.9958	1,2		1557.7441
						K.LYPIANGNNQSPIDIK.T	0.9958		2	1757.9841
						K.ADGLAILGVLMK.V	0.9958		2	1201.5102
						R.LTQFHFHWGNSNDHGSEHTVDGTR.Y	0.9958	2,3		2780.8918
						K.VGPANPSLQK.V	0.9958		1	1011.1661
638	CAH2_MOUSE	260	59.62	9	311	K.SIVNNGHSFNVEFDDSQDNAVLK.G	0.9958		2	2550.7007
						K.AVQQPDGLAVLGIFLK.I	0.9958		2	1670.0049
						R.EPITVSSEQMSHFR.T	0.9958		2	1648.8309
						K.VLEALHSIK.T	0.9958		1	1010.2217
						K.YAAELHLVHWNTK.Y	0.9958		2	1582.8021
						R.TLNFNEEGDAEEAMVDNWRPAQPLK.N	0.9944		2	2876.1267
						K.IGPASQGLQK.V	0.9958		1	999.1551
						K.DFPIANGDR.Q	0.9958		1	1005.0751
						R.QSPVDIDTATAQHDPALQPLLISYDK.A	0.9958		2	2838.1437
639	CAH3_MOUSE	260	38.08	5	27	K.YAAELHLVHWNPK.Y	0.9958		2	1578.8137
						K.EAPFTHFDPSCLFPACR.D	0.9958		2	2053.2135
						K.HDPSLQPWSASYDPGSAK.T	0.9958		2	1944.0673
						K.EWGYASHNGPDHWHELYPIAK.G	0.9958		2	2508.7141
						K.YNTFGEALKQPDGIAVVGIFLK.I	0.9937		2	2381.7771
640	CAH4_MOUSE	305	7.87	1	2	K.GFQPLVEALPSISKPHSTSTVR.E	0.9958		2	2352.6958
641	CAH7_MOUSE	264	5.68	1	7	K.FRSLLFTSEDDER.I	0.9927	1,2		1615.7398
642	CAHD1_MOUSE	1288	3.88	2	2	R.KMSTFVSSVKPSDSPTQHAVGFHR.A	0.9944		3	2631.9689

						R.MVEHYTAYLSDNTRLIANPGLK.F	0.9944		3	2507.867
643	CALCR_MOUSE	515	5.44	1	2	R.VVSAPRAVAFAEPDGLPIYICHQEPR.N	0.9958		3	2894.2689
644	CALM_MOUSE	149	66.44	5	64	R.EADIDGDGQVNYEEFVQMMTAK.-	0.9958		2	2491.7035
						R.VFDKDGNGYISAAELR.H	0.9944		2	1755.9249
						K.EAFSLFDKDGDGTITTK.E	0.9958		2	1846.0007
						K.DGNGYISAAELR.H	0.9958		1	1266.3531
						R.SLGQNPTEAELQDMINEVDADGNGTIDFPE	0.9958		3	4072.4795
645	CALR_MOUSE	416	55.05	13	61	K.IKDPDAAKPEDWDER.A	0.9958		2	1785.9078
						K.IDNSQVESGSLEDDWDFLPPK.K	0.9958		2	2392.5377
						K.GTWIHPEIDNPEYSPDANIYAYDSFAVLGLD	0.9924		3	4139.5665
						K.SGTIFDNFLITNDEAYAEEFGNETWGVTK.A	0.9958	2,3		3270.4895
						K.VHVIFNYK.G	0.9958		1	1020.2193
						K.DMHGDSEYNIMFGPDICGPGTK.K	0.9958		2	2442.6431
						K.HEQNIDCGGGYVK.L	0.9958	1,2		1477.5395
						K.EQFLDGDAWTNR.W	0.9958		1	1452.5229
						K.IDNSQVESGSLEDDWDFLPPKK.I	0.9958		2	2520.7118
						K.GQTLVVQFTVK.H	0.9924		1	1220.4545
						K.KVHVIFNYK.G	0.9958	1,2		1148.3934
						K.IDDPTDSKPEDWDKPEHIPDPDAK.K	0.9958		2	2761.9153
						K.KPEDWDEEMDGEWEPPVIQNPEYK.G	0.9958		2	2962.1702
646	CALU_MOUSE	315	40.32	6	13	K.EEFTAFLHPEEYDYMK.D	0.9958		2	2050.2465
						K.NADGFIDLEEYIGDMYSHDGNADEPEWVK	0.9958		3	3331.5043
						K.EEIVDKYDLFVGSQATDFGEALVR.H	0.9915		2	2702.9775
						K.DWILPSDYDHAEAEAR.H	0.9958		2	1888.9879
						R.VHHEPQLSDKVHNDAQNFDYDHDAFLGAE	0.9958		3	3678.8693
						K.VHNDAQNFDYDHDAFLGAEEAK.S	0.9958		2	2507.5914
647	CALX_MOUSE	591	22.17	8	31	K.TAELSLDQFHDK.T	0.9958		2	1404.5193
						R.KIPNPDFFEDLEPFK.M	0.9958		2	1837.082
						K.APVPTGEVYFADSFDR.G	0.9958		2	1771.9237
						K.CESAPGCGVWQRPMIDNPNYK.G	0.9958		2	2480.6895
						K.IPNPDFFEDLEPFK.M	0.9958		2	1708.9079
						K.WKPPMIDNPNYQGIWKPR.K	0.9958		2	2241.6183
						K.LNKPFLFDTKPLIVQYEVNFQNGIECGGAY	0.9958		3	3704.2263
						K.HHAISAK.L	0.9924		1	763.8747
648	CAMP1_MOUSE	1581	0.7	1	4	R.YAGEEESAK.L	0.9924		1	984.0074
649	CAN1_MOUSE	713	13.46	4	4	R.LPPGEYIVVPSTFEPNK.E	0.9958		2	1888.1705
						R.NWNTTFYEGTWR.R	0.9937		2	1575.6799

						R.CLQSGVLFQDEAFPPVSHSLGFK.E	0.9958		3	2564.8664
						K.AYAKVNGSYEALSGGCTSEAFEDFTGGVT	0.9958		3	3953.1867
650	CAN13_MOUSE	665	11.43	3	3	R.VSFPTLVCFLIRLETMAK.A	0.9958		3	2126.5715
						R.FPLQFQVFKVPQFQNVQGR.L	0.9907		2	2308.6909
						R.FWQCGQWVEVVIDDQLPVIGDNFLFVHPR	0.9958		3	3872.3435
651	CAN2_MOUSE	700	32.57	12	33	R.KPPPNLFKIIQK.A	0.9924		1	1423.7849
						R.SDTFINLREVLNR.F	0.9944		1	1577.7807
						K.LPPGEYVLVPSTFEPHK.D	0.9958		2	1911.2078
						R.FKLPPGEYVLVPSTFEPHK.D	0.9958		2	2186.5584
						R.NPWGQVEWTGK.W	0.9958		1	1302.4319
						K.RPTEICADPQFIIGGATR.T	0.9958		2	2003.2316
						R.NECLEAGALFQDPSFPALPSSLGYK.E	0.9924		2	2712.9819
						R.NYPNTFWMNPQYLIK.L	0.9958		2	1930.2311
						R.TDICQGALGDCWLLAAIASLTLNEEILAR.V	0.9958		2	3189.5654
						R.LPTKDGELLFVHSAEGSEFWSALLEK.A	0.9958		3	2905.2769
						R.KMGEDMHTIGFGIYEVPEELTGQTNIHLGK	0.9958		3	3346.7975
						K.LPCQLHQVIVAR.F	0.9958		2	1434.6909
652	CANB1_MOUSE	170	28.82	2	2	R.ISFEEFCAVVGGLDIHK.K	0.993		2	1922.1541
						K.LDLDNSGSLSVEEFMSLPELQQNPLVQR.V	0.9958		3	3160.5231
653	CAND1_MOUSE	1230	8.21	5	16	K.SPLMSEFQSQISSNPELAAIFESIQK.D	0.9958	2,3		2883.2428
						K.TVIGELPPASSGSALAANVCK.K	0.9944		2	2043.2909
						K.ITSEALLVTQQLVK.V	0.9924		1	1543.8443
						R.DLLDSVLPHLYNETK.V	0.9958		2	1757.9811
						K.FTISDHPQPIDPLLK.N	0.9952		2	1721.9939
654	CAND2_MOUSE	1235	23.64	16	35	R.SNPELTTLFESIQK.D	0.9958		2	1607.8009
						K.SFIAEFMESLQDPDLNVR.R	0.9958		2	2112.3619
						K.TVLSELPPAATGSGLAINVCR.K	0.9958		2	2127.4119
						R.LLDPEPYVGEMSTATLAR.L	0.9924		2	1964.2409
						K.FLISDQPHSIDPLLK.S	0.9958		2	1724.0098
						R.SAMRAVAALLTNPEVR.K	0.9958		2	1700.0092
						R.TLIQCLGSVGR.Q	0.9952		2	1204.3782
						K.LVFVNPPYLLPR.F	0.9958		2	1428.7605
						R.LDLQPILAEALPILASFLR.K	0.9958		2	2094.5455
						R.AVAALLTNPEVR.K	0.9944		2	1254.4722
						R.KSPTVADFSAQIR.S	0.9944		2	1420.6084
						K.VLAFLSLAEVGQVAGPGPQRELK.T	0.9917		2	2380.7929
						R.ATLTFFNSAVHNKPSLVR.D	0.9931		2	2003.3115

						R.KITGQLTSAIAQQEDVAVQLEALDILSDMLS	0.9958	3	3458.9495
						R.AISCVGHLVGHLGDR.L	0.9958	2	1591.7765
						K.CMAALISSRPDLLPDFHCTLAPALIR.R	0.9958	3	2940.406
655	CAP1_MOUSE	474	40.51	9	65	R.VENQENVSNLVIDDTELK.Q	0.9958	2	2060.2225
						R.SALFAQINQGESITHALK.H	0.9958	2	1929.1833
						K.LSDLLAPISEQIQEVITFR.E	0.9958	2	2173.5144
						K.VPTISINK.T	0.9944	1	872.0525
						R.GSKFFNHLSAVSESIQALGWVALAAKPGPF	0.9958	3	3358.9108
						R.ALLATASQCQQPAGNK.L	0.9958	2	1658.8181
						K.GAVPYVQAFDSLLANPVAEYLK.M	0.9958	2	2366.7191
						K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	0.9958	2	2813.1078
						R.LEAVSHTSDMHCGYGDSPSK.G	0.9958	2	2179.2887
656	CAP2_MOUSE	476	22.06	5	12	R.SALFAQLNQGEAITK.G	0.9958	2	1591.8045
						R.LEQLSAGLDGPPR.G	0.9958	2	1353.518
						R.VLAGDVETHAEMVHGAFQAQR.A	0.9958	2	2267.5242
						K.TEGCHLYLSEDALDCEIVSAK.S	0.9958	2	2411.5569
						R.AFLLMVSQYQQPQENEVAVLLKPISEK.I	0.9958	3	3104.6319
657	CAPS1_MOUSE	1355	3.47	3	3	R.FFVLVQVSQYTFAMCSYR.E	0.9944	2	2247.5825
						K.NCPDQDLKIK.L	0.9921	1	1231.3575
						R.IVYCTMEVEGGEK.L	0.9944	1	1515.6845
658	CAPS2_MOUSE	1297	2.62	2	2	K.DIATPIPAEEVK.K	0.9958	1	1283.4643
						R.EVLVAPGVSQRAPPAAAR.E	0.9912	2	1790.0757
659	CAPZB_MOUSE	277	32.49	5	33	R.KLEVEANNAFDQYR.D	0.9958	2	1697.8449
						K.GCWDSIHVVEVQEK.S	0.9958	2	1686.8279
						K.NLSDLIDLVPSLCEDLLSSVDQPLK.I	0.9958	2	2785.1273
						R.QMEKDETVSDCSPHIANIGR.L	0.9958	2	2288.4603
						R.RLPPQQIEK.N	0.9909	2	1109.3139
660	CASC3_MOUSE	697	6.46	3	3	R.EDEQAPKSR.Q	0.9958	1	1060.1087
						R.RTPQPVSIKPPPPEVVSR.G	0.9944	1	1985.3371
						R.MEEMGVQSGRAK.R	0.9958	1	1323.525
661	CASC4_MOUSE	435	5.75	2	2	R.IQTDTLK.Q	0.9958	1	818.9457
						K.RLEYESFQCGQQIK.E	0.9958	2	1786.9482
662	CASP_MOUSE	678	7.96	2	2	R.EQLSSANHSLQLASQIQK.A	0.9958	2	1983.1887
						K.ELNTLKSMEFAPSEGAGTQDSTKPLEVLLL	0.9958	3	3477.949
663	CASP1_MOUSE	402	10.45	2	2	K.DFIAFCSSTPDNVSWR.H	0.9945	2	1903.024
						K.QFINSVSIGTINGLLDELLEKR.V	0.9944	3	2460.8333
664	CASQ2_MOUSE	415	47.95	11	362	K.AFQEAAEHFQPYIK.F	0.9958	2	1679.8724

						R.YDLLCLYYHEPVSSDK.V	0.9921		2	2003.1817
						K.MNEVGFYEPFMDEPNVIPNKPYTEEELVEF	0.9958		3	3836.3194
						K.RYDLLCLYYHEPVSSDK.V	0.9958		2	2159.3692
						K.FFATFDK.A	0.9958		1	875.9995
						R.LRPEDMFETWEDDLNGIHIVAFAEK.S	0.9931		2	2977.3179
						R.DNTDNPDLSILWIDPDDFPLLVAYWEK.T	0.9958		2	3206.5323
						K.EIVLELVAQVLEHK.N	0.9958		2	1620.9298
						R.TIEFDGEFAADVLVEFLLDLIEDPVEIVNNK.	0.9958		3	3508.9441
						R.TIEFDGEFAADVLVEFLLDLIEDPVEIVNNKL	0.9958		3	4482.0406
						K.NIGFVMVDSR.K	0.9958		2	1138.3269
665	CASR_MOUSE	1079	5.84	2	2	R.WLQAMIFAIEEINSSPALLPNMTLGYR.I	0.9958		3	3080.6301
						R.IWLASEAWASSSLIAMPEYFHVVGGTIGFG	0.9944		3	3439.9966
666	CASZ1_MOUSE	1761	2.95	2	2	K.GLISPMMARLAAAALKPSATFDPGSGQQP	0.9958		3	3312.8701
						R.SSGALGLPASLLGAK.D	0.9958		1	1342.5785
667	CATA_MOUSE	527	61.86	20	244	K.FYTEDGNWDLVGNNTPIFFIR.D	0.9958		2	2519.7753
						R.ASQRPDVLTTGGGNPIGDK.L	0.9958		2	1884.0562
						R.GPLLVQDVVFTDEMAHFDR.E	0.9909		2	2190.4785
						R.ASQRPDVLTTGGGNPIGDKLNIMTAGSR.G	0.9958		3	2828.1729
						K.GAGAFGYFEVTHDITR.Y	0.9958		2	1741.9005
						R.SALEHSVQCAVDVK.R	0.9958		2	1543.6831
						K.NPVNYFAEVEQMAFDPSNMPPGIEPSPDK	0.9958		3	3222.5679
						K.EAETFPFNPFDLTK.V	0.9958		2	1656.8321
						R.IQALLDK.Y	0.9958		1	800.9737
						R.DAILFPSFIHSQK.R	0.9958		2	1503.741
						K.NAIHTYTQAGSHMAAK.G	0.9958		2	1701.8975
						R.LCENIAGHLK.D	0.9931		2	1155.3055
						R.LGPNYLQIPVNCPYR.A	0.9944		2	1805.0527
						K.DAQLFIQK.K	0.9958		1	963.1216
						K.LVNADGEAVYCK.F	0.9944		1	1339.4541
						K.NFTDVHPDYGAR.I	0.9958	1,2		1392.4704
						R.LFAYPDTHR.H	0.9958		2	1120.2529
						R.HMNGYGSHTFK.L	0.9958		2	1279.4155
						R.VANYQRDGPMCMHDNQGGAPNYYPNSFS	0.9944		3	3902.1464
						K.VWPHKDYPLIPVGK.L	0.9958		2	1649.9762
668	CATB_MOUSE	339	22.71	5	87	K.NGPVEGAFTVFSDFLTYK.S	0.9958		2	1993.2231
						R.GENHCGIESEIVAGIPR.T	0.9958		2	1838.9812
						R.EQWSNCPTIGQIR.D	0.9958		2	1589.7142

						K.HEAGDMMGGHAIR.I	0.9958	2	1382.5549
						K.EIMAEIYKNGPVEGAFTVFSDFLTYK.S	0.9958	2	2971.3943
669	CATC_MOUSE	462	6.49	2	5	K.NSWGSNWGESGYFR.I	0.9958	2	1647.7031
						R.NVQGVNYVSPVR.N	0.9958	2	1332.5021
670	CATD_MOUSE	410	47.56	11	257	K.AIGAVPLIQGEYMIPCEK.V	0.9944	2	1990.3314
						K.NYELHPDK.Y	0.9958	1	1016.0984
						K.FDGILGMGYPHISVNNVLPVFDNLMQQK.L	0.9958	2	3148.6649
						R.DPEGQPGGELMLGGTDSK.Y	0.9923	2	1788.9239
						K.AYWQVHMDQLEVGNELTLCK.G	0.9941	2	2435.723
						K.NYLDAQYYGDIGIGTPPQCFTVVFDTGSSN	0.9958	3	4422.8263
						K.GGCEAIVDTGTSLLVGPVEEVK.E	0.9958	2	2231.4712
						K.NIFSFYLNR.D	0.9958	1	1174.3445
						K.NIFSFYLNRDPEGQPGGELMLGGTDSK.Y	0.9958	3	2944.2452
						K.ILDIACWVHHK.Y	0.993	2	1392.6097
						K.QPGIVFVAAKFDGILGMGYPHISVNNVLPVI	0.9958	3	4159.8971
671	CATG_MOUSE	261	14.56	1	3	K.SAFRGDSGGPLVCSNVAQGIVSYGSNNGN	0.9958	3	3626.9305
672	CATL1_MOUSE	334	17.07	2	5	K.NLDHGVLLVGYGYEGTDSNK.N	0.9931	2	2152.3251
						K.AVATVGPISVAMDASHPSLQFYSSGIYYEP	0.9958	3	3736.1104
673	CAV1_MOUSE	178	35.39	3	24	K.YVDSEGHLYTVPIR.E	0.9931	2,3	1649.8437
						R.EQGNIYKPNNK.A	0.9958	1	1305.4331
						R.LLSTIFGIPMALIWGIYFAILSFLHIWAVVPCI	0.9958	3	3905.8153
674	CAZA1_MOUSE	286	23.78	4	14	R.EGAAHAFAQYNMDQFTPVK.I	0.9958	2	2126.3508
						R.LLLNNDNLLR.E	0.9958	2	1198.408
						K.FITHAPPGEFNEVFNDVR.L	0.9958	2	2090.3024
						K.IQVHYYEDGNVQLVSHK.D	0.9958	2	2030.2474
675	CAZA2_MOUSE	286	27.97	4	53	K.FIIHAPPGEFNEVFNDVR.L	0.9958	2	2102.3568
						K.FTVTPSTTQVVGILK.I	0.9958	2	1591.8883
						R.EGAAHAFAQYNLDQFTPVK.I	0.9958	2	2108.3177
						K.KVDGQQTIIACIESHQFQAK.N	0.9958	2	2302.5585
676	CB029_MOUSE	505	4.75	1	2	R.GGQEPDRPPLSGFLPPITPPEK.F	0.9932	2	2330.6457
677	CB033_MOUSE	291	46.39	5	34	R.VLTLSERPLDFLDLERPLPTPQSEESR.A	0.9958	3	3139.5327
						R.IVVTGNNEDISFSRPADLDLIQSTPFKPLALI	0.9958	3	3501.0172
						R.YGISNLDAAIEGASDDMTVVDAASLR.R	0.9958	2	2655.8933
						R.GGSAAATSNPHHDNVR.Y	0.9958	2	1591.6401
						K.VAPPNADLEQEFQDGVPNASVIMQVPER.I	0.9958	2	3052.3857
678	CB037_MOUSE	519	3.08	1	4	K.ENLITVTASGRVVK.R	0.9958	2	1487.7397
679	CB5D1_MOUSE	228	5.26	1	2	R.FVHIPPPLPR.S	0.9944	1	1173.4465

680	CBG_MOUSE	397	24.69	6	27	K.FSMSDTYDLQDVLADVGIK.D	0.9958	2	2118.3631
						K.YNRPFIFLAFDK.Y	0.9958	2	1531.7972
						R.QMNLYIPKFSMSDTYDLQDVLADVGIK.D	0.9944	3	3106.5759
						R.DLAPTNVDFAFNLYK.R	0.9958	2	1728.9421
						K.HYYESEALTIPSK.D	0.9958	2	1538.6971
						K.NTLISPVSISMALAMLSLSTR.G	0.9958	2	2206.6643
681	CBP_MOUSE	2441	2.58	3	4	K.SPSSPQQQQQVLNILK.S	0.9958	2	1796.0336
						K.KKPSMPNVSNDLSQK.L	0.9912	2	1673.925
						R.AASPMNHSVQMNSMASVPGMAISPSR.M	0.9958	3	2660.0713
682	CBPC1_MOUSE	1218	4.19	3	5	K.DLQTVLNILSILIELVSSGGGRR.A	0.9958	2	2454.8729
						R.ELEEMGAK.F	0.9924	1	907.0265
						R.MGTDICYYKNHFSR.S	0.9924	1	1792.9728
683	CBPC2_MOUSE	862	4.06	2	2	R.ALCRSLAGNTVYLLTITNPSR.T	0.9921	2	2321.6482
						R.YMLNGSFGER.D	0.9958	1	1174.3166
684	CBPC4_MOUSE	972	0.82	1	2	K.ILEDIR.R	0.9958	1	758.8931
685	CBPD_MOUSE	1377	3.56	2	2	R.IFGLPRELVVTVSGATMSALILTACIIWCICS	0.9958	3	3795.4978
						K.RNPVVTQLVDR.T	0.9924	2	1297.5002
686	CBPM_MOUSE	443	8.13	2	2	R.KDPEITHLIDSTR.I	0.9958	2	1525.7019
						R.SLTPDDDVFQHLAYTYASR.N	0.9904	2	2200.3691
687	CBPN_MOUSE	457	7.44	2	2	K.NGGPNHHLPLPDNWK.S	0.9958	2	1696.8655
						R.EALIQFLEQVHQGIK.G	0.9958	2	1754.0391
688	CBR1_MOUSE	277	48.01	8	122	K.EYGGLDVLVNNAGIAFK.V	0.9958	2	1781.0184
						K.SPEEGAETPVYLALLPPDAEGPHGQFVQD	0.9958	3	3193.4937
						R.FHQLDIDNPQSIR.A	0.9937	2	1583.744
						R.SETITEEELVGLMNK.F	0.9958	2	1693.9068
						K.GVHAEEGWPNSAYGVTK.I	0.9958	2	1802.9408
						K.KGVHAEEGWPNSAYGVTK.I	0.9958	2	1931.1149
						K.VNDDTPFHIQAEVTMK.T	0.9958	2	1846.0649
						K.ILLNACCPGWVR.T	0.9958	2	1459.6636
689	CBR2_MOUSE	244	37.7	5	17	K.FAEVEDVVNSILFLLSDR.S	0.9958	2	2067.3465
						K.ALGGIGPVDLLVNNAALVIMQPFLEVTK.E	0.9958	2	2894.4858
						K.ECPGIEPVCVDLGDWDATEK.A	0.9958	2	2291.4054
						K.AMAMELGPHK.I	0.9958	2	1085.3246
						K.ALHASGAK.V	0.9958	1	754.8643
690	CBR4_MOUSE	236	36.02	6	46	K.TMIQQGGSIVNVGSIIGLK.G	0.9958	2	1916.2866
						K.VTAGELGGNHLAFR.C	0.9958	2	1442.6175
						K.HLGPVNFLVNAAGINR.D	0.9958	2	1692.9614

						R.NLEVAKVTAGELGGNHLAFR.C	0.9944		2	2097.3817
						K.TEDMISQLHTNLLGSMLTCK.A	0.9958		2	2293.6217
						R.TKTEDMISQLHTNLLGSMLTCK.A	0.9958		2	2522.9009
691	CBS_MOUSE	561	7.66	2	2	R.NYMSKFLSDK.W	0.9944		1	1233.4247
						R.AGNLKPGDTIIEPTSGNTGIGLALAAAVK.G	0.9958		3	2751.1527
692	CBX1_MOUSE	185	23.24	2	2	R.GLEPERIIGATDSSGELMFLMK.W	0.9914		2	2395.7914
						K.KVEEVLEEEEEEYVVEK.V	0.9958		2	2110.2763
693	CC020_MOUSE	933	2.25	1	2	K.QPPPAPPPTLMPAATSGGK.Y	0.9958		2	1816.1254
694	CC023_MOUSE	499	3.21	1	3	R.LSVYLENLQKPGFK.S	0.9958		2	1636.9316
695	CC026_MOUSE	276	7.61	2	2	R.SLTAFKGDAK.V	0.9958		1	1038.1888
						K.ISDILAK.S	0.9958		1	759.9212
696	CC041_MOUSE	562	3.56	1	11	K.LNFRLLEGIDGFPESAVK.V	0.9944		2	2006.3091
697	CC060_MOUSE	185	20.54	3	5	R.LHPQVLQAMR.Q	0.9958		1	1193.4527
						R.LHPQVLQAMRQR.G	0.9944		1	1477.7709
						R.GIAVEVQDTPNACATFNFLCHEGR.V	0.9958	2,3		2707.8915
698	CC063_MOUSE	1610	5.03	2	2	R.SYGHEQPQQTSEAAAAALPKGAEEPERPF	0.9958		3	3254.4997
						K.NHTYNELFVSGGFIVSDESILNLEVVTIESLK	0.9958		3	5274.971
699	CC108_MOUSE	1847	2.6	3	3	R.QNDVKK.R	0.9958		1	731.8271
						R.SLDFGEVTVSPMEGEVGPEEGAPILVTLK.A	0.9958		3	3002.4035
						K.DEEDIDK.D	0.9958		1	863.8535
700	CC110_MOUSE	848	1.77	1	3	K.KAMNTSEQPSATK.S	0.9944		1	1393.5548
701	CC123_MOUSE	791	1.01	1	2	R.VQEVVK.E	0.9958		1	701.8412
702	CC129_MOUSE	1034	3.38	2	2	R.EHLEEIEQHFMGQQALYPR.D	0.993		2	2356.6177
						R.DMSEEEREEAEYLR.T	0.9958		2	1786.8646
703	CC135_MOUSE	876	5.71	3	3	K.YLALEEKLYK.D	0.9924		1	1270.5114
						K.GNKIIMTPEMCISYEVEPMEHTK.K	0.9954		2	2739.1552
						R.EDMLELKHINK.T	0.9958		1	1370.6067
704	CC136_MOUSE	1136	4.05	3	3	R.RLQEEQGQLQEELHR.L	0.9952		2	1894.0543
						K.SYDSSTSANEAFEK.S	0.9909		2	1536.5487
						R.KLTQNQECVLK.E	0.9929		2	1361.5475
705	CC142_MOUSE	738	10.43	2	2	R.LGVSPAQNTHLLSTLGGGGRGGGGGGGP	0.9944		3	4484.9785
						R.LGGPGALWSQYWTLLWAACAKCLDLR.V	0.9931		3	3008.4248
706	CC50A_MOUSE	364	5.22	1	3	R.DDSQLNGDPSALLNPSK.E	0.9917		2	1771.8785
707	CC88B_MOUSE	1481	4.86	4	5	R.DEVAQLR.R	0.9958		1	830.9163
						R.EGALHGGPRLGADGAGSTESLGGPLETEL	0.9944		3	3189.4227
						R.DLGAQRLAELLLER.E	0.9958		2	1597.8552
						R.EAPQGELVHK.A	0.9917		1	1108.2395

708	CC90A_MOUSE	340	7.94	2	2	K.MQQEIALQQVLSK.I	0.9958		1	1516.7961
						R.KIETEVAGLK.T	0.9958		2	1088.2896
709	CC90B_MOUSE	256	29.69	4	33	R.KLTFDTHALVQDLETHGFDK.T	0.9958		3	2316.5755
						K.TQAQTIVSVLSTLSNVSLDTIYK.E	0.9958		2	2482.8339
						K.AQQEITVQQLMAHLDSIR.K	0.9958		2	2082.3825
						R.RPVDITPLEQR.K	0.9958		2	1324.5229
710	CCD15_MOUSE	810	1.6	1	2	R.NAIRNFASAHR.R	0.9958		1	1257.3975
711	CCD18_MOUSE	1455	3.3	2	2	K.TELEKTTNSVK.E	0.9944		2	1250.3916
						K.LHANLTVNQLSQNVANDSQECGKVNTLET	0.9958		3	3652.9635
712	CCD21_MOUSE	761	3.68	2	2	K.QSVEEANGENLR.V	0.9924		1	1346.3965
						R.ETALQQMRTAVK.E	0.9958		1	1376.614
713	CCD39_MOUSE	937	3.31	2	2	K.NETQLLEKEMAIIR.E	0.9944		2	1688.98
						R.DQEIDNCALALSR.I	0.9905		1	1505.5909
714	CCD43_MOUSE	222	7.21	1	14	K.KEDEVQAIATLIEK.Q	0.9958		2	1587.8107
715	CCD44_MOUSE	294	52.72	9	74	R.GPGGSSLLIEALSNSGPK.C	0.9958		2	1684.887
						K.LDSLGLCPVSCSMEFIPHSK.V	0.9958		2	2278.5576
						K.VQLAEPELEQAAHLIQALNNYEDVIHVYDNI	0.9958		3	3693.0612
						K.FICDASSLHQVR.K	0.9944	1,2		1433.5731
						K.KLDSLGLCPVSCSMEFIPHSK.V	0.9958		2	2406.7317
						R.ALELAIEAGAEDVKEAEDEEEK.N	0.9958		2	2389.5292
						K.GIYLLYEGR.G	0.9958		1	1084.2603
						K.EGGPNPENNSSLANILELCR.S	0.9958		2	2185.3215
						K.KGVVVVGVEDR.E	0.9943		2	1157.3555
716	CCD51_MOUSE	406	8.87	2	2	K.RPEAAALGLFHR.L	0.9958		2	1338.5552
						R.GLVHAEQGQGSGSPTGSSTR.G	0.9958		2	1913.9987
717	CCD57_MOUSE	1016	1.28	1	2	R.ARELQDLEAVK.D	0.9958		1	1272.4441
718	CCD58_MOUSE	144	41.67	4	74	R.IVHELNTTVPTASFAGK.I	0.9958		2	1786.0379
						K.WMQSELNVEEVVNDR.S	0.9958		2	1849.0252
						K.QLYESLMAAHVSR.D	0.9958		2	1505.7319
						R.VHFKPPK.N	0.9958		1	853.0549
719	CCD66_MOUSE	935	7.06	2	6	R.NNPENLSQNRGISPLATSHR.E	0.9958		2	2206.3829
						R.LSSQLTHQHLESLCVSPDTQELADVNGVF	0.9958		3	4544.9392
720	CCD79_MOUSE	768	3.52	2	2	R.RAVDLAHK.Y	0.9958		1	910.0641
						K.RMSVYVLLVLVSNNR.N	0.9958		2	1764.1393
721	CCD80_MOUSE	949	2.32	1	2	R.RITNEGQILEQPLDPNLIPK.L	0.9944		3	2289.6371
722	CCD99_MOUSE	608	8.22	2	2	R.LFAMIEQKNGEIK.H	0.9958		2	1521.8151
						R.EVLPLNITTPEETEETAAASATEDGVSRLPF	0.9958		3	3532.8431

723	CCDC5_MOUSE	278	6.83	1	4	R.GMDASLSHRSLAALSEK.L	0.9958	2	1774.0019
724	CCHL_MOUSE	272	18.75	3	23	R.KGCPVTAATSDLTSESK.A	0.9958	2	1752.8823
						K.WEALHAHECPCGPSLVR.F	0.9958	2	2020.1871
						R.IHNQNNEQAWK.E	0.9958	1	1382.4783
725	CCL28_MOUSE	130	8.46	1	2	K.QWMRASEVK.K	0.9958	1	1135.3263
726	CCM2_MOUSE	453	11.04	2	2	K.YLGQLTSIPGYLNPSSR.T	0.9958	2	1867.1118
						R.DDAAHLVVLKTAQDPGISPSQSLCAESSR.(	0.9944	3	3054.3068
727	CCNB3_MOUSE	1396	3.87	2	5	K.ETEITIQDDSDSLERIEK.E	0.9948	2	2122.2475
						R.FICEMTLQEYEYIEERPSKLAAASFILALYMI	0.9944	3	3888.4947
728	CCND1_MOUSE	295	5.42	1	3	R.LQLLGATCMFVASK.M	0.9945	2	1539.8396
729	CCND3_MOUSE	292	3.77	1	4	R.ETTPLTIEK.L	0.9958	1	1032.1791
730	CCPG1_MOUSE	753	4.91	2	4	R.ENQVLKQYLEVEK.Q	0.9958	2	1620.8431
						R.RVCSGMFECAGQEAISPVNK.A	0.9958	2	2241.4561
731	CD018_MOUSE	517	5.42	2	3	R.MRLLADSEVASILPISK.S	0.9958	2	1844.2201
						K.LIDVIER.R	0.9924	1	858.0257
732	CD019_MOUSE	313	11.5	1	3	R.LHQVDNSSWASSPWVATIDSAHLAQPFLE	0.9944	3	3829.1333
733	CD037_MOUSE	561	3.74	1	2	R.QEFLKYSGPGPGQYDIIQK.R	0.9929	2	2169.4417
734	CD151_MOUSE	253	7.11	2	4	R.YHQSGHEGVSSAVDK.L	0.9958	2	1601.6726
						K.RYHQSGHEGVSSAVDK.L	0.9958	2	1757.8601
735	CD2L7_MOUSE	1484	2.02	2	5	R.SSGPALTESLVQTPVK.N	0.9926	2	1614.8363
						K.AITPPQQPYK.K	0.9944	2	1143.3281
736	CD34_MOUSE	382	9.16	2	11	R.LAQGICLELSEASSCEEFKK.E	0.9958	2	2300.5001
						K.EKGEDLIQILCEK.E	0.9937	1	1575.7656
737	CD36_MOUSE	472	30.3	9	56	R.TYLDVEPITGFTLQFAK.R	0.9958	2	1944.2347
						R.FVLPANAFASPLQNPDNHCFCTEK.V	0.9958	2	2779.0131
						R.QFWIFDVQNPDDVAK.N	0.9958	2	1823.0147
						R.LQVNILVKPAR.K	0.9958	2	1251.5583
						K.ELLWGYK.D	0.9958	1	909.0727
						K.EGKPVYISLPHFLHASPDVSEPIEGLHPNE[	0.9958	3	3848.223
						R.SIYAVFGSEIDLK.G	0.9943	2	1442.6519
						R.LQVNILVKPARK.I	0.9958	2	1379.7323
						K.QRGPYTYR.V	0.9931	2	1041.1545
738	CD4_MOUSE	457	3.5	1	3	K.GAWEKGSFPLIINK.L	0.9958	2	1560.8363
739	CD45_MOUSE	1291	5.73	4	11	R.TQHIGNQGENK.K	0.9924	1	1226.2913
						R.MIWEQKATVIVMVTR.C	0.9944	2	1806.2348
						K.NVINVQTDLGIPETPKPSCGDPAARK.T	0.9958	3	2779.0887
						R.AQTNYTCVAEILYR.G	0.9915	2	1702.8707

740	CD47_MOUSE	303	5.28	1	2	K.ISVSDLINGIASLK.M	0.9958	2	1430.6848
741	CD72_MOUSE	354	4.8	1	3	K.DTEQQLQACQAERAK.T	0.9944	1	1776.8669
742	CD81_MOUSE	236	32.63	3	14	K.QFYDQALQQAVMDDDANNAK.A	0.9958	2	2286.4345
						K.TFHETLNCCGSNALTTLTTTILR.N	0.9958	2	2625.8708
						R.NTLCPSGGNILTPLLQQDCHQKIDELFSGK	0.9958	3	3385.7309
743	CD9_MOUSE	226	11.95	1	3	K.AIHMALDCCGIAGPLEQFISDTCPK.K	0.9958	3	2806.1014
744	CD99_MOUSE	175	28	1	2	R.GSGDEGGHGGAGGAEPEGTPQGLVPGV\	0.9958	3	4265.6427
745	CDC23_MOUSE	597	4.02	2	2	K.FLSLPDTWMK.E	0.9944	1	1238.4871
						K.ALSIFNELRK.Q	0.9924	1	1191.416
746	CDC37_MOUSE	379	11.35	3	29	K.RLGPGGLDPVEVYESLPEELQK.C	0.9958	2,3	2426.7289
						R.LGPGGLDPVEVYESLPEELQK.C	0.9958	2	2270.5414
						K.EGEEAGPGDPLLEAVPK.A	0.9944	2	1708.8627
747	CDC42_MOUSE	191	13.61	2	22	K.TPFLLVGTQIDLR.D	0.9958	2	1473.7557
						K.WVPEITHHCPK.T	0.9958	1,2	1404.5774
748	CDCA2_MOUSE	982	5.3	2	2	R.FIAQQRNLK.K	0.9958	1	1118.3243
						K.EENLENIEPPQGSFANLSLSKSSLSETPPG	0.9944	3	4179.4609
749	CDCA5_MOUSE	264	3.41	2	12	K.KVPEILK.S	0.9958	1	827.055
						K.VPEILK.S	0.9903	1	698.8809
750	CDGAP_MOUSE	1425	7.16	3	3	K.HRPSSLNLDSATPIADLFRLENGAPFSSPG	0.9944	3	4254.7001
						K.LEPVCSLLESESQQELSPDPASLAPLEMLL	0.9924	3	4299.8435
						R.AQDSTLPGEHPLQLQLK.N	0.9958	1	1876.1197
751	CDK4_MOUSE	303	6.27	1	4	R.YEPVAEIGVGAYGTVYK.A	0.9912	2	1817.0484
752	CDK7_MOUSE	346	5.2	1	6	R.DLKPNNLLLDENGVLK.L	0.9958	2	1796.0739
753	CDS1_MOUSE	461	5.64	2	3	K.VLQQLLVLQPEQQLNIYR.T	0.9944	2	2196.598
						R.GPNPSKVLQQLLVLQPEQQLNIYR.T	0.9952	3	2777.2394
754	CE033_MOUSE	452	17.7	3	4	R.SRCWDACMVVDGGTSFEFNDGAIASMMIN	0.9958	3	3371.7112
						R.LYLEGTGINPTPVDLHEQQLSLNQHSR.A	0.9958	3	3061.3812
						K.NVEHIIDSLRDEGIEVR.L	0.9958	2	1995.1997
755	CE034_MOUSE	639	6.26	2	2	K.MAPGVSVSTILPVLLK.E	0.993	2	1626.0509
						K.VSQRPDSSGILSETQNQDPK.N	0.9958	2	2187.3281
756	CE290_MOUSE	2472	3.96	6	6	K.FEDSTGSMPDPSLPLPNQLEIALR.K	0.9904	2	2628.9569
						K.EKEGEAHGLAK.Q	0.9924	1	1169.2798
						K.ESALRLAEQNILSR.D	0.9958	2	1600.8155
						K.SQLALK.E	0.9924	1	659.8039
						K.EMEKNTFIIEDLK.N	0.9958	1	1610.8628
						K.DSDVKGGETSLIIPSLER.L	0.9932	2	1917.1235
757	CECR5_MOUSE	419	8.11	2	10	R.VPVVFVTNAGNILQHNK.A	0.9958	2	1851.1588

						R.LAFPELDMVDLQR.R	0.9958	2	1547.8096
758	CELF4_MOUSE	486	9.05	3	3	K.DHDAIKLFIGQIPR.N	0.9909	2	1623.8955
						R.KLFVGMLNK.Q	0.9924	1	1050.3477
						R.LFEAFGNIEECTILR.G	0.9929	2	1813.0265
759	CELF6_MOUSE	460	3.91	1	3	K.LFVGMLGKQQGEEDVR.R	0.9958	2	1807.0747
760	CELR1_MOUSE	3034	2.83	3	3	R.NPGPLSASATVHIVVEDENDNYPQFSEKR.	0.9958	3	3215.4601
						K.FGQPAAVPCPKGSVGNAVR.H	0.9958	3	1913.1528
						R.DSGPNGRLLYTFQGGDDGDGDFYIEPTSG	0.9958	3	3420.6299
761	CELR2_MOUSE	2920	1.95	2	3	R.ALDNNRPLEAIMSVLVSDGVHSVTAQCSLF	0.9958	3	3254.652
						K.SLDLTGPLLLGGVPDLPESFPVR.M	0.9958	2	2393.7857
762	CELR3_MOUSE	3301	3.7	3	3	K.ADTTYVEVMVNDVNDNAPQFVASHYTGLV	0.9958	3	5087.5367
						R.LTMAHPYHFQGNGTLSWDFGNDMAVSVP	0.9931	3	4374.9404
						R.LEYSLTGVASDTPFVINSATGWVSVSGPLD	0.9958	3	3240.5939
763	CENB1_MOUSE	740	2.03	1	2	R.RVQEAEEAGTALR.T	0.9958	1	1430.5607
764	CEND1_MOUSE	1703	1.7	2	2	K.ELYPYWVSALDTQDEK.E	0.9924	2	1958.1315
						R.KTLLASLTK.E	0.9944	1	975.2169
765	CENG1_MOUSE	1186	3.2	1	2	R.QLWAAVEAQDVAAVLLLLAHARHGPLDTS'	0.9944	3	3905.4489
766	CEP70_MOUSE	616	7.79	2	2	R.LMIEKQQEEAEWESINGLLMTHGFKPLCLV	0.9931	3	3674.2741
						K.QVLGPEDLQSIIK.K	0.9958	1	1440.6799
767	CERU_MOUSE	1061	26.77	18	134	K.EFYLFPTVFDENESLLLDDNIR.M	0.9958	2	2690.966
						R.AEDEHLGILGPPIHANVGDK.V	0.9958	2	2083.3085
						K.TIDKPAWLGFLGPVIK.A	0.9958	2	1756.1411
						K.LISVDTEQSNFYLQNGPDR.I	0.9958	2	2197.366
						K.HYFIGITEAVWDYASGTEEK.K	0.9958	2	2317.5163
						R.EDSACIPWAYYSTVDR.V	0.9907	2	1934.0351
						K.GTFDVECLTTDHYTGGMK.Q	0.9958	2	2033.183
						K.KLISVDTEQSNFYLQNGPDR.I	0.9958	2	2325.5401
						R.GPDEEHLGILGPVIWAEVGDTIK.V	0.9958	2	2446.7625
						K.VLPGQQYVYVLHANEPSPGEGDSNCVTR.I	0.9944	3	3088.3264
						K.DLYSGLIGPLIVCR.K	0.9958	2	1576.8425
						R.SSQQAASHVAPK.E	0.9958	2	1211.3201
						R.RAEDEHLGILGPPIHANVGDK.V	0.9958	2	2239.496
						K.QRGPDEEHLGILGPVIWAEVGDTIK.V	0.9958	3	2731.0807
						R.IYHSHVDAPK.D	0.9924	1,2	1167.3097
						K.DIFTGLIGPMK.I	0.9958	1	1192.4589
						K.DIASGLIGPLILCK.K	0.9958	1	1470.7589
						R.IYTFHAHGVTYTK.E	0.9958	2	1538.7459

768	CES3_MOUSE	565	28.67	8	60	K.AVIGDHGDEIFSVFGSPFLK.D	0.9958	2	2136.4118
						K.DLFQDLMADVVFGVPSVIVSR.S	0.9944	2	2308.6978
						R.GNWGHLDQVAALR.W	0.9958	1,2	1437.601
						K.QEFGWIIPTLMGYPLAEGK.L	0.9958	2	2151.528
						K.ESYPFLPTVIDGVVLPK.A	0.9958	2	1875.2151
						R.FAPPQPAEPWSFVK.N	0.9958	1,2	1601.8449
						R.NGNPNGGGLPHWPEYDQK.E	0.9958	2	1981.091
						K.ENIPLQFSEDCLYLNIYTPADLTK.N	0.9958	2	2859.1683
769	CF066_MOUSE	173	9.25	1	5	K.ITVVEALTLLNNHK.L	0.9958	2	1565.8534
770	CF113_MOUSE	577	3.64	1	7	K.QYQIVAVEGVLSPEEKVAR.K	0.991	2	2116.4221
771	CF125_MOUSE	136	35.29	2	2	K.LILSTDTLEEFQEMNK.S	0.9958	2	1912.1621
						R.VAQAFREGENTQIAEPEACDQMYESLAR.L	0.9958	3	3215.4414
772	CF142_MOUSE	269	20.07	3	37	K.SLAISSSLASDVVRPK.V	0.9958	2	1630.8821
						R.QGEQGPPGGPGNIATRPKSLAISSSLASDV	0.9944	3	3373.7941
						K.TSSHPEIPHGIAPQQK.H	0.9958	2	1727.9175
773	CF174_MOUSE	945	4.02	2	2	K.EGCLQSELIQFHLK.K	0.9958	1	1702.914
						R.DTFFEEDACQLQEMRHELER.A	0.9909	2	2584.7425
774	CF190_MOUSE	636	7.08	2	50	K.DIKLENLIIK.Q	0.9958	1	1199.4765
						R.VLEIQSGIYFEGSVYEMFGNECCLSTGEVIH	0.9958	3	3560.9267
775	CF201_MOUSE	227	15.86	2	3	R.DITSACKAVSAFQSMSGGSMFQCSWQHR	0.9958	3	3166.4422
						R.FMAKNK.T	0.9958	1	738.9231
776	CFAB_MOUSE	761	27.33	10	23	R.FLCTGGVDPYADPNTCK.G	0.9958	2	1916.0266
						R.DFHINLFQVLPWLK.D	0.9931	2	1771.1149
						K.GGSFQLLQGGQALEYLCPSGFYPYPVQTR	0.9944	2,3	3235.5891
						K.YGQTLRPICLPCTEGTTR.A	0.9958	2	2124.3338
						R.YGLLTYATVPK.V	0.9958	2	1226.4582
						K.GHETCMGAVVSEYFVLTAAHCFMVDDQKH	0.9944	3	3670.0812
						R.DLEIEEVLFHPK.Y	0.9915	2	1469.6775
						K.KAEGIPEFYDYDVALVK.L	0.9958	2	1958.2182
						R.EDYLDVYVFGVGPLVDSVNINALASK.K	0.9958	2	2799.1498
						K.SLSLCGMVWEHK.K	0.9958	2	1447.6582
777	CFAD_MOUSE	259	32.82	4	6	R.GDSGSPLVCGDAVEGVVTWGSR.V	0.9958	2	2206.3398
						K.EVEPGTLCDVAGWGVVTHAGR.R	0.9958	2	2211.4051
						R.RPDVLHQLR.V	0.9958	2	1134.3267
						K.RWYDVQSVVPHPGSRPDSLEDDLILFK.L	0.9958	3	3170.5517
778	CFAH_MOUSE	1234	18.8	11	57	R.LYYEESLRPNFPVSIGNK.Y	0.9958	2	2127.4045
						R.CVEILCTPPRVENGDGINVKPVYK.E	0.9944	3	2759.1072

						R.IVSGAAETDQEYYFGQVVR.F	0.9958	2	2133.322
						K.TSCPPPPQIPNTQVIETTVK.Y	0.9958	2	2208.4828
						R.VGPDSVQCYHFGWSPGFPTCK.G	0.9958	2	2427.61
						R.ECGADGWINDIPLCEVVK.C	0.9958	2	2076.2429
						K.KPCGHPGDTPFGSFR.L	0.9958	2	1660.7955
						K.IPCSQPPTIEHGSINLPR.S	0.9958	2	2017.2585
						K.VQCYNGYSLQNGQDTMTCTENGWSPPPK	0.9958	3	3663.8955
						K.IYSHSGEDIEFGCK.Y	0.9958	2	1642.7284
						R.CTLKPCEFPQFK.Y	0.9958	2	1555.7462
779	CFDP1_MOUSE	295	7.8	1	5	R.EKPQALVTSPATPLPAGSGIK.R	0.9958	2	2063.402
780	CFTR_MOUSE	1476	1.49	2	4	K.NEHVKK.S	0.9924	1	754.8643
						K.NNPVNSGNNGTK.I	0.9924	1	1216.2529
781	CG053_MOUSE	128	6.25	1	2	K.DIDDLK.K	0.9924	1	718.782
782	CH038_MOUSE	333	12.01	2	3	R.SVPAEAFPAFLQTVSLEDYLK.K	0.9958	2	2326.6513
						R.DVVYDIASQAHLHLK.H	0.9958	2	1709.9426
783	CH041_MOUSE	512	4.69	2	5	K.SSGQGGARNAALK.D	0.9958	1	1217.3273
						K.LDSAEEK.S	0.9958	1	791.8333
784	CH053_MOUSE	249	7.23	1	13	R.YLMGETQLCTTRCVLK.E	0.9958	1	1974.2551
785	CH070_MOUSE	324	6.79	1	6	K.ASSVNSPLGNKPQTLSPSHR.A	0.9958	2	2078.2925
786	CH10_MOUSE	102	60.78	6	164	K.DYFLFR.D	0.9958	1	860.9878
						K.VVLDDKDYFLFR.D	0.9958	2	1530.7637
						K.VLQATVVAVGSGGK.G	0.9958	1	1286.5143
						K.GGIMLPEK.S	0.9924	1	845.0447
						K.VLLPEYGGTK.V	0.9924	1	1077.2658
						K.GKSGEIEPVSVK.V	0.9958	2	1230.4038
787	CH3L4_MOUSE	402	5.97	1	31	K.SADLNVDSIITYWKDHGAASEK.L	0.9945	2	2421.6256
788	CH60_MOUSE	573	67.71	28	4198	K.LVQDVANNTNEEAGDGTTTATVLAR.S	0.9958	2	2561.7221
						K.ILQSSSEVGYDAMLGDFVNMVEK.G	0.9958	2	2533.8709
						R.TALLDAAGVASLLTTAEAVVTEIPK.E	0.9958	2	2455.8517
						R.AAVEEGIVLGGGCALLR.C	0.9958	1,2	1685.9274
						K.QSKPVTTPEEIAQVATISANGDK.D	0.9958	2	2385.6335
						K.ISSVQSIVPALEIANAHR.K	0.9958	1	1906.1924
						R.KPLVIIAEDVDGEALSTLVLNR.L	0.9958	2	2366.7606
						K.KQSKPVTTPEEIAQVATISANGDK.D	0.9958	2	2513.8076
						K.RIQEITEQLDITTSEYEK.E	0.9958	2	2197.4039
						K.KISSVQSIVPALEIANAHR.K	0.9958	2	2034.3665
						K.TLNDELEIIEGMK.F	0.9958	1	1505.7235

						K.CEFQDAYVLLSEK.K	0.9958	2	1602.7473
						R.TVIIEQSWGSPK.V	0.9958	1	1345.5382
						R.IQEITEQLDITTSEYEK.E	0.9924	2	2041.2164
						R.TALLDAAGVASLLTTAEAVVTEIPKEEK.D	0.9958	3	2842.2567
						R.ALMLQGVDLLADAVAVTMGPK.G	0.9958	2	2114.5666
						R.GVMLAVDAVIAELK.K	0.9958	2	1429.7583
						R.CIPALDSLKPANEDQK.I	0.9958	1,2	1799.9849
						K.DPGMGAMGGMGGGMGGGMF.-	0.9958	1	1675.9659
						K.DIGNIISDAMK.K	0.9958	1	1177.3581
						K.VGEVIVTK.D	0.9958	1	845.0269
						K.DMAIATGGAVFGEEGLNLNLEDVQAHDLGI	0.9958	3	3086.4003
						K.VGLQVVAVK.A	0.9958	1	913.1484
						K.LSDGVAVLK.V	0.9944	1	902.0788
						R.VTDALNATR.A	0.9958	1	961.0629
						R.GVMLAVDAVIAELKK.Q	0.9958	2	1557.9323
						R.IQEITEQLDITTSEYEKEK.L	0.9944	2	2298.506
						R.RGVMLAVDAVIAELK.K	0.9958	2	1585.9457
789	CHCH1_MOUSE	118	15.25	1	14	R.SIQESLGQSESLSPHK.M	0.9958	2	1727.8687
790	CHCH2_MOUSE	153	16.99	2	31	R.APAAQPPAAAAPSAVGSPAAAPR.Q	0.9958	2	1998.2492
						R.RAPAAQPPAAAAPSAVGSPAAAPR.Q	0.9958	2	2154.4367
791	CHCH3_MOUSE	227	52.86	11	377	R.RVTFEADENENITVVK.G	0.9958	2	1865.0501
						K.RYEYHPVCADLQTK.I	0.9958	2	1780.9439
						R.YSSVYGASVSDEDLK.R	0.9958	2	1620.71
						R.VTFEADENENITVVK.G	0.9958	1,2	1708.8627
						R.VAEELALEQAK.K	0.9958	1	1201.3623
						R.LSENVIDR.M	0.9958	1	946.0483
						R.YEYHPVCADLQTK.I	0.9958	1,2	1624.7565
						R.QNTQQTLSCSALASQYMHCVNHAK.Q	0.9958	2	2778.9887
						R.ISSEEERMK.A	0.9958	1	1109.2396
						R.RVAEELALEQAK.K	0.9944	1	1357.5498
						R.KQDAFYK.E	0.9958	1	900.022
792	CHCH6_MOUSE	273	27.47	5	25	R.RVEPVCSGLQAQILR.C	0.9958	2	1726.9829
						K.VPSAESGGGLQSSAVK.E	0.9958	2	1474.6109
						R.DHLHEVLLCSDLVK.A	0.9958	2	1678.892
						K.ASLTHEQQQSAR.L	0.9958	1	1356.4379
						K.AYQHCVSTAR.K	0.9944	1	1193.2707
793	CHCH7_MOUSE	85	54.12	3	4	R.LRDPDINPCLSESDASTR.C	0.9932	2	2047.1523

						R.FWNSVMIQR.R	0.9958	2	1181.3978
						R.RQNGVQPSMPTAAER.D	0.9958	2	1642.8302
794	CHCH8_MOUSE	87	26.44	1	2	R.SGCAASHFAVQECMAQHQDWR.Q	0.9958	2	2477.6051
795	CHD9_MOUSE	2885	2.32	3	3	K.ENSEYGVAPEWGDVVK.Q	0.9924	1	1779.9005
						K.DELAELSEAESEGEEKPK.L	0.9929	2	1991.0698
						K.AVPASGTSIQPTLGANGAILDSQPIVK.K	0.9958	2	2606.9793
796	CHIO_MOUSE	332	4.82	1	2	R.AALTHNDNHFNYEK.T	0.9909	2	1674.7697
797	CHKB_MOUSE	394	5.84	1	4	R.ARPEELSVCPVSGGLSNLLFR.C	0.9958	2	2302.6018
798	CHL1_MOUSE	1209	4.63	3	3	R.IIAANNSGTFKIPNEGHISHFQGK.Y	0.9958	3	2581.8937
						K.DTATLSWGLPKK.L	0.9924	2	1317.5278
						R.GDLYFANVEENDSR.N	0.9958	2	1629.68
799	CHM4B_MOUSE	224	20.98	2	2	K.QLAQIDGTLSTIEFQR.E	0.9958	2	1821.0403
						K.NLLEISGPETVPLPNVPSVALPSKPAK.K	0.9958	2	2769.2542
800	CHMP5_MOUSE	219	18.72	2	4	R.DNLAQQSFNMEQANYTIQSLK.D	0.9958	2	2444.6783
						K.APPPSLTDCIGTVDSR.A	0.9958	2	1686.8255
801	CHRD1_MOUSE	331	25.38	5	26	K.FQEHIIQAPKPVEAIK.R	0.9958	2	1849.1833
						R.KAEPMQWASLELPTTK.K	0.9958	2	1831.137
						K.RPSPDEPMTNLELK.I	0.9958	2	1627.8529
						K.TSDFNTFLAQEGCTR.G	0.9958	2	1747.8249
						R.HNSEKPPEPVKPEVK.T	0.9958	2	1715.9469
802	CHSP1_MOUSE	148	44.59	3	33	K.GHGFITPADGGPDIFLHISDVEGEYVPVEGI	0.9944	3	3862.1975
						K.LQAVEVVITHLAPGTK.H	0.9958	2	1676.9969
						K.HETWSGHVISN.-	0.9924	1	1267.3433
803	CHST2_MOUSE	530	13.21	3	3	K.LYPGDAVSLQGAAR.D	0.9945	2	1418.5925
						K.WHKEPLQQCNPDGPLGAAVGAAGAGWGI	0.9944	3	3830.226
						K.EVVGLVDDRVCK.K	0.9944	1	1389.5579
804	CI085_MOUSE	155	7.1	2	2	K.YKPLSKPK.K	0.9944	1	961.1924
						K.YKPLSKPKK.C	0.9924	1	1089.3665
805	CI128_MOUSE	487	6.98	1	2	K.YESPVSEVQKEPLEVSPTASIPESSHELTSI	0.9944	3	3501.7797
806	CIC_MOUSE	2510	3.59	3	3	R.SSPPPPLPAEERPGTKGPETASK.F	0.9958	2	2331.5877
						R.EPAAPESELEGQPTPPAPPPPTETWPPTAI	0.9944	3	4791.2848
						K.IIQLTPVPVSTPSGLVPPLSPATMPGPTSQF	0.9958	3	3337.9428
807	CINP_MOUSE	212	9.43	1	2	K.GFTTASSIANLKVSLLSK.E	0.9958	2	1838.1546
808	CIP4_MOUSE	603	24.05	7	46	K.FSQQQSFVQLLQEVNDFAGQR.E	0.9958	2	2470.7037
						R.LGAGYGLLSEAELQVVPIIGK.C	0.9958	2	2128.5169
						R.DQAHFYFSQMPQIFDK.L	0.9958	2	2003.2391
						R.KQGAEGYVPTSYLR.V	0.9958	2	1569.7575

						R.VPSDSSLGTPDGRPELR.A	0.9958		2	1783.9359
						R.HARPPDPPTTAPPDSSSSSTNSGSQDNK.E	0.9958		3	2836.9023
						R.SGRDPLAILSEISK.S	0.9958		2	1486.7086
809	CIR1A_MOUSE	686	7.58	2	2	R.CIVWGVAFLSDGTVISVDSVGK.V	0.9958		2	2310.6184
						R.TDGTVEIYNLSANYFQEKFFPGHESR.G	0.9958		2	3051.2982
810	CISD1_MOUSE	108	50.93	6	265	K.HNEETGDNVGPLIIK.K	0.9958		1	1636.8021
						K.VVHAFDMEDLGDK.A	0.9958		2	1476.6441
						K.FPFCDGAHIK.H	0.9958	1,2		1192.3257
						K.AMVNLQIQK.D	0.9941		2	1045.2854
						K.KFPFCDGAHIK.H	0.9958		1	1320.4998
						K.HNEETGDNVGPLIIKK.K	0.9944		2	1764.9762
811	CISD2_MOUSE	135	12.59	1	12	K.HNELTGDNVGPLILK.K	0.9924		2	1620.8461
812	CISY_MOUSE	464	52.8	16	405	K.GLVYETSVLDPDEGIR.F	0.9958	1,2		1763.9421
						R.DYIWNTLNSGR.V	0.9908	1,2		1339.4502
						R.ALGFPLERPK.S	0.9958		2	1128.3598
						K.LRDYIWNTLNSGR.V	0.9958		2	1608.7971
						R.AALPSHVVTMLDNFPTNLHPMSQLSAAITA	0.9957		3	4168.7321
						K.GGEEPLPEGLFWLLVTGQMPTEEQVSWLS	0.9958		2	3387.8317
						R.LDWSHNFTNMLGYTDPQFTELMR.L	0.9958		2	2818.1506
						K.LPCVAAK.I	0.9958		1	758.9024
						K.IVPNILLEQGK.A	0.9958	1,2		1224.4863
						K.TVVGQITVDMMYGGMR.G	0.9958		2	1759.1067
						K.DVLSNLIPK.E	0.9958	1,2		999.1955
						R.ALGVLAQLIWSR.A	0.9958		2	1327.6127
						R.VVPGYGHAVLR.K	0.9958	1,2		1168.3842
						K.YWELIYEDCMDLIAK.L	0.9921		2	1963.2185
						K.AKGGEEPLPEGLFWLLVTGQMPTEEQVSV	0.9958		2	3587.0845
						R.GYSIPECQK.M	0.9958		1	1082.1645
813	CJ006_MOUSE	1278	1.17	1	6	R.YLVQMKPSDLLKK.M	0.9958		2	1563.9391
814	CJ018_MOUSE	2382	0.63	1	4	K.QGENIDKLMEYVK.N	0.9958		1	1567.7974
815	CJ058_MOUSE	218	8.26	1	6	K.EFGDRVNPLSVLEAVK.K	0.9958		2	1774.0269
816	CJ119_MOUSE	642	3.27	1	3	K.YRDVAECGPQQELDLSSPR.S	0.9944		2	2221.3545
817	CK054_MOUSE	315	14.6	2	13	K.YHDFGCALLANLFASEGQPGK.V	0.9958		2	2296.5103
						K.AHIMPAEFSSCPLNSDEAVNK.W	0.9958		2	2318.5293
818	CK059_MOUSE	161	27.95	3	6	R.LAVLSSSLTHWK.K	0.9958		2	1342.5809
						K.ALNGAEPNYHSLPSAR.T	0.9958		2	1697.8479
						R.TDEQALLSSILAK.T	0.9958		1	1389.5889

819	CK067_MOUSE	122	14.75	1	2	R.ETGTEHSPGVQPADVK.E	0.9958	2	1652.7581
820	CK5P2_MOUSE	1822	6.81	5	12	K.SASETPLLSGTDVDSLSCDSTSSATSPTSM	0.9958	3	4468.7942
						K.KMQEGDLEMTLALEEK.D	0.9958	2	1866.1519
						K.ENFNLK.L	0.9958	1	764.8565
						K.KVSDLIQLVK.D	0.9944	1	1143.4123
						K.TGLLIQLKTPELLENLYNLPASPEVVVAQLQ	0.9944	3	4330.0679
821	CK5P3_MOUSE	503	8.75	2	2	K.MLSLVSTLQQLIGRLTSLR.M	0.9958	2	2130.5975
						K.QQEALQEQAALEPKLDLLLEK.T	0.9958	2	2408.7545
822	CKAP4_MOUSE	575	13.91	5	10	K.VQSLQATFGTFESLLR.N	0.9958	2	1798.0489
						R.LAMLQEHVGNLGSSSDLASTVR.S	0.9958	2	2286.5652
						K.VGAHGSEEGAVFK.D	0.9958	1	1288.4026
						R.RLEEELQQLK.V	0.9958	1	1286.471
						R.HTESLESLLSK.S	0.9958	2	1244.3873
823	CKP2L_MOUSE	745	4.97	2	2	R.STEAVTSDTSAAGTNTTSAEELAK.E	0.9958	2	2343.4174
						R.QCPDIQELK.T	0.9958	1	1131.2372
824	CL004_MOUSE	552	7.25	2	2	R.ERQGIEMEK.V	0.9924	1	1120.2659
						R.HSNLSEIHVAFHLCVDDNVKSGNITAR.D	0.9958	3	3035.3122
825	CL005_MOUSE	269	31.97	4	42	R.ESVLPGAPGSGLESSLAEVFPVGK.H	0.9958	2	2328.6244
						K.IIQGQGVDAPLSETGFR.Q	0.9958	2	1788.9982
						R.QAAAAGQFLSNVQFTHAFSSDLTR.T	0.9958	2	2568.8082
						R.GKDFFDFICQLILGK.A	0.9958	2	1802.0894
826	CL030_MOUSE	972	7.3	3	3	K.VQSSYLHSLLETGELLR.K	0.9958	2	1946.2108
						R.LRPIYDYLDNGNNK.M	0.9929	2	1695.8723
						R.EAGEETAVWQALTLLEEGLTHSPSNAQFKI	0.9931	3	3753.2469
827	CL035_MOUSE	1521	2.24	2	2	K.IHHSEASRTHSVSNNNK.G	0.9911	3	1919.0237
						R.EESHDLGMLDPEK.D	0.9958	2	1500.6203
828	CL055_MOUSE	816	2.57	1	6	R.SNGKLDFPQTSLLEHVVEK.R	0.9958	2	2142.4167
829	CL16A_MOUSE	1036	2.99	2	2	R.IAVRTITLNVYK.V	0.9958	1	1391.697
						K.RPNYKNVGEEEDEER.G	0.9924	2	1864.9231
830	CLAP1_MOUSE	1535	1.24	1	9	R.VLSTSTDLEAAVADALK.K	0.9958	1	1704.9152
831	CLAP2_MOUSE	1286	2.49	2	5	K.MQTKVIER.V	0.9958	1	1005.2206
						R.NHFPGEAETLYNSLEPSYQK.S	0.9958	2	2325.4961
832	CLH_MOUSE	1675	33.13	30	203	R.TSIDAYDNFDNISLAQR.L	0.9958	2	1944.0648
						K.SVNESLNNLFITEEDYQALR.T	0.9958	2	2356.5511
						R.KFNALFAQGNYSEAAK.V	0.9958	2	1759.9591
						K.LLYNNVSNFGR.L	0.9958	1,2	1297.4563
						R.LASTLVHLGEYQAAVDGAR.K	0.9952	2	1972.2083

						R.FQEHLQLQNLGINPANIGFSTLTMESDK.F	0.9958		2	3147.5298
						R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.	0.9958		2	3189.6384
						R.ISGETIFVTAPHEATAGIIGVNR.K	0.9958		2	2354.6683
						K.VSQPIEGHAASFAQFK.M	0.9932		2	1717.9218
						K.NNRPSEGPLQTR.L	0.9944		2	1369.4801
						R.LAELEEFINGPNNAHIQQVGDR.C	0.9958		2	2465.6848
						K.YESLELCRPVLQQGR.K	0.9943		2	1849.063
						R.RPLIDQVVQTALSETQDPEEVSVTVK.A	0.9958	2,3		2883.2255
						R.RPISADSAIMNPASK.V	0.9944		2	1558.793
						K.ADDPSSYMEVVQAANASGNWEELVK.Y	0.9958		2	2711.9166
						K.FNALFAQGNYSEAAK.V	0.9958		2	1631.785
						K.LHIIEVGTPPTGNQPFPK.K	0.9945		2	1946.2566
						R.LLEMNLMHAPQVADAILGNQMFTHYDR.A	0.9944		3	3130.6247
						K.WLLLTGISAQQNR.V	0.9958		2	1500.7409
						R.NLQNLLILTAIK.A	0.9958		2	1354.6762
						R.HSSLAGCQIINYR.T	0.9958		2	1519.6665
						R.GQCDLELINVCNENSLFK.S	0.9958		2	2154.3137
						R.KFDVNTSAVQVLIEHIGNLDR.A	0.9958	2,3		2369.6829
						R.AYEFAERCNEPAVWSQLAK.A	0.9958		3	2270.4724
						K.YHEQLSTQSLIELFESFK.S	0.9958		2	2200.4528
						K.DPELWGSVLLESNPYR.R	0.9958		2	1876.0758
						R.IHEGCEEPATHNALAK.I	0.9958		2	1777.8975
						R.GYFEELITMLEAALGLER.A	0.9958		2	2056.3814
						R.AHIAQLCEK.A	0.9958		1	1070.1999
						R.KVSQPIEGHAASFAQFK.M	0.9958		2	1846.0959
833	CLIC1_MOUSE	241	36.51	5	13	R.KFLDGNELTLADCNLLPK.L	0.9958		2	2062.3368
						K.LAALNPESNTSGLDIFAK.F	0.9958		2	1862.0899
						K.FLDGNELTLADCNLLPK.L	0.9958		2	1934.1627
						K.LCPGGQLPFLLYGTEVHTDTNK.I	0.9958		2	2461.743
						R.EEFASTCPDDEEIELAYEQVAR.A	0.9958		2	2602.6906
834	CLIC4_MOUSE	253	46.64	7	42	K.LDEYLNSPLPDEIDENSMEDIK.F	0.9958		2	2580.7768
						K.HPESNTAGMDIFAK.F	0.9915		2	1518.6843
						K.NSRPEANEALER.G	0.9958		2	1386.4642
						K.TDVNKIEEFLEEVLCPPK.Y	0.9958		2	2161.423
						R.FLDGDEMTLADCNLLPK.L	0.9958		2	1953.1806
						R.RFLDGDEMTLADCNLLPK.L	0.9958		2	2109.3681
						R.KPADLQNLAPGTHPPFITFNSEVK.T	0.9958		2	2622.9835

835	CLIP1_MOUSE	1391	21.42	15	49	K.ATSHVGEIEQELALAR.D	0.9958	2	1724.9114
						K.TKHEEILQNLQK.M	0.9958	2	1481.6921
						R.VWVNGNKPGFIQFLGETQFAPGQWAGIVL	0.9958	3	3815.366
						K.ELVLTGLQDSLNQVNQVK.E	0.9958	2	1999.2719
						K.SLHSVVQTLESDK.V	0.9958	1,2	1443.5969
						K.SKLETAIASHQQAMEELK.V	0.9958	2	2015.2891
						K.ASGPPSSETQEEFVDDFR.V	0.9958	2	1999.0545
						K.AAQTAEDAMQIMEQMTK.E	0.9958	2	1898.1715
						K.YTEQSEVIGNFTSQLSAVK.E	0.9958	2	2102.3055
						K.ALHTATEK.L	0.9958	1	870.9811
						R.RLESSKPPGDVDMSLSLLQEISALQEK.L	0.9958	3	2972.3808
						R.TASPLSTAAATMVSSSPATPSNIPHKPSQS	0.9958	3	3225.5982
						K.YGLFAPVHK.V	0.9929	2	1032.2303
						R.DGHDQHVLELEAK.M	0.9958	2	1491.6005
						K.LEAIHTDHQGEMTSLK.E	0.9958	2	1811.0197
836	CLIP2_MOUSE	1047	4.58	2	2	R.GGKHSSPVGRPSVGSASSSVVASTSGSK.	0.9958	3	2558.7678
						K.LQEVQEELAGLQQHWR.E	0.9958	2	1965.1759
837	CLPB_MOUSE	677	14.48	6	19	K.TANEQGVHSLEVLVTR.E	0.9958	2	1753.9529
						K.FIGSPPGYIGHEEGGQLTK.K	0.9958	2	1988.2071
						K.LKQCPNAVVLFDEVDK.A	0.9958	1	1876.126
						R.KLDIQAPLHPEK.V	0.9932	2	1389.6377
						R.HNITLLWDR.E	0.9958	2	1168.3408
						K.AHPDVLTIMLQLFDEGR.L	0.9957	2	1956.2671
838	CLPP_MOUSE	272	12.13	2	12	K.VLVHPPQDGEDEPELVQK.E	0.9958	2	2030.242
						R.IMIHQPSGGAR.G	0.9958	2	1167.3715
839	CLPX_MOUSE	634	2.37	1	4	R.LPVVVPLHSLDEK.T	0.9952	2	1446.73
840	CLUS_MOUSE	448	14.96	4	16	K.LFDSDPITVVLPEEVSK.D	0.9958	2	1889.1529
						R.VSTVTTHSSDSEVPSR.V	0.9958	2	1689.7765
						K.EIQNAVQGVK.H	0.9944	1	1086.2333
						R.ELHDPHYFSPIGFPHK.R	0.9941	2	1922.1527
841	CLYBL_MOUSE	338	47.34	10	149	K.TLEDFDLGTTEK.C	0.9958	2	1369.4681
						R.INSVSSGLAEVDLETFLQAR.V	0.9958	2	2150.3935
						R.KLEQPMNLIPFVETAMGLLNFK.A	0.9958	2	2535.0779
						K.QAQNIVTLATSIK.E	0.9958	2	1387.6194
						K.LEQPMNLIPFVETAMGLLNFK.A	0.9958	2	2406.9038
						K.IQWAEELIAAFK.E	0.9909	2	1419.6635
						K.QVIHPNQIAVVQEQFTPTPEK.I	0.9958	2	2404.7282

						K.DTQDILYAR.Q	0.9924		1	1095.1973
						K.TGPQVGLCLDAVVFGGEDFR.A	0.9931		2	2138.3508
						K.AFGLQAIDLVYIDFR.D	0.9958		2	1742.0275
842	CMBL_MOUSE	245	41.63	5	40	R.NGYTTIVPDFFVGQEPWDPAGDWSTFPAV	0.9958		2	3543.9159
						K.NPTLFIFAENDTVIPLEQVSTLTQK.L	0.9958	2,3		2820.2121
						K.TFSGQTHGFVHR.K	0.9958		2	1374.5015
						K.LEYGGMGHEVQVEHIK.A	0.9958		2	1827.0649
						R.NLIEWLNK.Y	0.9944		1	1030.212
843	CMC1_MOUSE	677	30.13	12	49	R.IADLPPANPDHIGGYR.L	0.9958		2	1706.8986
						K.FGLYLPK.F	0.9958		1	838.0373
						R.YLGLYNDPNSNPK.I	0.9945		2	1495.6317
						K.SPSVAVAQPK.A	0.9958		1	984.1405
						R.VSALNVLQDLGLFGLYK.G	0.9917		2	1851.1961
						R.VGGINLLTAGALAGVPAASLVTPADVIK.T	0.9958		2	2590.0788
						K.HLNYVEFTQFLQELQLEHAR.Q	0.9958		2	2516.8186
						R.YGQVTPLEIDILYQLADLYNASGR.L	0.9931		2	2714.0471
						K.FKSPSVAVAQPK.A	0.9958		2	1259.4911
						R.NIFLQYASTEVDGEHYMTPEDFVQR.Y	0.9904		2	2991.2581
						R.WFYIDFGGLKPSGSEPTPK.S	0.9958		2	2127.4039
						R.GDPHELRNIFLQYASTEVDGEHYMTPEDF\	0.9944		3	3796.1187
844	CMC2_MOUSE	676	45.86	16	73	R.WFYVDFGGVKPVGSEPVPK.S	0.9944		2	2109.432
						R.ITLPAPNPDHVGGYK.L	0.9944		2	1579.796
						R.FGLGSIAGAVGATAVYPIDLVK.T	0.9958		2	2120.4967
						R.IAPLEEGMLPFNLAEAQR.Q	0.9958		2	2000.3203
						K.ASGDAARPFLLQLAESAYR.F	0.9958		2	2037.2828
						R.SSPQFGVTLLTYELLQR.W	0.9958		2	1953.2456
						K.ASFANEDGQVSPGSLLLAGAIAGMPAASL\	0.9958	2,3		3541.054
						K.LAVATFAGIENKFGLYLPLFKPSASTSK.V	0.9911		3	2972.4973
						K.ASFANEDGQVSPGSLLLAGAIAGMPAASL\	0.9944		3	3798.3465
						K.FGLYLPLFKPSASTSK.V	0.9958		2	1757.0825
						R.GLLPQLLGVAPEK.A	0.9958		1	1335.6298
						K.FGQVTPMEVDILFQLADLYEPR.G	0.9958		2	2582.974
						R.DIMVTIRPHVLTPFVEECLVAAAGGTR.S	0.9958		3	2954.4236
						K.YASIEKNGEFFMSPHDFVTR.Y	0.9958		2	2376.6483
						R.SHQVSFSYFNGFNSLLNNMELIR.K	0.9958	2,3		2719.0466
						R.KIYSTLAGNR.K	0.9944		2	1123.2975
845	CN045_MOUSE	533	4.88	2	2	K.EIGMIQTELKTIK.Q	0.9925		2	1504.8255

						K.HRLEQEAEK.R	0.9944	1	1140.2413
846	CN124_MOUSE	308	17.21	3	19	R.VLVGGGTGFIGTAVTQLLR.G	0.9958	2	1860.2071
						R.GGGAISHMLLPFR.L	0.9958	2	1356.6287
						R.RTLATGYQYSFPELR.A	0.993	2	1803.0275
847	CN145_MOUSE	1102	3.99	2	2	K.KLNDIESHQAELELEVK.N	0.9958	2	1996.2249
						R.LHLKDQLLCLETEQESILGVIGK.E	0.9933	3	2638.0429
848	CN159_MOUSE	617	40.19	14	41	K.HLVDPIDDIFLAAQK.I	0.9958	2	1695.9561
						R.GPLPLLGQSEAVK.T	0.9958	2	1309.5486
						K.DPLHYSIVSAPAAQK.V	0.9958	1	1597.8113
						R.SLAPAFESFCQGNR.G	0.9958	2	1584.6947
						K.APLAFASPPGCMVMVPK.D	0.9958	2	1774.1556
						K.IPGISSTGVGDGGNELGMGK.V	0.9958	2	1847.0503
						R.AGEQSWIQALPSVAK.E	0.9958	2	1585.8003
						K.TPIPILTYQGR.S	0.9958	2	1259.4911
						R.SGVSGIVGMEVDGLPFHDVHAEMIR.K	0.9952	2	2654.0308
						R.RDLTGPSHAGAYK.T	0.9958	2	1373.5113
						K.DELLQAALSLSHAR.S	0.9958	2	1524.7171
						R.DLTGPSHAGAYK.T	0.9926	2	1217.3238
						K.DTASSASCLTPEMVPEVHAISKDPLHYSIVS	0.9958	3	3910.3541
						R.SVLVTTGFPTHFNHEPPEETDGPPGAIALA	0.9958	3	3932.4247
849	CN166_MOUSE	244	15.98	2	2	K.LTALDYHNPSGFNCK.D	0.9958	2	1737.8755
						K.HILGFDTGDAVLNEAAQILR.L	0.9958	2	2154.4307
850	CNBP_MOUSE	178	25.84	3	7	R.GFQFVSSSLPDICYR.C	0.9958	2	1776.9525
						K.CYSCGEFGHIQK.D	0.9958	2	1486.5562
						R.CGETGHVAINCSK.T	0.9958	2	1433.4932
851	CNDP2_MOUSE	475	32.63	9	86	R.LVPDMIPEVVSEQVSSYLSK.K	0.9958	2	2221.5708
						R.YPSLSLHGIEGAFSGSGAK.T	0.9958	2	1879.0795
						K.LPDGSEIPLPPILLGK.L	0.9958	2	1660.0068
						K.GPVAGWMNALEAYQK.T	0.993	2	1635.878
						K.KFAELQSPNK.F	0.9958	2	1162.3311
						K.KLAEWVAIQSVSAWPEK.R	0.9958	2	1943.2529
						K.NVMLLPVGSADDGAHSQNEK.L	0.9958	2	2083.2805
						K.QKLPDGSEIPLPPILLGK.L	0.9958	2	1916.3116
						R.FCLEGMEESGSEGLDELIFAQK.D	0.9958	2	2490.7072
852	CNKR3_MOUSE	555	1.44	1	3	K.VLNVVK.V	0.9924	1	671.8583
853	CNN2_MOUSE	305	5.9	1	2	R.SMQNWHQLENLSNFIK.A	0.9958	2	1990.2439
854	CNN3_MOUSE	330	13.33	2	3	K.KVNESSLNWPQLENIGNFIK.A	0.9958	2	2331.6335

						K.MQTDKPFDQTTISLQMGTNK.G	0.9958		2	2285.5923
855	CNOT8_MOUSE	292	15.75	2	10	K.NLKGGLQEVADQLDLQR.I	0.9958		2	1898.1264
						K.FNLTEDMYSQDSIDLLANSGLQFQK.H	0.9958		2	2879.1677
856	CNPY2_MOUSE	182	42.86	4	9	K.TIQMGSFRINPDGSQSVVEVPYAR.S	0.9944		3	2652.9849
						K.EYGEQIDPSTHRK.N	0.9958		1	1560.6634
						R.SEAHLTELLEEVCDR.M	0.9958		2	1801.9141
						K.FACESIVEEYEDELIEFFSR.E	0.9958		2	2513.6827
857	CNTN6_MOUSE	1028	5.06	2	2	R.LDGGSLAISSPR.T	0.9924		1	1173.3115
						R.EGQGVVLLCGPPPHFGELSYAWTFNDSPL	0.9958		3	4108.5219
858	CNTP1_MOUSE	1385	4.62	3	4	R.LNLENEIFIGGLVGAARK.N	0.9949		2	1915.2431
						R.GCIENVIYNRINIAEMAVMR.H	0.9944		2	2367.7529
						R.NSWNTISFHTGAALRFPPIR.A	0.9958		3	2286.601
859	CO024_MOUSE	241	18.67	2	4	R.AVVPGVKPQDWISAAR.V	0.9958		2	1694.9743
						K.TDGSFVVHDIPSGSYVVEVISPAYK.F	0.9958		2	2667.9751
860	CO039_MOUSE	1023	4.2	2	2	K.AEAATGEGSRNPSPSSGASTSPPGPTLR.A	0.9944		3	2640.7831
						R.EEVALDLSVKK.T	0.9924		1	1231.4319
861	CO1A1_MOUSE	1453	2.75	2	2	K.GSPGEAGRPGEAGLPGAK.G	0.9944		2	1608.7513
						R.GETGPAGPAGPIGPAGAR.G	0.9958		2	1533.6841
862	CO2_MOUSE	760	5.92	2	2	K.DHENATGANTYEVLIRVYSMMQTQMDR.L	0.9958		3	3175.5331
						K.ALQQIFEHMLDVSK.L	0.9944		2	1659.9409
863	CO2A1_MOUSE	1487	9.89	4	4	K.KHIWFGETMNGGFHFSYGDGNLAPNTAN\	0.9958		3	3960.4358
						R.GEPGNPGSPGPAGASGNPGTDGIPGAKG:	0.9958		3	3836.1289
						R.GEQGAPGPSGFQGLPGPPGPPGEGGKQ(	0.9958		3	4088.4423
						R.GDVGEKGPEGAPGK.D	0.9944		1	1298.3953
864	CO3_MOUSE	1663	46	44	434	R.IILQGSPVVQMAEDAVDGER.L	0.9958		2	2128.4052
						K.QKPDGVFQEDGPVIHQEMIGGFR.N	0.9958		3	2585.8969
						R.SGIPIVTSPYQIHFTK.T	0.9958		2	1789.0843
						R.MELKPGDNLNVNFHLR.T	0.9924		2	1898.1901
						K.VHQYFNVGLIQPGSVK.V	0.9958		2	1787.0715
						R.EPGQDLVVLSLPITPEFIPSFR.L	0.9958		2	2455.8565
						K.AAVFNHFISDGVK.K	0.9958	1,2		1405.5962
						K.VFSLAANLIAIDSHVLCGAVK.W	0.9958		2	2199.5646
						K.VLMEGVRPSNADALVGK.S	0.9958		2	1757.0581
						R.DNHLAPGQQTTLR.I	0.9952		2	1451.5821
						R.DILSSNNQHGILPLSWNIPELVNMGQWK.I	0.9944		2	3205.6587
						K.TVLTGASGHLR.S	0.9958		2	1112.2742
						R.KVLMEGVRPSNADALVGK.S	0.9958		2	1885.2322

						R.SHFPQSWLWTIEELKEPEK.N	0.9958	2	2385.6812
						K.HLIVTPAGCGEQNMIGMTPTVIAVHYLDQTI	0.9958	3	3969.4855
						R.VELLHNPAFCSMATAK.N	0.9958	2	1790.0534
						K.VYSYYNLEESCTR.F	0.9958	2	1684.7657
						R.VEPTETFYYIDDPNGLEVSIIAK.F	0.9958	2	2614.9086
						K.VDVPAADLSDQVPDTDSETR.I	0.9958	2	2131.2145
						R.VVIEDGVGDAVLTR.K	0.9958	2	1443.6402
						K.TVAIHTLDPEK.L	0.9958	1	1224.3995
						R.VSIRPAPETAK.K	0.9958	2	1169.3665
						R.SELEEDIIPEEDIISR.S	0.9958	2	1888.0356
						K.TIYTPGSTVLYR.I	0.9958	1	1371.5761
						K.DLNMDVSFHLPSR.S	0.9944	2	1531.7265
						R.DHVLGLAR.S	0.9958	1	881.0225
						R.IFTVDNNLLPVGK.T	0.9958	2	1430.6873
						R.WEEPDQQLYNVEATSYALLALLLLK.D	0.9958	2	2922.3477
						K.EADVSLTAFVLIALQEAR.D	0.9958	2	1947.2389
						K.NYAGVFMDAGLAFK.T	0.9958	2	1504.7436
						R.FYHPEKDDGMLSK.L	0.9958	2	1567.7565
						K.FFKPAMPFDLMVFVTNPDGSPASK.V	0.9958	2	2645.1061
						K.TELTNIKLLDDFDEYTMTIQQVIK.S	0.9958	2	2873.288
						R.QPLTITVR.T	0.9944	1	928.1197
						K.VLVVTQGSNAK.A	0.9958	1	1116.303
						R.LESEETIVLEAHDAQGDIPVTVTVQDFLK.R	0.9958	3	3198.5512
						K.TVVILIETPDGIPVK.R	0.9958	2	1594.9323
						K.TVVILIETPDGIPVKR.D	0.9958	2	1751.1197
						R.VMQDFFIDLR.L	0.9958	2	1284.5157
						K.DTWVEHWPEAEECQDQK.Y	0.9958	2	2188.2373
						R.LLWENGNLLR.S	0.9924	1	1228.4367
						K.AFIDCCNHITK.L	0.9958	2	1379.4877
						K.RQEALELIK.K	0.9958	2	1100.3036
						K.TMEAHPYSTMHNSNNYLHLSVSR.M	0.9958	2	2690.9679
865	CO4A2_MOUSE	1707	1.82	2	2	K.GAPGVAGAPGPK.G	0.9958	1	979.124
						K.AHNQDLGLAGSCLAR.F	0.9958	2	1583.7105
866	CO4A3_MOUSE	1669	3.3	2	2	K.GNPGSPGSAGLPGFAGFPGDQGHPGLK.G	0.9958	3	2477.6982
						R.GNPGLPGPKGLEGLPGLPGPPGPR.G	0.9958	3	2232.5907
867	CO4A4_MOUSE	1682	4.58	3	8	R.GDSGSPGPPGEK.G	0.9944	1	1085.1155
						K.GPLGSPGLNGLHGLK.G	0.9958	1	1417.6511

						R.LDCAPGKPGKPGLPGLPGAPGPEGPPGSI	0.9931		3	4396.9034
868	CO4B_MOUSE	1738	8.86	6	17	R.TLEIPGSSDPNIVPDGDFSSLVR.V	0.9958		2	2416.647
						R.GHIFVQTDQPIYNPGQR.V	0.9958		2	1971.1826
						R.EELVYNLDPLNNLGR.T	0.9958		2	1759.9567
						R.VTASEPLETMGSEGALSPGGVASLLR.L	0.9958		2	2530.853
						K.ILSLAQEQVGNSPEKLQETASWLLAQQLGI	0.9958		3	4672.1773
						R.YVSHFETDGPHVLLYFDSVPTTR.E	0.9958		2	2681.9641
869	CO5A1_MOUSE	1838	8.87	5	5	R.GETGFQGKTGPPGPPGVVGPQGPTGETG	0.9958		3	3135.4351
						R.GPAGPMGLTGRPGPMGPPGSGGLKGEPC	0.9958		3	3326.7908
						R.GDDGEVGPRGLPGEPGPR.G	0.9924		1	1762.8766
						R.GLPGPVGALGLKGSEGPPGPPGPAGSPGI	0.9958		3	2663.9933
						K.GNVGPQGEPGPPGQQGNPGAQGLPGPQ	0.9924		3	3300.5717
870	CO6A1_MOUSE	1025	15.41	8	43	K.GEKGEAGADGEAGRPGNSGSPGDEGDPC	0.9931		3	3320.3373
						R.VLLFSDGNSQGATAEAIEK.A	0.9958		2	1951.1406
						K.VFSVAITPDHLEPR.L	0.9958		2	1581.8119
						R.DAEEVISQTIDTIVDMIK.N	0.9958		2	2021.2874
						R.NLVWNAGALHYSDEVEIIR.G	0.9958		2	2200.4588
						K.KGLEELLIGGSHLK.E	0.9912	1,2		1494.7746
						K.AIAFQDCPVDLFFVLDTSESVALR.L	0.9958		2	2715.0412
						K.GLEELLIGGSHLK.E	0.9958		2	1366.6005
871	CO6A2_MOUSE	1034	13.73	7	94	R.YGGLHFSDQVEVFSPPGSDR.A	0.9958		2	2195.3525
						R.ATYLNSFSHVGTGIVHAINNVVR.G	0.9958		2	2470.7935
						R.VGVVQYSHEGTFEAIR.L	0.9958		2	1792.989
						K.NLEWIAGGTWTPSALK.F	0.9958		2	1744.9878
						K.GVVNFAVVITDGHVTGSPCGGIK.M	0.9958		2	2285.5713
						K.GDPGSRGPDGYPGEAGSPGER.G	0.9947		2	2016.0477
						K.HEAYGECYK.V	0.9958		1	1157.1908
872	CO7A1_MOUSE	2944	5.64	7	8	R.GSPGVPGSPGLPGPVGPK.G	0.9929		2	1557.7899
						R.GFPGPEGPPGSPGLPGVPGSPGIK.G	0.9958		3	2156.446
						K.LFAVGIKNADPEELK.R	0.993		2	1644.9084
						K.KGDMGEPGLPGQSGAPGK.E	0.9958		1	1683.8767
						K.GEKGAPGDLAGALLGEPGAK.G	0.9945		2	1809.0293
						K.GSTGRPGPRGEQGER.G	0.9924		1	1541.6236
						R.GLPGPVGAVGLPGPPGPSGLVGPQGSPG	0.9944		3	3905.4489
873	CO8A_MOUSE	587	6.13	2	6	K.SHSAGVTVGVAPVK.S	0.9958		2	1309.5082
						K.YNPVVIDFEMQPIYQLLR.H	0.9958		2	2239.6373
874	CO8B_MOUSE	589	6.62	2	20	R.LASGINLFTNTFEGPVLDHR.Y	0.9958		2	2202.4747

						R.YYAGGCSPHYILDTNFR.K	0.9958		2	2035.1889
875	CO8G_MOUSE	202	11.39	1	2	R.AEATTLHAAPQGAAMAVSTFR.K	0.9958		2	2102.3727
876	CO9_MOUSE	548	11.31	4	12	R.DNIIDDVISFIR.G	0.9958		2	1420.6054
						R.KPWNVVSLIYETK.A	0.9958		2	1577.8638
						K.TDFANWASSLANAPALISQR.M	0.9958		2	2134.3561
						R.MSPIYNLIPLK.I	0.9926		2	1289.619
877	CO9A1_MOUSE	921	19.22	5	5	R.GIQGSRGIPGSPGPK.G	0.9958		2	1408.6004
						R.GFPGRGIPGPPGPPGTTGLPGELGR.V	0.9958		2	2342.6627
						R.GPPGPPGPPGPSGTIGFHDGDPLCPNSCF	0.9958		3	4166.5489
						R.GPKGPPGPPGPPGDPGKPGAPGKPGTPG	0.9958		3	3948.3439
						K.RPDTGASGLPGRPGPPGPPGPPGENGFP	0.9958		3	3845.3739
878	COAA1_MOUSE	680	13.53	3	3	R.LSGMPLVSANHGVTGMPVSAFTVILSKAYF	0.9944		3	4703.5147
						R.GPAGHPGEPGLPGSPGNMGPQGPK.G	0.9924		3	2194.4295
						R.GFPGEKGAQGAPGVNGR.K	0.9924		1	1599.7464
879	COASY_MOUSE	563	13.5	3	6	R.HLDVRILLTNIQTK.S	0.9924		1	1664.9889
						R.AYAPGGPAYQPVVEAFGTDILHK.D	0.9958		2	2402.7117
						R.LQSQMSGQQLVEQSNVVLSTLWESHVTQ	0.9958		3	3730.1413
880	COBA1_MOUSE	1804	3.82	2	3	R.GIPGPVGEQGLPGAAGQDGPPGPLGPPGI	0.9958		3	2956.3714
						R.RHTESIQGDAGDNILDYSDGMEEIFGSLNS	0.9958		3	3513.7712
881	COBL1_MOUSE	1273	6.36	4	6	R.SNTISKPYISNTLPSDAPK.K	0.9958		2	2034.2737
						K.THTVNKPTVGSQHGDGDK.Q	0.9958		2	1878.9963
						R.VTTDTGTIPFAPNLEDINNILESK.F	0.9904		2	2603.8859
						R.ASGHYVTSAAAK.S	0.9958		1	1163.2755
882	COCA1_MOUSE	3120	2.6	3	3	K.IVDDLTINLCNSVK.G	0.9944		2	1604.8071
						K.SLYDDIEAGETTLPGDAIHTMIENLQPETKY	0.9958		3	3594.9692
						K.ISVFATYSSGEGEPVTGDATTELSQDSKILF	0.9958		3	3260.5359
883	CODA1_MOUSE	751	6.79	2	2	K.LLPLLNSVRLAPPPVIK.R	0.9954		2	1841.3341
						R.GFPGFPGPIGLDGRPGHPGPKGEMGLVGI	0.9958		3	2955.4099
884	COEA1_MOUSE	1797	4.9	4	4	K.ETLLDAIR.H	0.9958		1	931.077
						R.WDAVPGATGYLILYAPLTEGLAGDEKEMK.	0.9958		3	3110.5489
						R.ILPDTPQEPFALWEILNKNSEPLVGIILDNG	0.9958		3	3633.1791
						K.MMEMFGLVEK.D	0.9958		1	1215.5264
885	COF2_MOUSE	166	63.25	9	358	K.QILVGDIGDTVEDPYTSFVK.L	0.9958		2	2197.4467
						R.YALYDATYETK.E	0.9958	1,2		1338.4565
						K.MIYASSK.D	0.9926		1	799.9605
						K.KEDLVFIFWAPESAPLK.S	0.9958		1	1991.3373
						K.HEWQVNGLDDIK.D	0.9958		2	1454.5822

						K.LGGSVVVSLEGKPL.-	0.9958		2	1355.6176
						K.HEWQVNGLDDIKDR.S	0.9937		2	1725.8583
						K.EDLVFIFWAPESAPLK.S	0.9958		2	1863.1632
						R.KSSTQEEIK.K	0.9924		1	1050.154
886	COFA1_MOUSE	1367	7.32	5	11	R.AFLSSHLQDLSTVVR.K	0.9958		2	1673.9096
						K.GEFGLPGRPGRPGLNGLK.G	0.9958		2	1823.108
						K.GQVLFNNWDSIFSGDGGQFNTHIPIYSFDG	0.9958		3	3490.7722
						R.VILYYTEPGSHVSR.E	0.9958		2	1621.8333
						K.VVWHGSNPHGVR.L	0.9958		2	1345.5063
887	COG1_MOUSE	980	4.08	2	24	K.FYSMAAQIKLLLEIPEK.I	0.9944		2	1995.4278
						K.VKLDDLLAYLPSSDTPLLK.D	0.9958		2	2102.476
888	COG4_MOUSE	785	2.68	1	4	R.ALSSSNIDCLCAMINLATR.E	0.9958		2	2111.3504
889	COGA1_MOUSE	1580	3.16	2	2	K.GEKGDQGIPGVPGFDNCAR.C	0.9958		1	1975.0911
						K.GDIGVGIAGENGLPGPPGPQGPPGYGK.M	0.9931		2	2459.7209
890	COHA1_MOUSE	1470	6.26	4	4	R.GPPGPAGDPGKPGLTGPQGPQGLPGSPG	0.9944		3	2988.3329
						R.GLTGEPGIRGLPGAVGEPGAK.G	0.9958		2	1934.2028
						R.WTELDEVKR.L	0.9958		1	1176.3146
						R.GPPGVSAALSTYAAENSDNFR.S	0.9958		2	2125.2591
891	COIA1_MOUSE	1774	6.65	4	5	K.GEPGAQGPPGPAGPQGPAGPVVQSPNSQ	0.9958		3	4056.4435
						R.EVPEGWLIFVAEREELYVR.V	0.9958		3	2335.6647
						R.DGEPGDPGEDGRPGDTGPQGFPGTPGD\	0.9944		3	2964.0447
						R.AFLSSRLQDLYSIVR.R	0.9931		2	1769.0537
892	COJA1_MOUSE	1136	1.5	1	19	K.EEAGLPGTLRSIGHK.G	0.9937		2	1565.7697
893	COMD3_MOUSE	195	20.51	2	3	R.GIQTLADPGSFDSNAFALLLR.A	0.9958		2	2207.4912
						K.HCHAAAATCILEAGK.H	0.9944		2	1610.7424
894	COMD5_MOUSE	224	8.48	1	4	R.LAVLLAGTHTLLQQALR.L	0.9958		2	1819.2009
895	COMD8_MOUSE	183	24.59	2	2	K.VKPYTVEMSKEELQSLISSLEAANK.V	0.9958		3	2796.2055
						K.IATLQMPLLNLHLDVK.E	0.993		2	1820.2439
896	COMP_MOUSE	755	6.62	2	18	R.LVPNPGQEDNDRDGVGDACQGDFDADK.\	0.9958		3	2905.9281
						K.DTDLDGRGDACDDDIDGDR.I	0.9927		2	2096.9929
897	COMT_MOUSE	265	38.87	6	34	R.LLTMEINPDYAAITQQMLDFAGLQDK.V	0.9958	2,3		2941.384
						K.GTVLLADNVIVPGTPDFLAYVR.G	0.9958		2	2331.7172
						K.AVYQGPGSSPVK.S	0.9958		1	1190.3415
						R.GSSSFECTHYSSYLEYMK.V	0.9958		2	2177.3126
						R.KGTVLLADNVIVPGTPDFLAYVR.G	0.9958		2	2459.8913
						K.KYDVDTLDMVFLDHWK.D	0.9958		2	2026.3142
898	COOA1_MOUSE	1733	5.42	5	5	K.TLTYLSSLLSSIK.N	0.9944		2	1426.6934

						K.GWNGQIFEENTLLEPQVLSDDCK.I	0.9944		3	2693.8927
						K.GDPGLSPGQAASGEKGDPGLLGLVGPPGI	0.9944		3	2999.3507
						R.ENPAR.I	0.9958		1	586.6255
						K.RFTEQDSLPK.G	0.9924		1	1221.3555
899	COPA1_MOUSE	666	7.81	3	3	K.GTPSFHPLSDTVDELK.A	0.9958		2	1743.9109
						K.GGLGLPGLPGANGVK.G	0.9944		1	1307.5357
						K.GSIGAPGTPGMDGQK.G	0.9944		1	1373.5237
900	COPB_MOUSE	953	2.2	1	7	K.LVEKPSPLTLAPHDFANIK.A	0.9931		2	2091.4582
901	COPB2_MOUSE	905	5.97	3	8	K.VWQLGSSSPNFTLEGHEK.G	0.9943		2	2017.2053
						K.AAESLADPTEYENLFPGLK.E	0.9958		2	2066.272
						R.FELALQLGELK.I	0.9958		1	1261.504
902	COPD_MOUSE	511	18.4	5	8	K.NSNILEDLETLR.L	0.9931		2	1417.559
						K.VHAPPINMESVHMKIEEK.I	0.9932		2	2090.4633
						K.GVQLQTHPNVDK.K	0.9944		2	1336.4905
						K.APGFGGFGSSAVSGGSTAAMITETIIETDKF	0.9958		3	3086.4407
						K.KLFTAESLIGLK.N	0.9956		2	1320.6152
903	COPE_MOUSE	308	35.71	4	4	K.NAFYIGSYQQCINEAQR.V	0.9958		2	2063.1999
						K.CSPTLLLLNGQAACHSAQGRWETAEGVLQ	0.9958		3	3726.0699
						K.MQDQDEDATLTQLATAWVNLAVGGEK.L	0.9958		3	2806.0735
						K.DSGHPETLINLIVLSQHLGKPPEVTNR.Y	0.9944		2	2966.3671
904	COPG2_MOUSE	871	8.27	2	2	K.RWINEAQEAASSDNIMVQYHALGVLYHLR.	0.9944		3	3386.8125
						R.QMALNATYIFNGLTVSIPGMEKALHQYTLEI	0.9958		3	4416.1245
905	COPZ1_MOUSE	177	18.08	2	4	R.GEDVPLTEQTVSQVLQSAK.E	0.9958		2	2030.2395
						K.AFEKNIFNK.T	0.9958		1	1111.2859
906	COQ3_MOUSE	370	25.68	7	57	R.AQEHQEPAESALK.G	0.9937		2	1438.537
						K.GETGALHANTSGSPSVR.E	0.9958		2	1641.7379
						K.FAPLHSMNDLR.V	0.9944		2	1301.5059
						K.NFQALAHTWWDEYGK.F	0.9958		2	1867.03
						K.ILDVGCGGGLLTEPLGR.L	0.9944		1	1727.9647
						R.AQEHQEPAESALKGETGALHANTSGSPSV	0.9958		3	3061.2517
						R.LGASVVGIDPVAENIK.I	0.9958		1	1582.8375
907	COQ4_MOUSE	266	13.16	2	3	R.LLYPDHIPTTPLQK.M	0.9944		1	1636.9316
						R.HDMVAVLGETTGCHTLK.F	0.9945		2	1870.0968
908	COQ5_MOUSE	327	51.99	10	82	R.FLSYVQAQHQR.R	0.9958		2	1377.5455
						R.NVTHIDQALQEAHR.V	0.9944	1,2		1632.7763
						K.MHPLPGTQLLDMAGGTGDIAFR.F	0.9958	2,3		2299.6679
						R.LYDLYSFQVIPVIGEVIAGDWK.S	0.993		2	2526.9348

						K.KYQNEEDSLGGSLATVCDINR.E	0.9958		2	2370.5011
						R.FLCLEFGQVNDPLISR.L	0.9958		2	1909.1584
						R.VTYENLTTGIVAIHSGFK.L	0.9958		2	1951.2297
						K.KYDLMNDMMSLGIHR.A	0.9958		2	1825.169
						K.RAAETHFGFETVSEGEK.G	0.9958		2	1896.0233
						R.AAETHFGFETVSEGEK.G	0.9958		2	1739.8358
909	COQ7_MOUSE	217	32.72	3	17	R.MLMEEDPEKYEELLQVIK.Q	0.9958		2	2238.6162
						K.EGAMACTVAVEESIANHYNNQIR.M	0.9958		2	2578.7822
						K.QFRDEELEHHDTGLDHDAELAPAYALLK.R	0.9958		2	3235.4937
910	COQ9_MOUSE	313	43.13	7	81	R.MLIPYIEHWPR.A	0.9958		2	1455.7607
						K.STGEALVQGLMGAAVTLK.N	0.9958		2	1747.06
						K.LVQLGQAEK.R	0.9958		1	986.1564
						R.INDAMNMGHTAK.Q	0.9958		2	1303.4938
						K.QQPPHSSSQQHSETQGPEFSRPPPR.Y	0.9958		3	2827.9895
						R.YTDQSGEEEEDYESEEQLQHR.I	0.9958		2	2602.5543
						R.AVLAGIYNTTELVMMQDSSPDFEDTWR.F	0.9944		2	3091.4341
911	COR1A_MOUSE	461	6.94	2	2	R.YFEITSEAPFLHYLSMFSSK.E	0.9958		2	2398.7352
						R.HVFGQPAK.A	0.9958		1	884.0256
912	COR1B_MOUSE	484	11.98	2	2	R.YFEITDEPPYIHFLNTFTSK.E	0.9958		2	2463.7485
						R.SGASTATAVTDVPSGNLAGAGEAGKLEEV	0.9944		3	3318.6373
913	CORA1_MOUSE	1845	2.76	2	2	R.ELALVLSLCSHRVNHAFLFAIR.S	0.9931		3	2568.0061
						R.TQDPQQLPIVSVDNLPPVSSGKQYR.L	0.9901		2	2768.099
914	CORO7_MOUSE	922	23.43	8	18	R.VPPGGLENVLTTPETVLTGHTEK.I	0.9958		2	2390.6959
						R.LSGTGEALPSVPGVVLGPEELPVEVLQFHF	0.9958		3	4197.8157
						R.VAVPLLSSGGQVAVLELQKPGR.L	0.9958		2	2219.6328
						K.LQGHQDQIFSLAWSPDGK.Q	0.9958		2	2028.2315
						R.IWDLQTGAER.L	0.9958		1	1189.3134
						R.LAWTGIQEHLVSTGFNQMR.E	0.9958		2	2189.4967
						K.AVEFHEDLFPDTAGSVPASDAHMWWAGD	0.9958		3	3786.0827
						R.HVTYLGCHSDLVTDLDFSPFDDFLLASGSA	0.9958		3	3572.8323
915	COTL1_MOUSE	142	12.68	1	2	K.FALITWIGEDVSGLQR.A	0.9943		2	1806.0715
916	COX17_MOUSE	63	47.62	2	18	K.GEEHCGHLIEAHK.E	0.9909		2	1517.6073
						K.KPLKPCCACPETK.K	0.9958		2	1589.7707
917	COX2_MOUSE	227	32.16	3	181	R.MLISSEDVLHSWAVPSLGLK.T	0.9958		2	2183.5707
						R.VVLPMELPIR.M	0.9958	1,2		1167.4955
						R.LNQATVTSNRPGLFYGQCSEICGSNHSFM	0.9958		3	4397.9835
918	COX41_MOUSE	169	78.11	12	325	R.DYPLPDVAHVTMLSASQK.A	0.9958		2	1973.2513

						K.SEDYAFPTYADR.R	0.9958	1	1435.4894
						K.ANPIQGFSAK.W	0.9944	1	1033.1723
						K.WDYDKNEWK.K	0.9958	1,2	1284.3703
						R.RDYPLPDVAHVTMLSASQK.A	0.9958	2	2129.4387
						R.IQFNESFAEMNR.G	0.9958	1	1486.6422
						R.GTNEWKTVVGMAMFFIGFTALVLIWEK.S	0.9944	3	3090.7114
						R.ALSLIGK.R	0.9958	1	701.8845
						R.AHGSVVKSEDYAFPTYADR.R	0.9958	2	2114.2786
						K.SYVYGPIPHTFDRDWVAMQTK.R	0.9958	2	2512.845
						K.SEDYAFPTYADRR.D	0.993	2	1591.6769
						R.AHGSVVK.S	0.9958	1	697.8124
919	COX5A_MOUSE	146	63.01	9	576	R.WVTYFNKPDIDAWELR.K	0.9929	2	2054.3122
						K.GMNTLVGYDLVPEPK.I	0.9958	1,2	1633.9
						R.LNDFASAVR.I	0.9958	1	993.1075
						K.EIYPYVIQELRPTLNELGISTPEELGLDKV.-	0.9958	3	3430.9201
						K.EIYPYVIQELRPTLNELGISTPEELGLDK.V	0.9958	3	3331.7876
						R.RLNDFASAVR.I	0.9958	2	1149.295
						K.IIDAALR.A	0.9958	1	771.9352
						R.KGMNTLVGYDLVPEPK.I	0.9958	1,2	1762.0741
						R.ILEVVKDK.A	0.9958	1	944.1595
920	COX5B_MOUSE	128	76.56	8	118	K.GLDPYNMLPPK.A	0.9958	1	1245.4791
						K.EDPNLVPSISNK.R	0.9958	1	1313.4503
						K.AASGTKEDPNLVPSISNK.R	0.9952	2	1829.0171
						R.EIMIAAQK.G	0.9958	1	904.1125
						R.IVGCICEEDNCTVIWFWLHK.G	0.9958	2	2580.841
						R.SMASGGGVPTDEEQATGLER.E	0.9958	2	1993.1095
						K.LVPHQMAH.-	0.9958	1	933.1161
						R.CPNCGTHYK.L	0.9924	2	1137.1695
921	COX6C_MOUSE	76	38.16	4	46	K.AGIFQSAK.-	0.9924	1	821.9517
						K.AYAEFYR.N	0.9958	1	920.0123
						R.NYDSMKDFEEMR.K	0.9958	1,2	1565.7126
						R.KAGIFQSAK.-	0.9958	1,2	950.1258
922	COX7C_MOUSE	63	17.46	1	3	K.NLPFSVENK.W	0.9958	1	1048.1839
923	COX7R_MOUSE	111	42.34	2	12	K.LTSSVTAYDYSGK.N	0.9958	1,2	1392.5053
						K.LAGAWASEAYTPQGLKPVSTEAPPIIFATPT	0.9958	3	3314.8059
924	CP014_MOUSE	160	28.75	2	2	R.TGPTQQQVESRLGELLK.C	0.9958	2	1885.1277
						R.RPLTTSPSLEGTQETYTVAHEENVR.F	0.9958	3	2817.0416

925	CP035_MOUSE	569	2.11	2	2	R.SQLLMLFDK.F	0.9958		1	1095.3423
						R.RSQLLMLFDK.F	0.9944		1	1251.5297
926	CP045_MOUSE	203	5.42	1	2	K.EMADFLRIK.L	0.9958		1	1123.3557
927	CP061_MOUSE	79	15.19	1	6	K.FFGHCNDLDR.E	0.9958	1,2		1281.3361
928	CP062_MOUSE	963	3.63	2	5	R.ELIPRFYVEASILK.C	0.9958		1	1679.0123
						R.NNKLNQLSVNLWHLAQR.H	0.9958		2	2049.3432
929	CP110_MOUSE	2334	1.16	2	2	R.YIENLEK.C	0.9958		1	909.0269
						R.EQQLMAKSGELLALQK.E	0.9958		1	1788.1125
930	CP19A_MOUSE	503	3.78	1	3	R.LEYFPKPNEFTLENFEK.N	0.9945		2	2146.4039
931	CP1A1_MOUSE	524	2.48	1	6	R.YLPNSSLDAFK.D	0.9944		1	1255.413
932	CP24A_MOUSE	514	2.92	1	4	K.WSFESICLVLYEK.R	0.9929		2	1674.9001
933	CP2J5_MOUSE	501	3.99	1	2	R.MGNIVPLNSSREVTVDTK.F	0.9944		2	1961.2408
934	CP3AG_MOUSE	504	3.57	1	4	K.LALIKVLQNFSFQPCK.E	0.9958		2	1907.2726
935	CPEB3_MOUSE	716	3.49	1	2	R.AVGVGVGVGVGVPSPLNPISPLK.K	0.9958		3	2114.5363
936	CPIN1_MOUSE	309	36.25	5	40	R.LQELTGSEGQVFMENVTQLLQSSHK.E	0.9958		2	2805.1321
						R.EALSPEEVQSVQEHLGYHSDSLR.S	0.9958		2	2611.7844
						K.ESSFDVILSGVVPGSTSLHSAEVLAEMAR.I	0.9958	2,3		2990.3551
						K.SSSVKPVVDPAAAK.L	0.9958		2	1356.562
						K.KPNFEVGSSSQLK.L	0.9958		2	1421.5932
937	CPN2_MOUSE	547	15.17	5	8	R.HLEPDAFGGLPR.L	0.9958		2	1309.4673
						R.TLNLAQNLLTQLPK.G	0.9944		2	1567.8693
						K.GAFQSLTGLQMLK.L	0.9958		2	1394.6721
						K.QEQLICPVNPGHLSFR.A	0.9958		2	1896.1223
						R.LVSLTLSHNAITDLPEHVFR.N	0.9958		2	2263.6017
938	CPNE1_MOUSE	536	11.57	3	20	R.ETLAQTVLAEVPTQMVSYFR.A	0.9958		2	2284.6325
						R.LYGPTNFAPIINHVAR.F	0.9945		2	1784.0708
						R.FSVSLQHFCGGDLSTPIQVR.C	0.9958		2	2249.4974
939	CPNE3_MOUSE	533	15.57	3	7	R.QAIVNAAKLPMSIIIVGVGGADFSAMEFLDG	0.9944		3	3722.3094
						R.LYGPTNFSPIINHVAR.F	0.9958		2	1800.0702
						K.TIELSDDDFLGECEVTLGQIVSSK.K	0.9958		2	2656.8665
940	CPNS1_MOUSE	269	42.38	4	39	R.YADESGNMDFDNFISCLVR.L	0.9958		2	2254.3987
						R.ILGGVISAISEAAAQYNPEPPPPR.S	0.9958	2,3		2448.7813
						R.SHYSNIEANESEEVR.Q	0.9958		2	1764.8027
						K.GGGGGGGGGGLGGGLGNVLGGLISGAAG	0.9944		3	3785.0777
941	CPSF1_MOUSE	1441	2.43	2	3	R.LHPMGIDGPIDSFAPFHNVNCPR.G	0.9944		3	2592.9007
						R.RILQNAVR.N	0.9958		1	970.163
942	CPSF2_MOUSE	782	5.63	2	2	R.GDGNVLIAVDTAGRVLELAQLLDQIWR.T	0.9958		3	2937.3689

						K.IQQLKFSQIVNLK.G	0.9958		2	1559.8925
943	CPSF6_MOUSE	551	8.17	2	3	R.AVSDASAGDYGSAIETLVTAISLIK.Q	0.9958		2	2453.7491
						K.VLISSLQDCLHGIESK.S	0.9958		2	1800.0283
944	CPSF7_MOUSE	471	5.73	1	2	K.AVSGASAGDYSDAIETLLTAIAVIK.Q	0.9958		2	2437.7497
945	CPT1B_MOUSE	772	21.63	11	96	R.TSPDAFVQIALQLAHFR.D	0.9958		2	1915.2022
						R.ILDDPSPPQPGEEK.L	0.9944		1	1522.6519
						K.ALADDVELYCFQFLPFGK.G	0.9958		2	2134.4022
						R.YLDSVRPLLDDEAYYR.M	0.9944		2	1989.1919
						K.KQDLQDLFR.K	0.9952		2	1163.3189
						R.HIYLSGINSWK.K	0.9958	1,2		1318.518
						R.AAFFVTLDEDSHCYNPDDETSLSLYGK.A	0.9958		2	3096.2533
						K.LPVPSVPATIHR.Y	0.9958		2	1287.5479
						R.HVAVYHK.G	0.9958		1	853.9993
						K.ALLHGNCYNR.W	0.9958		1	1218.3238
						K.SFTLISCK.N	0.9944		1	956.093
946	CPT2_MOUSE	658	41.49	18	287	R.YLSAQKPLLNDSQFR.K	0.9958	1,2		1781.0214
						K.YILSDSSPVPEFPLAYLTSENR.D	0.9958		2	2499.7796
						R.AGLLEPEVFHLNPAR.S	0.9958		2	1663.9169
						K.YHGQLTK.E	0.9958		1	846.9615
						K.GHFYVFDVLDQDGNIVNPSEIQAHLK.Y	0.9958		3	2957.2719
						R.GVTLPELYQDPAYQR.I	0.9924	1,2		1750.9487
						K.LSPDAVAQLAFQMAFLR.Q	0.9958		2	1879.2274
						K.RYLSAQKPLLNDSQFR.K	0.9913		2	1937.2089
						K.DLVHLSHTMLHGDGTNR.W	0.9958		2	1904.1106
						K.ELHAHLLAQDK.Q	0.9958		2	1275.4502
						K.HSVGELQHMMAECSK.Y	0.9943		2	1744.9442
						K.HTSYISGPWFDMYLTAR.D	0.9958		2	2046.3075
						R.IPKPSRDELFTDTK.A	0.9931		2	1647.8687
						K.DGTAAVHFEHAWGDGVAVLR.F	0.9944		2	2109.3085
						K.LIHGGNEETLR.K	0.9958		2	1239.3738
						R.KVDSAVFCLCLDDFPMK.D	0.9958		2	2046.3181
						K.RCSEAFVR.E	0.9958		1	1025.1186
						R.KGHFYVFDVLDQDGNIVNPSEIQAHLK.Y	0.9958	2,3		3085.446
947	CPZIP_MOUSE	412	10.19	2	6	K.LQANLAFDPAALLPGASPK.S	0.9958		2	1895.2089
						K.AIVSPFHSPPSTPSSPGIR.S	0.9958		2	1935.19
948	CQ061_MOUSE	113	26.55	1	2	R.LGALSGAGALGLASYGAHGAQFPDAYGK.I	0.9958		2	2621.9121
949	CQ062_MOUSE	187	5.35	1	13	R.SDVEAIAK.L	0.9944		1	832.9292

950	CQ090_MOUSE	201	8.46	1	4	K.ALAILEEHVTDENLK.A	0.9958	1,2	1695.9103
951	CQ10B_MOUSE	240	5	1	3	K.LFNHLETIWR.F	0.9944	2	1329.5443
952	CR3L4_MOUSE	370	4.05	1	2	R.VAACSEQNQKLQR.K	0.9958	1	1532.6629
953	CRADD_MOUSE	199	18.09	2	2	K.GLQAVEADPSLLQHMLE.-	0.9944	2	1852.1126
						K.AFDTFLDSLQEFPWVR.E	0.9958	2	1972.2072
954	CRBB3_MOUSE	211	33.18	3	3	K.VGSIQVESGPWLAFERR.A	0.9944	3	1932.1893
						R.SDILLSLRPLHIDGPDHKLHLFENPAFSGR.I	0.9958	3	3396.8765
						R.HWNEWDANQPQLQSVRR.I	0.9944	3	2165.3353
955	CREG1_MOUSE	220	9.09	1	11	R.FVTHVSDWGSLATISTIK.E	0.9958	1,2	1963.2407
956	CREL1_MOUSE	420	14.76	2	3	R.SDFECHRLLELSEELVENWWFHR.Q	0.9958	3	3033.2952
						K.LCCPSGTFGPSCLPCPGGTERPCGGYGQ(	0.9958	3	3820.9019
957	CRIM2_MOUSE	1550	1.16	1	2	K.DCHGEDFSVHVTNDDR.G	0.9958	1	1903.8823
958	CRIP1_MOUSE	77	38.96	1	3	K.TLTSGGHAEHEGKPYCNHPCYSAMFGPK.	0.9958	3	3135.3694
959	CRIP2_MOUSE	208	32.69	3	171	K.GVNIGGAGSYIYEKPQTEAPQVTGPIEVPV'	0.9958	2	3327.7618
						K.GVNTGAVGSYIYDK.D	0.9958	2	1444.5841
						K.ASSVTTFTGEPNMCPR.C	0.9958	2	1755.9062
960	CRIP3_MOUSE	243	7.82	1	10	R.HLDPSPIPSDLHPLANK.A	0.993	2	1852.1002
961	CRK_MOUSE	304	23.68	4	29	R.IGDQEFDSLPALLEFYK.I	0.9958	2	1986.2286
						R.DSSTSPGDYVLSVSENSR.V	0.9958	2	1900.9506
						R.ALFDFNGNDEEDLPFK.K	0.9909	2	1871.9977
						K.IHYLDTTTLIEPVAR.S	0.9958	2	1743.0129
962	CRKL_MOUSE	303	24.09	4	11	R.VSHYIINSLPNR.R	0.9958	2	1413.6194
						K.IGDQEFDHLPALLEFYK.I	0.993	2	2036.2915
						K.IHYLDTTTLIEPAPR.Y	0.9958	2	1740.997
						R.YPSPPVGSVSAPNLPTAEENLEYVR.T	0.9958	2	2687.9659
963	CRML_MOUSE	1285	5.37	3	3	R.NNHAWARVQSLAQNPR.L	0.9958	2	1863.0487
						K.DFEAIQNNIALK.Y	0.9944	2	1376.5523
						R.NPPRPLLVAGPSSTGSSDSDGGLFAVPTTI	0.9931	3	3463.829
964	CROCC_MOUSE	2009	1.64	2	6	R.DLRAQLEEATAAHAQTVK.E	0.9912	2	1953.1625
						R.ESQRQVEALER.A	0.9958	1	1345.4551
965	CRRY_MOUSE	483	10.35	3	4	K.TPSDPENGLVHVHTGIQFGSR.I	0.9958	2	2249.4477
						K.GASSVHCQSLNK.W	0.9958	2	1288.3691
						K.YKEVGIHLNYK.E	0.9958	1	1364.5871
966	CRSPL_MOUSE	253	5.53	1	2	R.MPNTTLVQGRPK.N	0.9944	1	1342.5993
967	CRUM2_MOUSE	1282	4.91	2	2	K.DTRDSLELVLVGAVLQATLSR.H	0.9944	3	2257.5925
						R.CVCAPGYAGANCQLDVDECQSQPCAHGG	0.9958	3	4281.3948
968	CRYAA_MOUSE	196	11.73	1	2	K.HFSPEDLTVKVLEDFVEIHGK.H	0.9925	2	2440.7582

969	CRYAB_MOUSE	175	80.57	11	1580	R.IPADVDPLTITSSLSSDGVLTVNGPR.K	0.9958	2	2625.9359
						R.APSWIDTGLSEMR.L	0.9958	2	1463.6483
						K.VLGDVIEVHGK.H	0.9958	1,2	1166.3629
						K.YRIPADVDPLTITSSLSSDGVLTVNGPR.K	0.9958	3	2945.2994
						K.HFSPEELK.V	0.9958	1	987.1002
						R.LFDQFFGEHLLESDLFSTATSLSPFYLRPP	0.9944	3	3980.5115
						R.APSWIDTGLSEMRLEK.D	0.9958	2	1834.0973
						R.EEKPAVAAAPK.K	0.9924	1	1111.2835
						K.DRFSVNLDVK.H	0.9958	1,2	1193.3451
						K.VLGDVIEVHGKHEER.Q	0.9915	2	1717.9224
						R.RPFFPFHSPSR.L	0.9958	2	1375.5754
970	CRYL1_MOUSE	319	23.82	3	28	K.HVLSTFGPVPEFSGATVER.V	0.9958	2	2031.2755
						K.LYDIEQQQITDALENIR.K	0.9958	2	2063.2719
						R.LQYAVISEAWRLVEEEIVSPSDLDLVMSDG	0.9944	3	3823.3681
971	CRYM_MOUSE	313	17.57	2	2	R.TAAVSAIATK.L	0.9958	1	933.0929
						K.LVTFYEGHSNTAVPSHQASVLLFDPSNGS	0.9944	3	4559.1535
972	CS021_MOUSE	648	7.87	2	2	R.EGLQVGRASTPDWPSQDPQPGLQR.S	0.9944	3	2620.8411
						R.NAFFPEVFSPVPAEDESHEQDSR.S	0.9958	3	2635.7625
973	CS052_MOUSE	266	34.21	3	7	R.VVAPHQLHSEANER.L	0.9958	2	1587.7354
						R.ARPGRAALYVGLLGGAAACCALAPSEAAF	0.9958	3	4785.4303
						K.YKPIILTDDQVDQALWEEQVLQK.E	0.9958	2	2774.1431
974	CSAD_MOUSE	493	14.2	3	3	R.TLDGDPVAVEALLQDVFGIVVDEAILK.G	0.9944	3	2841.2714
						R.FFNQLFSGLDPHALAGR.I	0.9958	2	1891.1393
						K.EPEELKQLLDLELQSQGESR.E	0.9912	2	2342.5651
975	CSK21_MOUSE	391	21.48	5	31	R.FVHSENQHLVSPEALDFLDK.L	0.9958	2	2326.5706
						R.LIDWGLAEFYHPGQEYNVR.V	0.9958	2	2308.5578
						R.TPALVFEHVNNTDFK.Q	0.9958	2	1732.9335
						R.GGPNIITLADIVKDPVSR.T	0.9958	2	1866.168
						K.ILENLR.G	0.9924	1	757.9083
976	CSK2B_MOUSE	215	18.6	2	4	K.FNLTGLNEQVPHYR.Q	0.9958	2	1688.8833
						R.LYGFKIHPMAYQLQLQAASNFK.S	0.993	2	2570.027
977	CSKI1_MOUSE	1431	2.38	2	3	K.NGHIDIIRLLLQAGIDINR.Q	0.9924	2	2145.513
						R.VATVLASVKHK.E	0.9944	1	1153.4105
978	CSMD1_MOUSE	3564	2.22	2	2	K.VISCGSLSFPPNGNKIGTLTIYGATAIFTCN	0.9944	3	4446.9795
						K.VEGSDFRWGASISYSCVDGYQLSHSAILS	0.9924	3	3695.913
979	CSN1_MOUSE	471	17.62	4	9	K.MAAAFNTTVAALEDELTQLILEGLINAR.I	0.9958	2,3	2990.4419
						K.VSVYLQNWSHVLSYVSK.A	0.9958	2	2010.3

						R.IDSHSKILYAR.D	0.9944	1	1303.5039
						R.RGHDDLGDHYLDCGDLSNALK.C	0.9958	2	2372.4791
980	CSN2_MOUSE	443	23.25	6	16	R.IDQVNQLLELDHQK.R	0.994	2	1693.8974
						K.TNHSNIMDDPFIR.E	0.9958	2	1560.7246
						K.NDPEILAMTNLVSAYQNNDITEFEK.I	0.9958	2	2871.1451
						K.WTNQLNSLNQAVVSK.L	0.9923	2	1702.9077
						K.VLELEGEKGEWGFK.A	0.9958	2	1621.8303
						K.AHTDFFEAFK.N	0.9958	2	1213.3348
981	CSN3_MOUSE	423	31.68	5	34	K.YNNPAMLHNIDQEMLK.C	0.9958	2	1932.2196
						R.YATDTFAGLCHQLTNALVER.K	0.9958	2	2281.4962
						R.FIKPLSNAYHELAQVYSTNNPSELR.N	0.9958	2	2893.2285
						K.SGELLAKNLSHLDTVLGALDVQEHSLGVLA	0.9944	3	3688.3024
						K.YVLHMIEDGEIFASINQKDGMVSFHDNPEK	0.9958	3	3465.877
982	CSN4_MOUSE	406	39.66	9	62	R.LYLEDDDPVQAEAYINR.A	0.9958	2	2025.1791
						K.LYNNITFEELGALLEIPAAK.A	0.9944	2	2220.5707
						R.QLLTDFCTHLPNLPDSTAK.E	0.9958	2	2172.4089
						R.AVIEHNLLSASK.L	0.9958	2	1282.4826
						R.NAAQVLVGIPLETGQK.Q	0.9958	2	1638.9047
						R.GNQLQEFAAMLMPHQK.A	0.9958	2	1844.1566
						R.QDLAQLMNSSGSHK.D	0.9952	2	1516.669
						R.ASLLQNESTNEQLQIHYK.V	0.9941	2	2117.3232
						K.QIQSLCFQVNNLLEK.I	0.9952	2	1835.0765
983	CSN5_MOUSE	334	31.44	5	22	K.TTIEAIHGLMSQVIK.D	0.9958	2	1641.9665
						K.GYKPPDEGPSEYQTIPLNK.I	0.9924	2	2134.3501
						K.KQQQEILAAKPWTK.D	0.9958	2	1669.9645
						K.TWELANNMQEAQSIDEIYK.Y	0.9958	2	2284.5024
						K.YWVNTLSSSSLLTNADYTTGQVFDLSEK.L	0.9958	3	3141.415
984	CSN6_MOUSE	324	32.1	5	13	R.MTATGSGENSTVAEHLIAQHSAIK.M	0.9944	2	2454.7173
						R.EAYALCHCLPVLSTDK.F	0.9958	2	1878.0645
						K.ELEFLGWYTTGGPPDPSDIHVHK.Q	0.9958	2	2596.8584
						R.NIEVMNSFELLSHTVEEK.I	0.9958	2	2120.382
						K.ASEAGEVPFNHEILR.E	0.9958	2	1669.8345
985	CSN7A_MOUSE	275	24.36	4	11	K.VTTAAAAAATSQDPEQHLTELR.E	0.9958	2	2282.4722
						K.VTGQNQEQFLLLAK.S	0.9958	2	1589.832
						K.VTTAAAAAATSQDPEQHLTELREPASGTN(	0.9958	3	3223.4404
						R.QLEDLVIEAVYADVLR.G	0.9944	2	1847.1186
986	CSN8_MOUSE	209	30.62	3	35	R.KPASGTLDVSLNR.F	0.9958	2	1358.5375

						R.FIPLSEPAPVPPIPNEQQLAR.L	0.9924		2	2314.6897
						R.DFPGIYTTINAHQWSETVQPIMEALR.D	0.9958		2	3019.4015
987	CSPG2_MOUSE	3357	2.11	3	12	R.VSVPTHPDDVGDASLTMVK.L	0.9958		2	1969.2171
						R.LQGAHLTSILSHEEQMFVNR.V	0.9958		2	2311.6207
						K.TTGDILPGESVTQHPVTTLIDIVAMK.T	0.9915		2	2738.1688
988	CSPG4_MOUSE	2327	0.95	1	3	R.SGNEVHYHVTAGPQWGQLLR.D	0.9958		2	2250.4813
989	CSRP1_MOUSE	193	31.09	3	10	K.GYGYGQGAGTLSTDKGESLGIK.H	0.9958		2	2160.3452
						K.NLDSTTVAVHGEEIYCK.S	0.9958		2	1937.0796
						K.HEEAPGHRPTTNPNASK.F	0.9958		2	1843.9535
990	CSRP3_MOUSE	194	65.98	8	535	K.NFGPTGIGFGGLTQQVEK.K	0.9958		2	1851.0691
						K.TVYHAEEIQCNGR.S	0.9958		2	1577.6599
						K.GIGFGQGAGCLSTDTGEHLGLQFQQSPKP	0.9958	2,3		3216.5035
						K.ALDSTTVAAHESEIYCK.V	0.9958		2	1896.0271
						K.SLESTNVTDK.D	0.9958	1,2		1094.1638
						K.SLESTNVTDKDGELYCK.V	0.9958		2	1960.0681
						K.TCFHCMACR.K	0.9944	1,2		1243.3212
						K.VMGGGKPWHK.T	0.9944		1	1097.3232
991	CSTP1_MOUSE	312	25.32	4	10	K.QAQDHWLDQQLNIAEQK.Q	0.9958		2	2066.2376
						K.FFVLCGDLVHAMPGTPWR.Q	0.9958		2	2104.4431
						K.AWSTGNCDAGGDEWGQEIR.L	0.9958		2	2110.1266
						R.YYSLDELSQGGVEEDLK.E	0.9958		2	1946.0747
992	CT007_MOUSE	343	11.37	2	2	R.DFPLALDIGCGR.G	0.9958		1	1334.4809
						R.EGGFSPHISPFTAVNDLGHLLGR.A	0.9958		2	2422.7055
993	CT011_MOUSE	228	18.86	2	10	R.MESGIEPSVDLETLDER.I	0.9924		2	1921.0833
						K.GQIQEAIALINSLHPELLDTNR.Y	0.9911		2	2446.766
994	CT012_MOUSE	778	8.87	2	2	R.SSLVSAYSQSVSDTPESIK.K	0.9958		2	1986.14
						R.LPPPEGAQMGLCAECGSMVPMNTPICVVC	0.9958		3	5054.7945
995	CT029_MOUSE	170	9.41	1	2	R.LLTPAVSTGAAYCR.A	0.9958		2	1480.6703
996	CT059_MOUSE	439	8.2	1	2	K.VILLSASAWGFITVTTPLLAHLGSGHLAFLTI	0.9944		3	3599.2566
997	CT075_MOUSE	733	3.55	2	3	R.QFYDTHLVAFK.N	0.9958		1	1369.5627
						K.HLQTPCAELQR.R	0.9958		2	1353.4869
998	CT094_MOUSE	413	11.62	2	3	R.HLVTNNPGQAQQSDSAAITEQLATDQGGP	0.9958		3	3293.5315
						R.SQQQLHPGEWLK.T	0.9958		1	1451.6249
999	CTBP1_MOUSE	441	16.33	4	22	R.GAALDVHESEPFSFSQGPLK.D	0.9929		2	2117.3226
						K.VLNEAVGALMYHTITLTR.E	0.9958		2	2003.3673
						R.GGLVDEK.A	0.9958		1	717.7972
						K.AFGFNVLFYDPYLSDGIER.A	0.9958		2	2224.4772

1000	CTGE5_MOUSE	779	4.62	2	2	K.SGLENTAALDNQPKGALK.K	0.9945		2	1828.0324
						R.TIHSYQGQVISHEK.K	0.9958		2	1627.7972
1001	CTHR1_MOUSE	245	8.57	2	2	R.IIIEELPK.-	0.9958		1	955.1827
						K.GDASTGWNSVSRIIIEELPK.-	0.9952		2	2173.4307
1002	CTLA4_MOUSE	223	8.52	1	3	R.QTNDQMTEVCATTFTEK.N	0.9958		2	2005.1268
1003	CTNA1_MOUSE	906	22.19	9	27	R.VIHVVTSEMDNYEPGVYTEK.V	0.9958		2	2311.5684
						K.AHVLAASVEQATENFLEK.G	0.9958		2	1958.1784
						K.QLQQAVTGISNAAQATASDDAAQHQGGSC	0.9958		3	4120.3519
						R.LLEPLVTQVTTLVNTNSK.G	0.9958		2	1971.3018
						R.MSASQLEALCPQVINAALALAAKPQSK.L	0.9958		3	2812.2635
						R.VLTDAVDDITSIDDFLAVSENHILEDVNK.C	0.9958		3	3202.4962
						K.AVMDHVSDSFLETNVPLLVLIEAAK.N	0.9945	2,3		2713.1615
						R.VLTDAVDDITSIDDFLAVSENHILEDVNKCV	0.9958		3	4144.5855
						K.KAHVLAASVEQATENFLEK.G	0.9958		2	2086.3525
1004	CTNA2_MOUSE	953	3.36	2	7	K.AHVLAASVEQATQNFLEK.G	0.9958		2	1957.1937
						R.LVYDGVRDIR.K	0.9958		1	1206.3873
1005	CTNA3_MOUSE	895	5.47	2	2	K.LLEPLIIQVTTLVNCPQNPSNR.K	0.9915		2	2520.8981
						R.VAHIVAGEMDSYEPGAYTEGVMR.N	0.9958		2	2483.7731
1006	CTNB1_MOUSE	781	10.63	3	7	K.AAVSHWQQQSYLDSGIHSGATTTAPSLSG	0.9958		3	3087.3323
						K.HAVVNLINYQDDAELATR.A	0.9958		2	2043.2437
						R.AAMFPETLDEGMQIPSTQFDAAHPTNVQR	0.9958		3	3204.5562
1007	CTND1_MOUSE	938	5.12	2	3	K.NGNGGPGPYVGQAGTATLPRNFHYPPDG	0.9944		3	3189.4331
						K.GIPILVGLLDHPK.K	0.9958		2	1372.6939
1008	CTP5B_MOUSE	1292	3.02	2	3	K.HIGYTCDCTNSPYEGPFCKK.E	0.9958		2	2435.5503
						K.TTALSGVFLENLGVK.N	0.9958		1	1549.8076
1009	CTSR2_MOUSE	588	1.87	1	4	R.RMGHITHSR.R	0.9944		1	1095.2675
1010	CTSRB_MOUSE	1109	4.51	3	3	K.VTKSPCANDVALIGFMMKPSSNGVFIGK.T	0.9958		3	2970.4812
						R.GNLWYNEK.C	0.9958		1	1024.121
						R.DLYPEVNDIKVTK.S	0.9958		1	1534.7496
1011	CUBN_MOUSE	3623	1.9	2	2	R.FCGIYTPSTLFTSDNEMFIQFISDNSNGGQ(	0.9944		3	3725.0432
						R.LVFSSFYLEFHYNCANDYLEVYDTIAQTSL(	0.9958		3	3838.1873
1012	CUED1_MOUSE	388	4.12	1	7	R.SSSGSGGGGATGAR.G	0.9958		1	1109.0977
1013	CUL1_MOUSE	776	5.15	2	2	K.HQQLLGEVLTQLSSR.F	0.9958		2	1709.9431
						K.YNALVMSAFNNDAGFVAALDK.A	0.9958		3	2232.5158
1014	CUL2_MOUSE	745	8.32	2	4	R.MYTDMSVSADLNNKFNNFIR.N	0.9931		3	2381.6833
						R.NQDTVIDLGISFQIYVLQAGAWPLTQAPSS	0.9944		3	4391.9647
1015	CUL4A_MOUSE	759	4.87	2	4	R.YNLEELYQAVENLCSHK.V	0.9958		2	2111.2818

						K.TLGHNLLVSELYNQLK.F	0.9958	2	1843.1332
1016	CUL5_MOUSE	780	9.62	5	5	K.ETILAECQGMIK.R	0.9944	1	1393.6045
						K.LMLDTWNESIFSNIK.N	0.9958	2	1812.0906
						K.DFTEGTLFSVNQDFSLIK.N	0.9958	2	2062.2836
						R.KLMLDTWNESIFSNIK.N	0.9958	2	1940.2647
						K.VFVSLPTELEDLIPEVEEFYK.K	0.9958	2	2497.8445
1017	CUL7_MOUSE	1689	2.07	2	5	R.QFHVYQLQQLDQELLKLEDTEK.K	0.9958	2	2747.0771
						K.SQSRSSLEK.E	0.9958	1	1022.1032
1018	CUTA_MOUSE	177	20.34	2	3	R.LAACVNLIPQITSIYEWK.G	0.9958	2	2120.4626
						K.TQSSLVPALTEFVR.S	0.9958	2	1548.7795
1019	CUTC_MOUSE	272	22.43	3	9	R.NSSVAMGASLAHSEYSLK.V	0.9958	2	1853.057
						R.ILEGSGATEFHCSAR.S	0.9949	2	1635.7399
						R.AFDMVHDPMAALETLLTLGFER.V	0.9958	2	2478.8837
1020	CUX1_MOUSE	1515	2.31	2	10	K.RELDATATVLANR.Q	0.9958	1	1430.6041
						R.RPSSLQSLFGLPEAAGAR.D	0.9958	2	1858.1075
1021	CUX2_MOUSE	1426	3.58	3	4	K.RCPEPPSAR.E	0.9958	1	1070.1595
						R.TPETGSDDAIK.S	0.9958	1	1134.1852
						R.SVPPSPPERPSPATASQNGALTCVK.Q	0.9958	2	2549.8095
1022	CV028_MOUSE	505	26.93	7	24	R.GLGHQVATDALVAMEK.A	0.9958	2	1640.8951
						K.QIGNVAALPGIVHR.S	0.9958	2	1445.7079
						K.EQLAQAMFDHIPVGVGSK.G	0.9958	2	1928.2133
						K.VFNTTPDDLDLHVIYDVSHNIAK.V	0.9958	2	2627.9133
						R.GLPQLGTLGAGNHYAEIQVVDEIFNEYAAK	0.9958	3	3219.578
						R.NYNDELQFLDK.I	0.9921	1	1399.4998
						K.GQVCVMIHSGSR.G	0.9958	2	1331.4987
1023	CX6A2_MOUSE	97	45.36	2	7	K.GDHGGAGANTWR.L	0.9934	2	1199.2278
						R.TKPFAWGDGNHTLFHNPHVNPLPTGYEHF	0.9958	3	3282.6041
1024	CX6B1_MOUSE	86	76.74	7	384	K.NCWQNYLDFHR.C	0.9958	2	1553.6427
						K.SLCPVSWVSAWDDR.I	0.9958	2	1678.8077
						K.GGDVSVCEWYR.R	0.9924	1	1328.3899
						R.IAEGTFPGK.I	0.9924	1	920.0532
						R.IAEGTFPGKI.-	0.9958	1	1033.2126
						R.FPNQNQTK.N	0.9903	1	977.0647
						K.TAPFDSRFPNQNQTK.N	0.9958	2	1751.8961
1025	CX7A1_MOUSE	80	21.25	2	151	K.LFQADNDLPVHLK.G	0.9958	2	1510.7331
						K.QKLFQADNDLPVHLK.G	0.9924	2	1767.0379
1026	CX7A2_MOUSE	83	18.07	1	19	K.LFQEDNGMPVHLK.G	0.9958	2	1528.7662

1027	CXG2_MOUSE	440	8.64	1	2	R.GASAAGPGPTPRPPPCAFPAAAAGLACPP	0.9958	3	3518.9294
1028	CY1_MOUSE	325	46.46	8	206	K.LSDYFPKPYPNPEAAR.A	0.9958	2	1866.0831
						R.GLLSSLDHTSIR.R	0.9958	2	1299.4697
						R.HGGEDYVFSLLTGYCEPPTGVSLR.E	0.9958	2	2655.8897
						R.HLVGVCYTEEEAK.A	0.9958	2	1535.6599
						K.LSDYFPKPYPNPEAARAANNGALPPDLSYI	0.9958	3	3518.9536
						K.ALAEEVEVQDGPNDDGEMFMRPGK.L	0.9958	2	2635.88
						R.EGLYFNPYFPGQAIGMAPPIYTEVLEYDDG	0.9958	3	4383.9309
						R.AANNGALPPDLSYIVR.A	0.9958	1,2	1671.8937
1029	CY24B_MOUSE	570	5.09	1	10	K.TIASEHPNTTIGVFLCGPEALAETLSK.Q	0.9958	2	2858.1841
1030	CYB5_MOUSE	134	45.52	4	9	K.FLEEHPGGEEVLR.E	0.9958	2	1512.6622
						K.TYIIGELHPDDR.S	0.9958	1,2	1429.5724
						R.EQAGGDATENFEDVGHSTDAR.E	0.9952	2	2207.1882
						K.STWVILHHK.V	0.9958	1	1121.3274
1031	CYB5B_MOUSE	146	27.4	2	2	R.FLSEHPGGEEVLLEQAGADATESFEDVGH	0.9944	3	4100.4163
						R.FLSEHPGGEEVLLEQAGADATESFEDVGH	0.9924	2	3598.7747
1032	CYBP_MOUSE	229	41.05	4	19	K.NYSMIVNNLLKPISVESSSK.K	0.9958	2	2224.5775
						K.EKPSYDTEADPSEGLMNVLK.K	0.9958	2	2224.4444
						K.IYITLTGVHQVPTENVQVHFTER.S	0.9958	2	2683.0391
						K.KPELDNEKPAAVVAPLTTGYTVK.I	0.9958	2	2442.815
1033	CYC_MOUSE	105	55.24	6	1215	K.GITWGEDTLMEYLENPK.K	0.9958	2	1997.2269
						K.GITWGEDTLMEYLENPKK.Y	0.9958	2	2125.401
						K.TGPNLHGLFGR.K	0.9958	1,2	1169.3286
						K.TGQAAGFSYTDANK.N	0.9958	1,2	1431.5016
						R.ADLIAYLK.K	0.9958	1	907.0978
						R.KTGQAAGFSYTDANK.N	0.9958	2	1559.6757
1034	CYC2_MOUSE	105	39.05	5	59	K.KYIPGTK.M	0.9944	1	806.9805
						K.GVIWSEETLMEYLENPK.K	0.9958	2	2039.3075
						K.GVIWSEETLMEYLENPKK.Y	0.9958	2	2167.4816
						K.MIFAGIK.K	0.9944	1	780.016
						K.KIFVQK.C	0.9924	1	762.9707
1035	CYFP2_MOUSE	1253	0.88	1	2	R.QDGKDEIIK.N	0.9958	1	1046.1656
1036	CYH1_MOUSE	398	11.06	2	3	R.LKEEIAEVANEIESLGSTEER.K	0.9958	2	2347.5383
						R.VVEGNHTVYRISAPTPEEK.E	0.9958	3	2127.3617
1037	CYH3_MOUSE	399	7.52	2	4	K.VLQAFVELHEFADLNLVQALR.Q	0.9958	2	2426.821
						K.VLQAFVELHEFADLNLVQALRQFLWSFR.L	0.9944	3	3391.9432
1038	CYLD_MOUSE	952	2.94	2	2	K.GLQVDVGSPVKVQLR.S	0.9924	2	1595.8827

						R.IYGYVCATK.I	0.9944	1	1075.2158
1039	CYTB_MOUSE	98	23.47	1	23	R.VFQPLPHENKPLTLSSYQTNK.E	0.9958	2	2442.7771
1040	CYTC_MOUSE	140	14.29	1	18	K.SQTNLTDCPFHDQPHLMR.K	0.9958	2	2198.3839
1041	CYTSA_MOUSE	1118	4.92	3	8	K.AALAATLEEYKATVASDQIEMNR.L	0.9944	3	2496.7949
						K.LTKELEEIK.S	0.9958	1	1103.3012
						K.GSSGNASEVSVACLTER.I	0.9958	2	1724.7882
1042	D19L4_MOUSE	722	4.57	1	2	K.LCTGWTVTSLPLYSDDDLLQRNENIYQIYSI	0.9944	3	3708.0821
1043	D2HDH_MOUSE	535	33.83	10	83	K.VLLRPQTSEEVSQILR.H	0.9958	2	1869.1716
						K.GSCHIGGNVATNAGGLR.F	0.9958	2	1641.7502
						R.LPFSTVSEEDLAAFECIIPGR.V	0.9958	2	2352.6123
						R.VITDPEQLQTCNVDWLK.T	0.9958	2	2060.2775
						K.DVLGYSKPPVAVTLMQQLK.A	0.9958	2	2088.5133
						K.LTNVLEQVLNSGLVTDGTMATDQR.K	0.9958	2	2576.8817
						R.ELLGALEPYVYAWTAEQR.G	0.9958	2	2110.3739
						R.GSVSAEHGLGFK.K	0.9958	2	1189.3134
						K.AVNVAFLGCPGFAEVLQTFR.T	0.9958	2	2197.5078
						K.GSCHIGGNVATNAGGLRFLR.Y	0.9944	3	2058.2737
1044	D3D2_MOUSE	289	64.36	16	652	R.EADIQNFTSFISK.D	0.9958	1	1500.6482
						K.VGVVDEVVPEDQVHSK.A	0.9958	1,2	1736.9194
						R.VLVETEGPAGVAVMK.L	0.9958	1	1500.7937
						K.RVLVETEGPAGVAVMK.L	0.9958	2	1656.9812
						R.NPAHYAEYWK.N	0.9958	2	1279.3971
						K.WLAIPDHSR.Q	0.9958	1,2	1095.2461
						K.SLHMYLEK.L	0.9958	1,2	1021.2195
						R.NPPVNSLSLECLTEFTISLEK.L	0.9941	2	2392.6747
						K.YTIGLNESLLGIVAPFWFK.D	0.9958	2	2169.5713
						K.YTIGLNESLLGIVAPFWFKDMYVNTIGHR.E	0.9944	3	3356.9098
						R.GVILTSECPGIFSAGLDLLEMYGR.N	0.9958	2	2599.968
						K.NVQELWLR.L	0.9958	1,2	1058.2254
						K.DMYVNTIGHR.E	0.9958	1	1206.3617
						R.NPPVNSLSLECLTEFTISLEKLENDK.S	0.9944	3	2992.3161
						R.KATADNLIK.Q	0.9924	1	974.1454
						K.LRNPPVNSLSLECLTEFTISLEK.L	0.9926	2	2662.0216
1045	DAAM1_MOUSE	1077	3.71	3	14	R.YEFLMLGIQPVIDK.L	0.9958	2	1667.0161
						K.ELSVIDGRR.A	0.9958	1	1045.1838
						K.EEMMQTLNKMK.E	0.9924	1	1383.6791
1046	DAB2_MOUSE	766	9.27	3	3	K.VEEANKAEENGSEALMTLDDQANK.L	0.9911	2	2607.7626

						R.TGKPEAQGGPWPYPSSQTQQAVR.T	0.9958		2	2471.6915
						R.AFGYVCGGEGQHQFFAIK.T	0.9958		2	2017.217
1047	DACT1_MOUSE	778	2.96	1	2	K.MSQKNSLQAVPALDRPALDFK.S	0.9923		2	2330.7075
1048	DAK_MOUSE	578	17.82	5	18	K.TDLPTWSAAMDAGLESMQK.Y	0.9958		2	2053.3095
						R.ICTTLIGLEEHLNALDR.A	0.9958		2	1969.2115
						R.ASYISSAQLDQPDPGAVAAAAIFR.A	0.9958		2	2420.6842
						K.SPGASLLPVLTK.A	0.9958		2	1183.4337
						R.VALLSGGGSGHEPAHAGFIGK.G	0.9958		2	1963.2034
1049	DAZP1_MOUSE	406	4.43	1	11	K.IFVGGIPHNCGETELR.E	0.9958		2	1799.9903
1050	DBF4A_MOUSE	663	8.6	2	2	K.DLQEKGFHVVIGHASDLVALNTSK.E	0.9958		3	2579.9157
						K.HRNFAQSNQYQVVDDIVSQLVFDFVEYGR	0.9958		3	3475.8015
1051	DBNL_MOUSE	436	13.07	3	5	K.SPTDWALFTYEGNSNDIR.V	0.9958		2	2087.2096
						K.FVLINWTGEGVNDVR.K	0.9958		2	1719.9377
						R.VAGTGEGGLEELVEELNSGK.V	0.9958		2	1989.1437
1052	DBPA_MOUSE	361	18.01	4	7	R.VFPHPNRMQAGEIGEMK.D	0.9932		2	1942.2611
						R.SVGDGETVEFDVVEGEK.G	0.9958		2	1796.8823
						R.SRPLNAVSQDGK.E	0.9958		2	1272.4037
						K.EDVFVHQTAIK.K	0.9958		1	1287.4582
1053	DC1I2_MOUSE	612	17.32	5	11	R.LDLWNLNNDTEVPTASISVEGNPALNR.V	0.9958		2	2954.223
						K.SVSTPSEAGSQDSGDGAVGSR.R	0.9958		2	1951.9555
						K.QQILHSEEFLSFFDHSTR.I	0.9944		2	2222.4215
						K.APPHELTEEEKQQILHSEEFLSFFDHSTR.I	0.9958		3	3483.7753
						K.ICSWSLDMLSHPQDSMELVHK.Q	0.9958		2	2514.8398
1054	DC1L1_MOUSE	523	33.46	10	60	K.IGILHENFQTLK.V	0.9958	1,2		1413.6597
						K.AGATSEGVLANFFNSLLSK.K	0.9958		2	1927.1644
						R.KPASVSPTTPTSPTEGEAS.-	0.9958		2	1844.9702
						K.NVLLLGEDGAGK.T	0.9958		1	1186.3507
						R.SVSSNVASVSPIPAGSK.K	0.9958		2	1587.7703
						K.VEDNFEDIITKPPVR.K	0.9958		2	1772.9958
						K.TGSPGGPGVGGSPGGGAAGASPSLPPSA	0.9958		2	2333.5199
						K.SGQKPVLSDVHAELDR.I	0.9958		2	1751.9371
						R.DTLVMLVVDMSKPWTALDSLQK.W	0.9958		2	2491.9637
						K.KIGILHENFQTLK.V	0.9958		1	1541.8338
1055	DC1L2_MOUSE	492	10.16	2	9	K.NNAASEGVLASFFNSLLSK.K	0.9958		2	1970.1894
						K.IAILHENFTTVKPEDAYEDFIVKPPVR.K	0.9958		3	3143.6097
1056	DCA15_MOUSE	600	3.67	1	3	K.SERNSGAGSAGGGPGGTGGK.R	0.9944		2	1661.6853
1057	DCLK2_MOUSE	756	4.23	1	3	K.LEFPAPYWDNITDSAKELISQMLQVNVEAR	0.9958		3	3479.9294

1058	DCMC_MOUSE	492	18.7	4	26	R.LAQGFGVDHGQVAEQSAGVLQLR.Q	0.9958	2,3		2381.6536
						K.SMLSEWFSSGFLNLER.V	0.9958		2	1904.1474
						K.TPAPAEGQCADFVSFYGGLAEASQR.A	0.9958		2	2630.7962
						R.GYALNPVANFHLQNGAVMWR.I	0.9958		2	2259.5932
1059	DCNL1_MOUSE	259	7.34	1	4	K.LDVATDNFFQNPELYIR.E	0.9958		2	2056.2823
1060	DCOR_MOUSE	461	10.63	2	2	K.QIQSHGFPPEVEEQDDGTLPMSCAQESGM	0.9911		3	3477.6786
						K.FEEITSVINPALDK.Y	0.9958		2	1576.7869
1061	DCP1B_MOUSE	578	5.88	2	2	K.LMKNLTQSEQLK.A	0.9924		2	1433.7063
						R.ANEWEKTGVEGTLFVYTR.S	0.9907		2	2101.3232
1062	DCPS_MOUSE	338	22.78	4	35	K.TPFQVEHVAQLLTGSPELK.L	0.9958		2	2095.4032
						R.IVFENPDPSDGFVLIPDLK.W	0.9958		2	2116.4186
						K.WNQQQLDDLYLIAICHR.R	0.9958		2	2187.4289
						R.AHLLAQVIENLECDPK.H	0.9958		2	1851.0759
1063	DCR1A_MOUSE	1026	7.99	3	3	R.ESASEGPNVSPVVSPNQK.R	0.9924		1	1826.9579
						K.RIPGTGFTVDAFQYGEIEGCTAYFLTHFHSI	0.9944		3	4295.6795
						R.FVQWLKPQKIIPTVNVGSFR.S	0.9958		3	2358.835
1064	DCST1_MOUSE	732	14.07	3	3	R.QPGEFPVTAFLLGAGTGGLLAIGLFQLLVNI	0.9958		3	4148.85
						R.YVIRELLETLPIVLLLLVLCAIDWALYSVFDT	0.9958		3	4035.8524
						R.DYFKASLPTLLLVCLCLAQAFGYR.L	0.9944		3	2821.2642
1065	DCTN1_MOUSE	1281	18.42	13	68	K.LNQLSTHTHVVDITR.S	0.9958		2	1734.9529
						K.YFTCDEGHGIFVR.Q	0.994		2	1601.7247
						R.LVLTQEQLHQLHSR.L	0.9958		2	1702.9541
						K.RVEAAQETVADYQQTIK.K	0.9958		2	1951.1436
						K.ETVTQRPGATVPTDFATFPSSAFLR.A	0.9958	2,3		2698.0074
						K.SPSAQLMEQVAQLK.S	0.9958		2	1530.7796
						K.DSPLLLQQISAMRLHISQLQHENSILR.G	0.9944		3	3142.6469
						R.GGAPGQAPGALPGPGLVKDSPLLLQQISAI	0.9958		3	2998.5138
						K.DFEETMDALQADIDQLEAEK.A	0.9958		2	2312.464
						K.EQVDAALGAEEMVEMLTDR.N	0.9958		2	2108.3431
						K.LSLPPHEGPGGNLVAGALYR.K	0.9958		2	2019.3109
						R.LHISQLQHENSILR.G	0.9958		2	1688.9272
						R.AESLQQEVEALK.E	0.9952		2	1345.4924
1066	DCTN2_MOUSE	402	41.79	10	44	K.LLGPDAAINLADPDGALAK.R	0.9958		2	1836.0953
						R.WSPVASTLPELVQR.L	0.9958		2	1583.8277
						R.LLHEVQELTTEVEK.I	0.9958	1,2		1668.8846
						K.RTGYESGDYEMLGEGLGVK.E	0.9958		2	2062.2586
						R.TGYESGDYEMLGEGLGVK.E	0.9958		2	1906.0711

						R.ENLATVEGNFASIDAR.M	0.9958	2	1707.8375
						R.CDQDAQNPLSAGLQGACLMETVELLQAK.\	0.9958	2	3062.3511
						K.VHQLYETIQR.W	0.9958	1,2	1287.4612
						K.ATAGAPPDSSLVTYELHSRPEQDK.F	0.9944	2	2570.7753
						K.RLTELEATVR.C	0.9918	2	1188.3695
1067	DCTN4_MOUSE	467	8.99	2	5	R.LLQPDLQPVSASQLYPR.H	0.9958	2	1926.223
						K.IQLVAVNYIPEVRIMSIPNLR.Y	0.9944	3	2439.9653
1068	DCTN6_MOUSE	190	10.53	1	2	R.VQTERPQPQTLQLDFLMK.I	0.9958	2	2173.5353
1069	DCUP_MOUSE	367	11.72	2	6	R.YIANLGHGLYPDMDPER.V	0.9958	2	1962.1871
						K.AVTLQGNLDPCALYASEEEIGR.L	0.9957	2	2407.6056
1070	DDAH2_MOUSE	285	23.16	3	34	R.GVPESLASGEGAGAGLPALDLAK.A	0.9958	2	2081.3305
						R.DFAVSTVPVSGSSHLR.G	0.9958	2	1659.8393
						R.IVEMGDENATLDGTDVLFTGR.E	0.9952	2	2254.4737
1071	DDB1_MOUSE	1140	14.56	9	43	R.EATADDLIKVVEELTR.I	0.9958	2	1803.0196
						R.NGIGIHEHASIDLPGIK.G	0.9931	2	1772.014
						R.IGRPSETGIIGIIDPECR.M	0.9958	2	1984.2261
						K.YLAIAPPIIK.Q	0.9937	2	1099.402
						K.KVTLGTQPTVLR.T	0.9958	2	1313.5833
						R.SVLLLAYKPMEGNFEEIAR.D	0.9958	2	2181.5549
						R.KTEPATGFIDGDLIESFLDISRPK.M	0.9958	2	2650.9885
						R.LEIYVVTAEGLRPVK.E	0.9958	2	1688.0202
						R.KICYQEVSQCFGVLSSR.I	0.9958	2	2062.2623
1072	DDC_MOUSE	480	7.71	2	2	K.GSNELNETLLQRINSAK.K	0.9958	1	1888.0879
						K.AVPSDGNFSMRASALR.E	0.9958	2	1679.8913
1073	DDHD1_MOUSE	547	5.85	2	2	R.LEPLILK.H	0.9944	1	826.0672
						R.LQESFFYLPQLLFPENVMQSK.D	0.9944	3	2559.9825
1074	DDI2_MOUSE	399	10.28	3	3	R.VLVEQQQDR.A	0.9958	1	1115.2315
						R.TQAQHSSPGEMASSPQGLDNPALLR.D	0.9929	2	2593.8309
						K.FSRVLVEQQQDR.A	0.9905	1	1505.6737
1075	DDT4_MOUSE	229	10.48	1	2	R.LAYSEPCGLRGALLDVCVEQGK.S	0.9925	2	2436.6997
1076	DDX1_MOUSE	740	23.24	9	36	K.GHVDVLAPTVQELAALEK.E	0.9958	2	1891.1747
						K.EAQTSFLHLGYLPNQLFR.T	0.993	2	2135.4301
						R.DQLSVLDNGVDIVVGTPGR.L	0.9958	2	1955.1753
						K.TGAFSIPVIQIVYETLK.D	0.9958	2	1880.2347
						K.GEDSVPDTVHHVVVPVNPK.T	0.9958	2	2026.2566
						R.FLVLDEADGLLSQGYSDFINR.M	0.9944	2	2373.6244
						R.TKIDCDNLEQYFMQQGGGPDK.K	0.9958	2	2445.6289

						K.HYYEVSCHDQGLCR.V	0.9958	2	1824.8793
						K.IMHFPTWVDLK.G	0.9958	2	1387.6825
1077	DDX10_MOUSE	875	2.17	1	6	R.LVTEIQKQTIGLALQGK.D	0.9958	2	1841.2016
1078	DDX11_MOUSE	880	2.73	1	3	R.FAIPAAQLVVLPYPMLLHAATR.Q	0.9958	2	2393.939
1079	DDX17_MOUSE	650	5.38	2	2	K.ENKTIIFVETK.R	0.9958	1	1322.5443
						K.TLAYLLPAIVHINHQPYLER.G	0.9958	2	2362.7801
1080	DDX18_MOUSE	660	8.79	2	5	K.TGSGKTLAFLIPVIELIVK.L	0.9958	2	2000.4729
						K.QIFNVNNLNLPQVALSFGFKVPPFVDLNVS	0.9958	3	3857.4038
1081	DDX21_MOUSE	851	3.64	1	18	K.HVVLDEVDQMLDMGFADQVEEILCVAYKK.	0.9911	3	3396.8613
1082	DDX39_MOUSE	427	19.2	4	13	K.LTLHGLQQYYVK.L	0.9958	2	1463.7196
						K.LFDLLDVLEFNQVVIFVK.S	0.9958	2	2152.5817
						K.GSYVSIHSSGFR.D	0.9958	2	1297.4129
						R.AIVDCGFEHPSEVQHECIPQAILGMDVLCQ	0.9958	3	3654.0275
1083	DDX3X_MOUSE	662	6.5	2	5	K.HVINFDLPSDIEEYVHR.I	0.9958	2	2084.2957
						K.TAAFLLPILSQIYADGPGEALR.A	0.9958	2	2317.6903
1084	DDX46_MOUSE	1032	5.14	3	7	R.SVKGGAGNEK.K	0.9958	1	947.036
						R.GGTILAPTVSAKTIAEQLAEK.I	0.9958	3	2099.4325
						R.KIYLAIESANELAVQK.A	0.9958	2	1791.0978
1085	DDX50_MOUSE	734	5.18	2	2	R.HHSESEERTETR.E	0.9917	1	1498.5088
						K.GAVDALAAALAHISGASSFEPR.S	0.9944	3	2112.35
1086	DDX51_MOUSE	639	6.73	2	3	R.FLIIDEADR.M	0.9958	1	1092.2371
						R.ANGITSYFPVQAAVIPALLESADHGFLIGR.(	0.9958	2	3129.5859
1087	DDX58_MOUSE	926	3.56	2	3	K.WIEENPALSFLKPGILTGR.G	0.9958	2	2142.5058
						R.GPSNENPKLR.D	0.9944	1	1112.2309
1088	DDX59_MOUSE	619	6.3	2	4	K.QSSVSLSGIKIVVVDEADTMLK.M	0.9924	2	2320.7039
						K.EGEGSLRPSSPQR.V	0.9958	1	1400.4911
1089	DDX6_MOUSE	483	8.9	2	2	K.SIEEQLGTEIKPIPSNIDK.S	0.9945	2	2112.3849
						K.ASAGPGGGGTQPQPQLNQLK.N	0.9958	2	1907.0934
1090	DECR_MOUSE	335	56.12	13	557	K.VAGHPDVVINNAAGNFISPSER.L	0.9958	2	2265.4905
						R.DPDMVHNTVLELIK.V	0.9958	1	1624.8927
						K.AMTTFLSTLGAQCVIASR.N	0.9958	2	1928.2202
						R.FDGGEEVFLSGEFNSLK.K	0.9958	2	1876.0295
						K.FFQPVLKPMLPPDAFQGK.V	0.9958	2	2061.4925
						K.TITDIVLNGTAYVTLEIGK.Q	0.9958	2	2022.3465
						K.EEWDIIEGLIR.K	0.9958	2	1373.5486
						K.VAFITGGGTGLGK.A	0.9958	1	1178.3739
						R.FNIIQPGPIK.T	0.9918	1,2	1127.372

						K.VTKEEWDIIEGLIR.K	0.9958		2	1701.9603
						R.LGTMEELANLATFLCSDYASWINGAVIR.F	0.9958		2	3117.5098
						R.FDGGEEVFLSGEFNSLKK.V	0.9958		2	2004.2035
						R.CDVRDPDMVHNTVLELIK.V	0.9958		2	2155.4401
1091	DEF5_MOUSE	93	40.86	1	2	K.TDEETNTEEQPGEEDQAVSISFGGQEGSA	0.9911		3	3879.9483
1092	DEK_MOUSE	380	13.95	4	15	K.KLLADANLEEVTMK.Q	0.9958		2	1575.8609
						K.NVGQFSGFPFEK.G	0.9958		2	1357.5083
						K.LLYNRPGTVSSLK.K	0.9944		2	1448.7055
						R.IHFFLSK.K	0.9958		1	892.0886
1093	DEN1A_MOUSE	1016	1.48	1	8	K.QFLQNATQLQLFK.Q	0.9958		2	1579.8393
1094	DEN1B_MOUSE	425	3.53	1	3	K.QFLETAVNLQLFK.Q	0.9958		2	1551.8259
1095	DEN4B_MOUSE	1499	2.67	2	2	R.EILFLTMAALGKDHVDIVAFDK.K	0.9944		3	2447.8951
						R.NVVLGAAQFRQPLK.D	0.9909		2	1541.8368
1096	DEND3_MOUSE	1274	3.61	2	2	K.KHMQLNDFVK.R	0.9958		1	1260.4967
						K.DASFLAFQLLPEEQQLWAASTGVSELYMW	0.9944		3	3661.1634
1097	DENR_MOUSE	198	9.09	1	4	K.WPEVDDDSIEDLGEVK.K	0.9958		2	1846.9421
1098	DEPD2_MOUSE	1598	0.69	1	2	K.ISSGNIQER.V	0.9924		1	1004.0879
1099	DEPP_MOUSE	205	7.8	1	2	R.SRLLLPVPHLPTIR.E	0.9909		2	1613.0023
1100	DESM_MOUSE	469	27.93	6	52	R.ELQAQLQEQQVQVEMDMSKPDLTAALRDI	0.9958		3	3485.9526
						R.APSYGAGELLDFSLADAVNQEFLATR.T	0.9958		2	2757.0288
						R.TFGGAPGFSLGSPLSSPVFPR.A	0.9958		2	2079.3629
						R.FLEQQNAALAAEVNR.L	0.9958		2	1674.854
						R.HQIQSYTCEIDALK.G	0.9958		2	1706.8591
						R.RIESLNEEIAFLK.K	0.9958		2	1562.8064
1101	DEST_MOUSE	165	44.85	5	150	K.EILVGDVGATITDPFK.H	0.9958		2	1675.9195
						R.KEELMFFLWAPEQAPLK.S	0.9958		2	2078.4767
						K.HEYQANGPEDLNR.T	0.9958		2	1543.5925
						R.YALYDASFETK.E	0.9944		1	1308.4302
						K.HFVGMLPEK.D	0.9958	1,2		1058.2836
1102	DGAT1_MOUSE	498	9.64	2	3	R.LLKLAVPNHLIWLIFFYWFFHSCLNAVAELL	0.9958		3	4394.1761
						R.LFLENLIK.Y	0.9924		1	990.2309
1103	DGKG_MOUSE	788	4.44	1	7	R.KFHYLLNPEQVFNLDNGGPTPGLNFFHDTI	0.9929		3	3849.256
1104	DGKZ_MOUSE	929	4.31	2	6	R.STAPLHSDQQPVPEQLR.I	0.993		2	1904.0898
						R.AEPNPEAGPEERDDGATDR.L	0.9958		2	2027.0251
1105	DGUOK_MOUSE	277	28.16	3	6	K.THPEWQVATEPIAAWQNIQAAGAQK.D	0.9958		3	2747.0421
						K.LHFEALQHVPVLVLDVTEDFSENAAR.Q	0.9958		2	2951.3085
						K.GIELAYLQQLHSQHEDWFINK.T	0.9958		2	2570.8669

1106	DHB4_MOUSE	735	37.28	13	92	K.NNIHCNTIAPNAGSR.M	0.9958	2	1639.7343
						K.ALHGEQYLELYKPLPR.S	0.9958	2	1928.2413
						R.ILMTSSASGIYGNFGQANYSAAK.L	0.9958	2	2352.6239
						R.FAKPVYPGQTLQTEMWK.E	0.9958	2	2025.3728
						K.LPSFSSSYTELQSIMYALGVGASVK.N	0.9958	2	2637.0198
						K.SMMNGGLAEVPGLSFNFAK.A	0.9958	2	1971.2966
						K.AAVAVPNRPPDAVLR.D	0.9958	2	1546.813
						K.VHETGDVVISNAYVDLVPASGVSTQTPSEC	0.9958	3	4487.9213
						R.TSHAAPAATSGFVGAVGHK.L	0.9958	2	1766.9541
						R.AYALAFAERGALVIVNDLGGDFK.G	0.9904	2	2411.763
						K.ICDFSNASKPQTIQESTGGIVEVLHK.V	0.9958	2	2860.1596
						K.RNQPMTPEAVR.D	0.9944	2	1299.4906
						R.KNNIHCNTIAPNAGSR.M	0.9958	2	1767.9084
1107	DHB5_MOUSE	323	17.03	2	5	R.VCLEQSLKQLQLDYVDLYLIHFPMAMKPGE	0.9944	3	4196.9187
						K.ENMQVFEFQLTSEDMK.V	0.9958	2	1977.2111
1108	DHB8_MOUSE	260	27.69	4	29	K.HAAFQADVSQGPAAR.R	0.9958	2	1526.6517
						R.CNSVLPGFIATPMTQK.M	0.9958	2	1765.0437
						K.GTFLVTQAAAQALVSSGGR.G	0.9917	2	1835.0702
						R.DEFLLHMSEEDWDR.V	0.9958	2	1822.9434
1109	DHDDS_MOUSE	333	4.2	1	2	R.EGLQASGDAQLR.R	0.9958	1	1245.3347
1110	DHDH_MOUSE	333	27.03	4	52	K.ESPVVPLAESELLAEILEEAR.K	0.9958	2	2295.5921
						R.WGIVSAGLIANDFTTVLSSLPSSEHQVVAV	0.9958	3	3397.8559
						R.AEFGFDLSHIPR.A	0.9958	2	1389.5535
						K.AVLCEKPMGVNAAEVR.E	0.9958	2	1745.0131
1111	DHE3_MOUSE	558	36.38	13	79	K.HGGTIPVVPTAEFQDR.I	0.9958	2	1724.9139
						K.IIAEGANGPTTPEADK.I	0.9958	2	1584.7233
						K.VYEGSILEADCDILIPAASEK.Q	0.9958	2	2294.5269
						K.KGFIGPGIDVPAPDMSTGER.E	0.9958	2	2045.3178
						R.DSNYHLLMSVQESLER.K	0.9958	2	1922.1199
						K.TFVVQGFGNVGLHSMR.Y	0.9958	2	1750.0282
						K.GFIGPGIDVPAPDMSTGER.E	0.9958	2	1917.1437
						R.GVFHGIENFINEASYMSILGMTPGFGDK.T	0.9958	2	3033.4433
						K.LQHGSILGFPK.A	0.9958	2	1197.4227
						K.VYEGSILEADCDILIPAASEKQLTK.S	0.9958	3	2765.0962
						R.RDDGSWEVIEGYR.A	0.9958	2	1582.6695
						K.NLNHVSYGR.L	0.9958	2	1060.1575
						K.DIVHSGLAYTMER.S	0.9958	2	1492.6898

1112	DHI1_MOUSE	292	5.14	1	2	K.SPLTPILLGNPGR.K	0.9958	2	1335.5895
1113	DHI2_MOUSE	386	4.92	1	2	R.GLGLMYFIHHYLPEGLR.R	0.9958	2	2017.399
1114	DHPR_MOUSE	241	70.54	8	231	K.RPNSGSLIQVVTTDGK.T	0.9958	2	1672.879
						K.MTDSFTEQADQVTADVGK.L	0.9958	1,2	1944.0772
						K.GAVHQLCQSLAGK.N	0.9958	2	1369.5297
						K.QSMWTSTISSHLATK.H	0.9958	2	1678.9006
						K.SMPEADFSSWTPLEFLVETFHDWITGNK.R	0.9958	3	3286.6393
						K.NSGMPPGAAAIAVLPVTLDTPMNR.K	0.9958	2	2394.8097
						R.NWWVASIDVVENEEASASVVVK.M	0.9958	2	2432.6922
						K.EGGLLTLAGAKAALDGTPGMIGYGMAK.G	0.9944	3	2565.018
1115	DHR11_MOUSE	260	50	8	31	R.LALVTGASGGIGAAVAR.A	0.9958	2	1484.7391
						R.NIDDGHIININSMCGHR.V	0.9958	2	1967.1327
						R.CDLSNEEDILSMFSAVR.S	0.9957	2	1987.1549
						K.SAGYPGTLIPYR.C	0.9944	1	1295.4808
						R.QELLEAQTHIR.A	0.9943	2	1338.5064
						R.ATCISPGLVETQFAFK.L	0.9958	2	1770.0014
						R.SQHSGVDICINNAGMARPDTLLSGSTSGW	0.9944	3	3161.4395
						R.DRLALVTGASGGIGAAVAR.A	0.9944	2	1756.0152
1116	DHRS1_MOUSE	313	12.46	2	3	K.MKPDFSSAESPEMSGK.C	0.9958	2	1728.9295
						R.HGVSYVSLWPGLVQTEMVK.E	0.9958	2	2131.4974
1117	DHRS4_MOUSE	260	48.85	9	82	R.AVATLQGEGLSVTGIVCHVGK.A	0.9958	2	2097.3856
						R.FPSLGPYNVSK.T	0.9958	2	1209.3873
						R.LAEDGAHVVVSSR.K	0.9958	2	1340.4789
						K.TALLGLTK.N	0.9958	1	817.0165
						R.VNCLAPGLIK.T	0.9937	2	1085.2982
						R.RLAEDGAHVVVSSR.K	0.9958	2	1496.6664
						R.GGGSVVIVGSVAGFTR.F	0.9909	2	1463.6768
						R.LGKPEDCAGIVSFLCSEDASYINGETVVVG	0.9958	3	3857.1953
						R.RLGKPEDCAGIVSFLCSEDASYINGETVVV	0.9958	3	3900.2233
1118	DHRS9_MOUSE	319	7.21	1	3	K.YVFITGCDTGFGNLAARTFDK.K	0.9912	2	2354.5903
1119	DHRSX_MOUSE	335	8.06	2	2	R.ILDAR.G	0.9958	1	587.697
						R.QLARLGMCVVVAGNDEHR.G	0.9952	2	2026.2873
1120	DHSA_MOUSE	664	79.52	36	1609	R.ACALSIAESCRPGDK.V	0.9958	2	1635.7467
						K.VRVDEYDYSKPIQGQQK.K	0.9924	2	2054.267
						K.HVNGQDQIVPGLYACGEAACASVHGANR.I	0.9958	3	2953.1327
						K.SMQNHAAVFR.V	0.9958	1,2	1161.3238
						R.AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	0.9958	3	3368.6687

						K.EPIPVLPTVHYNMGGIPTNYK.G	0.9958		2	2341.7302
						R.AAFGLSEAGFNTACLTK.L	0.9958	1,2		1758.9348
						K.ISQLYGDLK.H	0.9944		1	1037.201
						K.GSDWLGDQDAIHYMTEQAPASVVELENYG	0.9958		2	3816.1647
						K.VSDAISTQYPVVDHEFDAVVVGAGGAGLR.	0.9958	2,3		2931.2316
						R.TYFSCTSAHTSTGDGTAMVTR.A	0.9958		2	2252.3833
						R.LPGISETAMIFAGVDVTK.E	0.9958		2	1850.1804
						R.LGANSLLDLVVFGR.A	0.9958		2	1474.7434
						R.GMVWNTDLVETLELQNLMLCALQTIYGAE/	0.9958	2,3		3555.0646
						K.VTLEYRPVIDK.T	0.9958	1,2		1333.5706
						K.HTLSYVDIK.T	0.9958		1	1076.2377
						R.WHFYDTVK.G	0.9958		2	1096.2303
						K.TLNEADCATVPPAIR.S	0.9958		1	1628.7888
						K.NTVIATGGYGR.T	0.9958		2	1109.2272
						R.VDEYDYSKPIQGQQK.K	0.9924		1	1798.9469
						R.AFGGQSLK.F	0.9924		1	807.9249
						K.ANAGEESVMNLDK.L	0.9958		1	1378.4968
						R.VGSVLQEGCEK.I	0.9958		1	1206.3044
						R.SHTVAAQGGINAALGNMEEDNWR.W	0.9958		2	2442.625
						K.DHVYLQLHHLPPEQLATR.L	0.9958		2	2168.463
						R.TGHSLLHTLYGR.S	0.9958	1,2		1355.5393
						R.GCGPEKDHVYLQLHHLPPEQLATR.L	0.9958		2	2797.1119
						R.ACALSIAESCRPGDKVPSIK.A	0.9958		2	2160.4077
						R.KHTLSYVDIK.T	0.9958		1	1204.4117
						R.LPGISETAMIFAGVDVTKEPIPVLPTVHYNM	0.9958		3	4172.8874
						K.KPFGEHWR.K	0.9958	1,2		1057.1997
						R.GVIALCIEDGSIHR.I	0.9958		2	1540.7258
						R.YDTSYFVEYFALDLLMENGECR.G	0.9958		2	2736.9754
						R.AKNTVIATGGYGR.T	0.9958		2	1308.4801
						K.VTLEYRPVIDKTLNEADCATVPPAIR.S	0.9958		3	2943.3361
						R.AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	0.9958		3	4680.0859
1121	DHSB_MOUSE	282	49.65	14	372	K.DLVPDLSNFYAQYK.S	0.9958		2	1673.8627
						K.LQDPFSVYR.C	0.9958	1,2		1125.2694
						R.MQTYEVDLNK.C	0.9958		1	1241.4015
						K.IKNEVDSTLTFR.R	0.9958	1,2		1423.6091
						K.YLGPAVLMQAYR.W	0.9958	1,2		1382.6635
						R.CHTIMNCTQTCPK.G	0.9958		2	1651.7733

						K.IYPLPHMYVIK.D	0.9937	2	1374.7271
						R.WMIDSR.D	0.9944	1	807.9427
						R.IDTDLSK.V	0.9924	1	791.8767
						K.CGPMVLDALIK.I	0.9958	1	1217.4755
						K.NEVDSTLTFR.R	0.9958	1	1182.2755
						R.GAQTAAAAAPR.I	0.9958	1	985.0879
						R.WDPDKTGDKPR.M	0.9958	2	1315.4282
						R.RIDTDLSK.V	0.9945	2	948.0641
1122	DHSO_MOUSE	357	31.09	7	55	K.GENLSLVVHGPGDIR.L	0.9958	2	1563.7538
						R.LENYPIPELGPNDVLLK.M	0.9958	2	1925.2322
						K.AMGAAQVVVTDLSASR.L	0.9958	2	1576.8083
						K.KPMVLGHEAAGTVTK.V	0.9958	2	1539.8333
						K.VLVCGAGPVGMVTLLVAK.A	0.9958	2	1785.2049
						K.KPMVLGHEAAGTVTKVGELVK.H	0.9958	2	2165.5994
						K.MHSVGICGSDVHYWEHGR.I	0.9958	2	2128.2953
1123	DHTK1_MOUSE	921	5.21	2	3	R.YPAAVSTLEEMAPGTAFKPVIGDSSVDPKN	0.9958	3	3320.7822
						R.NFRKPLIVASPK.M	0.9958	1	1370.6811
1124	DHX29_MOUSE	1365	4.98	4	4	R.VCEELGCESGPGGRNSLCGYQIR.M	0.9958	3	2599.7151
						K.LTPLGQHLAALPVNVKIGK.M	0.9958	2	1970.4092
						K.KKPAPATEAESALNLNLFEK.S	0.9958	2	2172.4863
						K.LTPLGQHLAALPVNVK.I	0.9958	2	1672.0238
1125	DHX30_MOUSE	1217	5.83	3	3	R.LESKPPARGGALLFCTVGILLR.K	0.9924	3	2369.8223
						K.DSGPLSDPITGKPYMPLSEAEEVRLSQSLL	0.9958	3	3816.3179
						R.LQSDDILPLGKDSGPLSDPITGKPYMPLSEA	0.9944	3	3770.2434
1126	DHX57_MOUSE	1388	5.33	3	8	R.ATLQVILMSATLDAGLFSK.Y	0.9958	2	1980.3704
						K.IIISTNIAETSITIDDVVYVIDSGKMK.E	0.9958	3	2940.4193
						K.YPYQAPLVAFYSTNENLPLACR.L	0.9958	2	2588.8884
1127	DHX9_MOUSE	1380	2.54	2	2	K.NELTYQMEQDHNLQSVLQER.E	0.9958	2	2476.6801
						K.VFDPVPDGVTK.V	0.9944	1	1174.3391
1128	DI3L1_MOUSE	1053	3.04	2	6	R.NRSIHGDVVVVEMLPK.S	0.9956	2	1794.1223
						K.EEVQSQGKNAQK.I	0.9958	1	1346.4398
1129	DIAC_MOUSE	366	13.93	2	5	R.FHQVWYDNPQSISLK.A	0.9958	2	1863.0825
						R.GIGMWNANCLDYSDDALAREQTQEMWGA	0.9958	3	3699.0731
1130	DIAP3_MOUSE	1171	4.7	2	2	K.MSSFVISANEQYEK.L	0.9924	2	1633.8133
						R.VSLTSHPVSWVQSFGHEGLGLLLDILEKLIN	0.9944	3	4087.7087
1131	DIDO1_MOUSE	2256	2.39	2	11	R.AAPEKSAAPLLDVFSSMLK.D	0.9958	1	1976.3386
						K.VSATERPADFTTDASSASLVEQQKMLEELN	0.9958	3	3397.7357

1132	DIXC1_MOUSE	711	1.13	1	2	K.EMEEAK.K	0.9958	1	736.8151
1133	DJB11_MOUSE	358	22.63	4	6	R.GDDLYTNVTVSLVEALVGFEMDITHLDGHK	0.9958	3	3290.6692
						K.FQDLGAAYEVLSDSEK.R	0.9921	2	1772.9061
						K.QLLKQGPVQK.V	0.9958	1	1139.3836
						K.LALQLHPDRNPDDPQAQEK.F	0.9932	2	2186.3891
1134	DJB12_MOUSE	376	4.79	1	2	K.FHPDKNHAPGATEAFK.A	0.9944	2	1767.9413
1135	DJC11_MOUSE	559	12.52	4	17	K.GWGELEFGAGDLQGPLFGLK.L	0.9958	2	2092.3587
						R.LFNLVHQAYEVLSDPQTR.A	0.9958	2	2131.3959
						R.GVLHQVMVPDSEALR.I	0.9958	2	1651.9213
						R.LCMLYHPDK.H	0.9952	2	1177.3699
1136	DKC1_MOUSE	509	9.63	2	5	R.LHNAIEGGTQLSRALETLTGALFQRPPLIAA	0.9958	3	3488.0708
						K.SQQSAGKEYVGIVR.L	0.9958	2	1522.7013
1137	DLDH_MOUSE	509	75.44	27	3207	R.LGADVTAVEFLGHVGGIGIDMEISK.N	0.9958	2	2529.911
						K.VVHVNGFGK.I	0.9958	1	957.1203
						R.RPFTQNLGLEELGIELDPK.G	0.9944	3	2170.4704
						K.ALTGGIAHLFK.Q	0.9958	2	1128.3598
						K.IPNIYAIGDVVAGPMLAHK.A	0.9958	2,3	1980.3758
						K.NETLGGTCLNVGCIPSK.A	0.9958	1,2	1820.9697
						K.SEEQLKEEGIEFK.I	0.9958	1	1566.7051
						K.GRIPVNNR.F	0.9931	2	926.0665
						R.VLGAHILGPGAGEMVNEAALALEYGASCEI	0.9958	2,3	3356.7413
						R.VCHAHPTLSEAFR.E	0.9958	2	1525.6733
						R.EANLAAAFGKPINF.-	0.9958	1	1463.6763
						R.GIEIPEVR.L	0.9958	1	913.0617
						K.NILVATGSEVTPFPGITIDEDTIVSSTGALSL	0.9958	3	3347.7845
						K.AEDEGIICVEGMAGGAVHIDYNCVPSVIYTH	0.9958	3	4245.6823
						K.FPFAANSR.A	0.9958	1	910.0201
						K.LVVIGAGVIGVELGSVWQR.L	0.9958	2,3	1953.3353
						R.FQTKIPNIYAIGDVVAGPMLAHK.A	0.9958	3	2484.9623
						K.IDVSVEAASGGK.A	0.9958	1	1133.2438
						R.IPVNNR.F	0.9958	1	712.8271
						K.AEVITCDVLLVCIGR.R	0.9944	2	1718.9636
						K.ALLNNSHYYHMAHGK.D	0.9958	2	1756.9793
						K.NQVTATKADGSTQVIDTK.N	0.9958	2	1878.0465
						K.ALTGGIAHLFKQNK.V	0.9958	2	1498.7684
						K.IGKFPFAANSR.A	0.9958	2	1208.4056
						K.STDRVLGAHILGPGAGEMVNEAALALEYGA	0.9958	3	3816.2007

						K.ALLNNSHYYHMAHGKDFASR.G	0.9958	2	2333.5889
						K.TVCIEKNETLGGTCLNVGCIPSK.A	0.9958	2	2551.7952
1138	DLG1_MOUSE	905	12.93	6	7	K.QIIEEQSGPYIWVPAKEK.L	0.9958	3	2116.4216
						K.GLGFSIAGGVGNQHIPGDNSIYVTK.I	0.9958	2	2502.7893
						R.YQDEEVLPPEHISPQVTNEVLGPELVHVSE	0.9958	3	3513.8829
						K.SMENIMEMNK.R	0.9958	1	1227.4513
						K.HCILDVSGNAIK.R	0.9958	2	1327.4894
						R.ALHLLEEYR.S	0.9943	2	1144.3158
1139	DLG3_MOUSE	849	0.94	1	2	K.DIQDNK.F	0.9958	1	732.7685
1140	DLG7_MOUSE	808	3.22	2	6	K.QLQKLK.E	0.9924	1	757.9517
						R.EVESLPATAPAQGKER.K	0.991	2	1683.8589
1141	DLRB1_MOUSE	96	55.21	3	21	K.STMDNPTTTQYANLMHNFILK.A	0.9958	2	2441.7792
						K.GVQGIIVVNTEGIPIK.S	0.9958	2	1637.9603
						R.EIDPQNDLTFLR.I	0.9945	2	1461.6146
1142	DMD_MOUSE	3678	3.26	6	10	R.RPQLEELITAAQNLK.N	0.994	2	1724.9981
						R.WTEDRWIVLQDILLK.W	0.9958	2	1929.2694
						K.ALRGEIAPLK.E	0.9944	1	1068.3048
						K.SILMYITSLFQVLPQQVSIEAIQEVEMLPRTS	0.9958	3	3881.5783
						K.WIIHADELLDESEK.K	0.9958	2	1698.87
						R.DFGPASQHFLSTSVQGPWER.A	0.9958	2	2247.4313
1143	DMXL2_MOUSE	3032	0.96	2	2	R.NLASPEGTLATLGLK.T	0.9945	2	1485.7209
						R.NSQLKCQWLK.T	0.9958	1	1305.4857
1144	DNER_MOUSE	737	4.48	2	18	R.QDANSLLILLWK.V	0.9924	1	1414.6879
						R.QLQPVPATQEPDIILPR.S	0.9958	2	1916.2279
1145	DNJA1_MOUSE	397	18.14	3	15	R.TIVITSHPGQIVK.H	0.9958	2	1393.6695
						K.ITFHGEGDQEPGLEPGDIIIVLDQKDHAVFT	0.9944	3	3548.9341
						K.ETTYYDVLGVKPNATQEELKK.A	0.9958	2	2427.7136
1146	DNJA2_MOUSE	412	33.25	7	33	K.LYDILGVPPGASENELK.K	0.9958	2	1816.0612
						K.LSELEDLLPSRPEVPNVIGETEEVELQEFDS	0.9958	3	3772.1114
						R.ITFTGEADQAPGVEPGDIVLLLQEK.E	0.9958	2	2641.9781
						K.VSLEDLYNGK.T	0.9944	2	1138.2627
						K.EISFAYEVLSNPEK.R	0.991	2	1626.8034
						K.FDVQFPENNWINPDK.L	0.9954	2	1864.0239
						K.VIEPGCVRVVR.G	0.9924	1	1284.5107
1147	DNJA3_MOUSE	480	41.67	12	91	K.FSQLAEAYEVLSDEVK.R	0.9958	1,2	1829.0136
						K.AQGLYETINVTIPAGIQTDQK.I	0.9958	2	2261.537
						K.QYDAYGSAGFDPGTSSSGQGYWR.G	0.9958	2	2458.5187

						R.GSIITNPCVVCR.G	0.9958	2	1376.528
						K.RVTIPVPAGVEDGQTVR.M	0.9958	2	1795.0488
						R.DGADIHSDLFISIAQAILGGTAK.A	0.9958	2	2314.6005
						K.IFGEFSSSPFGDFQNVFDQPQEYIMELTFN	0.9958	3	3934.3247
						R.KIFGEFSSSPFGDFQNVFDQPQEYIMELTF	0.9958	3	4062.4988
						R.VTIPVPAGVEDGQTVR.M	0.9944	2	1638.8613
						R.INSYGYGDHYIHIK.I	0.9958	2	1680.8601
						K.FSQLAEAYEVLSDEVKR.K	0.9958	2	1985.2011
						K.VQHCHYCGGSGMETINTGPFVMR.S	0.9958	2	2639.8954
1148	DNJA4_MOUSE	397	31.23	6	10	K.IQLSEALCGFK.K	0.9958	2	1266.4461
						K.NVVHQLSVTLEDLYNGITK.K	0.9958	2	2144.4325
						K.ILFHGEGDQEPELDPGDVIIVLDQK.D	0.9958	2	2778.0881
						K.LPQLEALLPPR.Q	0.9956	2	1247.5235
						R.GMQVHIQQIGPGMVQQIQTVCIECK.G	0.9944	3	2884.3139
						K.ETQYYDILGVKPSASPEEIKK.A	0.9958	2	2396.6996
1149	DNJB4_MOUSE	337	22.85	4	10	R.EGDETPNSIPADIVFVIK.D	0.9958	2	1945.1767
						R.LKQDPPIIHELK.V	0.9924	2	1431.7184
						R.NLPMSVTDIVKPGMR.R	0.9957	2	1659.0149
						R.DSEEMEIDGDPFSAFGFSMNGYPR.D	0.9958	2	2699.8795
1150	DNJC3_MOUSE	504	5.95	2	2	K.AISDLKAASK.L	0.9944	1	1004.1717
						K.LALQWHPDNFQNEEEK.K	0.9958	2	1999.1467
1151	DNJC5_MOUSE	198	9.6	1	2	R.SLSTSGESLYHVLGLDK.N	0.9958	2	1807.0105
1152	DNL3_MOUSE	1015	9.16	3	3	K.HVLDALDPNAYEAFKASR.N	0.9944	2	2018.2364
						K.DYIPKAFPGGQSMILDSEVLLIDNNTGKPLF	0.9958	3	4184.8402
						R.KFSGFSAAKPNNSEQAPSSPAPGTSLSASI	0.9958	3	2952.2071
1153	DNLZ_MOUSE	177	6.78	1	2	K.RNIEEILAAR.G	0.9958	2	1185.3689
1154	DNM1L_MOUSE	742	41.24	16	203	K.GHAVNLLDVPVPVAR.K	0.9958	2	1557.8362
						K.LQDVFNTVGADIIQLPQIVVVGTQSSGK.S	0.9958	2,3	2928.3556
						R.TLESVDPLGGLNTIDILTAIR.N	0.9958	2	2212.5486
						K.VPSALAPASQEPPPAASAEADGK.L	0.9958	2	2162.3611
						K.SSLLDDLLTESEDMAQR.R	0.9958	2	1924.087
						K.VFSPNVVNLTLVDLPGMTK.V	0.9958	2	2045.4449
						K.LYTDFDEIRQEIENETER.I	0.9958	2	2301.4283
						K.LDLMDAGTDAMDVLMGR.V	0.9958	2	1825.1202
						K.ALQGASQIIAEIR.E	0.9958	2	1370.5919
						R.IIQHCSNYSTQELLR.F	0.9958	2	1863.0465
						K.SVTDSIRDEYAFLQK.K	0.9958	2	1772.9524

						K.SKPIPIMPASPQK.G	0.9958		2	1394.7155
						K.LHDAIVEVVTCLLR.K	0.9958		2	1638.914
						R.INVLAAQYQSLLNSYGEPVDDK.S	0.9958		2	2438.6965
						K.AVMHFLVNHVK.D	0.9958	1,2		1295.5883
						R.RPLILQLVHVSPEDK.R	0.9958		2	1745.0751
1155	DNM3A_MOUSE	908	1.87	1	3	R.SWSVPVIRHLFAPLK.E	0.9958		2	1751.1276
1156	DNMBP_MOUSE	1580	3.04	2	2	R.GPATDITTASQGDSLDLDSKLTQQLIEFEK.	0.9958		3	3223.5151
						K.QDDPSRAETLETLR.S	0.9958		2	1631.7398
1157	DNMT1_MOUSE	1620	4.44	3	5	K.EYEPIFGLMQEK.I	0.9944		1	1484.707
						R.VPALASPAGSLPDHVR.R	0.9958		2	1587.8191
						R.TLDVFSGCGGLSEGFHQAGISETLWAIEM\	0.9944		3	4157.5691
1158	DOCK1_MOUSE	1865	3.27	2	2	K.FAATPSLALFVNLKNVVCK.I	0.9958		2	2093.4833
						K.GNMADYGNLMENQDMMVSPTSPPPPPPQ	0.9944		3	4146.7153
1159	DOCK2_MOUSE	1828	0.88	1	2	K.VQSMNEIVQSNLFK.K	0.9924		2	1637.8914
1160	DOCK3_MOUSE	2027	4.24	3	3	K.LSPACSGTSTPRGNVLASHSPMSPENIK.M	0.9931		3	2897.1988
						R.EMMLLLPTHRDRPSSAMYPAAILENGQPPI	0.9944		3	3783.376
						K.ELMQEQVHVLGVGLAVHEK.F	0.9958		3	2117.4711
1161	DOCK6_MOUSE	2080	3.13	3	3	K.MLVTMSLSSLVGTTQNFSEEHLRK.S	0.9958		2	2710.1359
						R.WAADLALPQLGRLLDLLYLCLAAFEYK.G	0.9958		3	3138.6862
						R.RPSSLLRR.L	0.9924		1	985.1776
1162	DOCK9_MOUSE	2055	3.31	4	4	R.YELIADIYK.L	0.9924		1	1128.3104
						R.NPEKSNSLDK.Q	0.9944		1	1132.2157
						R.VAFFGQAAQYQFTDSETDVEGFFEDEDGK	0.9958		3	3976.2111
						R.YPDNKVK.L	0.9958		1	863.989
1163	DOHH_MOUSE	302	29.14	3	6	R.HEAGEALGAIGNPEVLGLLK.Q	0.9958		2	1989.2792
						R.HEVGYVLGQLQHEAAVPGLAATLAR.T	0.9958		2	2601.9682
						R.EHIEDPEQVVRESCEVALDMYEYESSQDF	0.9958		3	4468.6823
1164	DOK7_MOUSE	504	7.34	1	2	R.DPSPASQGSSDHGSATDLGGQAPTGCPS	0.9958		3	3469.5884
1165	DOP2_MOUSE	2295	3.62	5	10	K.AATEWGVDQVVVELVGSK.E	0.9958		2	1888.1277
						R.ILEPMLLLLLQPK.T	0.9958		1	1521.9855
						R.NAKNAILEELPR.I	0.9958		2	1368.576
						K.EAAQLNLAPPGYFLLLSMLNDFVTRTPNLE	0.9958		3	3565.1218
						K.EAAQLNLAPPGYFLLLSMLNDFVTR.T	0.9958		3	2795.269
1166	DOPD_MOUSE	118	21.19	1	2	K.STEPCAHLLVSSIGVVGTAEQNR.T	0.9958		2	2426.655
1167	DP13A_MOUSE	707	18.67	6	12	R.IYDAQNELSAATHLTSK.L	0.9958		2	1863.0343
						R.VNQSALEAVTPSPSFQQR.H	0.9958		2	1960.1539
						K.SETEDSILHQLFIVR.F	0.9958		2	1788.0104

						K.LPIEETLEDSPQTR.S	0.9958		2	1628.7765
						R.LIAASSRPNQAGSEGQLVLSSSQSEESDLC	0.9924		3	3462.6629
						K.EILTLKEVFQIASNDHDAAINR.Y	0.9944		2	2498.7984
1168	DP13B_MOUSE	662	4.98	2	3	K.LNQTALQAVTPITSFGK.K	0.9958		2	1790.0697
						R.QIYLTDNPEAVAIK.L	0.9957		2	1575.8021
1169	DPEP1_MOUSE	410	48.29	10	144	K.AGFVGGQFWSAYMPCDTQNK.D	0.9958		2	2265.4707
						K.VASLIGVEGGHLIDSSLGVLR.T	0.9944	2,3		2093.4313
						R.LGVMIDLSHVSVATMK.D	0.9958		2	1702.0803
						R.YLTLTHNCNTPWADNWLVDR.G	0.9958		2	2490.7033
						R.TTPVIDGHNDLPWQLLNLFNNQLLRPDADL	0.9958		3	3687.1497
						R.YLTLTHNCNTPWADNWLVDRGDDEAESH(	0.9958		3	4018.2702
						K.VAGAGAVGLGGDYDGVTMLPVGLEDVSK\	0.9958		3	3833.3888
						K.LAQTHTNIPK.L	0.9944		2	1123.2975
						K.KVAGAGAVGLGGDYDGVTMLPVGLEDVSI	0.9958	2,3		2777.1621
						K.RILEQMDVIHR.M	0.9958		2	1410.6775
1170	DPH2_MOUSE	489	10.84	2	2	R.LLLGWTPGRPFFSCCPDTGQTQDQGAKA(	0.9958		3	3323.6245
						R.VTLQFPDQLLGDAGAVAAR.L	0.9958		2	1943.2101
1171	DPH5_MOUSE	281	14.23	2	2	R.YMSVNQAAQQLLEIVQNHR.A	0.9944		2	2243.5456
						R.ARGEEPAITEETLCVGLAR.V	0.9944		2	2073.2769
1172	DPOG1_MOUSE	1239	6.54	2	2	R.YSWTSQLSPADLIPLGGSTSASSSTKQDG(	0.9924		3	4552.9121
						R.ALVFDVEVCLAEGTCPTLAVAISPSAWYSW	0.9944		3	3874.2833
1173	DPOLA_MOUSE	1465	7.71	4	4	K.DMVQKMNLEVIYGDTDSIMINTNSTNLEEV	0.9958		3	3694.1783
						R.STGALLNPFSVHTPKAIPSGKPASPVLR.N	0.9958		3	2844.3298
						K.DCIFPCDFKEVISK.K	0.9944		1	1758.9411
						R.ICEPIDGIDAVLIALWLGLDSTQFRVHQYHK	0.9944		3	3610.1162
1174	DPOLB_MOUSE	335	2.99	1	2	R.IDIRLIPK.D	0.9958		1	968.2278
1175	DPOLL_MOUSE	573	5.41	2	2	R.ISAQAFNPGLLCVACGSYR.R	0.9917		2	2085.2996
						K.HYDDFLDR.M	0.9947		2	1081.1295
1176	DPOLM_MOUSE	496	7.26	2	5	R.RADAEALQQLIEAAVR.Q	0.9943		2	1754.9841
						R.YQTMKLFTQVFGVGVK.T	0.9944		3	1847.2256
1177	DPP10_MOUSE	797	5.65	2	17	R.YFLLENNSVMKETIQK.K	0.9958		2	1958.28
						K.EENLLIIHGTADTKVHFQHSAELIK.H	0.9944		3	2845.2279
1178	DPP3_MOUSE	738	29	12	29	K.RYEFQGNHFQVTR.G	0.9931		2	1682.8387
						K.NVSLGNVLAVAYAAK.R	0.9958		1	1490.7428
						K.GPSFDVQVGLHELLGHGSGK.L	0.9958		2	2035.2669
						K.ETVINPETGEQIQSWYR.S	0.9954		2	2051.22
						R.FPEDGPELEEVLIQLAAADAR.F	0.9958		2	2284.5279

						R.LASVLNTDPALDSELTSK.L	0.9958		2	1875.0832
						R.AGLLALEFYTPEAANWR.Q	0.9907		2	1923.1784
						K.LAQDFLDSQNLSAYNTR.L	0.9958		2	1957.1069
						R.YEFQGNHFQVTR.G	0.9932		2	1526.6512
						K.LIVQPNTRLEGSEVQLVEYEASAAGLIR.S	0.9958		3	3057.4741
						K.AYAANSHQEQMLAQYVESFTQGSIEAHK.F	0.9958		3	3140.4107
						R.LEGSEVQLVEYEASAAGLIR.S	0.9958		2	2135.3788
1179	DPP4_MOUSE	760	2.5	1	17	R.FRPAEPHFTSDGSSFYK.I	0.9958		2	1974.1393
1180	DPP9_MOUSE	862	8	3	5	R.LTFCHQGSAGVLDNPK.S	0.9958		2	1744.9109
						R.LQLVLLPPALFIPAVESEAQR.Q	0.9949		2	2305.7661
						R.FWASMMEAANCPPDYVPPEIFHFHTR.A	0.9958		3	3152.5374
1181	DPY30_MOUSE	99	47.47	3	17	K.ERPPNPIEFLASYLLK.N	0.9958		2	1888.2169
						K.VDLQSLPTRAYLDQTVVPILLQGLAVLAK.E	0.9958		3	3136.7459
						R.AYLDQTVVPILLQGLAVLAK.E	0.9958		2	2126.5877
1182	DPYL1_MOUSE	572	16.78	4	9	K.QIGENLIVPGGVK.T	0.9958		2	1324.5632
						K.MDENQFVAVTSTNAAK.I	0.9958		2	1726.8988
						R.NLHQSNFSLSGAQIDDNNPR.R	0.9958		2	2228.3427
						K.DLYQMSDSQLYEAFTFLKGLGAVILVHAEN	0.9958		3	4357.9221
1183	DPYL2_MOUSE	572	70.8	21	468	K.GTVVYGEPITASLGTDGSHYWSK.N	0.9958		2	2426.6446
						R.NLHQSGFSLSGAQIDDNIPR.R	0.9958		2	2170.3463
						K.AALAGGTTMIIDHVVPEPGTSLLAAFDQWR	0.9958		2	3139.5964
						R.ILDLGITGPEGHVLSRPEEVEAEAVNR.S	0.9958	2,3		2902.234
						R.KPFPDFVYK.R	0.9944		2	1141.355
						K.IVNDDQSFYADIYMEDGLIK.Q	0.9909		2	2350.602
						R.DIGAIAQVHAENGDIIAEEQQR.I	0.9958		2	2378.5608
						R.FQLTDSQIYEVLSVIR.D	0.9958		2	1912.1931
						K.IVLEDGTLHVTEGSGR.Y	0.9945		2	1683.8589
						K.DRFQLTDSQIYEVLSVIR.D	0.9958		2	2183.4692
						R.FQMPDQGMTSADDFFQGTK.A	0.9958		2	2152.3577
						R.ISVGSDADLVIWDPDSVK.T	0.9958		2	1917.1229
						R.MVIPGGIDVHTR.F	0.9958		2	1295.5425
						R.GLYDGPVCEVSVTPK.T	0.9958		2	1621.7937
						R.SITIANQTNCPLYVTK.V	0.9958		2	1824.0503
						K.THNSALEYNIFEGMECR.G	0.9958		2	2072.2227
						K.DNFTLIPEGTNGTEER.M	0.9958		2	1793.8846
						K.AAAFVTSPPLSPDPTTPDFLNSLLSCGDLQ	0.9958		3	4637.0456
						K.SAAEVIAQAR.K	0.9958		1	1016.1423

						R.GSPLVVISQGK.I	0.9944	1	1085.2889
						K.SCCDYSLHVDITEWHK.G	0.9958	2	2051.1518
1184	DPYL3_MOUSE	570	32.81	8	57	R.IAVGSDSDLVIWDPDALK.I	0.9958	2	1915.1504
						R.NLHQSGFSLSGTQVDEGVR.S	0.9958	2	2032.1771
						K.NHQSVAEYNIFEGMELR.G	0.9958	2	2038.2421
						K.AAAFVTSPPLSPDPTTPDYINSLLASGDLQI	0.9958	3	4536.9594
						R.AITVASQTNCPLYVTK.V	0.9958	2	1766.9983
						K.GNVVFGEPITASLGIDGTHYWSK.N	0.9958	2	2449.7252
						K.IMLEDGNLHVTQGAGR.F	0.9958	2	1711.9335
						K.MVIPGGIDVHTHFQMPYK.G	0.9958	2	2071.4627
1185	DPYL4_MOUSE	572	8.04	2	4	R.GVVVFGEPITASLGTDGSHYWSK.N	0.9958	3	2408.6727
						K.TIDAHGLMVLPGGVDVHTR.L	0.9952	2	1989.3
1186	DREB_MOUSE	706	5.52	2	2	K.LAASGEGGLQELSGHFENQK.V	0.9958	2	2073.2267
						K.YVLINWVGEDVPDAR.K	0.9909	2	1746.9603
1187	DRG2_MOUSE	364	11.26	2	3	R.VGLTHTMEHEDVIQIVK.K	0.9958	2	1950.2604
						K.GANIQLLDLPGIIEGAAQGR.G	0.9958	2	2007.2975
1188	DSC2_MOUSE	902	3.33	2	4	R.ELIDKYQLLIK.V	0.9958	1	1376.6793
						R.LGDKVQFCHTDDNQK.L	0.9958	2	1805.9079
1189	DSEL_MOUSE	1207	3.98	2	4	R.SGHFHLLRGWLQSLVQDTK.L	0.9958	2	2223.5424
						K.MFWFDHHGNSPVANIQEAEQAAEFK.K	0.9924	3	2905.1731
1190	DSG4_MOUSE	1041	3.17	2	2	K.ILDVNDNFPILEK.T	0.9924	1	1530.7612
						R.FAPVPEGGEGVMQPWR.I	0.9958	2	1758.0044
1191	DTBP1_MOUSE	352	5.11	1	3	K.ELEAFKAELDTEHTQK.A	0.9958	2	1890.0569
1192	DTD1_MOUSE	209	13.88	1	3	K.GNKPDFHLAMPTEQAESFYNSFLEQLR.K	0.9944	3	3171.5109
1193	DTD2_MOUSE	168	26.79	2	7	K.HVSILDLPGDVLIIPQATLGGR.V	0.9958	2	2285.6921
						R.LQVRPADGDAAAQWVEIRR.G	0.9909	2	2152.4208
1194	DTYMK_MOUSE	227	8.37	1	2	K.KTELEDHSVHLLFSANR.W	0.9958	2	1997.2181
1195	DUS10_MOUSE	483	10.77	3	5	K.GGLSSFKQNHGNLCDNSLQLQECR.E	0.9958	2	2763.9159
						R.IFSKEIIVYDENTNEPSR.V	0.9943	2	2155.3691
						K.EPLVLKGGLSSFK.Q	0.9918	2	1375.6512
1196	DUS2_MOUSE	318	6.6	1	3	R.APGTPAAALACLLPDRALR.A	0.9958	2	1935.2432
1197	DUS23_MOUSE	150	32	3	5	R.LPAHYQFLLDQGVR.H	0.9958	2	1657.9126
						R.LRPGSIETYEQEK.A	0.9958	2	1550.7087
						R.GPPHSDSCPGLTLHR.M	0.9958	2	1631.7545
1198	DUS27_MOUSE	1138	0.88	1	11	K.GEDTVLAK.K	0.9958	1	832.9292
1199	DUS3_MOUSE	185	55.14	6	45	R.VYVGNASVAQDITQLQK.L	0.9958	2	1835.0672
						K.LGITHVLNAAEGR.S	0.9958	2	1351.5485

						R.ATDFIDQALAHK.N	0.9958	2	1330.4832
						R.EIGPNDGFLAQLCQLNDR.L	0.9958	2	2061.2249
						R.SFMHVNTSASFYEDSGITYLGIK.A	0.9958	2	2568.8604
						K.ANDTQEFNLSAYFER.A	0.9932	2	1805.8981
1200	DVL1_MOUSE	695	4.32	1	5	K.AYAVVGGPPGGPPVRELAAVPPELTGSR.(	0.9958	2	2716.1124
1201	DX26B_MOUSE	861	1.86	1	5	K.MENGQSPPDGFLLK.S	0.9922	2	1533.7393
1202	DYH12_MOUSE	2954	2.17	2	2	R.IQETIDEWLKVQAQWLYLEPIFCSEDIMQQI	0.9958	3	4456.0073
						K.WVVFDGPIDTLWIESMNTVLDDNK.K	0.9944	3	2809.1628
1203	DYH17_MOUSE	4481	2.54	5	10	K.DVEALGK.K	0.9924	1	731.8241
						K.LIGAEENMALLTEFFDK.I	0.9943	2	1942.2342
						R.YFIDLLMEK.A	0.9958	1	1172.4248
						R.YSVMLEMFNTELDNAKLMYDAQMAASADC	0.9958	3	4045.6476
						K.GYHEYIDENLPPESPYLYGLHPNAEIGFLTV	0.9958	3	3995.3906
1204	DYH2_MOUSE	4456	2.06	4	4	R.EALLEVAEKYIIGVDLGTQENIHR.K	0.993	2	2712.0752
						K.ELVQRLETSMIHWTR.Q	0.9958	2	1900.2059
						K.RQLGEQNFIK.S	0.9924	1	1233.4129
						R.FYFEGFEINLVWSCGIFITMNPGYAGRTELI	0.9958	3	4115.6583
1205	DYH3_MOUSE	4083	1.64	4	5	K.FTTVDTYWKSLMAQAVNDTR.V	0.9958	2	2348.6355
						K.LEVRDPIIVFNPTFDDCWQLIK.N	0.9958	2	2720.1065
						K.SLMAQAVNDTRVMVAADQPR.M	0.9937	2	2174.4981
						R.DLVSFFMIHK.D	0.9924	1	1237.5023
1206	DYH5_MOUSE	4621	2.36	4	4	K.APGTGELFVNFDPQILVLFR.E	0.994	2	2234.603
						R.VWIKQMEQILAENSQLR.K	0.9958	2	2087.4448
						K.IVFEPHNIDNASPATVSRNGMVFMSSSVLD	0.9958	3	4408.0462
						K.LPNPAYTPEISARTSIIDFTVTVK.G	0.9958	3	2635.0325
1207	DYH8_MOUSE	4731	3.32	9	16	R.FQNIDKSWIK.I	0.9924	1	1279.4814
						K.LTQVIENWTYQNLSFAAFK.G	0.9958	2	2274.581
						K.EFLANNPSLTEIRSEILHYATLEQEIK.E	0.9958	3	3160.5511
						R.FEVKVTK.E	0.9913	1	851.0336
						K.LAIEGTIIMSENLRDALDNMYDAR.I	0.9958	3	2726.0919
						K.YTEPVILNLEK.T	0.9958	1	1319.5407
						K.IFGIIGCGYFDPCRK.F	0.9958	2	1804.0308
						K.ELAVASIK.A	0.9958	1	831
						K.LLFEVHNIENASPATVSR.M	0.9931	2	1998.2462
1208	DYHC1_MOUSE	4644	14.56	36	175	K.AISKDHLYGTLDPNTR.E	0.9958	2	1801.9969
						R.QPQGHLLLIGVSGAGKTTLSR.F	0.9958	2	2134.4868
						K.LVPLLLEDGGDAPAALEAALEEK.S	0.9958	2	2335.6568

						R.VLTLSEDSPYETLHSFISNAVAPFFK.S	0.9958		2	2914.2842
						K.FLSDPQVHTVLVER.S	0.9958		2	1640.8797
						R.SSLQSQCLNEVLK.A	0.9958		2	1506.6623
						K.IQGLTVEQAEAVVR.L	0.9958		2	1513.7343
						K.LSLSNAISTVLPLTQLR.W	0.9958		2	1827.1747
						K.MGAKLLQDVR.Q	0.9958		1	1131.3788
						R.FGNPLLVQDVESYDPVLNPVLNR.E	0.9958		2	2599.9463
						R.APVIDADKPVSSQLR.V	0.9958	1,2		1596.8241
						R.FTQDTQPHYIYSPR.E	0.9937		2	1753.9115
						K.EALELTDTGLLSGSEER.V	0.9958		2	1820.9482
						R.MLSAVSQQVQCIQEALR.E	0.9958		2	1962.2379
						K.FGQMLGSNMTEFHSQISK.S	0.9958		2	2043.3198
						R.SELEEQQMHLNVGLR.K	0.9958		2	1783.9971
						R.KLVPLLLEDGGDAPAALEAALEEK.S	0.9958		2	2463.8309
						R.VLRPQVTAVAQQNQGEAPEPQDMK.V	0.9958		2	2635.9549
						K.TKPVTGNLRPEEALQALTIYEGK.F	0.9958		2	2529.8962
						R.YPLIIDPSGQATEFIMNEYK.D	0.9958		2	2330.6576
						R.LFLTMEINPK.V	0.9958		1	1206.4858
						R.ALPDMEVVGLNFSSATTPELLLKTFDHYCE	0.9958		3	3719.1666
						R.ILVDDTIITTLENLK.R	0.9958		2	1701.9983
						R.KLEHLITELVHQR.D	0.9958		2	1616.904
						K.RAPVIDADKPVSSQLR.V	0.9958		2	1753.0115
						K.NVHLAPGWLMQLEK.K	0.9958		2	1636.9525
						K.VFYEEELDVPLVLFNEVLDHVLR.I	0.9958	2,3		2789.2005
						R.HYLDFINHYANLFHEK.R	0.9958		2	2062.2945
						R.YKEEYAVLISEAQAIK.A	0.9958		2	1856.1259
						K.SRQELEQHSVDTASTSDAVTFITYVQSLK.F	0.9958		3	3242.5236
						R.EAIVNSCVFVHQTLHQANAR.L	0.9958		2	2295.5291
						R.TLHTTASNWLHLIPQTLSPLK.R	0.9958		2	2372.7727
						K.RSELEEQQMHLNVGLR.K	0.9958		2	1940.1845
						R.ENFIPTIVNFSAEEISDAIR.E	0.9958		2	2266.5126
						R.NLHVVFTMNPSSEGLK.D	0.9958		2	1774.0447
						R.REEFVQWVELLPDAQTPSWLGLPNNAER.	0.9949		3	3296.6665
1209	DYHC2_MOUSE	4306	2.18	6	6	R.EIWSNELSPVLNLWK.K	0.9944		2	1829.1057
						K.SKVLLSNNVEAWLNDLALEMK.Q	0.9958		2	2388.7845
						R.SEAGLAFSNTIDFDDAKDK.V	0.9952		2	2045.1669
						K.ELMLER.E	0.9958		1	790.9531

						R.QLELK.V	0.9958		1	630.7624
						R.LQSAMALFACKALGLK.E	0.9958		2	1723.0931
1210	DYL1_MOUSE	89	41.57	2	14	R.NFGSYVTHETK.H	0.9958	1,2		1283.3831
						K.NADMSEEMQQDSVECATQALEK.Y	0.9958		2	2515.6462
1211	DYL2_MOUSE	89	40.45	2	2	K.NADMSEDMQQDAVDCATQAMEK.Y	0.9958		2	2489.6262
						K.YNIEKDIAAYIK.K	0.9944		1	1441.6671
1212	DYN1_MOUSE	867	5.88	2	2	K.LQSQLLSIEKEVDEYK.N	0.9958		2	1923.1705
						K.EFIFSELLANLYSCGDQNTLMEESAEQAQF	0.9958		3	3651.9497
1213	DYN2_MOUSE	870	14.6	8	18	R.VYSPHVLNLTLIDLPGITK.V	0.9958		2	2094.5022
						K.TLNQQLTNHIR.E	0.9937		2	1338.5094
						K.FFLSHPAYR.H	0.9958		2	1138.314
						K.GISPVPINLRVYSPHVLNLTLIDLPGITK.V	0.9958		3	3141.7679
						R.EISYAIKNIHGVR.T	0.9912		2	1500.7409
						K.LAKEVDPQGLR.T	0.9924		1	1226.4184
						K.LQDAFSSIGQSCHLDLPQIAVVGGQSAGK.S	0.9958		3	2985.2897
						K.YMLPLDNLKIR.D	0.9958		1	1376.7002
1214	DYRK3_MOUSE	586	5.8	2	2	K.SSESLSAVKCNLSSRPSK.V	0.9958		2	1938.1113
						R.FYRAPEIILGCR.Y	0.9924		1	1495.7307
1215	DYRK4_MOUSE	632	4.43	2	2	K.KLNVVPEK.F	0.9958		1	927.1319
						R.FTFSILKCLHMLYVEK.I	0.9958		2	2030.442
1216	DYSF_MOUSE	2083	11.67	13	29	R.QFHQLAAQGPQECLVR.I	0.9958		2	1883.0831
						K.SYQMASISSPSLVVECGGQTVQSCVIR.N	0.9958		3	2945.2466
						K.IPLQEVLATPSLSASFNAPLLDAK.Q	0.9958		2	2496.9066
						K.TANPQWNQNITLPAMFPSMCEK.M	0.9958		2	2579.9143
						K.NSVNPVWNEGFEWDLK.G	0.9958		2	1935.1027
						K.LLSDKPQDFQIR.V	0.9958		2	1460.6732
						K.IYPLPEDPAIPMPPRQFHQLAAQGPQECLV	0.9958		3	3571.1004
						K.TLLHDADAGHLSFVEEVFENQTR.L	0.9958		2	2629.8455
						R.LALHVLQQQGLVPEHVESRPLYSPLQPDIE	0.9958		3	3721.2511
						R.GAHFCLK.V	0.9958		1	832.9439
						R.RPVVGQCTIR.S	0.993		2	1186.3659
						R.KLLSDKPQDFQIR.V	0.9958		2	1588.8473
						K.WLLLSDPDDFSAGAR.G	0.9958		2	1663.8272
1217	DYTN_MOUSE	653	9.65	3	3	K.EEKFLSWAQSEPLVLLWLPTCYR.L	0.9943		2	2867.2831
						R.APELTLSLLMAMFDRTGSGILK.R	0.9958		3	2365.8519
						R.ELTTNQDNLWTK.L	0.9958		1	1463.5871
1218	DYXC1_MOUSE	420	11.9	2	2	K.EATEAKAVAK.R	0.9924		1	1018.1552

						R.GTAFCQLELYVEGLQDYEAALKIDPANTVV	0.9958		3	4015.3858
1219	E2AK4_MOUSE	1648	3.7	3	5	R.IPINPASRHFR.R	0.9949		1	1308.5289
						R.YYNAWIER.H	0.9958		1	1115.2334
						R.EEEDSIVIDILAEHVSGISLATHLSHSGPVPA	0.9958		3	3859.2877
1220	E2F4_MOUSE	410	10.73	2	4	R.HEKSLGLLTTK.F	0.9958		1	1227.4465
						K.VWVQQSIRNVTEDVQNSCLAYVTHEDICR.	0.9958		3	3521.8005
1221	E2IG5_MOUSE	155	31.61	4	24	K.EEEIPETISFEMLDAAK.N	0.9958		2	1953.1683
						R.HGVPLHKPTDFEK.K	0.9958		2	1505.7165
						K.RHESLTSLNLER.K	0.9958		2	1455.6139
						K.KEEEIPETISFEMLDAAK.N	0.9958		2	2081.3424
1222	E41L1_MOUSE	879	4.78	2	2	K.DFMTTPPCITTETISTTMENSLK.S	0.9958		3	2619.9248
						R.YYLCLQLRADIITGR.L	0.9958		2	1856.1412
1223	E41L2_MOUSE	988	9.01	5	7	K.DYFGLLFQDHPEQK.N	0.9944		2	1737.9091
						R.IVITGDAALDHDQALAQAIR.E	0.9958		2	2092.3598
						K.VRPAELEQFESTIGFK.L	0.9958		2	1852.0972
						R.KVEPVAHK.D	0.9958		1	908.0885
						R.QAGASVLPVETEAQEHVVAQK.L	0.9924		2	2192.4337
1224	E41L3_MOUSE	929	7.32	4	5	R.LLLPEAPPK.K	0.9944		1	978.2199
						K.GISQTNLITTVTPEKK.A	0.9958		2	1730.9994
						K.RIVITGDADIDHDQALAQAIK.E	0.9958		2	2264.5437
						R.DEVDAAESTPTDRR.H	0.9944		1	1562.5901
1225	ECE1_MOUSE	769	12.22	5	10	R.TPESSHEGLITDPHSPSR.F	0.9944		2	1948.0562
						R.WGTFSNLWEHNQAVIK.H	0.9958		2	1931.1607
						R.CWAARTSVEK.R	0.9944		1	1208.3257
						K.EYLRQVSTLINNTDK.C	0.9958		1	1795.0025
						K.RLVVLVTLLAAGLVACLAALGIQYQTR.T	0.9958		2	2884.4881
1226	ECH1_MOUSE	327	68.81	17	472	R.YCTQDAFFQIK.E	0.9958		1	1421.5585
						K.VIGNQSLVNELTFSAR.K	0.9958		2	1748.9768
						K.MFTSGIDLMDMASELMQPSGDDAAR.I	0.9958		2	2691.033
						K.DAMLNAAFALAADISSK.S	0.9944		2	1709.955
						K.RAPEEVSDHNYESIQVTSAQK.H	0.9958		2	2389.5407
						R.AVVVSGAGK.M	0.9924		1	787.9346
						R.DHSVDESLDYMATWNMSMLQTQDIIK.S	0.9958		2	3073.4343
						K.TFTVIEKCPKPVIAAIHGGCIGGGVDLVSAC	0.9958		3	3613.0902
						K.MMADEALDSGLVSR.V	0.9958	1,2		1495.7059
						R.APEEVSDHNYESIQVTSAQK.H	0.9958		2	2233.3532
						K.EVDMGLAADVGTLQR.L	0.9958		2	1575.7772

						K.SPVAVQGSK.I	0.9958		1	872.9969
						K.HVLHVQLNRPEK.R	0.993		2	1470.7177
						R.VFQDKDAMLNAAFALAADISSK.S	0.9958		2	2327.6575
						K.DAMLNAAFALAADISSKSPVAVQGSK.I	0.9958		3	2563.9287
						K.CPKPVIAAIHGGCIGGGVDLVSACDIR.Y	0.9958		2	2794.1219
						R.KMMADEALDSGLVSR.V	0.9958		1	1623.8799
1227	ECHA_MOUSE	763	76.15	41	5160	R.DSIFSNLIGQLDYK.G	0.9958	1,2		1613.8077
						K.KLDALTTGFGFPVGAATLADEVGVDVAQH	0.9933		3	3614.0465
						R.THINYGVK.G	0.9958		1	932.0672
						K.KMGLVDQLVEPLGPGIK.S	0.9958		2	1795.1907
						K.SLNSEMDNILANLR.L	0.9958		2	1590.7918
						K.MGLVDQLVEPLGPGIK.S	0.9958		1	1667.0167
						K.LDALTTGFGFPVGAATLADEVGVDVAQHV	0.9958		3	3485.8725
						K.TVLGVPEVLLGILPGAGGTQR.L	0.9943		2	2048.4337
						R.LPAKPEVSSDEDVQYR.V	0.9958		2	1833.9927
						K.ADMVIEAVFEDLGVK.H	0.9952		2	1636.9007
						K.VIGMHYFSPVDK.M	0.9958	1,2		1393.6434
						K.NVQQLAILGAGLMGAGIAQVSVDK.G	0.9958		2	2354.7704
						R.TIEYLEEVAVNFAK.G	0.9958		2	1626.8468
						K.EVESVTPEHCIFASNTSALPINQIAAVSK.R	0.9958	2,3		3114.4455
						K.DTTASAVAVGLR.Q	0.9958	1,2		1161.3005
						K.AGLEQGSDAGYLAESQK.F	0.9958	1,2		1724.8217
						K.EVQSEFIEVMNEIWANDQIR.S	0.9958		2	2451.7131
						K.MVGVPAAFDMMLTGR.N	0.9958	1,2		1596.9613
						R.KYESAYGTQFTPCQLLLDHANNSSK.K	0.9958	2,3		2874.1022
						K.ALMGLYNGQVLCK.K	0.9958		1	1467.7327
						K.GFYIYQEGSK.N	0.9958		1	1192.3135
						R.FVDLYGAQK.V	0.9958	1,2		1041.1919
						K.DTTVTGLGR.G	0.9944		2	920.0104
						R.FGGGSVELLK.Q	0.9958		2	1007.1747
						K.MQLLEIITTDK.T	0.9958		2	1305.5726
						R.FVNEAVLCLQEGILATPAEGDIGAVFGLGF	0.9958		3	4091.6283
						K.LTTYAMTVPFVR.Q	0.9958		2	1399.6911
						R.CLAPMMSEVMR.I	0.9958	1,2		1325.6083
						K.YESAYGTQFTPCQLLLDHANNSSK.K	0.9958	2,3		2745.9281
						R.SAVLISSKPGCFVAGADINMLSSCTTPQEA	0.9958		3	3370.7317
						K.GLYPAPLK.I	0.9924		1	859.0562

						K.SPKPVVAAISGSCLGGGLELAIACQYR.I	0.9958	2,3		2776.1377
						K.ALTSFERDSIFSNLIGQLDYK.G	0.9958		3	2418.7087
						K.VIIVVK.D	0.9924		1	670.9139
						R.KTVLGVPEVLLGILPGAGGTQR.L	0.9958	2,3		2176.6078
						K.TVLGVPEVLLGILPGAGGTQRLPK.M	0.9937		2	2386.8839
						K.FGELALTK.E	0.9958		1	879.044
						K.KALTSFER.D	0.9944		1	952.0983
						K.GFYIYQEGSKNK.S	0.9944		2	1434.5914
						K.TLLKDTTVTGLGR.G	0.9958		2	1375.6084
						K.ALMGLYNGQVLCKK.N	0.9958		2	1595.9068
1228	ECHB_MOUSE	475	73.05	30	1912	K.DVVDYIIFGTVIQEVK.T	0.9943		2	1839.1388
						K.KAQDEGHLSDIVPFK.V	0.9958		1	1684.8895
						K.AMDSDWFAQNYMGR.K	0.9958		1	1692.861
						K.DQLLLGPTYATPK.V	0.9958		1	1417.6451
						R.LNFLSPELPAVAEFSTNETMGHSADR.L	0.9915		2	2835.1175
						R.IPFLLSGTSYK.D	0.9958	1,2		1226.4582
						R.AALSGLLHR.T	0.9958		2	938.1178
						K.NIVVVEGVR.I	0.9958		1	985.1716
						K.FNIWGGSLSLGHPFGATGCR.L	0.9958		2	2135.3556
						R.DFIYVSQDPK.D	0.9958		1	1212.3446
						K.AQDEGHLSDIVPFK.V	0.9958	1,2		1556.7154
						K.DGGQYALVAACAAGGQGHAMIVEAYPK.-	0.9958	2,3		2706.9991
						R.LVMAAANR.L	0.9958		1	846.0355
						K.DLMPHDLAR.A	0.9924		1	1068.2359
						K.AQDEGHLSDIVPFKVPGK.D	0.9958		2	1938.1906
						K.AGLTMNDIDAFEFHEAFSGQILANFK.A	0.9958		2	2888.2238
						R.ALAMGYKPK.A	0.9944		2	979.2255
						K.DNGIRPSSLEQMAK.L	0.9958	1,2		1546.7387
						R.MEQDEYALR.S	0.9958	1,2		1155.2677
						R.LAAAFAVSR.M	0.9958		1	906.0727
						R.EAALGAGFSDK.T	0.9958		1	1066.1558
						K.LKPAFIKPYGTVTAANSSFLTDGASAMLIMS	0.9958		3	3605.1586
						R.KMMLDLNK.A	0.9958		1	993.2678
						R.KDGGQYALVAACAAGGQGHAMIVEAYPK.	0.9944		2	2835.1731
						R.DFIYVSQDPKDQLLLGPTYATPK.V	0.9958		2	2610.9665
						R.IPFLLSGTSYKDLMPHDLAR.A	0.9944		2	2275.6709
						K.FRLNFLSPELPAVAEFSTNETMGHSADR.L	0.9958		3	3138.4815

						K.AMDSDWFAQNYMGRK.T	0.9958		2	1821.0351
						K.VPGKDTVTK.D	0.9958		1	945.1039
						K.TLAKPNMK.N	0.9958		1	903.1278
1229	ECHD1_MOUSE	322	6.21	1	2	R.DVLETLWGGPANLEAIAK.K	0.9958		2	1898.1662
1230	ECHD2_MOUSE	296	26.35	4	38	R.NALGNVFVSELLEALAQLR.E	0.9958		2	2058.3855
						R.ALALAQEILPQAPIAVR.L	0.9958		2	1775.1447
						R.ELGLVNHAVAQNEEGNAAYHR.A	0.9958		2	2293.4605
						R.IAASSAVMGLIETTR.G	0.9958		2	1520.7845
1231	ECHM_MOUSE	290	70	15	989	K.AQFGQPEILLGTIPGAGGTQR.L	0.9958		2	2112.3934
						K.NSSVGLIQLNRPK.A	0.9929		2	1426.6591
						K.FLSHWDHITR.V	0.9958	1,2		1312.4734
						K.ALNALCNGLIEELNQALETFEQDPAVGAIVL	0.9958		2	3786.1939
						R.LFYSTFATDDR.R	0.9958		2	1336.4436
						K.LVEEAIQCAEK.I	0.9958		1	1290.4223
						K.SLAMEMVLTGDR.I	0.9958		1	1323.5653
						K.AFAAGADIK.E	0.9958		1	863.989
						R.TFQDCYSSK.F	0.9944	1,2		1136.1694
						K.ESVNAAFEMTLTEGNKLEK.R	0.9958		2	2112.3594
						K.KPVIAAVNGYALGGGCELAMMCDIIYAGEK	0.9944		3	3173.642
						K.RLFYSTFATDDR.R	0.9958		2	1492.6311
						K.ESVNAAFEMTLTEGNK.L	0.9958		2	1741.9104
						K.GKNSSVGLIQLNRPK.A	0.9958		2	1611.8851
						K.IVVAMAK.E	0.9944		1	731.972
1232	ECM29_MOUSE	1840	10.05	10	31	R.AIQTLGYFPVGDGVFPHQK.L	0.9958		2	2075.3745
						R.LGHAETDEQLQNIISK.F	0.9958		2	1796.975
						K.QTSSLVPPYLGMILSALMQGLAGR.T	0.9958		2	2505.0088
						K.QSLIDWNNPAIINKMYK.V	0.9909		2	2049.3954
						R.ELQLESLLGAFESLGK.A	0.9958		2	1734.9873
						R.FQEFSDIVIPLIK.K	0.9958		2	1549.8504
						K.FASTVFPSDHIPSR.Y	0.9958		2	1561.7373
						K.TKEGAVLKPELK.R	0.9944		1	1313.5803
						K.EEPVYK.T	0.9944		1	764.8535
						R.MCLAHSAGVVPTSQSLADMQDHAPAIGR.\	0.9958		3	2922.2697
1233	ECP5_MOUSE	155	11.61	1	3	K.TCKDGTSPNCHDSSSK.V	0.9932		2	1781.7627
1234	ECSIT_MOUSE	435	8.97	2	5	K.WIQGLQETNPTLAQIPVVFR.L	0.9958		2	2311.6891
						K.VPAMHEDLFKPSGNR.E	0.9958		2	1698.9372
1235	ECT2_MOUSE	738	8.94	3	5	R.VAVSLGTPIMKPEWIYK.A	0.9958		2	1933.3594

						R.GEQVTLFLFNDCLEIAR.K	0.9958		2	2026.2629
						R.GGPILAPEEIKTIFGSIPDIFDVHMK.I	0.9944		3	2826.3234
1236	EDC3_MOUSE	508	3.15	1	2	K.KPASSSSAPQSIPK.R	0.9958		2	1385.5602
1237	EDC4_MOUSE	1406	12.16	7	13	R.EPVLAQLRGLVSTLQSATEQMAATVSSSVI	0.9944		2	3131.5719
						R.GGQLQEQLTQQLSQALSSAVAGR.L	0.9958		2	2371.6127
						R.LCAQLEGLQSTVTDHVER.A	0.9958		2	2057.2341
						R.ELAELWHNQEELLQR.L	0.991		2	1909.1087
						R.QGPELGSQLGLDGGPGDGDR.H	0.9958		2	1926.0067
						K.GPGQVSTAASALSLDLQEVEPLGLPQASP	0.9944		3	3334.7111
						R.LTEHQVAEPPEDWPALIWQQQR.E	0.9958		2	2672.9597
1238	EDRF1_MOUSE	1239	3.55	2	3	R.KELVEECDQPK.N	0.9958		1	1375.4846
						K.NDFVRNILWTFEDIHMLVGSNMPIFGGGR.	0.9958		3	3337.8414
1239	EEA1_MOUSE	1411	11.34	9	21	K.NHALQQQLTQLTEK.L	0.9958		2	1652.8479
						K.ETSQQLKIELNSVK.G	0.9923		2	1617.84
						K.LQQQSSQAAQELAAEKGK.L	0.9958		2	1916.0983
						K.IQAGEGETAVLNQLQEK.N	0.9958		2	1829.0171
						K.SDGLVTDSSAELQALEQQLEEAQTENFNIK	0.9958		3	3309.5219
						K.LQSEHAHLEATINQLR.S	0.9907		2	1861.0677
						K.NAVSQKTVLENK.L	0.9958		1	1331.5119
						K.GEVSQAQNTLK.Q	0.9949		1	1175.2841
						K.TELLQRPGIEDVAVLK.K	0.9924		2	1782.0904
1240	EEPD1_MOUSE	569	1.76	1	15	R.EYIGGFKK.V	0.9958		1	942.1027
1241	EF1A1_MOUSE	462	37.01	12	741	K.QLIVGVNK.M	0.9958		1	871.0678
						R.VETGVLKPGMVVTFAPVNVTTEVK.S	0.9958		2	2516.999
						K.DGSASGTTLLEALDCILPPTRPTDKPLR.L	0.9958		3	2996.3539
						K.STTTGHLIYK.C	0.9958	1,2		1121.2786
						K.YYVTIIDAPGHR.D	0.9958		2	1405.5962
						K.THINIVVIGHVDSGK.S	0.9958		2	1589.835
						K.IGGIGTVPVGR.V	0.9958		2	1026.2241
						R.EHALLAYTLGVK.Q	0.9958		1	1315.5553
						K.NMITGTSQADCAVLIVAAGVGEFEAGISK.N	0.993		2	2911.263
						R.LPLQDVYK.I	0.9924	1,2		976.1607
						K.NMITGTSQADCAVLIVAAGVGEFEAGISKN	0.9958		3	3467.8421
						R.KDGSASGTTLLEALDCILPPTRPTDKPLR.L	0.9958		3	3124.5279
1242	EF1A2_MOUSE	463	42.12	9	923	K.YYITIIDAPGHR.D	0.9947		2	1419.6231
						R.VETGILRPGMVVTFAPVNITTEVK.S	0.9958		2	2573.0661
						K.EGNASGVSLLEALDTILPPTRPTDKPLR.L	0.9958		3	2962.3733

						R.KEGNASGVSLLEALDTILPPTRPTDKPLR.L	0.9958		3	3090.5473
						K.IGYNPATVPFVPISGWHGDNMLEPSPNMP'	0.9944	2,3		3601.1341
						K.ADPPQEAAQFTSQVIILNHPGQISAGYSPVI	0.9958		3	4444.8799
						K.RYDEIVK.E	0.9958		2	923.0568
						K.SGDAAIVEMVPGKPMCVESFSQYPPLGR.F	0.9944		2	3024.4427
						K.EGNASGVSLLEALDTILPPTRPTDKPLRLPL	0.9958		3	3919.5107
1243	EF1B_MOUSE	225	33.78	4	21	K.TPAGLQVLNDYLADK.S	0.9958		2	1618.8272
						K.KPAVVAK.S	0.9924		1	712.9108
						K.SSILLDVKPWDDETDMTK.L	0.9952		2	2094.3411
						K.SYIEGYVPSQADVAVFEAVSGPPPADLCH/	0.9944		3	3417.7657
1244	EF1D_MOUSE	281	26.33	5	52	R.ATAPQTQHVSPMR.Q	0.9958	1,2		1424.6177
						R.GVVQDLQQAISK.L	0.9958	1,2		1286.471
						K.SLAGSSGPGASSGPGGDHSELIVR.I	0.9958		2	2196.3384
						K.KPTLVAK.S	0.9958		1	756.9639
						R.ITSLEVENQNLR.G	0.9958		2	1416.5742
1245	EF1G_MOUSE	437	22.88	7	16	R.KLDPGSEETQTLVR.E	0.9958	1,2		1573.7435
						R.ILGLLDTHLK.T	0.9958		2	1123.3812
						R.EYFSWEGTFQHVGK.A	0.9917		2	1715.862
						R.KYSNEDTLSVALPYFWEHFDK.D	0.9958		2	2590.8511
						K.YSNEDTLSVALPYFWEHFDK.D	0.9924		2	2462.677
						K.KAAAPAPEEEMDECEQALAAEPK.A	0.9958		2	2486.676
						K.AKDPFAHLPK.S	0.9958		2	1124.328
1246	EF2_MOUSE	858	52.68	29	655	R.ALLELQLEPEELYQTFQR.I	0.9958		2	2221.5151
						K.IWCFGPDGTGPNILTDITK.G	0.9958		2	2106.349
						K.EGIPALDNFLDKL.-	0.9958		2	1445.6555
						K.ARPFPDGLAEDIDKGEVSAR.Q	0.9958		2	2144.3488
						R.GHVFEESQVAGTPMFVVK.A	0.9958		2	1963.2586
						K.KEDLYLKPIQR.T	0.9958		2	1403.6646
						R.NMSVIAHVDHGK.S	0.9958		1	1308.4979
						K.TGTITTFEHAHNMR.V	0.9958		2	1616.7918
						R.TFCQLILDPIFK.V	0.9958	1,2		1495.7681
						K.STAISLFYELSENDLNFIK.Q	0.9958		2	2205.4693
						K.AYLPVNESFGFTADLR.S	0.9948		2	1801.0086
						R.SNTGGQAFPQCVFDHWQILPGDPFDNSSF	0.9958		3	4247.5524
						R.WLPAGDALLQMITIHLPSPVTAQK.Y	0.9944		2	2602.1101
						R.GGGQIIPTAR.R	0.9944		1	970.1166
						R.KIWCFGPDGTGPNILTDITK.G	0.9958		2	2234.5231

						R.CELLYEGPPDDEAAMGIK.S	0.9921		2	2009.2014
						K.STLTDSLVCK.A	0.9958		1	1124.2427
						K.YEWDVAEAR.K	0.9944		1	1139.2096
						R.YLAEKYEWDVAEAR.K	0.9958		2	1743.9133
						R.VFSGVVSTGLK.V	0.9944		1	1094.2963
						K.DGSGFLINLIDSPGHVDFSSEVTAALR.V	0.9958		2	2819.1003
						K.ARPFPDGLAEDIDK.G	0.9958		2	1544.7044
						R.YVEPIEDVPCGNIVGLVGVDQFLVK.T	0.9958		2	2761.1536
						K.VFDAIMNFR.K	0.9958		1	1113.3196
						R.LMEPIYLVEIQCPEQVVGGIYGVLNR.K	0.9958		2	2991.4817
						R.CLYASVLTAQPR.L	0.9944		2	1379.5652
						R.IKPVLMMNK.M	0.9944		1	1074.4285
						K.DSVVAGFQWATK.E	0.9958		1	1309.4643
						K.RGHVFEESQVAGTPMFVVK.A	0.9958		2	2119.4461
1247	EFG1_MOUSE	751	25.3	10	68	K.LNHNAAFVQIPIGLEGDFK.G	0.9958		2	2084.3824
						R.FVLQDGAHHMVDSNEISFIR.A	0.9958	2,3		2316.5963
						K.GVQPLLDAVLEYLPNPSEVQNYAILNQNDS	0.9944		3	3443.8352
						K.YLEATGQLPVKK.G	0.9937		2	1347.5975
						R.ETIVAPVPFDFTHK.K	0.9944	1,2		1601.8425
						R.SFTPVFLGSALK.N	0.9944	1,2		1267.5107
						R.NIGISAHIDSGK.T	0.9944		2	1212.3482
						R.EYGCPCITGKPK.V	0.9958		2	1410.5421
						K.DNSDLSMESIHVPEPVISIAMRPSNK.N	0.9958		3	2868.2495
						K.RYNVPFLTFINK.L	0.9958		2	1512.7947
1248	EFG2_MOUSE	777	16.09	6	13	R.IYSGTLTPQLAVHNINR.N	0.9958		2	1898.1722
						R.NYSSAPAGSDVK.S	0.9958		1	1196.2591
						R.LLLPFADQHVEIPSLTAGNIALTVGLK.Q	0.9958		2	2832.3562
						R.EYGLETYLGPLQVAYR.E	0.9958		2	1873.1155
						R.SLGDVDDGDTVTDFMAQERER.G	0.9958		2	2357.4675
						R.HLVSAELEVRPAEEPCAVAK.I	0.9929		2	2206.4699
1249	EFHC2_MOUSE	750	2.27	1	4	K.VLLCDCDEFTKTYYR.T	0.9958		2	1984.1451
1250	EFHD2_MOUSE	240	7.5	1	10	R.RADLNQGIGEPQSPSR.R	0.9958		2	1725.8588
1251	EFTS_MOUSE	324	37.35	6	95	K.GFLNSSELSELAAGPDR.E	0.9955		2	1763.9017
						K.YGALVICETPEQIANLEEVGR.R	0.9958		2	2362.608
						R.LGQHVVGMAPLSVGSLDDEPGGETETR.M	0.9958		2	2753.013
						K.FQQLVQQVALGTMAHCQNLTDR.L	0.9958		2	2559.8689
						K.VPSGFYVGSYVHGVTQSPSLQNLVLGK.Y	0.9958		2	2835.2322

						R.RLGQHVVGMAPLSVGSLDDEPGGETETR.	0.9958		3	2909.2005
1252	EFTU_MOUSE	452	61.73	21	505	K.GEETPVIVGSALCALEQR.D	0.9958		2	1930.1315
						R.GITINAAHVEYSTAAR.H	0.9958		2	1674.854
						K.TIGTGLVTDVPAMTEEDK.N	0.9958	1,2		1878.1017
						K.LLDAVDTYIPVPTR.D	0.9944		1	1573.8296
						R.DLDKPFLLPVESVYSIPGR.G	0.9958		2	2146.4912
						R.TVVTGIEMFHK.S	0.9958		2	1262.5096
						R.HYAHTDCPGHADYVK.N	0.9958		2	1771.8523
						R.ELLTEFGYKGEETPVIVGSALCALEQR.D	0.9924		2	3011.3649
						K.ADAVQDSEMVELVELEIR.E	0.9958		2	2047.2849
						K.NMITGTAPLDGCILVVAANDGPMPQTR.E	0.9958		2	2814.2105
						K.QIGVEHVVVYVNK.A	0.9958	1,2		1484.7385
						R.EHLLLAK.Q	0.9958		1	824.011
						K.KYEEIDNAPEER.A	0.9958		2	1493.57
						R.GTVVTGTLER.G	0.9907		2	1033.1698
						K.KGDECELLGHNK.N	0.9958	1,2		1400.4974
						R.GLVMVKPGSIQPHQK.V	0.9915		2	1619.9659
						R.DKPHVNVGTIGHVDHGK.T	0.9943		2	1811.0103
						R.ELLTEFGYK.G	0.9958		1	1100.2567
						R.DKPHVNVGTIGHVDHGKTTLTAAITK.I	0.9958		3	2712.0812
						K.TIGTGLVTDVPAMTEEDKNIK.W	0.9944		2	2233.539
						K.GDECELLGHNK.N	0.9958		1	1272.3233
1253	EGF_MOUSE	1217	2.38	2	108	R.IDPDGTNHQQLVVDAGISADMDIHYK.K	0.9958		3	2854.1205
						R.IDPDGTNHQQLVVDAGISADMDIHYKK.E	0.9952		3	2982.2946
1254	EGFL6_MOUSE	550	3.45	1	2	R.DNDVGYYMAVPALAGHK.K	0.9943		2	1822.0454
1255	EGFLA_MOUSE	1017	3.34	2	8	K.CNTDIFIGGVPNYDDVK.K	0.9958		2	1928.0717
						K.KNSGILHPFSGSIQK.I	0.9944		2	1613.857
1256	EGFR_MOUSE	1210	9.42	7	37	R.LTQLGTFEDHFLSLQR.M	0.9958		2	1906.1485
						K.YCTAISGDLHILPVAFK.G	0.9958		2	1906.1981
						R.NYDLSFLK.T	0.9944		1	1000.1393
						R.FSNNPILCNMDTIQWR.D	0.9958		2	2010.2409
						K.AVNHVCNPLCSSEGCWGPEPR.D	0.9958		2	2427.5337
						R.IPLENLQIIR.G	0.9958		2	1209.4746
						R.NYVVTDHGSCVR.A	0.993		2	1407.4919
1257	EGLN_MOUSE	653	17	4	7	K.FQAPEIPLHLAYDSSLVIFQGQPR.V	0.9958		2	2728.1228
						K.VTAHVVSNEVIISFPSGSPPLR.K	0.9944	2,3		2307.6549
						K.GLVLPSVLGITFGAFLIGALLTAALWYIYSHT	0.9944		3	3536.2407

						K.GAITSIAALDDPQSIVLQLGQDPK.A	0.9958		2	2451.7795
1258	EH1L1_MOUSE	1716	11.13	9	10	K.TQEISSEGSGVPDLEAK.M	0.9958		2	1747.8535
						K.SWTLGQQEAEMEGFESPENK.S	0.9958		2	2298.4425
						K.AHSWQPGIQNPYR.G	0.9958		2	1554.7079
						R.STGQPGQTMVPTPAPR.L	0.9958		2	1625.8401
						R.AFCTGQELQLVQLEGGGGSGTYR.V	0.9958		2	2429.6147
						R.AFRGQGSEPAAITGGQVGPETPEPPPSPP	0.9958		3	3216.4912
						R.EQLLLEELVSLVNQR.D	0.9958		2	1784.0629
						K.VLATVDVNLAHHAGPVPAQVPLR.L	0.9958		2	2375.7794
						R.RQDQLQLLIEEQDLER.R	0.9958		2	2027.2419
1259	EHD1_MOUSE	534	53.37	19	81	K.DKPTYDEIFYTLSPVNGK.I	0.9958		2	2088.3215
						K.LADVDKDGLLDDEEFALANHLIK.V	0.9958	2,3		2555.8443
						R.EHQISSGDFPSLR.K	0.9944		2	1473.5852
						R.VYIGSFWSHPLLIPDNR.K	0.9945		2	2015.3219
						K.MQELLQTQDFSK.F	0.9926		2	1468.6648
						K.LDISDEFSEVIK.A	0.9958		2	1395.5493
						K.LLDTVDDMLANDIAR.L	0.9958		2	1675.8945
						K.FQALKPK.L	0.9924		1	832.0336
						R.IGPEPTTDSFIAVMHGPTEGVVPGNALVVD	0.9958		3	3274.7161
						R.FMCAQLPNPVLDSISIIDTPGILSGEK.Q	0.9958		2	2917.3535
						K.LLPLEEHYR.F	0.9944		2	1170.3537
						R.HLIEQDFPGMR.I	0.9958		2	1343.5432
						R.IILLFDAHK.L	0.9958		1	1070.3201
						R.KLNAFGNAFLNR.F	0.9958		2	1365.5778
						K.DGLLDDEEFALANHLIK.V	0.9958		2	1914.1223
						K.LEGHELPADLPPHLIPPSK.R	0.9958		2	2061.3885
						K.VKLEGHELPADLPPHLIPPSK.R	0.9958		2	2288.6952
						R.KMQELLQTQDFSK.F	0.9958		2	1596.8389
						R.FHEFHSPALEDADFDNKPMVLLVGQYSTG	0.9944		3	3394.7828
1260	EHD2_MOUSE	543	42.73	12	108	K.LEGHGLPTNLPR.R	0.9958		1	1304.4917
						K.IQLEHHISPGDFPDCQK.M	0.9958		2	2022.1907
						R.FGSFHSPALEDADFDGKPMVLVAGQYSTG	0.9958	2,3		3173.5238
						K.SKYDEIFYNLAPADGK.L	0.9958	1,2		1832.0197
						K.TSFIQYLLEQEVPGSR.V	0.9958		2	1868.0966
						R.QEELESVEAGVQGGAFEGTR.M	0.9958		2	2094.1992
						R.FMCAQLPNQVLESISIIDTPGILSGAK.Q	0.9958		2	2904.3577
						K.LLEALDDMLAQDIAK.L	0.9958		2	1659.9355

						K.LNPFGNTFLNR.F	0.9958		2	1293.4679
						R.KLNPFGNTFLNR.F	0.9958		2	1421.642
						R.DGMLDDEEFALASHLIEAK.L	0.9958		2	2105.324
						R.VGPEPTTDCFVAVMHGETEGTVPGNALVV	0.9958		3	3855.2771
1261	EHD3_MOUSE	535	9.53	4	4	R.YLLEQDFPGMR.I	0.9958		2	1369.5781
						K.LEGHELPSELPAHLLPPSK.R	0.9958		2	2065.3769
						K.VKLEGHELPSELPAHLLPPSK.R	0.9958		2	2292.6836
						K.DPEVFQTVSDGLK.K	0.9944		1	1435.5737
1262	EI2BA_MOUSE	305	5.9	1	2	K.MASAVAAIQTLLEFLK.R	0.9958		2	1707.0814
1263	EI2BB_MOUSE	351	5.7	1	2	R.LITDHHWNNAGDLMDLIR.R	0.9958		2	2135.4051
1264	EI2BE_MOUSE	717	8.93	3	3	R.VAAGAQIHQSLLCDR.A	0.9958		2	1639.818
						R.RWVYPLTPEVNFTDSTTQSYTHSR.H	0.9958		2	2887.1375
						K.LKGYNPAEVGLEGQGYLWK.A	0.9958		3	2123.4161
1265	EI2BL_MOUSE	369	27.1	4	11	R.AGAGGPGLAALVAFVR.D	0.9958		2	1427.6896
						R.LEHTFCTETRPYNQGAR.L	0.9929		2	2081.2182
						R.YSPGSLQILDQLQLPEHCHYEALSSVQQAS	0.9958		3	3870.2335
						K.VTVLTHCNTGALATAGYGTALGVIR.S	0.9958		2	2517.8541
1266	EID2_MOUSE	236	5.08	1	3	R.EAAFDIEYLR.N	0.9944		1	1227.3593
1267	EIF1_MOUSE	113	13.27	1	11	K.NICQFLIEIGLAK.D	0.9958		2	1519.7906
1268	EIF1B_MOUSE	113	38.05	2	2	K.TLTTVQGIADDYDK.K	0.9958		2	1540.6672
						K.KFACNGTVIEHPEYGEVIQLQGDQR.K	0.9958		3	2890.148
1269	EIF2A_MOUSE	581	7.92	2	4	R.NTVTQSASGDPEVDKK.I	0.9944	1,2		1676.7777
						K.NGPIYDVVWNSSSTEFCAVYGFMPAK.A	0.9944		3	2941.2503
1270	EIF3A_MOUSE	1344	4.46	4	25	K.DIDIEDLEELDPDFIMAK.Q	0.9958		2	2122.3485
						K.AIEVIRPAHILQEK.E	0.9945		2	1617.9321
						R.RVPPPALSR.D	0.993		2	993.1972
						K.AIEVIRPAHILQEKEEQHQLAVNAYLK.N	0.9944		3	3142.6285
1271	EIF3C_MOUSE	911	3.62	3	4	K.RFEELTNLIR.T	0.9958		2	1291.4929
						R.ILADLEDYLNELWEDK.E	0.9958		2	1980.1785
						R.ILADLEDYLNELWEDKEGK.K	0.9958		2	2294.52
1272	EIF3D_MOUSE	548	15.69	5	10	R.IFHTVTTTDDPVIR.K	0.9958		2	1615.8265
						R.NLAMEATYINHNFSQQCLR.M	0.9958		2	2311.5433
						R.NMVQFNLQTLPK.S	0.9958		2	1433.7087
						K.YSSQFGGGSQYAYFHEEDETSFQLVDTAR	0.9958		3	3678.8633
						K.RIFHTVTTTDDPVIR.K	0.9915		2	1772.014
1273	EIF3E_MOUSE	445	3.37	1	5	R.HLVFPLLEFLSVK.E	0.9958	1,2		1542.9047
1274	EIF3F_MOUSE	361	14.13	3	31	R.IQDALSTVLQYAEDVLSGK.V	0.9958		2	2051.3013

						R.LHPVILASIVDSYER.R	0.9958	2	1712.9866
						R.FLMSLVNQVPK.I	0.9958	2	1276.5799
1275	EIF3H_MOUSE	352	15.63	5	22	K.ASITFEHMFEEVPIVIK.N	0.9958	2	1991.3527
						K.HELLSLASSNHLGK.S	0.9944	2	1506.7019
						K.NSHLINVLMWELEK.K	0.9958	2	1727.0313
						K.SAVADKHELLSLASSNHLGK.S	0.9958	2	2078.3329
						K.KASITFEHMFEEVPIVIK.N	0.9958	2	2119.5268
1276	EIF3I_MOUSE	325	25.23	4	27	R.IHYFDPQYFEFEFEA.-	0.9958	2	1983.1431
						R.TERPVNSAALSPNYDHVVLGGGQEAMDV	0.9958	3	3575.889
						K.GHFGPINSVAFHPDGK.S	0.9958	2	1680.8631
						-.MKPILLQGHER.S	0.9958	1	1322.6115
1277	EIF3M_MOUSE	374	9.09	2	2	R.LQLLSNLFHGMDK.N	0.9958	2	1516.7985
						K.DPNAFLFDHLLTLKPVK.F	0.9958	2	1969.3342
1278	ELAV1_MOUSE	326	4.91	1	4	K.NMALLSQLYHSPAR.R	0.9958	2	1601.8639
1279	ELF2_MOUSE	593	3.2	1	4	K.TQQSPVSNGSPELGIKK.K	0.9958	2	1770.9805
1280	ELMO1_MOUSE	727	1.93	1	2	R.YIILTHVIRAQR.A	0.9924	1	1483.8001
1281	ELOA1_MOUSE	773	14.1	3	3	K.VVKTSSTALGEK.G	0.9958	1	1220.4087
						K.VPTDVLPALPDIPLPAIHANYRPLPSLELIPS	0.9944	3	4087.8412
						R.IKPAPYTTGSSHVPASNSSSNFHSSPEELA	0.9958	3	5534.8859
1282	ELOB_MOUSE	118	39.83	3	11	K.TLGECGFTSQTARPQAPATVGLAFR.A	0.9958	3	2637.9213
						K.ESSTVFELK.R	0.9924	1	1040.1583
						K.DDQLLDDGKTLGECGFTSQTARPQAPATV	0.9958	3	3637.9513
1283	ELOC_MOUSE	112	19.64	1	11	K.AMLSGPGQFAENETNEVNFR.E	0.9958	2	2212.3985
1284	ELP1_MOUSE	1333	4.73	3	3	K.YDRVDIIETSVKPSILEAQK.N	0.99	2	2305.6335
						R.FVHPCTQMEVATIGGEECVLGLTDRCR.F	0.9958	3	3137.433
						K.EYLPFLNTLK.K	0.9944	1	1238.4692
1285	ELP3_MOUSE	547	2.93	1	2	R.LVDIIAAVPPHYRK.I	0.9958	1	1592.9248
1286	EM55_MOUSE	466	37.77	8	28	R.SQYAHYFDLSLVNNSVDETLK.K	0.9958	2	2444.6599
						K.KLQEAFDQACSSPQWVPVSWVY.-	0.9958	2	2626.8939
						R.VASVAHSAPSEAPSCSPFGK.K	0.9958	2	1987.1425
						R.TALSDLYLEHLLQK.R	0.9958	2	1644.9084
						R.TAELSPFIVFIAPTDQGTQTEALQQLQK.D	0.9958	3	3076.4735
						K.HSSIFDQLDVVSYEEVVR.L	0.9958	2	2123.3269
						R.NRPETSLNQSNVTTEDMYTNGSPAPGSP	0.9958	3	3373.5921
						K.FETVHQIHK.Q	0.9924	1	1139.2993
1287	EMAL1_MOUSE	814	16.71	7	25	R.RLNITEEQQAVLNR.K	0.9958	2	1684.893
						K.IIEDPAQSSGFHPSGSVVAVGTLTGR.W	0.9958	2	2583.8607

						K.ARPLGQTLPLR.T	0.9945	2	1222.4764
						K.VHLFSYPCSQFR.A	0.9958	2	1541.7155
						K.KPSASLPAPSGAR.K	0.9944	2	1239.4172
						K.HATLWDAVGHRPVWDK.I	0.9958	2	1889.1264
						K.QEKPKFVLCVTFSENGDTITGDSSGNILVW	0.9958	3	3528.9068
1288	EMAL2_MOUSE	649	22.03	7	73	R.SAGFHPSGSVLAVGTVTGR.W	0.9958	2	1801.0122
						R.VWDSVSLSTLHVLGLGVFDR.A	0.9958	2	2201.5303
						R.ITQEVQGAHDGGVFALCALR.D	0.9958	2	2143.3733
						K.SHIYFWSLEGGSLSK.R	0.9958	2	1711.9145
						K.LVHLWSSETHQPVWSR.S	0.9958	2	1963.2058
						K.VVDSKCSNEAVLVATFHPTDPSLLITCGK.S	0.9958	3	3160.5239
						K.VHLFSYPCCQPR.A	0.9958	2	1564.7162
1289	EMI5_MOUSE	164	7.93	1	3	R.APDLEYLFEKPH.-	0.9958	2	1459.6415
1290	EMID2_MOUSE	440	15.91	3	4	K.ENGDSQLNPAVVDTVLTGIPGPR.G	0.9958	3	2350.5907
						K.ASAAEGEGVQQLR.E	0.9924	1	1316.4135
						K.ENGDSQLNPAVVDTVLTGIPGPRGPPGPP	0.9958	3	5065.5705
1291	EMIL1_MOUSE	1017	12.49	5	17	R.LQLVGSGLHEAEAAGEAQQAVLEGLQGLL	0.9958	2,3	3146.5278
						R.RPPQECCPPELGR.R	0.9958	2	1596.7155
						R.ASGPVPVPSGPSEELLR.Q	0.9944	2	1692.9096
						K.DFTGPSGKAGPPGPPGLQGPSGPAGPPG	0.9958	3	2835.1485
						R.RGSELGGAAGQGGHPPGYTSLASR.L	0.9958	2	2284.4532
1292	EMIL2_MOUSE	1074	11.08	4	4	K.QLQEAAQGPTVTMTTNELYQAYVDSKIDAI	0.9958	3	3456.8493
						K.VLVNDGDVYNPNTGIFTAPYDGRYLITATLT	0.9958	3	3758.1791
						K.DIKSELAEVK.D	0.9958	1	1132.2994
						R.APSRWTPALLALLALGGAGLCHASSQPGY	0.9944	3	3713.2058
1293	EMR4_MOUSE	689	7.11	2	3	K.VEHHILNENSDIPKK.D	0.9958	1	1773.9865
						K.TVRLIVAYLFTIINVLQGVLIFMVHCLLNR.Q	0.9944	3	3531.3362
1294	EMSY_MOUSE	1264	8.94	4	4	K.MIVTQPKGIGSAVQPAAK.I	0.9958	2	1797.1663
						K.IVYGQQGKTQVLIKPKPVTFQATVVSEQTR	0.9958	3	3345.9102
						R.VATTPGAATYVKTTSGSIITVVPK.S	0.9958	3	2363.7569
						K.NVVTTLLNAGGEKTLQTVPAGAKPAIITATR	0.9944	3	3547.1765
1295	ENOA_MOUSE	434	71.89	19	2625	K.SFVQNYPVVSIEDPFDQDDWGAWQK.F	0.9958	2	2972.1963
						K.DATNVGDEGGFAPNILENK.E	0.9958	1,2	1962.0801
						R.SGETEDTFIADLVVGLCTGQIK.T	0.9958	2	2354.5824
						K.DATNVGDEGGFAPNILENKEALELLK.T	0.9958	2	2759.0423
						R.AAVPSGASTGIYEALELR.D	0.9958	1,2	1806.0257
						K.VNQIGSVTESLQACK.L	0.9958	1	1634.7931

						K.FTASAGIQVVGDDLTVTNPK.R	0.9943	2	2034.2737
						R.YITPDQLADLYK.S	0.9958	1	1440.636
						K.LAQSNGWGVMVSHR.S	0.9958	2	1542.7557
						K.GVSQAVEHINK.T	0.9958 1,2		1182.3219
						R.HIADLAGNPEVILPVPAFNVINGGSHAGNK.	0.9958 2,3		3023.4215
						K.FGANAILGVSLAVCK.A	0.9948	2	1520.7784
						R.IGAEVYHNLK.N	0.9952	2	1144.3158
						R.GNPTVEVDLYTAK.G	0.9958	1	1407.5633
						K.AGYTDQVVIGMDVAASEFYR.S	0.9958	2	2193.4358
						K.LAMQEFMILPVGASSFR.E	0.9958	2	1898.2886
						K.LMIEMDGTENK.S	0.9924	1	1281.4817
						K.SKFGANAILGVSLAVCK.A	0.9944	2	1736.0307
						K.KVNVVEQEK.I	0.9958	1	1073.2346
1296	ENOB_MOUSE	434	67.51	23	2133	K.DATNVGDEGGFAPNILENNEALELLK.T	0.9958	2	2744.972
						K.LAMQEFMILPVGASSFK.E	0.9958	2	1870.2752
						K.FMIELDGTENK.S	0.9958 1,2		1297.4657
						K.VNQIGSVTESIQACK.L	0.9958	1	1634.7931
						K.VVIGMDVAASEFYR.N	0.9958	2	1557.8047
						K.TAIQAAGYPDK.V	0.9958	1	1135.2621
						R.IEEALGDK.A	0.9958	1	874.9665
						R.GNPTVEVDLHTAK.G	0.9958	2	1381.5284
						R.NGKYDLDFK.S	0.9958	1	1100.2163
						K.KLSVVDQEK.V	0.9958	1	1046.2089
						R.HIADLAGNPDLVLPVPAFNVINGGSHAGNK	0.9958	2	3009.3946
						R.IGAEVYHHLK.G	0.9958	2	1167.3531
						R.IAQAVEK.K	0.9944	1	758.8931
						K.RIAQAVEK.K	0.9925	2	915.0806
						K.NFIQNYPVVSIEDPFDQDDWATWTSFLSG\	0.9958	3	5102.5757
						K.VVIGMDVAASEFYRNGK.Y	0.9958	2	1857.1345
						K.TLGPALLEK.K	0.9924	2	942.1436
						K.AVEHINKTLGPALLEK.K	0.9958	2	1734.0489
						R.EILDSRGNPTVEVDLHTAK.G	0.9958	2	2095.3171
						K.YNQLMRIEEALGDK.A	0.9958	2	1680.9165
						K.KACNCLLLK.V	0.9952	2	1120.3099
						R.HISGEKLGELYK.N	0.9944	2	1374.5797
						K.EAMRIGAEVYHHLK.G	0.9958	2	1654.9274
1297	ENOG_MOUSE	434	23.73	5	38	R.DGKYDLDFK.S	0.9958	1	1101.2011

						R.HIAQLAGNSDLILPVPAFNVINGGSHAGNK.	0.9958		3	3026.4251
						R.NYPVVSIEDPFDQDDWAAWSK.F	0.9958		2	2483.6526
						K.LAMQEFMILPVGAESFRDAMR.L	0.9947		2	2413.8733
						K.LAQENGWGVMVSHR.S	0.9958		2	1584.793
1298	ENPL_MOUSE	802	26.81	13	140	R.FQSSHHSTDITSLDQYVER.M	0.9958		2	2251.3739
						R.ELISNASDALDK.I	0.9958		1	1276.3861
						K.NLLHVTDTGVGMTR.E	0.9944	1,2		1514.7399
						K.TVWDWELMNDIKPIWQRPSK.E	0.9958		2	2543.9458
						R.EEEAIQLDGLNASQIR.E	0.9958		2	1786.9365
						R.LISLTDENALAGNEELTVK.I	0.9958		2	2031.2677
						K.EFEPLLNWMKDK.A	0.9958		2	1550.8127
						K.YSQFINFPIYVWSSK.T	0.9958		2	1880.1528
						K.EFEPLLNWMK.D	0.9958	1,2		1307.55
						K.GVVDSDDLPLNVSR.E	0.9958		2	1486.6219
						K.LGVIEDHSNR.T	0.9958		1	1140.2413
						K.KGYEVIYLTEPVDEYCIQALPEFDGK.R	0.9958		2	3078.4084
						R.RVFITDDFHDMMPK.Y	0.9958		2	1753.0437
1299	ENPP1_MOUSE	906	8.28	3	4	K.SGTYFWPGSDVEIDGILPDIYK.V	0.9931		2	2473.7412
						K.SWVEETCESIDTPECPAEFESPPTLLFSLD(	0.9958		3	3848.0971
						R.AEYLHTWGGLLPVISK.L	0.9958		2	1785.0959
1300	ENPP3_MOUSE	874	5.72	2	3	K.ADRPSFYTIYVEEPDSAGHSSGPVSAGVIK	0.9958		3	3138.4173
						K.SMEAIFLAHGPSFIEK.T	0.9958		2	1778.0759
1301	ENSA_MOUSE	121	30.58	2	33	K.NLVTGDHIPTPQDLPQR.K	0.9958		2	1902.1173
						K.YPSLGQKPGGSDFLMK.R	0.9958		2	1726.0002
1302	ENTP2_MOUSE	495	8.48	2	5	R.AGQSLVECLEQALR.D	0.9958		2	1574.7405
						R.ILSGQDEGVFGWVTANYLLENFIK.Y	0.9929		2	2715.0777
1303	EP15_MOUSE	897	13.94	5	8	R.FHDSSSPLLTSGPSVAELPWAVK.S	0.9958		2	2426.7313
						K.AKYDAIFDSLSPVDGFLSGDK.V	0.9958		2	2246.4785
						K.AEITSQESQISSYEEELLK.A	0.9958		2	2185.3465
						K.AQLEPLQQHLQESQQEISSMQMR.L	0.9958		3	2741.0662
						K.NITGSSPVADFSAIKELDTLNNEIVDLQR.E	0.9944		3	3161.4931
1304	EP15R_MOUSE	907	6.95	3	4	K.LDPFESSDPFSSSSISSK.G	0.9958		2	1918.0209
						K.FDGIFESLLPVNGLLSGDK.V	0.9915		2	2022.3055
						R.STPSHGSVSSLNSTGSLSPK.H	0.9958		2	1931.0666
1305	EPB42_MOUSE	691	12.74	4	13	K.SVLPISQTQAAQEGALLYK.R	0.9944		2	2018.3177
						R.APTHTFLSALK.K	0.9958		2	1186.3965
						R.CLGIPARVVTTFDSAQGTVGSLLVDEYYNE	0.9958		3	4345.6893

						R.VVGALLHALK.K	0.9958		2	1021.2913
1306	EPC2_MOUSE	808	2.1	1	3	R.YHLGDYGGEILNEVK.V	0.9952		2	1707.8803
1307	EPHA5_MOUSE	877	5.93	2	2	K.ENQYIK.I	0.9958		1	794.8827
						K.FTSASDVWSYGIVMWEVVSYGERPYWEM	0.9958		3	4980.5338
1308	EPHA6_MOUSE	1035	8.21	3	3	K.FKPSQYIKIDTIAADESFTQMDLGDR.I	0.9958		3	2991.3423
						R.TNWISRDAAQK.I	0.9958		2	1290.4215
						K.LIRNPSALHTLVEDILVMPESPGDVPEYPLF	0.9944		3	4678.3974
1309	EPHA7_MOUSE	998	2	1	3	R.MTIDDVMSLGITLVGHQK.K	0.9958		2	1959.3265
1310	EPHB6_MOUSE	1014	7.5	2	2	R.AANSITVSWPQPEQTNGNILDYQLR.Y	0.9958		3	2817.0874
						K.VYFQTLPQGELSSQLPEKLSLVIGSILGALA	0.9931		3	5044.0722
1311	EPIPL_MOUSE	6548	1.79	4	8	K.GFFDPNTHENLTYLQLLER.C	0.9958		2	2308.5553
						K.FAGQTVSVWDLLSSQYFTEGR.R	0.9958		3	2392.6299
						R.GYFDQEMNSILADPGDDTKGFFDPNTHEN	0.9944		3	4405.7957
						R.LLEAQIATGGIIDPVHSHR.V	0.9958		2	2028.3188
1312	EPMIP_MOUSE	606	10.89	2	14	R.NQHTLSQPLTDEHLQALFR.V	0.9931		2	2249.4911
						K.AVSPNCWNVIHYSGFLHLELLSSYDVDINQ	0.9958		3	5020.7206
1313	EPN1_MOUSE	575	2.43	1	2	K.NIVHNYSEAEIK.V	0.9955		2	1417.5614
1314	EPN3_MOUSE	636	7.23	2	2	R.TPVLPSGPPIADPWAPSSPTR.K	0.9958		2	2144.435
						R.TPESFLGPSASSLVNLDSLVK.A	0.9958		2	2162.4448
1315	EPN4_MOUSE	631	2.54	1	10	K.HIHITQATETTTTR.H	0.9958		2	1610.7672
1316	ERAP1_MOUSE	930	2.69	2	2	K.LLKDLIDK.Q	0.9958		1	958.1863
						K.SGVKVSVYAVPDK.I	0.9924		1	1349.57
1317	ERC2_MOUSE	957	3.34	2	2	R.LLEILKEVENEK.N	0.9958		2	1457.7075
						R.GAEHFTIELTEENFRR.L	0.9924		2	1950.1179
1318	ERCC2_MOUSE	760	4.87	2	2	K.LLFIETQDGAETSVALEK.Y	0.9958		2	1965.2078
						R.QMPLPAGIYNLDDLK.A	0.9924		2	1688.9794
1319	ERCC3_MOUSE	783	5.62	2	2	K.RCICLEYPLLAEYDFR.N	0.9958		2	2119.3571
						K.LTAYSLYAAVSVGLQTSDITEYLR.K	0.9944		3	2635.9739
1320	ERG_MOUSE	486	9.67	2	2	K.MVGSPDTVGMSYGSYMEEK.H	0.9958		2	2069.3237
						R.VIVPADPTLWSTDHVRQWLEWAVK.E	0.9958		3	2848.2767
1321	ERG1_MOUSE	572	4.55	2	2	R.FIMSLR.K	0.9958		1	766.9769
						R.EYMAEQIYPQLPEHLK.E	0.9958		2	1990.2812
1322	ERGI1_MOUSE	290	8.97	1	2	K.LSFGDTLQVQNVHGAFNALGGADR.L	0.9958	2,3		2488.722
1323	ERLN1_MOUSE	346	13.01	2	6	K.IEEGHLAVYYRGGALLTSPSGPGYHIMLPF	0.9958		3	3866.4724
						K.TLIFNK.I	0.9958		1	735.9017
1324	ERO1A_MOUSE	464	1.72	1	6	R.ELENFR.H	0.9958		1	807.8815
1325	ES1_MOUSE	266	76.32	16	1652	K.NVLELTGK.-	0.9924		1	874.0251

						K.ITSLAQLNAANHDAAIFPGGFGAAK.N	0.9909	2	2456.7636
						R.GGAEVQIFAPDVPQMHVIDHTK.G	0.9958	2	2390.7191
						K.GVEVTVGHEQEEGGKWPYAGTAEAIK.A	0.9958	2	2743.9897
						K.NLSTFAVDGK.D	0.9958	1	1052.1723
						K.WPYAGTAEAIK.A	0.9958	1	1207.3715
						R.VALVLSGCGVYDGTEIHEASAILVHLSR.G	0.9958	2	2968.3459
						K.KPIGLCCIAPVLAAK.V	0.9943	2	1611.941
						R.NVLAESAR.I	0.9924	1	859.9578
						K.GVEVTVGHEQEEGGK.W	0.9958	1,2	1555.6415
						K.GVTEAHVDQK.N	0.9958	1	1084.1741
						K.VVTTPAFMCETALHHIHDGIGAMVK.N	0.9958	2,3	2737.1733
						R.GGAEVQIFAPDVPQMHVIDHTKGEPSER.E	0.9958	3	3046.3844
						R.GKITSLAQLNAANHDAAIFPGGFGAAK.N	0.9958	2	2641.9896
						K.VIKGVEVTVGHEQEEGGK.W	0.9958	2	1896.1075
						K.HCVKGVTEAHVDQK.N	0.9929	2	1608.7606
1326	ESAM_MOUSE	394	7.36	1	2	R.VLFLGLSTLAAFSRAQMELHVPPGLNK.L	0.9958	3	2911.4784
1327	ESPL1_MOUSE	2118	3.4	4	21	K.KVHTQK.G	0.9944	1	740.8808
						R.YTEALLQGWLGAGPGAPFLYYASQAR.Q	0.9952	2	2802.1613
						K.ERPGGVPLARIQR.L	0.9952	2	1449.6993
						K.LLRSIIILLMGSDVLSIQK.A	0.9958	3	2113.6507
1328	EST1_MOUSE	565	3.54	1	6	R.NGNPNGEGLPHWPEYDQK.E	0.9958	2	2053.1546
1329	ESTD_MOUSE	282	82.98	13	185	R.MYSYVTEELPQLINANFPVDPQR.M	0.9958	2	2726.076
						K.SGYQQAASEHGLVVIAPDTSPR.G	0.9958	2	2284.4905
						R.LQEGYDHSYYFIATFIADHIR.H	0.9958	2	2560.8278
						K.GEDDSWDFGTGAGFYVNATEDPWK.A	0.9958	2	2665.7449
						K.AYSGSQIDILIDQGK.D	0.9958	2	1608.7887
						R.SVSAFAPICNPVLCSWGK.K	0.9958	2	1994.23
						K.VFEHSSVELK.C	0.9958	1	1175.3269
						K.AYSGSQIDILIDQGKDDEFLSNGQLLPDNFI.	0.9958	3	4088.4371
						K.CPALYWLSGLTCTEQNFISK.S	0.9958	2	2389.6424
						K.DDEFLSNGQLLPDNFIAACTEK.K	0.9958	2	2498.6716
						R.FAVYLPPQAESGK.C	0.9958	2	1407.6091
						K.AFSGYLGPDESK.W	0.9958	1	1271.3691
						R.MSIFGHSMGGHGALICALK.N	0.9958	2	1988.3394
1330	ESTHL_MOUSE	556	5.04	1	2	K.QVHVGDTPIQVFLGIPFSKPPVGTRR.F	0.9958	3	2847.3359
1331	ESTN_MOUSE	554	47.65	15	176	K.ISEDCLYLNIYSPADLTK.S	0.9958	2	2116.3387
						K.AEEVAFWTELPAK.N	0.9958	1,2	1491.6837

						R.LKAEEVAFWTELPAK.N	0.9956		2	1733.0172
						R.YRPSFVSDK.R	0.9958	1,2		1099.2315
						K.RPQMVEGDHGDEIFSVFGAPLLK.E	0.9944		2	2543.9
						K.MNEETASLLLR.R	0.9958		2	1277.4785
						R.QKTESELLEISGK.L	0.9958		2	1462.6403
						K.EGYLQIGATTQQAQR.L	0.9911		2	1664.8155
						R.FHSELNISESMIPAVIEK.Y	0.9958		2	2045.3582
						R.LGIWGLFSTGDEHSQGNWAHLDQLAALR.\	0.9958		2	3094.416
						K.RPQMVEGDHGDEIFSVFGAPLLKEGASEE	0.9958		3	3819.1915
						K.YISLEGFEQPVAVFLGVPFAKPPLGSLR.F	0.9958	2,3		3033.5835
						R.DAGVSTYMYEFR.Y	0.9958		1	1439.5824
						R.NGNPNGEGLPHWPEYDEK.E	0.9958		2	2054.1393
						K.KNIQAVNEIIATLSQCNDTSSAAMVQCLR.Q	0.9958		3	3237.585
1332	ESYT1_MOUSE	1092	9.25	4	4	R.LTHGDSPSEAPVGPLGQVK.L	0.9958		2	1890.1033
						K.VLQAGVLDNWYPLQGGQGQVHLR.L	0.9958		2	2549.8949
						K.VQLDLAEIDLSQGAAQWYDLMDDR.D	0.9958		2	2767.0393
						R.LERLTPRPTAAELEEVLQVNSLIQTQK.S	0.9944		3	3078.5363
1333	ESYT2_MOUSE	845	2.84	2	2	R.VNGVK.V	0.9958		1	516.6182
						R.SSSSLLASPSHIAAK.E	0.9958		2	1456.639
1334	ETFA_MOUSE	333	75.08	18	2997	K.DPEAPIFQVADYGIVADLFK.V	0.9958		2	2209.5035
						R.AAVDAGFVPNDMQVGQTGK.I	0.9958		1	1906.1205
						K.APSSSSVGISEWLDQK.L	0.9958	1,2		1691.8351
						K.GLLPEELTPLILETQK.Q	0.9958	1,2		1795.1265
						R.GTSFEAAATSGGSASSEK.A	0.9958		2	1645.6769
						K.LNVAPVSDIIEIK.S	0.9958		1	1411.6818
						K.LLYDLADQLHAAVGASR.A	0.9958		2	1814.0513
						K.VLVAQHDAYK.G	0.9958		1	1144.3158
						K.QFSYTHICAGASAFGK.N	0.9958		2	1745.8981
						K.IVAPELYIAVGISGAIQHLAGMK.D	0.9958		3	2352.8407
						K.TIVAINKDPEAPIFQVADYGIVADLFK.V	0.9931		2	2949.4167
						K.SDRPELTGAK.V	0.9937		2	1074.179
						K.QFSYTHICAGASAFGKNLLPR.V	0.9958		3	2339.625
						R.LGGEVSCLVAGTK.C	0.9958		1	1291.4534
						R.TIYAGNALCTVK.C	0.9958		2	1311.487
						K.TIVAINK.D	0.9958		1	758.9365
						K.VVPEMTEILK.K	0.9958		1	1159.4266
						K.VVQDLCK.V	0.9924		1	861.98

1335	ETFB_MOUSE	255	75.69	17	1386	K.AGDLGVDLTSK.V	0.9958	1	1076.1919
						R.VIDFAVK.I	0.9924	1	791.9658
						K.HSMNPFCEIAVEEAVR.L	0.9958	2	1890.087
						R.GIHVEIPGAQAESLGPLQVAR.V	0.9924	2	2143.4508
						R.LKLPAVVTADLR.L	0.9921	2	1296.5962
						K.QAIDDDCNQTGQMTAGLLDWPQGTFASQ'	0.9958	3	3813.0639
						K.LPAVVTADLR.L	0.9958	1,2	1055.2627
						K.RVIDFAVK.I	0.9958	2	948.1533
						K.EKVDLLFLGK.Q	0.9958	2	1162.4148
						K.EIIAVSCGPSQCQETIR.T	0.9958	2	1949.1005
						K.QAIDDDCNQTGQMTAGLLDWPQGTFASQ'	0.9958	3	4040.3706
						K.VDLLFLGK.Q	0.9958	1	905.1253
						R.EIDGGLETLR.L	0.9958	1	1103.2175
						K.VSVISVEEPPQR.S	0.9958	1,2	1340.5193
						R.TALAMGADR.G	0.9944	1	906.0447
						K.VETTEDLVAK.L	0.9958	1	1105.2304
						K.KIEVVK.A	0.9958	1	715.9114
1336	ETFD_MOUSE	616	63.31	20	671	K.LTFPGGLLIGCSPGFMNVPK.I	0.9958	2	2106.4969
						R.FCPAGVYEFVPLEQGDGFR.L	0.9958	2	2189.3979
						K.AAQIGAHTLSGACLDPAAFK.E	0.9958	2	2000.228
						K.DPSQNINWVVPEGGGGPAYNGM.-	0.9958	2	2260.4425
						K.GAPLNTPVTEDR.F	0.9958	2	1270.3849
						R.FAEEADVVIVGAGPAGLSAAIR.L	0.9912	2	2114.4063
						R.ALNEGGLQSIPK.L	0.9958	2	1227.4032
						K.TTGLHVTEYEDNLK.Q	0.9958	1,2	1620.7563
						R.LQINAQNCVHCK.T	0.991	2	1485.6153
						K.VTVFAEGCHGHLAK.Q	0.9958	2	1526.7014
						K.DCTPIEYPKPDGQISFDLLSSVALSGTNHEI	0.9958	3	4433.8414
						R.LGHLVSWMGEQAEALGVEVYPGYAAAEVI	0.9958	3	3977.4371
						R.HTYGGSFLYHLNEGEPLVAVGFVVGLDYQ	0.9958	3	4158.6617
						R.IPVPILPGLPMNNHGNYIVR.L	0.9958	2	2215.6647
						K.DDSIPVNRNLSIYDGPEQR.F	0.9958	2	2189.3464
						R.VDHTVGWPLDR.H	0.9958	1,2	1295.4404
						K.RWEGVNMER.F	0.9917	1	1177.3232
						K.HHPSIQPTLEGGK.R	0.9958	1	1401.565
						K.HKGSDSDQLKPAK.D	0.9958	2	1411.5577
						K.TCDIKDPSQNINWVVPEGGGGPAYNGM.-	0.9958	2	2878.1085

1337	ETHE1_MOUSE	254	59.84	7	55	R.LSGAQADLHIGEGDSIR.F	0.9958	2	1739.8827
						K.VMDNLNLPKPQQIDIAVPANMR.C	0.9958	2	2478.9306
						K.IFTLPGNCLIYPAHDYHGLTVSTVEEER.T	0.9958	3	3233.5708
						R.ASPGHTPGCVTFVLNDQSMAFTGDALLIR.	0.9958	3	3077.4481
						R.EAVLIDPVLETAHR.D	0.9958	2	1563.7941
						K.LLYAVNTHCHADHITGTGVLR.S	0.9958	2	2349.6207
						K.TLYHSVHEK.I	0.9944	1,2	1114.2462
1338	ETUD1_MOUSE	1127	9.94	4	5	K.IHISVSEPIIPFR.E	0.9958	2	1508.8039
						K.IPEGIHVDSDGLITIPTPNK.L	0.9943	2	2117.4069
						R.ICDGCIIVVDAVEGVCPQTQAVLRQAWLEN	0.9911	3	4449.092
						R.VPLGFSAPLEDLPPVPHMACCTLENLYLLM	0.9958	3	3613.1997
1339	EVC_MOUSE	1005	3.48	2	12	R.INAYKLWK.K	0.9958	1	1036.2621
						R.LVQAHYQAVGKLLQAHEEQLLQR.L	0.9944	3	2674.0781
1340	EVG1_MOUSE	216	21.3	2	2	K.AASAIYLPPILATHSHLRPASLCQANGAYSF	0.9924	3	4394.9493
						R.EQFKPQATRDLEK.E	0.9958	2	1590.7764
1341	EVPL_MOUSE	2035	2.16	2	2	K.ELDEDIQAIHSARQGSGSPAHAR.T	0.9911	3	2446.5986
						R.QVLSWARSPLSQSSSLK.D	0.9958	3	1875.135
1342	EVX2_MOUSE	475	13.47	2	2	K.EMILMERGLHSPTAGK.R	0.9958	2	1771.1029
						R.GGGGSGGGGGGGAGTAGGSDFGCSAAA	0.9958	3	3805.9763
1343	EWS_MOUSE	655	4.89	2	2	K.QCGVVKMNK.R	0.9958	1	1064.2543
						K.APKPEGFLPPPFPPPGGDR.G	0.9958	2	1974.2694
1344	EXOC2_MOUSE	924	2.92	3	3	K.LVLSQLPNFWK.L	0.9937	2	1345.6274
						R.FKFLFNLPLNIK.R	0.9924	1	1494.8632
						K.FLFNLPLNIK.R	0.9958	1	1219.5125
1345	EXOS9_MOUSE	438	3.88	1	3	K.EGGKFGFAESIANQR.I	0.9944	1	1611.7544
1346	EZH2_MOUSE	746	2.82	1	2	K.DTDSDREAGTETGGENNDK.E	0.9944	2	2011.9213
1347	EZRI_MOUSE	586	28.33	14	84	K.SQEQLAAELAEYTAK.I	0.9958	1,2	1652.7985
						K.FYPEDVAEELIQDITQK.L	0.9958	2	2039.2463
						K.FVIKPIDK.K	0.9958	1	960.2047
						K.KAPDFVFYAPR.L	0.9958	2	1311.526
						R.RKPDTIEVQQMK.A	0.9947	2	1473.7307
						R.QLLTLSNELSQAR.D	0.9958	2	1473.6695
						K.APDFVFYAPR.L	0.9958	2	1183.3519
						K.KFVIKPIDK.K	0.9958	1	1088.3787
						R.ILQLCMGNHELYMR.R	0.9958	2	1779.0914
						K.DGILSDEIYCPPETAVLLGSYAVQAK.F	0.9958	2	2811.1243
						R.THNDIIHNENMR.Q	0.9958	2	1494.625

						R.IQVWHAEHR.G	0.9958		2	1176.3231
						K.IGFPWSEIR.N	0.9912		2	1105.2816
						R.KPDTIEVQQMK.A	0.9958	1,2		1317.5432
1348	F101A_MOUSE	204	13.24	1	2	K.IFYAPVPTVTAYSETIVAAPNCTWR.S	0.9958		3	2829.1908
1349	F10A1_MOUSE	371	12.94	3	67	R.LLGHWEEAAHDLALACK.L	0.9958		2	1935.1559
						K.LDYDEDASAMLR.E	0.9958		2	1399.5152
						K.KGAAIEALNDGELQK.A	0.9958		2	1557.7441
1350	F110A_MOUSE	296	34.12	3	3	R.TPGRPEGSAHKVPPATPPRPPPSTVAVR.F	0.9944		3	2858.276
						R.VDVRPLPASPARPYPSPGTTTTSSPGRPP(	0.9958		3	3630.1013
						R.GLGVAHLARASSDIVSLAGPSAGPCSSEG(	0.9958		3	3185.4101
1351	F110B_MOUSE	366	13.66	2	2	K.VYPTPGHGSPQESSSHVSR.R	0.9907		2	2010.1301
						K.SQEVINAKQEPVKPAVLAKPPVCPGTK.R	0.9958		3	2887.3587
1352	F111A_MOUSE	613	1.96	1	2	K.LFQVAAELPK.N	0.9958		1	1116.3458
1353	F113A_MOUSE	449	21.83	3	3	K.HDRLPDPWIEDWSEMDHSFQGSHK.Q	0.99		3	2951.1584
						R.MDQVLPDSCLLVWNLAMPLGERVTGGFLL	0.9958		3	4451.2515
						K.AKGELSFEQDQLVAGGQLGELHNGTQYR.	0.9958		3	3047.3109
1354	F1142_MOUSE	497	5.03	1	4	K.SLLSSASATVATVGQGISNVIEK.A	0.9958		2	2233.5242
1355	F115A_MOUSE	924	2.06	1	4	K.VLFTVGKLGPFLLNAVR.W	0.9958		2	1845.2816
1356	F122A_MOUSE	284	15.85	2	3	K.RIDFIPVSPAPSPTR.G	0.9958		2	1653.9218
						R.SNSAPLIHGLSDSSPVFQAEAPSARR.N	0.9958		3	2695.9517
1357	F133B_MOUSE	245	5.31	1	3	K.GSKALAEFEEK.M	0.9958		1	1209.3415
1358	F135A_MOUSE	1506	5.05	2	2	K.LHTFLSLSGPHLGTLYNSSALVNTGLWFM(	0.9958		3	3749.3679
						K.IGPWTELQEAELFVDNLLPDFEALDSNDKP	0.9958		3	4469.9892
1359	F136A_MOUSE	138	42.03	3	49	R.CHAPLAQAQALVTSELER.F	0.9958	2,3		1995.209
						R.CSANCCEDTQASMQQVHQCIER.C	0.9958	2,3		2713.7569
						K.CVDDHMHLIPTMTK.K	0.9958		2	1698.9589
1360	F13A_MOUSE	732	4.78	2	7	K.DYLNVTAVHLFK.E	0.9958		2	1420.6512
						K.ETLQNVWIHLDGPGVMRPK.R	0.9943		2	2191.556
1361	F16P2_MOUSE	339	21.24	4	23	R.TLVYGGIFMYPANQK.S	0.9958		2	1703.0087
						K.GTGELTQLLNSMLTAIK.A	0.9958		2	1791.1132
						R.VPLILGSPEDVQEYLSCVQR.N	0.9958		2	2303.5836
						R.SPFETDMLTLTR.Y	0.9923		2	1411.6129
1362	F261_MOUSE	471	8.49	2	2	K.IWIPHSSSSSLLQR.R	0.9958		2	1611.8411
						K.VFFIESICNDPDIIAENIKQVK.L	0.9958		2	2593.9459
1363	F91A1_MOUSE	837	3.94	2	2	R.CESLLGLDPATCSRVLNK.N	0.9958		2	2034.2495
						K.ESLQSLLHSSR.K	0.9958		1	1257.3891
1364	FA36A_MOUSE	117	34.19	3	5	R.ESILYGSLGSIVTGLGHFLVTSR.I	0.9958		2	2407.7722

					K.ILYESTHLDPER.K	0.9944	1,2		1473.6256
					K.ILYESTHLDPERK.M	0.9958		2	1601.7997
1365	FA49B_MOUSE	324	6.48	1	6 R.GLLGALTSTPYSPTQHLER.E	0.9958		2	2042.2993
1366	FA76B_MOUSE	339	12.39	2	3 K.QFGTPKPCQYCNIIAAFIGTKCQR.C	0.9944		3	2860.1836
					R.YPFEELSQGQQLCK.E	0.9958		2	1727.8774
1367	FA82B_MOUSE	305	20.33	4	5 K.KVLVYEALDYAK.R	0.9958		2	1412.669
					K.VLFANPPSSTYEEALR.Y	0.9958		2	1795.0019
					K.VEEILAQADYLYESGETEK.L	0.9958		2	2188.3496
					K.LYQLLIQYK.E	0.9958		2	1182.4484
1368	FA83H_MOUSE	1209	2.32	2	2 R.RSQSSSQGDNPLAPGYLPPHYK.E	0.9958		3	2400.6127
					R.SQSSSQGDNPLAPGYLPPHYKEYYR.L	0.9944		3	2856.0801
1369	FA96B_MOUSE	163	14.11	1	9 R.VAAALENTHLLEVVNQCLSAR.S	0.9958		2	2309.5939
1370	FA98A_MOUSE	515	17.48	3	6 R.GGRPNEIEPPPPEMPPWQK.R	0.9958		2	2157.4516
					K.HQGGWTDGGSGSGGGYQDGAYR.D	0.9958		2	2171.1631
					R.DSGFQPGGYHGGHSGGYQAGGYGGFQT	0.9958		3	4554.5945
1371	FAAA_MOUSE	419	36.75	8	53 R.IGVAIGDQILDLSVIK.H	0.9958		2	1654.9878
					R.DIQQWEYVPLGPFLGK.S	0.9944		2	1891.1766
					R.AFTSQASATMHLPATIGDYTDFYSSR.Q	0.9924		2	2840.0931
					K.HLFTGPALSK.H	0.9958		1	1071.2645
					R.ASLQNLLSASQAR.L	0.9958		2	1359.5253
					R.TFLLDGDEVIITGHCQGDGYR.V	0.9958		2	2367.5433
					K.ENALLPNWLHLPVGYHGR.A	0.9958		2	2087.3915
					K.HQHVFDETTLNNFMGLGQAAWK.E	0.9958		2	2545.8346
1372	FABD_MOUSE	381	32.02	6	16 R.VISGHLEALQFLR.R	0.9958		2	1483.7538
					R.AEAMQEASEAVPSGMLSVLGQR.Q	0.9958		2	2262.558
					K.KPLVAVHSNVSGQK.Y	0.9958		2	1464.7079
					R.TVHCQPAVFVASLAAVEK.L	0.9958		2	1928.2048
					K.GMEFPSTYEVGPGQQLGSILK.C	0.9958		2	2239.5482
					K.MLPVSGGFHTCLMEPAVDPLMK.V	0.9958		3	2431.8949
1373	FABP4_MOUSE	132	65.91	7	371 K.LGVEFDEITADDR.K	0.9958		2	1480.5713
					K.LVSSENFDDYMK.E	0.9958	1,2		1448.5873
					K.LGVEFDEITADDRK.V	0.9958		2	1608.7453
					K.SIITLDGGALVQVQK.W	0.9937		2	1542.8161
					K.NTEISFK.L	0.9944		1	838.9359
					K.VAGMAKPNMIISVNGDLVTIR.S	0.9944		2	2200.663
					K.LVVECVMK.G	0.9958		1	978.2013
1374	FABP5_MOUSE	135	54.81	5	21 K.TETVCTFQDGALVQHQQWDGK.E	0.9958		2	2449.6049

						R.KTETVCTFQDGALVQHQQWDGK.E	0.9958	2,3		2577.779
						K.TTVFSCNLGEK.F	0.9958	1,2		1256.3643
						R.LMESHGFEEYMK.E	0.9958		2	1501.712
						K.MAAMAKPDCIITCDGNNITVK.T	0.9944		2	2324.645
1375	FABP7_MOUSE	132	9.85	2	3	K.LIHVQK.W	0.9958		1	737.9205
						R.LDGDKLIHVQK.W	0.9924		1	1266.4832
1376	FABPH_MOUSE	133	96.24	17	13015	K.NTEINFQLGIEFDEVTADDR.K	0.9958		2	2327.4662
						-.MADAFVGTWK.L	0.9958		1	1126.3154
						K.WNGQETTLTR.E	0.9958		2	1206.3005
						K.NFDDYMK.S	0.9924		1	933.0234
						R.QVASMTKPTTIIEKNGDTITIK.T	0.9958		2	2390.798
						K.NTEINFQLGIEFDEVTADDRK.V	0.9949		2	2455.6403
						R.QVASMTKPTTIIEK.N	0.9958		2	1547.8505
						K.LILTLTHGSVVSTR.T	0.9958		2	1497.7782
						K.LIHVQKWNGQETTLTR.E	0.9958		2	1925.1979
						K.NGDTITIK.T	0.9915		2	861.9707
						K.SLVTLDGGK.L	0.9958		1	890.0245
						K.LVDSKNFDDYMK.S	0.9958		2	1475.6563
						K.SLGVGFATR.Q	0.9932		2	908.0452
						K.SLVTLDGGKLIHVQK.W	0.9958		2	1608.9218
						R.ELVDGKLILTLTHGSVVSTR.T	0.9958		2	2139.5003
						K.TQSTFK.N	0.9944		1	711.7929
						R.ELVDGK.L	0.9924		1	660.7453
1377	FAD1_MOUSE	492	17.28	5	6	R.LPQGSLVPYQPDAVEK.A	0.9958		2	1741.9817
						R.VSVVPDEVATIASEVNSFSR.R	0.9958		2	2107.3251
						R.SISPFPELEQFLQDTIK.R	0.9958		2	1993.264
						R.FPLVSVR.N	0.9924		1	818.0067
						K.DCTALLHLFHAAVQR.K	0.9958		2	1752.9799
1378	FADD_MOUSE	205	19.51	2	10	R.VQSGLDLFTVLLEQNDLER.G	0.9958		2	2190.4582
						R.LNLVADLVEEAQESVSK.S	0.9947		2	1845.0569
1379	FAF1_MOUSE	649	7.09	3	4	K.SLLEVNLFPQETLFLQAK.E	0.9958		2	2091.4552
						R.HFGSVIAQTIR.T	0.9958		2	1229.4245
						K.EENAEPVSKLR.I	0.9958		1	1272.4007
1380	FAH2A_MOUSE	313	57.83	9	108	R.LVQFQAPHLEEPHLGLESGVGGGVVDLNA	0.9958		3	3773.2371
						K.ATDVMAHVAGFTVAHDVSAR.D	0.9958		2	2056.3037
						K.TFDTFCPLGPALVTK.D	0.9958		2	1667.9086
						K.VICVGLNYADHCQEQNVR.V	0.9958		2	2176.3258

						K.FSSSIVGPYDEIILPPESK.E	0.9958	2	2079.3545
						K.TMVQFLEQGETTLSVAR.R	0.9958	2	1911.1804
						R.ALATQLPVIPR.S	0.9958	1,2	1179.4483
						K.KGDEVQCEIEELGVIINK.V	0.9958	2	2074.302
						K.EVDWEVEMAVVIGK.K	0.9941	2	1604.8585
1381	FAHD1_MOUSE	227	35.68	4	146	K.IITLEEGDLILTGTPK.G	0.9958	2	1714.0093
						K.SFTSSCPVSAFVPK.E	0.9958	2	1514.6844
						R.NLHHEVELGVLLGK.R	0.9958	2	1558.821
						R.STVLSEPVLFLKPSTAYAPEGSPVLMPAYC	0.9958	2,3	3382.9057
1382	FAM21_MOUSE	1334	4.27	2	2	K.SASLPSSQPPTSVSLFGDEDEEDSLFGSA/	0.9944	2	3356.5781
						K.SRPQTGNEADLFDSGDIFPK.S	0.9958	2	2195.3501
1383	FAM45_MOUSE	357	6.16	1	3	R.FPPATENFLYHLAAAEQMLK.V	0.9958	2	2292.6575
1384	FANCA_MOUSE	1439	1.74	1	2	R.EELLIALFFFSLMGLLSSYLTQR.D	0.9944	3	2693.2165
1385	FANCB_MOUSE	703	4.41	2	5	K.GDSLPSDEMVK.L	0.9958	1	1178.2995
						R.FFIVSFPSKACAVSEK.K	0.9924	1	1818.0888
1386	FANCI_MOUSE	1330	3.23	2	3	K.SPVTLLRDLSQDIHGQLGDIDQDVEIEK.T	0.9958	3	3135.4552
						K.EKAAVSTTMAK.V	0.9944	1	1137.3367
1387	FANCJ_MOUSE	1174	1.45	1	26	K.VRTIVLTSGTLSPLK.S	0.9923	2	1585.9279
1388	FAS_MOUSE	2504	11.18	16	60	R.LLLPEDPLISGLLNSQALK.A	0.9958	2	2035.4319
						R.LQVVDRPLPVR.G	0.9944	2	1292.5674
						R.TLLEGSGLESIINIIHSSLAEPR.V	0.9958	2	2450.7948
						R.DTSFEQHVLLHTGGK.G	0.9958	2	1669.8345
						K.AAMLGQEDPPQHGLPR.L	0.9958	2	1717.9402
						R.GYDYGPQFQGICEATLEGEQGK.L	0.9958	2	2448.5708
						R.IPALLNTQPMLQLEYTATDR.H	0.9958	2	2289.652
						K.FVFTPHMEAECLSESTALQK.E	0.9958	2	2326.5923
						K.SNMGHPEPASGLAALTK.V	0.9958	2	1681.9042
						K.AVAHILGIR.D	0.9958	2	950.1722
						K.VAEVLAGEGHLYSR.I	0.9958	2	1501.6823
						R.FPQLDDTSFANSR.D	0.9958	2	1498.592
						K.FDASFFGVHPK.Q	0.9958	2	1252.4148
						R.CILLSNLSNTSHAPK.L	0.9958	2	1655.8578
						K.LPESENLQEFWANLIGGVDMVTDDDRR.W	0.9944	3	3121.4052
						R.IRCILLSNLSNTSHAPK.L	0.9958	1	1925.2047
1389	FAT3_MOUSE	4555	2.52	4	4	K.VLDLNDNKPVFETSTYETIIMEGMPVGTK.L	0.9958	3	3243.7115
						R.VPVYNLIARATDGGGR.F	0.9944	1	1659.8857
						R.TTFCTVRVIVVDENDNAPQFMTVEYR.A	0.9944	3	3106.4432

						K.DLGSNGEVMYSVLTDTHQFIINSSTGIVYIA	0.9958	3	3974.3882
1390	FAT4_MOUSE	4981	1.14	2	2	R.QVFQVMEEQPPGTLVGTIPTRPGFTYR.L	0.9944	3	3050.5023
						R.VASALVPSQLIYNLIVSATDLGPERR.K	0.9952	2	2784.2285
1391	FBF1_MOUSE	1173	2.05	2	6	R.EERAGPPK.D	0.9958	1	883.9798
						K.DLDSMDDDLFGR.M	0.9958	1	1399.4718
1392	FBLI1_MOUSE	375	22.93	4	29	K.FAPVCSICENPIIPR.D	0.9943	2	1774.0021
						R.EVSTDVCGFCHKPVSPR.E	0.9948	2	1976.1285
						K.AFHPPCFTCVTCARCISDESFALDSQNQVY	0.9944	3	4494.7479
						R.ARPWEMLPTK.T	0.9944	2	1229.4827
1393	FBN1_MOUSE	2871	21.39	31	207	R.GQCVKPLFGAVTK.S	0.9958	2	1405.6464
						K.YQCACNPGYHPTHDR.L	0.9952	2	1876.9147
						K.CICKPGFQLASDGR.Y	0.9944	2	1609.7547
						K.ILCPGGEGFRPNPITVILEDIDECQELPGLC	0.9958	3	3884.2735
						K.GEGWGDPCELCPTEPDEAFR.Q	0.9958	2	2323.3663
						K.TLPGGNQCIVPICR.H	0.9958	2	1585.776
						K.GFVYKPDLK.T	0.9958	1	1067.2731
						R.QICPFGSGIIVGPDDSAVDMDECKEPDVCF	0.9958	3	3368.592
						K.ACEDIDECSLPNICVFGTCHNLPGLFR.C	0.9958	3	3196.405
						K.NCVDINECVLNSLLCDNGQCR.N	0.9958	2	2554.6377
						K.TCVDVNECDLNPNICLSGTCENTK.G	0.9958	2	2814.8815
						K.GTCWQTVIDGR.C	0.9958	2	1293.388
						R.GFSLDQSGASCEDVDECEGNHR.C	0.9944	2	2470.4139
						R.CECPVGFFYNDK.L	0.9958	1	1536.6131
						R.CECFPGLAVGLDGR.W	0.9958	2	1551.6716
						K.TGCTDINECEIGAHNCGR.H	0.9958	2	2065.059
						R.CWSPGVTVAPEMCPIR.S	0.9958	2	1861.0981
						R.CICPPGYSLQNDK.C	0.9958	2	1552.6564
						R.RPDGEGCIDENECQTKPGICENGR.C	0.9958	3	2792.8312
						K.GYIGTHCGQPVCESGCLNGGR.C	0.9958	2	2280.3571
						K.GSFICHCDMGYSGK.K	0.9958	2	1619.7213
						K.VIHDVCR.N	0.9958	1	899.0037
						R.GSYHCICK.T	0.9958	1	1025.0815
						R.GWGLHCEICPFEGTVAYK.K	0.9958	2	2125.3204
						R.CNHGFILSHNNDCIDVDECATGNGNLCR.N	0.9958	3	3264.3133
						R.AWNKPCEQCPIPSTDEFATLCGSQRPGFV	0.9924	3	5115.526
						R.AWGHPCEMCPAQPHPCR.R	0.9958	2	2092.2375
						R.RGQCVKPLFGAVTK.S	0.9958	2	1561.8339

						R.TGPCFTVVSNQMCQGQLSGIVCTK.T	0.9958	2	2673.9395
						K.VIHDVCRNGECVNDR.G	0.9958	2	1843.9263
						R.NYYADNQTCDGELLFNMTKK.M	0.9924	2	2426.6259
1394	FBN2_MOUSE	2907	1.51	2	5	R.NCIDIDECLVNR.L	0.9952	2	1521.5995
						R.MCCCTYNVGKAGNKPCEPCPTPGTADFK.	0.9958	3	3222.4242
1395	FBRL_MOUSE	327	22.32	3	4	R.DHAVVVGVYRPPPK.V	0.9958	2	1534.8014
						K.LAAAILGGVDQIHIKPGAK.V	0.9958	2	1873.2492
						K.VLYLGAASGTTVSHVSDIVGPDGLVYAVEF	0.9958	3	3719.1485
1396	FBSH_MOUSE	378	5.03	1	4	R.DLPFSRPQLRVSPATPK.A	0.9958	2	1910.2266
1397	FBW10_MOUSE	1030	3.69	2	3	R.ETTEGKGESSLQCIHEMNR.Q	0.9957	2	2207.343
						K.EEEVVKSSLNQMLDK.T	0.9958	2	1749.9739
1398	FBX10_MOUSE	950	4.84	3	3	R.GSGLQLLPRSDTK.V	0.9924	1	1372.5644
						R.GHGIITKGDGTAVVENDIIGNR.G	0.9944	3	2237.4777
						K.YLLGLIK.S	0.9924	1	820.0629
1399	FBX3_MOUSE	480	2.08	1	7	R.YWRITNAK.G	0.9958	1	1052.2211
1400	FBX38_MOUSE	1194	6.62	3	4	R.NRIIYLRPMQQVDTLTLEQK.L	0.9944	2	2460.8975
						K.SAKVCVMDSEVAEEMTADEEK.D	0.9958	3	2359.5455
						R.CNNSHQTGQAKPFPLEESSCEKGCQVTSE	0.9944	3	3680.8624
1401	FBX40_MOUSE	710	8.31	3	6	K.SQELPATMEMTGLAPWQDGVLER.L	0.9958	2	2560.8995
						K.NVHTDIQSSLDGWFQHR.C	0.9958	2	2041.1899
						K.EHAASVLTGSLGK.S	0.9958	2	1270.4282
1402	FBX41_MOUSE	873	1.49	1	4	R.SNEVISPEILK.M	0.9958	1	1229.4161
1403	FBX43_MOUSE	640	1.41	1	3	K.LYIIQLR.A	0.9944	1	919.1551
1404	FBX6_MOUSE	295	19.32	3	3	R.ASDSNTHEGFFWQGLWQR.L	0.9958	2	2167.3042
						R.NPCAEENLSSWRIDSNGGDR.W	0.9958	2	2278.3227
						R.LWRDLIDVVSLWK.R	0.9919	2	1643.9695
1405	FBX7_MOUSE	523	7.27	2	8	R.AHLSQVLLPTLGFSSDTR.F	0.9958	2	1943.2101
						K.RTQPLEVPESEPTLGQLR.A	0.9958	2	2051.3073
1406	FBX8_MOUSE	319	8.78	2	6	K.FIFCTRTLNWK.K	0.9945	2	1486.7228
						K.QAQGGIDIYHLLK.A	0.9924	1	1456.6848
1407	FBXL8_MOUSE	374	6.42	1	5	R.ALEVRASASPELHTALEELAAR.C	0.9943	3	2335.6225
1408	FCL_MOUSE	321	6.23	1	5	K.NVHINDNVLHSAFEVGAR.K	0.9958	2	1993.1893
1409	FCN2_MOUSE	314	3.5	1	4	K.SYANGVNWK.S	0.9958	1	1039.1356
1410	FDFT_MOUSE	416	4.33	1	2	R.NFIPKMDQDSLSSSLK.T	0.9958	2	1811.0601
1411	FERM1_MOUSE	677	5.02	2	33	K.AVADICKVLNIR.R	0.9958	1	1372.6171
						R.SLMEQSIQEDEQLQLRFK.Y	0.9958	2	2223.506
1412	FERM2_MOUSE	680	22.94	6	18	K.MQHLNPDPQLIPDQITTDVNPECLVSPR.Y	0.9944	3	3229.5983

						K.SREESSGTPAHQLNLR.G	0.9958	2	1782.9107
						K.TSTILGDITSIPELADYIK.V	0.9958	2	2051.3416
						K.EVDEVDAALSDLEITLEGGK.T	0.9958	2	2104.2726
						K.LLIPVAEGMNEIWLR.C	0.9958	2	1755.1284
						K.TMTPTYDAHDGSPLSPTSAWFGDSALSEG	0.9958	3	4916.4243
1413	FETUA_MOUSE	345	44.64	7	934	R.AQNVPLPVSTLVEFVIAATDCTAK.E	0.9958	2	2545.9019
						K.VGQPGAAGPVSPMCPGR.I	0.9958	2	1638.8481
						R.HAFSPVASVESASGETLHSPK.V	0.9958	2	2139.3293
						R.ELACDDPEAEQVALLAVDYLNNHLLQGFK.	0.9958	3	3287.6166
						K.ANLMHNLGGEEVSVACK.L	0.9958	2	1830.032
						R.QLTEHAVEGDCDFHILK.Q	0.9911	2	2013.1804
						R.VMHTQCHSTPDSAEDVR.K	0.9958	2	1971.0748
1414	FEZ1_MOUSE	392	10.2	3	4	R.QTFGSSGADR.Q	0.9924	1	1026.0507
						R.QYLNTVIPYEKK.S	0.9958	1	1496.7465
						K.RFSMEGISNILQSGIR.Q	0.993	2	1809.0935
1415	FEZF1_MOUSE	475	8.42	2	2	K.LVVPAVEKLPSGVAFK.D	0.9958	2	1655.0336
						R.GNVMSTSKPLAFSIERIMAR.T	0.9915	2	2209.63
1416	FFAR2_MOUSE	330	19.7	2	2	R.VEAVVFSSLNASLDPLLFYFSSSVVRR.A	0.9958	3	3004.4558
						R.AVGLAVVTLLNFLVCFGPYNMSHLVGFYLF	0.9944	3	4114.8097
1417	FGD4_MOUSE	766	1.57	1	2	R.YEMLLKDYLK.K	0.9958	1	1316.5983
1418	FGFR2_MOUSE	821	6.46	2	2	R.LSSTADTPMLAGVSEYELPEDPKWEFPR.D	0.9958	3	3167.5141
						K.DGVHLGPNNRTVLIGEYLQIK.G	0.9958	2	2337.6841
1419	FGR_MOUSE	517	6.19	1	6	R.SLSSGHRGYVPSNYVAPVDSIQAEEWYFG	0.9958	3	3345.6519
1420	FHL1_MOUSE	280	42.86	9	117	R.FTAVEDQYYCVDCYK.N	0.9958	2	1962.0517
						R.FVFHNEQVYCPDCAK.K	0.9958	2	1915.0443
						K.GEDFYCVTCHETK.F	0.9937	2	1646.6827
						K.GSSVVAYEGQSWHDYCFHCK.K	0.9958	2	2418.5159
						K.CLHPLASETFVSK.D	0.9958	2	1489.6776
						K.RFVFHNEQVYCPDCAK.K	0.9958	2	2071.2318
						K.NPITGFGK.G	0.9958	1	833.9627
						K.QVIGTGSFFPK.G	0.993	2	1181.3769
						K.AIVAGDQNVEYK.G	0.9958	1	1307.446
1421	FHL2_MOUSE	279	16.49	4	6	K.CAGCTNPISGLGGTK.Y	0.9958	1	1493.5891
						K.KCAGCTNPISGLGGTK.Y	0.9958	2	1621.7632
						R.FDCHHCNESLYGK.K	0.9958	2	1667.7071
						K.KPITTGGVTYR.E	0.9958	1	1193.3885
1422	FIBB_MOUSE	481	39.09	13	87	R.LYIDETVNDNIPLNLR.V	0.9958	2	1903.1424

						K.AHYGGFTVQNEASK.Y	0.9958	2	1509.6182
						K.KYCGLPGEYWLGNDK.I	0.9924	2	1800.9745
						K.HGTDDGVVWMNWK.G	0.9958	2	1545.7124
						R.MGPTELLIEMEDWK.G	0.9945	2	1692.9827
						K.ENENVINEYSSILEDQR.L	0.9958	2	2053.1467
						K.TENGGWTVIQNR.Q	0.9958	2	1375.4838
						R.DNDGWVTTDPR.K	0.9958	2	1276.3049
						K.YQVSVNK.Y	0.9958	1	837.9511
						K.YCGLPGEYWLGNDK.I	0.9958	2	1672.8005
						R.TPCTVSCNIPVVSGK.E	0.9958	2	1619.7877
						R.TMTIHNGMFFSTYDR.D	0.9958	2	1822.0632
						R.KGGETSEMYLIQPDTSIKPYR.V	0.9912	2	2414.7357
1423	FIGL1_MOUSE	683	8.35	2	2	K.GILLFGPPGTGK.T	0.9945	2	1157.3983
						K.EPTAFEVPQLSVCGGSEDADILSSSGHDTI	0.9958	3	4261.5226
1424	FINC_MOUSE	2477	5.45	8	14	K.CERHALQSASAGSGSFTDVR.T	0.9931	2	2137.2395
						K.HYQINQQWER.T	0.9958	2	1402.5119
						R.VVTPLSPPTNLHLEANPDTGVLTVSWER.S	0.9944	3	3044.4344
						R.HALQSASAGSGSFTDVR.T	0.9958	2	1691.7978
						K.LTCQCLGFGSGHFR.C	0.9958	2	1640.7711
						K.YSFCTDHAVLVQTR.G	0.9958	2	1697.8541
						K.DTLTSRPAQGVITTLENVSPPR.R	0.9924	2	2353.6377
						K.LGVRPSQGGEAPR.E	0.9958	2	1324.4825
1425	FIP1_MOUSE	581	7.23	2	3	R.MGLEVIPVTSTTNKITVQQGR.T	0.9958	3	2273.6531
						R.RLPGAIDVIGQTITISR.V	0.9958	2	1811.1349
1426	FIS1_MOUSE	152	18.42	2	18	R.KFQSEQAAGSVSK.S	0.9958	1	1367.5015
						R.GIVLLEELLPK.G	0.9924	1	1224.5266
1427	FKB10_MOUSE	581	9.12	2	2	R.NQDGKITAEELK.L	0.9958	2	1346.4802
						K.IIIPPFLAYGEKGYGTVIPPQASLVFYVLLLD'	0.9931	3	4084.8773
1428	FKB14_MOUSE	211	12.32	1	6	K.EFEKHGAVVNESHHDALVEDIFDK.E	0.9958	3	2766.9836
1429	FKB15_MOUSE	1216	2.8	2	2	R.YVEQSNLMMEK.R	0.9958	1	1372.5941
						K.VPRPTAQPEEEDEDEVSMK.G	0.9958	2	2187.3399
1430	FKB1A_MOUSE	108	64.81	5	60	R.GWEEGVAQMSVGQR.A	0.9929	2	1534.6867
						R.GQTCVVHYTGMLEDGK.K	0.9958	2	1795.971
						K.RGQTCVVHYTGMLEDGK.K	0.9958	2	1952.1585
						K.LIISSDYAYGATGHPGIIPPHATLVFDVELLK	0.9958	3	3652.2249
						K.LIISSDYAYGATGHPGIIPPHATLVFDVELLK	0.9958	3	3409.95
1431	FKBP3_MOUSE	224	28.13	3	82	K.FLQDHGSDSFLAEHK.L	0.9958	2	1731.862

						K.DHLVNAYNHLFESK.R	0.9958	2	1687.8522
						K.KGDVVHCWYTGTLPDGTVFDTNIQTSSK.K	0.9958	3	3128.3881
1432	FKBP4_MOUSE	458	32.53	8	79	K.AAENGAQSAPLPLEGVDISPK.Q	0.9958	2	2065.2878
						K.GEHSIVYLKPSYAFGSVGK.E	0.9958	2	2040.3263
						R.VFVHYTGWLLDGTK.F	0.9909	2	1636.8907
						R.GEGYARPNDGAMVEVALEGYHK.D	0.9945	2	2364.5945
						R.FQIPPHAELR.Y	0.9921	2	1208.4056
						R.RGEAHLAVNDFDLAR.A	0.9958	2	1684.8521
						K.VGEVCHITCKPEYAYGAAGSPPK.I	0.9958	2,3	2492.723
						K.VLQLYPSNK.A	0.9958	1	1062.2541
1433	FKBP9_MOUSE	570	14.74	2	2	R.GSIPGSAVLVFDIHVIDFHNPSDSISITSHYK	0.9958	3	4567.1212
						R.SLLLLLLWVTGQAAPVLGLAVSSELQIQQS	0.9911	3	4150.8145
1434	FKBPL_MOUSE	347	13.83	2	2	R.LLLTLPPPGPPER.T	0.9917	2	1400.7043
						K.CQVLALGFPFGSGMPEGWTELTIGIGQWR	0.9958	3	3466.9453
1435	FLNA_MOUSE	2647	19.68	27	119	R.LVSNHSLHETSSVFVDSLTK.V	0.9958	2	2201.4411
						K.ASGPGLNTTGVPASLPVEFTIDAK.D	0.9958	2	2343.6391
						R.RLTVSSLQESGLK.V	0.9912	2	1418.6335
						R.FGGEHVPNSPFQVTALAGDQPTVQTPLR.S	0.9958	2,3	2965.2951
						K.HTAMVSWGGVSIPNSPFR.V	0.9958	2	1944.2182
						K.YIPVQQGPVGVNVTYGGDHIPK.S	0.9958	2	2339.6561
						K.FNEEHIPDSPFVVPVASPSGDAR.R	0.9917	2	2468.6849
						K.VATVPQHATSGPGPADVSK.V	0.9958	2	1820.0122
						R.VTYTPMAPGSYLISIK.Y	0.9958	2	1742.0833
						K.AFGPGLQGGNAGSPAR.F	0.9958	2	1457.5888
						R.ALTQTGGPHVK.A	0.9944	2	1109.2706
						R.LIALLEVLSQK.K	0.9958	1,2	1227.5303
						K.GLVEPVDVVDNADGTQTVNYVPSR.E	0.9958	2	2545.7655
						R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTI	0.9958	3	3487.8848
						K.VTAQGPGLEPSGNIANK.T	0.9958	2	1653.8326
						K.VHSPSGALEECYVTEIDQDK.Y	0.9958	2	2278.4004
						K.YGGPYHIGGSPFK.A	0.9958	2	1380.5455
						R.APSVANIGSHCDLSLK.I	0.9958	2	1669.8413
						K.VTVLFAGQHIAK.S	0.9952	2	1284.5443
						R.VHGPGIQSGTTNKPNK.F	0.9958	2	1635.8203
						K.VTGPRLVSNHSLHETSSVFVDSLTK.V	0.9958	2	2712.0348
						K.GQHVPGSPFQFTVGPLGEGGAHK.V	0.9944	2	2305.5577
						K.KTHIQDNHDGTYTVAYVPDVPGR.Y	0.9958	2	2584.8076

						K.THEAEIVEGENHTYCIR.F	0.9958	2	2059.1657
						R.YSPSEAGLHEMDIR.Y	0.9958	2	1605.7625
						R.VNVGAGSHPNK.V	0.9958	2	1080.1887
						K.FNGTHIPGSPFK.I	0.9958	2	1302.4753
1436	FLNB_MOUSE	2602	7.26	9	15	K.AEGPGLSKAGVENGKPTHFTVHTK.G	0.9958	2	2463.7556
						K.IPYLPITNFNQNWQDGK.A	0.9958	2	2049.2933
						K.APLIVQFSSPLPGEAVK.D	0.9958	2	1754.0795
						K.YGGELVPHFPAWVK.V	0.9958	2	1600.8601
						K.LENVSVALEFLDHESIK.L	0.9945	2	1944.1919
						R.GQHVTGSPFQFTVGPLGEGGAHK.V	0.9958	2	2309.5461
						K.AHGPGLEGGLVGKPAEFTIDTK.G	0.9958	2	2195.4802
						R.YAPTEVGLHEMHIK.Y	0.9958	2	1625.8829
						K.AGSNMLLIGVHGPTTPCEEVSMK.H	0.9958	2	2429.775
1437	FLNC_MOUSE	2726	20.62	29	165	R.VEESTQVGGDPFPAVFGDFLGR.E	0.9958	2	2325.5395
						R.APLQVAVLGPTGVAEPVEVR.D	0.9958	2	2003.3494
						K.FNDEHIPDSPFVVPVASLSDDAR.R	0.9958	2	2528.7374
						R.RLTVTSLQETGLK.V	0.9958	2	1446.6872
						R.LSGGHSLHETSTVLVETVTK.S	0.9943	2	2096.3452
						K.YGGPQHIVGSPFK.A	0.9958	2	1387.5809
						R.YWPTEPGEYAVHVICDDEDIR.D	0.9958	2	2565.7211
						R.AFGPGLEGGLVNK.A	0.9943	2	1259.4478
						R.GPGLSQAFVGQK.N	0.9924	2	1189.3567
						R.SLTATGGNHVTAR.V	0.9958	2	1285.4025
						R.FVPQEMGPHTVTVK.Y	0.9958	2	1570.8468
						K.HVTNSPFK.I	0.9958	1	930.0513
						K.HTIIVSWGGVNVPK.S	0.9958	2	1507.7758
						K.YDGNHIPGSPLQFYVDAINSR.H	0.9958	2	2364.5791
						R.SPFPVHVAEACNPNACR.A	0.9958	2	1927.0589
						K.DGTCTVSYLPTAPGDYSIIVR.F	0.9958	2	2286.5097
						R.VHTPSGAVEECYVSELDSDK.H	0.9958	2	2223.321
						R.GAGTGGLGLAIEGPSEAK.M	0.9958	2	1585.7545
						K.SPFVVNVAPPLDLSK.V	0.9958	2	1583.8681
						R.ECPEGHVVTYTPMAPGNYLIAIK.Y	0.9958	2	2561.9215
						K.VPQLPITNFNR.D	0.9931	2	1299.5155
						R.TGVEVGKPTHFTVLTK.G	0.9944	2	1715.0025
						K.VNQPASFAVQLNGAR.G	0.9958	2	1572.7641
						K.FNGAHIPGSPFK.I	0.9958	1	1272.449

						R.HIGISFTPK.E	0.9958		2	1000.1857
						R.DSPFIAHIQPAPPDCFPDK.V	0.9958		2	2153.3649
						K.IECQDNGDGSCAVSYLPTEPGEYTINILFAE	0.9958		3	4399.7433
						K.SPFRVNVGEGSHPER.V	0.9958		3	1668.8093
						R.QQEGEASSQDMTAQVTSPSGKTEAAEIVE	0.9958		3	3975.1543
1438	FLOT1_MOUSE	428	13.32	3	20	K.LPQVAEEISGPLTSANK.I	0.9958		2	1754.9781
						R.LTGVSISQVNHNKPLR.T	0.9958		2	1764.0378
						K.KAEAFQMYQEAAQLDMLLEK.L	0.9929		2	2358.7297
1439	FLOT2_MOUSE	379	13.98	3	9	R.LLAELPASVHALTGVDLSK.I	0.9958	1,2		1935.2713
						R.KIGEAEAAVIEAMGK.A	0.9958		2	1517.7809
						K.IRQEEIEIEVVQR.K	0.9958		2	1641.865
1440	FLT3L_MOUSE	232	5.6	1	2	R.FVQTNISHLLK.D	0.9944		1	1300.5437
1441	FM1AB_MOUSE	654	3.98	1	4	K.EPDDSAQFTKAIAIILHLLYLLEK.V	0.9944		3	2743.2157
1442	FMN2_MOUSE	1578	2.72	2	2	R.GQADGFGLDILPKLK.D	0.993		2	1572.8449
						K.NGPGVMQVLGLVLAFGNYMNAGNKTR.G	0.9958		3	2723.1835
1443	FN3K_MOUSE	309	6.15	1	2	K.VIDLPGGGAVFVMEHLK.M	0.9958		2	1783.1388
1444	FNBP1_MOUSE	616	10.71	4	20	K.FEAWLAEVEGR.L	0.9924		1	1307.4484
						K.AAESIDQKNDSQLVVEAYK.S	0.9958		2	2109.2976
						K.LGVTPEDFSNFPPEQRR.K	0.9912		2	1990.1827
						K.HTQWGIDILEK.Y	0.9958		2	1340.5217
1445	FNBP2_MOUSE	1071	3.92	2	3	K.TIIIQHENIFPNPR.E	0.9958		2	1692.9584
						K.YYIHDLSDIIDQCCDLGYHASLNR.A	0.9958		3	2943.1311
1446	FND3A_MOUSE	1134	3.7	2	2	R.QCQDPTGHQDLVGPYSTTVFFISQR.T	0.9944		3	2883.1126
						K.YVVEMAEGSNGNK.W	0.9958		1	1398.5304
1447	FNIPL_MOUSE	1108	9.3	3	3	R.CKRPEQNSEASSMGFQEAEPDSSWIPQGI	0.9958		3	3947.1673
						K.LGQDVLVSSQVSSLLQSILQLYKLHLPADF(	0.9958		3	4369.0449
						R.SPEPTVVAEISEGVNTSELGHKPEK.N	0.9958		3	2635.8877
1448	FOX1_MOUSE	396	9.09	2	2	K.ILDVEIIFNER.G	0.9944		1	1361.581
						K.TRSHADDVGLVLSSLQASIYR.G	0.9944		3	2289.5534
1449	FOXB2_MOUSE	428	5.61	1	2	K.GSFWALHPDCGDMFENGSFLRR.R	0.99		2	2600.8365
1450	FP100_MOUSE	879	11.83	3	6	K.TCQAPGSEPTGAASLRAK.Y	0.9924		2	1802.9482
						K.MQLFERPCAGEEPLPRGQIGEVELSTCTPI	0.9958		3	4460.9815
						R.RDSPWNPEKPDGAIGGLPSVLCPASLNICS	0.9944		3	4165.6345
1451	FPPS_MOUSE	353	17.56	3	5	R.GLTVVQAFQELVEPK.K	0.9958		2	1658.9353
						K.QNFIQHFSQIVK.V	0.9957		2	1489.7171
						R.RGQICWYQKPGIGLDAINDALLLEASIYR.L	0.9958		3	3335.7967
1452	FPRP_MOUSE	879	4.89	2	6	R.RNDDVVASELLAVMDGDWTLR.Y	0.9944		2	2376.6465

						R.DSLVHSSPHVALSHVDTR.S	0.9958		2	1958.1411
1453	FRAS1_MOUSE	4010	2.54	4	5	R.CLSCAEKTILHDGK.C	0.9946		2	1632.7865
						K.ITHSRPQFGEVVLLMNLPADSPAGPAEEGH	0.9958		3	3847.3
						R.LSSGVAISNSSLSLQDLDTPDNELIFVLMK.H	0.9958		3	3208.6484
						R.VSYSHDGSNSLKDR.F	0.9958		1	1565.6396
1454	FRDA_MOUSE	207	28.5	2	107	K.NWVYSHDGVSLHELLAR.E	0.9958		2	1997.2205
						R.LAEETLDSLAEFFEDLADKPYTLEDYDVSF	0.9958		3	4271.6717
1455	FREM3_MOUSE	2123	2.12	2	2	K.TCQVLIINDSLYEEEESFSIALSLPTGGQLG	0.9958		3	4157.6301
						K.DESEKTCQVLIINDSLYEEEESFSIALSLPTG	0.9924		3	4173.5373
1456	FRIH_MOUSE	182	66.48	11	186	R.QNYHQDAEAAINR.Q	0.9944		2	1530.5968
						K.MGAPEAGMAEYLFDK.H	0.9958		2	1630.8709
						K.YFLHQSHEER.E	0.9941		2	1346.4447
						K.NDPHLCDFIETYYLSEQVK.S	0.9958		2	2372.5592
						K.ELGDHVTNLR.K	0.9924		1	1154.2681
						K.LATDKNDPHLCDFIETYYLSEQVK.S	0.9958	2,3		2901.1652
						K.SVNQSLLELHK.L	0.9958		2	1268.4557
						K.KPDRDDWESGLNAMECALHLEK.S	0.9958		2	2615.8433
						R.DDWESGLNAMECALHLEK.S	0.9957		2	2119.2765
						R.IFLQDIK.K	0.9958		1	877.0715
						R.KMGAPEAGMAEYLFDK.H	0.9958		2	1759.0449
1457	FRIL1_MOUSE	183	68.85	9	131	K.NLNQALLDLHALGSAR.T	0.9958		2	1706.9425
						R.VAGPQPAQTGAPQGSLGEYLFER.L	0.9958		2	2374.6152
						R.QNYSTEVEAAVNR.L	0.9958	1,2		1481.562
						R.ALFQDVQKPSQDEWGK.T	0.9958		2	1877.0636
						K.MGNHLTNLR.R	0.9958	1,2		1056.2279
						R.DDVALEGVGHFFR.E	0.9957		2	1462.6048
						R.ASYTYLSLGFFFDR.D	0.9958		2	1687.892
						R.RVAGPQPAQTGAPQGSLGEYLFER.L	0.9958		2	2530.8027
						K.TQEAMEAALAMEK.N	0.9958		2	1423.6393
1458	FSCN1_MOUSE	493	17.24	5	28	R.DVPWGVDSLITLAFQDQR.Y	0.9958		2	2061.3018
						R.LVARPEPATGFTLEFR.S	0.9958		2	1805.0867
						R.YLAADK.D	0.9924		1	680.7789
						R.SSYDVFQLEFNDGAYNIK.D	0.9907		2	2111.272
						R.DCEGRYLAPSGPSGTLK.A	0.9924		2	1808.9519
1459	FSD2_MOUSE	692	12.72	3	4	K.LEALYGQLVSCGENLDACRELMETVEEMC	0.9911		3	3945.2574
						R.SEPATVHTTGSYFQLNK.D	0.9958		2	1881.052
						R.ASEEYECYVIPEEEDEEEPADVFCITCKTP\	0.9958		3	3896.0587

1460	FTHFD_MOUSE	902	12.53	5	5	K.YQALGAELNVLPFCSQFIPMEVINAPR.H	0.9958	3	3079.5501
						R.LFVEDSIHDQFVQK.V	0.9958	2	1705.9078
						R.ANATEFGLASGVFTRDINK.A	0.9958	3	2012.2297
						K.SGAASVDVVRLVEEVK.E	0.9952	2	1658.8925
						K.ELCDGLELENEDVYMATTFGDFIQLLVRK.L	0.9958	3	3420.8221
1461	FUBP1_MOUSE	651	6.45	2	3	K.MVMIQDGPQNTGADKPLRITGDPYK.V	0.9958	3	2747.1567
						R.CQHAAEIITDLLR.S	0.9958	2	1540.7258
1462	FUBP2_MOUSE	748	10.56	3	6	K.IGGDAATTVNNNTPDFGFGGQK.R	0.9958	2	2182.311
						R.GGGGPGGGGPGGGGASGGPSQPPGGG(	0.9958	2	2328.4226
						K.LASQGDSIGSQLGPIHPPPR.T	0.9958	2	2028.2755
1463	FUMH_MOUSE	507	57.79	20	2693	R.SGLGELILPENEPGSSIMPGK.V	0.9958	2	2126.4297
						R.IYELAAGGTAVGTGLNTR.I	0.9958	1	1764.9762
						K.EFAQVIK.I	0.9949	1	834.9909
						K.ETAIELGYLTAEQFDEWVKPK.D	0.9958	2	2468.7656
						K.RAAAEVNQEYGLDPK.I	0.9958	2	1661.8119
						K.LHDALSAK.S	0.9945	1,2	854.9817
						K.LMNESLMLVTALNPHIGYDK.A	0.9958	2	2260.6717
						K.SQSSNDTFPTAMHIAAAVEVHK.V	0.9958	2,3	2342.5884
						R.AAAEVNQEYGLDPK.I	0.9958	2	1505.6244
						R.AIEMLGGELGSK.K	0.9958	1	1205.4119
						K.YYGAQTVR.S	0.9944	1	958.0617
						K.LNDHFPLVVWQTGSGTQTNMNVNEVISNR	0.9958	3	3272.6195
						R.VEFDTFGELK.V	0.9958	1	1185.319
						R.MPIPVIQAFGILK.R	0.9958	2	1427.8315
						K.FEALAAHDALVELSGAMNTAACSLMK.I	0.9958	2	2723.0976
						K.VLLPGLQK.L	0.9937	2	868.1075
						K.KPVHPNDHVNK.S	0.9958	1	1285.4483
						K.VAALTGLPFVTAPNK.F	0.9958	2	1499.7935
						K.AADEVAEGKLNDHFPLVVWQTGSGTQTN	0.9922	3	4143.5341
						K.VAALTGLPFVTAPNKFEALAAHDALVELSG	0.9958	3	4203.8679
1464	FUS_MOUSE	518	5.02	1	2	K.APKPDGPGGGPGGSHMGGNYGDDR.R	0.9958	2	2254.355
1465	FXL13_MOUSE	790	7.34	3	3	R.CHYLHILDISGCIQLTDQIIQDLQIGCK.Q	0.9958	3	3356.742
						R.EDDLISKHELQLK.K	0.9958	2	1568.7673
						K.MDKAIAHDNFR.C	0.9958	1	1318.4931
1466	FXL16_MOUSE	479	10.23	2	3	R.LLSCWEITNHGVVNVVHSLPNLTSLSLSGC	0.9958	3	5035.5953
						K.VTDDGVELVAENLRK.L	0.9944	2	1658.8491
1467	FXL19_MOUSE	674	6.23	2	2	K.KVGGDACLLR.G	0.9944	2	1089.2463

						R.ADNGEEGANLGGGWKLTEEPPPPPPLPR.	0.9924	3	2897.1735
1468	FXR1_MOUSE	677	13.29	5	5	R.KDELSDWSLAGEDDR.E	0.9958	2	1736.7893
						R.EDLMGLAIGTHGSNIQQAR.K	0.9958	2	2012.2481
						R.KVPGVTAIELDEDTGTFR.I	0.9958	2	1949.1681
						R.IFYHPETTQLMILSASEATVK.R	0.9958	2	2380.7614
						K.RVNILSDMHLR.S	0.9944	2	1354.6133
1469	FYCO1_MOUSE	1437	12.53	8	17	K.AAEEAASSFSGLQAQLAQAEQLAQSLQET.	0.9958	3	4000.2817
						R.QLQESLAHLSSVEEELAEAR.Q	0.9926	2	2240.4319
						K.LNCTSSHLAECQATLLR.K	0.9958	2	1975.1413
						K.LQSQLGVAETVLR.E	0.9958	2	1414.6451
						K.TPPDTELHQEPVPADLVLK.F	0.9958	2	2100.3764
						K.GQQGLSLPQVNTDQLALSQAQLEIHQGEA	0.9958	3	3359.6805
						R.AHVQELLQCSER.E	0.9958	1	1470.5914
						R.HLGNQMEASLLAVK.K	0.9958	2	1511.7796
1470	FYV1_MOUSE	2052	3.8	3	6	R.QAPLKVSLLQDLK.D	0.9958	1	1453.7654
						R.LEVQSFLDFAPHYFNYITNAVQQKRPTALA	0.9944	3	3612.1253
						R.DIIVSLVCQVVQTVRPDVKHQDDDMDIR.Q	0.9944	3	3295.7015
1471	G3BP1_MOUSE	465	27.96	8	36	K.LPNFGFVVFDDSEPVQK.V	0.9958	2	1939.1748
						K.FYVHNDIFR.Y	0.9958	2	1211.3653
						K.VLSNRPIMFR.G	0.9958	2	1233.5175
						K.NLPPSGAVPVTGTPPHVVK.V	0.9958	2	1868.1863
						R.HPDSHQLFIGNLPHEVDK.S	0.9958	2	2084.2987
						R.HPDSHQLFIGNLPHEVDKSELK.D	0.9929	2	2541.8259
						R.RFMQTFVLAPEGSVANK.F	0.9958	2	1896.2145
						R.HVDAHATLNDGVVVQVMGLLSNNNQALR.	0.9958	3	2987.3635
1472	G3BP2_MOUSE	482	8.92	2	3	K.LPNFGFVVFDDSEPVQR.I	0.9958	2	1967.1882
						R.YPDSHQLFVGNLPHDIDENELK.E	0.9958	2	2581.8009
1473	G3P_MOUSE	333	78.38	16	8209	K.GILGYTEDQVVSCDFNSNSHSSTFDAGAG	0.9958	3	4052.2795
						K.WGEAGAEYVVESTGVFTTMEK.A	0.9958	2	2292.522
						K.LISWYDNEYGYSNR.V	0.9925	2	1780.8907
						R.GAAQNIIPASTGAAK.A	0.9958	1	1370.5485
						R.VIISAPSADAPMFVMGVNHEK.Y	0.9958	2	2214.6026
						K.LVINGKPITIFQER.D	0.9958	2	1628.9554
						K.VIHDNFGIVEGLMTTVHAITATQK.T	0.9944	2	2597.0044
						K.LVINGKPITIFQERDPTNIK.W	0.9958	2	2297.7031
						K.RVIISAPSADAPMFVMGVNHEK.Y	0.9958	2	2370.7901
						R.VVDLMAYMASK.E	0.9958	2	1228.5073

						K.VEIVAINDPFIDLNYMVYMFQYDSTHGK.F	0.9958		3	3324.7903
						K.VIPELNGKLTGMAFR.V	0.9958		2	1646.9885
						K.YDNSLK.I	0.9924		1	739.8033
						K.AENGKLVINGKPITIFQER.D	0.9924		3	2128.4795
						R.LEKPAKYDDIK.K	0.9944		2	1320.5285
						K.IVSNASCTTNCLAPLAK.V	0.9958		2	1821.0131
1474	G3PT_MOUSE	440	5.23	2	266	R.VPTPNVSVVDLTCR.L	0.9956		2	1557.7533
						K.LTGMAFRVPTPNVSVVDLTCR.L	0.9958		3	2334.7052
1475	G45IP_MOUSE	222	24.77	3	10	R.ELEAEEQEWYPSLATMQESLR.L	0.9958		2	2540.7608
						R.HGAISGVPPASLWPTPEQLR.E	0.9958		2	2114.4117
						R.FQELLQDLDK.Q	0.9958		1	1249.4063
1476	G6PD1_MOUSE	515	10.68	3	6	R.DLQSSNQLSNHISSLFR.E	0.9943		2	1947.1148
						K.KPGMFFNPEESELDLTYGNR.Y	0.9958		2	2345.5885
						R.EAWRIFTPLLHK.I	0.9924		1	1511.81
1477	G6PI_MOUSE	558	62.19	21	1367	K.TLASLSPETSLFIIASK.T	0.9958	1,2		1779.0838
						R.FAAYFQQGDMESNGK.Y	0.9958	1,2		1693.8279
						K.TFTTQETITNAETAK.E	0.9958	1,2		1656.7869
						K.IEPELEGSSAVTSHDSSTNGLISFIK.Q	0.9958		2	2719.9623
						K.ILLANFLAQTEALMK.G	0.9958		2	1677.0551
						K.VFEGNRPTNSIVFTK.L	0.9958		2	1709.9426
						R.VWFVSNIDGTHIAK.T	0.9958		2	1587.8186
						K.KIEPELEGSSAVTSHDSSTNGLISFIK.Q	0.9958		2	2848.1363
						K.IFVQGIMWDINSFDQWGVELGK.Q	0.9958		2	2583.9642
						R.FNNFSLNLNTNHGHILVDYSK.N	0.9958	2,3		2448.7001
						K.MIPCDFLIPVQTQHPIR.K	0.9958		2	2066.4352
						R.VDHQTGPIVWGEPGTNGQHAFYQLIHQGT	0.9958		3	3317.6475
						K.EFGIDPQNMFEFWDWVGGR.Y	0.9958		2	2331.5665
						K.EVMQMLVELAK.S	0.9958	1,2		1291.6069
						K.HFVALSTNTAK.V	0.9958		1	1189.3567
						R.AVLHVALR.N	0.9958		2	879.0934
						K.SITDIINIGIGGSDLGPLMVTEALKPYSK.G	0.9958	2,3		3004.5091
						K.EWFLEAAK.D	0.9958		1	994.1351
						K.DVMPEVNR.V	0.9924		1	960.093
						K.LTPFILGALIAMYEHK.I	0.9958		2	1818.2274
						K.NLVNKEVMQMLVELAK.S	0.9958		2	1860.2807
1478	GA2L1_MOUSE	678	6.49	2	2	R.DQLPPLPRSR.R	0.9958		1	1179.3646
						R.ATPQVSSVPAAEEDVTEIATVPGVPTRTPR	0.9924		3	3077.4185

1479	GA2L2_MOUSE	860	3.26	3	4	R.ELVQGPPPLLK.V	0.9944		1	1191.4563
						R.EQALYDNLK.E	0.9958		1	1094.2096
						R.ELVQGPPPLLKVDLK.A	0.9958		1	1647.011
1480	GAB1_MOUSE	695	5.9	2	4	R.RPVPVADCEPPPVDR.N	0.9958		2	1704.8895
						K.VKPAPLDIKPLSEWEELQAPVR.S	0.9958		2	2516.9432
1481	GABR1_MOUSE	960	3.96	2	2	R.MAWTLIEQLQGGSYK.K	0.9958		2	1726.0002
						K.VFLTGGDLPALDGARVDFR.C	0.9958		3	2020.2957
1482	GABT_MOUSE	500	19.4	6	11	K.IDIPSFDWPIAPFPR.L	0.9958		2	1772.0563
						K.NLLLAEVINIIK.R	0.9958		2	1353.6885
						K.REDLLNNVAR.V	0.9924		2	1200.3402
						R.MLDLYSQISSVPIGYNHPALAK.L	0.9958	2,3		2418.8133
						K.MMTGGFFHK.E	0.9958		2	1056.2855
						K.HGCAFLVDEVQTGGGCTGK.F	0.9958		2	1994.1005
1483	GADL1_MOUSE	502	12.15	2	2	R.HGLWLHVDASWGGSALVSRK.H	0.9954		2	2177.4733
						K.QIWQARQEGAVPFLVCATSGTTVLGAFDP	0.9958		3	4336.7774
1484	GAK_MOUSE	1305	0.92	1	3	R.CPPGIWPSHK.R	0.9958		1	1179.33
1485	GALM_MOUSE	342	10.82	2	7	K.ASDVVLGFAELEGYLQK.Q	0.9958		2	1840.0832
						K.VLWTPQVLTNGVQFFR.V	0.9958		2	1906.2376
1486	GALT_MOUSE	379	22.16	5	25	R.HDPLNPLCPGATR.A	0.9958		2	1448.5877
						R.YNPLQDEWVLVSAHR.M	0.9958		2	1828.0373
						K.RPWQGQVEPQLLK.T	0.9958		2	1579.8423
						R.ALPEVHYCLAQK.D	0.9958		2	1429.6251
						K.VMCFHPWSDVTLPLMSVPEIR.A	0.9958		2	2515.9571
1487	GANAB_MOUSE	944	11.86	6	10	R.LSFQHDPETSVLILR.K	0.9958		2	1756.0116
						R.VVIMGAGKPAAVVLQTK.G	0.9958		2	1683.1058
						K.THSDSKPYGPTSVGLDFSLPGMEHVYGIP	0.9958		3	3899.2831
						R.GLMAFEHQR.A	0.9958		2	1089.2573
						K.GHLETPIWIER.V	0.9958		2	1351.5479
						R.FPQPLNMLEHLASK.R	0.9958		2	1625.9262
1488	GAPD1_MOUSE	1458	1.37	1	5	R.LPNFGSHVLTAAEMEAFK.Q	0.9958		2	1963.2586
1489	GAPR1_MOUSE	154	14.94	1	2	R.YFPAGNIVNQGFFEENVPPPKK.-	0.9958		2	2493.8241
1490	GARL3_MOUSE	1038	9.15	3	3	K.DLLVLEEQEGSVNFKFGVLFAK.D	0.9937		2	2483.8669
						K.VITPPTSIGLGVAAIPVTHSLSLSRMEIK.E	0.9958		3	2989.5872
						R.SASSDRIPSGILESPASEANPEGHNHWAS	0.9944		3	3935.0825
1491	GAS6_MOUSE	674	3.71	2	2	R.AYQVFEEAK.Q	0.9958		1	1085.2017
						K.TCQDVDECQQDR.C	0.9924		2	1554.4994
1492	GASP1_MOUSE	1347	5.12	3	3	K.AVCEPESSAEHEPDPSR.R	0.9945		2	1897.9159

						R.FHVLKLLLNLSENLVMTK.R	0.9958	3	2113.6098
						K.AENKPGDENANAAEVEPEAPLVVRPKVR.T	0.9958	3	3001.3262
1493	GASP2_MOUSE	826	7.87	2	2	K.MFQNISNIVKSGAMSLLDDDFSLEPLVSAFI	0.9958	3	4274.8471
						K.KPQEEVAGGAERESEAPLVVRPK.V	0.9924	3	2477.7801
1494	GATB_MOUSE	557	6.82	2	3	R.VDANISVHHPGEPLGVR.T	0.9958	2	1798.0115
						K.LCQTTIDGHPQVVMDVK.K	0.9958	2	1942.2037
1495	GATCL_MOUSE	155	32.26	2	2	R.VSPAVIEHLERLALVNFGSR.E	0.9911	2	2208.5687
						K.AIAFADQLHAVDTDGVEPLESVLEDR.C	0.9958	2	2812.0624
1496	GATM_MOUSE	423	5.44	2	2	R.RPDPIDWSLKYK.T	0.9924	1	1518.7557
						K.YWPFYQK.N	0.9958	1	1032.1864
1497	GBB1_MOUSE	340	25.88	5	28	K.ACADATLSQITNNIDPVGR.I	0.9958	2	2017.1693
						K.VHAIPLR.S	0.9944	1	805.9987
						R.LLLAGYDDFNCNVWDALK.A	0.9958	2	2128.3551
						K.IYAMHWGTDSR.L	0.9958	2	1337.4955
						R.VSCLGVTDDGMAVATGSWDSFLK.I	0.9958	2	2417.6589
1498	GBB2_MOUSE	340	20	4	15	K.ACGDSTLTQITAGLDPVGR.I	0.9958	2	1933.0918
						R.LLLAGYDDFNCNIWDAMK.G	0.9958	2	2160.4151
						R.ADQELLMYSHDNIICGITSVAFSR.S	0.9958	2	2742.0419
						R.KACGDSTLTQITAGLDPVGR.I	0.9958	2	2061.2659
1499	GBG5_MOUSE	68	42.65	1	16	K.QFCLQNAQHDPLLTGVSSSTNPFRPQK.V	0.9958	3	3072.3733
1500	GBLP_MOUSE	317	44.79	7	172	K.GHNGWVTQIATTPQFPDMILSASR.D	0.9958	2	2628.9653
						K.HLYTLDGGDIINALCFSPNR.Y	0.9958	2	2277.5078
						K.TNHIGHTGYLNTVTVSPDGSLCASGGK.D	0.9958	2	2744.9439
						K.YTVQDESHSEWVSCVR.F	0.9958	2	1983.0674
						R.YWLCAATGPSIK.I	0.9958	2	1367.5536
						R.FSPNSSNPIIVSCGWDK.L	0.9958	2	1909.0717
						K.IIVDELKQEVISTSSK.A	0.9958	2	1790.0642
1501	GBP1_MOUSE	589	6.11	2	3	R.TGFSLGSTVQSHTK.G	0.9943	2	1450.5913
						K.AGQTLVLLDTEGLEDVEK.G	0.9958	2	1931.1473
1502	GBP2_MOUSE	589	5.09	1	2	K.IQMPTETLQELLDLHRPIESEAIEVFLK.N	0.9958	3	3294.831
1503	GBP4_MOUSE	620	7.9	3	3	R.LPTDTLQELLTVHAACEK.E	0.9958	2	2040.2873
						R.LLLQIENVPENQLER.N	0.9958	2	1809.0727
						K.EAIAVFMEHSFK.D	0.9958	2	1409.6428
1504	GC3M_MOUSE	398	4.02	1	6	R.VVSALPIQHQDWMR.G	0.9958	2	1680.9653
1505	GCAA_MOUSE	330	28.79	5	27	R.VVSALPIQHQDWMSGK.E	0.9958	2	1797.082
						R.APQVYVLPPPEEEMTK.K	0.9921	2	1829.1181
						K.DLPAPIERTISKPK.G	0.9958	1	1565.8534

						K.TTAPSVYPLAPVCGDTTGSSVTLGCLVK.G	0.9958	2	2853.1714
						R.GPTIKPCPPCK.C	0.9952	2	1255.4321
1506	GCAB_MOUSE	335	8.06	1	2	K.EFSLTCMITGFLPAEIAVDWTSNGR.T	0.9958	2	2817.1519
1507	GCBM_MOUSE	404	10.4	2	21	K.CPAPNLEGGPSVFIFPPNIK.D	0.9958	2	2155.4675
						K.KLEPSGPISTINPCPPCK.E	0.9958	2	1996.2434
1508	GCC1_MOUSE	778	5.78	2	2	R.FLTLPDSLGRQQTLTAILTILHFSPEEK.Q	0.9935	3	3170.6763
						K.ELEAAQEQLAELK.D	0.9958	1	1472.6354
1509	GCC2_MOUSE	1679	5.12	4	4	R.DLEALQAQQDFAHKEHVAEFEK.K	0.9944	2	2584.8046
						K.GELEASQQQVEVYKIQLAEMTSEK.H	0.9944	3	2740.0546
						R.DLEALQAQQDFAHK.E	0.9924	1	1614.7551
						R.EEGEGMETTDSESVSSAGTHIQSLEQLLS	0.9958	3	3581.7517
1510	GCDH_MOUSE	438	21	4	20	R.SMMSVQSSLVMHPIYTYGSEEQR.Q	0.9958	2	2662.0225
						R.HAMNLEAVNTYEGTHDIHALILGR.A	0.9958	2	2677.0099
						K.SSRPVFDWKDPLILEEQLTADEK.L	0.9958	2	2718.0355
						R.HNPSNQSYTLSGTK.T	0.9944	1	1534.6255
1511	GCF_MOUSE	769	5.2	2	2	R.ELSGSCDHQEGMSSDDELSPAEMTNFHK.	0.9944	3	3140.2565
						K.MDSIGLDK.M	0.9958	1	879.0161
1512	GCNT7_MOUSE	433	12.47	2	3	R.LARGLHFITRPLSAEEGNFSLAYVIHAPR.E	0.9958	3	3237.7348
						K.QSPPHNLTISSGSAHYALTRK.F	0.9944	2	2266.5216
1513	GCSH_MOUSE	170	35.88	2	42	K.MTLSDPSELDELMSEEAYEK.Y	0.9958	2	2318.5265
						K.HEWITTEEGIGTVGISNFAQEALGDVVYCS	0.9958	3	4009.3815
1514	GDE1_MOUSE	331	3.63	1	2	K.DFVSPDYLKK.W	0.9924	1	1212.388
1515	GDE5_MOUSE	675	10.67	5	7	K.LSHVTALK.T	0.9958	1	869.0519
						R.KYEADPVELFEIPVK.E	0.9958	2	1778.0551
						R.HSQPECGYGLQPDR.W	0.9958	2	1644.7069
						R.SAGILTLPIMSR.N	0.9958	2	1259.5499
						R.LHFSEKPPVSISK.K	0.9958	2	1469.7239
1516	GDF15_MOUSE	303	7.92	1	2	R.LRLTPPPDLAMLPSGGAQLELR.L	0.9958	2	2346.7936
1517	GDF7_MOUSE	461	7.38	1	2	R.GAQGSGGGGGGGGGGGGGGGGGGGA	0.9946	3	2252.2038
1518	GDIA_MOUSE	447	38.93	9	55	R.NPYYGGESSSITPLEELYK.R	0.9958	2	2148.3307
						K.VPSTETEALASNLMGMFEK.R	0.9958	2	2056.3535
						K.SPYLYPLYGLGELPQGFAR.L	0.9958	2	2142.4619
						R.KFDLGQDVIDFTGHALALYR.T	0.9958	2	2280.5883
						K.FLVFVANFDENDPK.T	0.9958	2	1655.8474
						R.TDDYLDQPCLETINR.I	0.9958	2	1853.9465
						R.DWNVDLIPK.F	0.9958	1	1100.2597
						K.YIAIASTTVETAEPEKEVEPALELLEPIDQK.	0.9944	3	3428.8555

						K.RFQILEGPPESMGR.G	0.9958		2	1617.8633
1519	GDIB_MOUSE	445	44.27	15	144	K.VLHMDQNPYYGGESASITPLEDLYK.R	0.9958		2	2842.1493
						K.RMTGSEFDFEEMK.R	0.9958		2	1607.7933
						K.EIRPALELLEPIEQK.F	0.9958		2	1779.0868
						R.MTGSEFDFEEMK.R	0.9958		2	1451.6058
						K.VPSTEAEALASSLMGLFEK.R	0.9958		2	1981.2684
						K.FVSISDLFVPK.D	0.9958		2	1252.4961
						R.AYDATTHFETTCDDIK.D	0.9958		2	1888.9483
						K.FDLGQDVIDFTGHSLALYR.T	0.9958		2	2168.4136
						K.KFDLGQDVIDFTGHSLALYR.T	0.9944	2,3		2296.5877
						K.KVLHMDQNPYYGGESASITPLEDLYK.R	0.9958	2,3		2970.3234
						K.DLGTDSQIFISR.A	0.9958		2	1352.4869
						R.LSAIYGGTYMLNKPIEEIIVQNGK.V	0.9958		2	2653.1089
						R.AYDATTHFETTCDDIKDIYK.R	0.9958		2	2408.5464
						R.VICILSHPIK.N	0.9958		2	1180.4424
						R.TDDYLDQPCCETINR.I	0.9958		2	1900.9258
1520	GDIR1_MOUSE	204	52.94	7	114	R.LTLVCSTAPGPLELDLTGDLESFK.K	0.9958		2	2577.8977
						K.SIQEIQELDKDDESLR.K	0.9958		2	1919.0526
						R.AEEYEFLTPMEEAPK.G	0.9958		2	1784.9753
						R.VAVSADPNVPNVIVTR.L	0.9958		2	1651.9035
						R.LTLVCSTAPGPLELDLTGDLESFKK.Q	0.9958		2	2706.0717
						R.FTDDDKTDHLSWEWNLTIK.K	0.9958		2	2365.5609
						K.YIQHTYR.K	0.9958	1,2		981.0989
1521	GDIR2_MOUSE	200	31.5	4	12	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	0.9958		3	2946.3009
						K.TLLGDVPVVADPTVPNVTVTR.L	0.9958		2	2164.5071
						K.LNYKPPPQK.S	0.9944		2	1085.2914
						K.KTLLGDVPVVADPTVPNVTVTR.L	0.9958		2	2292.6811
1522	GELS_MOUSE	780	33.08	12	79	R.DPDQTDGPGLGYLSSHIANVER.V	0.9958		2	2342.4839
						R.SQHVQVEEGSEPDAFWEALGGK.T	0.9958		2	2401.5511
						K.KGGVASGFK.H	0.9958		1	850.9933
						R.AQVHVSEEGGEPEAMLQVLGPKPALPEGT	0.9958		3	3516.9019
						K.TPSAAYLWVGAGASEAEK.T	0.9958		2	1808.9854
						R.QGFEPPSFVGWFLGWDDNYWSVDPLDR./	0.9958		2	3231.5066
						R.QTQVSVLPEGGETPLFK.Q	0.9958		2	1831.0758
						K.FDLVPVPPNLYGDFFTGDAYVILK.T	0.9958		2	2702.1217
						K.NWRDPDQTDGPGLGYLSSHIANVER.V	0.9958		3	2798.9884
						K.VSNGAGSMSVSLVADENPFAQGALR.S	0.9958		2	2478.7393

						K.HVVPNEVVVQR.L	0.9958		2	1276.4813
						R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.	0.9958	2,3		2875.1139
1523	GEMI2_MOUSE	269	11.9	1	3	R.DFTPELGRWFYALLACLEKPLLPEAHSLIR.	0.9958		3	3558.1266
1524	GEPH_MOUSE	769	14.17	4	21	R.STLLATIQEHGYPTINLGIVGDNPDDLLNALI	0.9944		3	3936.3678
						R.VFMKPGLPTTFATLDIDGVR.K	0.9925		2	2179.5823
						K.FPVVAVMSTGNELLNPEDDLLPGK.I	0.9958		2	2556.9337
						K.AFITVLEMTPVLGTEIINYR.D	0.9958		2	2281.7155
1525	GFOD1_MOUSE	390	8.46	2	2	R.IDEVLLHQDVDLVCINLPPPLTR.Q	0.9912		2	2671.0753
						K.VHGLLK.T	0.9944		1	666.8417
1526	GFRA1_MOUSE	468	6.2	2	4	R.SAYITPCTTSMSNEVCNRR.K	0.9958		3	2248.4048
						R.QCVAGK.E	0.9924		1	662.7301
1527	GGN_MOUSE	673	11.74	2	2	K.SGPHLSPTSASGPLAAKASPGAGGGGLFA	0.9958		3	3728.1534
						R.EPNTAPVTDSSSGGGGGGSNGTSTAGASI	0.9958		3	3009.0434
1528	GGNB2_MOUSE	696	1.58	1	2	R.KSFEMTVEK.V	0.9958		1	1099.2873
1529	GGT1_MOUSE	568	2.99	1	7	R.QGKVLQEGETVTMPK.L	0.9958	1,2		1645.9116
1530	GGT5_MOUSE	573	12.74	3	9	R.SQDPFPWPALANTLETVAK.E	0.9932		2	2086.3519
						R.GQIQSQSQRPVFLNAVQAVFQEGPCVYAA	0.9958		3	3666.0539
						R.TGILLNNELLDLCWR.H	0.9958		2	1831.0881
1531	GHC1_MOUSE	323	16.72	2	2	K.LTLPKEMLAGCGAGTCQVIVTTPMEMLK.I	0.9924		3	3051.6177
						K.LINGGIAGLIGVTCVFPIDLAK.T	0.9958		2	2242.6733
1532	GHITM_MOUSE	346	8.67	1	2	K.HLAWMLHSGVMGAVVAPLTILGGPLLLR.A	0.9958		2	2924.6251
1533	GIMA4_MOUSE	219	35.62	4	37	R.SSHELGNQDQGIPQLR.I	0.9958		2	1779.9071
						K.FFQEVMHEFQNR.Y	0.9958		2	1612.8028
						K.ELVVVDTPGIFDTEVPDADTQR.E	0.9909		2	2417.6318
						R.YVALTSPGPHALLLVVPLGR.Y	0.9958		2	2074.5174
1534	GL8D4_MOUSE	444	4.73	1	3	R.DFPFQDNLFQSMYYPLQLK.F	0.9946		2	2395.7345
1535	GLB1L_MOUSE	646	10.53	2	2	K.IYPFLYHNGGNIISIQVENEYGSYK.A	0.9958		2	2920.2506
						K.MKFGPLTMSLDGNLLSFLDFLCPQGPIHSV	0.9958		3	4336.116
1536	GLCNE_MOUSE	722	10.25	3	3	K.KYTQFNPK.T	0.9958		1	1026.1802
						K.LAPIMFGIKTEPAFFELDVVVLGSHLIDDYGI	0.9958		3	3943.5495
						R.TPLSDTLHLPVWVDNDGNCAAMAER.K	0.9932		2	2784.0388
1537	GLGB_MOUSE	702	25.78	10	49	R.LLEIDPYLKPFAADFQR.R	0.9958		2	2037.366
						K.FSQVLHDIGENEGGIDK.F	0.9958		2	1859.0025
						K.IVLDSDAAEYGGHQR.L	0.9958		2	1631.7422
						R.IYESHVGISSHEGK.I	0.9958		2	1543.6763
						K.KFSQVLHDIGENEGGIDK.F	0.9958		2	1987.1766
						K.EWAPGAEGVFLTGEFSGWNPFSHPYK.K	0.9958		2	2912.1895

						R.LITHGLGGEGYLNFMGNEFGHPEWLDFPR	0.9958		3	3305.6941
						K.CVAYAESHDQALVGDK.T	0.9958		2	1763.8676
						K.SPLIPHGSK.L	0.9944		1	936.0989
						K.EFKDEDWNMGNIVYTLTNR.R	0.9958		2	2346.5763
1538	GLI3_MOUSE	1583	1.14	1	2	R.SDLSGVDFTVLNTLNR.R	0.9947		2	1751.9341
1539	GLNA_MOUSE	373	18.23	4	64	R.LTGFHETSNINDFSAGVANR.G	0.9958		2	2151.2999
						R.RPSANCDPYAVTEAIVR.T	0.9958		2	1920.0985
						K.ITGTNAEVMPAQWEFQIGPCEGIR.M	0.9958		2	2706.0113
						R.RLTGFHETSNINDFSAGVANR.G	0.9958		2	2307.4874
1540	GLO2_MOUSE	260	40.38	8	36	K.FARHVEPGNAAIQEK.L	0.9945		2	1667.8649
						K.VYCGHEYTVNNLK.F	0.9958		2	1597.7338
						R.HVEPGNAAIQEK.L	0.9911		2	1293.4221
						K.VTHLSTLQVGSLSVK.C	0.9958		2	1569.8418
						K.LVKLEPGLK.V	0.9924		1	997.2663
						K.ALLEVLGR.L	0.9924		1	871.0678
						K.TVQQHAGETDPVTTMR.A	0.9958		2	1771.9427
						K.LTTVLTTHHHWDHAGGNEK.L	0.9924		2	2155.3371
1541	GLOD4_MOUSE	298	51.68	10	133	K.VAEGIFETEAPGGYK.F	0.9958		2	1568.7234
						K.LLDDAMEADKSDEWFATR.N	0.9946		2	2114.291
						K.SLNYWSNLLGMK.I	0.9958		2	1426.6733
						K.LELQGIQGAVDHAAAFGR.I	0.9958	1,2		1854.0757
						R.ESHSILTPLVSLDTPGK.A	0.9958		2	1795.0428
						R.FQTVHFFR.D	0.9958		2	1082.2498
						K.RESHSILTPLVSLDTPGK.A	0.9958		2	1951.2303
						K.LGNDFMGITLASSQAVSNAR.K	0.9958		2	2053.2976
						K.ATVQVVILADPDGHEICFVGDEAFR.E	0.9924		2	2760.0417
						R.KLEWPLSK.V	0.9958	1,2		1001.2138
1542	GLOD5_MOUSE	148	14.86	1	7	R.LDHIVMTVKNIEDTTMFYSK.I	0.9958		3	2386.7835
1543	GLP3L_MOUSE	285	18.95	2	3	K.ATEPTETVQTWIELLTGETWNPFK.L	0.9958		3	2793.1022
						K.GILTTEKQNFLLFDMTTHPVTNTTEK.Q	0.9958		3	2981.3906
1544	GLPK_MOUSE	524	9.92	3	22	K.TAELLSHHQVEIK.Q	0.9958		2	1505.7141
						K.CVFSEHGLLTTVAYK.L	0.9958		2	1725.9483
						K.AVLGPLVGAVDQGTSSTR.F	0.9958		2	1728.9432
1545	GLRX1_MOUSE	107	61.68	4	71	R.KTQEILSQLPFK.Q	0.9958		2	1432.7031
						K.QGLLEFVDITATNNTSAIQDYLQQLTGAR.T	0.9958		3	3182.5144
						K.DCIGGCSDLISMQQTGELMTR.L	0.9958		2	2373.5876
						K.TQEILSQLPFK.Q	0.9958		2	1304.5291

1546	GLRX3_MOUSE	337	38.87	8	112	K.YEISSVPTFLFFK.N	0.9958	2	1578.848
						K.TYSNWPTYPQLYVSGELIGGLDIIK.E	0.9958	2	2829.2219
						K.HNIQFSSFDIFSDEEVR.Q	0.9958	2	2071.2102
						R.HVSSGAFPPSTNEHLK.E	0.9958	2	1708.8711
						R.GDLVGGLDIVK.E	0.9924	1	1086.2737
						K.DNGELLPILK.G	0.9944	1	1112.3116
						K.TFSNWPTYPQLYVR.G	0.9914	2	1773.0007
						R.LDGAHAPELTK.K	0.9958	2	1152.2926
1547	GLRX5_MOUSE	152	28.29	3	42	K.GTPEQPQCGFSNAVVQILR.L	0.9958	2	2102.3208
						R.DYAAYNVLDDPELR.Q	0.9931	2	1654.7735
						K.VVVFLK.G	0.9958	1	704.931
1548	GLT10_MOUSE	603	4.81	1	2	R.LLQAVALALAALVLLPNVGLWALYRER.Q	0.9958	3	2948.6114
1549	GLT12_MOUSE	576	5.38	1	2	K.DFKWFLDTVYPELHVPEDRPGFFGMLQNF	0.9958	3	3556.035
1550	GLT13_MOUSE	556	7.37	2	3	K.ENEKVGIFNCHGMGGNQVFSYTADK.E	0.9944	2	2804.029
						R.DFLKLTLENYVK.T	0.9958	1	1483.7478
1551	GLTD2_MOUSE	321	11.21	2	2	R.HAIPFAILTLLLLYISIWFFYEWPFPLPAQR.T	0.9958	3	3778.5633
						R.WFRHAIPFAILTLLLLYISIWFFYEWPFPLPA	0.9958	3	4268.1406
1552	GLU2B_MOUSE	521	19	4	11	K.MPPYDEETQAIIDAAQEAR.S	0.9917	2	2149.3368
						R.GVSLSNHHFYEESKPFTCLDGTATIPFDQV	0.9958	3	4469.6732
						K.HGGSPTSLGTWGSWAGPDHDK.F	0.9958	2	2151.259
						K.EKESLQQLAEVTR.E	0.9958	2	1531.7062
1553	GLYAL_MOUSE	296	3.04	1	3	K.YLPESLK.V	0.9924	1	850.0025
1554	GLYG_MOUSE	333	40.24	6	80	R.TKPWNYTYNPQTK.S	0.994	2	1641.8235
						K.RPELGITLTK.L	0.9958 1,2		1128.3573
						K.DASSYLMMEHVSGALSDLSFGEAPAAPQP	0.9958	3	3787.1362
						K.VLETVFDDVIMVDVLDSGDSAHLTLMK.R	0.9958	3	2964.4158
						R.WEQGQADYMGADSFDNIK.R	0.9958	2	2076.2012
						K.CVFMDADTLVLSNIDDLFER.E	0.9958	2	2374.6339
1555	GMCL1_MOUSE	524	7.63	2	6	K.ELSINVMK.Q	0.9944	1	934.1388
						K.YIYQTLFLNGENSDIKICALGEEWSLHK.I	0.9958	3	3343.7266
1556	GMPPB_MOUSE	360	10	2	6	R.FVEKPQVFVSNK.I	0.9917	2	1422.6671
						R.ISMSHEEEPLGTAGPLALAR.D	0.9952	2	2080.3636
1557	GMPR1_MOUSE	345	25.51	5	18	K.GHIISDGGCTCPGDVAK.A	0.9958	2	1744.8311
						K.FICLDVANGYSEHFVEFVK.L	0.9944	2	2275.5317
						K.GDVENTILDILGGLR.S	0.9958	2	1585.7978
						K.TGVGYPQLSAVIECADSAHGLK.G	0.9958	2	2274.5017
						K.DVLLRPK.R	0.9958	1	841.0415

1558	GNAI2_MOUSE	355	39.15	7	13	R.LWADHGVQACFGR.S	0.9958	2	1517.6531
						R.EYQLNDSAAYYLNDLER.I	0.9958	2	2078.1993
						R.IAQSDYIPTQQDVLR.T	0.9958	2	1747.9457
						K.ITQSSLTICFPEYTGANK.Y	0.9958	2	2031.236
						K.TTGIVETHFTFK.D	0.9958	2	1381.5712
						R.QYRAVVYSNTIQSILAIVK.A	0.9958	3	2167.5565
						K.KWIHCFEGVTAIIFCVALSAYDLVLAEDEEM	0.9958	3	3902.386
1559	GNAL_MOUSE	381	8.66	2	4	K.VNFHMFDVGGQR.D	0.9958	2	1407.5896
						K.HYCYPHFTCAVDTENIR.R	0.9958	2	2184.3045
1560	GNAO_MOUSE	354	5.37	1	2	R.MEDTEPFSAELLSAMMR.L	0.9958	2	1959.2546
1561	GNAS1_MOUSE	1133	3.97	2	2	R.ILHVNGFNGEGGEEDPQAAR.S	0.9952	2	2111.2352
						R.SNEYQLIDCAQYFLDKIDVIK.Q	0.9958	2	2576.872
1562	GNL1_MOUSE	607	2.47	1	7	K.VDLAPPALVVAWK.H	0.9958	1	1379.6854
1563	GNPI_MOUSE	289	36.33	4	5	K.IQAAGGIELFVGGIGPDGHIAFNEPGSSLVS	0.9958	3	3167.5486
						K.YFTLGLPTGSTPLGCYQK.L	0.9958	2	2004.2562
						K.AIEEGVNHMWTVSAFQQHPR.T	0.9958	2	2338.6055
						K.HIDIHPENTHILDGNAADLQAECDAFEEK.I	0.9958	3	3304.4767
1564	GNPTA_MOUSE	1235	3.4	2	2	R.DNIAGKSFQNR.L	0.9958	2	1250.3567
						R.DHALNPPPVLETNARLAQPTLGVTVSK.E	0.9958	3	2840.2523
1565	GNRHR_MOUSE	327	2.14	1	2	K.NNIPR.A	0.9944	1	613.6945
1566	GNS_MOUSE	544	6.62	2	2	K.NFNIHGTNK.H	0.9958	1	1045.1429
						R.RPNVLLLLTDDQDAELGGMTPLK.K	0.9958	2	2510.9085
1567	GO45_MOUSE	403	3.72	1	4	R.DAQSAIQDLLSER.E	0.9958	2	1446.5571
1568	GOGA3_MOUSE	1487	6.12	5	6	R.LEEDTEETSGLLEQLRQDLAVK.S	0.9917	2	2517.7497
						K.LENVSLSHQLTETQHR.S	0.9958	2	1893.0665
						K.DQLINELK.A	0.9958	1	973.1143
						K.DMSLVHQQMAELEGHLQSVQK.E	0.9958	2	2409.7376
						R.LQAQVEHSHSSQQK.Q	0.9958	2	1607.7232
1569	GOGA4_MOUSE	2238	7.28	9	14	K.SLNLK.S	0.9958	1	574.6982
						K.QLMREFNTQLAQK.E	0.9958	1,2	1607.8681
						K.CVEVLEDRPEENSQSHEIQSNVGTVDGLR	0.9944	3	3958.1645
						R.EQVHNLEDRLK.R	0.9958	2	1381.5314
						K.EQQESLALEELELQKK.A	0.9924	1	1916.1357
						K.RQENLLQR.C	0.9958	1	1057.1978
						R.EEEMTGKVTDLQTQLEELQK.K	0.9917	2	2350.6001
						R.LQSLSQQHQAAVEELR.E	0.9956	2	1838.0305
						K.AQEVEAELLESHQEETQQLHR.K	0.9958	2	2505.6604

1570	GOGA5_MOUSE	729	5.62	2	2	R.NEVQSLNQEMASLLQR.S	0.9958		2	1861.0801
						R.LRNVPVLFNDTETNLAGMYGK.V	0.9924		3	2353.6984
1571	GOLI4_MOUSE	655	5.19	2	3	K.LTGELQEVQPNHEAGPR.R	0.9946		2	1876.036
						K.AHQDIHTQLQDVK.T	0.9958		2	1533.6841
1572	GOLM1_MOUSE	393	4.07	1	3	R.IQSSHSFQLENVNK.L	0.9958		2	1631.7856
1573	GORS2_MOUSE	451	9.09	2	7	R.EASVTPSNLWGGQGLLGVSIR.F	0.9958		2	2142.4197
						K.ISLPGQMTGTPITPLK.D	0.9958		2	1655.0057
1574	GP108_MOUSE	569	5.27	2	8	K.DNHVIHPSPTEMSAVK.E	0.9958	1,2		1762.9781
						K.ENQTAPQVSGDK.T	0.9958		1	1274.3299
1575	GP115_MOUSE	698	6.73	2	2	K.HEFRPRQGK.C	0.9915		2	1155.3047
						K.SRMMAIGFAIGYGCPLVIAVITVTVTEPGEG	0.9958		3	3632.2369
1576	GP124_MOUSE	1329	7.67	3	3	R.NSPGDGLPLEGEPMLTPSEGSDTSAAPIAE	0.9958		3	3693.9782
						R.REVGVSGAQPSSVGQDAPVEPEPLADQQ	0.9958		3	3118.3873
						K.ACSGIVGALERIGGAALSPHAQHISVNSR.N	0.9958		3	2930.2627
1577	GP128_MOUSE	785	8.79	3	7	K.ATRLCNVSEFGNIELQNVTK.G	0.9945		2	2294.5359
						K.GSSNSLVSGRILINK.T	0.9958		2	1545.7794
						K.SLDILSNIGCALSIAGLALTILFQILTR.K	0.9929		2	2988.5475
1578	GP142_MOUSE	365	4.38	1	2	R.YDGVDGHWPESPER.S	0.9958		2	1644.6971
1579	GP149_MOUSE	732	7.65	2	2	R.RLSHEENQKPDLSDWEWCR.S	0.9929		2	2486.6287
						K.HVVGFQSLPVDMLSFLLSLLASSVTPVFVL	0.9958		3	3589.3172
1580	GP158_MOUSE	1200	3.75	2	2	K.EKTLGLAGK.T	0.9958		1	917.0935
						R.AEVCPWEFEPLEQPNAERSVTLPASSALS	0.9931		3	3529.8512
1581	GP175_MOUSE	369	7.86	1	2	R.FFLLAIELSVIILGLAFGHLESKSSIK.R	0.9958		3	2947.5743
1582	GP177_MOUSE	541	5.36	2	6	K.YYLLNIRLPVNEK.K	0.9958		2	1635.9469
						R.WLAPWGPNKCDK.I	0.9958		1	1472.6525
1583	GPC1_MOUSE	557	17.06	5	41	R.ALQATLATQLHGIDDHFQR.L	0.9958		2	2136.375
						R.DIQDFWISLPGTLCSEK.M	0.9958		2	2010.2171
						R.TPLTHALPGLSEQEGQK.T	0.9958		2	1807.0135
						K.LALQEKPSTGTLEK.L	0.9958		2	1515.7471
						K.GFSLSDVPQAEISGEHLR.I	0.9958		2	1943.1234
1584	GPC2_MOUSE	579	5.18	1	2	R.SRNLGSSVGLHTPLVLLLLPSALTLLVLR.-	0.9958		3	3054.7336
1585	GPC4_MOUSE	557	9.16	2	4	R.YLFAVTGNGLANQGNNPEVQVDTSKPDILI	0.9958		3	3458.8962
						K.VFQGCGPPKPLPAGR.I	0.9958		2	1581.8241
1586	GPD1L_MOUSE	351	23.93	6	20	R.KLTDIINNDHENVK.Y	0.9958		2	1653.8326
						K.VCIVGSGNWGSAVAK.I	0.9958		2	1505.68
						K.ELLNGQKLQGPQTSAEVYR.I	0.9958		2	2132.3812
						R.QKGLLDK.F	0.9944		1	801.9615

						K.ALGITLIK.G	0.9944	1	829.0709
						K.MWVFEETVNGR.K	0.9926	2	1368.5499
1587	GPDA_MOUSE	349	46.99	12	66	R.KLTEIINTQHENVK.Y	0.9958	2	1667.9029
						R.ELHSILQHK.G	0.9958	1	1105.2822
						K.KVCIVGSGNWGSAIAK.I	0.9958	2	1647.881
						K.VCYEGQPVGEFIR.C	0.9958	2	1554.7088
						K.FPLFTAVYK.V	0.9921	1,2	1086.3189
						K.VCIVGSGNWGSAIAK.I	0.9958	2	1519.7069
						K.LTEIINTQHENVK.Y	0.9958	2	1539.7288
						K.DLMQTPNFRITVVQEVDTVEICGALK.N	0.994	2	2978.3968
						K.ANTIGISLIK.G	0.9957	2	1030.2529
						K.VCIVGSGNWGSAIAKIVGSNAGR.L	0.9958	2	2274.5511
						K.LPPNVVAIPDVVQAATGADILVFVVPHQFIG	0.9944	3	3326.9499
						R.VTMWVFEEDIGGR.K	0.9958	2	1539.7461
1588	GPDM_MOUSE	727	15.27	5	8	K.NVVPICQPSAGVHIVMPGYYSPENMGLLDF	0.9958	3	3844.3151
						R.VIFFLPWEK.M	0.9958	1	1179.4472
						R.NHVVDISDSGLITIAGGK.W	0.9958	2	1797.0183
						K.MTIAGTTDTPTDVTHHPIPSEEDINFILNEVF	0.9958	3	3565.9337
						R.ALEHFPMLQK.D	0.9924	2	1214.4681
1589	GPM6A_MOUSE	278	5.76	1	2	K.SKEEQELHDIHSTR.S	0.9944	2	1709.8131
1590	GPR44_MOUSE	382	8.38	2	2	K.ALAVSKFLLAFMVPLAIIASSHVAVSLR.L	0.9958	3	2926.6201
						R.QKALAVSK.F	0.9958	1	845.0299
1591	GPR56_MOUSE	687	8.15	3	10	R.QMVYFLLSLFSLVQGAHSGSPR.E	0.9924	2	2438.8499
						K.NNSDSAKLPISSGSTSSSR.I	0.9958	2	1895.978
						R.FQAQGGPSPLKNNSDSAK.L	0.9944	2	1846.9945
1592	GPR61_MOUSE	449	10.69	2	7	K.QFVCFFKAAPEEELR.L	0.9958	2	1872.0967
						R.EGSIEENFLQFLQGTSENWVSRPLPSPKR.	0.9958	3	3347.7117
1593	GPR97_MOUSE	542	5.54	1	4	K.LSLLAWGLPVLVVIGAGSSNSYGVYTIR.D	0.9958	3	2907.4258
1594	GPR98_MOUSE	6298	2.86	8	13	K.TILDSCPYLSILALHWNPQQINGHK.F	0.9958	3	2920.3068
						K.SDSPFGIIR.F	0.9944	1	992.1197
						K.VSYETTAGSAKPPEDFEAVQKGEVFFQR.F	0.9958	3	3119.4143
						R.SGGHFGRLLLCYGTSDIDVVAR.A	0.9958	3	2394.6586
						R.WNGNNFAWHQTLPVRGVLGMALFSR.G	0.9958	3	2873.3103
						K.GAVRLHWAIEEK.A	0.9944	1	1409.631
						R.GPGVSGEITVNWKILPPSR.G	0.9944	2	2008.328
						R.RHHSGTDVLYFSGLEGAFGTVDPK.Y	0.9931	2	2591.8424
1595	GPSM1_MOUSE	650	12	4	5	R.GPTMPDEDFFSLIQR.V	0.9958	2	1753.9672

						R.ITLNNVGHLR.G	0.9958		2	1137.3273
						R.AAQSSVTASPQTEEFFDLIASSQSR.R	0.9958		2	2658.8382
						R.CPLEEGQAGAAEATAAPSVEDR.A	0.9958		2	2230.316
1596	GPX1_MOUSE	201	43.28	5	91	K.YVRPGGGFEPNFTLFEK.C	0.9958		2	1959.2114
						R.GLVVLGFPCNQFGHQENGKNEEILNSLK.Y	0.9958	2,3		3143.4925
						R.TIDIEPDIETLLSQQSGNS.-	0.9958		2	2061.2072
						R.NALPTPSDDPTALMTDPK.Y	0.9958		2	1885.0961
						R.GLVVLGFPCNQFGHQENGK.N	0.9958		2	2102.3233
1597	GPX3_MOUSE	226	8.41	1	34	K.YVRPGGGFVPNFQLFEK.G	0.9958		2	1956.2541
1598	GPX41_MOUSE	197	19.8	3	6	K.TDVNYTQLVDLHAR.Y	0.9958		2	1645.8125
						R.ILAFPCNQFGR.Q	0.9958		2	1323.5035
						R.SMHEFSAK.D	0.9958		1	937.0582
1599	GRAA_MOUSE	260	23.08	2	2	K.SAPSETLREVNITVIDR.K	0.9958		1	1901.1271
						R.GPSLATLLFLLLIPEGGCERIIGGDTVVPHSI	0.9944		3	4206.9862
1600	GRAM2_MOUSE	320	4.69	1	2	K.LFKDIPLEEVVLK.V	0.9944		1	1543.8871
1601	GRB2_MOUSE	217	27.19	3	12	R.DIEQMPQQPTYVQALFDFDPQEDGELGFR	0.9958		3	3415.712
						K.FNSLNELVDYHR.S	0.9958		2	1507.6457
						K.GACHGQTGMFPR.N	0.9958		2	1319.4467
1602	GRHL1_MOUSE	618	5.18	2	10	K.RPVLVLQNEALYPQRR.S	0.9944		2	1953.298
						K.ESEEVFDALMLK.T	0.9958		1	1411.6099
1603	GRHPR_MOUSE	328	53.35	10	133	R.NTMSLLAANNLLAGLR.G	0.9958		2	1672.9836
						K.DLEQGVVGAHGLLCR.L	0.9958		2	1624.8034
						R.VISTLSVGVDHLALDEIK.K	0.9958		2	1910.2181
						R.GDVVNQEDLYQALASGQIAAAGLDVTTPEI	0.9958		3	4241.7851
						R.KDLEQGVVGAHGLLCR.L	0.9958		2	1752.9775
						K.NCVILPHIGSATYK.T	0.9944		2	1573.7985
						R.AALAQAADCEVEQWNSDDPIPR.K	0.9958		2	2457.5817
						R.VISTLSVGVDHLALDEIKK.R	0.9958		2	2038.3922
						R.VGYTPGVLTDATAELAVSLLLTTCR.R	0.9958		2	2622.9849
						K.VFVTGPLPAEGR.A	0.9958		2	1243.4484
1604	GRIA2_MOUSE	883	6.57	3	4	K.FAYLYDSDRGLSTLQAVLDSAAEK.K	0.9924		3	2634.9024
						K.GSSLGNAVNLAVLK.L	0.9944		2	1343.5663
						R.YEGYCVDLAAEIAK.H	0.9944		2	1602.7473
1605	GRID2_MOUSE	1007	4.87	2	2	R.GVVLRVVTVLEEPFVMVSENVLGKPK.K	0.9958		3	2840.4375
						K.VSQQGMDVALQKVENNINK.M	0.9949		2	2116.3972
1606	GRIK5_MOUSE	979	7.05	2	2	R.ASGAGAPPRGLGTPAEATSPPRPRPGPTG	0.9958		3	2935.2753
						R.ENCEASTYPGPALSAALMFDAVHVVVSAVI	0.9944		3	3676.1047

1607	GRIN1_MOUSE	932	2.04	2	5	K.KDPQLLGK.K	0.9958		1	899.0782
						K.EDPRSSR.R	0.9944		1	846.8753
1608	GRIP1_MOUSE	1127	3.02	2	2	K.EGTTLGLTVSGGIDK.D	0.9924		2	1448.6134
						K.SASQTKPPDGALAVR.R	0.9944		2	1498.6793
1609	GRIPE_MOUSE	2035	1.38	2	34	K.QENDVINAILK.Q	0.9958		1	1257.4295
						K.TQMQQGLISIAAR.T	0.9958		1	1417.6665
1610	GRM1_MOUSE	1199	3.09	2	2	R.EEPISPPGEDDDDDSSER.F	0.9958		1	1989.9116
						K.LQSPEVRSFDDYFLK.L	0.9944		2	1845.0618
1611	GRM3_MOUSE	879	6.14	2	2	K.SYDSVIR.E	0.9944		1	839.9237
						K.VDEAEYMCPDGSYAIQENIPLLIAGVIGGSY	0.9958		3	4615.1751
1612	GRM4_MOUSE	912	2.52	2	5	R.MDPVDGTQLLK.Y	0.9924		1	1217.4229
						R.YNDTPIVK.A	0.9924		1	950.0795
1613	GRM7_MOUSE	915	8.74	2	2	K.VQFVIDAVYAMAHALHHMNKDLCADYR.G	0.9944		3	3190.6308
						R.LISPTSQLAITSSLISVQLLGVFIWFGVDPPN	0.9958		3	5470.3027
1614	GRM8_MOUSE	908	5.29	2	5	K.VYIIIFHPEQNVQK.R	0.9949		2	1729.0318
						K.ELLGYIRAVNFNGSAGTPVTFNENGDAPGF	0.9958		3	3138.4233
1615	GRP1_MOUSE	795	5.16	2	2	R.NHRAPPLTPSKPPVVVDWASGVSPKPDPK	0.9958		3	3075.5406
						K.IESLQLGK.S	0.9924		1	888.0519
1616	GRP2_MOUSE	608	5.1	2	2	R.HCKALILGIYK.Q	0.9958		1	1316.5957
						R.HSSLIDIESVPTYKWK.R	0.9958		3	1904.1729
1617	GRP75_MOUSE	679	67.01	32	3118	K.VQQTVQDLFGR.A	0.9958	1,2		1291.4496
						K.STNGDTFLGGEDFDQALLR.H	0.9958		2	2057.1809
						R.VINEPTAAALAYGLDKSEDK.V	0.9958		2	2106.3373
						K.VIAVYDLGGGTFDISILEIQK.G	0.9958		2	2252.6128
						K.ERVEAVNMAEGIIHDTETK.M	0.9958	2,3		2143.3765
						K.LLGQFTLIGIPPAPR.G	0.9958		2	1593.9529
						R.AQFEGIVTDLIK.R	0.9958		1	1334.5553
						K.RQAVTNPNNTFYATK.R	0.9958		2	1725.9016
						R.EQQIVIQSSGGLSK.D	0.9958		1	1474.6543
						K.NAVITVPAYFNDSQR.Q	0.9958		2	1695.8723
						R.QAVTNPNNTFYATK.R	0.9958		2	1569.7141
						R.TTPSVVAFTADGER.L	0.9958		2	1451.5761
						R.VEAVNMAEGIIHDTETK.M	0.9958	2,3		1858.0735
						R.QAASSLQQASLK.L	0.9944		2	1232.3793
						R.ASNGDAWVEAHGK.L	0.9958		1	1342.4105
						R.GVPQIEVTFDIDANGIVHVSAK.D	0.9958		2	2310.6121
						K.SQVFSTAADGQTQVEIK.V	0.9958		2	1809.9707

						R.VINEPTAAALAYGLDK.S	0.9958	1,2		1646.8809
						K.ETAENYLGHTAK.N	0.9958		1	1334.4283
						K.CELSSSVQTDINLPYLTMDASGPK.H	0.9958		2	2627.8892
						K.GAVVGIDLGTTNSCVAVMEGK.Q	0.9958		2	2079.3393
						R.EQQIVIQSSGGLSKDDIENMVK.N	0.9958		2	2419.7094
						K.DAGQISGLNVLR.V	0.9958	1,2		1243.4056
						K.SDIGEVILVGGMTR.M	0.9958		2	1447.6898
						K.LFEMAYK.K	0.9923	1,2		902.0961
						K.LYSPSQIGAFVLMK.M	0.9958		2	1554.8878
						R.LVGMPAK.R	0.9958		1	715.9293
						K.AVNPDEAVAIGAAIQGGVLAGDVTDVLLLD	0.9958		3	4592.2842
						K.MEEFKDQLPADECNK.L	0.9943		2	1854.9924
						K.KSQVFSTAADGQTQVEIK.V	0.9958		2	1938.1448
						K.AKCELSSSVQTDINLPYLTMDASGPK.H	0.9958		2	2827.1421
						K.MKETAENYLGHTAK.N	0.9958		2	1593.7949
1618	GRP78_MOUSE	655	63.05	26	770	R.IINEPTAAAIAYGLDK.R	0.9958		1	1660.9078
						K.KSDIDEIVLVGGSTR.I	0.9958		1	1589.7862
						R.VEIIANDQGNR.I	0.9958	1,2		1229.3353
						K.IEWLESHQDADIEDFK.A	0.9958		2	1976.1064
						K.KVTHAVVTVPAYFNDAQR.Q	0.9958		2	2017.295
						K.TKPYIQVDIGGGQTK.T	0.9958		2	1605.8314
						K.SQIFSTASDNQPTVTIK.V	0.9958		2	1838.0245
						K.DNHLLGTFDLTGIPPAPR.G	0.9958		2	1935.19
						K.VTHAVVTVPAYFNDAQR.Q	0.9958		2	1889.1209
						R.IEIESFFEGEDFSETLTR.A	0.9958		2	2150.3032
						R.GVPQIEVTFEIDVNGILR.V	0.9958		2	2000.3024
						K.ELEEIVQPIISK.L	0.9958		1	1398.6397
						R.GINPDEAVAYGAAVQAGVLSGDQDTGDLV	0.9958		3	4902.4885
						K.KTKPYIQVDIGGGQTK.T	0.9958		2	1734.0055
						K.NILVFDLGGGTFDVSLLTIDNGVFEVVATNC	0.9958		3	4569.9825
						R.ITPSYVAFTPEGER.L	0.9958		2	1567.7386
						K.TFAPEEISAMVLTK.M	0.9944		1	1537.8115
						K.NQLTSNPENTVFDAK.R	0.9958		2	1678.796
						R.TWNDPSVQQDIK.F	0.9958		1	1431.5449
						R.AKFEELNMDLFR.S	0.9958		2	1513.7515
						K.VYEGERPLTK.D	0.9958		2	1192.3574
						K.FEELNMDLFR.S	0.9914		2	1314.4987

						R.NELESYAYSLK.N	0.9958	1	1317.4381
						K.LYGSGGPPPTGEEDTSEKDEL.-	0.9958	2	2179.2555
						K.KSQIFSTASDNQPTVTIK.V	0.9958	2	1966.1986
						R.ALSSQHQAR.I	0.991	2	998.0867
1619	GRPE1_MOUSE	217	35.94	5	51	K.FDPYEHEALFHTPVEGK.E	0.9958	2	2017.2047
						R.TLRPALVGVVK.D	0.9944	2	1153.4538
						K.DLLEVADILEK.A	0.9958	1	1258.4546
						K.ATQSVPKEEISNNNPHLK.S	0.9958	2	2007.2107
						K.SLYEGLVMTEVQIQK.V	0.9958	2	1739.0369
1620	GRSF1_MOUSE	479	28.6	7	14	R.AQGLPWSCTVEDVLNFFSDCR.I	0.9958	2	2502.6747
						K.TTYLEDLPPLPEYELSPSK.L	0.9958	2	2193.4553
						K.SLQVKPSPVLSDGVVR.L	0.9917	2	1681.9731
						R.NSENGIHFLLNR.D	0.9958	2	1414.5638
						R.GLPFQANAQDIINFFAPLKPVR.I	0.9958	2	2457.8809
						K.LPEAVDFGTLPSLHFVHMR.G	0.9958	2	2167.5334
						R.RGDALIEMESEQDVQK.A	0.9958	2	1849.0228
1621	GSDM1_MOUSE	446	10.99	2	2	R.SSTLEVQTLSVAPTALENLHKER.K	0.9958	3	2524.8339
						K.AEGCFSLPFFAPLGLQGSVNHK.E	0.9943	2	2377.6709
1622	GSH0_MOUSE	274	6.57	1	12	R.ASTLHLQTGNLLNWGR.L	0.9958	2	1782.0121
1623	GSH1_MOUSE	637	6.44	2	5	K.EATSVLGEHQALCTITSFPR.L	0.9958	2	2218.4375
						K.VQLLLNGGDVLETLQEK.G	0.9958	2	1870.1534
1624	GSHB_MOUSE	474	12.66	3	8	R.EGGGNNLYGEEMVQALEQLK.D	0.9958	2	2180.3942
						K.QIEINTISASFGGLASR.T	0.9958	2	1764.9762
						R.VGLLEALLPGQPEAVAR.L	0.9943	2	1734.0489
1625	GSHR_MOUSE	500	23.8	6	20	R.NFDSLISSNCTEELENAGVEVLK.F	0.9958	2	2569.748
						K.ADFDNTVAIHPTSSEELVTLR.-	0.9958	2	2316.5297
						K.KTSSGLELQVVTSVPGR.K	0.9958	2	1759.0128
						R.KPTTTMIPDVDCLLWAIGR.D	0.9958	2	2188.5562
						K.IYSTAFTPMYHAVTTR.K	0.9958	2	1860.1376
						K.GHILVDEFQNTNVK.G	0.9958	2	1614.7984
1626	GSK3B_MOUSE	420	9.76	2	3	R.TTSFAESCKPVQQPSAFGSMK.V	0.9958	2	2289.5312
						R.LTPLEACAHSFFDELR.D	0.9958	2	1907.0991
1627	GSLG1_MOUSE	1175	6.64	5	9	R.VAELSSDDFHLDR.H	0.9958	2	1504.5963
						K.ADIFVDPVLHTACALDIK.H	0.9958	2	1999.2806
						K.FCHGILTK.A	0.9958	1	976.1296
						R.GEIEHHCSGLHR.K	0.9958	2	1432.5046
						K.HTWSNNLAVLECLQDVR.E	0.9958	2	2056.2518

1628	GSTA1_MOUSE	223	5.83	1	3	K.SHGQDYLVGNR.L	0.9958		2	1246.3249
1629	GSTA3_MOUSE	221	30.77	3	5	R.SDGSLMFQQVPMVEIDGMK.L	0.9958		2	2113.4666
						R.WLLAAAGVEFEEKFLK.T	0.9924		1	1852.1833
						R.ADIALVELLYHVEELDPGVVDNFPLLK.A	0.9958		2	3023.4962
1630	GSTA4_MOUSE	222	62.61	7	108	K.EKEESYDLILSR.A	0.9958		2	1482.6305
						R.KPPPDGPYVEVVR.T	0.9958	1,2		1453.6811
						K.DHGEAFLVGNQLSWADIQLLEAILMVEELS.	0.9958		3	4870.6149
						R.YFPVFEK.I	0.9958		1	930.0911
						R.ISNIPTIK.K	0.9958		1	886.0794
						K.DGHLLFGQVPLVEIDGMMLTQTR.A	0.9958		2	2572.0125
						R.WLLAAAGVEFEEEFLETR.E	0.9958		2	2111.3587
1631	GSTK1_MOUSE	226	60.18	10	26	K.AGMSTAQAQHFLEK.I	0.9958		2	1519.7155
						K.ISTQQVKNK.L	0.9958		1	1046.2119
						K.YGAFGLPTTVAHVDGK.T	0.9958		1	1633.8443
						K.TYMLFGSDRLELLAYLLGEK.W	0.9958		2	2333.7479
						R.LELLAYLLGEK.W	0.9958		2	1262.5321
						K.LQLRPTLIAGIMK.D	0.9958		2	1454.8577
						R.FLTTVSMEQPEMLEK.V	0.9958		1	1784.0926
						K.QFFQVPLNIPK.D	0.9958		2	1331.6005
						R.VWSRDEDITEYQSILAAAVK.A	0.9958		2	2295.5541
						K.LIENTDAACK.Y	0.9936		2	1135.2256
1632	GSTM1_MOUSE	218	56.88	12	308	K.VTYVDFLAYDILDQYR.M	0.9958		2	1995.239
						K.LYSEFLGK.R	0.9924		1	957.1143
						K.LGLDFPNLPYLIDGSHK.I	0.9958		2	1900.1845
						R.MLLEYTDSSYDEK.R	0.9958		2	1594.7303
						R.ADIVENQVMDTR.M	0.9958		2	1391.5389
						K.RPWFAGDK.V	0.9958		2	977.1105
						R.YTMGDAPDFDR.S	0.9958		2	1288.3741
						R.YIATPIFSK.M	0.9958		1	1040.2475
						K.RYTMGDAPDFDR.S	0.9958		2	1444.5615
						K.FKLGLDFPNLPYLIDGSHK.I	0.9945		2	2175.5352
						K.CLDAFPNLR.D	0.9958		2	1106.2329
						K.MAHWSNK.-	0.9958		1	874.005
1633	GSTM2_MOUSE	218	43.58	8	262	K.VTYVDFLVYDVLDQHR.I	0.9958		2	1983.231
						K.KKPEYLEGLPEK.M	0.9957		2	1431.672
						R.LLLEYTDTSYEDK.K	0.993		2	1590.7241
						R.FLSKPIFAK.M	0.9914		2	1051.3171

						R.VDILENQAMDTR.I	0.9958		2	1405.5658
						K.KPEYLEGLPEK.M	0.9958		2	1303.4979
						R.IQLAMVCYSPDFEK.K	0.9958		2	1701.9411
						K.CLDAFPNLK.D	0.9958		1	1078.2195
1634	GSTM5_MOUSE	224	33.04	4	11	K.FKLDLDFPNLPYLMDGK.N	0.9958		2	2027.3857
						K.LTFVDFLTYDVLDQNR.I	0.9958		2	1960.1937
						R.LCYNSNHENLKPQYLEQLPAQLK.Q	0.9958		2	2802.1254
						K.SMVLGYWDIR.G	0.9958		2	1240.4626
1635	GSTO1_MOUSE	240	62.92	10	220	K.SFLGGDSPSMVDYLTWPWFQR.L	0.9958		2	2490.795
						K.NKPEWFFEK.N	0.9958		1	1225.3892
						K.VPPLIASFVR.S	0.9958		2	1099.3616
						K.NPLGLVPVLENSQGHLVTESVITCEYLDEA	0.9958		3	3816.2196
						R.HEVININLK.N	0.9954	1,2		1080.2724
						K.GSAPPGPVPEGQIR.V	0.9958	1,2		1362.5284
						R.EYLNLYLQDSPEACDYGL.-	0.9958		2	2164.296
						K.LWMAAMQQDPVASSHK.I	0.9958		2	1801.0882
						K.KLFPDDPYK.K	0.9948		2	1123.2939
						K.NPLGLVPVLENSQGHLVTESVITCEYLDEA	0.9944		3	3944.3937
1636	GSTP1_MOUSE	210	62.86	9	180	K.FEDGDLTLYQSNAILR.H	0.9958		2	1856.0422
						R.EAAQMDMVNDGVEDLR.G	0.9958		2	1793.9612
						K.YVTLIYTNYENGKNDYVK.A	0.9958		2	2198.4369
						K.AFLSSPEHVNRPINGNGKQ.-	0.9958		2	2066.284
						K.AFLSSPEHVNRPINGNGK.Q	0.9958		2	1938.1533
						K.YVTLIYTNYENGK.N	0.9958		2	1578.7619
						K.EEVVTIDTWMQGLLKPTCLYGQLPK.F	0.9944	2,3		2921.3877
						R.MLLADQGQSWK.E	0.9958		1	1277.4809
						K.ALPGHLKPFETLLSQNQGGK.A	0.9958		2	2136.4587
1637	GSTT1_MOUSE	240	24.17	4	5	R.VDEYLAWQHTGLR.R	0.9958		2	1588.763
						R.KGEHLSDAFAR.V	0.9958		2	1231.3537
						K.NNIPFQMHTVELR.K	0.9958		2	1599.848
						K.YKVPDHWYPQDLQAR.A	0.9958		2	1917.1338
1638	GT2D1_MOUSE	1104	4.08	3	3	R.KILEASNSIQFVIK.R	0.9944		2	1590.9035
						R.KIACDPEAVEIVGIPDK.I	0.9958		2	1855.1047
						R.LGEKVILR.E	0.9924		1	928.1631
1639	GT2D2_MOUSE	936	1.5	1	2	K.TEPMEDSGTSPR.A	0.9924		1	1307.3747
1640	GTF2I_MOUSE	998	5.71	2	2	K.FTVIRPFPGLVINNQLVDQNESEGPVIQES	0.9958		3	4966.5536
						K.AGISFIIK.R	0.9924		1	849.0611

1641	GTPBA_MOUSE	366	6.56	1	2	K.ALEFQHIVPISTVTGEGIAELK.S	0.9958	2	2353.7209
1642	GTR12_MOUSE	622	9	2	2	R.VAIGVSISLSSIATCVYIAEIAPQHRR.G	0.9958	3	2913.3562
						K.YMFGLVIPLGVLQAIAMYFLPPSPR.F	0.9958	3	2795.4597
1643	GTR4_MOUSE	509	4.13	3	12	K.RLTGWADVSDALAELK.D	0.9958	2	1745.9731
						R.LTGWADVSDALAELKDEK.R	0.9929	2	1962.1638
						R.LTGWADVSDALAELK.D	0.9958	2	1589.7857
1644	GUAA_MOUSE	693	24.68	7	19	R.ELFVQSEIFPLETPAFAIK.E	0.9958	2	2180.5487
						K.EPPTDVTPTFLTTGVLSTLR.Q	0.9958	2	2146.4454
						K.VINAAHSFYNGTTTLPISDEDR.T	0.9958	2	2422.6134
						K.IANEVIGEMSLKPEEVFLAQGTLRPDLIESA	0.9958	3	4014.6239
						K.KLYGVQFHPEVGLTENGK.V	0.9958	2	2017.292
						K.ISQMPVILTPLHFDRDPLQK.Q	0.9958	2	2349.7967
						K.VLVLLSGGVDSTVCTALLNR.A	0.9958	2	2088.4186
1645	GUAD_MOUSE	454	28.85	6	15	R.LATLGGSQALGLDSEIGNFEVGK.E	0.9958	2	2277.5364
						R.GASIAHCPNSNLSLSSGLLNVLEVLK.H	0.9958	2	2695.0545
						R.FTLSCTETLMSELGNIAK.T	0.9958	2	2016.2801
						R.GTFVHSTWTCPMEVLR.D	0.9958	2	1922.175
						R.ASDSPIDLFYGDFVGDISEAVIQK.F	0.9958	2	2587.8426
						K.THDLYIQSHISENR.E	0.9958	2	1713.8473
1646	GUF1_MOUSE	651	4.76	2	2	K.LGTNVDSVLQAVIER.I	0.9907	2	1614.8393
						R.NFSIIAHVDHGK.S	0.9958	2	1338.5088
1647	GYS1_MOUSE	738	29.13	12	99	K.RSNSVDTGPSSSLSTPTEPLSPTSSLGEEF	0.9958	3	3077.2426
						K.VIFHPEFLSSTSPLLPVDYEEFVR.G	0.9958	2	2823.2176
						K.RKPDIVTPNGLNVK.K	0.9924 1,2		1551.8295
						K.AFPDHFTYEPHEVDATQGYR.Y	0.9944	2	2381.5224
						R.GHFYGHLDFNLDK.T	0.9958	2	1563.7123
						K.FSAMHEFQNLHAQSK.A	0.9958	2	1775.9793
						R.KLYESLLVGSLPDMNK.M	0.9958	2	1808.1431
						R.KPDIVTPNGLNVK.K	0.9958	2	1395.642
						R.SLDDSCSQLTSFLYSFCQQSR.R	0.9958	2	2530.6393
						R.SLSVSSLPGLEDWEDEFDPENAVLFEVAW	0.9958	3	3824.1457
						K.KFSAMHEFQNLHAQSK.A	0.9958	2	1904.1534
						K.MLDKEDFTMMK.R	0.9958	2	1389.6828
1648	H10_MOUSE	194	19.07	3	12	K.YSDMIVAAIQAEK.N	0.9945	2	1439.6667
						K.RLVTTGVLK.Q	0.9956	2	987.2309
						K.GVGASGSFR.L	0.993	2	837.9108
1649	H11_MOUSE	213	10.33	2	42	K.KPAGPSVSELIVQAVSSSK.E	0.9958	2	1885.168

						R.KKPAGPSVSELIVQAVSSSK.E	0.9958	2	2013.3421
1650	H12_MOUSE	212	28.77	8	43	K.KPAAAAVTKK.V	0.9924	1	985.215
						K.ASGPPVSELITK.A	0.9958	1	1199.3898
						K.ALAAAGYDVEK.N	0.9944	1,2	1108.2365
						K.KALAAAGYDVEK.N	0.9958	2	1236.4105
						K.KPAAAAVTK.K	0.9958	1	857.0409
						R.KASGPPVSELITK.A	0.9943	2	1327.5639
						K.KATGAATPK.K	0.9958	1	844.9865
						K.KPAGAAK.K	0.9958	1	642.7764
1651	H13_MOUSE	221	5.43	2	2	K.KPAAAAGAK.K	0.9924	1	784.934
						K.KPAAAAGAKK.V	0.9958	1	913.1081
1652	H14_MOUSE	219	6.85	2	4	K.TSGPPVSELITK.A	0.9958	1	1229.4161
						R.KTSGPPVSELITK.A	0.9958	1,2	1357.5901
1653	H1BP3_MOUSE	395	14.94	3	12	R.LTIFDEEVDPDAGLFSSDK.K	0.9958	2	2099.2555
						K.LYSCYPAASLPPLPR.K	0.9958	2	1705.9605
						R.KPTLPASVGPSEPGSGPQK.Q	0.9958	2	1835.0672
1654	H2A1F_MOUSE	130	60.77	6	282	R.AGLQFPVGR.V	0.9952	2	945.1093
						R.VTIAQGGVLPNIQAVLLPK.K	0.9958	1	1932.3573
						R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D	0.9958	2	2917.3751
						R.HLQLAIR.N	0.9948	2	851.0396
						R.HLQLAIRNDEELNK.L	0.9958	2	1693.9004
						R.NDEELNK.L	0.9958	1	861.884
1655	H2A2A_MOUSE	130	23.85	1	67	R.VGAGAPVYMAAVLEYLTAEILELAGNAAR.D	0.9958	3	2935.4083
1656	H2A2B_MOUSE	130	19.23	1	75	K.LLGGVTIAQGGVLPNIQAVLLPK.K	0.9944	3	2272.7801
1657	H2AV_MOUSE	128	36.72	2	9	R.VGATAAVYSAAILEYLTAEVLELAGNASK.D	0.9958	2	2897.2952
						K.ATIAGGGVIPHIHK.S	0.9958	1,2	1371.6255
1658	H2AW_MOUSE	372	9.68	2	5	K.LSLTQSDISHIGSMR.V	0.9944	2	1645.8712
						R.HILLAVANDEELNQLLK.G	0.9944	2	1934.2431
1659	H2AY_MOUSE	372	27.96	5	104	R.IGVGAPVYMAAVLEYLTAEILELAGNAAR.D	0.9958	2	2977.4889
						K.GVTIASGGVLPNIHPELLAK.K	0.9958	2	1987.35
						K.GKLEAIITPPPAK.K	0.9958	2	1335.6298
						K.FVIHCNSPVWGADK.C	0.9958	2	1630.8095
						K.NGPLEVAGAAISAGHGLPAK.F	0.9958	2	1831.0818
1660	H2B1B_MOUSE	126	23.02	2	111	K.AMGIMNSFVNDIFER.I	0.9958	2	1745.0211
						R.KESYSVYVYK.V	0.9958	1	1266.4363
1661	H31_MOUSE	136	45.59	4	23	K.DIQLAR.R	0.9924	1	715.8277
						K.STELLIR.K	0.9944	1	831.9878

						R.FQSSAVMALQEACEAYLVGLFEDTNLCAIH	0.9958		3	3588.9865
						R.YRPGTVALR.E	0.9921		2	1033.2186
1662	H32_MOUSE	136	25.74	2	68	R.FQSSAVMALQEASEAYLVGLFEDTNLCAIH	0.9929	2,3		3515.9259
						R.FQSSAVMALQEASEAYLVGLFEDTNLCAIH	0.9958		3	3672.1133
1663	H33_MOUSE	136	27.94	2	84	R.FQSAAIGALQEASEAYLVGLFEDTNLCAIH/	0.9958	2,3		3439.8127
						K.TDLRFQSAAIGALQEASEAYLVGLFEDTNL(	0.9958		3	3925.3533
1664	H4_MOUSE	103	66.99	6	55	K.VFLENVIR.D	0.9944		1	990.1906
						R.DNIQGITKPAIR.R	0.9958		1	1326.5387
						R.TLYGFGG.-	0.9958		1	714.796
						K.RISGLIYEETR.G	0.9958		2	1337.5186
						K.TVTAMDVVYALK.R	0.9958		2	1311.5793
						R.DAVTYTEHAK.R	0.9924	1,2		1135.2187
1665	HA10_MOUSE	325	26.77	5	12	R.APWMEQEGPEYWER.E	0.9958		2	1808.9623
						K.GNEQSFHVSLR.T	0.9958		2	1274.3787
						R.YFETSVSRPGLGEPR.F	0.9958		2	1695.8723
						K.THVTHHPGSEGDVTLR.C	0.9958		2	1743.8765
						K.GNEQSFHVSLRTLLGYYNQSESGSHTIQW	0.9958		3	3980.3259
1666	HA11_MOUSE	362	8.29	2	4	K.AYLEGECVEWLHR.Y	0.9958		2	1662.8083
						R.VYHEGLPEPLTLR.W	0.9958		2	1524.7599
1667	HA12_MOUSE	365	12.33	2	2	K.NGNATLLRTDPPK.A	0.9958		2	1397.5742
						K.TNTVIIAVPVVLGAVVILGAVMAFVMKR.R	0.9958		3	2883.6539
1668	HA1L_MOUSE	362	4.7	1	8	R.YFETAVSRPGLGEPR.Y	0.9958		2	1679.8729
1669	HA2J_MOUSE	254	3.94	1	4	K.YNLEILIK.D	0.9958		1	1006.2303
1670	HA2Q_MOUSE	221	13.57	1	2	K.ETVWMLPEFGQLTSFDPQGGLQNIATGK.H	0.9958	2,3		3066.4553
1671	HAND2_MOUSE	217	6.91	1	2	R.RTQSINSAFAELR.E	0.9958		2	1493.6627
1672	HASP_MOUSE	754	2.52	1	50	R.QQMGNRLTDPDLTSPGK.R	0.9937		2	1859.0643
1673	HAX1_MOUSE	280	6.79	1	3	R.SSALDDPFSILDLLLGR.W	0.9943		2	1833.0917
1674	HBA_MOUSE	142	92.25	14	4164	K.FLASVSTVLTSK.Y	0.9958		2	1253.4814
						R.MFASFPTTK.T	0.9958		1	1030.2268
						K.IGGHGAEYGAEALER.M	0.9958		2	1530.6371
						K.LRVDPVNFK.L	0.9958	1,2		1088.295
						K.TYFPHFDVSHGSAQVK.G	0.9958		2	1821.0019
						K.KVADALASAAGHLDDLPGALSALSDLHAHK	0.9958		3	2966.3237
						K.AAWGKIGGHGAEYGAEALER.M	0.9958		2	2044.2339
						K.FLASVSTVLTSKYR.-	0.9958		2	1572.8449
						K.VADALASAAGHLDDLPGALSALSDLHAHK.I	0.9958		3	2838.1497
						K.VADALASAAGHLDDLPGALSALSDLHAHKL	0.9958		3	3107.4966

						K.IGGHGAEYGAEALERMFASFPTTK.T	0.9958	2,3		2541.8407
						K.TYFPHFDVSHGSAQVKGHGK.K	0.9958		2	2200.4209
						R.VDPVNFKLLSHCLLVTLASHHPADFTPAVH	0.9958		3	3852.3941
						K.LLSHCLLVTLASHHPADFTPAVHASLDK.F	0.9958		3	3052.4693
1675	HBAZ_MOUSE	142	6.34	1	5	R.VDPVNFK.L	0.9944		1	818.9481
1676	HBB0_MOUSE	147	9.52	1	4	K.LVVGVATALSHK.Y	0.9924		1	1195.4477
1677	HBB1_MOUSE	147	91.84	16	6124	R.YFDSFGDLSSASAIMGNAK.V	0.9958		1	1982.1719
						K.VITAFNDGLNHLDSLK.G	0.9958		2	1757.9841
						K.DFTPAAQAAFQK.V	0.9958		1	1295.4374
						K.VNSDEVGGEALGR.L	0.9958		1	1303.3714
						R.LLVVYPWTQR.Y	0.9958		2	1275.5363
						K.GTFASLSELHCDK.L	0.9952		2	1465.5689
						K.AAVSCLWGKVNSDEVGGEALGR.L	0.9958		2	2276.4772
						K.LHVDPENFR.L	0.9911		2	1127.2449
						K.KVITAFNDGLNHLDSLK.G	0.9944	2,3		1886.1582
						K.VVAGVATALAHK.Y	0.9958		2	1137.3677
						K.GTFASLSELHCDKLHVDPENFR.L	0.9958		2	2573.7906
						K.AAVSCLWGK.V	0.9958		1	992.129
						K.DFTPAAQAAFQKVVAGVATALAHK.Y	0.9958		2	2413.7819
						K.VVAGVATALAHKYH.-	0.9958		2	1437.6847
						R.LLGNMIVIVLGHHLGK.D	0.9937		2	1715.1534
						K.VITAFNDGLNHLDSLKGTFASLSELHCDK.L	0.9958		3	3204.5298
1678	HBB2_MOUSE	147	55.78	8	777	R.YFDSFGDLSSASAIMGNPK.V	0.9956		2	2008.2098
						K.VNPDEVGGEALGR.L	0.9958		1	1313.4099
						K.NLDNLK.G	0.9958		1	716.8125
						K.KVITAFNEGLK.N	0.9924		1	1220.4545
						K.VITAFNEGLK.N	0.9924		1	1092.2804
						K.SAVSCLWAKVNPDEVGGEALGR.L	0.9958		2	2316.542
						K.SAVSCLWAK.V	0.9958		2	1022.1553
						R.LLGNAIVIVLGHHLGK.D	0.994		2	1655.0396
1679	HBE_MOUSE	147	26.53	3	9	K.LSELHCDK.L	0.9958		1	1002.0783
						K.LVAGVATALSHK.Y	0.9912		2	1167.394
						K.VNVEEVGGEALGR.L	0.9958		1	1329.4527
1680	HBS1L_MOUSE	682	5.72	2	4	K.SERAVCAGQPSK.G	0.9958		1	1290.3849
						K.SALPPPSLQTSEELGSTPTPVRK.S	0.9958		3	2393.6995
1681	HCD2_MOUSE	261	47.13	8	119	K.KLGESCIFAPANVTSEK.E	0.9958		2	1852.0607
						R.NFLASQVPFPSR.L	0.9958		1	1363.5589

						R.VVTIAPGLFATPLLTTLPEK.V	0.9958		2	2082.5315
						R.VINVNLIGTFNVIR.L	0.9958		2	1572.8912
						R.LGDPAEYAHLVQTIIENPFLNGEVIR.L	0.9958		2	2910.2994
						R.VVTIAPGLFATPLLTTLPEKVR.N	0.9958		2	2337.8516
						R.LVAGEMGQNEPDQGGQR.G	0.9958		1	1786.914
						K.IHTLEDFQR.V	0.9958	1,2		1159.2871
1682	HCDH_MOUSE	314	64.01	10	593	K.LGAGYPMGPFELLDYVGLDTTK.F	0.9958		2	2358.7113
						K.TLSCLSTSTDAASVVHSTDLVVEAIVENLK.I	0.9958	2,3		3161.4969
						K.FAAEHTIFASNTSSLQITNIANATTR.Q	0.9958	2,3		2781.0544
						K.LKNELFQR.L	0.9912	1,2		1048.2303
						K.FILDGWHEMEPENPLFQPSPSMNNLVAQK	0.9958	2,3		3370.822
						K.TFESLVDFCK.T	0.9944		1	1246.3686
						K.DTPGFIVNR.L	0.9958		1	1019.1454
						K.HVTVIGGGLMGAGIAQVAAATGHTVVLVDQ	0.9958		3	3615.1828
						K.KTGEGFYK.Y	0.9944		1	930.0483
						K.LVEVIK.T	0.9924		1	700.8968
1683	HDA10_MOUSE	666	5.11	1	7	R.SLAQALHGETPPSLGPFSKATPEEIQALMF	0.9911		3	3410.9532
1684	HDDC2_MOUSE	199	22.11	2	5	K.FSHPEIVQLVSELETER.N	0.9958		2	2014.2426
						R.LALVHDMAECIVGDIAPADNIPK.E	0.9958		2	2463.8177
1685	HDGF_MOUSE	237	19.41	3	27	K.GFSEGLWEIENNPTVK.A	0.9958		2	1820.9964
						K.YQVFFFGTHETAFLGPK.D	0.9958		2	1990.2683
						K.DLFPYEESK.E	0.9958		1	1128.2237
1686	HDGR2_MOUSE	669	2.84	1	5	K.YPIFFFGTHETAFLGPK.D	0.9958		2	1973.2811
1687	HDHD2_MOUSE	259	40.15	6	58	K.DGLALGPGPFVTALEYATDTK.A	0.9958		2	2137.3941
						K.KLEFEISEDEIFTSLTAAR.N	0.9958		2	2200.4503
						R.LLLDGAPLIAIHK.A	0.9909		2	1374.7098
						R.KDGLALGPGPFVTALEYATDTK.A	0.9958		2	2265.5682
						K.AMVVGKPEK.T	0.9958		1	959.1919
						R.ALPEFTGVQTQDPNAVVIGLAPEHFHYQLL	0.9958		3	3923.4227
1688	HDHD3_MOUSE	251	54.58	6	17	R.AQSHNFPNYGLSR.G	0.9958		2	1491.6059
						K.EHILPSLSHLLPALDLLEASSPMS.-	0.9958		2	2571.9917
						R.RLEDILTGLGLR.E	0.9958		2	1356.6084
						R.ACVEPAVAAHVGDSYLCDYQGSQAVGMH	0.9958		3	4523.907
						R.EHFDFVLTSEAVGCPKPDPR.I	0.9958		2	2302.5145
						R.AHGVVVEDITVEQAFR.Q	0.9958		2	1770.9829
1689	HEBP1_MOUSE	190	38.95	4	22	K.FATVEVTDKPVDEALR.E	0.9958		2	1791.0111
						R.IPNQFQGSPPAPSDESVK.I	0.9958		2	1899.0673

						R.NSLFGSVETWPWQVLSTGGK.E	0.9958	2	2194.4515
						K.EADYVAHATQLR.T	0.9958	1	1374.496
1690	HECD3_MOUSE	861	9.99	5	7	R.VQYFWEALNNFTNEDR.S	0.9958	2	2047.1907
						R.LGSRPQPAEAYTEAIQR.L	0.9958	2	1888.0904
						K.VVPQAVLDLLTWQELEK.K	0.9958	2	1982.3275
						K.KLLLTVDTTDDNFMPK.R	0.9924	1	1852.1529
						K.EQVAAMQAGLLKVVPQAVLDLLTWQELEK	0.9958	3	3222.8108
1691	HECW1_MOUSE	1604	3.3	2	3	R.NGAHDAITIPRSTSDTDLVTSDSR.S	0.9958	2	2530.6677
						K.DNNITDILDLTFTVNEEVFGQVTER.E	0.9958	3	2884.126
1692	HECW2_MOUSE	1578	2.85	2	2	R.TTTFIDPRLPLQSSRPTSALVHR.Q	0.9958	3	2594.9767
						K.LYVTFVGEEGLDYSGPSR.E	0.9926	2	1990.1767
1693	HEM1_MOUSE	642	8.1	3	4	K.FHVELEQALADLHGK.D	0.9958	2	1707.9267
						R.HNIYVQAINYPTVPR.G	0.9944	2	1786.0433
						K.ASLELQEDVQEMHAVR.K	0.9958	2	1856.0606
1694	HEM2_MOUSE	330	40	6	193	R.YGVNQLEEMLRPLVEAGLR.C	0.9932	2,3	2188.5499
						R.SWQTAASTVSASNLIYPIFVTDVPDDVQPIA	0.9958	3	3988.4864
						R.DIQEGADMLMVKPGLPYLDMVR.E	0.9958	2	2492.9693
						R.CVLIFGVPSR.V	0.9924	1	1148.3569
						R.AGADIIITYFAPQLLK.W	0.9958	2	1735.0764
						K.DEQGSAADSEDSPTIEAVR.L	0.9958	2	1977.9903
1695	HEM3_MOUSE	361	18.56	3	14	R.AKDQDILDLVSVLHDPETLLR.C	0.9958	2	2391.727
						R.GAQLAAENLGISLASLLLNK.G	0.9958	2	1997.3427
						R.KLDELQEFSAIVLAVAGLQR.M	0.9958	2	2201.5712
1696	HEM4_MOUSE	265	29.81	4	11	K.LSHPEGFGGLIFTSPR.A	0.9958	2	1715.9493
						K.EDDSGLDPYIQELR.L	0.9958	2	1650.7393
						K.LAEYICSKPSSELPLLFPCGTIK.G	0.9958	2	2625.0095
						K.YSLEYIQALSGSSFDQIK.F	0.9958	2	2050.2726
1697	HEM6_MOUSE	443	31.38	7	17	K.NPYAPTMHFNYR.Y	0.9958	2	1511.6977
						R.GIGGIFFDDLDSPSKEEAFR.F	0.9958	2	2201.3972
						K.AGVSISVVHGNLSEEAANQMR.G	0.9958	2	2170.4051
						K.LPFTAMGVSSVIHPK.N	0.9958	2,3	1584.9171
						K.WCDDYFFIVHR.G	0.9958	2	1558.7021
						K.MELMIMETQAQVCR.A	0.9958	2	1741.0549
						R.YFEVEEADGNTHWWFGGGCDLTPTYLNQ	0.9958	3	4300.5281
1698	HEMO_MOUSE	460	56.74	14	180	K.ELGSPPGISLETIDAAFSCPGSSR.L	0.9958	2	2449.6429
						R.CSPDPGLTALLSDHR.G	0.9958	2	1639.7717
						K.LFQEEFPGIPYPPDAAVECHR.G	0.9958	2	2473.7131

						K.VNSILGCSQ.-	0.9958		1	978.0563
						K.SGAQATWTEVSWPHEK.V	0.9958		2	1814.9518
						R.KWFWDFATR.T	0.9958		2	1257.4368
						R.VAEVENGTKPDSDVPEHCLDTWSFDAATM	0.9958		3	5189.6615
						R.DYFVSCPGR.G	0.9924		1	1101.17
						K.SLGPNTCSSNGSSLYFIHGPNLYCYSSIDK.	0.9958		3	3340.5593
						R.YYCFQGNK.F	0.9958		1	1080.1511
						K.NPITSVDAAFR.G	0.9958		2	1191.3293
						R.GECQSEGVLFFQGNR.K	0.9958		2	1728.8248
						K.VYLIQGTQVYVFLTK.G	0.9958		2	1773.1253
						R.GATYAFTGSHYWR.L	0.9958		2	1517.6433
1699	HERC4_MOUSE	1057	7.1	4	17	K.LIQPDHPQISQQVAASLEK.N	0.9958		2	2103.383
						K.SVASLFDAFHAGFHK.V	0.9958		2	1634.8345
						R.IYSFGLGGNGQLGTGSTSNR.K	0.9958		2	1987.1362
						K.IFWEVFHELPLEK.K	0.9958		2	1687.9787
1700	HEXB_MOUSE	536	11.57	3	6	R.VIPEFDTPGHTQSWGK.G	0.9958		2	1799.9805
						K.GSYSLSHVYTPNDVR.M	0.9958		2	1695.829
						K.FNVLHWHIVDDQSFPYQSTTFPELSNK.G	0.9958		3	3251.5817
1701	HIBCH_MOUSE	385	44.68	12	180	K.INSCFSANTVEQIIENLR.Q	0.9931		2	2109.3099
						K.SPSAEDVAGVLESYHAK.S	0.9958	2,3		1760.8981
						R.SLFAMPETGIGLFPDVGGGYFLPR.L	0.9958		2	2542.955
						R.GCGGVITLNRPK.F	0.9958	1,2		1272.4564
						R.AGIATHFVDSEK.L	0.9958	1,2		1275.4038
						R.ITQACMEGHDFHEGVR.A	0.9958		2	1888.0308
						K.TWEQDPDTFLIIIK.G	0.9958		2	1719.9751
						K.DVTDEDLNSYFK.S	0.9958		2	1446.5102
						R.VLEEELLALK.S	0.9958		1	1157.3929
						K.TLQEVLIMEYR.I	0.9958	1,2		1395.6569
						K.SIIFEEHMDK.I	0.9958		2	1249.4241
						K.SIIFEEHMDKINSCFSANTVEQIIENLR.Q	0.9958		3	3339.7108
1702	HIF1A_MOUSE	836	9.93	4	4	R.KLLDAGGLDSEDEMK.A	0.9958		2	1621.7999
						K.TIASQNAQR.K	0.9958		1	989.0763
						R.SLNLSATLNQRNTVPEEELNPK.T	0.9958		3	2468.7263
						R.ITELMGYEPEELLGRSIYEYYHALDSDHLTK	0.9958		3	3688.0999
1703	HIF1N_MOUSE	349	3.72	1	2	R.SYSFPTRPIPR.L	0.9958		2	1321.5217
1704	HINT1_MOUSE	126	70.63	5	291	K.AQVAQPGGDTIFGK.I	0.9958		2	1389.551
						K.HISQISVADDDDESLLGHLMIVGK.K	0.9958		2	2593.9116

						R.CLAFHDISPQAPTHFLVIPK.K	0.9958		2	2292.6519
						R.MVVNEGADGGQSVYHIHLHVLGGR.Q	0.9958		2	2546.8663
						K.KHISQISVADDDDESLLGHLMIVGK.K	0.9952		2	2722.0857
1705	HINT2_MOUSE	163	43.56	4	210	R.ISQAEEDDQQLLGHLLLVAK.K	0.9958		2	2221.5156
						R.DVAPQAPVHFLVIPR.K	0.9958		2	1659.9719
						R.SLPADILYEDQQCLVFR.D	0.9958		2	2068.3001
						K.AAPGGASPTIFSR.I	0.9944		1	1232.3818
1706	HIP1R_MOUSE	1068	8.05	5	5	K.EMAATSAAIEDAVRR.I	0.9915		2	1591.7796
						R.ILNSCTDLMK.A	0.9924		1	1195.3827
						R.EAELLAAQSLVREK.E	0.9944		1	1557.7874
						R.QKLLDEQLAVLR.S	0.9958		1	1426.6994
						K.AAGTDVNNIFQLTVEMFDYMDCELK.L	0.9958		2	2926.2486
1707	HLX_MOUSE	476	3.57	1	4	R.TEGTERSLHQTTVIK.A	0.9924		2	1700.8894
1708	HMGA1_MOUSE	107	16.82	1	10	R.KQPPVSPGTALVGSQK.E	0.9958		2	1594.8515
1709	HMGB1_MOUSE	215	21.86	5	95	K.IKGEHPGLSIGDVAK.K	0.9958	2,3		1521.7569
						K.HPDASVNFSEFSK.K	0.9957		2	1465.5621
						K.KLGEMWNNTAADDK.Q	0.9944		2	1593.7515
						K.GEHPGLSIGDVAK.K	0.9958		2	1280.4233
						K.KHPDASVNFSEFSK.K	0.9958		2	1593.7361
1710	HMGB3_MOUSE	200	16	2	2	K.KLGEMWNNLSDNEK.Q	0.991		2	1678.8572
						K.KNPEVPVNFAEFSK.K	0.9944		2	1606.8186
1711	HMGCL_MOUSE	325	24	4	9	K.LLEAGDFICQALNR.K	0.9958		2	1620.812
						R.FAGVMQAAQAASISVR.G	0.9952		2	1607.8681
						K.EVSVFGAVSELFTR.K	0.9958		2	1541.7441
						K.GASGNLATEDLVYMLNGLGIHTGVNLQK.L	0.9958		2	2887.2805
1712	HMMR_MOUSE	794	7.05	3	3	K.EVELEKHIAAHAQAILIAQEK.Y	0.9958		2	2342.7007
						K.EEEIKEITSSFLEK.I	0.9945		2	1682.8651
						K.EIEDLKLENLTLQEK.V	0.9915		2	1816.0587
1713	HMOX2_MOUSE	315	17.14	4	16	K.DHPAFAPLYFPTELHR.K	0.9958		2	1912.1576
						R.NKDHPAFAPLYFPTELHR.K	0.9958		2	2154.4355
						R.IHYVGQNEPELLVAHAYTR.Y	0.9958		2	2211.485
						R.ARMNALDLNLK.T	0.9958		1	1259.5095
1714	HN1_MOUSE	154	68.18	4	39	R.VLRPPGGGSNFSLGFDEPAEQPVR.K	0.9958		2	2527.799
						R.SNSSEASSGDFLDLK.G	0.9958		2	1557.611
						K.MASNIFGTPEENPPSWAK.S	0.9958	1,2		1977.1987
						K.GEGDMHENVDTDFQANLAQMEEKPVPAA	0.9958		3	4397.8782
1715	HN1L_MOUSE	190	15.26	1	3	R.SMKPPGGESSDLFGSPEEGISSSKPNR.M	0.9958		3	2779.0075

1716	HNMT_MOUSE	295	27.12	4	15	R.FLNNSTEHQCMQEFMDK.K	0.9958	2	2160.3468
						K.FFHGLLAASAK.I	0.9958	1	1162.3769
						K.AEIKILSVGGGAGEVDLQILSK.V	0.9958	2	2198.5651
						R.DDLCQYVTSSDLAQILDDLGIK.Y	0.9958	2	2483.6979
1717	HNRDL_MOUSE	301	9.3	2	2	R.GFGFVLFK.D	0.9944	1	915.1228
						K.VFVGGLSPDTSEEQIK.E	0.9958	2	1706.8901
1718	HNRH1_MOUSE	449	12.47	3	19	R.ATENDIYNFFSPLNPVR.V	0.9958	2	1998.2023
						R.STGEAFVQFASQEIAEK.A	0.9958	2	1843.0001
						K.HTGPNSPDTANDGFVR.L	0.9958	2	1685.7501
1719	HNRH2_MOUSE	449	8.91	2	5	R.ATENDIYNFFSPLNPMR.V	0.9929	2	2030.2623
						R.YGDGGSSFQSTTGHCVHMR.G	0.9924	2	2085.1811
1720	HNRL1_MOUSE	859	7.33	4	8	K.YNILGTNAIMDK.M	0.9958	1	1353.5762
						R.IGWSLDSCSTQLGEEPFSYGYGGTGKK.S	0.9958	3	2926.1316
						K.KYNILGTNAIMDK.M	0.9958	1	1481.7503
						R.RPLDMEPQQQVYHPELK.T	0.9909	2	2109.4076
1721	HNRPD_MOUSE	355	11.83	4	7	K.KIFVGGLSPDTPEEK.I	0.9958	2	1617.8394
						K.YHNVGLSK.C	0.9958	1	918.0403
						K.MFIGGLSWDTTK.K	0.9958	1	1356.5793
						K.KYHNVGLSK.C	0.9958	1	1046.2144
1722	HNRPF_MOUSE	415	8.92	2	5	K.HSGPNSADSANDGFVR.L	0.9958	2	1631.6585
						K.ITGEAFVQFASQELAEK.A	0.9958	2	1869.0813
1723	HNRPK_MOUSE	463	33.69	9	91	R.GSYGDLGGPIITTQVTIPK.D	0.9958	2	1918.1974
						R.LLIHQSLAGGIIGVK.G	0.9958	1,2	1519.8711
						K.KIIPTLEEGLQLPSPTATSQLPLESDAVECLI	0.9958	3	4185.6839
						K.IIPTLEEGLQLPSPTATSQLPLESDAVECLN`	0.9958	3	4057.5098
						R.IITITGTQDQIQNAQYLLQNSVK.Q	0.9958	2	2590.9365
						K.IILDLISESPIK.G	0.9958	1	1341.6311
						R.ILSISADIETIGEILK.K	0.9907	2	1716.0251
						K.DLAGSIIGK.G	0.9958	1	874.0251
						K.RPAEDMEEEQAFK.R	0.9958	2	1580.7094
1724	HNRPM_MOUSE	729	13.03	5	31	R.MGPLGLDHMASSIER.M	0.9958	2	1614.875
						R.GNFGGSFAGSFGGAGGHAPGVAR.K	0.9958	2	2036.1734
						K.FNECGHVLYADIK.M	0.9944	2	1566.7198
						K.GIGMGNLGPAGMGMEGIGFGINK.I	0.9958	2	2179.5752
						R.MGAGLGHGMDR.V	0.9958	2	1102.2714
1725	HNRPQ_MOUSE	623	4.33	2	2	K.EFNEDGALAVLQQFK.D	0.9958	2	1709.8962
						K.LYNNHEIR.S	0.9958	2	1059.1698

1726	HOOK1_MOUSE	728	4.12	2	2	K.YFHVQLQLEQLQEENYR.L	0.9958		2	2238.4643
						R.NVIKTLDPK.L	0.9944		1	1028.237
1727	HOOK2_MOUSE	716	2.51	1	5	R.EYIEELEPPTDSSTAR.R	0.9958		2	1837.9348
1728	HOP_MOUSE	73	34.25	1	18	K.HPDPTTLCLIAAEAGLTEEQTQK.W	0.9929		2	2524.7534
1729	HOT_MOUSE	465	43.23	9	79	K.AANLYASSPHSEFLDYVNAPIGK.G	0.9958		2	2465.7246
						R.HLETAGILGANIR.T	0.9958	1,2		1365.5754
						K.NLSQLPPVQIVMDSLSK.N	0.9958		2	1870.2146
						R.SPCPSNPIQRPAYQGSNPISDIWAVHALQI\	0.9958		3	4021.5774
						R.VEPTDGSFMDAIEFAK.K	0.9958		2	1757.9526
						K.FLFDLNVDDGLAALGYSK.D	0.9958		2	1959.206
						R.IQDAGLVLADALR.K	0.9958		2	1355.5773
						K.TADYAFEMAVSNIR.Y	0.9958		2	1588.7754
						K.GKPVTVPLKPLIAVPTTSGTGSETTGVAIFD	0.9958		3	3726.3049
1730	HPLN4_MOUSE	400	3.5	1	3	R.DGLDWCNAGWLR.D	0.9958		2	1463.5585
1731	HPRT_MOUSE	218	28.44	3	11	R.SVGYRPDFVGFEIPDK.F	0.9958		2	1827.0465
						R.SPSVVISDDEPGYDLDLFCIPNHYAEDLEK.	0.9958		3	3439.6766
						K.FFADLLDYIK.A	0.9958		1	1245.4607
1732	HPS6_MOUSE	805	8.32	3	159	K.LAQQQGGPGWGAEGPSLPLYRR.A	0.9913		2	2339.6187
						R.LLSDLSNFTGAARLR.E	0.9909		2	1634.8759
						K.RPEALELELLLGSGRPKAVLQAVR.Q	0.9925		2	2617.1105
1733	HPT_MOUSE	347	6.34	1	5	R.HGLTTGATLISDQWLLTTAK.N	0.9931		2	2128.4331
1734	HRSL3_MOUSE	162	20.99	2	2	K.HDEEYTPLPLSKIIQR.A	0.9958		2	1940.2065
						R.LTSENCEHFVNELR.Y	0.9958		2	1748.856
1735	HRX_MOUSE	3966	1.11	2	44	K.RMDQGSYVSVLEFSDDIVK.I	0.9929		2	2189.4449
						K.FCLEENERPLEDQLENWCCRR.C	0.9958		3	2854.9912
1736	HS105_MOUSE	858	21.56	10	40	R.NHAAPFSK.V	0.9944		1	871.9713
						K.IEVPLHSLMAQTQLK.A	0.9958		2	1709.0569
						R.RGPFELEAFYSDPQGVPYPEAK.I	0.9958		2	2498.7539
						K.NQQITHANNTVSSFK.R	0.9958		2	1689.8253
						R.VNTHGIFTISTASMVEK.V	0.9958		2	1836.1132
						K.ELNNVCEPVVTQPKPK.I	0.9958		2	1853.0918
						R.GCALQCAILSPAFK.V	0.9958		2	1536.7437
						K.KPVTDCVISVPSFFTDAER.R	0.9958		2	2169.4052
						R.LLTETEDWLYEEGEDQAK.Q	0.9958		2	2170.291
						K.KLMSSNSTDLPLNIECFMNDK.D	0.9937		2	2458.7702
1737	HS2ST_MOUSE	356	3.37	1	6	R.YHVLHINTTK.N	0.9944		1	1226.4209
1738	HS71A_MOUSE	641	19.19	6	136	K.QTQTFTTYSDNQPGVLIQVYEGER.A	0.9958	2,3		2775.9885

						R.TTPSYVAFTDTER.L	0.9924		1	1488.5939
						R.VCSPIISGLYQGAGAPGAGGFGAQAPK.G	0.9958		2	2532.8248
						R.GVPQIEVTFDIDANGILNVTATDK.S	0.9944		2	2531.8223
						K.VEIIANDQGNRTTPSYVAFTDTER.L	0.9958		3	2698.906
						K.AQIHDLVLVGGSTR.I	0.9958	1,2		1466.6805
1739	HS71L_MOUSE	641	5.3	2	3	K.IHDIVLVGGSTR.I	0.9958		1	1267.4709
						R.DNNLLGRFDLTGIPPAPR.G	0.9958		2	1967.2351
1740	HS74L_MOUSE	838	12.65	6	18	R.INIHGIFSVASASVIEK.Q	0.9958		2	1786.0813
						K.KIQLVLK.V	0.9958		1	842.113
						K.EPFELEAFYTNLHEVPYPDPR.I	0.9958		2	2564.8132
						K.KPVADCVISIPSFFTDAER.R	0.9958		2	2153.4058
						K.ELDNFCNPIVYKPKPK.V	0.9958		2	1963.25
						R.SVMAAAQVAGLNCLR.L	0.9948		2	1561.8059
1741	HS90A_MOUSE	733	47.34	23	327	K.HNDDEQYAWESSAGGSFTVR.T	0.9958		2	2257.2939
						R.RAPFDLFENR.K	0.9958		2	1265.4141
						K.VILHLKEDQTEYLEER.R	0.9958		2	2016.2585
						K.HLEINPDHSIIETLR.Q	0.9958		2	1788.0134
						K.HSQFIGYPITLFVEK.E	0.9958		2	1780.0764
						K.YIDQEELNK.T	0.9958		1	1152.2463
						R.GVVDSEDLPLNISR.E	0.9944		1	1514.6757
						K.ADLINNLGTIAK.S	0.9958		2	1243.4459
						R.TLTIVDTGIGMTK.A	0.9958		1	1350.6135
						K.SLTNDWEEHLAVK.H	0.9958		2	1542.6885
						K.HFSVEGQLEFR.A	0.9958		2	1349.4887
						K.KLSELLR.Y	0.9958		1	859.0568
						R.NPDDITNEEYGEFYK.S	0.9958		2	1834.8902
						K.LGIHEDSQNR.K	0.9932		2	1169.2394
						K.ELHINLIPSK.Q	0.9958		1	1164.3903
						K.HIYFITGETK.D	0.9958		1	1209.3873
						R.YYTSASGDEMVSLK.D	0.9958		2	1551.7083
						R.YESLTDPSK.L	0.9958		1	1040.1149
						R.VFIMDNCEELIPEYLNFIR.G	0.9958		2	2416.7603
						K.IRYESLTDPSK.L	0.9958		2	1309.4619
						K.LGLGIDEDDPTVDDTSAAVTEEMPPLEGDI	0.9958		3	3577.717
						K.HGLEVIYMIEPIDEYCVQQLK.E	0.9958		2	2578.9491
						K.EIFLRELISNSSDALDK.I	0.9958		1	1951.1839
1742	HS90B_MOUSE	724	41.85	20	741	R.GFEVVYMTEPIDEYCVQQLK.E	0.9958		2	2449.7439

						R.TLTLVDTGIGMTK.A	0.9958		1	1350.6135
						K.LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEI	0.9958		2	3537.7235
						R.YHTSQSGDEMTSLSEYVSR.M	0.9958		2	2178.2916
						R.VFIMDSCDELIPEYLNFIR.G	0.9958		2	2375.7078
						K.SLTNDWEDHLAVK.H	0.9958		2	1528.6616
						K.LGIHEDSTNR.R	0.9937		2	1142.2138
						R.RAPFDLFENK.K	0.9958		2	1237.4007
						K.HLEINPDHPIVETLR.Q	0.9958		2	1784.025
						K.HSQFIGYPITLYLEK.E	0.9958		2	1810.1027
						R.NPDDITQEEYGEFYK.S	0.9958	1,2		1848.9171
						K.SIYYITGESK.E	0.9944		1	1161.297
						R.RLSELLR.Y	0.9958		2	887.0702
						K.KHLEINPDHPIVETLR.Q	0.9944		2	1912.1991
						K.CLELFSELAEDKENYK.K	0.9958		2	1989.1524
						K.DLVVLLFETALLSSGFSLEDPQTHSNR.I	0.9958		2	2990.3397
						R.VKEVVK.K	0.9958		1	701.8845
						R.LVSSPCCIVTSTYGWTANMER.I	0.9958		2	2433.6706
						R.LVSSPCCIVTSTYGWTANMERIMK.A	0.9944		3	2806.1967
						K.RGFEVVYMTEPIDEYCVQQLK.E	0.9958		2	2605.9313
1743	HSC20_MOUSE	234	13.68	2	3	R.LADAQSEAAMEEIEATVR.A	0.9958		2	1935.1132
						R.LVHPDFFSQK.S	0.9958		2	1218.3977
1744	HSDL2_MOUSE	490	53.47	14	104	K.SFTGNFIIDENILK.E	0.9958		2	1611.8351
						K.LQLQEESQLQK.Q	0.9958		1	1344.5077
						K.SFTGNFIIDENILKEEGIK.N	0.9958		2	2168.4515
						R.TAIHTAAMDMLGGSGVENQCR.K	0.9958		2	2220.4463
						R.ATQAVYQFELSGEDGGTWFLDLK.S	0.9958		2	2576.8218
						K.NFDVYAIAPGHPLLPDFFLDEHPDAVMEEK	0.9958		3	3428.8403
						K.LLGTIYTAAEEIEAAGGTALPCVVDVR.D	0.9958		2	2791.1371
						K.LKPTMAFMSGK.L	0.9942		1	1211.5232
						K.LAGCTVFITGASR.G	0.9941		2	1353.5273
						R.KVDIIADAAYSIFK.R	0.9958		2	1554.8266
						K.AVEKFGGIDILVNNASAISLTNTLDTPTK.R	0.9958		3	3004.4075
						R.QQPQPFVQSMLPQKPHFGAVEETFR.I	0.9958		3	2928.3379
						K.VGHILNLSPPLNLNPLWFK.Q	0.9958		2	2173.609
						K.FGGIDILVNNASAISLTNTLDTPTK.R	0.9914		2	2576.9066
1745	HSP72_MOUSE	633	12.16	6	97	K.STAGDTHLGGEDFDNR.M	0.9958		2	1692.6958
						R.FEELNADLFR.G	0.9958		1	1254.3849

						R.ARFEELNADLFR.G	0.9958	2	1481.6512
						R.GPAIGIDLGTTYSCVGVFQHGK.V	0.9958	2	2278.5359
						K.LLQDFFNGK.E	0.9924	1	1082.2444
						K.RNTTIPTK.Q	0.9958	1	931.08
1746	HSP74_MOUSE	841	30.8	14	105	K.SNLAYDIVQLPTGLTGIK.V	0.9958	2	1904.2139
						R.WNSPAEEGLSDCEVFPK.N	0.9944	2	1966.0772
						K.NKEDQYEHLDAADVTK.V	0.9958	2	1876.9744
						K.LEDTENWLYEDGEDQPK.Q	0.9958	2	2082.1413
						K.VLATAFDTTLGGR.K	0.9958	1,2	1322.504
						R.EFSITDVVPYPISLR.W	0.9958	2	1737.0056
						K.KPVVDCVVSVPSFYTDAER.R	0.9958	2	2169.4052
						K.STNEAMEWMNSK.L	0.9958	2	1428.5745
						R.AGGIETIANEYSDR.C	0.9958	2	1496.5737
						K.EDIYAVEIVGGATR.I	0.9958	2	1493.6567
						R.KFDEVLVNHFCEEFGK.K	0.9958	2	1999.1963
						K.ELSTTLNADEAVTR.G	0.9952	2	1520.6366
						K.ELTSICSPIISKPKPK.V	0.9958	2	1799.1272
						K.HAEQNGPVDGQGDNPGSQAAEHGADTAV	0.9958	3	3330.3354
1747	HSP7C_MOUSE	646	56.81	21	3306	K.SINPDEAVAYGAAVQAAILSGDK.S	0.9958	2	2261.4937
						K.NQVAMNPTNTVFDAK.R	0.9958	1	1650.8468
						R.TLSSSTQASIEIDSLYEGIDFYTSITR.A	0.9958	2	2999.2549
						K.NQTAEKEEFEHQQK.E	0.9958	2	1746.8308
						R.GVPQIEVTFDIDANGILNVSAVDK.S	0.9958	2	2515.8229
						K.SQIHDIVLVGGSTR.I	0.9958	2	1482.6799
						K.GPAVGIDLGTTYSCVGVFQHGK.V	0.9958	2	2264.509
						K.DAGTIAGLNVLR.I	0.9958	1	1200.3805
						R.RFDDAVVQSDMK.H	0.9958	2	1411.5725
						R.NVLIFDLGGGTFDVSILTIEDGIFEVK.S	0.9944	2	2913.3374
						K.SFYPEEVSSMVLTK.M	0.9958	1,2	1617.8543
						K.NSLESYAFNMK.A	0.9958	1	1304.4602
						R.MVNHFIAEFK.R	0.9958	2	1236.4742
						K.CNEIISWLDK.N	0.9958	1,2	1278.4137
						K.HWPFMVVNDAGRPK.V	0.9958	2,3	1654.9298
						K.EIAEAYLGK.T	0.9958	1	994.1326
						K.SENVQDLLLLDVTPLSLGIETAGGVMTVLIK	0.9958	3	3240.8207
						K.TVTNAVVTVPAYFNDSQR.Q	0.9958	2	1983.1882
						R.FDDAVVQSDMK.H	0.9958	1	1255.3851

						K.DNNLLGKFELTGIPPAPR.G	0.9937	2	1953.2486
						R.NVLIFDLGGGTFDVSILTIEDGIFEVKSTAGD	0.9958	3	4587.01
1748	HSPB1_MOUSE	209	76.56	10	336	K.YTLPPGVDPTLVSSSLSPEGTLTVEAPLPK.	0.9924	2	3067.5035
						K.AVTQSAEITIPVTFEAR.A	0.9958	2	1834.0795
						R.VSLDVNHFAPEELTVK.T	0.9958	2	1799.0337
						R.KYTLPPGVDPTLVSSSLSPEGTLTVEAPLPI	0.9958	3	3195.6776
						R.LPDEWSQWFSAAGWPGYVRPLPAATAEG	0.9958	3	4314.8492
						R.LFDQAFGVPR.L	0.9958	1	1150.3225
						K.EGVVEITGK.H	0.9958	1	932.0617
						R.SPSWEPFRDWYPAHSR.L	0.9958	2	2019.1857
						R.QLSSGVSEIR.Q	0.9956	2	1076.1949
						R.LFDQAFGVPRLPDEWSQWFSAAGWPGYV	0.9958	3	5446.1485
1749	HSPB2_MOUSE	182	31.87	3	64	R.TVPHAHPATAEYEFANPSR.L	0.9958	2	2096.2663
						K.FQAFLDVSHFTPDEVTVR.T	0.9944	2	2109.3458
						R.AALSHDGILNLEAPR.G	0.9958	2	1577.7807
1750	HSPB6_MOUSE	162	88.89	9	954	R.APSVALPTAQVSTDSGYFSVLLDVK.H	0.9958	2	2566.9109
						R.ASAPLPGFSAPGR.L	0.9958	1	1228.3934
						K.VVDDHVEVHAR.H	0.9958	2	1276.3946
						R.LPPGVDPAAVTSALSPEGVLSIQATPASAQ	0.9958	3	3807.3361
						K.HFLPEEISVK.V	0.9958	2	1199.3922
						R.HEERPDEHGFIAR.E	0.9958	2	1593.6988
						R.FGEGLLEAELASLCPAAIAPYYLR.A	0.9924	2	2625.9905
						R.RASAPLPGFSAPGR.L	0.9917	2	1384.5809
						R.YRLPPGVDPAAVTSALSPEGVLSIQATPAS	0.9958	3	4126.6995
1751	HSPB7_MOUSE	169	59.17	5	48	K.CQLPEDVDPTSVTSALR.E	0.9958	2	1889.0356
						K.LAADGTVMNTFAHK.C	0.9932	2	1476.6904
						R.DFSPEDIIVTTFNNHIEVR.A	0.9944	2	2247.4692
						K.ALSMFSDDFGSFMLPHSEPLAFPARPGGQ	0.9958	3	3524.0058
						K.TLGDAYEFTVDMR.D	0.9958	2	1518.6813
1752	HSPB8_MOUSE	196	23.47	2	5	R.LLDDGFGMDPFPDDLTAPWPEWALPR.L	0.9958	2	2973.3289
						K.VCVNVHSFKPEELMVK.T	0.9958	2	1917.2397
1753	HTR5A_MOUSE	2038	2.4	2	2	R.ILANGFTDTVVNILK.A	0.9936	2	1618.9139
						R.LSLQRTQAGWLLVAALMTLGPAVVSHHLTI	0.9958	3	3241.8687
1754	HTRA2_MOUSE	458	19	5	21	R.LPSGDTYEAMVTAVDPVADIATLR.I	0.9958	2	2506.8304
						R.SQYNFIADVVEK.T	0.9958	2	1413.57
						K.TAPAVVYIEILDR.H	0.9944	2	1460.7135
						R.EPSFPDVQHGVLIHK.V	0.9944	2	1703.9383

						R.AGLRPGDVILAIGEK.L	0.9958		2	1509.7892
1755	HUCE1_MOUSE	457	2.84	1	5	K.WPLHPVDRIAK.D	0.9944	1,2		1332.5913
1756	HUWE1_MOUSE	4377	9.34	20	57	R.LLGPSAAADILQLSSSLPLQSR.G	0.9944		2	2238.5895
						K.VPIVNHLEFLRDEELEER.R	0.9958		2	2238.5052
						R.HADHSSLTLGSGSSTTR.L	0.9958		2	1714.7892
						K.TTPLKPSSLPVIPDTIK.E	0.9958		2	1808.1687
						R.GILEEPLPSTSSEEEDPLAGISLPEGVDPSF	0.9958		3	4334.7779
						K.GPNAVQLVKTTPLKPSSLPVIPDTIK.E	0.9958		3	2715.2493
						R.REPQVNQQQLQQLMDMGFTR.E	0.9958		3	2448.7772
						K.SVPVSSGGEGETSPHSLEASPLGQLMNML	0.9958		3	3603.0595
						K.YPPSATTLHFEFYADPGAEVK.I	0.9958		2	2341.5817
						R.LPSAHTCFNQLDLPAYESFEK.L	0.9958		2	2468.6911
						R.LFGHSSTSALSAILR.S	0.9943		2	1560.7935
						R.LLSLISIALPENK.V	0.993		2	1411.7251
						K.VPIVNHLEFLR.D	0.9909		2	1337.6078
						K.FLQFVTGTSK.V	0.9958		1	1128.3134
						R.GILEEPLPSTSSEEEDPLAGISLPEGVDPSF	0.9958		3	4178.5904
						R.EHAMEALLNTSTMEQATEYLLTHPPPIIGG\	0.9958		3	3621.161
						R.KYPYHLMLQK.F	0.9944		1	1321.6232
						R.SAPSSNSSAPAVVGNPGVTEVSPEFLAALF	0.9958		3	4217.6794
						R.SHHAASTTTAPTPAAR.S	0.9958		2	1577.6969
						K.SCASSSHENRPLDLLHK.M	0.991		2	1952.1003
1757	HVM12_MOUSE	117	17.09	1	7	-.EVQLQQSGPELVKPGASVK.M	0.9958		2	1995.2835
1758	HVM36_MOUSE	116	15.52	1	4	K.LLESGGGLVQPGGSLK.L	0.9958		2	1512.7465
1759	HXA4_MOUSE	285	4.21	1	3	K.EPVVYPWMKK.I	0.9958		2	1277.5671
1760	HXB4_MOUSE	250	4.8	1	14	K.EPVVYPWMRK.V	0.9909		2	1305.5805
1761	HXD9_MOUSE	339	20.65	2	2	R.FGPPGPGTQGRPAGVADGPAAATAEFAS(	0.9958		3	3246.5292
						R.HYGIKPETGAAPAPAAASTSSSSSTSSSSS	0.9958		3	2998.1437
1762	HXK1_MOUSE	974	18.89	9	28	R.MCINTEWGAFGDDGSLEDIR.T	0.9958		2	2287.4286
						K.SQNVSMESEVYDTPENIVHGSGSQLFDHV	0.9958		3	4388.7007
						K.FTTSDVAAIETDKEGVQNAK.E	0.9958		2	2125.297
						K.ATDCVGHDVATLLR.D	0.9958		2	1528.6715
						R.SANLVAATLGAILNR.L	0.9958		2	1484.7391
						R.NILIDFTK.K	0.9958		1	964.1497
						R.GLDHLNVTVGVDGTLYK.L	0.9958		2	1802.0373
						R.LSDEILIDILTR.F	0.9958		2	1401.6433
						R.LGVEPSHDDCVSVQHVCTIVSFR.S	0.9958		2	2642.8604

1763	HXK2_MOUSE	917	14.94	8	36	K.GLGATTHPTAAVK.M	0.9958	1	1224.4025
						R.STPDGTEHGEFLALDLGGTNFR.V	0.9958	2	2335.4918
						R.VEMENQIYAIPEDIMR.G	0.9958	2	1952.2477
						R.TVFDVAVDELSLNPGK.Q	0.9958	2	1704.9176
						R.LGLSPLQEDCVATHR.I	0.9958	2	1696.8669
						K.KLPLGFTFSFPCHQTK.L	0.9958	2	1909.2042
						R.MKVEMEQGLSK.E	0.9958	1	1280.5403
						R.STIGVDGSVYKK.H	0.9958	2	1254.4258
1764	HYDIN_MOUSE	5099	2.24	4	4	K.LKPHFSISPEEGYIISGTEVALEVTYHPTEIG	0.9911	3	3644.1156
						K.WDVKK.L	0.9958	1	675.8057
						K.VYYLPGIPEVFQRNFQIQIAHLVPENITLYGE	0.9958	3	4334.0227
						K.QALNVWAYPTAVGIFEDSIVCCIKENPEPAI	0.9958	3	3782.26
1765	HYES_MOUSE	554	73.65	23	828	R.SIPVFNYQLYFQEPGVAEAELEK.N	0.9958	2	2672.9941
						R.DFLLGAYQTEFPEGPTEQLMK.G	0.9907	2	2415.7199
						K.ATEIGGILVNTPEDPNLSK.I	0.9958	2	1969.1992
						K.WLQTEVQNPSVTSK.I	0.9958	2	1617.7991
						K.ITFSQWVPLMDESYR.K	0.9958	1	1873.1334
						K.GYGDSSSPPEIEEYAMELLCK.E	0.9958	2	2376.56
						K.ACGANLPENFSISQIFSQAMAAR.S	0.9958	2	2484.7553
						R.YQIPALAQAGFR.V	0.9958	1	1335.5485
						R.DMGMVTILVHNTASALR.E	0.9958	2	1830.1707
						K.AKPNEVVFLDDFGSNLKPAR.D	0.9958	2	2218.5174
						R.VAAFDLDGVLALPSIAGAFR.R	0.9957	2	2004.3366
						R.ASDETGFIAVHK.A	0.9958	1	1275.4038
						R.AVASLNTPFMPPDPDVSPMK.V	0.9958	2	2115.4671
						K.ITTEEEIEFYIQQFK.K	0.9958	2	1919.1382
						R.RSEEALALPR.D	0.9958	1,2	1142.3005
						K.VTGTQFPEAPLPVPCNPNDVSHGYVTVKP	0.9958	3	3448.8694
						K.ILVPALMVTAEK.D	0.9958	1	1285.6281
						K.GFTTCIVTNNWLDDGDKR.D	0.9907	2	2113.2573
						R.GHIEDCGHWTQIEKPTEVNQILIK.W	0.9958	3	2847.1663
						R.SINRPMLQAAIALK.K	0.9958	2	1526.8809
						R.GPLNWYR.N	0.9958	2	906.0317
						K.RGHIEDCGHWTQIEKPTEVNQILIK.W	0.9931	2,3	3003.3538
						K.DIVLRPEMSK.N	0.9958	1,2	1188.4277
1766	HYI_MOUSE	277	15.16	2	2	R.EFLPTVGHVQVAQVPDR.G	0.9958	2	1893.1527
						K.HAAGVLAQENLVGLLEPINTR.I	0.9958	2	2216.5455

1767	HYOU1_MOUSE	999	15.62	6	13	K.ESGDKPEAQKPNEK.G	0.9945	2	1557.6573
						K.VAIVKPGVPMEIVLNK.E	0.9958	2	1708.1559
						K.AHFNLDESGVLSLDRVESVFETLVEDSPEE	0.9925	3	4024.3381
						R.VEFEELCADLFDRVPGPVQQALQSAEMSL	0.9958	3	4761.3241
						R.YSHDFNFHINYGDLGFLGPEDLR.V	0.9929	2	2727.9518
						K.LPATEKPVLLSK.D	0.9958	2	1296.5932
1768	HYPK_MOUSE	129	13.18	2	4	K.EDLELIMTEMEISR.A	0.9958	1	1709.9674
						K.KEDLELIMTEMEISR.A	0.9958	2	1838.1415
1769	I12R1_MOUSE	738	10.03	2	3	R.HVSVRNQTGDSVSVEWTASQLSTCPGVLT	0.9958	3	3763.1247
						R.FSFEVQISRLSIIFASLGSFASVLLVGSLGYI	0.9944	3	3863.5352
1770	I12R2_MOUSE	874	3.66	3	4	K.YPILEEK.I	0.9958	1	892.0398
						K.QDAMYIANPQATGTLTAETR.Q	0.9923	2	2153.3716
						K.KYPILEEK.I	0.9958	1	1020.2139
1771	I2C1_MOUSE	857	5.02	2	3	R.IIFYRDGVPEGQLPQILHYELLAIR.D	0.9958	3	2955.4728
						K.YPHLPCLQVGQEQK.H	0.9931	2	1697.8975
1772	I2C2_MOUSE	860	6.86	3	4	K.KPSIAAVVGSMDAHPNR.Y	0.9958	2	1751.0135
						K.VSIKWVSCVSLQALHDALSGR.L	0.9944	2	2327.6549
						R.TIKLQANFFEMDIPK.I	0.9958	2	1796.1346
1773	I2C3_MOUSE	860	5.7	2	3	K.IDVYLYEVDIKPDK.C	0.9958	1	1710.9647
						K.AQPVIQFMCEVLDIHNIDEQPRPLTDSHRVI	0.9958	3	3688.1621
1774	I2C4_MOUSE	861	2.09	1	7	K.YAQGADSVEPMFKHLK.M	0.9952	2	1822.0887
1775	IAPP_MOUSE	93	44.09	3	5	R.LANFLVRSSNNLGPVLPPTNVGSNTYGK.R	0.9958	3	2931.3213
						R.SSNNLGPVLPPTNVGSNTYGK.R	0.9958	2	2117.3232
						R.KCNTATCATQR.L	0.9958	1	1311.3698
1776	IBP1_MOUSE	272	15.44	1	2	R.LGLCPPVPASCPEISRPAGCGCCPTCALPM	0.9958	3	4202.5752
1777	IC1_MOUSE	504	19.64	4	11	K.GVTSVSQIFHSPDLAIR.D	0.9958	2	1828.0782
						R.VLGPDSAANLELINTWVAENTNHK.I	0.9944	3	2607.8827
						K.TNMAFSPFSIASLLTQVLLGAGDSTK.S	0.9958	2	2671.0809
						K.HETVLELTESGVEAAAASAISFGR.S	0.9958	2	2446.6763
1778	ICAL_MOUSE	788	34.64	12	66	K.LSAAISEVVSQTPAPSTHAAAPLPGTEQK.D	0.9958	2,3	2860.1937
						K.ESQEQLAPLSDDFLLDALSQDFSSPANISSI	0.9958	3	4059.3399
						R.KVEEEVINDQALQALSDSLGTR.Q	0.9958	2	2416.6476
						K.EQKPFTPASPVQSTPSKPSDK.S	0.9958	2	2257.5053
						K.AASLGSSQPSRPHVGEAATATK.V	0.9931	2	2124.3182
						K.SLSESELIGELSADFDR.S	0.9958	2	1868.9922
						K.GVVPEDAVETLAGSLGTR.E	0.9958	2	1771.9652
						K.VEEEVINDQALQALSDSLGTR.Q	0.9958	2	2288.4735

						K.FQDVPSAGGESVAGGGTVATALDK.V	0.9958		2	2235.4124
						K.NEGITQPLPDSPKPMGTDQAIDALSSDFTC	0.9958		3	3765.0603
						K.DKELDDALDELSDSLGQRPPDPDENKPLDI	0.9958		3	3481.6624
						K.ELDDALDELSDSLGQRPPDPDENKPLDDK.	0.9944		3	3238.3997
1779	ICAM5_MOUSE	917	1.42	1	6	R.GAMLTARVLAR.R	0.9958		1	1159.4356
1780	ICB1_MOUSE	663	11.31	3	15	R.YFMLSGAYQGKLK.R	0.9958		1	1506.8029
						K.VVCEYPETGQTLELNPNFTGLFSPLTSLR.S	0.9944		3	3284.6563
						R.LEEKLTEPFLVVSLDSQPEMCFEIPPR.W	0.9958		3	3205.6565
1781	ICT1_MOUSE	206	7.77	1	14	R.FHLASADWIEEPVR.Q	0.9958		2	1670.865
1782	IDE_MOUSE	1019	5.89	4	12	R.FIIQSEKPPHYLESR.V	0.9923		2	1845.1081
						R.YNDKQPILLK.K	0.9958		1	1232.4655
						K.WQNADLNGK.F	0.9958		1	1046.1277
						K.NVPLPEFPEHPFQEEHLR.Q	0.9944		2	2216.4606
1783	IDH3A_MOUSE	366	50	17	832	R.ENTEGEYSGIEHVIVDGVVQSIK.L	0.9958		2	2503.7252
						K.TPYTDVNIVTIR.E	0.9958		2	1392.595
						R.NVTAIQGPGGK.W	0.9958	1,2		1042.1802
						K.TFDLYANVRPCVSIEGYK.T	0.9958		2	2133.3747
						R.SNVTAVHK.A	0.9958		1	855.9694
						K.TPIAAGHPSMNLLLR.K	0.9958		2	1591.9121
						R.HMGLFDHAAK.I	0.9958		2	1127.3061
						R.IAEFAFEYAR.N	0.9958	1,2		1217.3666
						K.APIQWEER.N	0.9958		1	1029.1405
						R.KTFDLYANVRPCVSIEGYK.T	0.9958		2	2261.5487
						K.DMANPTALLLSAVMMLR.H	0.9958		2	1848.2875
						R.MSDGLFLQK.C	0.9958	1,2		1039.2347
						K.IFDAAK.A	0.9924		1	664.7795
						K.RIAEFAFEYAR.N	0.9958		2	1373.5541
						K.IEAACFATIK.D	0.9958		2	1124.2885
						K.APIQWEERNVTAIQGPGGK.W	0.9958		2	2052.2975
						K.CSDFTEEICR.R	0.9958		1	1317.3271
1784	IDH3G_MOUSE	393	48.35	12	556	R.ENTEGEYSSLEHESVAGVVESLK.I	0.9958		2	2494.6281
						R.TSLDLYANVIHCK.S	0.9958		1	1534.7185
						K.KVTAVHK.A	0.9958		1	782.9615
						K.NIANPTATLLASCMMLDHLK.L	0.9958		2	2215.5972
						K.AVLASMDNENMHTPDIGGQGTTSQAIQDIII	0.9958	2,3		3285.6283
						K.GNIETNHNLPPSHK.S	0.9958	1,2		1558.6939
						R.HACVPVDFEEVHVSSNADEEDIR.N	0.9958		2	2655.7601

						K.LHSYATSIR.K	0.9958		1	1048.1869
						R.HTVTMIPGDGIGPELMLHVK.S	0.9923		2	2146.5708
						K.DIDILIVR.E	0.9958		1	957.1582
						R.KAVLASMDNENMHTPDIGGQGTTSQAIQD	0.9958		3	3413.8023
						R.HACVPVDFEEVHVSSNADEEDIRNAIMAIR	0.9958		3	3425.7205
1785	IDHP_MOUSE	452	66.37	31	2268	R.DQTNDQVTIDSALATQK.Y	0.9958		1	1848.9616
						K.LNEHFLNTTDFLDTIK.S	0.9958		2	1922.1449
						K.NYDGDVQSDILAQGFGSLGLMTSVLVCPD	0.9958		3	3258.5905
						K.DIFQEIFDK.H	0.9958		1	1155.2927
						K.YFDLGLPNR.D	0.9958		1	1095.2431
						R.LIDDMVAQVLK.S	0.9958	1,2		1245.52
						R.NILGGTVFR.E	0.9958		1	977.1515
						K.DLAGCIHGLSNVK.L	0.9958		2	1384.5413
						K.TIEAEAAHGTVTR.H	0.9958		2	1356.4783
						R.GKLDGNQDLIR.F	0.9958		2	1229.3787
						K.LILPHVDVQLK.Y	0.9958		2	1275.5773
						K.KWPLYLSTK.N	0.9958		1	1136.3794
						K.WPLYLSTK.N	0.9958		1	1008.2053
						K.VEKPVVEMDGDEMTR.I	0.9958		2	1735.9649
						R.IKVEKPVVEMDGDEMTR.I	0.9958		2	1977.2984
						K.VCVQTVESGAMTK.D	0.9958		2	1410.5916
						K.ATDFVVDR.A	0.9958		1	923.0135
						R.FKDIFQEIFDK.H	0.9958		2	1430.6433
						R.NILGGTVFREPIICK.N	0.9958		2	1718.0154
						R.HAHGDQYK.A	0.9931	1,2		956.0055
						R.LVPGWTKPITIGR.H	0.9958		1	1438.7562
						K.GRPTSTNPIASIFAWTR.G	0.9958		2	1876.1252
						K.LDGNQDLIR.F	0.9912		2	1044.1527
						K.LVFTPK.D	0.9924		1	704.8876
						K.YFDLGLPNRDQTNDQVTIDSALATQK.Y	0.9958		3	2925.1815
						K.SSGGFVWACK.N	0.9958	1,2		1099.1975
						K.CATITPDEAR.V	0.9944		1	1134.1975
						R.FAQTLEK.V	0.9924		1	836.9634
						K.VCVQTVESGAMTKDLAGCIHGLSNVK.L	0.993		2	2776.1097
						K.EKLILPHVDVQLK.Y	0.9958		2	1532.8668
						K.LILPHVDVQLKYFDLGLPNR.D	0.9958		2	2351.7972
1786	IF2G_MOUSE	472	9.53	2	4	K.IVSLFAEHNDLQYAAPGGLIGVGTK.I	0.9958		2	2571.9359

						R.QATINIGTIGHVAHGK.S	0.9958	2	1617.8484
1787	IF2M_MOUSE	727	16.51	6	6	K.ILNEAYPSMPVGIIGWR.D	0.9958	2	1917.2763
						R.KQQRPLKPK.E	0.9958	1	1123.3872
						R.ETQVAAMEVGGITQHIGAFLVSLPSGEK.I	0.9958	2	2871.2781
						R.LPHTLEEYPIGEASILATFTVTEGK.K	0.9958	2	2718.0759
						R.DLPSAGDEILEVESEPR.A	0.9958	1	1856.9812
						R.SPVVTVMGHVDHGK.T	0.9957	2	1463.6947
1788	IF3EI_MOUSE	564	6.21	2	5	R.LHSLLGDYYQAIK.V	0.9936	2	1521.7563
						K.FLSPVVPNYDNVHPNYHK.E	0.9924	2	2141.3934
1789	IF4A1_MOUSE	406	34.48	6	53	R.GIYAYGFEKPSAIQQR.A	0.9958	2	1829.0654
						K.LQMEAPHIIVGTPGR.V	0.9958	2	1619.9225
						R.DIETFYNTSIEEMPLNVADLI.-	0.9958	2	2428.7132
						R.SRDNGPDGMEPEGVIESNWNEIVDSFDDM	0.9958	3	4169.4513
						R.GIDVQQVSLVINYDLPTNR.E	0.9958	2	2145.4203
						K.LNSNTQVVLLSATMPSDVLEVTK.K	0.9958	2	2460.8457
1790	IF4A2_MOUSE	407	17.69	3	46	K.LQAEAPHIVVGTPGR.V	0.9958	2	1545.7819
						R.DIETFYNTTVEEMPMNVADLI.-	0.9958	2	2446.7463
						R.EHGGPEGMDPDGVIESNWNEIVDNFDDMI	0.9958	3	3475.6962
1791	IF4A3_MOUSE	411	7.06	2	2	R.DELTLEGIKQFFVAVER.E	0.9944	3	1995.2829
						K.EFRSGASR.V	0.9958	1	909.9773
1792	IF4B_MOUSE	611	10.97	3	5	K.SPPYTAFLGNLPYDVTEDSIK.D	0.9958	2	2328.5805
						K.GFGYAEFEDLDSLLSALSLNEESLGNR.R	0.9912	3	2948.1694
						R.ESEKSLENETLNK.E	0.9912	2	1521.6213
1793	IF4E3_MOUSE	207	9.18	1	2	K.AVFYKPHEEHHAFEGGR.G	0.9958	2	2012.1942
1794	IF4G1_MOUSE	1600	4.44	4	40	K.ITKPGSIDSNNQLFAPGGR.L	0.9958	2	1973.1961
						K.VPTTEKPTVTVNFR.K	0.9958	2	1589.832
						K.IHNAENIQPGEQK.Y	0.9958	2	1478.6047
						R.EFLAEGQDVGSFVAEKK.V	0.9958	2	1855.0545
1795	IF4G2_MOUSE	906	4.97	2	2	K.LCLELLNVGVESKLILK.G	0.9958	2	1942.3563
						K.SQGLSQLYHNQSQGLLSQLQGQSK.D	0.9958	2	2630.8772
1796	IF4G3_MOUSE	1579	1.14	1	5	R.QTPGGRGVPLLNVGPR.R	0.9958	1	1618.8795
1797	IF4H_MOUSE	248	12.5	1	2	K.ELPTEPPYTAYVGNLPFNTVQGDIDAIFK.D	0.9958	2,3	3211.5952
1798	IF5_MOUSE	429	17.25	5	6	K.ALNRPPTYPTK.Y	0.9944	2	1258.463
						K.FVLCPECENPETDLHVNPK.K	0.9958	2	2299.4744
						K.AMGPLVLTEVLFDEK.I	0.9958	2	1662.9819
						R.YLLHGLECVVAMHQAQLISK.I	0.9944	2	2311.7137
						K.KFVLCPECENPETDLHVNPK.K	0.9958	2	2427.6485

1799	IF5A1_MOUSE	154	53.25	6	399	R.NDFQLIGIQDGYLSLLQDSGEVR.E	0.9958	2	2581.8419
						K.VHLVGIDIFTGK.K	0.9958	2	1299.5559
						K.RNDFQLIGIQDGYLSLLQDSGEVR.E	0.9958	2,3	2738.0293
						K.KYEDICPSTHNMDVPNIK.R	0.9958	2,3	2162.3882
						K.YEDICPSTHNMDVPNIK.R	0.9958	2	2034.2141
						K.YDCGEEILITVLSAMTEEAAVAIK.A	0.9958	3	2627.9729
1800	IFNB_MOUSE	182	7.69	1	15	R.KCQELLEQLNGK.I	0.9958	2	1460.6367
1801	IFNE1_MOUSE	192	19.79	2	17	-.MVHRQLPETVLLLLVSSTIFSLEPK.R	0.9958	3	2852.4485
						K.SGGSSAQNLR.L	0.9944	1	977.0219
1802	IFRD1_MOUSE	449	4.23	1	2	R.NVFELGPPVMLDAATLK.T	0.9924	2	1816.1657
1803	IGBP1_MOUSE	340	19.12	3	4	K.YLMVPALQGALTMKQVNPSK.R	0.9952	2	2190.6673
						K.KLLEDVEVATEPTGSR.T	0.9958	2	1744.9396
						K.VFGTGYPSLATMTVSDWYEQHQK.Y	0.9944	2	2646.9337
1804	IGF1R_MOUSE	1373	4.88	3	4	K.YGSQVEDQR.E	0.9924	1	1082.1149
						K.AENGPGPGVLVLR.A	0.9958	2	1279.4819
						R.SLRPEVEQNNLVLIPPSLSKMIQMAGEIADC	0.9958	3	4257.9687
1805	IGF2_MOUSE	180	9.44	1	2	R.DVSTSQAVLPDDFPR.Y	0.9958	1	1647.782
1806	IGH1M_MOUSE	393	17.3	3	44	K.VTCVVVDISKDDPEVQFSWFVDDVEVHTA(	0.9958	3	3948.3008
						R.SVSELPIMHQDWLNGK.E	0.9958	2	1855.1187
						R.VNSAAFPAPIEK.T	0.9958	2	1244.4331
1807	IGHA_MOUSE	344	11.05	1	12	R.WLHGNEELSPESYLVFEPLKEPGEGATTYI	0.9958	3	4063.553
1808	IGS10_MOUSE	2594	3.51	4	7	R.DIDGSGLEEPKPSVLLK.Q	0.9958	2	1798.0435
						R.ITVHQNGTLEIRNIR.L	0.9944	3	1765.0255
						K.YLYLSDNFLTSLPK.E	0.9958	2	1674.9341
						R.SESTHMTPTEASMISAPTSISLGKTPIDTSG	0.9958	3	3858.3456
1809	IGS21_MOUSE	468	15.81	2	2	R.ASCLLLAAILDLARGYLTVNIEPLPPVVAGD.	0.9958	3	3749.4357
						R.EKVVLASGNIFLNVMAPPTSIEVVAADSPAF	0.9958	3	3529.0888
1810	II2A_MOUSE	445	6.52	2	2	K.EQHNINYEK.G	0.9958	1	1175.2431
						R.LVCFELTSNADEWFLR.A	0.9958	2	2001.2122
1811	IL18R_MOUSE	537	9.12	3	4	R.FWKNLVYLMPAK.A	0.9924	1	1510.8804
						R.LIIVLSQSYLTNGARR.E	0.9958	2	1805.1307
						R.YNITKTVNITVIEGR.S	0.9958	1	1721.9945
1812	IL7RA_MOUSE	459	7.19	2	2	K.TSEFLLIGSSNICVK.L	0.9945	2	1668.8939
						R.SPETSVSPPETVRR.E	0.9912	2	1542.6891
1813	ILEUA_MOUSE	379	11.08	2	2	K.TFHFDSVEDIHSR.F	0.9958	2	1590.6921
						K.IPELLSVGVVDSMTKLVLVNAIYFK.G	0.9958	3	2750.3527
1814	ILF2_MOUSE	390	14.87	2	2	R.AQDPSEVLTMLTNETGFEISSSDATVKILIT	0.9958	3	4090.6325

						R.VKPAPDETSFSEALLK.R	0.9909		2	1732.9714
1815	ILF3_MOUSE	898	4.01	2	2	K.YEILQSVDDAAIVIKNTK.E	0.9958		2	2021.3183
						K.EPPLSLTIHLTSPVVR.E	0.9958		2	1760.0867
1816	ILK_MOUSE	452	12.17	3	17	R.GDDTPLHLAASHGHR.D	0.9958		2	1584.6914
						R.GMAFLHTLEPLIPR.H	0.9958		2	1595.9433
						K.VALEGLRPTIPPGISPHVCK.L	0.9937		2	2142.5157
1817	ILKAP_MOUSE	392	6.63	2	3	K.FAAQNLHQNLIR.K	0.9958		2	1425.6334
						K.QASSQKPAWK.D	0.9958		1	1131.2767
1818	ILRL1_MOUSE	567	4.76	2	2	K.DLSLEYDCLALNLHGMIR.H	0.9944		2	2134.4212
						R.ITGVTEK.D	0.9924		1	747.8669
1819	IMA3_MOUSE	521	5.95	1	10	K.AQNVTLEAILQNATSDNPVVQLSAVQAAR.I	0.9958		3	3023.3732
1820	IMA4_MOUSE	521	9.6	2	3	K.DAQVVQVVLDGLSNILK.M	0.9958	1,2		1812.1167
						R.VQNTSLEAIVQNASSDNQGIQLSAVQAAR.I	0.9958		2	3014.2791
1821	IMB1_MOUSE	876	20.43	11	44	R.AAVENLPTFLVELSR.V	0.9958		2	1659.9231
						R.VLANPGNSQVAR.V	0.9958		2	1226.3781
						K.LAATNALLNSLEFTK.A	0.9958		2	1606.8595
						R.LQQVLQMESHIQSTSDR.I	0.9958		2	2001.2219
						K.GALQYLVPILTQTLTK.Q	0.9958	1,2		1760.1271
						K.ESTLEAIGYICQDIDPEQLQDK.S	0.9958		2	2566.7443
						R.HFIMQVVCEATQCPDTR.V	0.9958		2	2093.2942
						K.TVSPDRLELEAAQK.F	0.9958		2	1557.7441
						R.IQFNDLQSLLCATLQNVLR.K	0.9958		2	2247.5658
						K.YMEAFKPFLGIGLK.N	0.9958		2	1614.9861
						R.LELEAAQKFLER.A	0.9958		1	1447.6744
1822	IMB3_MOUSE	1097	9.3	4	8	R.VQAHAAAALINFTEDCPK.S	0.9958		2	1957.1596
						R.QVQTSGGLWTECIAQLSPEQQAAIQELLNS	0.9958		3	3372.6795
						K.LVLEQVVTSIASVADTAEEKFVPYYDLFMPS	0.9944		3	3705.2979
						R.KQAEETYENIPGR.S	0.9958		1	1535.6537
1823	IMDH2_MOUSE	514	25.1	8	25	K.KYEQGFITDPVVLSPK.D	0.9958		2	1822.1113
						R.HGFCGIPITDTGR.M	0.9958		2	1431.5572
						K.YPSLQVIGGNVVTAAQAK.N	0.9958		2	1817.0953
						R.FGVPVIADGGIQNVGHIAK.A	0.9958		2	1893.1961
						K.LPIVNENDELVAIIAR.T	0.9958		2	1780.0745
						R.TSSAQVEGGVHSLHSYEK.R	0.9958		2	1917.0422
						K.REDLVVAPAGVTLK.E	0.9958		2	1468.7367
						R.RFGVPVIADGGIQNVGHIAK.A	0.9958		2	2049.3835
1824	IMMT_MOUSE	757	50.46	30	759	R.TSSVTLQTITAQNAAVQAVK.A	0.9958		2	2032.3018

						K.LSTDDLNSLIAHAHR.R	0.9958		2	1663.8307
						K.VVSQYHELVVQAR.D	0.9958		2	1528.7513
						R.KELDSITPDITPGWK.G	0.9958		2	1700.9292
						R.EIAGATPHITAAEGR.L	0.9958	1,2		1494.6475
						R.LHNMIVDLDNVVK.K	0.9958		2	1510.7918
						K.LFGMVLGSAPYTVPLPK.K	0.9958		2	1791.2018
						K.ELDSITPDITPGWK.G	0.9958	1,2		1572.7551
						K.ISSVSEVMK.D	0.9944		1	980.1645
						K.LPVAQSQK.T	0.9952	1,2		871.0244
						K.IAGAGLLFVGGGIGGTILYAK.W	0.9958		2	1949.3439
						K.TIPYSDKLFGMVLGSAPYTVPLPK.K	0.9958		2	2596.0998
						K.AHQLWLSVEALK.Y	0.9958		2	1395.6445
						K.AVDEAADALLK.A	0.9958		1	1116.2566
						R.GIEQAVQSHAVAEEEAR.K	0.9958	1,2		1824.945
						K.TKGDTPASAASTGAAQIISAAGDTLSVPAP/	0.9958		3	3750.1113
						K.AHSNILK.T	0.9958		1	782.9181
						K.TSSAEMPTIPLGSAVEAIR.V	0.9958		2	1931.2115
						K.KPVQSGPLK.I	0.9958		1	954.1576
						R.YSTSSSSGLTAGK.I	0.9958		1	1246.3165
						K.KVQAAQSEAK.V	0.9958		1	1060.1955
						R.KAVDEAADALLK.A	0.9958		1	1244.4307
						R.LHNMIVDLDNVVKK.V	0.9958		2	1638.9659
						R.QAAAHTDHLR.D	0.9911		2	1120.2131
						K.REIAGATPHITAAEGR.L	0.9958		2	1650.835
						R.KAHQLWLSVEALK.Y	0.9958		1	1523.8185
						R.SQEQMDSFTLDINTAYAR.L	0.9958		2	2091.2568
						K.QLKPPAELYPEDINTFK.L	0.9958		2	2004.2903
						R.RIDQLNR.E	0.9944		2	915.0402
						K.RTFDSAVAK.A	0.9958	1,2		995.1234
1825	IMPA1_MOUSE	277	6.86	1	6	K.YPCHSFIGEESVAAGEK.T	0.9958		2	1882.0027
1826	IMPG1_MOUSE	798	7.39	2	2	R.STAAQGLNLEIESYSLDIEPADQADPCKLLD	0.9958		3	3723.9992
						K.SSLEYQALEQRFTDLLVPYLR.S	0.9958		3	2542.8944
1827	IN35_MOUSE	286	9.09	1	3	R.VQVQPLELPVVTNIQVSSQPDNHR.V	0.9924		2	2699.0391
1828	INADL_MOUSE	1834	6.05	4	4	K.TSQNSQGDQHSAHSSCRPSFAPVITSLQN	0.9958		3	3641.9023
						R.IILQVVADTNISAIATQLEIMSAGSQLGSPTA	0.9958		3	3485.9751
						R.DEENLEVFLVDLQK.K	0.9958		2	1691.8755
						K.QLKGQLSHIPSDCSANFDFSR.K	0.9931		2	2408.5988

1829	INCE_MOUSE	880	6.25	2	3	R.ASWGLQDSPGSTDSPWQERVLSPILLNNIL	0.9944		3	3794.256
						R.EFSNEPELMPKTPSQK.N	0.9944		2	1863.0925
1830	INO1_MOUSE	557	4.85	1	7	K.TMSIVSYNHLGNNDGQNLSAPLQFR.S	0.9958	2,3		2778.0716
1831	INOC1_MOUSE	1559	4.43	3	3	K.LYALDVLLTRLK.S	0.9958		1	1418.763
						K.IEILTYCQLTSRQK.L	0.9917		2	1754.0026
						K.EEPPNSLLGETSGASSSGLLNPYSLNGVLQ	0.9958		3	3794.0747
1832	INP4A_MOUSE	939	5.01	2	7	R.SSLQVDWHEEEWQK.V	0.9958		2	1801.9097
						R.QIVTQYQTIILTYQENLTDLHQYKGPSFK.A	0.9958		3	3471.9347
1833	INP4B_MOUSE	924	4.65	2	2	K.TLEFVPVNLHLQR.M	0.9958		2	1566.8436
						R.AKQSLTFVLLQELAYSLPQCLMLTLR.R	0.9912		3	3038.6252
1834	INPP_MOUSE	396	10.61	3	9	R.SPDTGLDLPQLLYHVENK.G	0.9943		2	2040.2805
						K.FPGLGK.K	0.9926		1	618.7538
						K.TLADVLVQEVIK.Q	0.9958		2	1328.592
1835	INT1_MOUSE	2195	2.14	2	2	K.EPPMEEDIGETDALQGYQWLLRDLPR.L	0.9958		3	3073.404
						R.TFVDNIQTAFNTKMPPK.S	0.9958		1	1953.2635
1836	INT7_MOUSE	966	6.21	2	2	K.ISEMIQGLATPVDLKLK.L	0.9958		1	1857.2592
						R.VEPHNDYFSTQFLLNFAVLGTHSITVESSVI	0.9924		3	4393.9023
1837	INVO_MOUSE	467	6.85	2	4	K.ELSDQPLDQALVKK.G	0.9945		2	1584.8101
						K.QQQSHEPDMAGDQK.E	0.9958		2	1599.6721
1838	INVS_MOUSE	1062	5.37	2	3	R.VDLVDQDGHSLLHWAALGGNADVCQILIEN	0.9958		3	4631.0844
						R.LIVGNSALRDK.E	0.9958		1	1186.397
1839	IP3KC_MOUSE	678	2.65	1	2	R.GSLSEAEAGALPAEAR.M	0.9958	1,2		1529.6469
1840	IPKA_MOUSE	76	30.26	1	8	R.NAIHDILVSSASGNSNELALK.L	0.9958		2	2154.3849
1841	IPO7_MOUSE	1038	4.05	2	24	R.NPVWYQALTHGLNEEQR.K	0.9958		2	2056.2449
						R.EMPVKVEAAIALQVLISNQEK.A	0.9944		2	2311.7424
1842	IPO9_MOUSE	1041	8.45	3	3	K.EALVDTLTGILSPVQEVR.A	0.9958		2	1941.2322
						R.IAAQDLLLAVATDFQNESAVALATAATRHLQ	0.9958		3	3911.3611
						K.ICPFTIAIFLKYSNDPVVASLAQDIFK.E	0.9958		3	3072.5806
1843	IPSP_MOUSE	405	2.47	1	10	K.FSIEATYK.L	0.9958		1	959.0868
1844	IPYR_MOUSE	289	54.67	10	160	K.VLGILAMIDEGETDWK.V	0.9958		2	1791.0693
						K.GQYISPFHDVPIYADK.D	0.9958		2	1851.0685
						K.VPDGKPENEFAFNAEFK.N	0.9958		2	1940.1192
						R.LKPGYLEATVDWFR.R	0.9958		2	1695.9585
						K.GYIWNYGAIPQTWEDPGHSDK.H	0.9958		2	2435.614
						K.VIAINVDDPDAANYK.D	0.9958		2	1618.7838
						K.DFAVDIIK.S	0.9958		1	921.0813
						R.YVANLFPYK.G	0.9924		1	1115.3171

						K.DVFHMVVEVPR.W	0.9958		2	1328.5719
						K.HTGCCGDNDPIDVCEIGSK.V	0.9958		2	2135.1471
1845	IPYR2_MOUSE	330	59.39	14	177	K.ESNVEEEVWHFLR.N	0.9958	1,2		1674.8101
						K.GYIWNYGALPQTWEDPHLR.D	0.9958		2	2317.5681
						K.AFALDVINSAHER.W	0.9958		2	1443.6023
						K.MEIATEEPLNPIK.Q	0.9958		2	1485.7357
						K.IIAINVNDPEAEKFHDIDDVK.K	0.9958		3	2396.6592
						R.NDEYENLFNMVVEIPR.W	0.9958		2	1983.203
						K.GAISCVNVHICDSPFHCTMEEAR.S	0.9958		2	2691.8735
						K.FKPGYLEATLNWFR.L	0.9958	1,2		1743.0177
						K.ILGTLALIDQSETDWK.I	0.9958		2	1804.0502
						R.YTPNIFPHK.G	0.9924		1	1117.2926
						K.ARNDEYENLFNMVVEIPR.W	0.9958		2	2210.4693
						K.HVAGHYISPFHDIPLK.A	0.9958		2	1832.1148
						R.LFFKHVAGHYISPFHDIPLK.A	0.9944		3	2367.8015
						K.FHDIDDVK.K	0.9958		1	989.0727
1846	IQCA_MOUSE	857	3.97	2	2	R.QVAIEPMPSLLDVR.Q	0.9924		2	1568.8719
						K.YPGKTGLQMMIHLVFK.V	0.9958		2	1864.3173
1847	IQCE_MOUSE	778	2.96	2	3	K.EDMYDEIIELK.K	0.9958		1	1398.5678
						R.EEVEALTK.K	0.9924		1	919.0196
1848	IQCF1_MOUSE	182	10.44	1	3	R.RQSMLDTFQQEQWAVVR.L	0.9958		2	2123.3941
1849	IQCH_MOUSE	1071	5.14	2	3	K.GKSLVSLLPEFELK.N	0.9915		2	1560.8742
						K.FLHMFLTQGGVIEAYPPADSVTNLTVDMLIE	0.9958		3	4077.6565
1850	IQEC1_MOUSE	961	10.3	4	4	K.SESDYSDGDNDSINSTSNSNDTINCSSESS	0.9958		3	3433.238
						R.MQFSFEGPEK.V	0.9958		1	1200.3515
						K.SPAPSSDFADAITELEDAFSRQVK.S	0.9915		2	2582.7833
						K.SLAESIDDALNCRSLHSEEVPASDTAR.A	0.9958		3	2945.0924
1851	IQEC3_MOUSE	1195	1.34	1	2	K.ELKSNEDHVTYVTK.V	0.9958		2	1663.8247
1852	IQGA1_MOUSE	1657	6.88	6	25	R.ILAIGLINEALDEGDAQK.T	0.9958		2	1884.1369
						K.LEGVLAEVAQHYQDTLIR.A	0.9958		2	2056.3262
						K.TLQALQIPAAKLEGVLAEVAQHYQDTLIR.A	0.9958		3	3191.6982
						R.QNVAYEYLCHLEEAK.R	0.993		2	1868.0191
						R.HTDNVIQWLNAMDEIGLPK.I	0.9958		2	2195.498
						R.FQPGETLTEILETPATNEQEAEHQR.A	0.9958		2	2870.0587
1853	IQUB_MOUSE	788	6.35	2	2	K.KLQQTTNTTSTQMTK.I	0.9918		2	1711.9281
						R.IEGLSEGSQIITVTIQTSIDRYEEVAVEIIK.S	0.9944		3	3435.8939
1854	IRAK3_MOUSE	609	6.9	2	2	R.ENDPGPLEPANVTVDNVLVPEHNEK.G	0.9937		2	2727.9445

						K.RFLSELEVLLLFR.H	0.9958		1	1635.9902
1855	IRAK4_MOUSE	459	3.49	1	5	K.KLGAMVEISTEELK.Q	0.9958		2	1548.8353
1856	IREB2_MOUSE	963	8	2	2	K.TIHFPSGQTLDVFEAAELYQKEGIPLIILAGK	0.9958		3	3501.06
						R.LCDCDRANYLASPPLVVAYAIAGTVNIDFQ	0.9944		3	4415.83
1857	IRF3_MOUSE	419	8.83	2	5	K.TVDLHISNSQPISLTSDQYK.A	0.9958		2	2247.4668
						K.ELLEMAREGGASSLK.T	0.9944		2	1591.8199
1858	IRF5_MOUSE	497	2.62	1	5	R.FPSPEDIPSDK.Q	0.9958		1	1232.3324
1859	IRGM_MOUSE	409	8.07	2	2	K.YPPVFLVSSLDPLLYDFPK.L	0.9958		2	2211.6055
						R.LLQNIQENIR.E	0.9958		1	1241.4331
1860	IRK10_MOUSE	379	3.96	1	2	K.YIADFSLFDQVVK.V	0.9958		2	1545.7753
1861	IRK16_MOUSE	419	2.63	1	3	R.MTMAFKDLK.L	0.9958		1	1085.365
1862	IRK3_MOUSE	501	4.59	1	2	K.EQEEMLLMSSPLIAPAITNSK.E	0.9911		2	2303.6913
1863	IRK5_MOUSE	419	11.69	2	2	R.LFLVSPLIISHEINEK.S	0.9958		2	1853.212
						K.CPEGIILLLVQPILGSIVNAFMVGCMFVK.I	0.9958		3	3220.9151
1864	IRS1_MOUSE	1233	8.35	4	4	R.HSSASFENVWLRPGDLGGVSK.E	0.9929		2	2244.4716
						K.AHHDGAGGGCGGSCSGSSGVGEAGEDL	0.9958		3	3567.566
						R.AGNTVPFGAGAAVGGSGGGGGGGSEDV	0.9924		2	2291.3959
						R.HSSETFSAPTRAGNTVPFGAGAAVGGSG	0.9958		3	3492.6567
1865	IRS4_MOUSE	1216	5.43	2	4	K.NVSSKPSTEASFSKPEDK.G	0.9924		2	1939.0862
						R.DFPAASAVIAAPAEAPLLAVSRALAVVSAL	0.9947		3	4223.9053
1866	ISC2A_MOUSE	206	56.8	6	101	R.LLDVPILLTEQYPEGLGPTVPELGAQGIRP	0.9958		3	3502.0887
						R.ILPESSILFLCDLQEK.F	0.9958	1,2		1906.1927
						K.FRPSIAYFPQIVSVAAR.M	0.9958	2,3		1923.2681
						K.TCFSMVPALQK.E	0.9958		2	1282.5067
						R.QSGAFLATSESLILQLVR.D	0.9958		2	1934.2431
						R.GLQVHVVVDACSSR.S	0.9944		2	1527.6867
1867	ISCA2_MOUSE	154	14.29	1	2	R.LLTRWETTSSIPEAGEGQIR.L	0.9946		2	2245.4973
1868	ISCU_MOUSE	168	27.98	4	9	K.TFGCGSAIASSSLATEWVK.G	0.9958		2	1973.156
						K.LHCSMLAEDAIK.A	0.9958	1,2		1388.5879
						K.KVVDHYENPR.N	0.9958		2	1257.3915
						K.VVDHYENPR.N	0.9943		2	1129.2175
1869	ISLR2_MOUSE	745	11.14	3	6	R.VSLPEPDSIACASPPELQGVPVHRLPALPC	0.9958		3	3816.3246
						R.LSAEPPPEAPGTPLR.A	0.9924		1	1532.7367
						R.LQWQLQIPGGTVVLVPPVLSKEEDGGDK.	0.9958		3	3004.4533
1870	ISOC1_MOUSE	297	22.56	4	18	K.GLGSTVQEIDLTGVK.L	0.9958		2	1517.7197
						R.ILGIPVIITEQYPK.G	0.9958		2	1584.9396
						K.FSMVLPEVEAALAEIPGVR.S	0.9958		2	2029.4021

						K.FLSLYGDQLDMHR.K	0.9958	2	1595.8132
1871	ITA1_MOUSE	1179	4.58	3	5	R.CVSDLTLDVSTTEKNLLIVR.S	0.9944	3	2277.5866
						K.WVLIGSPLVGQPK.A	0.9958	2	1394.7001
						K.FVEEIKSIASEPTEK.H	0.9924	2	1707.9183
1872	ITA2B_MOUSE	1033	8.62	3	3	R.YCEAGFSLAVTQAGELVLGAPGGYFFLGLI	0.9958	3	3349.82
						R.FTYDNSNPVFFDGYR.G	0.9909	2	1842.9616
						K.LSPIVLSLNVSLPPEETGGAPAVVLHGETH\	0.9944	3	3777.2694
1873	ITA4_MOUSE	1039	10.97	4	5	K.ATAFPEPHPKVIELNK.D	0.9958	2	1792.088
						R.MFGQSISGQIDADNNGYVDVAVGAFQSDS	0.9958	3	3546.8903
						K.IMVPNSFLPQDDKLFNVLDVQTTTGQCHFK	0.9944	3	3494.9533
						K.QINCEVTESSGIVKLACSLGYIYVDR.L	0.9924	3	2976.2856
1874	ITA5_MOUSE	1053	3.89	2	2	K.HVPNSIGFEVELQLDWQKQK.G	0.9944	3	2396.708
						K.APMDSHGLRPVLHYQSK.S	0.9944	2	1937.2267
1875	ITA7_MOUSE	1179	10.69	5	22	R.ELGQPEPQEPPEKVEPSTSWWPVSSAEK.	0.9958	3	3150.4253
						K.VFIYHGSSLGVVVKPSQVLEGEAVGIK.S	0.9958	2	2814.2975
						K.ICQSNLQLER.Y	0.9958	1	1261.3868
						K.DSATRLIPEVVLSGER.L	0.9952	2	1742.9701
						R.SNWGNSQWEGSDAHPILAADWHPELGPD	0.9958	3	3819.0569
1876	ITAD_MOUSE	1168	6.34	2	4	R.CDIPSLGTLDELDFILKGNLSFGWISQTLQK	0.9944	3	3510.9752
						R.AQVSTMLEEYVVYEPVFLMVFSSVGGLLLL	0.9958	3	4309.2051
1877	ITAM_MOUSE	1153	4.94	3	5	R.NDGEDSYGTQVTVYYPSGLSYR.K	0.9937	2	2472.5835
						K.VIQHQYQFNNLGQR.S	0.9958	2	1745.9382
						R.ENAAKILVVITDGEK.F	0.9958	2	1600.8528
1878	ITAV_MOUSE	1044	6.9	4	5	R.GVSSPDHIFLPIPNWEYK.E	0.9946	2	2100.3813
						K.TMTVFRGGQMQCEELVAYLR.D	0.9948	2	2390.7438
						R.MFLLVGAPK.A	0.9924	1	976.2653
						R.QAHILLDCGEDNVCKPK.L	0.9924	2	1998.1756
1879	ITB1_MOUSE	798	19.42	8	70	K.LRPEDITQIQPQQLLLK.L	0.9958	2	2034.4068
						K.NVLSLTDRGEFFNELVGQQR.I	0.9958	2	2323.5705
						K.LPQPVQVDPVTHCK.E	0.9958	2	1618.8395
						K.FQGPTCETCQTCLGVCAEHK.E	0.9929	2	2384.4691
						K.CNCQSHGIPASPK.C	0.9958	2	1456.5305
						K.LSENNIQTIFAVTEEFQPVYK.E	0.9944	2	2471.7692
						R.EKLPQPVQVDPVTHCK.E	0.9958	2	1876.129
						K.LGGIVLPNDGQCHLENNVYTMSHYYDYPS	0.9958	3	4148.6051
1880	ITB2_MOUSE	771	2.46	1	14	K.LNFTGPGEPDSLRCDTR.A	0.9958	2	1936.0545
1881	ITB5_MOUSE	798	2.01	1	2	R.KPISTHTVDFAFNK.F	0.9944	2	1605.8339

1882	ITB6_MOUSE	787	4.96	2	2	K.LIPGATVGLLQK.D	0.9944	1	1210.5027
						K.CSHMKVGDTASFNVTVSVSNCEK.R	0.9944	3	2558.7549
1883	ITBP2_MOUSE	350	19.14	2	5	K.LLPLLISQALGVALEQK.E	0.9958	2	1807.2273
						K.ELDQEPGAGLDNSLIWTGSSCQNPGCDAV	0.9958	3	5178.3591
1884	ITFG3_MOUSE	555	11.17	3	34	R.GSLGVDGDGVALLHVTR.T	0.9958	2	1666.8747
						R.HAAYVLLTGPASSDVPGLVSVTK.H	0.9944	2	2283.6299
						R.VIHLGEGSSDSDQAIR.D	0.9958	2	1684.8033
1885	ITIH2_MOUSE	946	18.08	9	43	K.LVNNSPLPQSVVFDVQIPK.G	0.9958	2	2095.4466
						K.KFYNQVSTPLLR.N	0.9958	2	1466.7233
						R.NVQFNYPQASVTDVTQNNFHNYFGGSEIV	0.9958	3	3646.9543
						K.IQPSGGTNINEALLR.A	0.9958	2	1583.7849
						R.FLHVPDTFEGHFQGVPVISK.G	0.9958	2	2255.581
						K.FYNQVSTPLLR.N	0.9958	2	1338.5492
						K.LTEVQSIITATSANTELVLETLSQMDDLEEFI	0.9958	3	3771.2227
						K.AHVSFKPTVAQQR.K	0.9958	2	1469.6865
						K.VQFELHYQEVK.W	0.9958	2	1420.6079
1886	ITIH3_MOUSE	889	15.52	7	14	K.NIHDQSMTNINDGLLK.G	0.9958	2	1814.0233
						R.ESPGNVQIVNGYFVHFFAPQGLPVVPK.N	0.99	2	2942.3898
						R.NAIGGKFPLYNLGFGNNLNYNFLETLALEN	0.9958	3	3867.3586
						K.FPLYNLGFGNNLNYNFLETLALENHGLAR.F	0.9958	3	3326.7386
						R.FAHNVVTTR.A	0.9932	2	1045.1863
						R.STSIIIMLTDGDANTGESRPEK.I	0.9958	2	2336.5763
						R.NSYPHFYDGSEIVVAGR.L	0.9958	2	1912.0685
1887	ITM2B_MOUSE	266	6.77	1	6	K.DDVILNEPSADAPAAR.Y	0.9958	2	1654.774
1888	ITPA_MOUSE	198	41.41	5	95	K.LEEVIQILGDNFPCTLEAQK.I	0.9944	3	2318.5952
						K.LKPEGLHQLLAGFEDK.S	0.9958	2	1796.0764
						K.KLEEVIQILGDNFPCTLEAQK.I	0.9958	2	2446.7693
						K.IDLPEYQGEPDEISIQK.C	0.9958	1,2	1975.1596
						R.DFGWDPCFQPDGYEQTYAEMPK.S	0.9956	2	2682.8429
1889	ITPR1_MOUSE	2749	4	5	5	R.NMGAHAVVLELLQIPYEK.A	0.9943	2	2026.4015
						K.LLEDLVYFVTGGTNSGQDVLEVVFSKPNR.	0.9958	3	3198.6
						K.ELVEVIK.K	0.9958	1	830.0123
						R.ESLTSFGNGPLSPGGPSKPGGGGGGPGS	0.9944	3	2932.0898
						K.EELLPAEETEQDK.E	0.9958	2	1531.6135
1890	ITPR2_MOUSE	2701	2.74	3	3	K.MSSFLYIGDIVSLYAEGSVNGFISTLGLVDD	0.9958	3	3440.8897
						K.CNSLLPLDDIVRVVTHDDCIPEVK.I	0.9958	3	2809.1213
						R.CVSDESLPFDLR.A	0.9958	1	1438.5433

1891	ITPR3_MOUSE	2670	2.96	3	5	K.NAMRVTLDATGNEGSWLFIQPFWK.L	0.9958	3	2783.1767
						R.IGEQAEAMFGVGKTSSMLEVDDEGGR.M	0.9944	3	2714.979
						R.VLLHLTMHDYPSLVSGALQLLFK.H	0.993	2	2597.1339
1892	ITSN1_MOUSE	1714	3.21	3	5	R.IAEITHLQQQLQESQQMLGR.L	0.9958	2	2352.6708
						R.RQELLNQR.N	0.9924	1	1057.1978
						K.HDQQFLSLKPIAGFITGDQAR.N	0.9958	2	2343.6475
1893	ITSN2_MOUSE	1658	3.26	2	3	K.MPVQMIGDILAAELSHMQAYIRFCSCQLNG	0.9944	3	4238.9005
						K.EYQNKLIYLVPEK.Q	0.9958	2	1637.9164
1894	IVD_MOUSE	424	68.63	18	138	K.QLGSLGVLGITAPVQYGGSGLGYLEHVLV	0.9958	3	3645.2085
						K.KGDHYVLNGNK.F	0.9958	2	1245.3805
						K.TDLTAVPASR.G	0.9944	1	1031.1539
						K.VPAANVLSQESK.G	0.9958	1,2	1243.4026
						K.IGQFQLMQGK.M	0.9958	1	1150.3813
						R.GSNTCELVFEDCK.V	0.9958	2	1559.6021
						R.EAFGQKIGQFQLMQGK.M	0.9915	2	1811.1089
						R.ASGAVGLSYGAHSNLCVNQIVR.N	0.9958	2	2274.5077
						K.FWITNGPDADILVVYAK.T	0.9958	2	1923.2188
						K.LISGEFIGALAMSEPNAGSDVVSMK.L	0.9944	2	2524.9069
						K.FLQENLAPK.A	0.9912	2	1060.2383
						K.GVYVLMSGLDLER.L	0.9958	2	1452.7088
						K.GMPGFSTSK.K	0.9944	1	912.0484
						K.MADMYTRLMASR.Q	0.9958	1	1446.7407
						K.DCAGVILYAAECATQVALDGIQCLGGNGYI	0.9958	3	3992.3476
						R.LVLAGGPLGIMQAVLDHTIPYLHVR.E	0.9958	2	2685.2463
						R.GSNTCELVFEDCKVPAANVLSQESK.G	0.9958	2,3	2783.9814
						K.AQEIDQTNDFK.N	0.9958	1	1309.3751
1895	IZUM1_MOUSE	397	10.83	2	2	R.VWENSSETLIAKGK.E	0.9958	1	1562.763
						R.LLILLTLGFVVLVASIIISVLHFRK.V	0.9944	3	2779.5553
1896	JAD1A_MOUSE	1690	3.67	3	3	K.SHYERILYPYELFQSGVSLMGVQMPDLDL	0.9958	3	3531.0786
						R.HSMANLENIVNEAK.N	0.9944	1	1570.7607
						K.LEKVEQLFGEGK.Q	0.9958	1	1377.5804
1897	JAD1C_MOUSE	1554	4.89	3	3	K.ARAWIADVDEIQNGDHYPCLDDLEGLVAV	0.9958	3	3469.7583
						R.EAFELLPDDERQCIK.C	0.9958	2	1864.0283
						K.SGICKIRPPADWQPPFAVEVDNFR.F	0.9949	2	2801.1431
1898	JAD1D_MOUSE	1548	2.2	2	2	R.QSVQPSKFSCYSR.R	0.9924	1	1574.6996
						R.QALASEDVTALLKQLEK.S	0.9958	1	1858.1424
1899	JAK3_MOUSE	1100	9.09	4	9	R.AILRDLNGLITSDYELLSDPTPGIPSPR.D	0.9958	3	3025.4289

						R.REVVDGETHDSEVLLK.V	0.9958	2	1827.0013
						R.LVTVTRMDGHILEAEFPGLPEALSFVALVD	0.9944	3	3765.3619
						K.IADFGLAKLLPLGK.D	0.9958	1	1456.8119
1900	JHD2C_MOUSE	2350	2.47	2	2	R.QNLQGGNVPTMNGVSQVLQNVLHHSNK.T	0.9944	3	2915.2566
						K.TDYLKPEAGETGRIILPNVNLESAHVK.S	0.9952	2	2966.3641
1901	JHD3B_MOUSE	1086	2.95	1	2	R.KFNAAAALSEPYCAICTLFYPYSQSVQTER	0.9944	3	3487.8226
1902	JHD3C_MOUSE	1054	3.98	2	2	R.WIDYGKVAK.L	0.9944	1	1080.2719
						K.RPKPEEDEEFAEFSGEEGANPAMGPRHLK	0.9958	3	3256.5304
1903	JIP3_MOUSE	1337	6.13	4	5	K.EVGNLLLENSQLLETK.N	0.9958	2	1801.0471
						K.NVPVPVYCRPLVEK.D	0.9958	2	1670.9586
						K.ERPTSLNVFPLADGMVR.A	0.9958	2	1903.2066
						R.SHALCQISAGSRPLEFFPDDDCTSSAR.R	0.9958	3	3026.1781
1904	JIP4_MOUSE	1321	17.64	11	59	K.NLPVPVYLRPLDEK.D	0.9958	2	1653.9621
						K.YNAPTSHVTPSVK.K	0.9958	2	1401.562
						K.ERPISLGIFPLPAGDGLLTPDTQK.G	0.9958	2	2536.931
						R.MGDEGGESELLGEDLPLEPSVTK.A	0.9958	2	2403.6173
						K.LHQLSGSDQLEATAHSR.I	0.9958	2	1850.9859
						R.LYHAHTYQHLQDVDIEPYVSKMLGTGK.L	0.9958	3	3145.5597
						R.MGDEGGESELLGEDLPLEPSVTKAER.S	0.9958	3	2759.9991
						K.ELMPLVVAVLENLDSVFAQDQEHQVELELL	0.9958	3	3579.1029
						K.AFDFLSEETEASLASR.R	0.9958	2	1773.8938
						K.HIEVQVAQETR.N	0.9958	2	1310.4526
						R.LWVGTGNGVIISIPLTETNKTSGTPGNRPGS	0.9944	3	3493.9883
1905	JKIP3_MOUSE	844	4.03	2	17	K.QVEEALTMVIQADK.I	0.9958	2	1575.8175
						K.HEVQDAKDQNELLEFR.I	0.9957	2	1972.1216
1906	JMJD5_MOUSE	414	2.66	1	2	K.ELRTLLPDK.E	0.9944	1	1085.2889
1907	JMJD6_MOUSE	403	1.99	1	7	K.LLEDYK.V	0.9958	1	780.8962
1908	JMY_MOUSE	983	3.66	2	3	K.DNGASTTAETLEK.D	0.993	2	1337.3831
						K.SASAPAAHLFDSSQLVSAR.K	0.9947	2	1916.1008
1909	JPH2_MOUSE	696	21.55	9	18	K.ELAPDFYQPGPEYQK.R	0.9958	2	1782.947
						R.LLQEILENSESLLEPPER.G	0.9912	2	2110.3691
						R.RSPARPASEHMAIEALQPPPAPSQEPEVAI	0.9958	3	3515.9868
						R.RSDSAPPSPVSATVPEEEPPAPR.S	0.9958	2	2374.5694
						K.AEAAEQAALAANQESNIAR.T	0.9958	2	1929.0537
						R.ETPQPEGGPPSPAGTPPQPK.R	0.9958	2	1970.1461
						R.GLGTGLPERPR.E	0.9944	2	1153.3267
						K.ELAPDFYQPGPEYQKR.R	0.9958	1	1939.1345

						R.RLLQEILENSESLLEPPER.G	0.9958		2	2266.5565
1910	K0020_MOUSE	647	2.94	1	3	K.QAFQELQGDLVELSKAK.Y	0.9958		2	1905.1583
1911	K0100_MOUSE	2234	1.48	2	2	R.QLIATDDAVPLGSGK.G	0.9958		1	1485.6775
						R.GAETEGCVIVSAAK.A	0.9958		1	1392.5151
1912	K0157_MOUSE	415	10.6	2	2	R.ISLAIPNLGNTSQQEYK.V	0.994		2	1877.1045
						R.SVFMPRPQAVGSSSYASTSGGLK.F	0.9909		2	2315.6061
1913	K0226_MOUSE	956	3.77	2	2	K.LLPIPDSLPISPDDGQHADIYKLR.I	0.9929		2	2675.0569
						R.EIQELKQK.I	0.9924		1	1016.1827
1914	K0241_MOUSE	649	8.47	2	2	K.GQEPSDSGRYLELPPRPSPESSESDWETL	0.9958		3	4402.6826
						R.QADITRETVQK.S	0.9958		1	1289.4313
1915	K0284_MOUSE	1574	6.04	4	4	R.APGMAPQMEQQSLLVPGSPGGQKWVSR.	0.9944		3	2838.2721
						K.EPTSGPPAPGK.L	0.9924		1	1038.1454
						R.KQEEDDSLSDAGTYTIETEAQDQEVEEAR.	0.9958		3	3288.3271
						R.DEHWVKDLGSLNGTFVNDVR.I	0.9937		2	2302.5083
1916	K0423_MOUSE	1759	2.62	2	14	K.LSKALFTQMGQNLLNQAASQPPHIK.K	0.9958	2,3		2737.1925
						K.VNLVALETMHKMIPLLR.D	0.9958		2	1979.4932
1917	K0528_MOUSE	1016	1.87	1	2	R.AHVAALGGNAVVSYIMK.Q	0.991		2	1702.0245
1918	K0556_MOUSE	1610	4.47	2	2	K.SLIFDGVLEKGGGEAPSDCTIPVDLQR.E	0.9958		3	2875.1713
						R.HYVGLNGIEIFSSSGEPVQISSITADPPDINI	0.9958		3	4369.8749
1919	K0562_MOUSE	926	5.51	3	3	K.LMEMPVGTQK.E	0.9958		1	1134.3943
						K.EVKSLQLIPSYLVQPLK.A	0.993		2	1956.3763
						R.QVVEISSLTEHLLTECDR.R	0.9944		2	2130.3258
1920	K0754_MOUSE	979	2.76	1	2	R.EPQSESVTLEHMSKSVDIPEVQNVK.N	0.9958		3	2812.1212
1921	K0776_MOUSE	793	2.9	2	2	R.CVPQIIAFLHSK.I	0.9958		1	1413.669
						R.LFEKGMK.Y	0.9958		1	853.0673
1922	K0831_MOUSE	492	15.45	3	3	R.DLVDSVDDAEGLYVAVERCPLCNTTR.R	0.9958		3	2969.1641
						R.KLNANILYLCSSQHVNLDQLQPLHTLR.N	0.9958		3	3190.639
						R.SHILELTSIIFPIDEVK.T	0.9947		2	1955.3019
1923	K0913_MOUSE	1832	1.75	3	4	K.EQDNLMLEK.A	0.9958		1	1120.2629
						R.EKGDLALALMITYK.D	0.9931		2	1566.8963
						K.GDLALALMITYKDDQAK.L	0.9944		1	1867.1676
1924	K1033_MOUSE	1173	5.12	2	3	R.KDLALFFSLNPIR.F	0.9954		2	1534.8418
						K.LEGQLLDGMIFQACIEQQFDSLNGGISVSK	0.9958		3	4790.2814
1925	K1045_MOUSE	400	9.25	2	2	K.ALLPTEQESRYVDWPTFLR.E	0.9958		3	2322.6256
						R.GTVEGSVQEVQEEK.E	0.9958		2	1519.6055
1926	K1107_MOUSE	1369	4.89	3	3	K.SAPPTLAQAQGSQGESPHSVKSSVSSR.Q	0.9944		3	2681.879
						R.LTFHGAAQSQLPDNCATEDSK.C	0.9958		2	2291.4021

						R.ELSSNIPKISSVK.S	0.9958	1	1402.6311
1927	K1109_MOUSE	5005	2.18	5	15	R.MNRGVVEETANNVDAGK.T	0.99	2	1804.9726
						K.IDPVGVDYILQK.L	0.9924	1	1360.5932
						R.LWFLWPDDTLKNK.R	0.9924	2	1676.9555
						R.IGETDELPEIRVDAASPGPR.V	0.9958	3	2123.3275
						K.LEELTPSSSSAFSSTSAESDMYYGQSLLQF	0.9958	3	4042.414
1928	K1219_MOUSE	1484	5.73	5	5	R.RPKVNSILNLFGSWLFDAAFVHCK.L	0.9958	3	2821.2634
						K.EVPVIFIHPLNTGLFR.I	0.9958	2	1853.2175
						R.LPTINK.H	0.9958	1	685.8418
						K.FSNDDSSSYDKPITFLSLK.L	0.9944	2	2165.3612
						K.HRPFPEEVDK.I	0.9907	2	1254.3879
1929	K1279_MOUSE	617	10.7	2	5	R.QLEHNAYHPMEWAINAATLSQFYINK.L	0.9958	3	3091.4705
						R.LAVVEFHLGVNHIDTEELSAGEEHLVRCLS	0.9958	3	4174.7154
1930	K1310_MOUSE	903	3.88	1	2	R.LVATSPGSSLPGTASASSLLQGLSFSLQDI	0.9958	3	3208.5902
1931	K1370_MOUSE	1075	4.74	2	3	K.TQSGCFDLDASLLHLRSLSSK.S	0.9958	2	2336.5731
						K.HTWTMAPVSALHVRSGMPPEYTAAIR.N	0.9944	3	2881.3429
1932	K1409_MOUSE	2596	1.93	2	9	K.RHLYVLLGYDQQEGCFMIAPQK.M	0.9958	2	2668.0516
						K.LKSPLPDTNLLLLVQFICADAGTK.L	0.9958	3	2629.0784
1933	K1462_MOUSE	1320	6.67	5	5	R.TSSAINQASMSK.G	0.9944	1	1225.3593
						K.ELESRGMAQAYSLPVHVR.E	0.9958	3	2044.3361
						R.RPWDLISQLESFNK.E	0.9958	2	1733.9646
						R.SPPQHIPNPYLEDPVPR.H	0.9958	2	1957.1961
						K.FEGLYPFVHGEHTSQNR.K	0.9944	2	2019.1833
1934	K1539_MOUSE	538	4.28	1	3	R.RLLPAGETLDVSSEDEGPAPR.R	0.9943	2	2210.4057
1935	K1546_MOUSE	1912	2.14	2	2	K.RTVSEPSLSGLHPNK.I	0.9958	2	1622.8216
						R.EGSCFGQIKVEESFCVGNQYSK.S	0.9944	3	2554.7047
1936	K1600_MOUSE	764	9.69	3	5	K.EAQKTAAVALAK.A	0.9958	1	1201.4087
						K.RLLGLEPEGPIVDHITLLEGVIVLEEFCK.E	0.9958	3	3290.8341
						K.LTSILQHAVEALAPSLPLQEDFVYHWK.A	0.9958	3	3107.5792
1937	K1602_MOUSE	1323	3.33	2	2	R.REEMPSEDSLAEPVSTTHFTACGSLTR.T	0.9958	3	3010.2251
						R.TSTPQGPAFGGSR.T	0.9958	1	1263.3525
1938	K1622_MOUSE	875	4.8	3	4	R.FLDTCEFIIEIFSR.S	0.9958	2	1791.0198
						R.GPGNTADPKSSGSK.D	0.9958	1	1303.3714
						K.DVLAIVKK.T	0.9958	1	886.1228
1939	K1632_MOUSE	2572	2.14	2	2	K.AVKSGLPIGCYLALAVTAVGHSLEK.F	0.9944	2	2555.9867
						R.LFNVYVLWLEDENFQKGDTYIPSLPK.H	0.9958	3	3130.5671
1940	K1731_MOUSE	2412	2.36	2	4	R.LPPPVPSPFENIDVNR.I	0.9958	2	1792.0446

						R.DGQETLLLYKESCSEDSEAGPVESLSSVV\	0.9944		3	3995.2227
1941	K1751_MOUSE	788	2.92	2	2	R.RMDAVLSLK.N	0.9958		1	1033.2744
						R.KPVGGSKMEK.D	0.9924		1	1061.2848
1942	K175L_MOUSE	547	9.14	2	2	K.RMSEEMR.Q	0.9944		1	939.0925
						R.EDTLVYLVSQAPEQEQLTSVDWPESFAAC	0.9944		3	4508.007
1943	K1841_MOUSE	718	8.64	2	2	K.DCEIPALEPGNVISILISSEFLK.M	0.9958		2	2545.8989
						R.FDELKSCGSSPVDNQYNPLMATGEGPVET	0.9958		3	3834.2094
1944	K1881_MOUSE	1403	14.18	11	32	K.DTVTTGLTGAINVAK.G	0.9958		2	1461.6555
						K.DTVTTGLTGAVNVAK.G	0.9958	1,2		1447.6286
						K.DTVTTGLTGAMNVAK.G	0.9944		1	1479.6886
						K.DMGSFSVTSSEDAFSGVFGIMDAAK.G	0.9958		2	2557.8062
						K.VSTNSQMAGDAAGLLQPSEQTAGDK.D	0.9958		2	2477.6624
						K.GMVQGGLGATQSALVGTK.E	0.9958		2	1675.9409
						R.NLVSHTHSSTSTK.D	0.9958		2	1399.5033
						K.GAVQGGLDTTK.S	0.9958		1	1047.1533
						R.AFEHALSHIQHNQFQAR.A	0.9958		2	2035.232
						K.TLSSFFGSLPGFSSAR.N	0.9958		2	1661.8547
						K.DTVTTGLTGALNVAK.G	0.9958		2	1461.6555
1945	K1946_MOUSE	825	4.24	2	2	K.IYSGGKELK.V	0.9944		1	995.1637
						R.AWFVSLDGKPVAQVRHSFIDLK.K	0.9943		3	2514.9328
1946	K1C13_MOUSE	437	5.72	1	3	R.YALQLQQIQGLISSIEAQLSELR.S	0.9958		2	2602.9909
1947	K1C14_MOUSE	484	5.17	1	2	R.YCMQLAQIQEMIGSVEEQLAQLR.C	0.9958		2	2740.1281
1948	K1C17_MOUSE	433	16.17	3	4	R.GQVGGEINVEMDAAPGVDLSR.I	0.9958		2	2115.3227
						R.YCVQLSQIQGLIGSVEEQLAQLR.C	0.9958		2	2633.9708
						R.QFTSSSSIKGSSGLGGGSSR.T	0.9958		2	1888.0012
1949	K1C18_MOUSE	423	8.04	3	5	K.IIEDLR.A	0.9958		1	758.8931
						R.AEGQRQAQEYEALLNIK.V	0.9909		2	1962.1698
						R.DWGHYFKIIEDLR.A	0.9958		2	1692.9145
1950	K1C19_MOUSE	403	7.69	2	3	R.SLLEGQEAHYNNLPTPK.A	0.9958		2	1912.1094
						R.TKFETEHALR.L	0.9958		2	1232.3818
1951	K1C23_MOUSE	422	3.32	1	7	R.KDYSQYEENISR.L	0.9945		2	1532.6067
1952	K1KB1_MOUSE	261	7.28	1	15	K.DLQCVNLKLLPNEDCDK.A	0.9958		2	2075.2557
1953	K2C1_MOUSE	637	3.61	2	3	K.RTNAENEFVTIK.K	0.9958		2	1422.5809
						R.TKYEDEINK.R	0.9944		1	1140.2353
1954	K2C1B_MOUSE	572	4.55	2	12	R.FLEQQNQVLQTK.W	0.9958		2	1476.6726
						K.WELLQQVNTSTR.T	0.9958		2	1475.6445
1955	K2C5_MOUSE	580	2.41	1	3	R.SLDLDSIIAEVK.A	0.9958	1,2		1303.4955

1956	K2C7_MOUSE	457	7	2	2	R.ASFGSRSLYGLGSSRPR.V	0.9958		1	1798.9993
						R.AYSIKTTSTTR.R	0.9905		1	1229.3757
1957	K2C71_MOUSE	524	3.63	1	3	K.LDELEGALHQAKEELAR.M	0.9958		2	1923.1332
1958	K2C72_MOUSE	520	4.42	1	12	K.QCSNLETAIADAEQRGDCALK.D	0.9952		2	2351.4645
1959	K2C8_MOUSE	490	2.86	1	4	K.SLNNKFASFIDK.V	0.9958		2	1384.5749
1960	K6PF_MOUSE	780	53.08	28	791	R.GITNLCVIGGDGSLTGADTFR.S	0.9958		2	2125.3093
						K.GQIEEAGWSYVGGWTGQGGSK.L	0.9958		2	2155.2878
						R.DLQVNVEHLVQK.M	0.9958		2	1422.6243
						R.IVEIVDAITTTAQSHQR.T	0.9958		2	1883.1118
						R.IGLIQGNR.V	0.9958	1,2		871.0274
						R.VFFVHEGYQGLVDGGEHIR.E	0.9958		2	2160.3965
						K.NVLGHMQQGGSPTPFDR.N	0.9958		2	1842.0392
						R.SEWSDLLNDLQK.D	0.9944		1	1448.5725
						K.AIAVLTSGGDAQGMNAAVR.A	0.9944		2	1803.0435
						R.VLVVHDGFEGLAK.G	0.9958	1,2		1384.6182
						K.KNLEQISANITK.F	0.9958		2	1359.5657
						R.VTVLGHVQR.G	0.9958		2	1009.1966
						R.LPLMECVQVTK.D	0.9958		2	1318.5806
						K.AMNWMSGK.I	0.9958		1	925.1084
						K.YEIDLDTSDHAHLEHISR.K	0.9958		2	2152.2847
						K.RGITNLCVIGGDGSLTGADTFR.S	0.9958		2	2281.4967
						R.IFANTPDSGCVLGMR.K	0.9958		2	1638.8451
						R.ALVFQPVTELK.D	0.9958		1	1245.5046
						K.GGLHTVAVMNVGAPAAGMNAAVR.S	0.9958		2	2165.5365
						R.SFMNNWEVYK.L	0.9924		2	1318.4895
						K.RFDEAIK.L	0.9944		1	879.0037
						K.CNENYTTDFIFNLYSEEGK.G	0.9958		2	2345.4469
						K.NLEQISANITK.F	0.9944		1	1231.3916
						K.EQWWLK.L	0.9944		1	890.0293
						K.SSYLNIVGLVGSIDNDFCGTDMTIGTDSALH	0.9958	2,3		3430.734
						R.LNIIIVAEGAIDK.N	0.9958		2	1369.6445
						K.LLAHVRPPVSK.G	0.9945		2	1217.5002
						R.LNIIIVAEGAIDKNGKPITSEDIK.N	0.9944		2	2552.9713
1961	K6PL_MOUSE	780	25.51	10	57	K.AIGVLTSGGDAQGMNAAVR.A	0.9958		2	1789.0166
						R.TNVLGHLQQGGAPTPFDR.N	0.9958		2	1909.1117
						R.ISMADYVSGELEHVTR.R	0.9958		2	1808.0161
						R.IMEVIDAITTTAQSHQR.T	0.9958		2	1915.1718

						K.GQVQEVGWHDVAGWLGR.G	0.9958		2	1895.0873
						R.TGISEGHTVYIVHDGFEGLAK.G	0.9958		2	2231.4698
						R.LAAAYNLLQHGITNLCVIGGDGSLTGANIFF	0.9958		3	3231.6452
						R.VFANAPDSACVIGLRK.K	0.9958		2	1718.9598
						R.TLPKPHLEAIVENLR.T	0.9958		2	1731.0482
						R.HGKPISSSYVK.D	0.9958		2	1203.3836
1962	K6PP_MOUSE	784	9.31	4	26	R.RFEGNLNTYK.R	0.9915		2	1242.3769
						K.NVLGHMQQGGAPSPFDR.N	0.9958		2	1812.0129
						K.EIGWADVGGWTGQGGSILGTK.R	0.9958		2	2090.3
						R.IIEVVDAIMTTAQSHQR.T	0.9944		2	1913.1993
1963	KAD1_MOUSE	194	71.65	13	2339	K.VNAEGTVDTVFSEVCTYLDSLK.-	0.9958		2	2448.6521
						R.LETYYNATEPVISFYDK.R	0.9926		2	2054.2604
						K.GELVPLDTVLDMLR.D	0.9923		2	1571.8725
						K.VDSSNGFLIDGYPR.E	0.9958	1,2		1540.6726
						K.IGQPTLLLYVDAGAETMTQR.L	0.9958		2	2178.5084
						K.RLETYYNATEPVISFYDK.R	0.9958		2	2210.4479
						K.IIFVVGGPGSGK.G	0.9915		2	1131.3604
						R.KVNAEGTVDTVFSEVCTYLDSLK.-	0.9958		2	2576.8262
						K.YGYTHLSTGDLLR.A	0.9958		2	1496.6628
						K.KLSAIMEK.G	0.9958		1	920.1553
						K.LSAIMEK.G	0.9958		1	791.9812
						R.LETYYNATEPVISFYDKR.G	0.9958		2	2210.4479
						K.IGQPTLLLYVDAGAETMTQRLLK.R	0.9958		2	2533.0014
1964	KAD2_MOUSE	232	63.79	11	101	R.LEAYHTQTTPLVEYYR.K	0.9958	1,2		1985.2035
						R.GIHCAIDASQTPDIVFASILAAFSK.A	0.9958		2	2633.9703
						R.AVLLGPPGAGK.G	0.9958		1	980.1955
						K.LAENFCVCHLATGDMLR.A	0.9958		2	2008.2319
						K.EKLDSVIEFSIQDSLLIR.R	0.9958		2	2106.424
						K.TRLEAYHTQTTPLVEYYR.K	0.9958		2	2242.4961
						K.LVSDEMVVELIEK.N	0.9958		2	1504.7791
						R.SYHEEFNPPK.E	0.9958	1,2		1248.3373
						R.SYHEEFNPPKEPMK.D	0.9958		2	1733.9361
						K.LDSVIEFSIQDSLLIR.R	0.99		2	1849.1345
						K.NLETPSCKNGFLLDGFPR.T	0.9958		2	2066.2873
1965	KAD3_MOUSE	227	48.02	7	38	K.TVGIDDLTGEPLIQR.E	0.9958		1	1627.8351
						K.VYQIDTVINLNVPFEVIK.Q	0.9952		2	2105.4821
						K.TLTQCSWLLDGFPR.T	0.9958		2	1694.8939

						K.AYEAQTEPVLQYYQK.K	0.9958	1,2		1832.0197
						R.QNMLQGTEIGVLAK.T	0.9958		2	1502.7692
						K.KGVLETFSGTETNK.I	0.9915		2	1511.672
						K.HLSSGDLLR.Q	0.9958	1,2		998.127
1966	KAD4_MOUSE	223	50.22	6	77	R.GVLHQFSGTETNR.I	0.9958		1	1446.5626
						R.SAQHWLLDGFPR.T	0.9958		2	1427.6053
						R.AVILGPPGSGK.G	0.9958		1	996.1949
						R.VYNLDFNPPQVQGIDDITGEPLVQQEDDKF	0.9958		3	3983.3373
						R.IAQNFGLQHLSSGHLLR.E	0.9958		2	1892.1709
						K.GLLVPDHVITR.L	0.9958	1,2		1220.4575
1967	KANK2_MOUSE	843	4.86	2	17	R.LDLDFLKYVDDIEK.G	0.9958		2	1726.9641
						R.SHEVVETMCPLPTATTGNVHTAK.K	0.9958		2	2481.7492
1968	KAP0_MOUSE	381	33.86	8	96	R.LTVADALEPVQFEDGQK.I	0.9958		2	1861.0587
						K.VSILESLDKWER.L	0.9958		2	1475.6848
						R.RSENEEFVEVGR.L	0.9957		2	1451.5357
						K.IVVQGEPGDEFFIILEGTAAVLQR.R	0.9958		2	2602.9903
						K.HNIQALLK.D	0.9929		2	937.1301
						K.NVLFSHLDDNER.S	0.9958	1,2		1459.5583
						R.LGPSDYFGEIALLMNRPR.A	0.9912		2	2050.3831
						R.GAISAEVYTEEDAASYVR.K	0.9958		2	1932.0508
1969	KAP2_MOUSE	401	36.66	9	100	K.NLDQEQLSQVLDAMFEK.I	0.9958		2	2009.2385
						R.NISHYEEQLVK.M	0.9958		1	1360.5095
						K.GQYFGELALVTNKPR.A	0.9958		2	1693.9432
						K.MFESFIESVPLFK.S	0.9958		2	1574.875
						K.TDEHVIDQGDDGDNFYVIER.G	0.9958		2	2338.4057
						K.RNISHYEEQLVK.M	0.9958		2	1516.697
						R.GSFGELALMYNTPR.A	0.9929		2	1556.7766
						R.VSVCAETFNPDEEEEDNDPRVVHPK.T	0.9958		3	2914.0345
						K.SNKNGGNQEVEIAHCHK.G	0.9958		2	1923.0184
1970	KAPCA_MOUSE	351	31.62	7	48	K.KWETPSQNTAQLDQFDR.I	0.9958		2	2065.2065
						R.ILQAVNFPFLVK.L	0.9948		2	1389.7239
						R.FPSHFSSDLK.D	0.9958		2	1165.2908
						R.NLLQVDLTK.R	0.9944		1	1044.2364
						R.TWTLCGTPEYLAPEIILSK.G	0.9958		2	2193.5109
						R.FYAAQIVLTFEYLHSLDLIYR.D	0.9937		2	2576.9977
						R.KVEAPFIPK.F	0.9944		1	1029.2676
1971	KAPCB_MOUSE	351	9.4	2	2	R.ILQAVEFPFLVR.L	0.9958		2	1432.7489

						R.KWENPPPSNAGLEDFER.K	0.9924		2	1987.1357
1972	KAT1_MOUSE	424	27.59	6	37	K.ILVLNTPNNPLGK.V	0.9944		2	1393.6695
						K.SSMPDLPGAMDEPYDTR.F	0.993		2	1883.0547
						R.RLEGIDHNPWVEFTR.L	0.9958		2	1870.0775
						K.GQLGSSNDWQLDPTELASK.F	0.9958		2	2047.1858
						K.GLSAIPVSTFYSQPHHK.D	0.9958		2	1870.1179
						R.TVHQNSIFHCPTQAQAAVAQCFER.E	0.9958		2	2802.0106
1973	KAT3_MOUSE	455	24.4	7	38	K.LAADPSVVNLGQGFPDISPPSYVK.E	0.9958		2	2472.8003
						K.AIILNTPHNPLGK.V	0.9958		2	1388.653
						R.GFGHPALVK.A	0.9924	1,2		926.1063
						R.MAGAVPVFIPLR.S	0.9958		2	1271.6067
						K.RIEGLDSNVWVEFTK.L	0.9958		2	1794.0171
						K.DSTLDAAEEIFR.A	0.9944		1	1367.4552
						K.KLTAIPVSAFCDSK.S	0.9944		2	1537.7625
1974	KCC1A_MOUSE	374	12.3	4	7	K.YLHDLGIVHR.D	0.9958	1,2		1223.4202
						R.FTCEQALQHPWIAGDTALDK.N	0.9958		2	2302.5145
						K.NIHQSVSEQIK.K	0.9958		2	1283.427
						K.RFTCEQALQHPWIAGDTALDK.N	0.9958		2	2458.702
1975	KCC2A_MOUSE	478	2.93	1	2	R.DLKPENLLLASK.L	0.9958		2	1341.5907
1976	KCC2D_MOUSE	499	18.64	4	6	R.FTDEYQLFEELGK.G	0.9958		2	1619.768
						K.ICDPGLTAFEPEALGNLVEGMDFHR.F	0.9958		2	2790.0859
						K.VTEQLIEAINNGDFEAYTK.I	0.9958		2	2156.3538
						R.EYYSEADASHCIQQILESVNHCHLNGIVHR.	0.9958		3	3581.8151
1977	KCNC1_MOUSE	511	3.33	1	3	K.HIPRPPQLGSPNYCK.S	0.9944		2	1764.9909
1978	KCNH1_MOUSE	989	3.34	2	2	K.QLSEILR.I	0.9958		1	859.0134
						R.GSAQSPQETGEISRPQSPESDR.D	0.9958		2	2344.4136
1979	KCNK3_MOUSE	409	12.47	2	2	K.AGVQWRFAGSFYFAITVITTIGYGHAAPSTI	0.9958		3	3548.9823
						R.YNLSEGGYEELER.V	0.9958		1	1559.6293
1980	KCNQ4_MOUSE	696	8.76	2	2	K.DANSDFSSYADSLWWGTITLTTIGYGDK.T	0.9944		3	3086.2947
						R.LGLLGSPLPPGAPLPGPGSGSGSACGGQF	0.9958		2	2615.9152
1981	KCNV1_MOUSE	503	2.58	1	2	R.FSACYFTLKLK.E	0.9924	1,2		1378.6202
1982	KCRB_MOUSE	381	65.09	16	304	K.TDLNPDNLQGGDDLDPNYVLSSR.V	0.9958		2	2519.6409
						K.LAVEALSSLDGDLSGR.Y	0.9958		2	1603.7697
						K.RGTGGVDTAAVGGVFDVSNADR.L	0.9958		2	2122.259
						R.FPAEDEFPDLSSHNNHMAK.V	0.9958		2	2187.3478
						R.GIWHNDNK.T	0.9958		1	984.0592
						K.TFLVWINEEDHLR.V	0.9958		2	1672.8809

						R.HGGYQPSDEHKTDLNPDNLQGGDDLDPN	0.9958		3	3755.9066
						K.SMTEAEQQQLIDDHFLFDKPVSPLLLASGM	0.9958		3	3590.1036
						R.LEQGQAIDDLMPAQK.-	0.9958	1,2		1657.8792
						R.LGFSEVELVQMVVDGVK.L	0.9958		2	1850.1804
						K.LRFPAEDEFPDLSSHNNHMAK.V	0.9958		2	2456.6947
						R.GTGGVDTAAVGGVFDVSNADR.L	0.9958		2	1966.0715
						R.FCTGLTQIETLFK.S	0.9958		2	1558.7809
						K.NYEFMWNPHLGYILTCPSNLGTGLR.A	0.9944	2,3		2955.3265
						K.VLTPELYAELR.A	0.9958		2	1304.5291
						K.SMTEAEQQQLIDDHFLFDKPVSPLLLASGM	0.9958		3	4330.8769
1983	KCRM_MOUSE	381	89.76	31	6554	K.ETPSGFTLDDVIQTGVDNPGHPFIMTVGCV	0.9958		3	4432.8221
						K.LSVEALNSLTGEFK.G	0.9944		1	1508.7117
						R.LGSSEVEQVQLVVDGVK.L	0.9958		2	1787.0202
						K.GGDDLDPNYVLSSR.V	0.9958		2	1508.5847
						R.GTGGVDTAAVGAVFDISNADR.L	0.9958	1,2		1994.1253
						K.GQSIDDMIPAQK.-	0.9958	1,2		1303.473
						K.DLFDPIIQDR.H	0.9909	1,2		1232.3788
						K.FEEILTR.L	0.9958		1	908.0422
						K.LNYKPQEEYPDLSK.H	0.9958		2	1724.9079
						K.RGTGGVDTAAVGAVFDISNADR.L	0.9944		2	2150.3127
						K.TDLNHENLK.G	0.9958	1,2		1084.1741
						R.FCVGLQK.I	0.9958		1	851.9873
						K.LANLSK.H	0.9944		1	645.777
						K.SFLVWVNEEDHLR.V	0.9958		2	1644.8271
						R.DKETPSGFTLDDVIQTGVDNPGHPFIMTVG	0.9944		3	4676.0848
						K.SMTEQEQQQLIDDHFLFDKPVSPLLLASGM	0.9958		3	3647.1555
						K.GYTLPPHCSR.G	0.9958		2	1188.2945
						R.HGGYKPTDK.H	0.9944		2	1003.1026
						K.HKTDLNHENLK.G	0.9958		2	1349.4893
						K.SMTEQEQQQLIDDHFLFDKPVSPLLLASGM	0.9944		3	4387.9289
						K.VLTPDLYNK.L	0.9958		1	1063.2389
						K.LMVEMEK.K	0.9958		1	880.1054
						K.FKLNYKPQEEYPDLSK.H	0.993		2	2000.2585
						R.GGVHVKLANLSK.H	0.9958		2	1223.4611
						R.RFCVGLQK.I	0.9952		2	1008.1748
						K.IEEIFK.K	0.9958		1	778.9237
						K.IEEIFKK.A	0.9944		1	907.0978

						K.HNNHMAK.V	0.9958	1,2		851.9585
						K.AGHPFMWNEHLGYVLTCPSNLGTGLR.G	0.9958		2	2929.2916
						R.VISMEK.G	0.9924		1	706.8755
						K.GKYYPLK.S	0.9958		1	869.0513
1984	KCRS_MOUSE	419	71.12	29	9081	K.RGTGGVDTAAVADVYDISNIDR.I	0.9956		2	2266.4295
						R.LGYILTCPSNLGTGLR.A	0.9958		1	1735.9873
						R.REVENVAITALEGLK.G	0.9958	1,2		1642.8931
						R.GTGGVDTAAVADVYDISNIDR.I	0.9958		2	2110.242
						R.EVENVAITALEGLK.G	0.9958		2	1486.7056
						K.TFLIWINEEDHTR.V	0.9958		2	1674.8534
						K.VPPPLPQFGR.K	0.9958		2	1108.3286
						K.LSEMTEQDQQR.L	0.9958		1	1365.4577
						K.TVGMVAGDEESYEVFADLFDPVIK.L	0.9958		2	2632.9417
						K.MTPSGYTLDQCIQTGVDNPGHPFIK.T	0.9958		2	2778.0749
						R.LIDDHFLFDKPVSPLLTCAGMAR.D	0.9958		2	2618.0321
						R.SEVELVQIVIDGVNYLVDCEK.K	0.9958		2	2422.7009
						K.HNNCMAECLTPTIYAK.L	0.9958		2	1924.111
						K.ITHGQFDER.Y	0.9958		1	1103.1796
						R.GIWHNYDK.T	0.9958		1	1033.1313
						R.GWEFMWNERLGYILTCPSNLGTGLR.A	0.9958		3	2972.357
						K.LFPPSADYPDLR.K	0.9958		1	1391.5663
						R.GWEFMWNER.L	0.9958		1	1255.3929
						R.GLSLPPACSR.A	0.9958		2	1058.1889
						K.LFPPSADYPDLRK.H	0.9913		2	1519.7404
						R.EVENVAITALEGLKGDLAGR.Y	0.9958		2	2056.3238
						R.SEVELVQIVIDGVNYLVDCEKK.L	0.9958		2	2550.875
						K.HPTDLDASK.I	0.9944		1	984.0538
						R.EQHKLFPPSADYPDLR.K	0.9958		2	1914.1277
						K.LRHNGYDPR.V	0.9924		1	1128.2357
						R.KHNNCMAECLTPTIYAK.L	0.9958		2	2052.2851
						K.HPTDLDASKITHGQFDER.Y	0.9958		2	2068.2101
						R.VMKHPTDLDASK.I	0.9958	1,2		1342.553
						R.YYKLSEMTEQDQQR.L	0.9958		2	1819.9837
1985	KCRU_MOUSE	418	11.96	2	23	K.SEVELVQLVIDGVNYLIDCER.R	0.9958		2	2464.7412
						K.TTPTGWTLDQCIQTGVDNPGHPFIK.T	0.9958		2	2785.0515
1986	KCTD4_MOUSE	259	6.56	1	2	R.ENQLLAQEAEFFQLK.G	0.9958		2	1809.0288
1987	KCY_MOUSE	196	49.49	7	58	K.YGYTHLSAGELLR.D	0.9956		2	1480.6634

						K.RIQTYLESTKPIIDLYEEMGK.V	0.9958		2	2528.9233
						R.IQTYLESTKPIIDLYEEMGK.V	0.9958		2	2372.7358
						K.SVDEVFGEVVK.I	0.9958		2	1208.3538
						K.IVPVEITISLLK.R	0.9958		1	1325.6751
						R.KNPDSQYGELIEK.Y	0.9939	1,2		1521.6671
						-.MKPLVVFVLGGPGAGK.G	0.9958		2	1570.9769
1988	KEAP1_MOUSE	624	2.56	1	5	R.HHRSALGITVHQGK.I	0.9924		1	1541.7561
1989	KERA_MOUSE	351	1.99	1	2	R.NMPPR.L	0.9958		1	614.7405
1990	KGP2_MOUSE	762	3.94	2	2	K.QTVAIAELTEELQSK.C	0.9944		1	1660.862
						R.QNPTERLGNLK.N	0.9924		1	1270.4312
1991	KGUA_MOUSE	198	52.02	5	19	K.LFQEHSSIFGFSVSHTTR.N	0.9958		2	2081.2951
						R.NPRPGEEDGKDYYFVTR.E	0.9958		2	2044.1876
						R.DIAAGDFIEHAEFSGNLYGTSK.E	0.9958		2	2343.5114
						K.KTDLCPIYIFVQPPSLDVLEQR.L	0.9958		2	2633.0259
						K.EPGLFDLVIINDDLDK.A	0.9947		2	1817.0459
1992	KHDR1_MOUSE	443	4.97	1	4	K.DSLDPSFTHAMQLLSVEIEK.I	0.9958		2	2261.5519
1993	KHK_MOUSE	298	14.09	2	2	R.GGNASNSCTVLSLLGAR.C	0.9958		2	1677.8211
						R.CAFMGSLAPGHVADFLVADFRQR.G	0.9958		2	2566.9061
1994	KI13A_MOUSE	1749	3.09	3	6	K.LEESEKLIK.E	0.9958		1	1089.2743
						R.QLESMGISLETSGIKVGDDK.C	0.9909		2	2108.3686
						K.CYLVNLNADPALNELLVYYLK.D	0.9958		2	2499.8756
1995	KI21A_MOUSE	1672	3.05	4	4	R.GGILKLWNVDTFVPVGEMR.G	0.9932		2	2132.5285
						R.EIAQLKK.D	0.9944		1	830.0153
						K.LQQDVMEMKK.T	0.9958		1	1250.514
						R.QREELTK.R	0.9958		1	904.011
1996	KI26A_MOUSE	1881	5.05	3	4	R.GGEASGGPLCLSLSALGSVILALVNGAK.H	0.9958		3	2612.9928
						R.NSPAKGVGATKPPAGGAK.G	0.9958		1	1608.8381
						R.AVVLDPDRSAPGLSGDPDYSSSSEQSCDT	0.9944		3	4430.7207
1997	KI26B_MOUSE	2112	5.3	5	8	K.YEWLMKELEATR.Q	0.9958		2	1569.8157
						R.ENAYSSEEGVK.C	0.9924		2	1213.2432
						K.SLPQSVGQSSNLPPSGK.H	0.9952		2	1683.8589
						R.YNADKPAASSVPAPQGSCVASETSTGTSV	0.9958		3	3591.8359
						K.SYTMIGRDDSMQNLGIIPCAISWLFK.L	0.9958		3	3018.4818
1998	KIF11_MOUSE	1052	4.37	3	23	R.NIQVVVRCRPFNLAER.K	0.9948		2	1972.2669
						K.AGSLELDKTIK.T	0.9958		1	1175.3678
						R.AKNIMNKPEVNQK.L	0.9948		2	1514.7832
1999	KIF17_MOUSE	1038	6.94	3	7	R.DSMLFQQLLEQVQPLIR.R	0.9958		2	2059.4314

						K.AILAQQMGPGNLSALLSTQTPPGPVQSEEI	0.9944	3	3064.4809
						K.INLSLSALGNVISALVDGR.C	0.9944	3	1913.2248
2000	KIF22_MOUSE	660	5.45	2	2	K.QRESSNQIQLLK.K	0.9958	1	1444.631
						R.HLLEGQNASVLAYGPTGAGK.T	0.9911	2	1984.2193
2001	KIF24_MOUSE	1356	3.02	2	3	K.AHPLASHVPNVPFTSGPK.T	0.9958	1	1857.1221
						R.TYCPLTPEQAQQVIIRAHK.E	0.9958	2	2254.5603
2002	KIF27_MOUSE	1394	3.01	3	5	R.QELEMLEEDLKK.R	0.9952	2	1505.7235
						R.DIPNTQQIIIGR.D	0.9958	2	1368.576
						K.ISEQVQALQRER.D	0.9958	1	1457.6297
2003	KIF3C_MOUSE	796	2.14	1	2	K.YLIIENFIPPEEKNK.I	0.9958	2	1848.1491
2004	KIF5A_MOUSE	1027	3.21	2	2	K.EVLQALEELAVNYDQK.S	0.9913	2	1863.0746
						R.HVAVTNMNEHSSR.S	0.9958	2	1482.614
2005	KIFC2_MOUSE	792	4.67	2	2	K.FAERVGQVELGPAR.R	0.9924	1	1529.7391
						R.VQHLTLENEALKQSLSLTR.D	0.9958	2	2181.4972
2006	KIME_MOUSE	395	5.82	1	3	R.VIHGNPSGVDNAVSTWGGALR.F	0.9958	2	2108.3213
2007	KINH_MOUSE	963	10.8	7	47	K.SLSALGNVISALAEGSTYVPYR.D	0.9958	2	2269.5596
						R.FRPLNESEVNR.G	0.9958	2	1361.5003
						K.KMEENEK.E	0.9958	1	908.0142
						K.LHDPEGMGIIPR.I	0.9958	2	1335.5639
						R.NTIQWLENELNR.W	0.9958	2	1530.6805
						R.FVCSPDEVMDTIDEGK.S	0.9958	2	1842.9784
						R.SHSIFLINVK.Q	0.9958	2	1158.3861
2008	KIRR3_MOUSE	778	4.24	1	2	R.VGAGEREVTLTVNGPPIISSTQTQHALHGE	0.9958	3	3228.5895
2009	KIT_MOUSE	975	5.54	2	2	R.DPAKLFLVGLPLFGK.E	0.9924	1	1615.9994
						R.QETLTISSARVDDSGVFMCYANNTFGSAN	0.9958	3	3801.1397
2010	KLC1_MOUSE	537	19.18	6	30	R.DHPAVAATLNNLAVLYGK.R	0.9958	2	1868.1429
						K.NEHNSILQSLLETLK.C	0.9958	2	1739.9664
						K.YKDAANLLNDALAIR.E	0.9958	2	1661.8986
						K.KYDDDISPSEDK.D	0.9944	1	1412.4497
						K.YDDDISPSEDK.D	0.9958	1	1284.2757
						K.DSDSSKEPLDDLFPNDEDEPGQGIQHSDS	0.9958	3	3702.7509
2011	KLC2_MOUSE	599	5.34	2	2	K.ACKVDSPTVNTTLR.T	0.9944	2	1562.7295
						K.LQGGGPQEPNSRMK.R	0.9958	2	1499.6849
2012	KLF15_MOUSE	415	6.51	1	2	R.ATLGSGGGSGGIGDSSGPVTWGSWR.R	0.993	2	2307.4411
2013	KLF7_MOUSE	301	6.31	1	2	K.VGGVAAAAAVTPAGAVK.S	0.9924	1	1410.6567
2014	KLHL1_MOUSE	751	3.33	2	8	K.LFVIGGRDGLK.T	0.9958	1	1175.4166
						R.RLQFGVAVIDDK.L	0.9958	1	1361.584

2015	KLHL2_MOUSE	593	6.91	2	2	R.AGMVYMAGLVFAVGGFNGSLRVR.T	0.9912	2	2373.8395
						K.LMVVVGGQAPKAIR.S	0.9944	1	1439.8027
2016	KLHL7_MOUSE	586	3.58	1	2	R.YHLLSPEDREELAGGTRPR.R	0.9958	2	2197.4153
2017	KLHL9_MOUSE	617	9.4	2	5	K.YVNNFILKNFPALLNTGEFLK.L	0.9958	2	2456.8901
						K.SLAPMDAPRYQHGIAVIGNFLYVVGGQSN\	0.9944	3	3584.0435
2018	KLK1_MOUSE	261	9.58	1	9	K.YQCGGILLNANWVLTAAHCHNDK.Y	0.9943	2	2656.8927
2019	KNG1_MOUSE	661	23	9	46	K.EVLGHSIAQLNAENDHPFYYK.I	0.9958	2	2446.6812
						K.KATSQVVAGTK.Y	0.9958	2	1090.2651
						R.DAETEQGPTHGHGWLHEK.Q	0.9958	2	2030.1203
						R.FPSLHGDCVALPNGDDGECR.G	0.9958	2	2217.2886
						R.DIPVDSPELKEVLGHSIAQLNAENDHPFYYI	0.9958	3	3540.9109
						R.ENEFFIVTQTCK.I	0.9958	2	1516.6569
						K.AYFPCIGCVHAISTDSPDLEPVLK.H	0.9958	2	2690.9851
						K.HLGQSLDCNANVYMRPWENK.V	0.9943	2	2433.6697
						K.ERFPSLHGDCVALPNGDDGECR.G	0.9931	2	2502.5916
2020	KNTC1_MOUSE	2207	1.95	2	3	K.HYCNADTGRLLFVVCQK.L	0.9958	2	2082.2989
						R.SLQLFLIFDTDVDVVGLCQEGK.F	0.9944	2	2497.8139
2021	KPB1_MOUSE	1241	5.24	4	4	R.ILSHIYSSLGCNSR.M	0.9944	2	1607.7729
						R.RFSTVPKPDVVVQVSILAETEEIK.A	0.9958	3	2686.121
						R.RLDGALNR.V	0.9958	1	915.0402
						K.HLTVGLPPEPR.E	0.9958	2	1216.4257
2022	KPB2_MOUSE	1235	4.29	3	4	R.ASADEQFFPLGQTMSNSLHSIK.S	0.9958	2	2409.6758
						K.SLNLVDSPQPLLKTTPEYDYQWPR.D	0.9924	3	2862.2115
						R.ASADEQFFPLGQTMSNSLHSIKSVR.S	0.9958	3	2752.0741
2023	KPCA_MOUSE	672	2.98	1	30	K.NLIPMDPNGLSDPYVKLK.L	0.9955	2	2015.3753
2024	KPCG_MOUSE	697	5.02	2	3	R.LGSGPDGEPTIR.A	0.9958	1	1199.3061
						R.LHISDFSFLMVLGKGSFGK.V	0.9958	2	2084.484
2025	KPRA_MOUSE	356	12.08	2	2	K.IYVMATHGILSAEAPR.L	0.9958	2	1730.0349
						R.IAIIVDDIIDDVESFVAAAEILK.E	0.9931	2	2473.8664
2026	KPRB_MOUSE	369	12.2	2	3	R.SVAAIHPSLEIPMLIPK.E	0.9958	2	1817.2402
						K.MNITKGGLVLFSANSNSSCMELSK.K	0.9958	3	2589.9479
2027	KPYM_MOUSE	531	70.62	32	2647	R.EATESFASDPILYRPVAVALDTK.G	0.9958	2	2494.804
						K.CDENILWLDYK.N	0.9958	1	1469.6001
						K.IYVDDGLISLQVK.E	0.9947	2	1463.7142
						R.LDIDSAPITAR.N	0.9958	2	1172.3238
						K.DAVLNAWAEDVDLR.V	0.9911	2	1587.7294
						K.VVEVGSK.I	0.9944	1	717.8406

						R.GDLGIEIPAEK.V	0.9958	1	1142.2945
						R.NTGIICTIGPASR.S	0.993	1,2	1360.5193
						R.APIIAVTR.N	0.9944	1	841.0415
						R.RFDEILEASDGIMVAR.G	0.9944	2	1823.0741
						K.KGVNLPGAAVDLPAVSEK.D	0.9958	2	1766.0477
						R.AGKPVICATQMLESMIK.K	0.9958	2	1878.2619
						R.LNFSHGTHEYHAETIK.N	0.9958	2	1885.0458
						K.GDVVIVLTGWRPGSGFTNTMR.V	0.9958	2	2264.6073
						R.AEGSDVANAVLDGADCIMLSGETAK.G	0.9934	2	2495.6839
						K.GADFLVTEVENGGSLGSK.K	0.9958	1,2	1780.9292
						K.ITLDNAYMEK.C	0.9958	1	1198.3765
						K.GVNLPGAAVDLPAVSEK.D	0.9958	1	1637.8736
						R.FDEILEASDGIMVAR.G	0.9958	2	1666.8866
						R.GIFPVLCK.D	0.9958	1	934.1327
						K.FGVEQDVDMVFASFIR.K	0.9958	2	1861.1224
						R.LAPITSDPTEAAAVGAVEASFK.C	0.9937	2	2146.4021
						R.EAEAAIYHLQLFEELR.R	0.9958	2	1933.1711
						R.RLAPITSDPTEAAAVGAVEASFK.C	0.9958	2	2302.5895
						R.MQHLIAR.E	0.9912	2	869.0727
						R.VNLAMDVGK.A	0.9958	1	947.1376
						R.AEGSDVANAVLDGADCIMLSGETAKGDYP	0.9958	3	3496.7909
						K.NVREATESFASDPILYRPVAVALDTK.G	0.9944	2	2864.2279
						K.DIQDLK.F	0.9958	1	731.8241
						K.EKGADFLVTEVENGGSLGSK.K	0.9958	2	2038.2188
						K.KPRPTRAEGSDVANAVLDGADCIMLSGET/	0.9944	3	3231.5714
						K.GADFLVTEVENGGSLGSKK.G	0.9958	2	1909.1033
2028	KRR1_MOUSE	380	2.89	1	3	K.NIHPIYNIK.T	0.9958	1	1112.317
2029	KRT84_MOUSE	603	2.99	1	12	R.LQAERNHLQDILEGFK.K	0.9958	2	1912.1557
2030	KS6A1_MOUSE	724	3.59	1	2	R.EASFVLHTISKTVEYLHSQGVVHR.D	0.9943	2	2739.1063
2031	KS6A2_MOUSE	733	3.96	2	2	R.NPCNRLGAGVDGVEEIK.R	0.9958	1	1828.9861
						K.EATDHDKR.A	0.9924	1	972.0024
2032	KSYK_MOUSE	629	5.41	1	2	K.QTWNLQGQALEQAIISQKPQLEKLIATTAHE	0.9958	3	3618.1277
2033	KT3K_MOUSE	309	11.97	2	3	R.MFEGEMASLTAILK.T	0.9958	1	1541.8611
						K.VVDAPGGGSMLVMEHLDMR.Y	0.9958	2	2015.3681
2034	KTN1_MOUSE	1327	16.5	13	49	K.QKPSLEEQVIKESDASK.I	0.9952	2	1917.1235
						R.LFPTVSVPSNLNYSEWLR.G	0.9958	2	2123.4161
						K.FQQVQEQMEAEIAHLK.Q	0.9958	2	1930.1859

						K.EITDLCNELESLK.N	0.9958	1	1564.696
						K.VEPVLVTK.Q	0.9958	1	885.0917
						K.HQQASFPSQEELQTVISEK.E	0.9958	2	2187.3709
						K.SVEELLEVELLKVANK.E	0.9958	2	1814.1296
						K.AHQLSVTSQVQELQNLLR.G	0.9958	2	2065.3371
						K.GELSGLLHQLQEK.E	0.9958	2	1452.6506
						K.ESDASKIPGK.K	0.9924	1	1032.1387
						K.AQIQQFHSQIAAQTSASVLAEELHK.V	0.9958	2	2737.0446
						R.EIIDMIKPDHVEGIQK.S	0.9958	2	1866.1828
						R.LLEEQLQHEVASK.M	0.9958	2	1524.7141
2035	KU70_MOUSE	608	5.92	1	2	K.QHYLRPSLFVYPEESLVSGSSTLFSALLTK(	0.9958	3	3888.4187
2036	KU86_MOUSE	732	6.56	3	3	K.KEDIQK.E	0.9944	1	760.8656
						K.DQYQNITVCRHLMLPDFDLLEDIGNK.I	0.9958	3	3149.5116
						K.TLFPLTEVIK.K	0.9958	1	1161.4271
2037	KV5A6_MOUSE	115	17.39	1	2	K.ASQDINSYLSWFQQKPGK.S	0.9958	2	2098.3226
2038	KV5A9_MOUSE	115	14.78	1	4	R.ASQSIGTSIHWYQQR.T	0.9958	2	1762.9224
2039	KV5AA_MOUSE	108	16.67	1	2	K.LLIYYTSSLHSGVPSR.F	0.991	2	1794.0605
2040	KV5AB_MOUSE	108	30.56	2	4	R.LHSGVPSR.F	0.9944	1	852.9688
						R.ASQDISNYLNWYQQKPDGTVK.L	0.9958	2	2456.6739
2041	KY_MOUSE	661	6.2	2	2	R.QFENSMYHKSEFYNK.G	0.9944	1	1953.1358
						K.SGLNELVSDLLQEAHSDLERVR.A	0.9924	2	2481.7251
2042	L2HDH_MOUSE	464	3.66	1	2	R.NAPSPAATSSLAISR.M	0.9958	2	1443.5999
2043	LA_MOUSE	415	4.34	1	7	K.ICHQIEYYFGDFNLPR.D	0.9958	2	2073.2812
2044	LACB2_MOUSE	288	20.83	3	5	K.ANIIYPGHGPVIHNAEAK.I	0.9958	2	1902.1631
						R.VLGCNPGPMTLQGTNTYLVGTGSRR.I	0.9958	2	2650.9788
						K.MAEHNLLLHLR.K	0.9958	2	1347.6213
2045	LACE1_MOUSE	480	10.83	3	19	K.ALAVCHGPLDHYDFLIK.S	0.9958	2	1970.2445
						K.NGVVVVATSNRPPEDLYK.N	0.9912	2	1959.2095
						K.QNDLTSPRILK.V	0.9944	1	1285.4862
2046	LACTB_MOUSE	551	21.96	7	12	R.HYASHTGGAVGASSVLLVLPEELDSEAVN	0.9958	3	3166.4717
						K.GGKNNEK.S	0.9958	1	746.7984
						R.GIIVSIICNMQSVGLNSTALKIALEFDK.D	0.9958	3	3036.5635
						R.LLISHLSGIR.H	0.9958	2	1109.3573
						K.LDLDLPVQHYVPEFPEK.E	0.9958	2	2040.3233
						K.LDLDLPVQHYVPEFPEKEYEGEK.V	0.9958	2	2776.0717
						R.VPCKPETVMR.I	0.9958	2	1217.4352
2047	LAD1_MOUSE	528	6.25	2	2	R.YHTAIQRSESVR.S	0.9958	2	1447.5937

						R.DSLGPEQTSSQPLVPKK.K	0.9958	2	1812.03
2048	LAMA1_MOUSE	3084	1.98	2	2	R.TLNADLMTLSHRDLR.D	0.9958	3	1757.0178
						R.CADGYYGNPTVPGGTCVPCNCSGNVDPLI	0.9958	3	4547.6399
2049	LAMA2_MOUSE	3106	4.73	5	8	R.KDFMIVLTNLGEILIQITYNLGMDAIFR.L	0.9958	3	3243.8904
						K.NGVEYHYVTITLDLQQVFQIAYVIVKAANSP	0.9944	3	4618.2951
						K.EGNDILDEANQLLGEINSVIDYVDDIK.T	0.9958	2	3006.247
						R.ISEISMEVAEPGHVLAGSPPAHLIER.C	0.9958	2	2741.1345
						R.HCDECKPETFGLQLGR.G	0.9958	2	1948.0748
2050	LAMA3_MOUSE	3333	2.88	5	6	R.MLINMNK.H	0.9958	1	864.109
						K.QMARPGGEGTDLPVGDWSR.E	0.9944	2	2030.2225
						R.QCDRCLSGAYDFPYCQGSGSVCHPAGTLI	0.9944	3	4364.4786
						R.EANGITSEVLDGLNPIQTDLGRIK.D	0.9958	3	2554.8601
						R.EANGITSEVLDGLNPIQTDLGR.I	0.9958	2	2313.5266
2051	LAMA4_MOUSE	1816	3.85	4	6	K.LSDLQESINQALDHVR.D	0.9958	2	1839.0153
						R.LNDAVK.Q	0.9958	1	659.7605
						K.ESMDTIDQATHLVEQAHNMR.D	0.9958	2	2327.5488
						K.KIPFTDIYIGGAPQEVLQSR.T	0.9958	2	2233.5724
2052	LAMA5_MOUSE	3718	1.32	2	2	R.VFADGAPHYVAFYSNVTGVWLYVDDQLQL	0.9944	3	3516.9775
						R.FGFNPLEFENFSWR.G	0.9912	2	1790.975
2053	LAMC1_MOUSE	1607	6.66	5	17	R.VSVPLIAQGNSYPSETTVK.Y	0.9958	2	1991.2487
						R.SRVESTEQLIEIASR.E	0.9958	2	1718.9047
						R.LHEATDYPWRPALSPFEFQK.L	0.9958	2	2433.7282
						K.LQELESLIANLGTGDDMVTDQAFEDR.L	0.9958	2	2882.1255
						K.AEQQTADQLLARADAAK.A	0.9924	1	1800.9664
2054	LAMC2_MOUSE	1191	0.67	1	2	K.NLENIR.D	0.9944	1	758.8527
2055	LAMC3_MOUSE	1581	3.04	2	5	R.YQEVQAAQTALGIAVAEALPKAEK.A	0.9958	3	2500.8547
						K.RTYASGPWEPYQYYSASCQK.T	0.9952	2	2443.6001
2056	LAMP1_MOUSE	406	7.39	2	2	K.MLSLNVFSVQVQAFK.V	0.9958	2	1712.06
						K.ALQATVGNSYK.C	0.9958	1	1152.2926
2057	LANC1_MOUSE	399	23.31	4	10	K.IPQSHIQQICENILTSGENLSR.K	0.9958	2	2538.7863
						K.LHSLVKPSVDFVCR.L	0.9958	2	1657.9195
						R.TADTPFSLFEGMAGTIYFLADLLVPTK.A	0.9958	2	2920.3901
						K.EERYLCDAQQCADVIWQYGLLK.K	0.9944	2	2760.0077
2058	LAP2_MOUSE	1402	8.84	5	7	K.LSLPDNDLTTLPASIANLINLR.E	0.9958	2	2365.7325
						R.QEDENFNSLLQNGVNLNNSPEEKFK.I	0.9958	2	2909.0954
						K.SATLLYDQPLQVFTAASSSSELLSGTK.A	0.9944	3	2816.1345
						K.LPDGFSQLLNLTQLYLNDAFLEFLPANFGR	0.9924	3	3428.9121

						R.EQLIDYLMLK.V	0.9958		2	1266.5384
2059	LAP2A_MOUSE	693	7.5	3	7	R.YGVNPGPIVGTTR.K	0.9924		1	1331.5143
						R.LEDKDDLDVTELSNEELLDQLVR.Y	0.9958		2	2702.9293
						R.NRPPLAAGANSK.G	0.9949		2	1196.3518
2060	LAP4_MOUSE	1612	3.16	2	4	R.VLSINGVDMTEARHDHAVSLLTAASPTISLL	0.9958		3	3632.1699
						R.HCSLQVVPEEIYR.Y	0.9948		2	1630.8071
2061	LAPM5_MOUSE	261	27.97	2	2	R.MADLLSSFLLIGVLFIISISLLFGVVK.N	0.9958		2	2910.6551
						K.LARPRPGPSKVPLMTLQLLDFCLSILTLCSS	0.9944		3	4872.7544
2062	LARG2_MOUSE	690	9.28	3	3	R.YDPRFVGFGWNK.V	0.9958		1	1486.6726
						K.AELLTLLDAGSLHTFRYHEWPQGHSSTDYS	0.9958		3	3589.9053
						R.KNPLHLHLITDAVAR.N	0.9917		2	1699.0091
2063	LARP1_MOUSE	1072	7.37	4	5	K.WTSQHSDTLTLRK.-	0.9944		2	1573.7489
						K.VGDFGDAVNWPTPGEIAHK.S	0.9924		2	2011.201
						K.HAPPPAAVNGQPPPEPSAPAK.V	0.9958		2	2031.2785
						R.FSHPTALPQQLPSQQLMSK.D	0.9958		2	2139.4772
2064	LARP5_MOUSE	741	3.24	2	2	K.SVQVNGAATELR.K	0.9958		2	1245.3781
						R.KPSYAEICQR.T	0.9958		2	1252.3789
2065	LARP7_MOUSE	570	4.91	1	2	K.DILATISEVVYIDLLEGDTECHARFK.T	0.9944		3	3009.3491
2066	LASP1_MOUSE	263	3.04	1	2	K.VNCLDK.Y	0.9924		1	748.8205
2067	LASS2_MOUSE	380	4.74	1	2	R.APPNATLEHFYQTSGK.Q	0.9958		2	1761.9316
2068	LBH_MOUSE	105	40	2	7	K.DRLPSIVVEPTEGEVESGELR.W	0.9958		2	2312.5389
						R.KDGLSYQIFPDPSDFDR.C	0.9958		2	2001.1595
2069	LBN_MOUSE	1220	0.82	2	4	K.LDNDLK.Q	0.9958		1	717.7972
						K.QKLDNDLK.Q	0.9958		1	974.102
2070	LBXCO_MOUSE	964	6.95	2	2	R.GEDGLTLDVTGTQLVEKDIENLAR.E	0.9944		3	2587.8437
						K.STAVAAALGPAASYLCTPETHEPDKEDNHS	0.9944		3	4144.3314
2071	LC7L2_MOUSE	392	7.4	2	3	K.SHLLNCCPHDVLSGTR.M	0.9958		2	1867.0039
						K.LHLGFIEIR.E	0.993		2	1098.3335
2072	LCAP_MOUSE	1025	9.95	6	32	R.NMIENSMFEEEPDVVDLAK.E	0.9958		2	2211.4635
						K.KYFAATQFEPLAAR.S	0.9958		2	1613.8565
						K.SSVPAEEGLIQDEFSESVK.M	0.9958		2	2052.1993
						R.NPYVLSDK.D	0.9958		1	936.0526
						R.ANLINNIFELAGLGK.V	0.9958		2	1587.8595
						K.EPCLHPLEPDEVEYEPR.G	0.9958		2	2110.2507
2073	LDB3_MOUSE	723	51.73	23	300	K.ASGAGLLGGSLPVK.D	0.9943	1,2		1227.4465
						R.TPLCGHCNNVIR.G	0.9958		2	1441.5622
						R.CYEQFFAPICAK.C	0.9958		2	1534.6839

						K.DLAVDSASPVYQAVIK.T	0.9924	1,2		1676.9072
						R.QYNNPIGLYSAETLR.E	0.9958		2	1739.9255
						K.DFNMPLTISR.I	0.9944		1	1194.3911
						K.AAQSQLSQGDLVVAIDGVNTDTMTHLEAQ	0.9958		3	3256.5689
						R.GAPAYNPTGPQVTPLAR.G	0.9958		2	1710.9303
						K.KPFGNSLFHMEDGEPYCEK.D	0.9944		2	2286.4866
						K.HAHAINV.-	0.9944		1	761.8588
						R.ILAQMTGTEYMQDPDEEALR.R	0.9958		2	2312.5715
						K.DPALDTNGSLATPSPSPEAR.A	0.9958		2	1997.1259
						K.TSLADVCFVEEQNNVYCER.C	0.9958		2	2334.4335
						R.SWHPEEFNCAYCK.T	0.9958		2	1728.7902
						K.DYINLFSTK.C	0.9958		1	1101.2444
						K.CHGCDFPVEAGDK.F	0.9958		2	1492.5171
						R.FPASSR.T	0.9944		1	664.7391
						R.QTWHTTCFVCAACK.K	0.9958		2	1770.8807
						K.SASYNLSLTLQK.S	0.9958		2	1325.5046
						R.GPFLVAMGR.S	0.9958	1,2		948.1711
						R.ASPGALEFGDTFSSSFSQTSVCSPLMEAS	0.9958		3	4115.5643
						K.TQSKPEDEADEWAR.R	0.9958		2	1662.7099
						K.IMGEVMHALR.Q	0.9958		2	1157.4345
2074	LDHA_MOUSE	332	71.99	21	701	K.GLYGINEDVFLSVPCILGQNGISDVVK.V	0.9958		2	2908.2873
						K.DLADELALVDVMEDK.L	0.9958		1	1676.8763
						K.SLNPELGTDADKEQWK.E	0.9958		2	1831.9769
						K.GYTSWAIGLSVADLAESIMK.N	0.9958		2	2113.4333
						R.VIGSGCNLDSAR.F	0.9958	1,2		1249.3324
						K.QVVDSAYEVIK.L	0.9929	1,2		1251.4222
						K.GEMMDLQHGSLFLKTPK.I	0.9958	1,2		1933.2911
						K.GEMMDLQHGSLFLK.T	0.9958		2	1606.8952
						K.LKGEMMDLQHGSLFLK.T	0.9958		2	1848.2287
						K.SADTLWGIQK.E	0.9924		1	1119.2627
						R.NVNIFK.F	0.9958		1	734.8735
						K.LLIVSNPVDILTYVAWK.I	0.9958		2	1945.3525
						K.VTLTPEEEAR.L	0.9944		1	1145.2548
						R.VHPISTMIK.G	0.9958		1	1026.2823
						K.DLADELALVDVMEDKLK.G	0.9958		2	1918.2098
						K.DQLIVNLLK.E	0.9958		1	1056.2908
						K.DQLIVNLLKEEQAPQNK.I	0.9958		2	1981.2566

						K.DYCVTANSK.L	0.9958	1	1058.0991
						K.SLNPELGTDADK.E	0.9958	1	1260.3434
						K.ITVVGVGAVGMACAISILMK.D	0.9958	2	1991.4647
						R.RVHPISTMIK.G	0.9958	2	1182.4698
2075	LDHB_MOUSE	334	70.66	20	2057	K.SLADELALVDVLEDK.L	0.9958	1	1630.8327
						K.GMYGIENEVFLSLPCILNAR.G	0.9958	2	2297.6405
						K.LIASVADDEAAVPNNK.I	0.9958 1,2		1627.7917
						K.SADTLWDIQK.D	0.9952 1,2		1177.2994
						K.GYTNWAIGLSVADLIESMLK.N	0.9958	2	2182.5396
						R.GLTSVINQK.L	0.9958	1	960.1185
						K.LKDDEVAQLR.K	0.9924	1	1187.3384
						K.SLADELALVDVLEDKLK.G	0.9958	2	1872.1663
						K.GEMMDLQHGSLFLQTPK.I	0.9958	2	1933.2477
						K.YSPDCTIIVVSNPVDILTYVTWK.L	0.9958	2	2685.0553
						K.DDEVAQLR.K	0.9958	1	946.0049
						K.MVVDSAYEVIK.L	0.9958	1	1254.484
						R.NVNVFK.F	0.9924	1	720.8467
						K.ITVVGVGQVGMACAISILGK.S	0.9958	2	1974.3759
						K.IVADKDYSVTANSK.I	0.9958	2	1511.672
						K.LKGEMMDLQHGSLFLQTPK.I	0.9958	2	2174.5812
						R.IHPVSTMVK.G	0.9958	1	1012.2555
						K.IVVVTAGVR.Q	0.9944	1	914.1362
						K.FIIPQIVK.Y	0.9944	1	958.2321
						K.YSPDCTIIVVSNPVDILTYVTWKLSGLPK.H	0.9924	3	3280.795
2076	LDHD_MOUSE	484	17.77	5	26	K.AVVGSPHVSTASAVR.E	0.9958	2	1438.6267
						R.ALALGGTCTGEHGIGLGK.R	0.9958	2	1712.9097
						R.GSQGGLSQDFVEALK.A	0.9958	1	1536.6818
						K.RQLLQEEVGPVGVETMR.Q	0.9958	2	1942.2408
						R.HNAWYAALALSPGSK.A	0.9958	2	1586.7905
2077	LDLR_MOUSE	864	7.64	2	2	R.GNEEQPHGMRFLSIFFPIALVALLVLGAVLL	0.9958	3	3709.4766
						R.LTGSDVNLVAENLLSPEDIVLFHKVTQPR.G	0.9958	3	3206.6665
2078	LEG1_MOUSE	135	67.41	6	116	K.DSNNLCLHFNPR.F	0.9912	2	1487.581
						R.LNMEAINYMAADGDFK.I	0.9958	2	1804.0425
						R.FNAHGDANTIVCNTK.E	0.9958	2	1662.7655
						K.SFVLNLGK.D	0.9958	1	878.0593
						R.EPAFPFQPGSITEVCITFDQADLTIK.L	0.9944	2	2926.2587
						K.LPDGHEFK.F	0.9944	1	943.0471

2079	LEGLA_MOUSE	172	43.02	3	7	R.VFVDGHQLFDFYHR.I	0.9958	2	1780.9829
						R.GEEQSAIPYFPFIPDQPFR.V	0.9957	2	2239.4919
						K.VLVMGIVDLNPESFAISLTCGDSEDPPADV/	0.9958	3	3717.1862
2080	LEPR_MOUSE	1162	2.24	1	23	K.YQFSLYPVFMEGVGKPKIINGFTK.D	0.9958	2	2765.2855
2081	LETM1_MOUSE	738	28.86	14	314	R.VQQMIGQIDGLITQLETTQQDGK.L	0.9924	2	2545.8676
						K.KLEEGGPVYSPPAQVVVR.K	0.9958	2	1926.223
						K.LGPSQSTPTGESVISITELISAMK.Q	0.9958	2	2447.8035
						K.RVQQMIGQIDGLITQLETTQQDGK.L	0.9958	2,3	2702.0551
						K.EDVQISTTQVAEIVATLEK.E	0.9909	2	2075.3208
						K.DIQPEVAEATLPGRPGPEPQPPVDDVILPS	0.9958	3	4602.1926
						K.EDVQISTTQVAEIVATLEKEEK.I	0.993	2	2461.7259
						K.LISLTSALDDNKDGNINIDDLVK.V	0.9944	2,3	2487.7667
						K.AKLEATLQEEAAIQQEHLEELK.R	0.9958	2	2522.815
						K.DIQPEVAEATLPGRPGPEPQPPVDDVILPS	0.9958	3	5259.9141
						K.LEATLQEEAAIQQEHLEELK.R	0.9958	2	2323.5621
						K.GEEITKEEIDILSDACSK.L	0.9958	2	2038.1793
						K.VIDLVNK.E	0.9958	1	800.9737
						K.LEATLQEEAAIQQEHLEELKR.A	0.9958	2	2479.7496
2082	LGI4_MOUSE	537	6.89	2	2	R.FRPEEELSAPSVVSCKPLVLGPR.L	0.9944	3	2568.9421
						R.CLILVWDYSLQRFRPEEELSAPSVVSCKPL	0.9958	3	4116.7254
2083	LGMN_MOUSE	435	20.23	4	19	K.DYTGEDVTPENFLAVLR.G	0.9958	2	1940.1168
						R.GTYLGDWYSVNWMEDSDVEDLTK.E	0.9958	2	2724.9118
						R.DHVFIYFTDHGATGILVFPNDDLHVK.D	0.9958	2,3	2972.3293
						R.HQADACHAYQIIHR.N	0.9958	2	1720.854
2084	LGR4_MOUSE	951	7.78	2	4	R.VDCSGKGLTAVPEGLSAFTQALDISMNNIT	0.9958	3	4040.4977
						R.LLCFFALGLLGSAGPSGAAPPLCAAPCSCI	0.9958	3	3380.6866
2085	LGUL_MOUSE	184	55.43	7	169	K.GLAFIQDPDGYWIEILNPNK.I	0.9958	2	2304.6073
						K.RFEELGVK.F	0.9958	1	978.1362
						K.DFLLQQTMLR.I	0.9958	2	1265.5133
						R.GFGHIGIAVPDVYSACK.R	0.9958	2	1792.0105
						K.ATLELTHNWGTEDDETQSYHNGNSDPR.G	0.9958	3	3089.1314
						R.VLGLTLLQK.L	0.9958	2	985.2553
						R.FEELGVKFVK.K	0.9958	1	1196.4319
2086	LHPP_MOUSE	270	11.48	1	3	K.FRPGDEHHPEVQADGYVDNLAEAVDLLLK	0.9944	3	3249.5639
2087	LHR2A_MOUSE	793	11.22	5	6	K.AFGENAVVQLISLQK.A	0.9958	2	1617.8858
						R.CFSFGIGQGASTSLIK.N	0.9958	2	1673.8725
						R.YLLPAILNPR.Y	0.9958	2	1170.4404

						K.ELNKPVQGPLAHR.V	0.9958	2	1459.6914
						K.AHSEYEEALSQGHQAYLLEEDDYSR.D	0.9958	2	2942.038
2088	LHX1_MOUSE	406	2.96	1	4	K.DSESANVSDK.E	0.9944	1	1052.0398
2089	LHX3_MOUSE	400	4.75	1	2	K.QLETLKSAYNTSPKPAR.H	0.9958	2	1905.1613
2090	LIAS_MOUSE	373	6.17	1	8	K.VALSGLDVYAHNVETVPELQR.K	0.9958	2	2311.5999
2091	LIFR_MOUSE	1092	8.7	4	4	R.TEPVALVLLNTMLSGK.D	0.9958	2	1687.0478
						K.NLIVYWKPLPINEANGK.I	0.9958	2	1970.3219
						K.IPALSPGDHEVTINYLNGFQSK.F	0.9958	2	2401.6812
						R.NSAGSSPPSKIASMEIPNDDITVEQAVGLGI	0.9958	3	3256.5689
2092	LIMA1_MOUSE	753	3.45	1	9	K.LSLGTYASLHGRIYCKPHFNQLFK.S	0.9944	3	2852.2774
2093	LIMC1_MOUSE	1057	13.91	8	18	K.VSMNGEMAPGDEEGKEK.E	0.9923	2	1808.9729
						K.SQMFEGVATVHDSPVQVK.Q	0.9958	2	1960.2121
						R.SHSTEPNVSSFPNDPSPMK.Y	0.9958	2	2059.2146
						R.LPTPIAGLDNTILFLR.G	0.9958	2	1755.1106
						K.SAVPFNQYLPNK.S	0.9945	2	1378.5706
						R.NQQIPNPPTSTSEDVKPK.T	0.9958	2	1981.1699
						R.TSVPESIASAGTGSPSK.I	0.9924	1	1576.7007
						R.CEEEAAVLPHSRAR.Q	0.9944	1	1625.7478
2094	LIMD1_MOUSE	668	5.99	2	5	R.VFKPLVDTQPWLQDGPK.S	0.9944	2	1969.2908
						K.IHLQQQQQQQLLQEEALPR.A	0.9958	2	2329.6212
2095	LIMK2_MOUSE	638	5.64	2	4	R.CDEETQKTFLTEVK.V	0.9947	2	1728.8597
						R.YTVVGNPYWMAPEMLNGK.S	0.9944	2	2071.4163
2096	LIN41_MOUSE	855	3.98	2	2	K.NGRAGGGPGGAGGHSNHR.H	0.9958	2	1616.6559
						K.ALEDRECELLWK.V	0.9958	2	1562.7289
2097	LIPB1_MOUSE	969	3.41	2	3	R.HLATHFNLLIGAEAQHQK.R	0.991	2	2029.309
						K.LELMAEISNLK.L	0.9924	1	1261.5194
2098	LIPB2_MOUSE	882	5.33	2	2	R.TQSGNFNTDAPGMAEFR.R	0.9958	2	1843.9653
						K.EIVMATQGPSERTLSINEDEIEGSFR.K	0.9958	3	2910.1823
2099	LIPL_MOUSE	474	22.15	5	75	R.SIHLFIDSLLNEENPSK.A	0.9958	2	1957.1907
						R.AQQHYPVSAGYTK.L	0.9958	2	1450.5938
						R.LSPDDADFVDVLHTFTR.G	0.9958	2	1949.1271
						R.SIGIQKPVGHVDIYPNGGTFQPGCNIGEAIF	0.9958	2	3296.6763
						R.ITGLDPAGPNFEYAEAPSR.L	0.9957	2	2006.1791
2100	LIPS_MOUSE	759	14.36	5	11	R.LLSLMDPLLPLSVLSK.C	0.9929	2	1740.1951
						R.IIQNLDVHFWKAFWNITEIEVLSSLANMAST	0.9958	3	3949.5597
						R.SSQGVLHMPLYTSPIVK.N	0.9958	2	1858.206
						K.NPFMSPLLAPDSMLK.T	0.9958	2	1662.015

						R.ASHNLAELEAYLAALTQLR.A	0.9958	2	2085.3677
2101	LIPT_MOUSE	373	7.77	2	2	K.KFDLLLDGQFK.I	0.9958	2	1324.5627
						R.HQNPWQECNLHLMR.Q	0.9958	2	1864.0576
2102	LIS1_MOUSE	410	28.78	5	8	K.GHTDSVQDISFDHSGKLLASCSADMTIK.L	0.9958	3	3022.2795
						R.MVRPNQDGTLIASCSNDQTVR.V	0.9958	2	2363.5738
						R.TMHGHDHNVSSVAIMPNGDHIVSASR.D	0.9958	3	2771.0576
						K.LNEAKEEFTSGGPLGQK.R	0.9915	2	1805.9823
						K.TLNAHEHFVTSLDFHK.T	0.9958	2	1897.1002
2103	LITD1_MOUSE	782	8.18	2	2	K.EVIEENFAELEDQSLEIVSAHRVPNSVDEHI	0.9958	3	3592.8577
						K.SSLDDLNSLACTIEARVSEQEDAVEGLTK.D	0.9924	3	3152.3595
2104	LKHA4_MOUSE	611	22.75	9	76	K.SLSNVIAHEISHSWTGNLVTNK.T	0.9958	2	2408.6762
						R.TLTGTAALTVQSQEENLR.S	0.9958	2	1933.1259
						K.DLSSHQLNEFLAQVLQK.A	0.9958	2	1971.2205
						K.ASMHPVTAMLVGR.D	0.9924	2	1370.6709
						K.NQEIVIEISFETSPK.S	0.9907	2	1734.9439
						K.SHDQAVHTYQEHK.A	0.9958	2	1580.6567
						R.RTLTGTAALTVQSQEENLR.S	0.9958	2	2089.3133
						K.EEDLSSFSIADLK.D	0.9911	2	1454.5737
						K.TWDHFWLNEGHTVYLER.H	0.9958	2	2204.4087
2105	LMA1L_MOUSE	374	12.57	2	2	R.LALGTREASIPPLNPK.A	0.9958	2	1677.9847
						K.HWKQQLGSTVQVRPEGGWGSSCPDGFR.	0.9958	3	3058.3085
2106	LMCD1_MOUSE	365	28.49	6	22	K.DPTFDTITYEWAPPGVTQK.L	0.9958	2	2167.3795
						K.GMCSGFEPHSWR.K	0.9958	2	1451.5653
						R.QLMHQLPIYDQDPSR.C	0.9949	2	1842.0795
						K.HFICEGCEQLLSGR.A	0.9921	2	1706.828
						K.DPTFDTITYEWAPPGVTQKLGLQYMELIPK	0.9924	3	3453.9747
						K.SEALGVGEVALPGQGGLPKEENK.T	0.9958	2	2280.5401
2107	LMNA_MOUSE	665	24.96	10	20	R.MQQQLDEYQELLDIK.L	0.9958	2	1895.1346
						R.IDSLSAQLSQLQK.Q	0.9958	1	1431.6292
						R.SLTMVEDNEDDDEDGEELLHHHR.G	0.9958	2	2736.7968
						K.AQNTWGCGSSLR.T	0.9958	2	1337.4008
						R.NSNLVGAAHEELQQSR.I	0.9958	1,2	1753.8692
						R.VRSLETENAGLR.L	0.9958	1	1345.4984
						K.AGQVVTIWASGAGATHSPPTDLVWK.A	0.9958	2	2550.8766
						R.TLEGELHDLR.G	0.9912	2	1183.3067
						R.LQEKEDLQELNDR.L	0.9929	2	1630.752
						K.LALDMEIHAYR.K	0.9958	2	1332.5603

2108	LMNB1_MOUSE	588	9.69	2	3	R.YVLKAGQTVTVWAANAGVTASPPTDLIWK.	0.9911	3	3059.5352
						K.SLEGDLEDLKDQIAQLEASLSAAK.K	0.9958	2	2545.8034
2109	LMTK1_MOUSE	1365	5.05	2	2	K.EIGHGWFGKVFLGEVHSGVSGTQVVVK.E	0.9944	3	2855.2688
						K.QVGTPDSLDSLDIPSSASDGGCEVLSPSA/	0.9958	3	3680.8842
2110	LONF3_MOUSE	753	2.92	1	2	K.YSKNVILEELIATFLPEEFK.E	0.9944	3	2384.7747
2111	LONM_MOUSE	949	34.77	18	72	R.GYQGDPSSALLELLDPEQNANFLDHYLDVI	0.9958	3	3875.2372
						R.VVDNPIYLSDMGAALTGAESHELQDVLEET	0.9958	3	3687.1103
						K.IVSGEAQTVQVTPENLQDFVGKPVFTVER.I	0.9958	2,3	3189.5926
						K.LALLDNHSSEFNVTR.N	0.9958	2	1716.8913
						K.RAGVTCIILPAENR.K	0.9904	2	1570.7985
						K.TKTENPLVLIDEVDK.I	0.9958	2	1714.9537
						R.NPVFPR.F	0.9958	1	729.857
						K.RDDNNESDVVESLDEIYHTGTFAQIHEMQD	0.9958	3	3923.1267
						K.ILCFHGPPGVGK.T	0.9958	2	1282.4943
						R.AQAVLEEDHYGMEDVK.K	0.9958	1	1834.9953
						K.EVEDELGPKPQLEMVTEAATDTSK.E	0.9944	2	2618.8696
						K.TENPLVLIDEVDKIGR.G	0.9958	2	1812.0733
						K.AQLSAAVLTLLIK.Q	0.9958	2	1341.6775
						K.EVLMVEVENVAHEDFQVTEEVK.A	0.9946	2	2574.8622
						K.DYSDLAPFITEGLEVHFVEHYR.D	0.9958	2	2638.8957
						R.KDYSDLAPFITEGLEVHFVEHYR.D	0.9957	3	2767.0697
						K.HVMDVVDEELSK.L	0.9958	2	1401.5744
						K.KEVEDELGPKPQLEMVTEAATDTSK.E	0.9958	2,3	2747.0437
2112	LOX12_MOUSE	663	9.2	3	3	R.DALQLWEVTAR.Y	0.9958	1	1302.4728
						R.SRTQLISDGGIFDQVVSTGGGGHVQLLTR.	0.9915	2	3000.3414
						R.NEQLDLPYEYLKPSR.I	0.9958	2	1866.0807
2113	LOXL2_MOUSE	776	2.84	1	2	R.LGQGIGPIHLNEVQCTGTEK.S	0.9958	2	2152.3783
2114	LOXL3_MOUSE	754	11.01	3	4	K.AGTWGTVCDRK.W	0.993	2	1251.3507
						R.AVSVWYCCPWGLLLLHCLCSFSVGSPSPS	0.9924	3	4024.5131
						R.VEVQIGIPGHLRWGLICGDDWGTLEAMVA	0.9958	3	3510.968
2115	LPHN1_MOUSE	1466	4.3	2	2	K.VLEPTSTHESEHQSGAWCKDPLQAGDR.I	0.9958	3	3037.195
						R.INELLLSVITWVGIVISLVCLAICISTFCFLR.G	0.9944	3	3725.4317
2116	LPHN3_MOUSE	1537	0.72	1	3	K.VFLCPGLLK.G	0.9924	1	1047.2921
2117	LPIN1_MOUSE	924	9.52	3	3	K.QASDNGARSANQSPQSVGGSGIDSGVEST	0.9958	3	3323.3849
						K.TPDKMNFQAIHSESSDTFSDQSPTMAR.G	0.9958	3	3030.2673
						K.LKNGPNDVVFSVTTQYQGTCR.C	0.9958	2	2385.6049
2118	LPP_MOUSE	613	7.99	2	11	R.METTHSFGNPSISVSTQQPPK.K	0.9958	2	2274.5103

						R.EAAYAPPASGNQNHPGMYPVSGPK.K	0.9958	2	2441.6801
2119	LPP60_MOUSE	564	3.19	1	6	K.LSYVLGQPGLSLNDRK.K	0.9958	2	1761.0311
2120	LPPR2_MOUSE	343	15.45	2	5	R.AFFPAPPSSSPVSGESTIVSGACCR.F	0.9958	3	2569.7627
						K.GSRLVKPSLCLALLCPAFLVGVVR.V	0.9914	2	2627.1645
2121	LPPRC_MOUSE	1392	14.66	11	19	K.DVGEPVPFPEPPESFAFYIK.Q	0.9958	2	2266.5549
						K.QAGIEPGPDTYLALLNAHAER.G	0.9944	2	2237.4771
						K.LQQLGVVYDVSHYNALLK.V	0.9958	2	2061.3885
						R.AGDMENAENILTVMK.Q	0.9958	2	1636.8757
						K.TSQVTSSDLESTLEK.L	0.9958	2	1625.7271
						K.NVQGIIDILK.I	0.9947	1	1113.3427
						K.GDLPAALEASIACHK.K	0.9958	2	1553.7216
						K.GICNLLNTYHVPELIK.D	0.9958	2	1885.1797
						R.MANQFALYKPVTDLFLQLVDSGKVDEAR.A	0.9958	3	3170.6508
						K.LFECDRDQMYYNLLK.L	0.9958	2	2009.2502
						K.LKAEGQPVGSALK.Q	0.9958	2	1298.5253
2122	LR16A_MOUSE	1374	3.57	3	17	R.FMPIPMYDAAQALKTNPEK.T	0.9958	2	2166.5581
						K.AEPRVDGGCR.S	0.9924	1	1117.1729
						R.YVQVMGSGLLAEMK.A	0.9958	1	1526.8494
2123	LR2BP_MOUSE	346	9.54	1	2	K.AFFWHSEACGNGSLESQGALGLMYFYGQ	0.9958	3	3455.7945
2124	LRC20_MOUSE	184	17.93	2	7	R.NVSDQIHLITLANNELK.S	0.9958	2	1923.1765
						R.LPNEVSSLQHLR.A	0.9945	2	1393.5858
2125	LRC24_MOUSE	521	1.92	1	4	K.SGLRLPTR.V	0.9958	1	900.0689
2126	LRC25_MOUSE	297	12.46	2	4	R.SPLQASHAQVLDLSK.N	0.9958	2	1594.8082
						K.AQMSPHDIPKPVTDFLPR.Y	0.9958	2	2050.3831
2127	LRC40_MOUSE	602	11.96	3	3	R.LLPALTVLDIHDNQLTSLPSAIR.E	0.9958	2	2501.9291
						R.LDLSNNDISSLPCSLGNLHLKFLALEGNPLF	0.9944	3	3422.8725
						R.SVPEEMALLQSLER.L	0.9958	1	1602.8432
2128	LRC47_MOUSE	581	11.53	4	5	R.NALGPGLSPELGPLPALR.V	0.9958	2	1773.0855
						R.RNALGPGLSPELGPLPALR.V	0.9958	1	1929.273
						K.VLHVSENPTPLTVR.V	0.9943	2	1562.8094
						R.LDAFPPELFRPGALPLLSELAAADNCLR.E	0.9958	3	3068.509
2129	LRC48_MOUSE	523	7.46	2	7	K.LLEIAINTLEKILK.G	0.9958	1	1612.0061
						R.FPCLRTLSLAGNPVSEAEEYK.M	0.9944	2	2382.6416
2130	LRC52_MOUSE	314	5.73	1	3	R.FANQIFRSNTHLGPIR.R	0.9958	2	1872.1398
2131	LRC59_MOUSE	307	18.24	3	27	R.LVNLQHLDLLNNR.L	0.9958	2	1562.8124
						K.LSTLPSDFCGLTHLVK.L	0.9958	2	1789.0478
						R.DKLDGNELDLSLSDLNEVPVK.E	0.9958	2	2314.5517

2132	LRC8E_MOUSE	795	3.77	3	4	R.GATLESLRELK.Q	0.9944	1	1217.4081
						R.LETLPEELGDCK.G	0.9958	1	1404.5231
						K.GNRLETLPEELGDCK.G	0.9944	2	1731.8664
2133	LRIG3_MOUSE	1117	3.04	1	3	K.DDSPLVVTERHFFAAGNQLLIIVDSDVSDA(	0.9958	3	3430.7961
2134	LRIT2_MOUSE	549	2.19	1	2	R.VMEEDEEVEK.E	0.9944	1	1237.321
2135	LRP1_MOUSE	4545	4.22	9	29	K.VPDEHMIPIENLMNPR.A	0.9958	2	1906.2251
						R.TNTQPFDLQVYHPSR.Q	0.9958	2	1803.9719
						K.NEPVDRPPVLLIANSQNILATYLSGAQVSTI	0.9958	3	3939.4582
						K.GYLFWTEWGHYPR.I	0.9958	2	1712.9072
						K.NAVVQGLEQPHGLVVHPLR.G	0.9958	2	2064.3982
						K.FGHSPLINLTGGLSHASDVVLYHQHK.Q	0.9958	3	2829.1905
						R.GTMYWSDWGNHPK.I	0.9909	2	1579.7295
						K.FCSEAQFECQNHR.C	0.9958	2	1713.7357
						R.SLFPGHPHSAYEQTFQGDESVR.I	0.9958	2	2490.6506
2136	LRP10_MOUSE	713	7.43	2	2	R.RWGLLPR.T	0.9958	1	898.0989
						K.TPIPTPSTLPALATVSEPPGPLPSVPVESSL	0.9944	3	4218.9243
2137	LRP4_MOUSE	1905	2.62	3	12	R.QVLVSHVSHPFALTQQDR.W	0.9912	2	2063.3237
						K.SPVLPNTLPTTLHSSTTKTR.T	0.9958	2	2152.4557
						K.FLLFAR.R	0.9924	1	766.9615
2138	LRP5_MOUSE	1614	0.81	1	2	R.IEVANLNGTSR.K	0.9924	1	1174.2993
2139	LRRC1_MOUSE	524	10.69	3	3	K.LGLSDNEIQRLPPEIANFMQLVELDVSR.N	0.9958	3	3198.6617
						K.LSNLNADRNK.L	0.9958	1	1145.2608
						R.ATPHPGELKNMK.K	0.9944	1	1323.5529
2140	LRRC2_MOUSE	371	6.47	2	2	K.ILDLPK.N	0.9958	1	698.8809
						K.SIPPELGDCEHLER.L	0.9911	2	1652.7674
2141	LRRF1_MOUSE	729	4.66	2	2	K.SEQQAEALDSPQK.K	0.9958	2	1431.4991
						K.CEQQVQSQDQENTSDLK.N	0.9926	2	2038.0552
2142	LRRK1_MOUSE	2014	2.28	2	3	K.LSHLPPGFLHLSKLQK.L	0.9943	2	1816.1997
						R.DADFSENSLKEVPLGLFQLDALMFLR.L	0.9958	3	2970.4101
2143	LRRK2_MOUSE	2527	2.14	3	4	K.CPSLKQLNLSYNQLSSIPENLAQVVEK.L	0.9958	3	3074.4675
						K.QTNTGSVLARK.V	0.9958	1	1175.3304
						R.YLHSAMIIYR.D	0.9958	1	1267.5316
2144	LRRN3_MOUSE	707	7.64	2	4	K.EGGLYTCIATNLVGADLK.S	0.9914	2	1896.1138
						R.SLVIAGINLTEIPDDALAGLENLESISFYDNR	0.9944	3	3464.8511
2145	LRWD1_MOUSE	648	8.18	2	2	R.VDGLAFVNEDVVASKGSGQGTIYLWSWS(	0.9958	3	3687.0624
						K.DLETQLWACAFEPAR.E	0.9924	2	1807.9666
2146	LSG1_MOUSE	644	4.81	2	2	K.EIDAAKENVILINK.A	0.9944	2	1570.8265

						R.GFMTAHGQPDQPR.S	0.9958		2	1442.592
2147	LSM11_MOUSE	361	7.48	2	2	R.KPKVDYQQVFTR.H	0.9958		1	1509.7483
						K.EDTDGTAGARR.Q	0.9958		1	1149.1625
2148	LSM12_MOUSE	195	13.33	2	5	K.EGSALSHVR.K	0.9958		1	956.0464
						R.LQGEVVAFDYQSK.M	0.9958		2	1484.6488
2149	LSM2_MOUSE	95	44.21	2	4	R.YVQLPADEVDTQLLQDAAR.K	0.9958		2	2146.3617
						K.NDLSICGTLHSVDQYLNIK.L	0.9958		2	2191.4119
2150	LSM8_MOUSE	96	38.54	2	4	K.GFDQTINLILDESHER.V	0.9958		2	1888.044
						K.GFDQTINLILDESHERVFSSSQGVEQVVLG	0.9958		3	3950.4405
2151	LTB1L_MOUSE	1713	2.8	2	3	R.LEPGQPQLSPGVSTIHLHPQFPVVVEK.T	0.9956		2	2935.3959
						K.EICPGGMGYTVSGVHRR.R	0.9944	1,2		1877.0943
2152	LTBP4_MOUSE	1666	2.76	2	3	R.GSYTGALSEPYEGLEAEECGILDGCPHGR.	0.9958		3	3126.249
						R.VLHDGGCSLPILR.N	0.9958		2	1437.6482
2153	LTV1_MOUSE	470	7.66	2	3	R.QEKELLNLK.K	0.9924		1	1115.3152
						R.SSAGFLSDGGDLSAPGSPQEAMK.K	0.9958		3	2210.3771
2154	LUM_MOUSE	338	25.44	6	142	K.SIPTVNENLENYYLEVNELEK.F	0.99		2	2511.7448
						K.LPAGLPTSLLTLYLDNNK.I	0.9958		2	1944.2786
						K.SLQDLQLTNNK.I	0.9949		1	1274.4166
						K.RFTGLQYLR.L	0.9957		2	1154.3573
						K.ISNIPDEYFK.R	0.9958		1	1226.3715
						K.ILGPLSYSK.I	0.9924		1	978.1766
2155	LX12B_MOUSE	701	3.85	2	2	R.YNVQINSIGRALLLNK.G	0.9929		2	1817.1417
						R.QEEIRAK.K	0.9958		1	873.9847
2156	LY6A_MOUSE	134	17.16	1	8	K.NNLCLPICPPNIESMEILGTK.V	0.9944	2,3		2414.7518
2157	LY6C_MOUSE	131	16.03	1	3	R.ASDGFCIAQNIELIEDSQR.R	0.9958		2	2167.3032
2158	LYAG_MOUSE	953	5.56	2	4	K.GQWLTLEAPLDTINVHLR.E	0.9915		2	2077.3909
						R.EVTVLGVATAPTQVLSNGIPVSNFTYSPDN	0.9958		2	3220.6037
2159	LYPA1_MOUSE	230	59.57	7	33	R.ASFSQGPINSANR.D	0.9958		1	1349.4459
						K.ATAAVIFLHGLGDTGHGWAEAFAGIK.S	0.9958	2,3		2611.9627
						K.ALINPANVTFK.I	0.9958	1,2		1188.4123
						K.IYEGMMHSSCQQEMMDVK.H	0.9958		2	2205.5047
						K.LAGVTALSCWLPLR.A	0.9958		2	1557.8425
						R.IILGGFSQGGALSLYTALTTQQK.L	0.9958		2	2368.7355
						R.DISVLQCHGDCDPLVPLMFGSLTVER.L	0.9958		2	2960.3041
2160	LYPA2_MOUSE	231	40.69	4	29	R.ETAAVIFLHGLGDTGHSWADALSTIR.L	0.9958	2,3		2740.0477
						K.MVMPSWFDLMGLSPDAPEDEAGIK.K	0.9958		2	2638.0403
						K.DLAILQCHGELDPMVPVR.F	0.9958		2	2064.3735

						K.TYPGVMHSSCPQEMAAVK.E	0.9958		2	1994.2539
2161	LYPL1_MOUSE	239	25.52	3	3	K.HVLNQDLTFQHIK.I	0.9958		2	1593.8259
						K.SLGVSTTFHSLPNLNHELNK.T	0.9958		2	2209.4667
						R.MLPELFQCHGSADNLVLHAWGK.E	0.9958		2	2524.8659
2162	LYRM1_MOUSE	122	10.66	1	2	K.NKNLTDPELIK.Q	0.9958	1,2		1285.4832
2163	LYRM2_MOUSE	88	11.36	1	11	R.QQVLLLYR.K	0.9944		1	1033.259
2164	LYRM7_MOUSE	104	20.19	1	30	R.TAVIQGIHTDHDTLQLVPR.K	0.9958		2	2115.397
2165	LYST_MOUSE	3788	2.27	4	8	R.ETAGELLLGK.C	0.9958		1	1031.1943
						K.LYLEGSAPSGQVSAKVNLFR.K	0.9958		2	2137.4435
						R.DGVPSEAAEHLKALINSVIK.I	0.9937		2	2092.4001
						R.VLQAALEFIRSTANHDSESPVHSPSAHR.H	0.9958		3	3058.3402
2166	LZIC_MOUSE	190	42.11	4	23	K.LTEDDETFLSANASAVLSQFEK.V	0.9958		2	2416.6007
						R.KVEILTALR.K	0.9958	1,2		1043.295
						K.ETLEQLSEFNDSLK.K	0.9958		2	1653.7833
						K.IMSGNMTLVDELSGMQLAIQAAISQAFK.T	0.9958		3	2969.4995
2167	LZTL1_MOUSE	299	11.37	2	4	R.VLQDLQLDQENQQDLLK.A	0.9958		2	2041.2658
						K.AQDLDDLENTVATLR.S	0.9958		2	1674.8052
2168	LZTS1_MOUSE	599	9.68	2	2	R.TKGLELEVCENELQR.K	0.994		2	1818.9879
						K.GAVRPTAFKPVLPRSGAILHSSPESTSHQL	0.9958		3	4170.8253
2169	M11D1_MOUSE	461	8.68	2	2	R.ITQPVLKRPR.H	0.9958		1	1208.4929
						R.QFLPVSPKVQFDVVVSAYALSELPSR.A	0.9944		3	2878.3409
2170	M2GD_MOUSE	869	1.61	1	3	K.IHELFPLLNMNK.I	0.9958		1	1469.7851
2171	M2OM_MOUSE	314	17.83	3	55	K.FLFGGLAGMGATVFVQPLDLVK.N	0.9958		2	2281.7613
						K.TSFHALTSILK.T	0.9958		2	1218.4386
						R.MIDGKPEYKNGLDVLLK.V	0.9958		2	1934.3013
2172	M3K10_MOUSE	940	4.36	2	3	R.LLEECWDPDPHGRPDFGSILK.Q	0.9958		3	2482.721
						K.GSDGASPPASPSIIPR.L	0.9944		2	1509.6591
2173	M3K12_MOUSE	888	4.84	1	4	R.AALPPHEPGGLGSPGGLGVGPSAWDACP	0.9958		3	4118.6567
2174	M3K4_MOUSE	1597	3.01	2	2	R.ISDAIDRVDHMFTLEFDAEVEESESATLQQ`	0.9944		3	3910.2141
						K.LFCDIAGMLLK.S	0.9958		1	1281.5623
2175	M3K6_MOUSE	1291	1.47	1	6	R.TLQAQLRAQSLGPALLK.G	0.9958		2	1809.1624
2176	M3K7_MOUSE	579	3.28	1	3	R.DLKPPNLLLVAGGTVLK.I	0.9958		1	1749.1472
2177	M4A6C_MOUSE	217	11.98	1	3	K.SGYPFIGALFFIASGILSIITERK.S	0.9958		3	2602.0917
2178	M4K2_MOUSE	821	4.51	2	2	R.DIKGANLLLTLQGDVK.L	0.9958		2	1699.0006
						R.LQHQAPLSIPTNRITQR.I	0.9918		2	1974.2735
2179	M4K3_MOUSE	894	4.03	2	2	K.LEPGEDFAVVQQEIIMMKDCK.H	0.9958		2	2481.8478
						K.TRSEINFGQVK.F	0.9944		1	1279.4386

2180	M4K5_MOUSE	847	6.49	2	2	K.LASELSFDFR.I	0.9924		1	1185.322
						R.QSSPSCVPVAETSSSIGNGDGISKLISENTE	0.9924		3	4158.4455
2181	M6PBP_MOUSE	437	69.57	15	229	K.AQETLQQLTSVLGLMESVK.Q	0.9958		2	2076.4131
						K.ELVSSTVSGAQEMVSSSVSSAK.E	0.9944		2	2171.3814
						K.LEPQIATASEYAHR.G	0.9958		2	1586.7447
						R.SQVNDLQATFSGIHSFQDLSAGVLAQTR.E	0.9958		3	2992.2749
						R.DITQQLQSMCVALGASIQGLPSHVR.E	0.9958		3	2711.0747
						K.SAMTSGVQSVMGSR.V	0.9958		2	1398.5922
						R.VTGAVDVTLGAVQNSVDK.T	0.9958		2	1773.9811
						R.VAGLPLISSTYGMVSAAYTSTK.E	0.9958		2	2218.5702
						K.TLTTAAVSTAQPILSK.L	0.9958		1	1602.8687
						K.SEAWADNRLPLTEAELALIATPPEDSDMAS	0.9958		3	3869.2519
						R.LQESLPILQQPTEK.V	0.9958		2	1624.8748
						R.LPLTEAELALIATPPEDSDMASLQQQR.Q	0.9958		3	2939.3075
						R.EALDNTVEYVAQNTPAMWLVGPFAPGITEI	0.9958		2	3263.6893
						K.LHQMWLSWNQK.T	0.9958	1,2		1471.7197
						R.NHAYEHSLGK.L	0.9958	1,2		1156.2431
2182	MA2A1_MOUSE	1150	3.04	2	3	R.ISSKINNQNR.Y	0.9958		2	1174.3023
						K.VLSDSGKPVEVQVSAVWNDMR.T	0.9958		2	2317.622
2183	MA2B1_MOUSE	1013	7.31	3	6	K.TVDQYYYGILSDVQHASVQYILDSVVSSLLE	0.9958		3	4145.6586
						R.SQGGSSLQDGSLELMVHR.R	0.9958		2	1902.0893
						R.HLVLLSSVSDAAAR.H	0.9958		2	1439.6548
2184	MA2B2_MOUSE	1018	3.73	2	2	R.KLMVSIALGGPPGSGTGAPK.D	0.9911		3	1839.2035
						R.LAHPSLAGELLCQR.I	0.9958		2	1565.7789
2185	MA2C1_MOUSE	1039	14.24	7	19	R.QFLQGQNFFLQEFGK.M	0.9958		2	1832.0685
						R.TNHSGFLFGFGDGGGGPTQTMLDR.L	0.9952		2	2470.6782
						R.LFGDSCSVTLSSFLTPER.L	0.9958		2	2017.2091
						R.VQLSSPGQLFTALER.D	0.9958		2	1646.8839
						R.SFQALHTANQMVNICDPAQPETYPAAK.A	0.9958		3	3004.31
						R.SAQFLYPAAQLQHLWR.L	0.9958		2	1930.2193
						R.KPVLGQAGTLAVGTEGGLR.G	0.9958		2	1825.1185
2186	MA7D1_MOUSE	846	15.48	7	10	K.DSMQKEELAPQEPQWSLPSK.E	0.9952		2	2329.5867
						K.EPAAPASPAPSPVPSPTPAQPQK.E	0.9958		2	2223.4906
						R.AAEEKEPAAPASPAPSPVPSPTPAQPQK.E	0.9958		3	2752.0532
						R.KPGAGGSPALAR.R	0.9924		1	1082.2479
						R.TAEGLLPFAEAEAFLK.K	0.9958		2	1707.9641
						K.EQSSTQIPAETAVPAVPAAPTAPPTAAPSV	0.9958		3	4688.1774

						K.EQSSTQIPAETAVPAVPAAPTAPPTAAPSV	0.9958	3	4101.5751
2187	MA7D2_MOUSE	781	17.16	5	6	R.SGGNGGGGGGGGGGGGGYGGSGGGGG	0.9944	3	3446.6316
						K.GAMAGGEPSQMEK.M	0.9944	1	1293.4523
						K.GAMAGGEPSQMEKMK.K	0.9952	2	1552.819
						K.EDPKVELQPPPDVENK.A	0.9907	2	1835.0209
						K.CSWAGSPGPGGRDGESENTPPLPLTLATS	0.9958	3	5017.2711
2188	MA7D3_MOUSE	876	1.48	1	2	R.KPEIMAEKLDK.V	0.9924	1	1302.5719
2189	MAAI_MOUSE	216	40.28	6	84	R.MISDLIASGIQPLQNLSVLK.Q	0.9958	2	2141.5744
						K.ELLALEVFQVSHPR.R	0.9958	2	1638.9071
						R.FKVDLSPYPTISHINK.E	0.9958	2	1860.1631
						K.VDLSPYPTISHINK.E	0.9952	2	1584.8125
						K.YCVGDEVSMADVCLVPQVANAERFK.V	0.9958	3	2859.1556
						R.RQPDTPAELR.T	0.9929	2	1183.3097
2190	MACD1_MOUSE	323	40.56	8	323	K.YVIHTVGPIAVGQPTASQAAELR.S	0.9958	2	2379.7214
						R.SVAFPCISTGVFGYPNEEAAEVVLASLR.E	0.9958	2	2985.3295
						R.SCYLSSLDLLLEHR.L	0.9958	2	1706.9024
						R.LIICVFLEKDEGIYR.E	0.9958	2	1869.1773
						R.GDITKLEVDAIVNAANSSLLGGGGVDGCIH	0.9958	2	3110.4173
						K.LEVDAIVNAANSSLLGGGGVDGCIHR.A	0.9958	2	2595.8382
						K.VDLSTSTDWK.E	0.9944	1	1152.2463
						R.LRSVAFPCISTGVFGYPNEEAAEVVLASLR	0.9958	3	3254.6764
2191	MACF1_MOUSE	5327	4.26	11	15	K.IDALLDWVGLLWGHLRESHR.L	0.9929	2	2387.7495
						R.DGHNLISLLEVLSGIKLPR.E	0.9943	2	2075.4593
						R.LFLNKIQALR.F	0.9958	1	1216.5125
						R.VDEIDAAIQRSQQYEQAADAELAWVAETK.	0.9931	3	3250.5029
						K.NDVLAHQATVATVNK.A	0.9958	2	1581.7691
						K.EIQDKLDQMVFFWEDIK.A	0.9944	2	2185.4993
						K.ITGQLESLER.R	0.9958	2	1146.2859
						R.TGTVQVLKR.S	0.9924	1	1002.2021
						R.TELVSISSSEDEGNLRFVYELLSWVEEMQM	0.9958	3	3651.0945
						K.QFHETAEPISDFLSVTANK.L	0.9944	2	2135.3379
						K.VEPQLAEDQPVHGDLDLVMNLMDAHK.V	0.9958	3	2916.2935
2192	MAG_MOUSE	626	5.59	2	5	K.NYPPVVFK.S	0.9958	1	964.1521
						R.VICTSRNLYGTQSLELPFQGAHR.L	0.9944	2	2648.9475
2193	MAGI1_MOUSE	1471	1.16	2	2	K.FIHTKLR.K	0.9924	1	915.1264
						R.EEAGLK.L	0.9958	1	646.7184
2194	MAGI2_MOUSE	1275	2.98	2	11	K.LIKDAGLSVTLR.I	0.9924	1	1286.5577

						R.QYPLSDYRQPQDFDYFTVDMEK.G	0.9909		2	2787.029
2195	MAN1_MOUSE	921	5.43	2	2	R.MLSVQEAAAYLKNLGPEYEDVFNTSLLWIF	0.9958		3	3592.1439
						K.VWDRAVDFLAANESR.V	0.9958		2	1749.9236
2196	MANA_MOUSE	423	49.41	12	152	R.LFAPAQSQDDPYLSIYDPPVPDFTVMK.M	0.9958		2	3056.4567
						K.LPFLFK.V	0.9958		1	764.986
						R.ISQQVFDGNNMEDIYGK.L	0.9958		2	1959.1377
						K.KVPEFQLLIGDDATAQLK.E	0.9958		2	1987.3037
						K.VLSVDTALSIQAHPNK.E	0.9958		2	1693.9407
						K.NTFNGKLPFLFK.V	0.9958		2	1426.7013
						K.SEVACLLASSDPLAQISEDKPYAELWMGTH	0.9958		3	3573.9655
						K.KVVVEQLNLLVK.R	0.9958		2	1382.73
						K.FIDVPTLCEMLNYTPSPSNNR.L	0.9924		2	2469.7377
						R.VFPLSCVVQQYAWGK.V	0.9958		2	1783.046
						K.DLLIFR.A	0.9958		1	776.9542
						K.TLGQWIAENPDCLGSK.V	0.9958		2	1789.9489
2197	MAON_MOUSE	604	46.36	14	132	K.SLIYTPDYDSFSLDTYSWPK.E	0.9958		2	2399.6154
						R.GIFASGSPFK.S	0.9958		1	1011.1656
						R.TFTPGQGNNAYVFPGVALGVIAGGIR.H	0.9958	2,3		2577.9456
						K.HNLASYYPEPK.D	0.9958	1,2		1319.4594
						K.GHIATMLNSWPEDNIK.A	0.9958		2	1827.0649
						R.HIPDEIFLLTAEQIAQEVSEQHLSQGR.L	0.9958		2	3090.4197
						K.EMFAQDHPEVNSLEEVVR.L	0.993		2	2130.3368
						K.LALYTACGGVNPQQCLPVLLDVGTNNEELI	0.9958		3	4329.913
						R.DMASFHERPIVFALSNPTSK.A	0.9958		2	2248.5615
						R.VRGEEYDDLLDEFMQAVTDK.F	0.9958		2	2374.5812
						R.ILGLGDLGCYGMGIPVGK.L	0.9952		2	1821.1512
						K.SVTLEDGRTFTPGQGNNAYVFPGVALGVIA	0.9958		3	3435.8644
						R.SHLNHEKEMFAQDHPEVNSLEEVVR.L	0.9958		3	2976.25
						R.LQLGIHGLIPPCFLSQDVQLLR.I	0.9958		2	2518.9714
2198	MAOX_MOUSE	572	46.33	13	98	R.ILGLGDLGCNGMGIPVGK.L	0.9909		2	1772.0791
						R.AIFASGSPFDPVTLPDGR.T	0.9958		2	1848.0654
						K.GHIASVLNAWPEDVVK.A	0.9958		2	1735.9805
						R.VRGPEYDAFLDEFMEAASSK.Y	0.9958		2	2263.4835
						R.GPEYDAFLDEFMEAASSK.Y	0.9958		2	2008.1634
						K.IKPTALIGVAAIGGAFTEQILK.D	0.9958		2	2212.6811
						K.YCTFNDDIQGTASVAVAGLLAALR.I	0.9958		2	2527.8029
						K.LALYTACGGVNPQQCLPITLDVGTENEELL	0.9958		3	3418.7982

						K.LSDQTVLFQGAGEAALGIAHLVVMAMEK.E	0.9958		3	2901.409
						K.YGMNCLIQFEDFANR.N	0.9958		2	1879.0632
						R.GLFISIHDK.G	0.9958		1	1030.212
						R.TLFPGQGNNSYVFPGVALGVVACGLR.H	0.9937		2	2695.0594
						R.QQLNIHGLLPPCIISQELQVLR.I	0.9958	2,3		2571.0043
2199	MAP1A_MOUSE	2776	1.98	2	2	K.TYGAPETELTYPPNMVAAPLAEEEHVSSAT	0.9944		3	4011.3231
						K.FSKPDLKPFTPEVR.K	0.9958		2	1661.9414
2200	MAP1B_MOUSE	2464	1.26	2	11	K.FYLLVVVGETVTEEHLR.R	0.99		2	2005.3214
						R.HNLQDFINIK.L	0.9958		1	1242.4203
2201	MAP4_MOUSE	1125	38.04	17	49	K.VAEFNNVTPLSEEEVTSVK.D	0.9958		2	2093.2952
						K.AAEQMSTLPIDAPSPLENLEQK.E	0.9958		2	2383.6759
						K.VGSLDNVGHLPAGGAVK.T	0.9958		2	1591.8075
						R.DFMAALEAEPYDDIVGETVEK.T	0.9958		2	2343.5642
						R.DDGLADLLFVSSGPTNASAFTER.D	0.9958		2	2384.5615
						K.DVAPPMEEEIVPGNDTTSPK.E	0.9958		2	2127.3277
						K.RNTTPTGAAPPAGMTSTR.V	0.9946		2	1787.9885
						K.DVTLPLEAERPLVTDMTPSLETEMTLGK.E	0.9958		3	3088.5557
						K.AAGSIASAQKPPAGK.V	0.9958		2	1354.5491
						K.TEGGGSEALPCPGPPAGEEPVIPEAAPDA(	0.9958		3	4770.0137
						K.AAVGVTGNDITTPPNKEPPPSPEK.K	0.9958		2	2417.6781
						K.KPTSTKPSSSAPR.V	0.9958	1,2		1344.5107
						K.KPMSLASGSVPAAPHK.R	0.9958		2	1578.87
						R.TSPSKPSSAPALKPGPK.T	0.9944		2	1650.9157
						R.VDYPDYQSSQNWPEDASFCFQPQQVLDT	0.9958		3	4590.7554
						K.KKPCLDTSQVEGIPSSKPTLLANGDHGME(	0.9958		3	4701.0987
						K.GQSTVPPCTASPEPVK.A	0.9958		1	1655.8114
2202	MAPK2_MOUSE	386	13.47	3	5	K.SIGEAIQYLHSINIAHR.D	0.9958		2	1923.182
						R.MTITEFMNHPWIMQSTK.V	0.9958		2	2096.4849
						K.KIEDASNPLLLK.R	0.9958		2	1341.5907
2203	MARCS_MOUSE	309	6.8	1	12	K.GEATAERPGEAAVASSPSK.A	0.9958	1,2		1815.9347
2204	MARE1_MOUSE	268	27.99	4	9	R.NIELICQENEGENDPVLQR.I	0.9958		2	2271.4119
						K.FQDNFEFVQWFK.K	0.9958		2	1635.8187
						R.QGQETAVAPSLVAPALSKPK.K	0.9958		2	1993.3109
						K.KPLGSSTAAPQRPIATQR.T	0.9958		2	1880.1575
2205	MARE2_MOUSE	326	26.38	5	52	R.FQDNLDFIQWFK.K	0.9958		2	1601.8015
						K.DLETQVIQLNEQVHSLK.L	0.9958		2	1995.2401
						R.EIELLCQEHGQENDDLVQR.L	0.9958		2	2326.4479

						K.SSPASKPGSTPSRPSSAK.R	0.9958		2	1729.8876
						K.LEHEYIHNFK.L	0.9958		2	1330.4857
2206	MARE3_MOUSE	281	19.57	3	3	R.LSNVAPPCILR.K	0.9947		2	1240.4546
						R.NGGHEADAQILELNQQLLDLK.L	0.9958		2	2320.5645
						R.HDMLAWVNDSLHLNYTK.I	0.9958		2	2058.319
2207	MARH6_MOUSE	909	9.13	2	2	K.SLLPNFLPYNVMLYSDAPVSELSLELLLLQV	0.9958		3	4808.6741
						R.RPLNFPLRIFLLIVFMCITLLIASLICLTLPVFA	0.9958		3	4204.2111
2208	MARK1_MOUSE	795	1.38	1	7	K.KLLVLNPIK.R	0.9958		1	1038.3622
2209	MARK4_MOUSE	752	1.99	1	3	K.AENLLLDAEANIK.I	0.9958		1	1414.5987
2210	MAST1_MOUSE	1570	1.46	2	2	R.FSALLEPSR.F	0.9944		1	1020.1735
						K.TWRGGSPEIK.R	0.9944		1	1131.2767
2211	MAST2_MOUSE	1734	1.38	1	2	R.KVSRPQAFEEATNPLQVPSLSR.S	0.9958		2	2455.7764
2212	MAST4_MOUSE	2618	2.22	2	2	K.AAAAEPSTSLHDTPRSATATTTAIATTTTTT	0.9958		3	4174.3612
						K.RSPSATVQSSLR.S	0.9924		1	1289.4343
2213	MAT2B_MOUSE	334	9.58	2	3	K.EFQQSNWHTVGCGFR.R	0.9958		2	1853.9573
						K.AVLENNLGAAVLR.I	0.9958		2	1340.5656
2214	MATN1_MOUSE	500	1.6	1	2	R.SPDISK.V	0.9958		1	646.7184
2215	MATR3_MOUSE	846	18.09	8	23	R.IGPYQPNVPVGIDYVIPK.T	0.9958		2	1970.3189
						K.ITPENLPQILLQLK.R	0.9958		2	1620.9731
						R.GPSLNPVLDYDHGSR.S	0.9958		2	1627.7538
						R.GAPPSSNIEDFHGLLPK.G	0.9958		2	1779.9903
						R.YQLLQLVEPFGVISNHLILNK.I	0.9958		2	2439.9035
						R.GDTDQASNILASFGLSAR.D	0.9958		2	1823.9573
						K.GYPHLCSICDLPVHSNK.E	0.9958		2	1998.178
						R.VIHLSNLPHSGYSDSAVLK.L	0.9958	2,3		2038.3109
2216	MAVS_MOUSE	503	21.67	4	45	R.EHQEQEPELGGAHAANVASVPIATYGPVSI	0.9958		3	4083.5065
						R.MSGGSLIPSPNQQALSPQPSR.E	0.9958		2	2153.4179
						R.VYQSYLPPGTSLR.S	0.9958		2	1481.6915
						R.SLEPLQLPDFPAAVSGPSAFAPGHNIPDHG	0.9944		3	3309.7086
2217	MBD1_MOUSE	636	4.56	1	2	K.RLLPSAGSGSGEGAGLRPYQTHQTHQK.R	0.9958		3	2835.1117
2218	MBNL1_MOUSE	341	15.84	2	4	K.YFHPPAHLQAK.I	0.9944		1	1309.5131
						K.AAQYQVNQAAAAQAAATAAAMGIPQAVLP	0.9958		3	3899.5468
2219	MCA2_MOUSE	320	25	4	14	K.SCENLAPFSTALQLLK.-	0.9958		2	1793.0362
						K.TTSPATDAGHVQETSEPSLQALESR.Q	0.9958		2	2613.7545
						K.DIVINANPASPPLSLLVLHR.L	0.9958		2	2140.5339
						R.VLSTVHTHSSVK.N	0.9929		2	1295.4813
2220	MCAF1_MOUSE	1306	0.92	1	6	R.QQLDAVHRVK.G	0.9944		1	1194.3793

2221	MCAT_MOUSE	301	16.94	3	9	R.LQTQPPSLSGQPPMYSGTLDCFR.K	0.9958	2	2581.869
						K.NLLAGGFGGMCLVFVGHPLDTVK.V	0.9958	2	2403.8109
						R.LQTQPPSLSGQPPMYSGTLDCFRK.T	0.9958	2	2710.0431
2222	MCCA_MOUSE	717	44.91	16	61	K.SIMAAAGVPVVEGYHGK.D	0.9958	1,2	1686.9665
						K.IPLSQEEIPLQGHAFEAR.I	0.9958	2	2036.2951
						K.YLSPVSAEGAQGGTIAPMTGTIEK.V	0.9958	2	2379.6875
						K.IIEEAPAPGINPEVR.R	0.9958	2	1605.8314
						R.IYAEDPDNNFMPGAGPLVHLSTPSADMSTI	0.9958	3	3205.541
						K.QEGIIFIGPPSSAIR.D	0.9958	2	1585.8436
						R.LQVEHPVTEMITGTDLVEWQLR.I	0.9958	2	2595.9733
						R.LSGHPEFEAGNVHTDFIPQHHK.D	0.9958	2	2498.7196
						K.KVFFSEGAQANR.H	0.9958	1,2	1354.5082
						R.VLGDLSSEDGCTYLK.S	0.9958	2	1657.7809
						R.NSMHVDMADEAYSIGPAPSQQSYLAMEK.I	0.9958	2	3072.4061
						K.SSAAQAIHPGYGFLSENMEFAELCK.Q	0.9958	2	2759.0285
						K.LHTQDQFSPFSFSSGR.R	0.9958	2	1841.9774
						R.HNFYFMEMNTR.L	0.9958	2	1490.6942
						R.RLNISYTR.N	0.9929	2	1023.1801
						R.HVEVQVFGDHHGNAVYLFER.D	0.9958	2	2354.5895
2223	MCCB_MOUSE	563	30.2	11	42	R.IFGYPVGIIGNNGVLFSESAK.K	0.9958	2	2183.512
						K.RFEEEGNPYYSSAR.L	0.9958	1,2	1705.7807
						K.QFSSAEEAALKEPIIK.R	0.9958	2	1762.0129
						K.ALVSQLHER.A	0.9958	2	1053.2064
						K.SGVTDHYALDDHHALHLTR.K	0.9958	2	2159.3255
						R.KSGVTDHYALDDHHALHLTR.K	0.9958	2	2287.4996
						K.KMDVTIEPSEEPLFPADELYGIVGANLK.R	0.9958	2	3077.5165
						R.LGTQPDSASSTYQENYEQMK.A	0.9958	2	2278.4089
						K.GAHFVQLCCQR.N	0.9958	2	1376.4901
						K.AATGEEVSAEDLGGADLHCR.K	0.9958	2	2059.1199
						K.AATGEEVSAEDLGGADLHCRK.S	0.9958	2	2187.294
2224	MCEE_MOUSE	178	50	4	169	K.MELLHPLGSDSPITGFLQK.N	0.9958	2	2084.4382
						R.DVLGAQVSEVVPLPEHGVSVVFVNLGNTK	0.9958	3	3005.4411
						R.LNHVAVAVPDLEK.A	0.9958	1	1405.6371
						K.AGGMHHVCIEVDNISAAVMDLK.K	0.9958	2,3	2368.6943
2225	MCES_MOUSE	465	3.44	1	2	R.MQALEQYPAHENSK.L	0.9958	1	1646.8151
2226	MCF2L_MOUSE	1149	2.61	2	2	K.YTVVMDDEKGGPDTLAMR.S	0.9958	2	1999.2612
						K.EDLQLALK.E	0.9924	1	930.0892

2227	MCFD2_MOUSE	145	43.45	2	3	K.EEGSEQAPVMSEDELVSIIDGVLR.D	0.9958	2	2603.8579
						K.STVHDQEHIMEHLEGVIDQPEAEMSPQEL(	0.9958	3	4147.5801
2228	MCM3_MOUSE	812	2.09	1	2	K.KASEDESDLEDEEEK.S	0.9958	2	1753.7247
2229	MCPH1_MOUSE	822	5.84	3	12	R.SISSISDLISKSASSLEKPVK.E	0.9929	2	2177.5004
						R.QPRPQK.A	0.9944	1	753.8796
						K.QLEDMGATVSKTLNK.Q	0.9944	1	1635.8731
2230	MCPT4_MOUSE	246	20.33	2	3	K.GDSGGPLLCAGVAHGIVSYGRGDAKPPAV	0.9958	3	3184.548
						K.YNFYSNLHDIMLLK.L	0.9958	2	1772.0717
2231	MD12L_MOUSE	2157	0.7	1	4	K.QKVSPWDLFEGQK.N	0.9958	2	1562.7655
2232	MDC1_MOUSE	1707	9.26	7	13	R.LDVPPPLVPRSLLTIEK.T	0.9958	2	1888.3012
						K.TALDVPLER.N	0.9944	1	1014.1668
						R.GRPSKSPNK.T	0.9958	1	971.1044
						K.DLEGLASAPIITGSQADGGKGDPLSPGR.Q	0.9958	3	2680.9316
						K.SQPQVLVEQSQSASGRDSDTDVEEESSGF	0.9944	3	3109.1577
						R.SQSGSPAAPVEQVVIHTDTSGDPTLPQRE(	0.9958	3	3774.0525
						R.SPDCSVALPFPSISK.Q	0.9944	1	1605.7943
2233	MDHC_MOUSE	334	80.54	18	2508	R.DIWFGTPEGEFVSMGVISDGNSYGVPDDL	0.9958	3	4152.6614
						K.EVGVYEALKDDSWLK.G	0.9912	2	1752.9616
						K.VIVVGNPANTNCLTASK.S	0.9958	1,2	1758.9787
						K.DLDVAVLVGSMPR.R	0.9958	2	1372.6226
						K.GEFITTVQQR.G	0.9958	1	1179.3183
						K.FVEGLPINDFSR.E	0.9958	1,2	1394.57
						K.ELTEEKETAFEFLSSA.-	0.9958	2	1831.9709
						K.LGVTADDVK.N	0.9958	1	918.0349
						K.NVIIWGNHSSTQYPDVNHAK.V	0.9958	2	2281.4923
						K.ENFSCLTR.L	0.9958	1	1027.0881
						K.FVEGLPINDFSREK.M	0.9958	2	1651.8595
						K.DQPIILVLLDITPMMGVLDGVLMELQDCALF	0.9958	3	5240.1975
						R.KLSSAMSAAK.A	0.9924	1	994.1944
						K.EVGVYEALK.D	0.9958	1	1008.1595
						R.VLVTGAAGQIAYSLLYSIGNGSVFGK.D	0.9958	3	2586.9909
						K.SQIALK.L	0.9944	1	659.8039
						K.DQPIILVLLDITPMMGVLDGVLMELQDCALF	0.9958	3	4522.3776
						K.SVKVIVVGNPANTNCLTASK.S	0.9958	2	2073.3636
2234	MDHM_MOUSE	338	85.21	26	4465	K.VDFPQDQLATLTGR.I	0.9958	1	1561.7349
						K.GYLGPEQLPDCLK.G	0.9958	1	1490.6624
						K.ETECTYFSTPLLLGK.K	0.9958	1	1759.9599

						K.VAVLGASGGIGQPLSLLLK.N	0.9958		2	1794.1881
						R.LTLYDIAHTPGVAADLSHIETR.A	0.9958		3	2394.6897
						K.HGVYNPNK.I	0.9958		1	929.0232
						R.VNVPVIGGHAGK.T	0.9958		1	1148.3506
						R.FVFSLVDAMNGK.E	0.9958	1,2		1328.5689
						K.IFGVTTLDIVR.A	0.9958		2	1234.4814
						K.TIIPLISQCTPK.V	0.9958		1	1371.6263
						K.NSPLVSR.L	0.9944		1	772.8796
						K.AGAGSATLSMAYAGAR.F	0.9958	1,2		1455.6287
						K.KGEDFVK.N	0.9958		1	822.9365
						K.GCDVVVIPAGVPR.K	0.9958	1,2		1339.5438
						K.EGVVECSFVQSK.E	0.9958	1,2		1369.4803
						K.MIAEAIPELK.A	0.9958		1	1115.3734
						R.DDLFNTNATIVATLTAACAQHCPEAMVCIIA	0.9958		3	5005.5901
						K.NLGIGK.I	0.9958		1	601.7239
						R.DDLFNTNATIVATLTAACAQHCPEAMVCIIA	0.9958		3	5133.7642
						K.NLGIGKITPFEEK.M	0.9958		2	1446.6867
						K.VAVLGASGGIGQPLSLLLKNSPLVSR.L	0.9958		2	2548.0445
						R.IQEAGTEVVK.A	0.9958		1	1074.2193
						K.ETECTYFSTPLLLGKK.G	0.9958		2	1888.134
						K.KHGVYNPNK.I	0.9958		1	1057.1973
						K.HGVYNPNKIFGVTTLDIVR.A	0.9958		2	2144.4813
						R.FVFSLVDAMNGKEGVVECSFVQSK.E	0.9958		2	2679.026
2235	MDM4_MOUSE	489	9	2	5	K.DDDLEDSRSLSDDTDVELTSEDEWQCTEC	0.9958		3	3594.5314
						K.DPSPLYDMLR.K	0.9924		1	1207.3869
2236	MDR1_MOUSE	1276	4	3	6	K.VKEHGTHQQLLAQK.G	0.9958		1	1617.8484
						R.EIIGVVSQEPVLFATTIAENIR.Y	0.9915		2	2400.7777
						K.GTQLSGGQK.Q	0.9924		1	875.9572
2237	MECP2_MOUSE	484	11.57	2	12	R.KPGSVVAAAAAEAK.K	0.9958		1	1270.4716
						K.APMPLLPSPPPPEPESSEDPISPPEPQDLS	0.9958		3	4111.5271
2238	MECR_MOUSE	373	48.26	7	29	R.LTAPSCSEVPLQGYQQALEASMKPFVSSK	0.9958		2	3155.5563
						K.LPAVGGNEGVGQVIAVGSSVSALKPGDWV	0.9958		3	3902.4453
						K.NLELTAVEGSDVHVR.M	0.9958		2	1639.8057
						R.MLAAPINPSDINMIQGNYGLLPK.L	0.9954		2	2471.9355
						R.MLVDFEQLQPGDSVIQNASNSGVGQAVIQ	0.9958	2,3		3658.1211
						R.ALVYGNHGDPAK.V	0.9958		2	1242.3769
						R.HLAPGGTMVTYGGMAK.Q	0.9944		2	1591.8836

2239	MED1_MOUSE	1575	2.92	2	2	K.LQNCTGIPLFETPPTYLPLYELITQFELSK.D	0.9958	3	3528.0455
						K.VSASGGSVDSSK.K	0.9924	1	1081.1247
2240	MED14_MOUSE	1459	1.64	2	2	K.MLFFLQLTQK.T	0.9958	1	1269.5878
						K.WANDAGKVEK.C	0.9958	1	1118.2346
2241	MED23_MOUSE	1367	4.75	2	2	K.SHAWGILHTLLEMFSHRMHHIQPHYR.V	0.9944	3	3236.7478
						K.YPEKLYFEGLAEQVDPPVPIQSPYLPIYFGN	0.9958	3	4114.6961
2242	MED24_MOUSE	987	5.67	2	2	R.LLSSSDDDANILSSPTDRSMNSSLSASQLH	0.9958	3	3752.0767
						R.GSILQFMPFTTVSELVK.V	0.9958	1	1898.2678
2243	MED28_MOUSE	178	4.49	1	4	K.FLDIAR.Q	0.9944	1	734.8735
2244	MEF2C_MOUSE	474	2.74	1	3	K.INEDIDLMISR.Q	0.9943	2	1319.5157
2245	MEFV_MOUSE	767	4.69	2	4	R.GDTCVQSSCSCSIAPGDPK.A	0.9958	2	2027.0475
						R.NMSSKTSLIGEER.C	0.9958	2	1452.6226
2246	MELPH_MOUSE	590	9.66	2	5	R.SLCGRLQGGGGSEPSLEEGNGDSEQTDE	0.9958	3	3839.8097
						K.YSPSSQGVDSGSFDRK.S	0.994	2	1717.7893
2247	MELT_MOUSE	833	3.12	1	3	K.VISSSLDYQTNNNDQAVVEICITR.I	0.9929	2	2740.9501
2248	MEP50_MOUSE	342	23.98	3	6	K.NASCTLSSAVHSQGVTR.L	0.9958	2	1775.8822
						R.LVFSPHSVPLLTSLSEDCSLAVLDSSLSEVF	0.9958	3	3506.941
						K.YEHDDIVSTVTVLSSGTQAVSGSKDCCIK.I	0.9931	3	3158.3755
2249	MERL_MOUSE	596	4.7	2	2	K.EFTIKPLDKK.I	0.9924	1	1219.4667
						K.AQITEEEAKLLAQK.A	0.9958	1	1572.7991
2250	MESD2_MOUSE	224	20.54	2	2	K.ETEEITSLWQGSLFNANYDVQR.F	0.9909	2	2601.7887
						R.LLEQWEKDDDIEEGDLPEHK.R	0.9929	2	2439.5945
2251	MET_MOUSE	1379	2.68	2	2	R.NETHNPTVKDLIGFGLQVAK.G	0.9958	3	2182.4844
						K.EALVKSEMNVNMK.Y	0.9944	1	1493.7767
2252	MET10_MOUSE	553	8.32	2	2	K.QHIQINLNGRVSLNFK.D	0.9925	2	1882.1758
						R.RPPPSSVNTGGITEIMAEGGELEFVK.R	0.9924	2	2717.0662
2253	METH_MOUSE	1253	2.87	2	6	R.VPPASVFEGHMLLSGLEPFR.I	0.9958	2	2184.5609
						K.IPLLIGGATTSR.T	0.9958	2	1199.4361
2254	METK1_MOUSE	396	7.58	2	13	K.IIVDTYGGWGAHGGGAFSGK.D	0.9958	2	1951.1485
						K.KPIYQK.T	0.9944	1	776.9542
2255	METK2_MOUSE	395	10.89	3	13	R.FVIGGPQGDAGLTGR.K	0.9958	2	1445.6182
						K.YLDEDTIYHLQPSGR.F	0.9958	2	1807.9573
						R.TAAYGHFGR.D	0.9958	2	980.0708
2256	METL2_MOUSE	389	3.86	1	2	K.VQENSSPLVCPEK.Q	0.9958	2	1487.6159
2257	MFAP1_MOUSE	439	2.73	1	2	R.DVFERPSAKK.R	0.9958	1	1177.3457
2258	MFAP2_MOUSE	183	6.56	1	3	R.TVCAHEELLR.A	0.9915	2	1228.3569
2259	MFAP4_MOUSE	257	7.78	1	5	R.ADGEYWLGLQNLHLLTLK.Q	0.9958	2	2085.4105

2260	MFAP5_MOUSE	164	8.54	1	4	R.QCVHQSCFTSLR.R	0.9958	2	1523.6209
2261	MFGM_MOUSE	463	2.59	1	2	R.AFGWYPHLGR.L	0.9958	2	1204.3763
2262	MFHA1_MOUSE	1048	9.83	3	3	R.GLRFIVYDLAGDESYEVIQPFFLSPGALYVL	0.9958	3	4637.3319
						R.DASLLLHKLLLGTNGEGEGEGESFPTIAVP	0.9944	3	3917.3648
						R.QIALQEKNDAEGLSHLAK.V	0.9958	2	1966.2016
2263	MFN1_MOUSE	741	18.22	7	12	R.CTNEVNASILQSQQEIIENLKPLLPAGIQNK.	0.9958	3	3464.9073
						K.VLPSGIGHTTNCFLSVEGTDGDK.A	0.9958	2	2405.5897
						R.LSVLVDEFCSEFHPTPSVLK.V	0.9958	2	2305.5989
						K.TVNQLAHALHMDK.D	0.9958	2	1478.7093
						K.AGCLVHVFWPK.A	0.9958	2	1314.5389
						K.AIQLESELENFSK.Q	0.9958	1,2	1508.6684
						R.CLHFLVEELK.V	0.9917	2	1288.4956
2264	MFN2_MOUSE	757	6.08	2	3	K.AGWLDSELNMFTHQYLQPSR.-	0.9958	2	2394.6666
						R.LSVLVDEYQMDFHPSPVVLKVYK.N	0.9958	3	2708.1878
2265	MFSD5_MOUSE	450	14	2	2	R.ALGGLSTALLFSAFEAWYIHEHVER.H	0.9944	3	2819.1919
						R.ACSNPSFLQFQLDFYQVYFLALAADWLQA	0.9958	3	4093.6363
2266	MGAT1_MOUSE	447	3.8	1	2	R.ACIRPEISRTMTFGR.K	0.9958	2	1796.0637
2267	MGDP1_MOUSE	164	69.51	7	105	R.TSEIQGANQLLELFDLGK.Y	0.9958	2	1977.2218
						R.DGMSLQTLTQGLETFAK.A	0.9958	2	1841.0863
						R.RGQNIQLYPEVPEVLGR.L	0.9958	2	1969.251
						R.GQNIQLYPEVPEVLGR.L	0.9958	2	1813.0635
						K.LAVFDLDYTLWPFWVDTHVDPPFHK.S	0.9958	3	3060.4809
						R.LQSLGVPVAAASR.T	0.9958	2	1269.4868
						K.TGVPFSQMVFFDDENR.N	0.9947	2	1890.0772
2268	MGLL_MOUSE	303	32.67	5	23	R.ELPEVTNSVLHEVNSWVSHR.I	0.9958	2	2333.5657
						R.TPQNVPYQDLPHLVNADGQYLFCR.Y	0.9958	2	2847.1254
						K.GLDMLVFAHDHVGHGQSEGER.M	0.9958	2	2292.4906
						K.MYEGAYHVLHR.E	0.9958	2	1376.5755
						K.ALIFVSHGAGEHCGR.Y	0.9958	2	1611.7667
2269	MGT4A_MOUSE	535	8.79	2	2	K.DYMKPLLLK.V	0.9958	1	1121.4235
						K.MFQAPDLALVVEFILMFYKEKPIDWLLDHIL	0.9958	3	4164.0548
2270	MIA3_MOUSE	1930	6.01	4	4	R.SIEEEEDVSVSSSHQRKPQPAAGYTDSED	0.9944	3	4438.5831
						K.FGSTADALVSDDEATR.L	0.994	2	1655.7154
						K.HSASDPGPAPVVNSSSR.S	0.9958	2	1665.7599
						K.DPNLSEEDKVEPPTWGDAFFSIVTGGEGK	0.9958	3	3989.3411
2271	MIA40_MOUSE	139	33.09	2	7	K.SAFSCFHYSTEDIK.G	0.9958	1,2	1692.7883
						K.YPDLYPQDEEEEEEAKPVEPVEETADTK.V	0.9958	3	3281.4182

2272	MICA1_MOUSE	1048	6.49	2	2	K.EADNNGSLESQELPTPGDSNMQPDPSSPF	0.9958	3	4571.8872
						R.LSSLNIIPDSGAEPPPKPPR.S	0.9958	2	2086.3959
2273	MICA2_MOUSE	960	3.02	2	3	K.FFQDLKEETGIDLENIVYYK.D	0.9958	2	2465.7619
						R.FPLER.W	0.9944	1	661.7789
2274	MIDN_MOUSE	465	5.81	1	4	K.LAATSSTSLLQGQSQIRMCKPPGDR.L	0.9958	3	2704.0399
2275	MIER2_MOUSE	541	2.96	1	4	R.SVGECVEYYYLWKK.S	0.9958	2	1825.0369
2276	MIF_MOUSE	115	33.04	3	26	R.LHISPDR.V	0.9944	1	837.9541
						K.LLCGLLSDR.L	0.9958	2	1047.206
						R.VYINYYDMNAANVGWNGSTFA.-	0.9958	2	2371.5855
2277	MILK1_MOUSE	870	5.63	2	2	R.QREEEEDK.M	0.9924	1	1063.066
						R.LQASSEVQFHTPTKPPLPSKPQELASPPG(	0.9958	3	3903.4331
2278	MIME_MOUSE	298	17.11	3	9	R.RLDFTGNLIEDIEDGTFSK.L	0.9958	2	2171.3685
						R.VIHLQFNSISSLTDDTFCK.A	0.9958	2	2226.4571
						K.RLPIGSYF.-	0.9944	1	953.1289
2279	MIMIT_MOUSE	168	44.05	4	9	K.EVDYEAGDIPTEWEAWIR.R	0.9958	2	2180.3349
						K.GHASAPYFGREEPSVAPTSTGK.T	0.9958	2	2247.4289
						K.ETSEELLPSPTATQVK.G	0.9958	1	1730.9097
						K.TFQPGSWTPEDGKR.Q	0.9958	2	1606.7349
2280	MINT_MOUSE	3644	1.81	3	3	K.EAGPAAASPQESESPQKGSGSSPQLANNF	0.9958	3	3349.4655
						K.IGGNKIK.V	0.9944	1	729.8979
						K.GSGSSPQLANNPADPDREAEEESASASTA	0.9958	3	3796.9109
2281	MIPEP_MOUSE	711	8.16	3	3	R.SCARDVSTSWSPVGAAFNVKPQSHLWNLI	0.9958	3	3571.9433
						K.HYQTGQPLPK.A	0.9958	2	1169.3256
						R.FSHLVGYGAK.Y	0.9958	1	1079.2437
2282	MIPO1_MOUSE	279	6.09	1	2	R.TAALVEEVYFAQRER.D	0.9958	2	1782.9939
2283	MIRO1_MOUSE	631	8.08	3	3	K.ISDQDNDGTLNDAELNFFQR.I	0.9958	2	2313.399
						K.AVLHPTGPLYCPEEK.E	0.9958	2	1711.9214
						K.TGVLQSLLGR.N	0.9917	2	1044.2394
2284	MIRO2_MOUSE	620	5.65	2	6	K.AVLHPTAPLYDPEAK.Q	0.9958	2	1622.8614
						K.SCFGHPLAPQALEDVK.R	0.9958	2	1769.9611
2285	MIST_MOUSE	435	2.3	1	2	R.FQNVSLLK.N	0.9958	1	949.1381
2286	MK01_MOUSE	358	12.01	2	10	K.RIEVEQALAHPYLEQYYDPSDEPIAEAPFK.	0.9958	3	3520.8768
						R.NYLLSLPHK.N	0.9944	1,2	1085.2914
2287	MK09_MOUSE	423	6.86	2	6	K.FEELFPDWIFPSESER.D	0.9958	2	2029.2127
						K.RISVDEALR.H	0.9945	2	1059.2107
2288	MK12_MOUSE	367	10.9	2	2	K.KDFASVLTNASPQAVNLLER.M	0.9915	2	2174.4618
						R.VTAAEALTHPYFESLR.D	0.9958	2	1806.0281

2289	MK14_MOUSE	360	21.67	4	7	K.HENVIGLLDVFTPAR.S	0.9958	2	1681.9322
						K.MNFANVFIGANPLAVDLLEK.M	0.9958	2	2177.5665
						R.YQNLSPVGSGAYGSVCAAFDTK.T	0.9958	2	2293.4608
						R.TLFPGTDHIDQLK.L	0.9909	2	1485.6799
2290	MK1I1_MOUSE	124	38.71	2	46	K.KLPSVEGLHAIVVSDR.D	0.9958	2	1721.0097
						K.VANDSAPEHALRPGFLSTFALATDQGSK.L	0.9958	3	2902.1931
2291	MK67I_MOUSE	317	7.89	2	3	K.EDISNNIPK.K	0.9958	1	1030.1228
						R.DSEGNQVLPDQK.E	0.9958	1	1330.3941
2292	MKL2_MOUSE	1080	5.56	3	12	R.GQQRPPDPQPSDPPHPFNTSDPK.H	0.9912	2	2540.7111
						K.KQPQGFPEILTAEDFEPFK.E	0.9918	2	2222.5023
						K.ECLEGSNQKSLK.E	0.9944	1	1393.5029
2293	MKNK2_MOUSE	459	2.61	1	2	K.DWSHISFAAK.D	0.9958	1	1162.2902
2294	MLE1_MOUSE	188	19.68	3	23	K.EAFLLFDR.T	0.9924	1	1011.1656
						R.HVLATLGEK.M	0.9958	1	968.1411
						R.VFDKEGNGTVMGAELR.H	0.9958	2	1723.9415
2295	MLL3_MOUSE	4903	0.82	2	2	K.DSSGSISEQLPSR.D	0.9958	1	1363.424
						K.RCNQENAGPVVSAIQGSTPLPAR.D	0.9958	3	2423.6573
2296	MLRB_MOUSE	172	68.6	7	54	R.ATSNVFAMFDQSQIQEFK.E	0.9958	2	2092.3307
						R.NAFACFDEEATGTIQEDYLR.E	0.9958	2	2351.4541
						R.FTDEEVDELYR.E	0.9958	2	1416.4839
						R.DGFIDKEDLHDMLASLGK.N	0.9958	2	2005.2501
						K.GNFNYIEFTR.I	0.9958	2	1261.3794
						K.NPTDAYLDAMMNEAPGPINFTMFLTMFGEI	0.9958	3	3368.8767
						K.KGNFNYIEFTR.I	0.9952	2	1389.5535
2297	MLRN_MOUSE	172	31.4	2	3	K.NPTDEYLEGMMNEAPGPINFTMFLTMFGE	0.9958	3	3426.9134
						R.NAFACFDEEASGFIHEDHLR.E	0.9958	2	2366.4742
2298	MLRV_MOUSE	166	81.33	13	1162	R.IEGGSSNVFSMFEQTQIQEFK.E	0.9958	2	2407.6569
						K.RIEGGSSNVFSMFEQTQIQEFK.E	0.9958	2	2563.8444
						K.NLVHIITHGEEKD.-	0.9958	2	1505.6707
						R.FSKEEIDQMFAAFPPDVTGNLDYK.N	0.9958	2	2764.0785
						K.EEIDQMFAAFPPDVTGNLDYK.N	0.9958	2	2401.6497
						R.DTFAALGR.V	0.9958	1	850.9499
						K.GADPEETILNAFK.V	0.9924	1	1405.5474
						K.EAFTIMDQNR.D	0.9958	1	1225.3618
						R.EMLTTQAER.F	0.9909	2	1079.2133
						K.EAPGPINFTVFLTMFGEK.L	0.9958	2	1999.3319
						K.LKGADPEETILNAFK.V	0.9958	2	1646.8809

						K.NLVHIITHGEEK.D	0.9958		2	1390.5821
						K.NEEIDEMIK.E	0.9958		1	1121.2476
2299	MLTK_MOUSE	802	8.35	3	5	K.DSGGEPEENEEKIVNLELVFGFHLKPGTGF	0.9944		3	3772.0827
						K.GMHYLHMEAPVK.V	0.9958	1,2		1413.6954
						R.SFAELLHQCWEADAK.K	0.9958		2	1805.9507
2300	MMAA_MOUSE	415	8.43	2	3	R.EFQHQMLASGELAAK.R	0.9958		2	1660.8853
						R.ACLAEAITLVESTHTR.K	0.9958		2	1772.9623
2301	MMAB_MOUSE	237	43.88	6	14	K.HTAFQEGPVLELER.W	0.9958		2	1626.8094
						R.RVVPLVQMGETDANVAK.F	0.9958		2	1828.1369
						K.YSSQLPPLKAFILPSGGK.S	0.9945		2	1904.2597
						K.DDQVFEAVGTTDELSSAIGFAMELVTEK.G	0.9958		2	3004.2893
						K.GHMFAEELQK.I	0.9929		2	1190.3593
						K.SSSALHFCR.A	0.9958		2	1065.14
2302	MMGL_MOUSE	304	7.57	1	7	R.LENSHLVVVNSLEEQNFLQNR.L	0.9958		2	2483.7434
2303	MMP16_MOUSE	607	4.61	1	2	R.SAETMQSALAAMQQFYGINMTGKVDR.N	0.9958		2	2850.2521
2304	MMP2_MOUSE	662	2.42	1	7	R.IHDGEADIMINFGR.W	0.9958		2	1588.7784
2305	MMP20_MOUSE	482	6.43	2	2	K.FATADPNLLAATPRTFR.S	0.9931		3	1863.1264
						K.LDQNTMNVIK.K	0.9958		1	1176.3734
2306	MMP37_MOUSE	337	10.68	2	2	R.RILAHFPEDLSLAFAYGSAVYR.Q	0.9958		3	2497.8589
						K.MHQGQLEIDK.S	0.9958		2	1199.3673
2307	MMR2_MOUSE	775	8.52	2	2	R.ESRASEIQPLQVTLCWASVASAPLLPPCSS	0.9958		3	3384.7865
						R.RPQTEAITHPVTGLILNTSTVTLPPTGNVTR	0.9944		3	3286.7562
2308	MMSA_MOUSE	535	64.49	22	542	K.AISFVGSNQAGEYIFER.G	0.9929		2	1889.0746
						K.IVNDNPYGNGTAIFTTNGATAR.K	0.9958		2	2268.4478
						K.WIDIHNPATNEVVGR.V	0.9958		2	1721.9132
						R.VNAGDQPGADLGPLITPQAK.E	0.9958		2	1963.1979
						R.AFPAWADTSILSR.Q	0.9948		2	1435.6225
						K.TITSQWKEEDATLSSPAVVMPTMGR.-	0.9958	2,3		2737.1152
						K.EEIFGPVLVVLETETLDEAIK.I	0.9958		2	2345.6923
						K.KWLPELVDR.A	0.9958		2	1156.3702
						K.LLQDSGAPDGTLNIIHGQHDAVNFICDHPDI	0.9958		3	3512.8267
						K.NHGVVMPDANK.E	0.9958		1	1182.3397
						R.GLQVVEHACSVTSLMLGETMPSITK.D	0.9958		2	2690.1086
						K.ENTLNQLVGAAFGAAGQR.C	0.9958		2	1817.9993
						R.CMALSTAILVGEAK.K	0.9958		2	1464.7266
						R.VCNLIDSGTK.E	0.9957		2	1107.2152
						K.YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	0.992	2,3		3116.6661

						K.GYENGNFVGPTIISNVKPSMTCYK.E	0.9958		2	2677.9979
						K.EEDATLSSPAVVMPTMGR.-	0.9958	1,2		1892.1494
						K.NHGVVMPDANKENTLNQLVGAAFGAAGQI	0.9958		2	2981.3159
						K.TLADAEGDVFR.G	0.9958		1	1194.2865
						K.LFIDGK.F	0.9958		1	692.8333
						K.WLPELVDR.A	0.9958		1	1028.1961
						K.SDKWIDIHNPATNEVVGR.V	0.9944		2	2052.2541
2309	MOCOS_MOUSE	862	6.61	2	2	R.LCLIQPFIDLQQRIMVIK.A	0.991		2	2229.7388
						K.SDCHSPQEGSCTDPSVCNGSYPDTNIMDL	0.9958		3	3895.0117
2310	MOES_MOUSE	577	30.16	12	107	K.KTQEQLASEMAELTAR.I	0.9958		2	1807.0289
						K.FYPEDVSEELIQDITQR.L	0.991		2	2083.2591
						R.IQVWHEEHR.G	0.9958		2	1234.3597
						K.TANDMIHAENMR.L	0.9958	1,2		1403.5708
						R.ILALCMGNHELYMR.R	0.9958		2	1722.0395
						R.EVWFFGLQYQDTK.A	0.9958		2	1661.8541
						K.TQEQLASEMAELTAR.I	0.9958	1,2		1678.8548
						R.KESPLLFK.F	0.9924		1	962.1772
						K.TAMSTPHVAEPAENEHDEQDENGAEASAE	0.9958		3	3337.426
						K.KAQQELEEQTR.R	0.9929		2	1360.4667
						K.KGSELWLGVDALGLNIYEQNDR.L	0.9958		2	2491.763
						K.KTANDMIHAENMR.L	0.9958		2	1531.7449
2311	MOG_MOUSE	246	28.46	2	2	K.VEDPFYWVNPGVLTLIALVPTILLQVPVGLV	0.9958		3	4588.5687
						K.ITLFVIVPVLGPLVALIICYNWLHRR.L	0.9944		3	3077.782
2312	MON1B_MOUSE	553	7.05	2	9	K.FELYTCLSPLVTKAGAILVVTK.L	0.9937		2	2424.8927
						R.LVEDGMHNLGALR.T	0.9958		1	1425.6458
2313	MON2_MOUSE	1715	1.4	2	4	R.DAFITAICK.G	0.9924		1	1039.1828
						K.EAAESGIIKVK.T	0.9958		1	1145.3415
2314	MOR2B_MOUSE	1022	1.08	1	2	R.EPVTDNMEK.F	0.9958		1	1063.1676
2315	MORC1_MOUSE	950	4.84	2	3	K.LALLLQKLQLGGPAGDPQQIDAYLEDLLK.E	0.9958		3	3135.6714
						K.SLPGVQMEDLSPR.S	0.9958		1	1429.6312
2316	MOS2L_MOUSE	189	24.87	2	21	R.LGLVPVSEASTVIAVSSAHR.A	0.9954		2	1994.2987
						R.QSVEDNASEPSGKDVDDVQEKPK.D	0.9956		2	2502.6079
2317	MOSC2_MOUSE	338	16.86	2	4	K.SIYQSSPLFGMYFSVEK.L	0.9958		2	1984.2739
						K.KLYPSESYLQNYEVAYPDCSPVHLISEASL	0.9958		3	4173.5886
2318	MOT1_MOUSE	493	4.26	1	5	K.AAQSPQQHSSGDPTEEESPV.-	0.9958		2	2082.1015
2319	MOT3_MOUSE	492	14.43	2	2	R.AGSPEQEPEEEAVPELDHESIGGHEARGQ	0.9958		3	3214.3428
						R.ARSYGTLVAFCIAFGLSYGMVGALQFEVLM	0.9958		3	3926.593

2320	MOXD1_MOUSE	613	5.71	1	2	K.ANVVSTVLPYFDLVNQNVPIPNKGTTYWC(	0.9958	3	3846.4017
2321	MP2K1_MOUSE	393	20.36	5	12	K.RLEAFLTQK.Q	0.9956	2	1106.3103
						K.LCDFGVSGQLIDSMANSFVGTR.S	0.9929	2	2375.6246
						K.KLEELELDEQQR.K	0.9958	2	1530.6751
						K.KPTPIQLNPAPDGSAVNGTSSAETNLEALQ	0.9958	3	3150.4698
						K.KKPTPIQLNPAPDGSAVNGTSSAETNLEAL	0.9958	3	3278.6439
2322	MP2K2_MOUSE	401	9.23	1	2	R.RKPVLPALTINPTIAEGPSPTSEGASEANLV	0.9958	3	3616.1063
2323	MP2K3_MOUSE	347	10.37	2	4	R.ISCVSKPPVSNPTPPR.N	0.9958	2	1736.9751
						R.MSYLELMEHPFFTLHK.T	0.9958	2	2024.4029
2324	MP2K4_MOUSE	397	8.56	2	17	R.FTLNPNTTGVQNPHIER.L	0.9958	2	1939.138
						K.WNSVFDQLTQVVK.G	0.9958	2	1564.7813
2325	MP2K7_MOUSE	535	9.91	2	2	K.LCDFGISGRLVDSK.A	0.9924	2	1567.7485
						K.QTGYLTIGGQRYQAEINDLENLGEMGSGT(	0.9958	3	3876.2123
2326	MPCP_MOUSE	357	27.17	6	34	R.IQTQPGYANTLR.E	0.9958	1	1362.5284
						K.MYKEEGLNAFYK.G	0.9958	1	1493.7174
						K.GIFNGFSITLK.E	0.9958	1	1197.4197
						K.ALYSNILGEENTYLWR.T	0.9958	2	1943.1662
						R.LPRPPPPEMPESLK.K	0.9958	2	1588.9055
						R.ANPFNAPHLQLVHDGLSGPR.S	0.9958	2	2141.397
2327	MPDZ_MOUSE	2055	4.72	4	4	K.SVLQSPLFSQILNLQTSLQQLK.D	0.9958	2	2486.9145
						R.KSPLPSLPHSLYPK.Y	0.9924	1	1564.8681
						R.GPDGLGFSIVGGYGSPHGDLPIYVK.T	0.9909	2	2503.8168
						R.IQIGDQIIAVDGTNLQGFTNQQAVEVLR.H	0.9958	3	3042.4191
2328	MPP4_MOUSE	635	5.35	2	2	K.ASGSPEIQELR.Q	0.9958	1	1187.2951
						K.ISDLTICAGLIPSNHLLKR.K	0.9944	2	2122.4821
2329	MPP5_MOUSE	675	4	2	2	K.VAEQEMQLEPITDER.V	0.9958	2	1788.9672
						R.ELGLSFQK.G	0.9958	1	922.0691
2330	MPP6_MOUSE	553	9.58	3	3	R.FIVLNPARFGTTVPFTSR.K	0.9924	2	2024.3732
						K.IDSILEVVQTGR.T	0.9958	1	1330.5241
						K.EPHFQSLLEAHDIVASK.C	0.9958	2	1922.1479
2331	MPPA_MOUSE	524	38.93	10	111	R.RFSSGATYPNIPLSSPLPGVPKPIFATVDG(	0.9958	3	3472.9659
						R.GKPAVAALGDLTDLPTYEHIQAALSSR.N	0.9958	2	2796.1527
						K.YLSGIAHFLEK.L	0.9955	2	1278.4936
						K.GLDTVVDLLADVVLHPR.L	0.9958	2,3	1833.1381
						R.MVLAGVGVEHEHLVECAR.K	0.9958	2	2007.2812
						K.HGGICDCQTSR.D	0.9958	2	1291.2953
						R.EVLHSYLK.N	0.9924	1	989.1595

						R.KYLVGAEPAWGAPGTVDVDR.S	0.9958		2	2102.3543
						R.MAVQFELEDLNMRPDPEPLLTEMIHEAAFF	0.9958		3	3545.0805
						R.KLPHELCTLIR.N	0.9958		2	1380.6397
2332	MPPB_MOUSE	489	30.67	8	30	R.IVLAAAGGVCHNELLELAK.F	0.9958		2	1979.2933
						K.TNMLLQLDGSTPICEDIGR.Q	0.9946		2	2134.3754
						K.SPAIAALGPIER.L	0.9958	1,2		1195.4044
						R.RIPIPELEAR.I	0.9957		2	1194.4196
						R.EMQEVETNLQEVVFDYLHATAYQNTALGR	0.9958		3	3371.7027
						K.FHFGDSLCSHK.G	0.9958		2	1335.4277
						R.SQLDLELEIENMGAHLNAYTSR.E	0.9958		2	2505.7619
						K.NNGTAHFLEHMAFK.G	0.9958		3	1617.8223
2333	MPPH1_MOUSE	1774	2.2	3	3	K.NKELLDLIEK.L	0.9958		1	1215.4325
						K.EYHTQEISR.E	0.9958		1	1163.2321
						K.EYHTQEISRENSFHASIEAIWEECK.E	0.9958		3	3095.2745
2334	MPRA_MOUSE	345	19.71	2	2	R.EDPHALPLFFIVLASFTYLSFSAVAHLLQAK	0.9958		3	3448.0447
						R.AQVPPLFWKPYIYAGYRPLHQNWCFYFRT	0.9958		3	4265.9237
2335	MPRD_MOUSE	278	12.95	2	12	K.SFESTVGQGSDTYSYIFR.V	0.9958		2	2045.1693
						R.HTLAANFNPVSEER.G	0.9958		2	1585.7165
2336	MPRI_MOUSE	2483	7.81	9	17	R.DGPQWTDGVTVLQYVDGDLCPDK.I	0.9958		2	2579.7455
						K.SATGQVQVLGLVHTQK.L	0.9958		2	1666.9181
						K.TKSVSSTIFFHCDPLVK.D	0.9958		2	1967.2384
						R.VTGPPIFNPVANEVYLNFESSTHCLADR.Y	0.9958		3	3149.4529
						R.TGATEHYLINVCK.S	0.9958		2	1506.6648
						K.EEGEKPDFCNGHSPAVTVTFVCPSER.R	0.9957		3	2951.1079
						R.DGPQWTDGVTVLQYVDGDLCPDKIR.R	0.9958		3	2849.0925
						R.AGINASYSEKGLVFMSICEENENCGPGVG/	0.9958		3	3912.1747
						K.GHIQLSYTDGDDCGSDK.K	0.9958		2	1868.8744
2337	MPZL3_MOUSE	237	23.63	2	4	K.DNGTFSCAVKNPPDVYHNIPLTELTVTER.C	0.9944		3	3289.5921
						R.GTVGGRGCALFPLLSILVVQGAR.I	0.9924		2	2342.7563
2338	MRC1_MOUSE	1456	2.4	2	21	R.YEQAFLTSLVGLRPEK.Y	0.9958		2	1852.1405
						K.MVSQSHAVVPEGADK.G	0.9958		2	1555.746
2339	MRC2_MOUSE	1479	4.87	3	15	R.GLQTPLWIGLASEEGSR.R	0.9956		2	1815.0361
						R.DSLEDCVTIWGPEGRWNDSPCNQSLPSIC	0.9958		3	3522.7048
						R.RGGCVALATGSAMGLWEVK.N	0.9958		1	1964.2562
2340	MRCKA_MOUSE	1719	1.63	2	3	K.QMVRNINNK.R	0.9958		1	1117.3116
						K.EEEVDLVMQKAESLR.Q	0.9958		2	1776.9996
2341	MRCKG_MOUSE	1551	3.55	2	2	R.KPWTSLSSESVSCPQGSLSPAASLIQVSEF	0.9931		3	3443.8047

						K.QSQALQQEVAELREELQAR.G	0.9958		2	2227.4392
2342	MRGBP_MOUSE	218	6.42	1	2	K.VVIEEEMKEEMK.E	0.9958		1	1494.7585
2343	MRIP_MOUSE	1024	6.35	3	5	K.SPEGTTVSGYDIMK.S	0.9958		2	1485.649
						K.VEPPTPQEPGPAKMAVTSSSGGSSGSSSS	0.9958		3	3330.602
						K.FQANIFNKSK.C	0.9944		1	1197.3793
2344	MRM1_MOUSE	320	4.38	1	2	K.AGLQGERAELLR.V	0.9958		1	1313.4996
2345	MRP7_MOUSE	1501	3	2	2	K.GFGLATQEPWIQCATIR.D	0.993		2	1949.1828
						K.ALKLGPSRPPTGEVLNLLGTDSER.L	0.9944		2	2521.8766
2346	MRP9_MOUSE	1366	6.15	3	3	R.LNTVLNCDLVLVMENGK.V	0.9958		2	1933.2367
						K.QVENISRSPWFSHITSSIQGLGVIHAYDK.K	0.9958		3	3271.6597
						K.SPPSYITQPEDPDTILLLANATLTWEQEINR	0.9958		3	3656.0838
2347	MRVI1_MOUSE	899	4.67	2	2	K.ELENFK.A	0.9958		1	779.8681
						K.ELTVEQKENFDPLQHVEATPMAQASGASIS	0.9944		2	3414.7687
2348	MSI1H_MOUSE	362	3.87	1	3	K.VCEIHFHEINNK.M	0.9958		2	1540.6849
2349	MSI2H_MOUSE	346	9.25	2	5	K.MFIGGLSWQTSPDSLR.D	0.9958		2	1796.0509
						K.VLGQPHHELDSK.T	0.9924	1,2		1360.5125
2350	MSLN_MOUSE	625	6.72	2	5	K.TYPQGYPESLIQQLGHFFR.Y	0.9958		2	2282.5633
						R.QMDLVNEIPFTYEQLSIFK.H	0.9958		2	2316.6741
2351	MSRA_MOUSE	233	53.22	8	154	R.SAVYPTSAVQMEAALR.S	0.9925		2	1694.9433
						K.HNFGPITTDIR.E	0.9958		2	1271.4184
						R.VVYRPEHISFEELLK.V	0.9958		3	1860.1631
						R.EGQVFYYAEDYHQQYLSK.N	0.9958		2	2269.4314
						K.VFWENHDPTQGMR.Q	0.9958		2	1617.779
						K.GVYSTQVGFAGGHTR.N	0.9958		2	1537.675
						K.VISAEEALPGR.T	0.9958		1	1142.2975
						R.RALQLLSSANPVR.R	0.9958		1	1425.6743
2352	MTA1_MOUSE	715	7.41	2	2	K.QVYIPNYNKPNPNQISASSVK.A	0.9958		2	2362.6475
						R.AGPGADTGEEGEVEEEVENPEMVDLPEK.	0.9944		3	2958.0877
2353	MTAP_MOUSE	283	46.64	7	39	K.YVDTPFGKPSDALILGK.I	0.9932		2	1822.1113
						K.IGIIGGTGLDDPEILEGR.T	0.9958		2	1826.0569
						K.SLLLTTIPQIGSMEWSETLR.N	0.9921		2	2276.6532
						R.EEIQPGDMVIIDQFIDR.T	0.9958		2	2019.2769
						R.TSLRPQTFYDGSHCSAR.G	0.9958		2	1984.1015
						R.TWGADVVNMTTVPEVVLAK.E	0.9958		2	2031.3747
						R.GVCHIPMAEPFCPK.T	0.9958		2	1643.8733
2354	MTBP_MOUSE	894	3.47	2	2	K.KPKTISVPDVAVK.G	0.9936		2	1382.6866
						R.CVSGLPLPGREASK.D	0.9958		2	1471.6629

2355	MTCH2_MOUSE	303	17.82	3	8	K.VLQYYQESEKPEELGSVTVQK.E	0.9958	2	2455.724
						R.LCSGVLGTVVHGK.V	0.9958	2	1327.5328
						R.SAATLITHPFHVITLR.S	0.9958	2	1778.1075
2356	MTCPB_MOUSE	107	9.35	1	3	R.GVQELLLK.L	0.9958	1	900.1063
2357	MTDC_MOUSE	350	9.43	2	2	K.NVVVAGR.S	0.9944	1	714.8429
						K.KAGYITPVPGGVGPMTVAMLMK.N	0.9958	3	2219.7671
2358	MTER3_MOUSE	385	7.01	2	2	K.ELGANK.T	0.9958	1	631.7068
						R.FLTTASSIFHNPVENNK.Q	0.9943	2	1920.132
2359	MTF2_MOUSE	593	4.38	2	6	K.EPEGTSHEFK.I	0.9958	1	1161.2133
						K.MIQKTAELPLDK.E	0.9958	1	1387.6776
2360	MTM1_MOUSE	603	9.62	3	3	K.LADAPASTSSSSQMVPHVQTHF.-	0.9958	2	2299.52
						K.HAFPLAHNLPLFAFVNEEK.F	0.9958	2	2195.5284
						R.LPVLSWIHPENK.M	0.9958	2	1433.6933
2361	MTMR5_MOUSE	1867	3.54	2	2	R.EEGVGGSGGGPALLPAEGAVFLTTYRVIFT	0.9958	3	4546.1951
						R.FVDKVCTESGVTSDHLK.G	0.9944	1	1923.0961
2362	MTMR9_MOUSE	545	8.81	2	2	K.EDEKLINATLR.A	0.9958	1	1302.4704
						K.TPRVDNVVLHRPFYTAVEGTLCLTGHHLIL	0.9958	3	3761.2877
2363	MTMRE_MOUSE	648	4.63	2	3	R.DDDSGLLVHCISGWDR.T	0.9924	1,2	1845.9293
						K.YICDLMVENK.K	0.9924	1	1285.464
2364	MTO1_MOUSE	669	10.01	2	7	K.LHLSRPQTIGAASRIPGVTPAAIINLLR.F	0.9929	2	2937.505
						K.HTPDDPSIPFSFLSDSVWIKPEDQLPCYLTH	0.9958	3	4112.5103
2365	MTP18_MOUSE	166	7.83	1	5	R.KLYPSVEKPSTP.-	0.9958	1	1346.5663
2366	MTPN_MOUSE	118	16.1	1	2	K.GPDGLTALEATDNQAIK.A	0.9958	2	1714.8699
2367	MTUS1_MOUSE	1210	2.81	2	3	K.FEALTVVIQHLLSER.E	0.993	2	1756.055
						K.NPQVMYLEQELESLK.A	0.9958	2	1822.0833
2368	MTX1_MOUSE	317	5.05	1	10	R.QYMERLQLLCGEHK.S	0.9958	2	1806.0558
2369	MTX2_MOUSE	263	20.15	3	61	K.VPFIHVGNQVVSELGPIVQFVK.A	0.9958	3	2407.8613
						R.RIEQHYFEDWGK.G	0.9929	2	1608.7532
						K.GHSLSDGLDEVQK.A	0.9924	1,2	1385.4735
2370	MUC18_MOUSE	648	18.36	6	9	K.VWVEVEPVGLLKEGDHVTIR.C	0.9958	3	2276.6408
						R.VHIQSSQIVESSGLYTLK.S	0.9945	2	1990.2639
						K.QPVPTPDLVEAEVGSTALLK.C	0.9958	2	2065.3715
						K.APEEPTIQANVVGIHVDR.Q	0.9958	2	1946.1704
						R.LSLQDSVATLALSHVTPHDER.M	0.9958	2	2290.5382
						R.LQDHYVELQVFK.A	0.9958	2	1519.7404
2371	MUG1_MOUSE	1476	41.33	35	431	R.LSSSDEEDFLYVDIK.G	0.9958	2	1760.8921
						R.AVDQSVLLLKPESELSPSWIYNLPGMQQNI	0.9958	3	3386.8878

						K.ESVVFVQTDKPVYKPGQSVK.F	0.9958		2	2236.5731
						R.AHFSVMGDILSSAIR.N	0.9958		2	1604.8645
						K.MLRPLNELLPLAYIEDPK.K	0.9958		2	2126.5622
						R.YVEDMGLTAFTNLMIK.L	0.9958		2	1847.1946
						R.FSTSQSLPASQTR.L	0.9958		1	1410.5266
						K.YLNETQQLTQKIK.T	0.9958		2	1607.8473
						K.ESGEKEEHSFTVMEFVLPR.F	0.9958	2,3		2252.5036
						K.HTNLVPHGTEK.D	0.9958		1	1233.3695
						K.YTYGKPVPGHVK.I	0.9958		2	1346.5718
						K.QMSFSLAAEPIQGPYK.I	0.9958		2	1768.0375
						K.FALEIPVEFSMVPMAK.M	0.9929		2	1810.2197
						K.MLSGFIPLKPTVK.K	0.9958		2	1431.8199
						R.AFIFIDESHITHAFTWLSQK.Q	0.9958		2	2392.7191
						K.LPIICFDYGMVPISAPR.V	0.9958		2	1950.3125
						R.KDPSSNDPLTETIR.K	0.9958		2	1573.7001
						R.HGIPFFVK.V	0.9958		2	945.1521
						R.LSEDQEDCILYSSWLAEK.H	0.9958		2	2187.3308
						K.QQNSNGGFSSTQDTVVALDALSK.Y	0.9958		2	2368.5193
						R.HTSSWLVTPK.S	0.9944		1	1156.3268
						R.VEFDLAFTPEISWSLR.T	0.99		2	1911.1644
						K.QEHTFSSLFCASDAEISEK.M	0.9944		2	2187.2904
						K.AQELSYTSATTTDQHGLAEFSIDTTCISGSS	0.9958		3	3772.0369
						R.NLQPAIVK.V	0.9944		1	883.0788
						K.VPNAMSVNDEVLSVTACGK.Y	0.9958		2	1992.2178
						K.MLRPLNELLPLAYIEDPKK.N	0.9958	2,3		2254.7363
						K.NLFDELVLDK.D	0.9958		1	1206.3813
						K.YMVLVPSQLYTETPEK.I	0.9958		2	1899.2092
						R.LQVTASPQSLCGLR.A	0.9952		2	1530.7307
						K.ENNSIHWKRPQK.S	0.9958		1	1537.7213
						R.LTAQPAPSPEDLTLSMSTIMWLTK.Q	0.9958		2	2633.0902
						K.VNHKEEDSCSYFYCMEER.H	0.9915		2	2384.4678
						K.GGVDDEMTLSAYITMALLESSLPATHPVVS	0.9958		3	3234.7041
						K.EEHSFTVMEFVLPR.F	0.9958		2	1721.9684
2372	MUG2_MOUSE	1451	5.79	4	5	R.GEAFMLKATVMNYLPTSMR.M	0.9958		3	2161.6003
						R.AHFSVMGDILSSAIK.N	0.9958		2	1576.8511
						R.AVDQSVLLLKPEDELSPSWIYNLPGMQHNI	0.9944		3	3423.9086
						K.YTYGKPVPGQVK.I	0.9944		2	1337.5614

2373	MUG4_MOUSE	1448	1.45	1	18	K.QSGEKEEHSFTVMEFVLPR.F	0.9912	2	2251.5188
2374	MUP1_MOUSE	180	18.89	2	22	K.INGEWHTIILASDK.R	0.9958	2	1597.8113
						R.LFLEQIHVLENSLVLK.F	0.9958	2	1896.2804
2375	MUSC_MOUSE	201	8.96	2	2	R.GADAGGAGGR.A	0.9958	1	788.7953
						R.GADAGGAGGRAGGAGK.K	0.9958	1	1230.2827
2376	MUSK_MOUSE	868	4.72	2	4	R.VSSPGPPPLSCAEQLCIARQVAAGMAYLSI	0.9931	3	3317.7169
						R.IHNVQK.E	0.9924	1	738.8649
2377	MUTA_MOUSE	748	34.76	12	119	R.ADTLDLPEELPGVKPFTR.G	0.9947	2	1999.2713
						K.NPEDLIWHTPEGISIKPLYSR.A	0.9958 2,3		2466.7991
						R.DQALAEQCLSALTQCAASGDGNILALAVDA	0.9924 2,3		3275.5293
						K.VADPWGGSYMMESLTNDVYEAALK.L	0.9958	2	2648.9619
						K.VIATGFADLGFDVDIGPLFQTPR.E	0.9956	2	2450.7967
						K.ELTALGRPDILVMCGGVIPPQDYEFLYEVG	0.9958	3	4368.9576
						K.GKNPEDLIWHTPEGISIKPLYSR.A	0.9958	2	2652.0251
						R.AHCQTSGWSLTEQDPYNNIVR.T	0.9958	2	2477.6183
						R.GDVGMAGVAIDTVEDTK.I	0.9958 1,2		1678.8518
						R.AAVQVLDDIEK.C	0.9958	1	1201.3623
						K.AGQQGLSVAFDLATHR.G	0.9958	2	1671.8533
						K.IIADIFQYTAQHMPK.F	0.9958	2	1777.0912
2378	MXI1_MOUSE	228	5.7	1	34	R.HTTLGLLNKAK.A	0.9939	1	1196.4355
2379	MXRA8_MOUSE	442	8.14	2	2	K.EVLVVAHGAPALMTCINR.A	0.9937	2	1952.2885
						R.VVHWDLSGGPGSQR.R	0.9958	2	1495.6377
2380	MYB_MOUSE	636	5.03	2	3	K.KLVEQNGTDDWK.V	0.9944	1	1433.5608
						R.IKELELLLMSTENELK.G	0.9958	2	1904.2696
2381	MYBA_MOUSE	751	6.26	3	8	R.EVLKEETGTDIFLK.E	0.9958	2	1622.8559
						K.VLNPELIKGPWTK.E	0.9958 1,2		1495.8051
						R.RYLSTYTATSSTSR.A	0.9924	1	1594.7215
2382	MYBPP_MOUSE	932	3.54	2	2	R.KQHVPQFEETGEKPVVTQK.F	0.9911	3	2210.4948
						R.ETTQRPWALK.S	0.9958	1	1230.4093
2383	MYCB2_MOUSE	4711	1.55	2	2	R.RESELFSSHLVSNTCGLLASIVSELTASALG	0.9944	3	4617.09
						R.LPSATDMQSRCSILSPELALPTGSR.A	0.9958	3	2689.0223
2384	MYCBP_MOUSE	103	33.01	2	5	K.VLVALYEEPEKPTSALDFLK.H	0.9958	2	2263.6361
						K.YEATVEENKK.L	0.9958	1	1211.3141
2385	MYCD_MOUSE	935	7.49	3	9	R.SQQMDELLDVLIESGEMPADAR.E	0.9958	2	2448.7224
						K.KPKDPKPK.V	0.9944	1	938.1582
						K.SSCSDQKPLPFLATTIKQEDVSSCPFAPQQ	0.9958	3	3712.037
2386	MYG_MOUSE	154	88.96	17	10312	R.HSGDFGADAQGAMSK.A	0.9944	2	1479.564

						K.VEADLAGHGQEVLIGLFK.T	0.9958	2	1897.1815
						K.HGCTVLTALGTILK.K	0.9958	2	1484.7454
						K.ALELFRNDIAAK.Y	0.9958	2	1361.584
						K.YLEFISEIIIEVLK.K	0.9958	2	1710.0637
						K.KHGCTVLTALGTILK.K	0.9958	2	1612.9195
						K.THPETLDKFDK.F	0.9958	1	1331.468
						K.GQHAAEIQPLAQSHATK.H	0.9958	2	1787.9731
						K.RHSGDFGADAQGAMSK.A	0.9944	2	1635.7515
						K.HGCTVLTALGTILKK.K	0.9958	2	1612.9195
						K.KGQHAAEIQPLAQSHATK.H	0.9958	2	1916.1471
						R.HSGDFGADAQGAMSKALELFR.N	0.9958	2	2209.4412
						R.NDIAAK.Y	0.9958	1	631.7068
						K.YLEFISEIIIEVLKK.R	0.9943	2	1838.2377
						-.MGLSDGEWQLVLNVWGKVEADLAGHGQE	0.9924	3	3811.3905
						K.YKELGFQG.-	0.9958	1	942.0593
						K.GQHAAEIQPLAQSHATKHK.I	0.9958	2	2053.2882
2387	MYG1_MOUSE	380	11.58	3	8	K.LSSAGLVYLHFGR.K	0.9958	2	1420.6542
						R.LNFYQHSWLPAR.A	0.9958	2	1532.7446
						K.EHLYHLESELSPK.V	0.9944	2	1582.7533
2388	MYH1_MOUSE	1942	13.23	21	374	K.LEQQVDDLEGSLEQEK.K	0.9958	1	1860.9696
						K.NLQQEISDLTEQIAEGGK.R	0.9958	2	1974.132
						K.AITDAAMMAEELK.K	0.9958	1	1394.6411
						K.DIDDLELTLAK.V	0.9944	1	1246.4002
						R.LQDLVDK.L	0.9944	1	830.9567
						R.SLSTELFK.I	0.993	2	925.0697
						R.LDEAEQLALK.G	0.9958	1	1130.2835
						K.HADSVAELGEQIDNLQR.V	0.9958	3	1896.0238
						K.ILAEWK.Q	0.9958	1	759.9237
						K.AITDAAMMAEELKK.E	0.9958	1	1522.8152
						R.TKYETDAIQR.T	0.9958	1	1225.3439
						K.IKLEQQVDDLEGSLEQEK.K	0.9958	2	2102.3031
						K.QIEQEKSELQAALEEAEASLEHEEGK.I	0.9921	2,3	2927.1052
						R.ADIAESQVNK.L	0.9958	1	1075.1637
						K.KHADSVAELGEQIDNLQR.V	0.9958	2	2024.1979
						K.VEAHFSLVHYAGTVDYNIAGWLDKNK.D	0.9944	3	2949.2951
						R.IEELEEEIEAER.A	0.9958	1	1489.5762
						K.LEQQVDDLEGSLEQEKK.I	0.9958	2	1989.1437

						K.ALQEAHQQTLDDLQAEEDK.V	0.9958		2	2183.2933
						K.YETDAIQR.T	0.9924		1	996.0648
						K.NKDPLNETVVGLYQK.S	0.9958		1	1718.9475
2389	MYH10_MOUSE	1976	22.93	27	97	K.QEVMISDLEERLK.K	0.9944		2	1590.8322
						K.ELACEVKVLQQVK.A	0.9958		2	1544.7979
						R.IAQLEEELEEEQSNMELLNDR.F	0.9958		2	2533.7235
						K.SLEAEILQLQEELASSER.A	0.9958		2	2046.2389
						R.TQLEELEDELQATEDAK.L	0.9958		2	1963.0594
						R.HATALEELSEQLEQAK.R	0.9958		2	1797.9597
						K.KQELEEILHDLESR.V	0.9958		2	1739.9231
						K.DAAGLESQLQDTQELLQEETR.Q	0.9958		2	2375.5083
						K.MQAHIQDLEEQLDEEEGAR.Q	0.9958		2	2242.3789
						K.LQNELDNVSTLLEEAEK.K	0.9958		2	1946.1186
						K.LDGETTDLQDQIAELQAQVDELK.V	0.9958		2	2573.7705
						R.QLLQANPILESFGNAK.T	0.9958		2	1744.0006
						R.LQQELDDLTVDLDHQR.Q	0.9958		2	1939.0892
						K.LQNELDNVSTLLEEAEKK.G	0.9958		2	2074.2927
						K.KVDDDLGTIESLEEAK.K	0.9958		2	1762.9085
						K.KFDQLLAEEK.G	0.9958	1,2		1221.3959
						K.VIQYLAHVASSHK.G	0.9958	1,2		1453.6841
						R.IAECSSQLAEEEEK.A	0.9958		2	1623.6771
						R.DLSEELEALK.T	0.9958		1	1147.2677
						R.DLSEELEALKTELEDTLDTTAAQQELR.T	0.9958		2	3063.2965
						K.NILAEQLQAETELFAEAEEMR.A	0.9958		2	2436.696
						K.VEDMAELTCLNEASVLHNLK.D	0.9958		2	2287.5562
						R.KLDGETTDLQDQIAELQAQVDELK.V	0.9958		2	2701.9445
						R.HAEQERDELADEIANSASGK.S	0.9958		2	2171.2419
						R.KLQAQMK.D	0.9958		1	847.0636
						K.LQQLFNHTMFILEQEEYQR.E	0.9923		2	2468.7894
						K.KLDAQVQELHAK.V	0.9944		2	1380.587
2390	MYH11_MOUSE	1972	16.23	18	96	K.QLLQANPILEAFGNAK.T	0.9958		2	1728.0012
						K.DVASLGSQLQDTQELLQEETR.Q	0.9958		2	2361.5248
						K.HTQAVEELTEQLEQFK.R	0.9958		2	1931.1094
						K.LDAFLVLEQLR.C	0.9958		1	1317.5712
						R.KATLQAEQLSNELATER.S	0.9958		2	1903.0996
						R.SGKLDAFLVLEQLR.C	0.9958		2	1589.8754
						R.HVSTLNIQLSDSK.K	0.9958		2	1442.6121

						K.LQNEVESVTGMLNEAEGK.A	0.9958	2	1949.1401
						R.DLGEELEALK.T	0.9958	1	1117.2414
						R.DLGEELEALKTELEDTLDSTATQQELR.A	0.9958	2,3	3049.2696
						K.SLEADLMQLQEDLAAAER.A	0.9958	2	2004.2195
						R.LQQELDDLVVDLDNQR.Q	0.9958	2	1914.0795
						K.KMAQQMLDLEEQLEEEEAAR.Q	0.9958	2	2392.6583
						R.IAQLEEELEEEQGNMEAMSDR.V	0.9958	2	2452.6241
						K.QADLEKEELAEELASSLSGR.N	0.9958	2	2176.3422
						K.KLEGDLK.D	0.9958	1	802.9463
						K.VDYNASAWLTKNMDPLNDNVTSLLNASSD	0.9944	3	3298.6056
						K.KQELEEILHEMEAR.L	0.9912	2	1755.9837
2391	MYH14_MOUSE	2000	5.5	6	11	R.TPNVGGPGGPQVEWTAR.R	0.9958	2	1723.8857
						R.RLDGESSELQEQMVEQK.Q	0.9958	2	2007.1798
						R.RLQQELDDATVDLGQQK.Q	0.9904	2	1958.1356
						R.RLESQLQEVQGR.S	0.9958	2	1443.6029
						R.HSQALVEMAEQLEQAR.R	0.9952	2	1841.049
						R.LQQHIQELESHLEAEEGAR.Q	0.993	2	2218.3879
2392	MYH3_MOUSE	1940	3.66	5	119	K.GTLEDQIISANPLLEAFGNAK.T	0.9958	2	2202.4692
						K.NALAHALQSSR.H	0.9958	2	1168.298
						K.LEQQVDDLESSLEQEK.K	0.9944	2	1890.9959
						K.AKNALAHALQSSR.H	0.9944	2	1367.5509
						R.KLAEQELLDSNER.V	0.9958	1	1545.6897
2393	MYH4_MOUSE	1939	5.42	7	161	R.DLEEATLQHEATAAALR.K	0.9958	2	1840
						K.NLTEEMAGLDENIAK.L	0.9958	2	1648.8255
						R.RDLEEATLQHEATAAALR.K	0.9958	2	1996.1875
						R.IHFGATGK.L	0.9958	1	830.9621
						K.TKLEQQVDDLEGSLEQEK.K	0.9958	2,3	2090.2487
						K.KMEGDLNEMEIQLNHANR.Q	0.9958	2	2143.3973
						K.WLPVYNPEVVAAYRGK.K	0.9958	1	1863.1692
2394	MYH6_MOUSE	1938	47.83	82	2873	R.VQLLHSQNTSLINQK.K	0.9958	1	1723.97
						K.GTLEDQIIQANPALEAFGNAK.T	0.994	2	2201.4411
						K.LELQSALEEAEASLEHEEGK.I	0.9958	2	2213.3599
						K.LTQESIMDLENDKLQLEEK.L	0.9958	2	2277.5488
						K.NLQEEISDLTEQLGEGGK.N	0.9958	2	1961.0899
						K.ALQEAHQQALDDLQAEEDK.V	0.9958	2	2153.267
						K.ALQEAHQQALDDLQAEEDKVNTLTK.S	0.9958	2	2810.0471
						R.ILNPAAIPEGQFIDSR.K	0.9903	1,2	1741.9847

K.NDLQLQVQAEQDNLNDAEER.C	0.9958	2	2343.4258
K.MEGDLNEMEIQLSQANR.I	0.9915	2	1979.1872
K.DTQLQLDDAVHANDDLK.E	0.9958	1	1912.0202
K.MVSLLQEKNDLQLQVQAEQDNLNDAEER.(	0.9958	3	3272.5683
R.LQDAEEAVEAVNAK.C	0.9958	1	1487.6067
K.NLTEEMAGLDEIIAK.L	0.9958	1	1647.8811
R.LEEAGGATSVQIEMNK.K	0.9958	1	1677.867
K.LELDDVTSNMEQIIK.A	0.9958	1,2	1748.9862
K.IEDEQALALQLQK.K	0.9924	1	1499.7044
K.MESDLTQLQTEVEEAVQECR.N	0.9958	2	2396.5514
R.LQNEIEDLMVDVER.S	0.9958	2	1703.9049
R.MVDSLQTSLDAETR.S	0.9944	1	1566.7235
R.IEELEEELEAER.T	0.9958	1	1489.5762
R.TECFVPDDKEEYVK.A	0.9958	1	1759.8732
R.NNLLQAELEELR.A	0.9958	1	1442.6121
K.MESDLTQLQTEVEEAVQECRNAEEK.A	0.9956	2,3	2968.1391
R.TLEDQANEYR.V	0.9958	1	1239.2841
R.AQLEFNQIK.A	0.9958	1	1091.2523
R.SLNDFTTQR.A	0.9958	1,2	1082.1582
K.LSYTQQMEDLK.R	0.9958	2	1356.5335
K.SAYLMGLNSADLLK.G	0.9958	1,2	1496.7619
K.EFDISQQNSK.I	0.9958	1	1196.2591
K.ENIAIVER.R	0.9958	1	944.0757
R.SNAAAAALDK.K	0.9958	1	932.0214
R.LDEAEQIALK.G	0.9958	1	1130.2835
K.VKLEQQVDDLEGSLEQEK.K	0.9958	2	2088.2762
K.DTQLQLDDAVHANDDLKENIAIVER.R	0.9958	2	2837.0727
K.LAEQELIETSER.V	0.9912	2	1418.5437
K.MVSLLQEK.N	0.9924	1	948.1657
K.KMEGDLNEMEIQLSQANR.I	0.9958	2	2107.3613
K.LSYTQQMEDLKR.Q	0.9958	1	1512.721
K.SEFKLELDDVTSNMEQIIK.A	0.9958	2	2240.5305
K.NAYEESLEHLETFK.R	0.9958	1	1710.8376
R.KLAEQELIETSER.V	0.9958	1	1546.7178
K.LLGSLDIDHNQYK.F	0.9958	2	1516.694
R.LQDLVDKLQLK.V	0.9958	1,2	1313.5803
K.RQAEEAEEQANTNLSK.F	0.9958	1,2	1818.8949

K.NAYEESLEHLETFKR.E	0.9958	2	1867.0251
K.KALQEAHQQALDDLQAEEDK.V	0.9958	2,3	2281.4411
K.KMESDLTQLQTEVEEAVQECR.N	0.9958	2	2524.7255
K.QLEVEKLELQSALEEAEASLEHEEGK.I	0.9952	2,3	2940.1877
K.GSSFQTVSALHR.E	0.9958	2	1290.4215
K.LTGAIMHYGNMK.F	0.9958	1,2	1336.6099
K.ERLEAQTRPFDIR.T	0.9958	2	1631.8319
R.QAEEAEEQANTNLSK.F	0.9958	2	1662.7075
R.SEAPPHIFSISDNAYQYMLTDR.E	0.9915	2	2556.809
R.RNNLLQAELEELR.A	0.9958	1,2	1598.7996
R.VIQYFASIAAIGDR.S	0.9958	2	1524.7599
K.APGVMDNPLVMHQLR.C	0.9931	2	1679.0081
K.RVIQYFASIAAIGDR.S	0.9943	2	1680.9474
K.FDKIEDMAMLTFLHEPAVLYNLK.E	0.9958	2	2740.2478
K.KGSSFQTVSALHR.E	0.9958	2	1418.5955
K.RNAESVK.G	0.9958	1	803.8937
K.LMATLFSTYASADTGDSGK.G	0.9958	2	1937.1285
K.EALISQLTR.G	0.9924	1	1031.1973
R.NYHIFYQILSNK.K	0.9958	2	1540.7618
R.KVQHELDEAEER.A	0.9958	2	1483.5779
K.QKYEESQSELESSQK.E	0.9924	1,2	1800.8737
K.LTQESIMDLENDK.L	0.9958	1	1536.6942
K.VQHELDEAEER.A	0.9958	1,2	1355.4038
K.ELTYQTEEDKK.N	0.9958	2	1384.4827
K.LAEKDEEMEQAK.R	0.9937	2	1421.5622
R.KAPGVMDNPLVMHQLR.C	0.9958	2	1807.1822
K.LKNAYEESLEHLETFK.R	0.9958	2	1952.1711
K.KNMEQTIK.D	0.9924	1	992.1785
R.SEAPPHIFSISDNAYQYMLTDRENQSILITG	0.9958	3	4042.423
K.HLKNSQAHLK.D	0.9924	1	1176.364
R.ELEEISERLEEAGGATSVQIEMNK.K	0.9958	2	2663.9135
K.YEESQSELESSQK.E	0.9958	2	1544.5689
K.EMANMKEEFGR.V	0.9958	1	1342.5275
K.VQHELDEAEERADIAESQVNK.L	0.9958	2	2411.5443
R.SNAAAAALDKK.Q	0.9958	2	1060.1955
R.VKLEEAQR.S	0.9927	2	973.1173
R.LEAQTRPFDIR.T	0.9958	1	1346.529

2395	MYH7_MOUSE	1935	8.79	10	32	K.MDADLSQLQTEVEEAVQECR.N	0.9958	2	2352.4982
						K.NLTEEMAGLDEIIVK.L	0.9958	2	1675.9349
						K.NLQEEISDLTEQLGSTGK.S	0.9943	2	1963.1058
						K.NDLQLQVQAEQDNLADAEER.C	0.9958	2	2300.4008
						R.GKLTYTQQLEDLK.R	0.9944	1	1537.7533
						K.QLEAEKLELQSALEEAEASLEHEEGK.I	0.9958	3	2912.1339
						R.IEDEQALGSQLQK.K	0.9924	1	1459.5963
						K.KMDADLSQLQTEVEEAVQECR.N	0.9958	2	2480.6723
						K.KMEGDLNEMEIQLSHANR.M	0.9958	2	2116.3717
						R.QLEEEVKAK.N	0.9958	1	1074.2193
2396	MYH9_MOUSE	1960	31.73	43	506	K.ANLQIDQINTDLNLER.S	0.9958	2	1871.0574
						R.LQQELDDLLVDLDHQR.Q	0.9958	2	1951.1436
						K.KVEAQLQELQVK.F	0.9958	1,2	1413.6573
						K.LQVELDSVTGLLSQSDSK.S	0.9958	2	1920.1241
						R.ELETQISELQEDLESER.A	0.9958	2	2049.1529
						K.HSQAVEELADQLEQTK.R	0.9958	1,2	1826.9579
						K.VSHLLGINVTDFTR.G	0.9958	1,2	1572.8045
						K.DFSALESQLQDTQELLQEENR.Q	0.9904	2	2494.6311
						K.KANLQIDQINTDLNLER.S	0.9958	2	1999.2315
						K.NFINNPLAQADWAAK.K	0.9958	2	1673.8687
						R.IIGLDQVAGMSETALPGAFK.T	0.9958	2	2019.3637
						R.VISGVLQLGNIAFK.K	0.9958	1,2	1459.7721
						R.FLSNGHVTIPGQQDK.D	0.9958	2	1641.8241
						K.QIATLHAQVTDMK.K	0.9958	2	1456.7002
						R.DLGEELEALKTELEDTLDSTAAQQELR.S	0.9958	2	3019.2433
						K.MQQNIQELEEQLEEEESAR.Q	0.9958	2	2334.4737
						K.SMEAEMIQLQEELAAAER.A	0.9958	2	2050.3064
						K.LQLQEQLQAETELCAEAEELR.A	0.9958	2	2502.7039
						K.VAAYDKLEK.T	0.9958	1	1037.201
						K.KQELEEICHDLEAR.V	0.9958	2	1770.903
						R.DELADEIANSSGK.G	0.9958	1,2	1349.3941
						K.LVWVPSSK.N	0.9958	1	916.1081
						K.IAQLEEQLDNETK.E	0.9958	1,2	1531.6598
						K.THEAQIQEMR.Q	0.9924	1,2	1243.3801
						K.KLVWVPSSK.N	0.9958	1	1044.2822
						R.VAEFTTNLMEEEEK.S	0.9958	2	1670.8286
						K.TELEDTLDSTAAQQELR.S	0.9958	2	1921.0251

						R.LTEMETMQSQLMAEK.L	0.9958		2	1771.0689
						K.NMDPLNDNIATLLHQSSDK.F	0.9958		2	2127.3337
						K.KLEEDQIIMEDQNCK.L	0.9958		2	1894.07
						R.KLEGDSTDLSDQIAELQAQIAELK.M	0.9958		2	2616.8822
						K.RALEQQVEEMK.T	0.9958		2	1361.556
						R.RGDLPFVVTR.R	0.9958		2	1160.3616
						K.DLEAHIDTANK.N	0.9958		1	1227.3165
						R.CQYLQAEK.K	0.9958		1	1040.1272
						K.GALALEEK.R	0.9944		1	830.9567
						K.EEVGEEAIVELVENGKK.V	0.9958		2	1873.0673
						K.KLEMDLK.D	0.9958		1	877.0869
						K.KMQQNIQELEEQLEEEESAR.Q	0.9958		2	2462.6477
						K.HLAAENR.L	0.9958		1	810.8881
						K.HSQAVEELADQLEQTKR.V	0.9958		2	1983.1454
						K.NKHEAMITDLEER.L	0.9952		2	1586.7601
						K.MEDGVGCLETAEEAK.R	0.9958		1	1639.7377
2397	MYL3_MOUSE	204	71.57	12	1116	K.DTGTYEDFVEGLR.V	0.9958	1,2		1502.5774
						K.LMAGQEDSNGCINYEAFVK.H	0.9944		2	2147.3302
						K.ITYGQCGDVLR.A	0.9958		1	1282.4051
						R.ALGQNPTQAEVLR.V	0.9944	1,2		1397.5742
						R.HVLATLGER.L	0.9958		1	996.1545
						K.AAPAPAAAPAAAPAAAPEPERPK.E	0.9958		2	2094.3781
						K.IKIEFTPEQIEEFK.E	0.9958	2,3		1752.0172
						K.MMDFETFLPMLQHISK.N	0.9958	2,3		1969.3823
						K.IEFTPEQIEEFK.E	0.9958	1,2		1510.6837
						K.IEFTPEQIEEFKEAFLLFDR.T	0.9958		2	2502.8261
						K.NKDTGTYEDFVEGLR.V	0.9958		2	1744.8553
						K.AAPAPAAAPAAAPAAAPEPERPKEAEFDAS	0.9958		3	2972.2841
2398	MYL4_MOUSE	193	24.87	3	39	K.EQGTYEDFVEGLR.V	0.9958		2	1543.6299
						K.TLDFEMFLPILQHISR.N	0.9958		2	1961.3294
						R.ALGQNPTNAEVLR.V	0.9958		2	1383.5473
2399	MYL6_MOUSE	151	38.41	5	106	K.VLDFEHFLPMLQTVAK.N	0.9958		1	1889.2629
						K.DQGTYEDYVEGLR.V	0.9958		1	1545.6024
						K.NKDQGTYEDYVEGLR.V	0.9958		2	1787.8803
						R.HVLVTLGEK.M	0.9958		1	996.1949
						R.VFDKEGNGTVMGAEIR.H	0.9958		2	1723.9415
2400	MYL6B_MOUSE	207	7.25	1	7	R.ALGQNPTNAEVLK.V	0.9958		2	1355.5339

2401	MYLK_MOUSE	1941	0.98	1	2	R.FESQPQSQEVTEGQTVK.F	0.9943		2	1923.0435
2402	MYLK3_MOUSE	795	25.66	9	31	R.ELSLAGSGSTPPTTAQAAWPEVLELVR.A	0.9944		2	2782.1229
						R.AITLVGSTFQNSK.V	0.9958		2	1366.5571
						K.NEVNIMNQLSHVNLIQLYDAFESK.S	0.9958		2	2821.1773
						R.TVEGLPLIINTSLK.G	0.9958		1	1498.8033
						K.DTLISAGYTVSQHEVLGGGR.F	0.9958		2	2061.259
						K.KLNVLTEK.V	0.9958		1	945.1472
						R.LSSGPLPQPLGPLTPDSDIHSGDALPR.I	0.9958	2,3		2739.0575
						K.LQCVCQGMDHLEQDLHR.L	0.9958		2	2140.3107
						K.GSLADGPEENKEQAEVAGVKPNHVLTTGG	0.9924		3	3633.9108
2403	MYO15_MOUSE	3511	2.08	2	2	R.MFAIYGPEQVQQYSGRALGENPPHLFAIAN	0.9944		3	3851.4174
						K.LILRFMGDPHLHGTQEMILGNYIVHQGLVEI	0.9958		3	3870.5689
2404	MYO1C_MOUSE	1028	9.44	5	29	R.VNNININQGSITFAGGPGR.D	0.9958		2	1930.1307
						R.GVSFYEVPPHLFAVADTVYR.A	0.9958		2	2268.5767
						R.NFHVFYQLLEGGEEETLR.R	0.9958		2	2182.3971
						R.LLQSNPVLEAFGNAK.T	0.9958		2	1601.843
						K.GAPVGGHILSYLLEK.S	0.9958		2	1554.8296
2405	MYO1D_MOUSE	1006	4.47	2	2	K.GIIAILDDACMNVGKVTDGMFLEALNSK.L	0.9929		3	2997.458
						K.NSMIALVDNLASK.E	0.9958		1	1376.611
2406	MYO1F_MOUSE	1099	1.09	1	3	R.EEASNILLNK.K	0.9958		1	1131.2713
2407	MYO5B_MOUSE	1818	4.13	4	4	R.NLVTDLKPQMLSGTVPCLPAYILYMCIR.H	0.9944		3	3268.8729
						R.EATIMIQKSVR.G	0.9958		1	1276.5371
						K.LGILDLLDEECKVPK.G	0.9924		1	1743.0167
						R.YENLRDEQTPGHR.K	0.9958		3	1615.7025
2408	MYO6_MOUSE	1265	3.79	3	3	K.NLEISIDALMAKFTSTMMTR.E	0.9958		2	2274.7139
						R.QARPTYATAMLQNLLK.-	0.9958		2	1820.1601
						R.REEDEER.R	0.9958		1	962.9487
2409	MYO7A_MOUSE	2215	0.99	2	2	K.YIDIHFNK.R	0.9944		1	1050.2022
						K.WAQLAIAAHK.K	0.9958		1	1109.3164
2410	MYO9B_MOUSE	2114	4.45	5	9	R.ELRQALQTDPAAVK.L	0.9958		1	1540.7599
						K.DTNLVLNVFQSLLDEFTR.S	0.9958		2	2125.3861
						K.FLDEFLLNKVNDLR.S	0.9958		1	1737.0086
						K.LASAVLSQSLDLSEK.H	0.9958		1	1561.7728
						R.TPVVQDLELGALSEEAAGGDEDR.E	0.9958		2	2372.5047
2411	MYOF_MOUSE	2048	5.57	6	9	R.DQLRPTQLLQNVAR.F	0.9912		2	1652.8942
						K.QKHSATTVFGANTPIVSCNFDR.V	0.9958		3	2451.6672
						R.YGGRDYHLDEFEANK.I	0.9944		1	1814.9084

						R.SLLTEADAGHTEFTDEVYQNENR.Y	0.9958		3	2640.7362
						K.NLVDPFVEVSFAGK.K	0.9958		1	1522.7411
						R.NKDGSNLPILPSQR.A	0.9958		1	1539.7318
2412	MYOM1_MOUSE	1666	11.22	9	34	K.ALNLTCNVWGDPPPEVSWLK.N	0.9943		2	2297.5817
						R.FPVTGLIEGR.S	0.9958	1,2		1089.2798
						K.TVDLSGQAFDEAFAEFQR.L	0.9958		2	2032.1736
						K.SHPSAPWTGQIIVTEEEPTEGVIPGPPTDLS	0.9958		3	3901.2757
						R.ATLTFSHLNKEDEGLYTIR.V	0.9958		2	2209.4637
						R.AVNQAGVGKPSDLAGPVVAETRPGTK.E	0.9958	2,3		2520.8485
						K.LHCSVAGWPEPR.L	0.9945		2	1409.5535
						K.LNEDHLLHAPEFIIKPR.S	0.9958		2	2043.3763
						K.KTLEETQTYHGK.L	0.9958		2	1435.5767
2413	MYOME_MOUSE	2224	2.88	3	4	K.EELETKFGHWQK.E	0.9952		1	1532.6958
						K.NEATEMETLVEAEKR.C	0.9924		1	1750.9183
						R.NTMLSLCLENAELKEQMGEAMSDGWEVEI	0.9958		3	3588.9183
2414	MYOZ2_MOUSE	264	30.3	5	23	R.SPPNPENIAPGYSGPLK.E	0.9958		2	1738.9377
						K.YTFENFQYESR.A	0.9958		2	1484.5645
						R.SPWEQAIGSDPELLEALYPK.L	0.9958		2	2244.5059
						K.VPDFELLLLTDPR.F	0.9958		2	1528.7887
						R.FLAFANPLSGR.R	0.9958		2	1193.3909
2415	MYPN_MOUSE	1315	3.04	2	3	R.ISMHQDTTGYVCLLIQPAKK.S	0.9958		2	2304.6759
						R.LEGRVIGMPPPVFYWK.K	0.9958		1	1890.2964
2416	MYPT1_MOUSE	1004	5.98	2	2	K.EKDSAPTAVTIPVAPTVVNAAAPSTTTLTTT	0.9958		3	3928.3831
						R.RSTQGVTLTDLQEAEK.T	0.9958		2	1776.9414
2417	MYSM1_MOUSE	819	3.66	2	4	R.GSADPCLNAVKIEK.L	0.9944		2	1502.6739
						K.YLNKTSVRPGLK.N	0.9958		1	1376.642
2418	MYST4_MOUSE	1872	2.46	3	5	K.EAERLMEQASCWEK.E	0.9958		2	1767.9172
						K.LILGHMEKLK.N	0.9958		1	1182.5102
						R.WTPMLISNAVVSEEER.E	0.9958		2	1862.1077
2419	MYT1_MOUSE	1127	1.51	1	5	K.CPVPGCVGLGHISGK.Y	0.9958		1	1538.7192
2420	MYT1L_MOUSE	1187	4.8	2	3	K.CPTPGCTGRGHVNSNR.N	0.9958		1	1770.8346
						R.YCKNASPSSSTTSSYAPSSSSNLSCGGGS	0.9958		3	3698.6988
2421	N4BP1_MOUSE	893	9.97	3	3	K.AMHCIFVGAQSLFLKSLIQDTCADLCVLDTC	0.9958		3	4038.6334
						R.VVLDEFTAPAEK.A	0.9958		1	1319.4973
						R.GASGHQQRNPAFPENGFQQQTEPLLPNN	0.9958		3	3893.1901
2422	N6MT2_MOUSE	214	23.36	2	4	K.YNVGVIEENWQLSQFWYSQDTALR.L	0.9958		3	2948.2206
						R.GKILLCTGAIMEEQAAQLLGVK.M	0.9958		2	2344.7816

2423	NAB2_MOUSE	525	6.48	2	2	K.SPLELGEKLSPLPGGPGAGDPR.I	0.9929	2	2145.4203
						R.KYSVIYGR.L	0.9958	1	986.1588
2424	NAC1_MOUSE	970	13.4	7	17	R.VGIIDDDIFEEDENFLVHLSNVR.V	0.9958	2	2689.9384
						K.EIEQLIELANYQVLSQQQK.S	0.9958	2	2275.5639
						K.ALLLNELGGFTLTGK.E	0.9958	2	1547.8351
						K.VVNSHVDNFLDGALVLEVDER.D	0.9958	2	2341.5828
						K.TFFIEIGEPR.L	0.9944	2	1209.3873
						R.GMIIEHEGDRPASK.T	0.9952	2	1540.7344
						R.IAEMGRPILGEHTK.L	0.9941	2	1552.8321
2425	NACAM_MOUSE	2187	43.26	46	395	K.GSALSGASSPLYPLEVSFLPEAGLAVQGPK	0.9958	2	2944.3544
						K.NLPISALVNVGAPVSPAQAGLPTR.K	0.9958	2	2343.7318
						R.SSSAPLSLVALAPHSVQK.S	0.9958	2	1793.0733
						K.APVAPSNEATIVPTEIPTSLK.N	0.9958	2	2136.4503
						K.DPASPVTSLVVPAAHK.Q	0.9958	2	1589.832
						K.ETPPGGVTAMPLEIPSAPQK.A	0.9958	2	2021.3362
						K.TTGGPAPVVRPAIAGVATTTSLR.A	0.9958	2	2194.5393
						K.GSNVALQPLVTQVPASQK.T	0.9958	2	1838.1142
						K.NILFVITKPDVYK.S	0.9958	2	1550.8815
						K.GAPNALAESPASPK.K	0.9932	2	1310.4496
						K.QIPTPEDAVTILAGSPLSPK.K	0.9958	2	2035.3452
						K.QFPAPPASATLGVPVSPLPATEGLK.N	0.9958	2	2446.8492
						K.ESPSSQSASSLEVLSEDTVTK.K	0.9958	2	2182.3001
						K.GPVGSQVATPLAAFTSDK.V	0.9958	2	1746.9579
						K.ETSLEGATAVPLEIPPSHK.K	0.9958	2	1977.2218
						K.EIPVSCIGATHHALDNPSAISVAPATHVPPP	0.9958	3	4004.4553
						K.GLPSAVALAPQTVPVEK.D	0.9958	2	1677.9817
						K.SVPFPDPPLAEISFSNAR.K	0.9958	2	1945.1821
						K.GAPVPSTGAPPSPK.G	0.9958	2	1263.4362
						R.ASTLPATTLPSLK.E	0.993	2	1300.5382
						K.IEDLSQQAQLAAAEK.F	0.9958	2	1615.7807
						K.DTTLQPLAPIALK.E	0.9958	1	1381.6555
						K.SPVSDTLSGALTSPPPK.G	0.9958	2	1654.8577
						K.GVTAVPLEISLPLK.E	0.9958	1	1437.763
						K.EFPASPSIKPVTTSLAQTAPPSLQK.A	0.9958	2	2596.9836
						K.NNSNDIVNAIMELTM.-	0.9958	2	1679.9007
						K.DSHISPVSDACSTGTTTPQASEK.L	0.9958	2	2377.4468
						K.ETPAPSPEGATTAPVQIPPSPR.K	0.9958	2	2201.4411

						K.GPPATLAETPTYPK.K	0.9958	1,2		1443.6397
						K.RASTLPATTLPSLK.E	0.9946		2	1456.7257
						R.KVDAVSHMESSGSSR.Q	0.9958		2	1577.7093
						K.KGPTAFTEMLAAPAPESALAITAPIQK.S	0.9958	2,3		2726.2036
						R.AFPSHLENPLASVQPGLMSCPQTLSNTSP	0.9958	2,3		3309.7279
						K.QPLLESAPGSVLESPSK.L	0.9958		2	1739.9634
						K.EAPATPSVGVIAVSGEISPSPK.K	0.9958		2	2094.3697
						K.VPVPAETQEVAVSSR.E	0.9958		2	1569.7551
						K.NTAPSTTSPLVPLASEGCPVASSMALSPQ	0.9958		3	4581.1122
						K.GAPIVPTESSISSK.Q	0.9924		1	1373.5462
						K.ENLAAPAVLPVSSK.S	0.9958		1	1396.6268
						K.AIETLLVSPAK.G	0.9958		1	1142.3812
						K.VPPEAVSASVAPKPAPAASLTLAPSPVAPL	0.9958		2	3129.7105
						K.KLSQTVGPK.E	0.9958		1	958.146
						K.ETPTTPSPEGVTAAPLEIPISSK.K	0.9958		2	2323.6025
						K.KAAATETPIETSTAPSLEGAPK.E	0.9958		2	2171.4094
						K.KTPATPSPEGVTAVPLEIPPCSK.K	0.9958		2	2377.7064
						K.TPATPSPEGVTAVPLEIPPCSK.K	0.9946		2	2249.5323
2426	NADC_MOUSE	299	6.02	1	2	R.CSGIASAAATAVEVAR.S	0.9958		1	1534.6757
2427	NADE1_MOUSE	725	5.38	1	2	R.GSLLVLGSANVDESLLGYLTKYDCSSADIN	0.9924		3	3829.2593
2428	NAGA_MOUSE	409	32.03	5	12	R.DPGIVGLLTSDQLPPGHCIFYGMIADGIHT	0.9958		3	4296.9031
						R.AHPQGLVLVTDAVPALGLGNGR.H	0.9958		2	2156.4929
						R.SHEVIQALTAQGIR.V	0.9958		2	1523.7324
						R.AAEVAVQSGATFITHLFNAMLPFHHR.D	0.9958		3	2867.3006
						R.LLSHGVTSFCPTLVTSPPEVYHK.V	0.9958		2	2570.9141
2429	NAGK_MOUSE	343	13.99	3	5	K.IVFDSIDNLEAAPHDIGHVK.Q	0.9958		2	2191.4484
						R.LGILTHLYR.D	0.9958		2	1086.3225
						R.HSSALGGASLGAR.H	0.9958		2	1184.2974
2430	NAL14_MOUSE	993	2.11	1	3	R.IPVGCVTLPNETLLRSLCK.A	0.9958		2	2171.5177
2431	NAL4A_MOUSE	982	1.93	1	3	K.QEVLQLGLKQVSWTEVK.K	0.9958		2	1986.3189
2432	NAL4C_MOUSE	982	6.62	3	3	K.IEDAGVKLLCDAIK.H	0.9958		1	1545.7827
						K.LLCDVLSQEECNIEKLMVAACNLSPDDCK.	0.9909		3	3426.7222
						R.RNGIMDSDIPTLLDVR.I	0.9909		2	1816.0826
2433	NAL4E_MOUSE	978	2.45	2	2	K.ETQEFLMAEK.E	0.9958		1	1226.3869
						K.FNIKDQDSLK.Q	0.9958		1	1208.3568
2434	NALCN_MOUSE	1738	0.69	1	12	R.NAQREDSEIK.M	0.9944		1	1190.2553
2435	NAMPT_MOUSE	491	41.34	12	219	K.DPVPGYSVPAAEHSTITAWGK.D	0.9958		2	2184.413

						R.STEAPLIIRPDSGNPLDTVLK.V	0.9958		2	2237.5584
						R.GVSSQETAGIGASAHLVNFK.G	0.9958		2	1974.1808
						K.KWSIENVSFGSGGALLQK.L	0.9958		2	1922.1912
						K.YLLETSGNLDGLEYK.L	0.9958		2	1715.8975
						R.VIQGDGVDINTLQEIVEGMK.Q	0.9958		2	2159.4596
						K.WSIENVSFGSGGALLQK.L	0.9958		2	1794.0171
						K.DAFEHIVTQFSSVPVSVVSDSYDIYNACEK.	0.9958		3	3408.6656
						R.TPAGNFVTLEEGKGDLEEYGHDLLHTVFK.	0.9958		3	3218.5469
						K.GDLEEYGHDLLHTVFK.N	0.9958		2	1874.0599
						R.EHFQDDVFNER.G	0.9958		2	1436.4802
						R.TPAGNFVTLEEGK.G	0.9958		2	1363.5101
2436	NAR3_MOUSE	420	10.24	2	4	K.EDDSVVLIPLSEVFQVSR.K	0.9958		2	2033.286
						K.SLTEVEERPTILVRNTSFSLK.N	0.9958		3	2420.7685
2437	NARG1_MOUSE	865	1.5	1	2	R.RLPLNFLSGEK.F	0.9958		2	1274.5058
2438	NASP_MOUSE	773	7.89	2	8	K.HLVMGDIPAAVNAFQEAASLLGK.K	0.9952		2	2353.7417
						K.LGEVSVESENYIQAVEEFQACLSLQEQYLE	0.9958		3	3986.2605
2439	NAT13_MOUSE	169	9.47	1	2	K.RLNQVIFPVSYNDK.F	0.9952		2	1693.9432
2440	NAV1_MOUSE	1875	3.41	3	4	K.NQASHPPATKLAELPPTPLR.A	0.9943		2	2139.4624
						K.TSLDVSNSVEPGFLAPGAR.S	0.9958		2	1918.1137
						K.TPPVAVTSPITHTAQSALK.V	0.9958		2	1920.2163
2441	NAV3_MOUSE	2359	3.18	4	39	R.FIHTDPSR.F	0.9958		1	973.0763
						R.AVSHSGSFRDSMEEVHGSSLSLVSSTSSL	0.9944		3	3791.0485
						K.KAEGDCDSHGDGAAK.W	0.9958		1	1518.5029
						R.EGLQMYGK.R	0.9958		1	926.0753
2442	NB5R3_MOUSE	301	13.62	2	6	K.SVGMIAGGTGITPMLQVIR.A	0.9958		2	1902.3209
						K.APDAWDYSQGFVNEEMIR.D	0.9923		2	2129.3081
2443	NBN_MOUSE	751	3.6	1	3	K.LLPAAGAAPGEPYRLLAGVEYVVGR.K	0.9958		2	2540.9682
2444	NCAM2_MOUSE	837	2.15	1	2	K.EENGKEVLNAETIEIK.V	0.9944	1,2		1817.0031
2445	NCKP1_MOUSE	1128	3.1	2	2	K.FLSESLMWHISSQVAELKK.L	0.9958		2	2234.6184
						K.RMTIIGVILSFR.S	0.9958		1	1406.7728
2446	NCOAT_MOUSE	916	6.99	3	6	K.RAPVIWDNIHANDYDQK.R	0.9958		2	2056.2449
						K.LALTEWLQEFGVPHQYSSR.Q	0.9958		2	2262.5297
						R.LLPIDGANDLFFQPPPLTPTSK.V	0.9958		2	2382.7619
2447	NCOR1_MOUSE	2453	2.04	3	5	R.SSANAKK.D	0.9944		1	705.7892
						K.HEAPSSPLSGQPCGDDQNASPSK.L	0.9944		3	2367.4137
						K.STLTPTQRESIPAK.S	0.9958		1	1529.7337
2448	NCPR_MOUSE	678	11.95	3	4	R.LPFKPTTPVIMVGPGTGVAPFMGFIQERAV	0.9958		3	3516.2458

						R.IFELGLGDDDGNLEEDFITWR.E	0.9956		2	2455.6397
						R.TNVLYELAQYASEPSEQEHLHK.M	0.9958		2	2587.8052
2449	NDF4_MOUSE	330	8.79	1	2	R.NYIWALSEVLETGQTLEGKGFVEMLCK.G	0.9958		3	3117.5502
2450	NDK3_MOUSE	169	20.12	2	2	R.EAELLCWEDSAGHWLYE.-	0.9958		2	2109.222
						K.NVIHGSDSVESAHR.E	0.9958		2	1508.5907
2451	NDKA_MOUSE	152	80.26	9	444	K.EISLWFQPEELVEYK.S	0.9958		2	1911.1614
						R.GLVGEIIK.R	0.9924		1	829.0275
						R.NIIHGSDSVKSAEK.E	0.9958		1	1485.6371
						R.VMLGETNPADSKPGTIR.G	0.9958	1,2		1787.0411
						R.TFIAIKPDGVQR.G	0.9958		2	1345.5846
						R.GDFCIQVGR.N	0.9958		1	1052.1412
						K.DRPFFTGLVK.Y	0.9958		2	1180.3922
						K.YMHSGPVVAMVWEGLNVVK.T	0.9958		2	2117.5317
						K.FLQASEDLLK.E	0.9958		1	1164.344
2452	NDKB_MOUSE	152	40.79	4	1253	K.YMNSGPVVAMVWEGLNVVK.T	0.9952		2	2094.4945
						R.NIIHGSDSVESAEK.E	0.9958		2	1486.5785
						K.EIHLWFKPEELIDYK.S	0.9958		2	1961.2677
						K.DRPFFPGLVK.Y	0.9958	1,2		1176.4038
2453	NDRG1_MOUSE	394	33.25	6	14	K.ISGWTQALPDMVVSHLFGK.E	0.9924		2	2087.4443
						K.YFVQGMGYMPSASMTR.L	0.9958		2	1827.1409
						K.EEIHNNVEVVHTYR.Q	0.9921		2	1739.8851
						R.DLEIERPMPGTHTVTLQCPALLVVGDNSPA	0.9958		3	4334.8178
						K.GNRPVILTYHDIGMNHK.T	0.9958		2	1966.2682
						K.MADCGGLPQISQPAK.L	0.9958		1	1573.7706
2454	NDRG2_MOUSE	371	67.65	13	854	R.FGDMQEIIQNFVR.V	0.9924		1	1597.8291
						K.LTGLTSSIPDMILGHLFSQEELSGNSELIQK.	0.9958		3	3359.8164
						R.YALNHPDTVEGLVLINIDPNAK.G	0.9958		2	2407.7288
						R.GIIQHAPNLENIELYWNSYNNR.R	0.9958		2	2659.9206
						R.ILLDQGQTHSVETPYGSVTFTVYGTPKPK.F	0.9958		3	3165.5701
						R.TASLTSAASIDGSR.S	0.9958	1,2		1337.4295
						K.GWMDWAAHK.L	0.9926		2	1102.2555
						K.RPAIFTYHDVGLNYK.S	0.9958		2	1795.0507
						R.TLSQSSESGTLPSGPPGHTMEVSC.-	0.9958		2	2447.599
						K.MADSGGQPQLTQPGK.L	0.9958		2	1515.6813
						K.CPVMLVVGDQAPHEDAVVECNSK.L	0.9958	2,3		2555.7946
						K.YFLQGMGYMASSCMTR.L	0.9958		2	1904.1899
						R.GIIQHAPNLENIELYWNSYNNRR.D	0.9924		2	2816.1081

2455	NDRG3_MOUSE	375	5.07	1	9	R.THSTSSSIGSGESPFSR.S	0.9958	2	1724.7813
2456	NDST3_MOUSE	873	3.32	2	2	K.VKTPENLSPPISK.H	0.9958	2	1410.6537
						R.LQTLPPAQLAHK.Y	0.9958	2	1317.5742
2457	NDUA1_MOUSE	70	17.14	1	2	R.VQYQWYLMER.D	0.9958	2	1416.6373
2458	NDUA2_MOUSE	99	45.45	5	96	K.TVSLNNLSADEVTR.A	0.9958	1,2	1519.6518
						R.YAFGQEK.T	0.9924	1	842.9267
						R.AMQNVLSGK.A	0.9924	1	948.1253
						K.AHPNLPILIR.E	0.9944	1,2	1144.4055
						K.KAHPNLPILIR.E	0.9958	2	1272.5796
2459	NDUA3_MOUSE	84	44.05	2	36	K.ATPYNYPVPVRDDGNMPDVPSHPQDPLGI	0.9952	3	3890.3185
						R.DDGNMPDVPSHPQDPLGPSLDWLK.N	0.9958	2	2631.8762
2460	NDUA4_MOUSE	82	50	5	104	R.LALFNPDVSWDR.K	0.9958	1	1433.6066
						K.FYSVNVDYSK.L	0.9958	1	1222.3397
						R.LALFNPDVSWDRK.N	0.9958	2	1561.7807
						K.NNPEPWNKLGPNEQYK.F	0.9958	2	1929.099
						R.KNNPEPWNK.L	0.9958	1,2	1127.2449
2461	NDUA5_MOUSE	116	66.38	8	1969	K.WKPWEPLVEEPPANQWK.W	0.9958	2	2135.4295
						K.TTGLVGLAVCDTPHER.L	0.9958	1,2	1726.8932
						K.KTTGLVGLAVCDTPHER.L	0.9958	2	1855.0673
						K.KLEALLQGGEVEEVILQAEK.E	0.9958	2	2197.534
						K.YTEQITNEKLDMVK.A	0.9937	2	1712.9556
						R.KYTEQITNEK.L	0.9958	1	1254.3825
						K.LEALLQGGEVEEVILQAEK.E	0.991	2	2069.3599
						K.YTEQITNEK.L	0.9958	1	1126.2084
2462	NDUA6_MOUSE	131	45.8	4	255	R.QAAAAAASTSVKPIFSR.D	0.9958	2	1676.9132
						R.VVDLLVIK.G	0.9944	1	899.1619
						R.EVPNTVHLMQLDITVK.Q	0.9937	2	1838.1724
						R.FFHETETPRPK.D	0.9958	2	1389.5535
2463	NDUA7_MOUSE	113	70.8	9	72	R.NWASGQDLQAK.L	0.9958	1	1218.3115
						K.LSNNYYCTR.D	0.9917	2	1191.2518
						R.REVVPPSIIMSSQK.A	0.9958	2	1571.8755
						K.AVTPAPPMK.R	0.9958	1	912.1351
						R.EVVPPSIIMSSQK.A	0.9958	1	1415.688
						K.KAVTPAPPMK.R	0.9958	1	1040.3092
						K.LRNWASGQDLQAK.L	0.9958	2	1487.6585
						R.TQPPPKLPVGPSHK.L	0.9958	1	1483.7538
						K.AAESSAMAATEK.K	0.9958	2	1167.2763

2464	NDUA8_MOUSE	172	67.44	9	897	K.TDRPLPENPYHSR.A	0.9958	2	1582.7159
						R.ARPEPNPVIEGDLKPAK.H	0.9958	2	1832.1099
						K.LVNGCALNFFR.Q	0.9917	2	1311.4925
						K.SHCAEPFTEYWTCLDYSNMQLFR.H	0.9958	3	2957.1752
						K.LGWVRPDLGQLSK.V	0.9958	2	1469.7269
						K.AAAHHYGAQCDK.T	0.9958	1,2	1329.3807
						K.FDQCVLDK.L	0.9958	1	1025.1126
						R.FFFWTV.-	0.9924	1	847.0037
						K.VKTDRPLPENPYHSR.A	0.9907	2	1810.0225
2465	NDUA9_MOUSE	377	44.03	11	362	K.AVQHSNVVINLIGR.E	0.9958	2	1520.7751
						R.SVFPEAIIIRPSDIFGR.E	0.9937	2	1918.2462
						R.WLSSEIEETKPAK.T	0.9958	1,2	1518.7069
						R.NFDFEDVFVNIPR.A	0.9958	2	1612.782
						R.IHISDVMPTDLPGLEDLGVQPTPLELK.S	0.9958	2,3	2929.3985
						R.FLNHFANYR.W	0.9958	1,2	1182.3268
						R.FIHVSHLNASMK.S	0.9958	2	1384.6391
						R.SSVSGVVATVFGATGFLGR.Y	0.9945	2	1813.0635
						R.WFLAVPLVSLGFK.T	0.9958	1,2	1477.8327
						R.CDVYDIMHLR.L	0.9958	2	1322.4877
						R.KAVQHSNVVINLIGR.E	0.9958	2	1648.9492
2466	NDUAA_MOUSE	355	66.2	18	294	R.LLQYADALEHLLSTGQGVVLER.S	0.9958	2	2426.7752
						K.TEVLNYTTIPVYLPEITIGAHQGSR.I	0.9958	2	2774.1461
						R.VITVDGNICSGK.N	0.9958	1	1263.3997
						K.VTSAYLQDIENAYKK.T	0.9958	2	1743.9543
						R.YGLLAAILGDK.T	0.9958	1,2	1134.3611
						K.HYPEAGIQYSSTTTGDGRPLDIEFSGSCSL	0.9958	3	3504.7113
						K.VTSAYLQDIENAYK.K	0.9958	1	1615.7802
						K.VVEDIEYLK.Y	0.9944	1	1108.2768
						K.EIAQQLGMK.H	0.9944	1	1018.2164
						K.MSEMCEVLVYDSWEAEDPTK.V	0.9958	2	2420.631
						K.YAPGYNAEVGDKWIWLK.-	0.9954	2	2011.2872
						R.LTLPEYLPPHAVIYIDVPVPEVQSR.I	0.9958	2	2847.3269
						K.LRYGLLAAILGDK.T	0.9944	2	1403.708
						K.YAPGYNAEVGDK.W	0.9958	1	1284.3678
						R.KYAPGYNAEVGDK.W	0.9958	1,2	1412.5419
						R.MLVQDKTEVLNYTTIPVYLPEITIGAHQGSR	0.9958	3	3489.024
						R.MLVQDK.T	0.9924	1	733.9012

						R.KQCVDHYNEIK.R	0.9958	2	1434.5579
2467	NDUAB_MOUSE	141	24.82	3	5	R.FFESYHEVPDGTQCHR.K	0.9958	2	2010.0955
						K.RFFESYHEVPDGTQCHR.K	0.9958	2	2166.2829
						K.IGKLEGWELFPTPK.V	0.9958	2	1615.9127
2468	NDUAD_MOUSE	144	37.5	5	27	K.VKQDMPPPGGYGPIDYK.R	0.9958	2	1863.1383
						K.QDMPPPGGYGPIDYK.R	0.9943	2	1635.8316
						K.VGESVFHTTR.W	0.9958	1	1133.2492
						R.IALMPLFQAEK.D	0.9944	1	1261.5652
						R.RLLIEDLEAR.I	0.9958	2	1228.4343
2469	NDUB3_MOUSE	104	26.92	2	14	K.MELPDYR.Q	0.9958	1	924.0594
						R.YMGGFAGNITFPSVILK.G	0.9958	2	1816.1682
2470	NDUB4_MOUSE	129	43.41	4	111	K.YKPAPLATLPSTLDPAEYDVSPETR.R	0.9929	2,3	2733.0472
						R.VSHIEDPALIR.W	0.9958	1	1250.4404
						K.RVSHIEDPALIR.W	0.9958	2	1406.6279
						R.SANIYPNFRPTPK.N	0.9958	2	1505.7165
2471	NDUB5_MOUSE	189	22.22	6	43	K.TLAILQIESEK.A	0.9958	1	1245.4588
						R.GDGPWYQFPTPEK.E	0.9958	1	1522.6568
						R.ARGDGPWYQFPTPEK.E	0.9958	2	1749.9231
						R.GDGPWYQFPTPEKEFIDHSPK.A	0.9958	2	2476.7069
						K.TLAILQIESEKAELR.L	0.9958	2	1715
						K.EFIDHSPK.A	0.9958	1	973.0733
2472	NDUB6_MOUSE	128	25.78	2	23	R.IFPGDTILETGEVIPPMR.D	0.9958	1	1986.3337
						R.DGAVWKNMVFK.A	0.9958	1	1295.542
2473	NDUB7_MOUSE	137	63.5	10	95	R.YLWDASVEPDPEK.I	0.9958	1	1549.677
						K.IPSFPPDLGFPER.K	0.9958	2	1472.6836
						K.HEQHDWDYCEHLDYVK.R	0.9958	2	2175.2439
						R.DSFPNFLACK.H	0.9958	1	1199.3148
						K.IPSFPPDLGFPERK.E	0.9958	2	1600.8577
						R.VAQGQGEGEVGPEVAL.-	0.9958	1	1540.6702
						R.DYCAHYLIR.L	0.9958	1,2	1211.3288
						R.RYLWDASVEPDPEK.I	0.9944	1,2	1705.8645
						R.YLWDASVEPDPEKIPSFPPDLGFPER.K	0.9958	2	3003.3374
						K.RDSFPNFLACK.H	0.9958	2	1355.5023
2474	NDUB8_MOUSE	186	24.73	3	6	K.DMLPGSYPR.T	0.9924	1	1036.1907
						R.SQHERDPWYQWDHSELR.M	0.9958	2	2270.3848
						R.MNWGEPIHWDLDMYIR.N	0.9958	2	2077.3827
2475	NDUB9_MOUSE	179	58.66	6	69	K.VPEWCLDYWHPSEK.A	0.9958	1	1847.0027

						K.QLQEETSPDGIMTEALPPAR.R	0.9958		2	2184.426
						K.AMYPDYFSK.R	0.9958		1	1122.2806
						R.EAEEEFWQNQHPQPYIFPDSPGGTSFER.\	0.9958		3	3324.5029
						R.HLESWCIHR.D	0.9958		2	1238.3574
						R.EGDLPPLWWHIVTRPR.E	0.9958		2	1973.2877
2476	NDUBA_MOUSE	176	50	6	280	R.TPAPSPQTSLPNPITYLTK.A	0.9958		2	2027.3251
						K.AYDLVVDWPVTLVR.E	0.9958	1,2		1646.9267
						R.RVPDITECK.E	0.9958		2	1118.2414
						K.VDQEIMNIIQER.L	0.9958	1,2		1488.699
						R.YLDLGAYYSAR.K	0.9958		1	1292.4338
						K.EGDVLCIYEAEMQWR.R	0.9958		2	1900.0791
2477	NDUBB_MOUSE	151	52.98	5	48	R.EVNGLPIMESNYFDPSK.I	0.9958		2	1941.1627
						R.AVIAPSGVEK.K	0.9958		1	971.1417
						K.IQLPEDD.-	0.9944		1	829.8822
						R.QREPTMQWQEDPEPEDENVYAK.N	0.9958	2,3		2720.8836
						K.NPDFHGYDSDPVVDVWNMR.A	0.9958		2	2264.4333
2478	NDUC2_MOUSE	120	21.67	3	183	K.KTYAEILEPFHPVR.-	0.9958		2	1700.978
						K.TYAEILEPFHPVR.-	0.9958		3	1572.8039
						K.LHPEDFPEKEK.K	0.9958		2	1369.5169
2479	NDUS1_MOUSE	727	74.42	36	1092	R.YDDIEETNYFQQASELAK.L	0.9958		2	2165.2745
						R.IASQVAALDLGYKPGVEAIR.K	0.9958		2	2072.4123
						K.VDSDNLCTEEIFPTEGAGTDLR.S	0.9958		2	2440.5458
						R.ALSEIAGITLPYDTLDQVR.N	0.9958		2	2076.3544
						K.LVNQEVLADPLVPPQLTIK.D	0.9958		2	2088.4955
						K.DCFIVYQGHHGDVGAPMADVILPGAAYTEI	0.9958		3	3233.5886
						R.FASEIAGVDDLGTTGR.G	0.9958		2	1609.7331
						R.DDGAAILAAVSNMVQK.I	0.9958	1,2		1603.8309
						K.DFYMTDSISR.A	0.9958		1	1235.3539
						K.GWNILTNSEK.S	0.9958		1	1162.2877
						K.MLFLLGADGGCITR.Q	0.9958	1,2		1524.7846
						K.VAVTPPGLAR.E	0.9944		2	981.1832
						R.NRLEEVSPNLVR.Y	0.9958		2	1426.6157
						R.KTESIDVMDAVGSNIVVSTR.T	0.9958		2	2122.3985
						K.ILQDIASGR.H	0.9958		1	973.1173
						R.LEEVSPNLVR.Y	0.9944		1	1156.3244
						R.EGVMEFLLANHPLDCPICDQGGECDLQDQ	0.9958		3	4274.5904
						R.VAGMLQNFEGNAVAAIAGGLVDAEALVALI	0.9958		2	2914.3899

						K.KPMVVLGSSALQR.D	0.9958		1	1386.6959
						R.TTGTAASNLIEVFVDGQSVMVEPGTTVLQA	0.9958		3	3454.8373
						K.GLLTYTSWEDALSR.V	0.9958		2	1612.7795
						R.FEAPLFNAR.I	0.9924		1	1065.2169
						R.GNDMQVGTYIEK.M	0.9944		2	1355.5054
						R.SNYLLNTTIAGVEEADVVLLVGTNPR.F	0.9924		2	2760.1167
						R.MHEDINEEWISDK.T	0.9958		2	1646.7687
						K.AVTEGAQAVEEPSIC.-	0.9958		1	1561.652
						K.VGMQIPR.F	0.9958		1	800.9946
						R.IASQVAALDLGYKPGVEAIRK.N	0.9909		2	2200.5864
						K.SWLHNDLK.V	0.9924		1	1013.1411
						R.KSWLHNDLK.V	0.9937	1,2		1141.3152
						R.MCLVEIEK.A	0.9958		1	1022.2111
						R.MHEDINEEWISDKTR.F	0.9958		2	1904.0613
						K.VALIGSPVDLTYR.Y	0.9958		2	1404.6494
						K.VMNILHR.I	0.99		2	883.0996
						K.SATYVNTEGR.A	0.9958	1,2		1098.1576
						K.AREGVMEFLLANHPLDCPICDQGGECDLQ	0.9958		3	4501.8567
2480	NDUS2_MOUSE	463	45.14	12	510	K.LYTEGYQVPPGATYTAIEAPK.G	0.9958		2	2270.5438
						R.QWQPDIEWAEQFSGAVMYPSK.E	0.9958		2	2498.7718
						K.APGFAHLAGLDK.M	0.9958		2	1197.3793
						K.ETAHWKPPPWNDVDILK.E	0.9958		2	2047.3207
						K.TQPYDVYDQVEFDVPIGSR.G	0.9958		2	2229.4076
						K.GEFGVYLVSDGSSRPYR.C	0.9914		2	1890.0623
						K.GHMLADVVAIIGTQDIVFGEIDR.-	0.9958		2	2470.8462
						K.TSMESLIHHFK.L	0.9958	1,2		1330.5444
						R.TVDIGVVTAEDALNYGFSGVMLR.G	0.9958		2	2428.7626
						K.AVTNMTLNFGPQHPAAHGVLR.L	0.9958		2	2232.5681
						R.KTQPYDVYDQVEFDVPIGSR.G	0.9958		2	2357.5817
						R.IIEQCLNK.M	0.9924		1	1018.1645
2481	NDUS3_MOUSE	263	43.35	11	341	R.KFDLNSPWEAFPAYR.Q	0.9958	1,2		1842.0636
						K.RVVAEPVELAQEFR.K	0.9944		1	1643.8833
						R.VVAEPVELAQEFR.K	0.9958		2	1487.6958
						K.FDLNSPWEAFPAYR.Q	0.9958		1	1713.8895
						K.QLSAFGEYVAEILPK.Y	0.9958		2	1665.9268
						K.YVQQVQVSCLDELEICIHPDGVIPTLTFLR.D	0.9958		3	3545.0022
						R.ILTDYGFEGHPFR.K	0.9958		2	1552.7294

						R.ILTDYGFEGHPFRK.D	0.9958		2	1680.9035
						R.KDFPLTGYVELR.Y	0.9958		2	1438.6665
						R.RILTDYGFEGHPFR.K	0.9958		2	1708.9169
						R.DHTNAQFK.S	0.9958		1	961.022
2482	NDUS4_MOUSE	175	54.29	8	188	R.WENPLMGWASTADPLSNMVLTFSAK.E	0.9958		2	2768.1745
						K.LDITTLTGVPEEHIK.T	0.9958		3	1666.9121
						R.ERWENPLMGWASTADPLSNMVLTFSAK.E	0.9958		2	3053.4774
						R.IFVPARNNMQSGVNNTK.K	0.9958		2	1891.1552
						R.DTQLITVDEK.L	0.9958		1	1162.2823
						K.SYGANFSWNK.R	0.9941		2	1174.2578
						R.DTQLITVDEKLDITTLTGVPEEHIK.T	0.9958		2	2810.1712
						K.KVPKPK.S	0.9924		1	696.9114
2483	NDUS5_MOUSE	106	54.72	6	248	K.IEFDDFEECLLR.Y	0.9958	1,2		1586.7046
						K.EWIECAHGIGGTR.A	0.9944		2	1486.5933
						R.HFMFLSAEQPYK.N	0.9958		2	1498.7393
						K.KLGISLDR.H	0.9944	1,2		902.0818
						R.HFMFLSAEQPYKNAAR.C	0.9958		2	1911.1883
						K.ECKIEFDDFEECLLR.Y	0.9958		2	2004.1329
2484	NDUS6_MOUSE	116	57.76	7	471	K.EVNENFAIDLIAQQPVNEVEHR.I	0.9924		2	2565.8021
						K.ITHTGQVYDEK.D	0.9958		1	1291.4032
						R.IIACDGGGGALGHPK.V	0.9958		2	1423.578
						K.VYINLDK.E	0.9958		1	865.0171
						R.QKEVNENFAIDLIAQQPVNEVEHR.I	0.9958		2	2822.1069
						K.VYINLDKETK.T	0.9958		1	1223.4118
						K.ITHTGQVYDEKDYR.R	0.9958		2	1725.8553
2485	NDUS7_MOUSE	224	17.86	2	5	K.LDDLINWAR.R	0.9958		1	1116.2621
						R.VHQSVATEGPSPSPSPSLSSTQSAVSK.A	0.9958		2	2653.8626
2486	NDUS8_MOUSE	212	57.55	9	835	K.LCEAICPAQAITIEAEPR.A	0.9958		2	2043.2569
						R.EPATINYPFEK.G	0.9958		1	1309.4613
						K.CIYCGFCQEACPVDAIVEGPNFEFSTETHE	0.9958		3	4329.5811
						R.ILMWTELIR.G	0.9958		1	1175.4748
						K.WEAEIAANIQADYLYR.-	0.9958		2	1927.1235
						K.LLNNGDKWEAEIAANIQADYLYR.-	0.9931		2	2681.9646
						R.GLGMTLSYLFREPATINYPFEK.G	0.9958		2	2548.9593
						R.YDIDMTK.C	0.9924		1	886.0075
						R.GLGMTLSYLFR.E	0.9958		2	1258.5212
2487	NDUV1_MOUSE	464	66.38	19	554	K.HAGGVTGGWDNLLAVIPGGSSTPLIPK.S	0.9958		2	2615.9921

						K.QIEGHTICALGDGAAWPVQGLIR.H	0.9958		2	2463.7649
						R.GAGAYICGEETALIESIEGK.Q	0.9958		2	2069.2391
						R.GEFYNEASNLQVAIR.E	0.9958		2	1711.8717
						K.GPDWILGEMK.T	0.9958		1	1146.3465
						R.IFTNLYGR.H	0.9952	1,2		984.1429
						R.GGTWFAGFGR.E	0.9923		2	1056.1686
						R.GGAGFPTGLK.W	0.9958		1	905.0415
						K.GDARPAEIDSLWEISK.Q	0.9958		2	1787.9671
						K.LFNISGHVNHPCTVEEEMSVPLK.E	0.9958		2	2638.9643
						K.WSFMNKPSDGRPK.Y	0.9958		2	1550.7753
						R.HFRPELEDR.M	0.9937		2	1199.3115
						K.TSFGSLKDEDR.I	0.9958		1	1255.3269
						R.LKPPFPADVGVFGCPTTVANVETVAVSPTI	0.9958		3	3401.8598
						K.KTSFGSLK.D	0.9958		1	868.0208
						K.LFNISGHVNHPCTVEEEMSVPLKELIEK.H	0.9958		3	3251.6882
						K.HESCGQCTPCR.E	0.9958		2	1392.3663
						K.SVCETVLMDFDALVQAQTGLGTAAVIVMDI	0.9944		3	3212.6669
						K.YLVVNADEGEPGTCK.D	0.9958		1	1652.7644
2488	NDUV2_MOUSE	248	66.53	11	487	K.NYPEGHQAAAVLPVLDLAQR.Q	0.9958		2	2163.441
						R.DTPENNPDTPFDFTPENYK.R	0.9958		2	2242.3166
						R.FCCEPAGGLTSLTEPPK.G	0.9958	1,2		1865.0223
						R.DSDSILETLQR.K	0.9924		1	1277.3739
						K.DIEEIIDELK.A	0.9958		1	1217.3587
						R.QNGWLPISAMNK.V	0.9958		2	1359.5859
						K.LFTLIEVECLGACVNAPMVQINDNYYEDLTI	0.9958		3	3732.1692
						K.VAEVLQVPPMR.V	0.9958		1	1239.5187
						R.FCCEPAGGLTSLTEPPKGPGFGVQAGL.-	0.9958		2	2749.0248
						K.YHIQVCTTTPCMLR.D	0.9958		2	1781.012
						K.GPGFGVQAGL.-	0.9958		1	903.0257
2489	NDUV3_MOUSE	104	48.08	3	342	K.TQSVLKEPEPTDTTTYK.N	0.9958		2	1939.1266
						K.NLQHHDYNTYTFLDLNLDLSK.F	0.9937		2	2565.8015
						K.FRLPQPSSGR.E	0.9943		2	1145.3066
2490	NEB2_MOUSE	817	3.18	2	2	K.EIEFLKK.E	0.9924		1	907.0978
						R.ASSLNENVDHSALLK.L	0.9944		2	1598.7532
2491	NECA1_MOUSE	352	14.49	2	8	R.QGPSKPEVLSIQWPGK.R	0.9952		2	1752.0232
						R.QMSVTEEDLEEFQLALKHYVESASAQSGC	0.9958		3	3557.877
2492	NED4L_MOUSE	1004	4.18	2	8	R.LWIEFESEKGLDYGGVAR.E	0.9958		2	2070.3092

						R.SKASLNPNDLGPLPPGWEER.I	0.9958	2	2178.4093
2493	NEDD1_MOUSE	660	6.21	2	2	R.EAPSPSIATVLPQPVTTALGK.G	0.9958	2	2078.4136
						K.AASSVTAGVASSLSEK.I	0.9958	1	1465.6005
2494	NEDD4_MOUSE	887	14.32	6	34	R.VTLYDPMSGILTSVQTK.T	0.9958	2	1854.1688
						R.DDFLGQVDVPLYPLPTENPR.M	0.9958	2	2286.5462
						R.LAVCGNPATSQPVTSSNHSSR.G	0.9958	2	2171.2976
						R.FIIDEELFGQTHQHELK.T	0.9958	2	2085.3238
						K.RPSPDDDLTDEDNDDMQLQAQR.A	0.9958	2	2575.6367
						R.GKTDSNDLGPLPPGWEER.T	0.9958	2	1969.1179
2495	NEIL2_MOUSE	329	6.69	1	3	K.YFSGLGNIIKNEALYR.A	0.9912	2	1859.135
2496	NEK1_MOUSE	1203	4.07	2	4	K.ESFEENGSLYIVMDYCEGGDLFKR.I	0.9944	3	2860.0872
						K.NSLLIGLSTGLFDANNPKMLR.T	0.9911	3	2275.6715
2497	NEK10_MOUSE	1111	2.34	1	2	R.DTTVLLGALLALASLAESSECREK.I	0.9958	3	2548.8597
2498	NEK9_MOUSE	984	4.17	3	3	R.GWHTILIVEK.V	0.9924	1	1196.4349
						K.DTLPYEELQGLK.V	0.9958	2	1406.5755
						K.KLEGGQQVGMHSR.G	0.9958	2	1427.6213
2499	NELFB_MOUSE	580	3.97	1	5	R.LLALGQGAWDLIDSQVFKEPK.M	0.9958	2	2329.7013
2500	NEO1_MOUSE	1493	3.35	2	6	R.VENTSQPGEMQVTIQNLMPATVYIFK.V	0.9958	3	2940.3993
						R.SRPPMPVVVPSAPEVQETTR.M	0.9958	2	2178.5114
2501	NEP_MOUSE	750	7.2	3	4	K.DGDLVDWWTQQSANNFK.D	0.9958	2	2025.1412
						R.EDEYFENIIQNLK.F	0.9958	2	1655.8016
						R.IIGTLQNSAEFADAFHCR.K	0.9958	2	2051.2323
2502	NEST_MOUSE	1864	3.7	3	3	K.TLENGVLELSKPLGEEEPR.M	0.9944	2	2111.3568
						R.ARADDELAALR.V	0.9924	1	1201.3249
						R.SSEEQNLESLITFKEESQYPLGGPEAEDQN	0.9958	3	3786.0694
2503	NETO1_MOUSE	533	7.5	2	2	K.HAEGGVFTSPNYPSKYPPDR.E	0.9944	3	2220.4057
						R.NFVAVYDGSSSVEDLK.A	0.9958	2	1730.8688
2504	NEUL_MOUSE	704	8.24	3	13	R.NLILKPGGSLDGMDMLQNFLQR.E	0.9958	2	2461.9001
						K.STSHVATFLDDLSQK.L	0.9947	2	1649.7979
						K.LVASRLVNTGLLTLR.Q	0.9911	2	1626.9834
2505	NEXN_MOUSE	607	19.93	5	16	K.EEEENESFGLSREYEELIK.L	0.9944	3	2331.4516
						K.EMLASDDEEESSPKIEK.A	0.9958	2	1938.0675
						R.EDEEEEEGSIVNGSTTEDEEQTR.S	0.9958	3	2613.5293
						R.AEQIEDINNTGTESASEEGDDSLLITVVPAK	0.9958	3	3247.448
						K.TVSQESLTPGKLEINFEQLLR.Q	0.9931	2	2403.738
2506	NF1_MOUSE	2841	2.11	3	3	K.FKEKPTDLETR.S	0.9958	1	1364.5413
						K.ALKTLSIFYQAGTSK.A	0.9926	2	1628.909

						K.LCKASTYINWEDNSVIFLLVQSMVVDLK.N	0.9944	3	3287.8049
2507	NFAC2_MOUSE	927	4.1	2	2	R.DAGLSPEQPALALAGVAASPR.F	0.9932	2	1992.2395
						K.VLEIPLEPKNNMR.A	0.9958	3	1553.8602
2508	NFAC3_MOUSE	1075	4.47	2	4	K.TSEDQAAILPGK.L	0.993	2	1230.3605
						R.EDTDLPSVPSLPVPHSAQAQRPSSETGHP	0.9958	3	3446.6744
2509	NFASC_MOUSE	1240	4.44	2	3	K.GPEPDTIIGYSGEDLPSAPR.R	0.9943	2	2072.2359
						R.LVCRANGNPKPTVQWMVNGEPLQSAPPN	0.9958	3	3443.8743
2510	NFH_MOUSE	1090	2.57	2	2	K.SPAEAKSPIEVK.S	0.9924	1	1256.4417
						R.DALKCDVTSALR.E	0.9944	1	1349.4931
2511	NFIB_MOUSE	570	6.32	2	2	R.AVKDELLSEKPEIK.Q	0.9949	2	1599.8651
						K.KPEKPLFSSTSPQDSSPR.L	0.9958	2	1989.1925
2512	NFKB1_MOUSE	971	4.22	2	3	R.GYNPGLLVHSDLAYLQAEGGGDR.Q	0.9958	2	2403.6133
						R.RLEPVVSDAIYDSK.A	0.9929	2	1592.7893
2513	NFRKB_MOUSE	1296	2.62	2	2	K.GKNTVASSEAKPAATIR.I	0.9958	2	1701.9205
						R.ITVPLSVISQPMK.G	0.9924	1	1413.7589
2514	NFS1_MOUSE	451	26.39	7	22	R.EMSPLWEMVQDGIDLK.S	0.9958	2	1892.1922
						K.ELEAAIQPDTSLVSVMTVNNEIGVK.Q	0.9958	2	2659.0241
						K.VYFHTDAAQAVGK.I	0.9958	2	1407.5687
						K.HLVTTQTEHK.C	0.9958	2	1194.3329
						R.KVYFHTDAAQAVGK.I	0.9958	2	1535.7428
						R.THAYGWESEAAMER.A	0.9958	1	1638.7515
						R.SGTVPTPLVVGLGAACELAQQEMEYDHK.I	0.9958	2	3002.3321
2515	NFU1_MOUSE	199	32.16	4	32	R.IRPTVQEDGGDVIYR.G	0.9958	2	1718.9071
						K.LQGSCTSCPSSIITLK.S	0.9958	2	1752.9349
						K.SVFFGPDFITVTK.E	0.9958	2	1458.6971
						R.TMDFPTPAAAFR.S	0.9958	2	1325.5249
2516	NGL1_MOUSE	640	6.41	1	2	R.ALFDPLLVVLLALQLLVVAGLVRAQTCPSV(	0.9958	3	4289.9876
2517	NGLY1_MOUSE	651	12.6	4	4	K.GTNVSDEDFLLLELLHWFK.E	0.9958	2	2277.5817
						K.VLQSNIQHVQLYENPVLQEK.A	0.9958	2	2380.7062
						K.EILFIPSENEK.I	0.9958	1	1319.4973
						R.HSGNQTGQLPSLPSAPMVVGDSTILK.V	0.9958	2	2635.9953
2518	NGN1_MOUSE	244	16.39	2	2	R.SAPALSGASNVPGAQDEEQERR.R	0.9944	3	2270.3775
						R.NRMHNLNAALDALR.S	0.9944	1	1609.8467
2519	NHLC2_MOUSE	725	24.41	8	23	R.GASLSGLLPAQTSLEYALLDAVTQQEKDEL	0.9958	3	4085.5976
						R.DPMNLFAFGDVDGAGINAK.L	0.9958	2	1953.1767
						K.LQHPLGVAWDEER.Q	0.9958	2	1550.7141
						R.YNITHPVVNDADASLWQELEVSCWPTLVIL	0.9958	3	3795.2525

						K.DGLLIVGVHSAK.F	0.9958		2	1209.4313
						K.AGFAQPSGLALASEEPWSCLFVADSESST	0.9958		3	3271.5305
						R.LLYVADTNNHQIK.V	0.9958		2	1529.7361
						K.HLVGGERDPMNLFAFGDVDGAGINAK.L	0.9958		3	2702.0166
2520	NHLC3_MOUSE	347	21.33	3	5	R.AWNYTVDTPHGMFVSGTPFEQSVWITDVC	0.9944		3	4170.6014
						R.GDNIPKVLVFSEDGYFLR.A	0.9958		3	2070.3525
						K.FNIPHSVTLDAVGR.V	0.9958		2	1526.7355
2521	NHRF2_MOUSE	337	51.34	10	22	K.RDPFQESGLHLSPTAAEAK.E	0.9958		2	2055.2547
						R.DPFQESGLHLSPTAAEAK.E	0.9958		2	1899.0673
						R.VVPTEEHVEGPLPSPVTNGTSPAQLNGGS	0.9958		3	3461.7332
						R.LLVVDPETDEHFK.R	0.9958		2	1542.7289
						R.SVDPGSPASHSGLR.A	0.9958		2	1367.4612
						R.RGPQGYGFNLHSDK.S	0.9958		2	1576.7116
						R.LVEVNGVNVEGETHHQVVQRIK.A	0.9931		3	2485.8057
						R.LVEVNGVNVEGETHHQVVQR.I	0.9958		2	2244.4721
						R.GEQGYGFHLHGEK.G	0.9958		2	1459.5608
						R.GLPPAHNPWEPKPDWACSGSLGSDTGQK	0.9958		3	2991.2121
2522	NID1_MOUSE	1245	4.74	2	15	K.SSNAGHQGVWVFEIGSPATAK.G	0.9958		2	2144.3513
						R.NTFQAVLASSNSSSYAIFLYPEDGLQFFTTI	0.9944		3	3811.2391
2523	NIF3L_MOUSE	376	11.7	2	5	R.VAVYSPHTAYDAAPQGVNSWLAK.G	0.9958		2	2446.7245
						R.GFLSELQEMLGVHFENK.I	0.9958		2	1979.258
2524	NIN_MOUSE	2035	3.64	3	5	R.LQTVVQNTQADLTHSREK.V	0.9945		2	2069.2822
						K.QDLLFDISVLK.K	0.9958		1	1291.5303
						K.ALDFSLDGNINLTELTLALENELLVTKNGIHC	0.9944		3	4199.7912
2525	NINLP_MOUSE	1276	1.65	1	2	K.ELYVENAHLMKAVQLTEEK.Q	0.9958		2	2246.5836
2526	NIPBL_MOUSE	2798	4.72	6	6	R.QYLDFKLLMEHLDPDEEEEEGEVSASTNAI	0.9924		3	3496.7377
						K.VLNILEKNIQDGSK.L	0.9909		2	1571.8143
						K.QGDTNK.S	0.9958		1	662.6775
						R.HFALNVIALTLNQGLIHPVQCVPYLIAMGTD	0.9944		3	4102.8116
						K.YGMTVVQHCVSCLGAVVNK.V	0.9909		2	2123.4072
						K.QVSGGEDEIQQLQK.A	0.9958		1	1559.6732
2527	NIPS2_MOUSE	281	40.21	9	272	K.LQFHNVKPECLDAYNK.I	0.9958		2	1977.1932
						K.LKENQEFVNFR.K	0.9958		2	1424.5993
						K.HGWEELVYYTVPLIQEMESR.I	0.9958		2	2480.7974
						R.YEGGYPALTEVMNK.L	0.9958	1,2		1572.773
						K.DAHSNLLAK.K	0.9958		1	969.0855
						R.SYQLRPGTMIEWGNYWAR.A	0.9958		2	2229.5206

						K.KETSSLYK.L	0.9958		1	956.0837
						R.KDAHSNLLAK.K	0.9958		2	1097.2596
						K.LQFHNVKPECLDAYNKICQEVLPK.I	0.9958		3	2945.3204
2528	NIT1_MOUSE	323	18.27	4	16	R.ASYGHSMVVDPWGTVVAR.C	0.9958		2	1933.1919
						R.RPDLYGSLGHPLS.-	0.9958	1,2		1412.5883
						K.IYNCHVLLNSK.G	0.9958		2	1361.5499
						R.IDLHFLQQMR.Q	0.9958		1	1301.5493
2529	NIT2_MOUSE	276	51.09	9	51	K.ESSIYLIGGSIPEEDAGK.L	0.9958		2	1866.0319
						R.AVDNQVYVATASPAR.D	0.9945		2	1562.7227
						K.ASYVAWGHSTVVDPWGQVLTK.A	0.9958		2	2302.5944
						K.TLSPGDSFSTFDTPYCK.V	0.9958		2	1924.0369
						K.LYNTCSVFGPDGSLLVK.H	0.9958		2	1871.1065
						K.AGTEETILYSDIDLK.K	0.9958		2	1668.8383
						K.IHLFDIDVPGK.I	0.9958		2	1254.4716
						K.ITFQESKTLSPGDSFSTFDTPYCK.V	0.9943		2	2757.9765
						K.RADLYTVESK.K	0.9958		2	1182.3189
2530	NK1R_MOUSE	407	12.04	2	2	R.YLQTQSSVYKVSR.L	0.9958		1	1559.7624
						K.FIQQVYLASMWLAMSSTMYNPIIYCCLNDR	0.9958		3	3994.6085
2531	NK3R_MOUSE	452	9.73	1	2	R.TVTNYFLVNLAFSDASVAAFNTLVNFIYGVI	0.9958		3	4844.3619
2532	NKD2_MOUSE	461	7.16	2	2	R.RSQVLAEHVIPANEPATR.A	0.9958		2	1989.2418
						K.GSLEVVLPPEK.S	0.9958		1	1168.3757
2533	NKG2D_MOUSE	232	8.19	1	2	R.LALTTSQPGENGIIRGR.Y	0.9904		2	1784.0256
2534	NKRF_MOUSE	690	6.23	3	3	R.EPISVKEQHK.R	0.9958		1	1195.361
						R.YLSTYDGQNPPKK.Q	0.994		2	1511.6745
						K.MGWTGGGLGKSGEGIR.E	0.9958		1	1563.7716
2535	NLF3_MOUSE	419	9.55	1	2	K.AATRHVIQIESAEDWTAEEATNADPQAQGA	0.9944		3	4022.3924
2536	NLRC3_MOUSE	1064	9.68	5	7	R.GNDVGAAGAKALANALK.L	0.9958		2	1541.7477
						R.GAIALAEALKVNQILENLDLQSNSISDMGVT	0.9944		3	3729.3424
						R.MALGGEGQDKEK.V	0.9958		1	1263.4082
						R.MALGGEGQDK.E	0.9944		1	1006.1187
						K.VNTTLIALYLQVASIGSQGAQALGEALTVNF	0.9958		3	3173.6371
2537	NLTP_MOUSE	547	20.11	8	104	K.KLEEEGEQFVK.K	0.9958		1	1336.4845
						K.KADCTITMADSDLLALMTGK.M	0.9958		2	2156.4806
						K.LQNLQLQPGK.A	0.9958		1	1139.3402
						K.MNPQSAFFQGK.L	0.9958		1	1255.4339
						K.ADCTITMADSDLLALMTGK.M	0.9958		2	2028.3065
						K.KIGGIFAFK.V	0.9958		1	981.226

						K.HSVNNTYSQFQDEYSLEEVMK.S	0.9958		2	2549.7278
						K.YGLSAHPITPQMFGYAGK.E	0.9958		2	1939.239
2538	NMD3B_MOUSE	1003	3.99	2	4	R.LAEDLAFDFELYIVGDGKYGALR.D	0.9944		2	2576.9085
						R.DGRWTGLVGDLLAGR.A	0.9958		1	1586.791
2539	NMI_MOUSE	314	10.51	2	3	K.VSAHPVPLNTGVR.F	0.9958		2	1347.5601
						R.GEQSMGLVHEIMSENK.E	0.9958		2	1790.0162
2540	NMNA3_MOUSE	245	8.57	1	3	R.YISDSPILQQFQHNIHLAR.E	0.9958		2	2281.5791
2541	NMRL1_MOUSE	309	10.36	2	2	K.KPEEYVGQNIGLSTCR.H	0.9958		2	1852.0203
						K.AQTLDQWLEQHK.G	0.9958		2	1497.6506
2542	NNTM_MOUSE	1086	36.46	31	904	R.KTTVLAMDQVPR.V	0.9958	1,2		1359.6269
						K.ILIVGGGVAGLASAGAAK.S	0.9958		2	1525.832
						R.SLGVGYAAVDNPIFYKPNTAMLLGDAK.K	0.9958		2	2827.2678
						K.GITHIGYTDLPSR.M	0.9944	1,2		1430.6035
						R.VTIAQGYDALSSMANISGYK.A	0.9958		2	2090.3557
						K.SLGAEPLEVDLK.E	0.9958		1	1271.4533
						R.AAALEQFK.S	0.9958		1	878.0159
						K.DDFDFGTMSHVIR.G	0.9958		2	1540.6905
						R.VALSPAGVQALVK.Q	0.9958	1,2		1253.5278
						R.FFTGQITAAGK.V	0.9958	1,2		1141.3122
						K.NIPEEAPVKPK.T	0.9958		1	1222.427
						K.AVVLAANHFGR.F	0.9958	1,2		1155.3451
						R.MATQASTLYSNNITK.L	0.9958		1	1643.8523
						R.AAGAQIQGMK.E	0.9958		1	975.151
						K.EVDILISTALIPGKK.A	0.9958		2	1597.9359
						K.SPVKPGIPYK.Q	0.9958	1,2		1086.3195
						K.RVALSPAGVQALVK.Q	0.9958	1,2		1409.7153
						K.EVLASDLVVK.V	0.9944		1	1073.2749
						K.FPDDLYR.A	0.9944		1	926.0165
						K.APVLFSK.E	0.9944		1	761.9395
						R.APMVNPTLGAHEADFLKPSGTLISFIYPAQI	0.9958		3	3982.5867
						K.VIFPAPTPK.N	0.9958		1	970.1998
						R.FGIHPVAGR.M	0.9944	1,2		954.1197
						K.QGFNVVVESGAGEASKFPDDLYR.A	0.9958	2,3		2486.7001
						K.AISPDKDNFHFEVK.D	0.9958	1,2		1647.8278
						R.APMVNPTLGAHEADFLKPSGTLISFIYPAQI	0.9958		3	4468.1273
						K.AQYPIADLVK.M	0.9958		1	1118.3183
						K.DNFHFEVK.D	0.9958		1	1036.132

						K.EGSVVVDLAAEAGGNFETTKPGELYVHK.G	0.9944	3	2919.2176
						K.EVDILISTALIPGK.K	0.9952	2	1469.7618
						K.RSLGVGYAAVDNPIFYKPNTAMLLGDAK.K	0.9958	3	2983.4553
2543	NOB1_MOUSE	403	15.38	2	2	R.ELQELLIDGREEEEEEEECEDSDDDGGGW	0.9944	3	4167.2271
						K.VSSSIQHPETALHISGFHLPSK.S	0.9958	2	2373.6738
2544	NOC3L_MOUSE	807	2.73	2	7	K.VISGFVK.G	0.9958	1	749.9285
						K.ELIHLLPIKDK.S	0.9958	2	1319.6304
2545	NOD2_MOUSE	1020	1.76	1	2	R.SLYEMQEEQLAQEAVR.R	0.9944	2	1925.1205
2546	NOL1_MOUSE	793	4.79	2	4	K.GAETELVRFLPAAGDENSK.R	0.9958	2	2005.1919
						R.VEDSGTPVPTPSEIR.A	0.9958	1	1584.7233
2547	NOL10_MOUSE	687	4.95	2	3	K.DEEEEEPEGKPSDAESSESSDDEK.G	0.9958	2	2655.5202
						R.LKLEAK.H	0.9958	1	701.8845
2548	NOL3_MOUSE	220	48.18	6	49	R.MPDPAWDWQHVGPGYR.N	0.9958	2	1913.1199
						R.GVLTGPEYEALDALPDAERR.V	0.9958	2	2173.3873
						R.GVLTGPEYEALDALPDAER.R	0.9958	2	2017.1999
						R.SYDPSCPGHWTPEAPSSGTTCPELPR.A	0.9958	3	2888.0083
						R.LVETLQADSGLLLDALVAR.G	0.9958	2	1998.3275
						R.ASEQEEVGGPEGSEALQPR.T	0.9958	2	1971.0447
2549	NOM1_MOUSE	854	8.08	3	3	R.TVGSGSGDQGGNVGLNDGPETRRPPTEV	0.9944	3	3405.6658
						K.DQQEREIVHILMDCCLQEK.T	0.9909	2	2445.6821
						K.DIELILLMLK.N	0.9958	1	1201.5506
2550	NOTC1_MOUSE	2531	4.31	4	5	R.LLDEYNLVRSPQLHGTALGGTPTLSPTLCS	0.9958	3	4153.6477
						R.DGLNGYKCDCAPGWSGTNCDINNNECESI	0.9944	3	4297.2587
						K.DIENNK.E	0.9958	1	732.7685
						R.HGGTCQDRDNSYLCLCLK.G	0.993	2	2198.2954
2551	NOTC2_MOUSE	2470	2.87	3	6	R.EPLPPIVTFQLIPK.R	0.9958	2	1592.9622
						R.QTGDFTLECNCLPGFEGSTCER.N	0.9911	3	2579.6346
						K.DCESGCASNPCQHGGTCYPQRQPPHYSC	0.9944	3	3468.4673
2552	NOTC3_MOUSE	2318	3.41	3	3	R.CAEGFEGTLCERNVDDCSPDPCHHGR.C	0.9958	3	3077.0714
						R.LLDAGADTNAQDHSGRTPLHTAVTADAQG	0.9944	3	3775.1728
						R.YGGKCLDLVDK.Y	0.9924	1	1268.4186
2553	NOX1_MOUSE	563	8.88	2	2	R.TFEQQHSPMPRIEVDGPFGTVSEDVFQYE	0.9944	3	5165.8696
						R.IEVDGPFGTVSEDVFQYEVAVLVGAGIGVT	0.9958	3	3826.3783
2554	NP1L1_MOUSE	391	24.55	4	19	K.NVDLLSDMVQEHDEPILK.H	0.9958	2	2096.36
						R.QLTVQMMQNPQILAALQER.L	0.9944	2	2213.6184
						K.FYEEVHDLER.K	0.9958	2	1337.4313
						K.TVSNDSFFNFFAPPEVPENGDLDDDAEAIL	0.9958	3	4544.8879

2555	NP1L4_MOUSE	375	27.2	6	59	R.LDNVSHTPSSYIETLPK.A	0.9958	2	1902.1113
						K.LTDQVMQNPQVLAALQER.L	0.9958	2	2055.3569
						R.NVDMLSELVQEYDEPILK.H	0.9958	2	2136.4218
						K.FSDPGQPMSFVLEFHFEPNDYFTNPVLTK.	0.9958	3	3405.8055
						R.KYAALYQPLFDK.R	0.9958	2	1457.7123
						K.YAALYQPLFDK.R	0.9958	1	1329.5383
2556	NP60_MOUSE	546	3.48	1	2	K.DLVLGPSGVLQGIRPGK.C	0.9958	2	1707.0262
2557	NPA1P_MOUSE	2274	4.44	4	5	K.EAVIQFLERILLTLVMNPYSYTDK.A	0.9944	3	2858.3655
						R.GLGALLPTLAEHELDTVFLQTLQK.D	0.9944	3	2609.0379
						R.LCPSVCQSSHFAVLLGTYSATLSVLDQKILL	0.9944	3	3805.4255
						K.TIEELLLAILK.H	0.9944	1	1256.5688
2558	NPAL2_MOUSE	383	2.87	1	2	K.YSHLHLAQK.E	0.9944	1	1097.262
2559	NPAS3_MOUSE	925	6.27	2	2	K.ENFEFYELAKLLPLPAAITSQLDK.A	0.9958	3	2752.1797
						K.NIIWVNYLLSNPEYKDTPMDIAQLPHLPEK.A	0.9944	3	3554.098
2560	NPC1_MOUSE	1278	1.1	1	2	K.SNLQLPLQFLSR.C	0.9958	2	1416.6634
2561	NPHP3_MOUSE	1324	3.47	2	7	K.EAETSLLGGKAPSR.Q	0.9924	1	1416.5742
						K.HFPNTLILSHFVGRPMSTSSESSLIIKR.L	0.9958	3	3156.6733
2562	NPL4_MOUSE	608	8.55	3	3	K.TGNQHFGYLYGR.Y	0.9958	2	1413.5351
						K.AFGAPNVVEDEIDQYLSK.Q	0.9958	2	1996.1809
						K.SGCEGHLPWPNGICTK.C	0.9958	2	1813.9398
2563	NPM_MOUSE	292	27.05	4	24	K.MSVQPTVSLGGFEITPPVVLR.L	0.9958	2	2228.655
						R.MTDQEAIQDLWQWR.K	0.9958	2	1821.0173
						K.DLKPSTPR.S	0.9958	1	914.0495
						R.TVSLGAGAKDELHIVEAEAMNYEGSPIK.V	0.9958	3	2931.2873
2564	NPTN_MOUSE	281	12.1	2	6	R.AEDSGEYHCVYHFVSAPK.A	0.9958	2	2097.214
						K.SVGYPHPEWIWR.K	0.9958	2	1527.7251
2565	NPTXR_MOUSE	493	10.95	2	2	K.FLAVLLAAGMLAFLGAVICIIASVPLAASPAR	0.9958	3	3198.9306
						R.VAELEHGSSAYSPPDAFK.V	0.9911	2	1906.0587
2566	NQO1_MOUSE	274	52.19	7	43	R.GWEVLESDLYAMNFNPIISR.N	0.9958	2	2355.6703
						R.ALIVLAHSEK.T	0.9958	1,2	1081.3005
						K.NFQYPSESSLAYK.E	0.9958	2	1534.6653
						R.FCGFQVLEPQLVYSIGHTPPDAR.M	0.9958	2,3	2632.9446
						K.LEAADLVIFQFPLQWFGVPAILK.G	0.9958	2	2617.1491
						R.LETVWEETPLYFAPSSLFDLNFQAGFLMK.I	0.9944	3	3395.8941
						K.FGLSVGHHLGK.S	0.9958	1	1152.3414
2567	NQO2_MOUSE	231	12.99	2	2	K.SIWKEEPIHCTPPWYFQE.-	0.9958	2	2348.5855
						K.KVAVEELSK.Q	0.9944	1	1003.1839

2568	NR1H4_MOUSE	488	8.81	2	3	K.GSAVEAMFLRSAEIFNK.K	0.9944	2	1871.1614
						K.SGISDEYITPMFSFYKSVGELK.M	0.9958	2	2499.8378
2569	NR1I3_MOUSE	358	16.2	2	2	R.FLYAKLMGLLADLR.S	0.9958	2	1625.0252
						K.ELVQILLGAHTRHVGPLFDQFVQFKPPAYL	0.9944	3	4770.6066
2570	NR2E1_MOUSE	385	4.68	1	2	K.TIGNVPITRLLSDMYK.S	0.9958	1	1822.173
2571	NR4A2_MOUSE	598	2.51	1	3	K.LEDLVPPPAIIDK.L	0.9954	1	1420.6891
2572	NRAP_MOUSE	1728	12.27	13	21	K.NNTFTSVYHTPLNLTLK.K	0.9958	2	1964.2285
						K.INAQQLSHVNYR.A	0.9958	2	1443.6053
						K.GSFPAMITPAYQIAK.R	0.9958	2	1595.8969
						R.HQYTMTLGLPEFIR.A	0.9944	2	1707.0001
						K.GTGWLALQSPQIESAK.K	0.9958	2	1686.9053
						K.FTTVVDSPDLIHAK.E	0.9958	2	1543.76
						R.GASVEPEAAAALGDHQSR.G	0.9917	2	1766.865
						K.GTGWVATGSLHVEQAK.K	0.9958	2	1641.8241
						K.LLHSLQVAK.M	0.9958	1	1009.237
						K.GAAHFHSLAAQDNLVLK.R	0.9958	2	1793.0354
						K.KAQTLASDQDYR.H	0.9929	2	1396.4997
						K.YTAVTDTPNLLHAK.Y	0.9943	2	1544.7477
						R.GVNPDASEILHIHK.K	0.9958	2	1530.7239
2573	NRCAM_MOUSE	1256	4.94	2	2	K.DGDDEWTSVVVANVSKYIVSGTPTFVPYLI	0.9958	3	3401.8377
						K.ILTFQGTKTHGMLPGLQPYSHYALNVR.V	0.9958	3	3044.5444
2574	NRDC_MOUSE	1161	1.55	1	2	K.SNFDLNPDLHLPAENK.Y	0.9958	2	1824.9878
2575	NRG2_MOUSE	756	8.86	3	24	R.EPPASGRVALVK.V	0.9944	1	1224.4459
						K.RVLTITGICVALLVVGIVCVVAYCK.T	0.9912	2	2778.3333
						R.IPEDDEYETTQECAPPPPPRPRTR.G	0.9917	2	2853.0405
2576	NRIP1_MOUSE	1161	2.67	2	22	K.LNSHQKVTLLQLLLGHK.S	0.9944	2	1943.3432
						R.DEAPQEHSER.A	0.9924	1	1198.1912
2577	NRP1_MOUSE	923	2.49	1	3	K.IENPGYLTSPGYPHSYHPSEK.C	0.9958	2	2374.5713
2578	NS1BP_MOUSE	642	5.61	2	4	K.VDAYIQEHLLQISEEEEFLK.L	0.9958	2	2434.7051
						R.LQVCGHEMLAHR.A	0.9958	2	1451.6526
2579	NSBP1_MOUSE	406	10.1	2	6	R.LSAMPVPFTPELKPK.R	0.9958	2	1656.0362
						K.DECNMENAENGEAKIMEAPIPK.M	0.9958	2	2491.7134
2580	NSD1_MOUSE	2588	0.73	1	2	K.KSDQPPTDATQLLPLSK.K	0.9958	2	1840.0837
2581	NSD2_MOUSE	1365	3.66	2	2	K.TYMNGKPLFESSICGDGAADVSQSEENEQ	0.9944	3	3293.4629
						K.TQNCEVNHECSVFLSK.A	0.9944	3	1953.0479
2582	NSF_MOUSE	744	7.26	4	9	K.DIEAMDPSILK.G	0.9958	1	1232.4345
						R.TPLVSVLLEGPPHSGK.T	0.9958	2,3	1631.9127

						R.LQILHIHTAR.M	0.9944	1	1202.4452
						K.MEIGLPDEK.G	0.9944	1	1032.1969
2583	NSF1C_MOUSE	370	27.84	6	14	K.ASSSILINEAEPTTNIQIR.L	0.9909	2	2058.2963
						R.LAHGGQVNLDMEDHR.D	0.9958	2	1692.8467
						K.LGSTAPQVLNTSSPAQQAENEAK.A	0.9958	2	2342.5248
						R.SYQDPSNAQFLESIR.R	0.9958	2	1755.8815
						K.SPNELVDDLFK.G	0.9958	1	1277.4167
						R.SGQQIVGPPR.K	0.9958	1	1039.1795
2584	NSMA_MOUSE	419	11.69	2	2	R.EVAIILCIPSVGLVLVAGAVYLFHKQEAK.G	0.9958	3	3139.7583
						R.GSEPHLAYCLQQEGDR.A	0.9924	2	1860.9439
2585	NSUN2_MOUSE	757	8.85	3	3	K.FHQFLVSETESGNISR.Q	0.9958	2	1852.0135
						K.VEVPQPLSWYPEELAWHTNLSR.K	0.9958	2	2652.9689
						K.YEPDSANPDTLQCPIVLCGWRGK.A	0.9958	3	2677.9056
2586	NSUN7_MOUSE	724	1.52	1	2	K.DYKLIFQDK.S	0.9958	1	1170.3507
2587	NT5C_MOUSE	200	7.5	1	3	R.RFPEEPHVPLEQR.R	0.9915	2	1634.835
2588	NT5D1_MOUSE	467	2.14	1	2	R.YNLPESAR.L	0.9944	1	950.0391
2589	NT5D3_MOUSE	546	3.85	1	2	R.RTPLQHELPAWSDSPSAFK.A	0.9957	2,3	2168.4166
2590	NTCP5_MOUSE	434	4.84	1	2	K.IVSTLLFILMPMSTGVIIK.H	0.9917	2	2077.6753
2591	NTF2_MOUSE	127	70.87	5	74	K.IQHSITAQDHQPTPDSCIISMVVGQLK.A	0.9958	3	3005.3821
						K.NINDAWVCTNDMFR.L	0.9958	2	1756.8964
						R.LALHNFG.-	0.9944	1	771.8943
						K.ADEDPIMGFHQMFLLK.N	0.9958	2	1893.2257
						R.TQLGAIYIDASCLTWEGQQFQGK.A	0.9958	2	2615.8683
2592	NU160_MOUSE	1402	2.43	1	2	K.FQNYNILPGGVHVSETQNHVIILILTNQTVHI	0.9944	3	3657.1697
2593	NU188_MOUSE	1759	1.25	1	3	K.ESLTQAVGLSTQAEGTRTLK.S	0.9958	2	2091.3262
2594	NUB1_MOUSE	614	10.1	3	17	K.ELLDTVDNYAVLQLDIVWCYFR.L	0.9929	2	2747.0858
						R.LYLLQGIQNYHSGNGEEAR.E	0.9958	2	2163.3543
						K.VHNLLQLGFTAQEAR.L	0.9958	2	1697.9346
2595	NUBPL_MOUSE	319	17.87	4	9	K.LAQTLDLDVLGDVPLHLSIR.E	0.993	2	2189.5602
						K.VNVPVLGLVQNMSVFQCPK.C	0.9958	2	2130.5195
						R.KLAQTLDLDVLGDVPLHLSIR.E	0.9958	2	2317.7343
						K.AYLHIASEVVR.R	0.9958	2	1258.463
2596	NUCB1_MOUSE	459	24.84	7	35	K.TFFILHDINSDGVLDEQELEALFTK.E	0.9958	2,3	2896.2231
						K.KVPEQPPELPQLDSQHL.-	0.9958	2	1956.2059
						R.YLQEVINVLETDGHFR.E	0.9958	2	1934.1589
						K.TFFILHDINSDGVLDEQELEALFTKELEK.V	0.9958	3	3395.7876
						R.LVTLEEFLASTQR.K	0.9958	2	1507.727

						K.LSQELDFVSHNVR.T	0.9958		2	1544.7074
						R.DLAQYDAAHHEEFKR.Y	0.9958		2	1830.9542
2597	NUCG_MOUSE	294	23.81	4	9	R.GALWVLEQLRPER.L	0.9958		2	1567.8313
						R.EGKAPGLLGR.V	0.9944		1	998.1704
						K.NHVAVPTHFFK.V	0.9958		2	1297.5021
						R.AMDDTFYLSNVAPQVPHLNQNAWNNLER.	0.9958		2	3259.5799
2598	NUCL_MOUSE	707	8.2	4	12	K.SEADAEKNLEEK.Q	0.9943		2	1363.421
						K.VEGSEPTTPFNLFIGNLNPNK.S	0.9958		2	2289.5499
						K.FAISELFAK.N	0.9958		1	1026.2206
						K.KVVVSQTK.K	0.9924		1	889.0831
2599	NUD12_MOUSE	462	15.58	3	5	R.ETCPSLQGVHNTSYPRVDPVVIMQVIHPDC	0.9924		3	3577.0155
						K.ESHPTTVYLLFSDLNPLVTLGGNK.E	0.9958		2	2616.9738
						R.HIANLLANAK.G	0.9958		2	1065.2608
2600	NUD13_MOUSE	352	18.47	3	4	K.IIYYPQMAPVVITLVSDGAR.C	0.9958		2	2207.6361
						R.KGSLALQPSEASPLLLPPK.L	0.9958		2	1947.3256
						K.TGVFYLFHDLDPLLQASGHR.Y	0.9958	2,3		2287.5828
2601	NUD19_MOUSE	357	17.65	3	3	R.RLENFASLSALYR.F	0.9945		2	1540.7623
						R.QPPFPGLSHGDADPAALPDDVALR.I	0.9909		2	2457.705
						R.VVIHSPYVYEIYMTLPSENK.H	0.9958		2	2383.7645
2602	NUDC_MOUSE	332	14.76	3	19	K.LKPNLGNGADLPNYR.W	0.9955		2	1642.8552
						R.KTDFFIGGEEGMAEK.L	0.9958		2	1659.8512
						K.LITQTFNHHNQLAQK.A	0.9957		2	1794.0231
2603	NUDC2_MOUSE	157	19.11	2	3	R.HVALAVGGR.E	0.9944		1	880.0378
						K.LFDSTIADEGTWTLEDR.K	0.9958		2	1970.0997
2604	NUDT3_MOUSE	168	11.31	1	2	K.VLQCHKPVQASYFETLR.Q	0.9958		2	2077.3569
2605	NUDT8_MOUSE	210	23.33	3	9	K.EHVWGVLQPVYDR.E	0.9958		2	1598.8015
						K.LLAPGFYQPSLAVPELPR.G	0.9958		2	1969.3342
						R.VWGLTAVITELTLK.L	0.9958		2	1544.8748
2606	NUMB_MOUSE	653	6.43	1	2	K.TVVGPSVAPGNTAPSPSSPTSPTPDGTAS	0.9958		3	3885.2109
2607	NUP50_MOUSE	466	9.87	2	4	R.YLATIEK.Q	0.9958		1	837.9915
						K.CNNSNQPPSSGPASSTACPGNAYHKQLAC	0.9944		3	3703.8623
2608	NUP93_MOUSE	819	7.45	3	8	K.QMTDVVLTPATDALK.S	0.9945		2	1603.8713
						R.SSLDSIEMAYARQIYIYNEK.I	0.9911		2	2395.6893
						K.SSGQSAQLLSHEPGDPPCMR.R	0.9958		2	2155.313
2609	NUPL_MOUSE	561	11.05	3	8	K.SLLGESAPALHLNK.G	0.9958		2	1450.6781
						K.SSSADFGTFSTSQSHQTASTVSK.V	0.9958		2	2349.4295
						K.APVGSVVSVPSHSSASSDK.Y	0.9958		2	1798.9475

2610	NVL_MOUSE	855	8.77	3	3	K.TLLAKAVANESGLNFISVK.G	0.9958		2	1976.3238
						K.FEDVGGNDATLKEVCK.M	0.9958		2	1782.911
						K.TLLAHAIAGELDLPILKVAAPEIVSGVSGESE	0.9944		3	3457.9897
2611	NWD1_MOUSE	1563	3.33	2	2	R.ACPYPMLVPLAGFLQPPGGPLRATLTGCH	0.9958		3	3221.7633
						R.VFAQGTLAISASKDHTLR.L	0.9944		2	1916.1875
2612	NXF1_MOUSE	618	7.93	2	2	R.FEEDDGDVAMNDPQDGPR.V	0.9958		2	2008.0369
						R.QGLLYAYHDGACCSLSIPYNPQNPVRK.N	0.9958		3	3123.4273
2613	NYX_MOUSE	476	11.55	2	2	R.VPGALRGLANLTHAHFER.S	0.9937		2	1960.2491
						R.SHAVMVFCYKATFLFTSCVLLSLAQYVVVG	0.9931		3	3810.4647
2614	O08614_MOUSE	3429	4.67	9	13	R.HPADNR.T	0.9958		1	709.7397
						K.QELPPPPPPK.K	0.9924		1	1100.303
						K.MLSESEKAAQASLNALNDPIAVEQALQEK.I	0.9958		3	3100.4681
						R.AQQLELEEGLSSHQPSLIK.V	0.9958		2	2108.3562
						K.QQTDNPKSMDEQLTSLK.V	0.9958		2	1964.1547
						K.DLAEMQEWMAQAEEDYLER.D	0.9958		2	2358.5563
						K.IQAEISAHELTLEELR.K	0.9958		2	1853.0825
						K.MSPIERLDHAFDK.A	0.9924		1	1559.7802
						K.FQLFQKPANFEQR.M	0.9958		2	1653.8809
2615	O08692_MOUSE	167	20.36	2	25	R.LLSATPPSSQNPATNIPLQFR.I	0.9958		2	2253.5632
						K.YDIIGNILK.N	0.9958		1	1049.2554
2616	O08797_MOUSE	374	10.16	2	2	K.LQEDYDMESLFQR.L	0.9958		2	1674.8225
						K.NVCYSPASISSALAMVLLGAK.G	0.9958		2	2153.5079
2617	O08804_MOUSE	377	35.28	7	36	R.DVHQGFQSLLTETNK.T	0.9958		2	1717.876
						R.LGMTDAFEEGMADFSGIASK.E	0.9919		2	2078.3162
						K.SFVEVNEEGTEAAAATAANIGFR.C	0.9944		2	2355.523
						R.NVLFSPISVSSALAMVFMGAK.G	0.9958		2	2170.6332
						K.ITELLSSGSVNSNTPLVLVNAIYFK.G	0.9958		2	2681.1015
						K.VIHKSFVEVNEEGTEAAAATAANIGFR.C	0.9958		2	2833.1301
						R.KFYEAEMEELDFK.G	0.9958		2	1679.8818
2618	O08806_MOUSE	377	4.24	1	3	R.LFVENTCELLPTFK.K	0.9958	1,2		1711.9617
2619	O08852_MOUSE	4293	1.14	2	2	R.VPIVSLECVSCK.A	0.9958		1	1391.58
						K.CVPEELWCPGANVCIPFDASCNSHVCINGS	0.9958		3	3793.9995
2620	O08934_MOUSE	530	1.7	1	3	K.ELEKMEK.K	0.9958		1	907.0698
2621	O35189_MOUSE	850	5.53	2	2	K.IVILCNKGSVIAFHVVLGYLGSLALGSFTLAF	0.9958		3	3722.4613
						R.FEIPKLNK.F	0.9958		1	989.2028
2622	O35452_MOUSE	4006	2.67	5	5	R.VVPVEGPDRSVVISPLDPNR.K	0.9944		2	2146.4514
						R.EVTVLDLDPAR.I	0.9958		1	1228.3879

						R.FLLYGLLGRK.R	0.9944	1	1180.4789
						R.EVTIEGLQPGR.K	0.9944	1	1199.3494
						K.RLGPISALGVTASEVDISAPDHTEPPHAPGI	0.9958	3	4519.0251
2623	O35483_MOUSE	812	2.71	1	3	R.RVGPGAGVDGGLLTFPPAVR.S	0.9958	2	1937.2522
2624	O35662_MOUSE	169	13.02	1	2	K.TLSYLLPAIVHINHQPFLER.G	0.9958	2	2362.7801
2625	O35727_MOUSE	597	6.7	2	18	R.LHEGFSSITYQHDLALLR.L	0.9958	2	2101.3696
						R.NKPGVYTDVANYLAWIQK.H	0.9944	2	2081.3788
2626	O54738_MOUSE	370	9.19	2	2	K.VLQTEENPLLPDEKPDR.S	0.9958	2	1994.209
						K.ANNPTPGLVPGPK.S	0.9958	2	1262.4514
2627	O54850_MOUSE	1281	1.48	1	2	K.ILQEELSILNIYAPNTR.A	0.9958	2	1988.2914
2628	O54997_MOUSE	444	11.94	2	2	K.ECLRPWLSHSALAPDVDCVGFQELDLSKE.	0.9944	3	4464.91
						R.LVGIMLLLYVK.Q	0.9944	1	1262.6801
2629	O55032_MOUSE	377	9.02	1	2	K.NYVTIMQNNPLTSGLEPSPPQCDYIRPSLT	0.9958	3	3593.0119
2630	O55124_MOUSE	1463	22.21	17	127	R.FLSELAQLEENVHLAR.S	0.9958	2	1870.1155
						R.FVVHGLTTGEQYIFR.V	0.9958	2	1768.0251
						R.IVSRGGVSDHSAFMFVR.D	0.9937	2	1866.1479
						R.FWLQAEHLSPDASFR.F	0.9958	2	1805.0025
						R.ILTVEGLTEGSLYEFK.I	0.9952	2	1800.0588
						K.IAATNLAGIGQPSDPSEHFK.C	0.9958	2	2054.267
						R.SLDLSGQAFDEAYAEFQQLK.A	0.9958	2	2261.4497
						K.IPDISPPQQAKPK.L	0.9924	2	1419.664
						K.VIGGLPDVVTIMEGK.T	0.9924	2	1528.8475
						R.NYVVLSWDPPSPR.G	0.9958	2	1530.7233
						R.LCFTVQGFPTPVVQWYK.D	0.9958	2	2071.3924
						K.TLNLTCTVFGNPDPEVVWFK.N	0.9958	2	2338.6313
						K.WTKMFFGEGQASLSFSHLNK.D	0.9944	3	2316.6391
						K.VQAALTVPSHPYGITLLNCDGHSMTLGWK.	0.9911	3	3168.6038
						K.HGLSDPSEITPPIQAQDMIVVPSAPGR.V	0.9958	2	2814.1859
						R.RLQAIHLEGEK.E	0.9958	2	1294.4966
						K.NWHEVNSSPVK.E	0.9958	1	1297.4129
2631	O88196_MOUSE	1979	1.36	2	2	R.QILEKAGGLK.S	0.9944	1	1057.2785
						R.KQDSDEMPFGCIK.V	0.9958	1	1555.7089
2632	O88493_MOUSE	2657	6.66	9	31	R.TDLQTITNDPR.L	0.9924	1	1274.3733
						R.EELSSLKPILTPSTGAGVGSK.K	0.9958	2	2072.3635
						R.SQRPYVLTADTLK.L	0.9958	2	1492.7153
						K.LLTPITTLTSQQIHQILASTR.Y	0.9958	2	2336.7373
						R.LNLLDLDYELAEQLDNIAEK.A	0.9958	2	2333.5976

						K.NANPSELEQIVLSPAFILAAESLPK.I	0.9929	2	2653.0477
						R.EFRELPNIEER.V	0.9912	2	1432.5761
						R.HAQVISSSGIVSLGIGDR.N	0.9909	2	1797.0213
						K.ISLSPEYVYSVSTFRELPR.L	0.9941	2	2244.5523
2633	O88738_MOUSE	4845	3.12	7	13	R.LPMLYPEVIQQVSAPVIASTTQEKPK.D	0.9958	3	2869.3893
						R.LSYLLPSARPELGVGPGR.S	0.9958	2	1883.2009
						R.TLHLPVSTTLSDVLDR.V	0.9958	2	1768.0202
						K.LPCPEGLDPDIEDASPVCR.A	0.9958	2	2141.2716
						K.AGVKPDAPDQEPEGLALLVPDIQR.T	0.9958	2	2529.8528
						K.SPATSPISSNSHR.S	0.9958	2	1341.4233
						K.EKHQEQHNIPFPCLLAGGLLTYK.S	0.9958	3	2695.0594
2634	O88783_MOUSE	2183	3.44	3	3	K.TSSPDLGQVPLSLDDNQK.T	0.9958	2	1915.0642
						K.FNPLVVVGLSRVDGDDVEIVPSEEPER.I	0.9911	3	2968.2903
						R.GESVTVTMDNVGTWMLTTMNSNPK.R	0.9958	2	2614.9632
2635	O89083_MOUSE	190	10	1	2	R.YNFLTEALDFVGVHQNR.T	0.9958	2	2024.2431
2636	O89096_MOUSE	252	3.97	1	2	K.LLGCFSPK.S	0.9944	1	922.0783
2637	OAT_MOUSE	439	53.99	11	133	K.KTEQGPPSSEYIFER.E	0.9958	2	1768.9207
						R.WLAVDHENVRPDMVLLGK.A	0.9958	2	2093.4515
						R.HQVLFIADEIQTGLAR.T	0.9958	2	1812.0788
						R.AFYNNVLGEYEEYITK.L	0.9958	2	1954.1431
						K.ALSGGLYPVSAVLCDDEIMLTIKPGEHGST	0.9958	3	4107.557
						R.QYFDFLSAYGAVSQGHCHPK.I	0.9931	2,3	2313.4999
						K.YGAHNYHPLPVALER.G	0.9958	2	1737.9584
						R.LAPPLVIK.E	0.9958	1	851.1203
						R.IAIAALEVLEEENLAENADK.M	0.9958	2	2156.3947
						R.TLSAISSSTDPTSYDGFGPFMPGFETIPYNI	0.9958	3	3996.3907
						R.LRDNGLLAKPTHGDIIR.L	0.9944	2,3	1890.196
2638	OBSCN_MOUSE	8891	1.78	6	8	R.ERPVDITKPLEDQR.T	0.9944	2	1696.901
						R.SDHSVTLSWVAPMSDGGGGLCGYRVEMK	0.9924	3	2998.3211
						R.SSAQLVVSDIPVVLTRPLEPK.A	0.9958	2	2249.6561
						K.DGVELGPSDKYDFLHK.A	0.9944	1	1820.9964
						R.GPGCPLPVPTVQGLGPGGSLGFGRGSLA	0.9958	3	2990.4014
						K.DEDIEWSLNGTPLYNDSFHEISHEGCLHTL	0.9958	3	4213.5726
2639	OCAD1_MOUSE	247	43.72	6	11	K.FDSNVSGQSSFGTSPAADNIEK.E	0.9958	2	2259.3477
						R.SVPLAATSMLITQGLISK.G	0.9958	2	1831.2213
						R.YEPIPFSASMNESTPTGITDHIAQGPEPNLE	0.9958	3	3786.1152
						R.ESYGVTLPHK.T	0.9958	1	1131.2737

						K.KLENSPLGEALR.S	0.9958		2	1327.5235
						R.YEPIPFSASMNESTPTGITDHIAQGPEPNLE	0.9958		3	3942.3027
2640	ODB2_MOUSE	482	46.89	15	184	K.IPHFGYCDEIDLTQLVK.L	0.9958		2	2049.2971
						K.LREELKPVALAR.G	0.9958		2	1395.6884
						R.TFPTPIAKPPVFTGK.D	0.9958		2	1601.9292
						K.EDILSFLEK.Q	0.9958		1	1094.2499
						K.AQIMNVSWSADHR.V	0.9923		2	1515.6867
						K.SYLENPAFMLLDLK.-	0.9958		2	1654.9617
						K.AASLGLLQFPILNASVDENCQNITYK.A	0.9958		2	2881.2213
						R.LYYNLDDIAYVGKPLIDIETEALK.D	0.9958		2	2771.1798
						K.ASHNIGIAMDTELGLIVPNVK.N	0.9958		2	2193.5664
						K.RLYYNLDDIAYVGKPLIDIETEALK.D	0.9958		3	2927.3673
						K.LSEVVGSGK.D	0.9958		1	875.9976
						K.DRTEPVTGFQK.A	0.9958	1,2		1278.4075
						K.SEITPPPPQPK.D	0.9958		1	1191.3696
						R.ILKEDILSFLEK.Q	0.9958		2	1448.7429
						R.LYYNLDDIAYVGKPLIDIETEALKDSEEDVVI	0.9958		3	5384.8702
2641	ODBB_MOUSE	390	39.49	9	135	R.VAHFTFHPDPESLQYGQTQK.M	0.9958		2	2331.5492
						K.MNLFQSITSALDNSLAK.D	0.9958	1,2		1854.1285
						K.ILYRAAVEQVPVEPYK.I	0.9952		2	1876.2059
						K.DPTAVIFGEDVAFGGVFR.C	0.9958		2	1898.1253
						R.LLISHEAPLTGGFASEISSTVQEECFLNLEA	0.9944		3	3818.2385
						R.AAVEQVPVEPYK.I	0.9957		2	1330.5236
						R.TIVPWDVDTVCK.S	0.9958		2	1433.6105
						K.IPLSQAEVIQEGSDVTLVAWGTQVHVIR.E	0.9958		3	3047.4814
						R.AAVEQVPVEPYKIPLSQAEVIQEGSDVTLV/	0.9944		3	4358.9817
2642	ODFP2_MOUSE	830	1.45	1	2	K.EEKDFTMLQK.K	0.9958		1	1269.4553
2643	ODO1_MOUSE	1023	61.58	45	2086	K.YAELLVSQGVVNQPEYEEEISK.Y	0.991		2	2525.7717
						R.FLDTAFDLDAFK.K	0.9924		1	1403.5743
						R.NTNAGAPPGTAYQSPLSLSR.S	0.9958		2	2003.179
						K.YPNAELAWCQEEHK.N	0.9958		2	1775.8811
						K.LGFYGLHESDLDK.V	0.9944	1,2		1494.6439
						K.NQGYYDYVKPR.L	0.9958		2	1403.537
						R.SSLATMAHAQSLVEAQPNVDK.L	0.9958		2	2198.4559
						R.TSFDEMLPGTHFQR.V	0.9958		3	1666.8487
						R.NITLSLVANPSHLEAADPVVMGK.T	0.9958	2,3		2377.7613
						K.VASSVPVENFTIHGGLSR.I	0.9958		2	1871.1032

						R.GHHVAQLDPLGILDADLDSSVPADIISSTDK	0.9958		2	3201.5145
						R.IEQLSPFPFDLLLK.E	0.9958		1	1660.994
						K.LVEDHLAVQSLIR.A	0.9958	1,2		1493.7465
						R.FLDTAFDLDAFKK.F	0.9924		1	1531.7484
						R.SMTCPSTGLEEDVLFHIGK.V	0.9958		2	2122.3638
						R.QKFETPGIMQFTNEEK.R	0.9958		2	1928.167
						R.QILLPFR.K	0.9924		1	887.113
						K.THLTELQR.F	0.9958		1	998.127
						K.RFGLEGCEVLIPALK.T	0.9958		2	1703.0007
						R.KPLIVFTPK.S	0.9958		2	1043.3378
						K.KTHLTELQR.F	0.9958		2	1126.3011
						K.YAELLVSQGVVNQPEYEEEISKYDK.I	0.9958		3	2932.2103
						R.RNGHNEMDEPMFTQPLMYK.Q	0.9958		2	2339.6638
						K.VFHLPTTTFIGGQEPALPLR.E	0.9958		2	2195.5693
						R.TVDWALAEYMAFGSLLK.E	0.9958		2	1916.2421
						R.VVNAPIFHVNSDDPEAVMYVCK.V	0.9958		2	2505.814
						R.KELEQIFCQFDSK.L	0.9958		2	1672.8414
						R.VIPENGPAAQDPHK.V	0.9958		1	1473.6286
						K.ELEQIFCQFDSK.L	0.9958		2	1544.6673
						R.FGLEGCEVLIPALK.T	0.9958		2	1546.8133
						K.SWDIFFR.N	0.9944		1	971.1033
						K.TIIDMSSANGVDYVIMGMPHR.G	0.9958		2	2308.6907
						K.HWLDSPWPGFFTLDGQPR.S	0.9946		2	2157.3953
						K.TKAEQFYCGDTEGK.K	0.9958	1,2		1634.7058
						R.AKPVWYAGRDPAAAPATGNK.K	0.9958		2	2042.3048
						K.FETPGIMQFTNEEK.R	0.9958	1,2		1671.8622
						R.NGHNEMDEPMFTQPLMYK.Q	0.9958		2	2183.4763
						R.FEEFLQR.K	0.9944		1	969.0849
						K.YHLGMYHR.R	0.9958		1	1077.2487
						R.HHVLHDQNVDK.R	0.9958		2	1342.4569
						R.SSLATMAHAQSLVEAQPNVDKLVEDHLAV	0.9958		3	3673.1791
						R.HHVLHDQNVDKR.T	0.9958		2	1498.6443
						R.QNGIVLLLPHGMEGMGPEHSSARPER.F	0.9958		3	2814.2097
						K.EAQKYPNAELAWCQEEHK.N	0.9958		2	2232.3801
						R.FLQMCNDDPDVLPDLQEENFDINQLYDCN	0.9958		3	5605.0655
2644	ODO2_MOUSE	454	52.64	14	476	K.ASAFALQEQPVVNAVIDDATK.E	0.9958		2	2188.4423
						K.NDVITVQTPAFAESVTEGDVR.W	0.9932		2	2249.4393

						R.GLVVPVIR.N	0.9944	1	853.0959
						R.NVETMNYADIER.T	0.9958	1	1455.5823
						R.VLLLDL.-	0.9944	1	685.8821
						K.AKPAETPAPAHK.A	0.9958	2	1218.3983
						K.EAQNTCAMLTTFNEVDMSNIQEMR.A	0.9958	2	2835.1142
						K.VEGGTPLFTLR.K	0.9924	1,2	1190.3849
						K.NELAIEDMDGGTFTISNGGVFGSLFGTPIIN	0.9958	3	5432.1879
						K.LGFMSAFVK.A	0.9958	1,2	1000.2439
						K.TSVQVPSPANGIIEALLVPDGGK.V	0.9952	2	2263.5963
						R.HKDAFLK.K	0.9958	1	859.0159
						R.DYIDISVAVATPR.G	0.9944	1	1420.6054
						R.LKEAQNTCAMLTTFNEVDMSNIQEMR.A	0.9958	2	3076.4477
2645	ODP2_MOUSE	642	49.38	22	1414	R.VAPAPAGVFTDIPISNIR.R	0.9958	2	1839.1448
						K.VPLPSLSPTMQAGTIAR.W	0.9958	1,2	1740.071
						K.GLETIASDVVSLASK.A	0.9955	1,2	1490.694
						R.DVPLGAPLCIIVEK.Q	0.9958	1	1524.8071
						R.VFVSPLAK.K	0.9958	1	861.0721
						K.LQPHEFQGGTFTISNLGMFGIK.N	0.9958	2	2423.7919
						R.DVPVGSIICITVEKPQDIEAFK.N	0.9958	2	2459.8084
						K.VPEANSSWMDTVIR.Q	0.9958	1	1605.8059
						R.VVDGAVGAQWLAEFK.K	0.9958	1,2	1590.8192
						K.DIDSFVPSK.A	0.9958	1	1008.1161
						K.GFDVASVMSVTLSCDHR.V	0.9958	2	1882.0644
						K.AAPAAAAAMAPPGPR.V	0.9958	1	1320.5523
						K.ISEGDLIAEVETDK.A	0.9958	2	1519.6458
						K.NFSAIINPPQACILAIGASEDK.L	0.9958	2	2330.6092
						K.YLEKPITMLL.-	0.9958	1,2	1221.5408
						K.NFSAIINPPQACILAIGASEDKLIPADNEK.G	0.9958	3	3211.6056
						K.KYLEKPITMLL.-	0.9958	2	1349.7149
						K.QTIPHYYLSVDVNMGEVLLVR.K	0.9923	2	2447.8548
						R.VVDGAVGAQWLAEFKK.Y	0.9958	2	1718.9933
						K.GIDLTQVK.G	0.9944	1	874.0251
						R.QNHVVDVSVAVSTPAGLITPIVFNAHIK.G	0.9958	2,3	2928.4044
						R.QNHVVDVSVAVSTPAGLITPIVFNAHIKGLE	0.9931	3	4400.0752
2646	ODPA_MOUSE	390	66.92	18	1066	R.LEEGPPVTTVLTR.E	0.9958	1,2	1412.6262
						K.GPILMELQTYR.Y	0.9958	2	1321.5774
						R.KEIEDAAQFATADPEPPLEELGYHIYSSDPF	0.9944	3	3963.3026

						K.RGDFIPGLR.V	0.9958		2	1031.2027
						R.MVNSNLASVEELK.E	0.9958		1	1434.6477
						R.AILAELTGR.R	0.9934	1,2		944.1191
						K.EIEDAAQFATADPEPPLEELGYHIYSSDPPF	0.9958		3	3835.1285
						R.AHGFTFTR.G	0.9958		1	937.0458
						R.YHGHSMSDPGVSYR.T	0.9958		2	1593.7136
						K.NFYGGNGIVGAQVPLGAGIALACK.Y	0.9958		2	2348.6733
						K.LPCIFICENNR.Y	0.9958		2	1436.583
						R.GFCHLCDGQEACCVGLEAGINPTDHLITAY	0.9958	2,3		3536.744
						R.VDGMDILCVR.E	0.9958		1	1178.3552
						R.MVNSNLASVEELKEIDVEVR.K	0.9958		2	2275.5793
						R.TREEIQEVR.S	0.9958	1,2		1160.2724
						K.YNGKDEVCLTLYGDGAANQGQIFEAYNMA	0.9958		3	3713.0786
						K.DEVCLTLYGDGAANQGQIFEAYNMAALWK	0.9958		2	3250.5728
						R.SKSDPIMLLK.D	0.9946		2	1132.4039
2647	ODPAT_MOUSE	391	11.25	2	15	R.GFCHLCDGQEACCVGLEAGINPTDHVITSY	0.9958		3	3538.7165
						K.SILAELTGR.K	0.9958		1	960.1185
2648	ODPB_MOUSE	359	62.95	14	2597	R.DNNPVVMLENELMYGVAFELPAEAQSK.D	0.9958		2	3010.4036
						R.IMEGPAFNFLDAPAVR.V	0.9958		1	1749.0374
						K.VFLLGEEVAQYDGAYK.V	0.9944		2	1803.0215
						K.DIIFAVK.K	0.9958		1	805.9927
						R.TIRPMDIEAIEASVMK.T	0.9958		2	1805.1579
						K.TNHLVTVEGGWPQFGVGAEICAR.I	0.9944		2	2499.7545
						K.DFLIPIGK.A	0.9958		1	903.1094
						K.TYYMSAGLQPVPIVFR.G	0.9958		2	1843.1938
						K.VLEDNSVPQVK.D	0.9958		1	1228.3879
						K.EGIECEVINLR.T	0.9958		2	1332.4626
						R.EAINQGMDEELERDEK.V	0.9958		2	1907.0161
						R.GPNGASAGVAAQHSQCFAAWYGHCPGLK	0.9958		3	2901.1022
						K.VVSPWNSEDAK.G	0.9958		1	1232.3354
						R.VTGADVPMPYAK.V	0.9958		1	1249.4675
2649	ODPX_MOUSE	501	40.92	11	390	K.STVPHAYATADCDLGAVLK.V	0.9944		2	1990.1865
						K.LTEDEEGNPQLQQHQLITVTMSSDSR.V	0.9931		2	2958.1835
						K.HSLDASQGTATGPR.G	0.9958	1,2		1398.4752
						K.VLMPSLSPTMEQGNIVK.W	0.9958	1,2		1845.2227
						K.NIQLGSLIALMVEEGEDWK.Q	0.9958		2	2146.4633
						K.GLITPIIK.D	0.9958		1	855.1087

						K.QMPGVNVTWDGEGPK.Q	0.9958	1,2	1615.801
						K.QLPSVDISVAVATDK.G	0.9958	2	1543.7575
						K.GIQEIADSVK.V	0.9958	1	1060.1925
						R.RSLGLAQGAAAWPVDR.G	0.9924	2	1668.8961
						K.DVSAPPPVSKPPAPTQPSPQPQIPCPAR.K	0.9958	3	2918.2885
2650	OGT1_MOUSE	1046	6.31	3	20	R.AIQINPAFADAHSNLASIHK.D	0.9958	2	2119.3879
						K.ALEVFPEFAAAHSNLASVLQQQGK.L	0.9958	2	2556.8809
						R.LCPTHADSLNNLANIK.R	0.9958	2	1781.9726
2651	OLA1_MOUSE	396	40.66	9	61	K.YDPGALVIPFSGALELK.L	0.9958	2	1791.0972
						K.IPAFLNVVDIAGLVK.G	0.9958	2	1569.9279
						R.AFEDDDITHVEGSVDPIR.D	0.9958	2	2016.1284
						R.FDFLCQYHKPASK.I	0.9958	2	1641.8328
						K.YEDFKDEGSENAVK.A	0.9958	2	1631.6929
						K.IGIVGLPNVGK.S	0.9958	2	1067.317
						K.STFFNVLTNSQASAENFPFCTIDPNESR.V	0.9958	3	3195.3918
						R.FYHDWNDK.E	0.9924	1	1125.1851
						K.GAHNGQGLGNAFLSHISACDGIFHLTR.A	0.9958	2	2852.1075
2652	OPA1_MOUSE	960	28.02	16	134	R.SIVTDLVSQMDPHGR.R	0.9958	2	1655.8663
						K.LDAFIEALHQEK.-	0.9958	1	1414.6011
						K.IDQLQEELLHTQLK.Y	0.9958	2	1708.9524
						K.VNDEHPAYLASDEITTVR.K	0.9958	2	2031.1864
						R.MVLVDLPGVINTVTSGMAPDTK.E	0.9958	2	2259.6815
						R.LKDTENAIENMIGPDWK.K	0.9957	2	1975.2238
						K.AVEVAWETLQEEFSR.F	0.9958	2	1794.9585
						K.QQWDAAIYFMEEALQGR.L	0.9958	2	2057.2879
						K.ALPSSEDLASLAPDLDK.I	0.9958	2	1742.9207
						K.VTLSEGPHHVALFK.D	0.9958	1,2	1535.7862
						K.EVLEDFAEDGEK.K	0.9958	1	1381.4357
						K.AKNEILDEVISLSQVTPK.H	0.9958	2	1985.2853
						K.SLIDMYSEVLDVLSDYDASYNTQDHLPR.V	0.9958	3	3261.5409
						K.HWEEILQQSLWER.V	0.9958	2	1754.9426
						K.EKIDQLQEELLHTQLK.Y	0.9958	2	1966.2419
						R.VIQHNALEDR.S	0.9958	2	1195.3207
2653	OPLA_MOUSE	1288	31.37	19	125	R.GGTFTDVFAQCPGGHVR.V	0.9958	2	1806.9415
						R.GRPLDTSHIASIR.M	0.9958	2	1423.6151
						R.LLPASFPCIFGPGEDQPLSPEASR.K	0.9958	2	2586.8701
						R.SQISTESFLHLR.Y	0.9958	2	1418.5925

						R.KGGPVTVTDANLVLGR.L	0.9958		2	1597.8552
						R.ELGFTHVSLSSEVMPMVR.I	0.9958		2	2020.3693
						R.SGLFVVGPESAGAHPGPACYR.K	0.9958		2	2130.3337
						K.LLSEDPANYADAPTEGIR.R	0.9958		2	1933.0819
						R.YAGEFEHVFEASTAGVTLQAPQLDINTVAA	0.9944		3	3565.8779
						R.MGYYETVAGGAGAGPGWHGR.S	0.9958		2	1995.1791
						K.GSILDPSPEAAVVGGNVLTSQR.V	0.9958		2	2168.4117
						R.GHTACADAYLTPTIQR.Y	0.9958		2	1775.925
						K.TSVTVYPGDAFCLHTPGGGGYGDPEDPAF	0.9958		3	4442.8073
						R.GGTFTDVFAQCPGGHVRVLK.L	0.9958		2	2147.4075
						R.HSGLLSALGLALADVVHEAQEPCSLSYTPE	0.9958		3	4126.5353
						K.LVQGGVFQEEAVTEALQAPGK.I	0.9958		2	2172.4429
						R.DIPLNQGCLAPVQVIIPK.G	0.9958		2	1976.3331
						K.LDPIQLSIFSHR.F	0.9958		2	1426.6585
						R.ALGMDTVHIHR.H	0.9958		2	1250.4613
2654	ORML2_MOUSE	153	13.73	1	6	R.LLTHWEQMDYGLQFTSSRK.F	0.9944		2	2341.6465
2655	ORN_MOUSE	237	14.35	2	6	K.ESTVTLQQAEYEFLSFVR.Q	0.9909		2	2148.377
						R.RWYPEDYEFAPK.K	0.9958		2	1601.7582
2656	OSBL1_MOUSE	950	4.74	3	4	R.TGKPFNPLLGETYELVR.D	0.9937		2	1935.2303
						K.ITMPVIFNEPLSFLQR.L	0.9958		2	1906.2934
						K.ECDVAK.D	0.9958		1	721.7515
2657	OSBL3_MOUSE	855	4.21	2	2	K.SSDDAWVSNGTYLELR.K	0.9915		2	1813.9182
						K.VAMPVELNEPLNTLQR.L	0.9958		2	1825.1333
2658	OSBL6_MOUSE	959	2.82	2	5	R.FAVELNELDPVLK.D	0.9958		1	1487.7362
						K.QVVSEQDHNK.G	0.9958		1	1184.2511
2659	OSBP2_MOUSE	908	3.85	2	4	R.LDPLTGEMACMYK.G	0.9952		2	1529.7726
						K.ASSEVDRQHWITALELAK.A	0.9947		2	2055.2981
2660	OSCP1_MOUSE	379	3.69	1	5	R.AQENIVPNPLAK.E	0.9958		1	1294.4936
2661	OSGEP_MOUSE	335	15.82	2	2	R.HHRAVILDLLQEALAEAGLTSK.D	0.9944		3	2386.7568
						R.LITGAVNPTVLYVSGGNTQVISYSEHR.Y	0.9958		2	2877.2267
2662	OSR1_MOUSE	266	4.51	1	2	R.YIHSKEKPFK.C	0.9958		1	1277.5089
2663	OST1_MOUSE	311	3.54	1	5	R.DGRLNLDYK.A	0.9958		1	1094.2126
2664	OSTF1_MOUSE	215	16.28	2	5	K.DIVEVLFTQPNVELNQQNK.L	0.9958		2	2229.4949
						K.GYADIVQLLLAK.G	0.9958	1,2		1304.5724
2665	OTOF_MOUSE	1997	3.81	4	4	K.ADPYIAIKLGK.T	0.9944		1	1189.4405
						R.LRNGGPSSRPTGEVVVSMEPEEPVK.K	0.9958		3	2652.9824
						R.NYTLLDEHQDLNEGLGEGVSFR.A	0.9924		2	2507.6757

						R.GWLKGQQEDK.Q	0.9924	1	1189.3134
2666	OTUB1_MOUSE	271	25.46	5	78	R.IQQEIAVQNPLVSER.L	0.9958	2	1724.9548
						R.AFGFSHLEALLDDSK.E	0.9958	2	1650.8284
						K.FFEHFIEGGR.T	0.9958	2	1239.3757
						R.GEGGTTNPHVFPEGSEPK.V	0.9958	2	1840.9439
						K.FFEHFIEGGRTVK.E	0.9958	1	1567.7874
2667	OX26_MOUSE	124	15.32	1	5	K.ASGPLGTLAEELSSYSR.R	0.9958	2	1738.8919
2668	OXA1L_MOUSE	433	11.78	2	3	R.VMPLVVLPVTIHFPSAVFMYWLSSNVFSLC	0.9958	3	4720.6529
						K.FSARIR.E	0.9958	1	749.8912
2669	OXND1_MOUSE	311	36.66	6	11	R.VGGEFFFDPQPTDAPR.N	0.9958	2	1780.9341
						K.QTAQISAELKPYVTDGR.I	0.9958	2	1878.0923
						K.AGQWVDFFIPGVSVVGGFSICSSPQR.L	0.9924	3	2799.1242
						K.HLESCHVPK.E	0.9917	2	1107.2206
						R.DHISAETLFYVCGPPPMTDFFSK.H	0.9958	2	2660.9668
						K.YADHPPAVWVHNK.C	0.9958	2	1534.7171
2670	OXSM_MOUSE	459	28.76	7	13	R.VVITGIGLVTPLGVGTQLVWDR.L	0.9958	2	2294.7428
						K.ILINMAAGQVSIR.Y	0.9956	2	1386.6959
						K.SMSSSTIMAVGAAELALK.D	0.9958	2	1768.0938
						K.SMSSSTIMAVGAAELALKDSGWHPK.R	0.9944	3	2575.9575
						K.GPNHSVSTACTTGAHAVGDSFR.F	0.9958	2	2230.3245
						R.GPHEGQFNEENFVSK.S	0.9958	1	1719.8076
						R.DGFVMGEGAAVLVLEEHEHAVQR.G	0.9958	2	2494.7845
2671	OXSR1_MOUSE	527	10.06	3	7	R.DTAEGVSQELISAGLVDGR.D	0.9958	2	1918.0679
						K.IPISLVLR.L	0.9924	1	911.1759
						K.VLMLTLQNDPPSLETGVQDK.E	0.9958	2	2199.5243
2672	OXYR_MOUSE	388	9.02	2	2	R.RNEALAR.V	0.9958	1	829.9345
						K.TAAAAAAAEGSDAAGGAGRAALAR.V	0.9958	3	2029.1771
2673	P_MOUSE	833	8.16	4	4	K.CMLGKEVADLSALASSEK.R	0.9924	1	1910.1561
						R.TFEIVSREAVSISIQASLQQTR.L	0.9944	3	2464.7813
						K.RDLAGSVHLR.A	0.9924	1	1124.2882
						R.EETAVRGLLLEK.V	0.9958	1	1358.5779
2674	P20D1_MOUSE	503	10.74	2	2	R.FNPLPLNPQDFSGVHGINEK.V	0.9958	2	2224.4808
						K.VNVIPPLAQATINCRIHPSQTVHEVLELVK.N	0.9958	3	3377.9213
2675	P20D2_MOUSE	431	16.94	4	57	K.ALAMTALDVIFKPALLEGVR.K	0.9944	2	2129.6092
						R.AIWSAPELAYEEHR.A	0.9958	2	1672.8375
						R.FFECEPPAASWAVQPHFGLPTAFR.A	0.9958	3	2764.0808
						R.IDEAAER.L	0.9958	1	803.8473

2676	P210L_MOUSE	1881	2.45	2	2	K.CFPNSSVIEEDGGGLLR.S	0.9958	2	1850.9892
						R.HSEVFLQLPAENNFAMVVHTKAAGR.T	0.9944	2	2768.1656
2677	P2RX3_MOUSE	397	5.04	1	3	R.FPLFNFEKGNLLPNLTDK.D	0.9958	2	2108.4448
2678	P2RY6_MOUSE	328	6.71	1	15	R.MAVVVAAVFAISFLPFHITK.T	0.9958	2	2162.6843
2679	P3C2A_MOUSE	1686	1.84	2	11	K.ASVCNLQISPKSEDINK.F	0.9932	2	1904.0936
						R.QDMLALQMIK.I	0.9944	1	1191.4896
2680	P3C2G_MOUSE	1506	3.19	2	2	K.SCRPLPVTKSFSLLVNWNEIINFPLEIK.S	0.9944	3	3316.8774
						R.YFSEFTSQSPDSSQLR.F	0.9958	2	1879.9775
2681	P3H2_MOUSE	703	4.98	2	2	R.RSPEPEPER.G	0.9958	1	1097.1729
						R.GPLQPFDLLYASGVAAYYSGDYER.A	0.9919	2	2653.9073
2682	P4HA1_MOUSE	534	11.05	2	2	R.INMRIQDLTGLDVSTAEELQVANYGVGGQ\	0.9958	3	4256.6929
						R.ATISNPVTGALETVHYR.I	0.9958	2	1830.0507
2683	P5CR2_MOUSE	320	6.25	1	2	R.VKLESPTVSTLAPPSSGK.L	0.9958	2	1799.0746
2684	P5CR3_MOUSE	274	14.23	2	15	R.TDVLTPAGTTIHGLHALER.G	0.9958	2	2003.2657
						K.QVLASAPTDNNLCHFR.A	0.9958	2	1844.0031
2685	P63_MOUSE	680	1.47	1	3	R.QTISFPPR.D	0.9944	1	946.0941
2686	P70355_MOUSE	1734	0.75	1	2	K.NKSEILALLK.A	0.9958	1	1129.3855
2687	P70356_MOUSE	669	5.68	1	2	R.APFSPPPGPPCCSGSSDSTSGCSRDCEEF	0.9958	3	3902.9823
2688	PA1B2_MOUSE	229	18.78	2	52	R.ELFSPLHALNFGIGGDTTR.H	0.9958	2	2046.2902
						K.ICKPLHELIMQLLEETPEEK.Q	0.9958	2	2451.847
2689	PA2G4_MOUSE	394	22.08	5	52	R.LVKPGNQNTQVTEAWNK.V	0.9958	2	1928.1551
						K.HELLQPFNVLYEK.E	0.9958	1,2	1630.884
						K.GIAFPTSISVNNCVCHFSPLK.S	0.9958	2	2349.624
						K.VAHSFNCTPIEGMLSHQLK.Q	0.9958	2	2170.4572
						K.AAHLCAEAALR.L	0.9958	2	1183.3189
2690	PABP1_MOUSE	636	23.58	7	39	R.SKVDEAVAVLQAHQAK.E	0.9958	2	1694.9285
						R.IVATKPLYVALAQR.K	0.9958	2	1543.8931
						K.ITGMLLEIDNSELLHMLESPESLR.S	0.9958	2,3	2742.1751
						K.GFGFVCFSSPEEATK.A	0.9958	2	1663.7901
						R.LFPLIQAMHPSLAGK.I	0.9958	2	1623.9971
						R.NPQQHLNAQPQVTMQQPAVHVQGQEPLT	0.9958	3	4459.999
						K.GYGFVHFETQEAAER.A	0.9958	2	1741.8571
2691	PACN2_MOUSE	486	19.55	6	23	R.ANHGPGMAMNWPQFEEWSADLNR.T	0.9958	2,3	2659.9129
						R.EANSKADPSLNPEQLK.K	0.9924	2	1741.8956
						K.HLDLSNVASYK.T	0.9958	2	1247.3934
						R.LDSGQVGLYPANYVEAIQ.-	0.9958	2	1938.1443
						R.ALYDYEGQEHDELSFK.A	0.9958	2	1945.049

						K.GRLDSGQVGLYPANYVEAIQ.-	0.9958	2	2151.3837
2692	PACN3_MOUSE	424	26.42	6	19	R.YMEDMEQAFESCQAAER.Q	0.9958	2	2096.2137
						R.ALYDYAGQEADELSFR.A	0.9958	2	1848.9635
						R.DLQQSIEAASDEEDLR.W	0.9915	2	1819.8767
						K.DVLLTLHQHLDLSSSDK.F	0.9958	2	1922.1454
						R.STHGPGMAMNWPQFEEWSLDTQR.A	0.9958	2,3	2706.9667
						K.AWHAFFTAAER.L	0.9958	1,2	1307.4539
2693	PACS2_MOUSE	862	3.13	2	5	R.LICTAKHQQNMLR.V	0.9958	1	1613.8847
						K.HQQNMLRVLIDGVECSDVK.F	0.9909	2	2242.5213
2694	PADI1_MOUSE	662	9.82	2	3	R.VGNTDYPLGRILIGGSFPKPSGR.R	0.9907	2	2402.7587
						R.ELGLSESDIVDIPQLFFLKGAYAEAFFPDM\	0.9958	3	4205.9137
2695	PADI2_MOUSE	673	2.97	1	2	K.AGHGEAVMFKGLGGMSSK.R	0.9958	2	1765.0552
2696	PAFA_MOUSE	440	9.55	2	2	K.IALMGHSFGGATVLQALSEDQRFR.C	0.9958	3	2605.9744
						R.ALSAILDIEHGDPK.E	0.9958	2	1479.6732
2697	PAHX_MOUSE	338	12.13	3	5	K.MYHGIQDYDPNSPR.V	0.9915	2	1693.8309
						R.NKTQGFR.K	0.9958	1	850.9529
						K.GDTVFFHPLLIHGSGR.N	0.9958	2	1754.0012
2698	PAIP1_MOUSE	400	7.75	2	7	K.GTNGQVTRADILQVGLR.E	0.9958	2	1799.0402
						K.QMLLKLVELR.S	0.9958	1	1243.5939
2699	PAIRB_MOUSE	407	24.57	7	40	R.FDQLFDDESDPFEVLK.A	0.9958	2	1945.0894
						K.SEEAHAEDSVMDHHFR.K	0.9958	2	1897.9733
						K.NPLPPSVGVADKK.E	0.9958	2	1322.5473
						R.SSFSHYSGLK.H	0.9944	1	1113.2151
						K.SKSEEAHAEDSVMDHHFR.K	0.993	2	2113.2255
						R.GGSGSHNWGTVKDELTESPK.Y	0.9958	2	2087.2102
						R.RPDQQLQGDGK.L	0.9958	1,2	1242.3341
2700	PAK2_MOUSE	524	17.56	4	15	K.ERPEISPPSDFEHTIHVGFDAVTGEFTGMP	0.9944	3	3972.3368
						K.DPLSANHSLKPLPSVPEEK.K	0.9929	2	2059.3269
						R.ECLQALEFLHANQVIHR.D	0.9958	2	2079.3324
						K.DGFPSGTPALNTK.G	0.9958	1	1305.4301
2701	PALLD_MOUSE	1408	3.2	2	2	K.SPISLCETPSHEEPKSGK.Q	0.9944	3	1984.1364
						R.ETNGVHPSHGVNGLINGKAYGNK.S	0.9958	3	2364.5827
2702	PALM_MOUSE	383	21.67	4	10	K.EIDVLEFGESAPAASK.E	0.993	2	1663.8217
						K.SETLVNAQQTPLGTPK.E	0.9958	2	1684.887
						K.ENSAAPSPGRPQSASPAK.E	0.9958	2	1752.8815
						K.VVHAVDGIAENGIQPLSSSEVDELIHK.A	0.9958	2	2858.1778
2703	PAN2_MOUSE	1200	2.92	2	2	R.AITPLQVHVDPAFLRFIPTYTSR.L	0.9958	3	2644.0916

						R.FLIDIGVK.F	0.9944		1	905.1253
2704	PAN3_MOUSE	691	10.56	2	2	R.RSHTPNPASFMVPPSASTPANNPAPQPPS	0.9958		3	3697.1198
						R.QHAGLLPESLIWAYIVQLSSALRTIHTAGLA	0.9958		3	3648.212
2705	PANK4_MOUSE	820	11.95	4	10	R.HANVDMLVQDIYGGAHQTLGLSGNLIASSF	0.9958		3	3315.7283
						R.QYWLTCFEEALDGVVK.R	0.9958		2	1959.1719
						R.LERPLVNLPLLLDPSSYVPDTVDLTDDALAI	0.9958		3	3422.9005
						R.HEGYLGAIGAFLK.G	0.9955		2	1376.5981
2706	PAPS2_MOUSE	621	4.83	2	2	K.KDLYEPTHGGK.V	0.9958		1	1245.3775
						R.NPVHNGHALLMQDTR.R	0.9958		2	1703.9163
2707	PAR3L_MOUSE	1203	4.74	3	3	K.SYDGPEEADADGLSDK.S	0.9958		1	1669.6526
						K.KSSSLESLQTAVAEVR.K	0.9958		2	1705.9059
						R.LGRKPSSPSLSPLMGFGSK.K	0.9958		3	1947.3031
2708	PARC_MOUSE	1865	6.38	3	3	R.SSLDQHVAAVLATVQISSLDTNLQLSGLCA	0.9958		3	4355.8096
						R.NSDLSPELLHQALLPLTSDNGPLTLEETQD	0.9958		3	4402.9054
						R.LGNAAAVGVACSSTDVLSCILHLLGQGYVE	0.9958		3	3388.7809
2709	PARK7_MOUSE	189	92.59	13	486	K.TQGPYDVVVLPGGNLGAQNLSESPMVK.E	0.9958		2	2772.1456
						R.GPGTSFEFALAIVEALVGK.D	0.9958		2	1907.2169
						K.VTTHPLAK.D	0.9944		1	867.036
						K.GAEEMETVIPVDVMR.R	0.9958		1	1676.9405
						K.APLVLKD.-	0.9958		1	755.9328
						K.MMNGSHYSYSESR.V	0.9944		2	1549.6729
						K.GLIAAICAGPTALLAHEVGFGCK.V	0.9958	2,3		2327.6612
						K.DGLILTSR.G	0.9958		1	875.0128
						K.VTVAGLAGKDPVQCSR.D	0.9958		2	1658.8614
						R.ALVILAK.G	0.9958		1	727.9658
						K.TQGPYDVVVLPGGNLGAQNLSESPMVKEII	0.9958		3	3255.754
						R.DVMICPDTSLEDAK.T	0.9958		1	1594.7401
						R.AGIKVTVAGLAGK.D	0.9958		1	1185.4526
2710	PARP6_MOUSE	630	3.97	1	2	R.HPQLDADIEAVKEIYSENSVSIR.E	0.9958		3	2614.8718
2711	PARVB_MOUSE	365	9.86	2	6	K.VLLDWINDVLAEER.I	0.9958		2	1685.9176
						K.QLEEDLYDGQVLQKLLEK.L	0.9958		2	2162.4448
2712	PAXI_MOUSE	591	16.92	4	10	K.KPIAGQVVTAMGK.T	0.9958		2	1300.6024
						R.YAHQQPPSPLPVYSSSAK.N	0.9958		2	1958.1809
						R.AILENYISALNTLWHPECFVCR.E	0.9958		2	2708.0211
						R.GLEDVRPSVESLLDELESSVPSPVPAITVN(	0.9958		3	4151.5891
2713	PBIP1_MOUSE	727	3.16	1	3	R.LLQAQLQAQKEELQSLLHQPK.G	0.9944	2,3		2444.8369
2714	PBX4_MOUSE	378	21.43	3	4	K.TAVSIQFQEEDPPDAQLLRLDNMLLAEGVS	0.9958		3	3812.2867

						R.TLAFLQPPTGGVCLQPLVHSNWQR.A	0.9958		3	2721.1003
						K.FQEEATMYTGKASTVTK.A	0.9958		1	1893.1187
2715	PCATA_MOUSE	544	3.86	1	5	R.IGIEEFAEYLKLPVSDVLR.Q	0.9958		2	2192.5603
2716	PCBP1_MOUSE	356	52.53	8	31	K.AFAMIIDKLEEDINSSMTNSTAASRPPVTLR	0.9944		3	3380.8561
						R.QVTITGSAASISLAQYLINAR.L	0.9958		2	2178.4936
						R.ESTGAQVQVAGDMLPNSTER.A	0.9958		2	2091.2573
						R.IITLTGPTNAIFK.A	0.9944		2	1389.6781
						R.INISEGNCPER.I	0.9958		1	1289.3538
						K.QICLVMLETLSQSPQGR.V	0.9931		2	1961.2501
						R.CSDAAGYPHATHDLEGPPLDAYSIQGQHT	0.9958		3	3948.2605
						R.QQSHFAMMHGGTGFAGIDSSSPEVK.G	0.9958		2	2607.8751
2717	PCBP2_MOUSE	362	21.55	4	7	R.AITIAGIPQSIIECVK.Q	0.9943		2	1714.0215
						R.IITLAGPTNAIFK.A	0.9958		2	1359.6518
						K.AFAMIIDKLEEDISSSMTNSTAASRPPVTLR	0.9958		3	3353.8305
						R.LVVPASQCGSLIGK.G	0.9924		1	1429.666
2718	PCCA_MOUSE	724	52.62	26	339	R.AQAVHPGYGFLSENK.E	0.9958		2	1618.7893
						K.YSSAGTVEFLVDSQK.N	0.9958		2	1631.7796
						R.VDSGIQPGSDISIYYDPMISK.L	0.9952		2	2286.5586
						R.LSQYQEPIHLPGVR.V	0.9958		2	1637.879
						R.GVTHNIPLLR.E	0.9958		2	1120.3402
						K.TVAIHSDVDASSVHVK.M	0.9958	2,3		1665.8436
						K.RLAAEDVTFIGPDTHAIQAMGDK.I	0.9958		2	2457.7637
						K.GHTLTLSER.N	0.9958		1	1014.1264
						R.FSSQEAASSFGDDR.L	0.9958	1,2		1504.5095
						R.HKQEDIPISGWAVECR.V	0.9945		2	1926.1052
						K.MADEAVCVGPAPTSK.S	0.9958	1,2		1533.7028
						K.LNVTSTWNLASPLLSVNVDGTQR.T	0.9958		2	2486.7874
						R.HIEIQVLGDK.H	0.9958	1,2		1152.336
						R.VPVIRPDVAK.W	0.9958		2	1094.3427
						K.HGNALWLNER.E	0.9958	1,2		1210.3377
						R.LQVEHPVTECITGLDLVQEMILVAK.G	0.9958	2,3		2837.3107
						R.LAAEDVTFIGPDTHAIQAMGDK.I	0.9958		2	2301.5763
						K.VVEEAPSIFLDPETR.Q	0.9958		2	1702.9017
						K.RMEDALDNYVIR.G	0.9958		2	1495.6935
						K.SYLNMDAIMEAIKK.T	0.9958		2	1627.9545
						R.LAAEDVTFIGPDTHAIQAMGDKIESK.L	0.9958		2	2759.1035
						K.SYLNMDAIMEAIK.K	0.9958		1	1499.7804

						R.QAMGEQAVALAK.A	0.9958		1	1217.4259
						K.LHDEDHTVVASNNGPAFTVEVDGSK.L	0.9958		2	2639.7948
						R.NQLLAIASSVFVASQLR.A	0.9958		2	1818.1264
						K.NFYFLEMNTR.L	0.9957		2	1335.52
2719	PCCB_MOUSE	541	62.85	20	233	K.THTTVSGVAHR.A	0.9958		2	1166.2821
						K.HLLGDTNYAWPTAEIAVMGAK.G	0.9958		2	2259.5848
						R.GFVDDIIQPSSTR.A	0.9958	1,2		1435.5767
						R.TVGIVGNQPNVASGCLDINSSVK.G	0.9958		2	2330.5664
						K.AYNMLDIIHAVIDER.E	0.9944		1	1774.0447
						R.LVYVFSQDFTVFGGSLSGAHAQK.I	0.9958		2	2459.7637
						R.HAALLGGGQR.R	0.9958	1,2		980.1147
						R.EFFNFLPLSSQDPAPIR.E	0.9958		2	1979.2426
						K.IMDQAITVGAPVIGLNDSGGAR.I	0.9958		2	2156.4619
						R.IQEGVESLAGYADIFLR.N	0.9921		2	1882.1235
						R.LVPELDTVVPLESSK.A	0.9958		2	1626.8877
						R.FCDAFNIPLITFVDVPGFLPGTAQEYGGIIR.	0.9958		2	3429.9062
						K.FANPFPAAVR.G	0.9958		2	1090.27
						K.SVTNEDVTQEQLGGAK.T	0.9958		2	1676.7777
						K.LLYAFAEATVPK.I	0.9958		2	1323.5749
						K.DTSYLFITGPEVVK.S	0.9958	1,2		1569.7949
						K.GHQDVEAAQAEYVEKFANPFPAAVR.G	0.9958		3	2746.011
						K.GHQDVEAAQAEYVEK.F	0.9958		2	1674.7643
						R.AFDNDVDALCNLR.E	0.9958		2	1523.6086
						R.ISLLLDPGSFMESDMFVEHR.C	0.9958		2	2324.6717
2720	PCD15_MOUSE	1943	5.76	3	7	R.GTVVGVISAAAINQSIVYSIVAGNEEDK.F	0.9958		3	2806.1424
						R.GESLGYTEGALLALAFIIILCCIPAILVVLVSY	0.9958		3	4113.8892
						K.GDFVINKTTGLVSIAPGVELIVGQTYALTVQ	0.9958		3	4214.7625
2721	PCD21_MOUSE	859	1.16	1	2	R.VGVMVPPR.A	0.9958		1	855.0862
2722	PCDA4_MOUSE	947	2.11	2	2	K.SDFITFGK.K	0.9924		1	915.0337
						R.QRLLVLVK.D	0.9944		1	969.2589
2723	PCLO_MOUSE	5038	1.75	4	4	K.ETPSIEKTPPAVATDQK.L	0.9958		2	1813.0147
						R.RHSWHDEDDETFDESPELK.F	0.9958		3	2373.4106
						K.QHLLYQQEEER.Q	0.9958		2	1473.5852
						R.QVISGVGISTPQYSTARMTPPPGPQYGVG	0.9924		3	3402.8932
2724	PCNT_MOUSE	1920	1.35	2	2	R.QMVQLQEELEK.Q	0.9958		1	1375.5799
						K.LDGFNELVIKK.D	0.9958		1	1276.5187
2725	PCSK1_MOUSE	258	19.77	3	3	K.EPRSLSAASAPLVETSTPLR.L	0.9958		2	2083.3494

						R.ILTGSSEPEAAPAPR.R	0.9958		2	1496.6604
						R.ALAHLLEAER.Q	0.9958		2	1123.2975
2726	PCSK9_MOUSE	694	1.15	1	3	R.RGYVIK.V	0.9944		1	735.9047
2727	PCTK3_MOUSE	451	7.54	2	2	R.MSAEAALNHPYFQSLGDR.V	0.9958		2	2008.2158
						R.VHQLHDTASIFSLK.E	0.9958		1	1596.8265
2728	PCX1_MOUSE	2344	3.71	3	3	K.IIMLNR.R	0.9958		1	759.9854
						K.HHTLVAFLGAEGGQGSATEAQPGNTSSPA	0.9958		3	3600.8893
						K.TAPEGNTPAGPPEAPDAQASEEMADQAAF	0.9944		3	3798.8953
2729	PCX3_MOUSE	1620	3.58	2	2	K.SVLGFVLYALAGAVGFFTHYLLPQLRK.Q	0.9958		3	2982.5846
						R.RHNAGSNPTPPASVMGSPPSSLQEAQR.G	0.9958		3	2775.0281
2730	PCY1A_MOUSE	367	19.35	4	9	R.TEGISTSDIITRIVR.D	0.9958		2	1661.8961
						R.NAPWTLTPEFLAEHR.I	0.9958		2	1782.9963
						R.EFIGSFLEMFGPEGALK.H	0.9958		2	1873.1737
						R.VYADGIFDLFHSGHAR.A	0.9958		2	1805.9902
2731	PCY1B_MOUSE	369	11.65	2	2	K.EFVNRVEEK.S	0.9924		1	1150.2767
						R.LTLTAPAPFADESSCQCQAPHEKLTVAQAF	0.9924		3	3299.5971
2732	PCY2_MOUSE	404	11.39	2	7	K.WVDEVVPAAPYVTTLETLDK.H	0.9958		2	2247.5499
						R.YVSEVVIGAPYSVTAELLNHFK.V	0.9958		2	2437.7979
2733	PCYOX_MOUSE	505	4.55	1	5	K.VQGHDYEAGGSVIHPLNLHMK.R	0.9958		2	2303.6006
2734	PDC6I_MOUSE	869	27.96	13	81	K.STSVVEQGGIQTVDQLIK.E	0.9958		2	1903.1399
						K.ATLVKPTPVNVPVSQK.F	0.9958		2	1679.0128
						R.EATTLANGVLASLNLPAAIEDVSGDTVPQS	0.9958		3	3410.8437
						R.EPTVDISPDTVGTLSLIMLAQAQEVFFLK.A	0.9958		3	3164.6814
						R.TPSNDLYKPLR.A	0.9958		2	1304.4887
						R.LQHAAELIK.N	0.9924		1	1023.2205
						K.FYNELTEILVR.F	0.9958		2	1397.614
						K.NIQVSHQEFSK.M	0.9944	1,2		1317.4441
						K.FLTALAQDGVINEEALSVTELDR.I	0.9944		2	2505.7845
						K.NLATAYDNFVELVANLK.E	0.9958		2	1896.1503
						K.MVPVSVQQSLAVFSQR.K	0.9958		2	1777.0917
						K.KTSEVDLAKPLVK.F	0.9952		2	1428.7123
						K.SLLSNLDEIKK.E	0.9952		2	1260.4735
2735	PDCD4_MOUSE	469	7.25	2	3	K.TLTPIIQEYFEHGDTNEVAEMLR.D	0.9944		2	2708.0149
						K.KGGAGGK.G	0.9958		1	574.6579
2736	PDCD5_MOUSE	126	33.33	3	4	K.VSEQGLIEILEK.V	0.9915		2	1358.5749
						R.NSILAQVLDQSAR.A	0.9958		2	1415.5895
						R.LSNLALVKPEK.T	0.9949		2	1212.4753

2737	PDDC1_MOUSE	220	18.64	2	2	R.YHALLIPSCPGALTDLASSGSLAR.I	0.9958	2	2471.7821
						K.AYASPAKLESIDGAR.Y	0.9958	1	1549.7239
2738	PDE1A_MOUSE	565	6.55	2	2	K.NYHMVGLTYPAAVIVTLKEVDK.W	0.9952	2	2462.9098
						R.NSLQQPEGIDR.A	0.9944	1	1257.3457
2739	PDE1B_MOUSE	535	6.92	2	3	K.SECAILYNDRSVLENHHISSVFR.M	0.9912	2	2747.9934
						K.QWSVHSRWTK.A	0.9924	1	1315.477
2740	PDE1C_MOUSE	706	13.03	4	4	R.SVLENHHLSAAYRLLQEDEEMNILVNLSK.D	0.9958	3	3367.8016
						R.TLVIEMVMATDMSCHFQQIK.A	0.9958	2	2383.8075
						K.ALSLMLHTADISHPAK.A	0.9958	2	1706.0129
						K.NLEYAATVLESVYIDETRR.L	0.991	2	2243.4784
2741	PDE3A_MOUSE	1141	2.8	1	2	R.SASIKPHEAPSPSAVNPDSWNAPGLTTLTK	0.9958	3	3075.4051
2742	PDE4A_MOUSE	844	5.45	2	2	K.TDQEDLLAQELENLSK.W	0.9958	2	1846.9861
						R.NSSVASEAHGEDLIVTPFAQVLASLR.N	0.9958	2	2713.0196
2743	PDE5A_MOUSE	865	6.94	3	3	K.QAILATDLALYIK.R	0.9924	1	1433.7313
						R.FPWTNENMGHVNTPCIGSLLCTPIK.N	0.9929	2	2888.2429
						K.GIVGHVAAFGEPLNIK.D	0.9958	1	1622.9077
2744	PDE6C_MOUSE	861	5.46	3	14	R.HGFNVGQTMFTLLMTGR.L	0.9958	2	1911.247
						K.KEDIVGVATFYNR.K	0.9958	2	1512.7056
						K.ATPDEISSILK.F	0.9958	1	1174.3367
2745	PDIA1_MOUSE	509	31.04	10	197	K.HNQLPLVIEFTEQTAPK.I	0.9958	2	1966.2444
						K.ILFIFIDSDHTDNQR.I	0.9958	2	1835.0263
						K.IKPHLMSQEVPEDWDK.Q	0.9958	2	1953.2201
						K.QFLLAAEAIDDIPFGITSNSGVFSK.Y	0.993	2	2641.9806
						R.TGPAATTLSDTAAAESLVDSSEVTVIGFFK.	0.9958	2	2987.2873
						K.YQLDKDGVVLFK.K	0.9958	2	1425.6677
						K.SNFEEALAAHK.Y	0.9958	2	1217.3238
						K.THILLFLPK.S	0.9958	2	1082.3745
						R.ILEFFGLK.K	0.9944	1	967.1961
						K.KSNFEEALAAHK.Y	0.9958	2	1345.4979
2746	PDIA3_MOUSE	505	42.38	17	164	K.ALEQFLQEYFDGNLK.R	0.9958	2	1816.0203
						R.FAHTNIESLVK.E	0.9958	2	1259.4478
						K.TFSHELSDFGLESTTGEVPVVAIR.T	0.9924	2	2592.8651
						K.RLAPEYEAAATR.L	0.9958	2	1348.5015
						K.DLLTAYYDVDYEK.N	0.9958	2	1608.7418
						K.GFPTIYFSPANK.K	0.9958	2	1342.537
						K.FIQDSIFGLCPHMTEDNK.D	0.9958	2	2153.3803
						K.LNFAVASR.K	0.9958	1	878.0189

						R.ELNDFISYLQR.E	0.9958		2	1398.5584
						R.DLFSDGHSEFLK.A	0.9958		2	1395.5114
						K.EYDDNGEGITIFRPLHLANK.F	0.9958		2	2303.5364
						K.KFIQDSIFGLCPHMTEDNK.D	0.9958		2	2281.5544
						R.EATNPPIIQEEKPK.K	0.9958		2	1594.8052
						K.KFLDAGHK.L	0.9958		1	916.0678
						R.TADGIVSHLK.K	0.9932		2	1041.1924
						R.KTFSHELSDFGLESTTGEVPVVAIR.T	0.9958		2	2721.0392
						K.FIQDSIFGLCPHMTEDNKDLIQGK.D	0.9958		2	2808.1445
2747	PDILT_MOUSE	588	5.27	2	7	R.FHVILDSVLVFK.K	0.9958		2	1417.7343
						R.FLMVIFHNPSLKQSR.K	0.9958		2	1818.1901
2748	PDIP2_MOUSE	368	11.96	3	4	K.APPFVAR.E	0.9924		1	757.9108
						K.THTYYQVLIDAR.D	0.9958		2	1480.6634
						R.DVASATPEKAENPAGHGSK.E	0.9924		1	1866.9823
2749	PDK1_MOUSE	434	33.41	7	21	K.GVYPPIQVHVTLGEEDLTVK.M	0.9958		2	2195.5205
						K.HIGSINPNCDVVEVIK.D	0.9958		2	1795.0117
						R.LCDLYYVNSPELELEELNAK.S	0.9958		2	2413.6497
						R.TPSVQLVQSWYIQSLQELLDFK.D	0.9958		2	2624.0087
						R.SLASASASGSGPASELGVPGQVDFYARFS	0.9944		3	3557.9569
						K.HIGSINPNCDVVEVIKDGYENAR.R	0.9958		3	2600.8138
						K.ANHEADDWCVPSR.E	0.9958		1	1557.5853
2750	PDK1L_MOUSE	341	14.08	2	2	K.VADFGLSKVCSASGQNPEEPVSVNK.C	0.9926		2	2620.842
						K.MSHGSNSSLYLQLVETSLK.G	0.9958		2	2095.3753
2751	PDK2_MOUSE	407	27.03	6	34	R.ATVESHESSLTLPPIK.I	0.9958	1,2		1709.9371
						K.HIGSIDPNCSVSDVVK.D	0.9911	1,2		1727.878
						R.ALLKNASLAGAPK.Y	0.9958	1,2		1254.5155
						R.HYQTIQEAGDWCVPSTEPK.N	0.9958		2	2247.3918
						R.MLINQHTLIFDGSTNPAHPK.H	0.9958		2	2235.5658
						R.HNDVVPTMAQGVLEYK.D	0.9958		1	1802.0551
2752	PDK3_MOUSE	415	9.4	2	2	R.HNDVVPTMAQGVIEYK.E	0.9958		2	1802.0551
						R.AAPLAGFGYGLPISRLYAR.Y	0.9958		3	1994.3469
2753	PDK4_MOUSE	412	25.49	5	7	R.ATVEHQENRPSLTPVEATVVLGK.E	0.9958		3	2476.7923
						K.DTCTVDPVTNQNLQYFLDR.F	0.9958		2	2300.4529
						K.SWYIQSLMDLVEFHEK.S	0.9958		2	2026.3142
						K.HYQMSSEADDWCIPSR.E	0.9958		2	1983.0852
						K.MLCDQYYLTSPELNLTQVNGK.F	0.9958		3	2488.7811
2754	PDLI1_MOUSE	327	30.58	5	34	K.MNLASEPQEVLHIGSAHNR.S	0.9958		2	2104.3483

						K.QSTSFLVLQEILESDGK.G	0.9958		2	1895.1168
						K.TSASGEEANSRPVVQPHPSGSLIIDK.D	0.9958		3	2677.931
						R.HPECYVCTDCGINLK.Q	0.9958		2	1866.9638
						K.GHFFVEDQIYCEK.H	0.9958		2	1672.8005
2755	PDLI5_MOUSE	591	16.07	5	15	K.ACMGSLNMTLQR.A	0.9958		2	1382.6021
						R.NTEFYHIPTHSDASK.K	0.9958		2	1747.8614
						R.IGDVVLSIDGISAQGMTHLEAQNK.I	0.9958		2	2497.8261
						R.ILAQITGTEHLTESENDNTK.K	0.9958		2	2215.3788
						R.SAAAFKPVGSTSVK.S	0.9958		2	1350.5577
2756	PDP1_MOUSE	538	38.29	10	25	K.NVSSILGFDSNQLPANAPIEDR.R	0.9958		2	2358.57
						K.MSSVFEDQNAATHLIR.H	0.9958		2	1820.0301
						K.VTLGQMHGLLTER.R	0.9958		2	1455.7154
						R.ALLPILQWHK.H	0.9958		2	1219.5155
						R.AMLGVQEEDGSWSAVTLSNDHNAQNERE	0.9958		3	3487.6959
						R.IVGEYLTGMHHQQPIAVGGYK.V	0.9958		2	2299.6525
						K.FIPPNYHTPPYLTAEPEVTYHR.L	0.9958	2,3		2643.961
						R.VAFSGATACVAHVDGVDLHVANTGDSR.A	0.9958	2,3		2727.9164
						R.HAVGNNEFGAVDHER.L	0.9944		2	1652.7232
						K.FLVLATDGLWETMHR.Q	0.9958		2	1790.0899
2757	PDS5A_MOUSE	1332	4.43	3	4	R.LESVKFASHCLMNHPDLAK.D	0.9958		3	2198.5109
						K.NKEINSDQSTQGNISSDR.G	0.9944		1	1994.0391
						K.LANPKQPTNPFLEMVK.F	0.9958		2	1828.1797
2758	PDXD1_MOUSE	787	4.83	2	2	R.QIPVVGSVLNWFSPVQASQK.G	0.9958		2	2185.5309
						K.SDPEGEKIHTGLLK.K	0.9944		1	1524.7141
2759	PDXK_MOUSE	312	25.96	5	18	K.TVSAMQHVLQR.T	0.9958		2	1270.4924
						K.AEAGEGQKPSPAQLELR.M	0.9958		2	1781.9633
						R.VLSIQSHVVR.G	0.9958		2	1138.3555
						K.VVPVADIITPNQFEAELLSGR.K	0.9958		2	2269.603
						K.SQELHELYEGLK.V	0.9911		2	1446.5999
2760	PE2R3_MOUSE	365	17.53	2	2	K.KSFLLCIGWLALTDLVGQLLTSPVVILVYLS(	0.9958		3	3718.4675
						K.TRATPVLLGVWLSVLAFALLPVLGVGR.Y	0.9924		3	2820.4807
2761	PEA15_MOUSE	130	37.69	3	58	K.DNLSYIEHIFEISR.R	0.9958		2	1736.9219
						R.RPDLLTMVVDYR.T	0.9958		2	1478.7497
						K.SEEITTGSAWFSFLESHNK.L	0.9958		2	2171.3275
2762	PEBP1_MOUSE	187	82.35	11	689	R.YVWLVYEQEQPLSCDEPILSNK.S	0.9958		2	2711.9942
						K.LYTLVLTDPDAPSR.K	0.9958		2	1561.7753
						R.VDYAGVTVDELGK.V	0.9924		1	1366.5108

						K.GNDISSGTVLSDYVGSGPPSGTGLHR.Y	0.9958		2	2531.6983
						K.YNLGAPVAGTCYQAEWDDYVPK.L	0.9958		2	2518.7077
						K.LYEQLSGK.-	0.9958		1	938.0685
						K.VLTPTQVMNRPSSISWDGLDPGK.L	0.9958	2,3		2499.8444
						K.LYTLVLTDPDAPSRK.D	0.9958		2	1689.9493
						K.FKVETFR.K	0.9958		1	927.091
						K.KYNLGAPVAGTCYQAEWDDYVPK.L	0.9958		2	2646.8817
						R.EWHHFLVVNMK.G	0.9944		2	1440.7057
2763	PEBP2_MOUSE	187	13.37	2	4	K.LYTLILTDPDAPSR.K	0.9947		2	1575.8021
						K.LYKQLSGK.-	0.9921		1	937.1271
2764	PECA1_MOUSE	727	9.63	3	5	R.ADNCHSHPAVFSEILR.V	0.9958		2	1853.9983
						K.IAEESDSGEYSCTAGIGK.V	0.9958		2	1874.919
						K.ISEPSVEANSHYGYDDVSGNDAVKPINQN	0.9958		3	3249.4314
2765	PEO1_MOUSE	685	16.2	4	4	R.ELDSLALSQSTGLPTLSLPRGTVCLPPALL	0.9958		3	4055.6703
						R.CSLVRPGNQQPRPLEALNQGLSLPRILR.T	0.9944		3	3184.6817
						K.TTGHFLCMTSLAEGSWEDLQASVEGRGD	0.9958		3	3312.5581
						R.DTEVVVTSRELDSLALSQSTGLPTLSLPR.C	0.9944		3	3086.4668
2766	PEPD_MOUSE	493	7.91	2	8	K.YAVDDVQYTDEIASVLTSR.N	0.9958		2	2146.3153
						K.FNVNNTILHPEIVECR.V	0.9958		2	1956.1748
2767	PEPL_MOUSE	1755	4.39	5	10	K.AESEVANLRLELVEQER.K	0.9945		2	1986.1894
						K.QVDLEGERASQEEK.I	0.9924		2	1618.6977
						K.ELDDLKK.M	0.9958		1	860.9829
						R.NSIEAHMEAVHAEWK.E	0.9958		2	1752.9421
						K.LHTEGDQLLTAEHPGR.N	0.9958		2	1774.9309
2768	PEPL1_MOUSE	524	13.36	3	6	K.YHAAVLTNSAEWEAACVK.A	0.9958		2	2021.203
						K.DNLHAVFCLAENAVGPNATRPDDIHLLYSG	0.9958		3	3409.7491
						K.ELGITPTIIRDEQLK.T	0.9952		2	1727.011
2769	PER1_MOUSE	1291	3.72	2	2	R.SGTGSAASGSLGSGLGSGSGSGSHEGGS	0.9944		3	2970.0067
						R.AGPVPVGAK.K	0.9944		1	795.9572
2770	PERI_MOUSE	475	2.53	1	2	K.NLQEAEEWYK.S	0.9958	1,2		1310.4057
2771	PERQ1_MOUSE	1044	1.44	1	2	K.EVESPYDVHDYIR.S	0.9958		2	1622.7313
2772	PESC_MOUSE	584	5.99	2	4	K.VFLSIK.G	0.9958		1	706.9035
						R.LLLPVAEYFPGMQLPPHLSPFVSEK.E	0.9944		3	2811.3545
2773	PEX1_MOUSE	1284	3.82	2	2	R.SEEAAEACVLK.V	0.9944		1	1207.2891
						K.AVVPIWVDQQTYIFIQIVTLMPAAPYGRLET	0.9958		3	3878.5647
2774	PEX14_MOUSE	376	9.04	1	2	K.SSSPSSPAAVNHHSSSDISPVSNESTSSSP	0.9958		3	3113.1919
2775	PEX19_MOUSE	299	39.8	6	44	R.ELEELLESALDDFDK.A	0.9958		2	1766.8963

						R.FEAMLDLMQQLQALGHPPK.E	0.9958	2	2168.5769
						K.YPEWLQSHQDSTPPEQFEK.Y	0.9952	2	2347.5023
						K.ELAEEEPHLVEQFQK.L	0.9958	2	1827.0007
						K.AKPSPEHAPTISAPDASGPQK.R	0.9958	2	2087.2969
						K.FFQELFDSELASQATAEFEK.A	0.9958	2	2338.5323
2776	PEX5_MOUSE	639	2.5	1	3	R.EAVEHFLEALNMQR.K	0.9909	2	1687.9109
2777	PF21B_MOUSE	487	4.11	1	3	K.TLIPDSLPVTPGRDRPPK.Q	0.9943	2	1960.284
2778	PFD2_MOUSE	154	9.09	1	4	K.IIETLSQQLQAK.G	0.9958	2	1372.6048
2779	PFD3_MOUSE	196	18.37	2	10	K.NLDSLEEDLDFLR.D	0.9958	2	1579.7038
						R.LHLGIPEAVFVEDVDSFMK.Q	0.9958	2	2147.4938
2780	PFD5_MOUSE	154	37.66	3	12	K.IQQLTALGAAQATVK.A	0.9958	2	1513.7776
						K.NQLDQEVEFLSTSIAQLK.V	0.9924	2	2064.3
						K.LHDVEHVLIDVGTGYYVEK.T	0.9958	2	2187.457
2781	PFTA_MOUSE	377	10.61	2	4	K.DLQEEMNYITAIIEEQPK.N	0.9958	2	2165.4199
						K.DPSQELEFIADILSQDAK.N	0.9958	2	2020.2005
2782	PFTK1_MOUSE	469	4.48	1	3	R.VQRTQSTFDPFEKPANQVK.R	0.9958	2	2221.4777
2783	PGAM1_MOUSE	254	78.74	13	712	R.ALPFWNEEIVPQIK.E	0.9958	2	1684.9756
						R.SYDVPPPPMEPDHPFYSNISK.D	0.9958	2	2418.6826
						K.HLEGLSEEAIMELNLPTGIPIVYELDK.N	0.9958	2	3025.4841
						R.VLIAAHGNSLR.G	0.9958	1,2	1151.3542
						R.HYGGLTGLNK.A	0.9958	2	1060.1979
						R.YADLTEDQLPSCESLK.D	0.9958	2	1869.9862
						R.FSGWYDADLSPAGHEEAK.R	0.9958	2	1981.085
						R.HGESAWNLENR.F	0.9958	1,2	1313.372
						K.NLKPIKPMQFLGDEETVR.K	0.9958	2	2116.4833
						R.HYGGLTGLNKAETAAK.H	0.9958	2	1631.8289
						R.TLWTVLDAIDQMWLPVVR.T	0.9958	2	2157.5787
						R.YADLTEDQLPSCESLKDTIAR.A	0.9958	2	2426.6056
						K.AMEAVAAQGK.V	0.9904	2	976.1357
2784	PGAM2_MOUSE	253	65.61	13	873	R.ALPFWNEEIAPK.I	0.9958	2	1415.6317
						R.YAGLKPEELPTCESLK.D	0.9958	1,2	1836.0583
						R.HGESLWNQENR.F	0.9958	1,2	1370.4239
						R.YAGLKPEELPTCESLKDTIAR.A	0.9944	2	2392.6777
						K.HNYYTSISK.D	0.9958	2	1113.2151
						R.RYAGLKPEELPTCESLK.D	0.9958	2	1992.2457
						R.FCGWFDAELSEK.G	0.9958	2	1489.5903
						R.SFDTPPPPMDEK.H	0.9958	1	1361.5091

						R.FLGDEETVR.K	0.9958	1	1066.1558
						K.IEFDICYTSVLK.R	0.9924	2	1488.6869
						R.TLWTILDVTDQMWVPVVR.T	0.9958	2	2173.5781
						R.RSFDTPPPPMDEK.H	0.9958	2	1517.6966
						K.HLEGMSDQAIMELNLPTGIPIVYELDQNLKF	0.9958	3	4094.7921
2785	PGAM5_MOUSE	288	17.71	2	2	K.FNKIVHSSMTR.A	0.9944	1	1320.5523
						R.QALQLAACGLAGGSAAVLFSAVAVGKPRG	0.9958	3	3414.8125
2786	PGBM_MOUSE	3707	9.68	17	38	R.DPSPGQPSNFIVPFQEQAWQRPDGQPATI	0.9958	3	3252.5296
						R.GMLEPVQKPDVILVGAGYR.L	0.9945	2	2043.432
						R.NSQLTGGFTVEPVHDGAR.L	0.9958	2	1886.0311
						R.NIGASVEFHCAVPNER.G	0.9958	2	1800.9347
						R.LPAIEPSDQGQYLCR.A	0.9958	2	1747.9116
						R.LYQLSPADSGEYVCQVAGSSHPEHEASFK	0.9958	2	3195.3918
						R.QPLVVLQGNNIVLEHHASR.D	0.9958	2	2125.4385
						R.HQGSELHFPSVQPSDAGVYICTCR.N	0.9958	2	2746.9282
						K.MASVGLSDIVMDTTVTHTTIHGR.A	0.9958	2	2443.7956
						K.CVVPGQAHAQVTWHK.R	0.9943	2	1718.9219
						R.RCESCAPGYEGNPIQPGGK.C	0.9958	2	2078.178
						R.IAHVELADAGQYR.C	0.9958	2	1443.6023
						K.CLIHEGAMPIK.V	0.9958	2	1269.5109
						R.LHHMSVADSGEYVCR.A	0.9958	2	1761.9159
						R.VAEGQTLDLNCVVPGHAHAQVTWHK.R	0.9958	3	2769.0581
						R.FLVHDAFWALPK.Q	0.9958	2	1444.719
						R.VAEGQTLDLSCVVPGQAHAQVTWHK.R	0.9958	2	2733.0221
2787	PGCB_MOUSE	883	1.13	1	7	R.YAVDTVLR.Y	0.9958	1	937.0837
2788	PGCP_MOUSE	470	18.51	4	11	R.LVLWTAEEQGGIGASQYYELHK.A	0.9958	2	2493.7783
						K.YSLVMEADSGTFLPTGLQFTGSDK.A	0.9952	2	2565.8543
						K.AIQIMYQNLQQDGLENVHLEQVR.I	0.9958	2	2741.0942
						K.AIINLAVYGK.Y	0.9958	1	1062.2975
2789	PGES2_MOUSE	384	28.39	6	32	R.AFLDFHSLPYQVVEVNPVR.R	0.9917	2	2231.559
						K.TYLVSGQPLEEVITYYPPMK.A	0.9958	2	2329.7132
						K.VPILVAQEGDSLQQLNDSSVIISALK.T	0.9958	2	2739.1387
						R.SAAQLPLSNSLQLTLYQYK.T	0.9934	2	2139.4564
						R.AIEEAPSVHHVNPSCKD.-	0.9944	2	1891.0136
						R.KVPILVAQEGDSLQQLNDSSVIISALK.T	0.9958	3	2867.3128
2790	PGH1_MOUSE	602	3.32	1	2	K.ALGHGVDLGHIYGDNLER.Q	0.9958	2	1937.1221
2791	PGH2_MOUSE	604	13.25	3	3	R.LDDINPTVLIK.R	0.9924	1	1241.4704

						R.AVLLCAALGLSQAANPCCSNPCQNRGECM	0.9958		3	4151.4247
						K.GCPFTSFNVQDPQPTKTATINASASHSR.L	0.9958		3	3021.239
2792	PGK1_MOUSE	417	77.46	24	1940	K.ITLPVDFVTADKFDENAK.T	0.9958		2	2024.2781
						K.VLNNMEIGTSLYDEEGAK.I	0.9958		1	1984.1853
						K.TGQATVASGIPAGWMGLDCGTESSK.K	0.9958		2	2482.6906
						K.DCVGPEVENACANPAAGTVILLENLR.F	0.9958		2	2784.0278
						K.YSLEPVAAELK.S	0.9958		1	1220.4081
						K.VNEMIIGGGMAFTFLK.V	0.9958		2	1729.1054
						R.VDFNVPMK.N	0.9958		1	950.1407
						K.LGDVYVNDAFGTAHR.A	0.9958		2	1635.7764
						K.TGQATVASGIPAGWMGLDCGTESSKK.Y	0.9958		2	2610.8647
						K.VSHVSTGGGASLELLEGK.V	0.9958	1,2		1741.9389
						K.KYAEAVGR.A	0.9924		1	894.0183
						K.ALESPERPFLAILGGAK.V	0.9958		2	1770.0819
						R.AHSSMVGVNLPQK.A	0.9958	1,2		1368.5939
						K.ITLPVDFVTADK.F	0.9958	1,2		1319.5407
						K.IQLINNMLDK.V	0.9958	1,2		1202.4546
						K.QIVWNGPVGVFEWEAFAR.G	0.9958		2	2106.391
						K.LTLDKLDVK.G	0.9958		1	1045.2645
						K.DVLFLK.D	0.9958		1	734.9139
						R.VDFNVPMKNNQITNNQR.I	0.9958		2	2033.2695
						R.FHVEEEGK.G	0.9924		1	975.0459
						K.SVVLMSHLGRPDGVPMPDK.Y	0.9958		2	2036.415
						R.GCITIIGGGDTATCCAK.W	0.9958		2	1755.8611
						K.VADKIQLINNMLDK.V	0.9958		2	1615.9287
						K.VLPGVDALSNV.-	0.9944		1	1084.2578
2793	PGK2_MOUSE	417	17.51	6	31	K.SVVLMSHLGRPDGIPMPDKYSLEPVADELK	0.9944		3	3295.8366
						K.SLLNKDVIFLK.D	0.9958		2	1290.5889
						K.DVIFLK.D	0.9958		1	734.9139
						K.ALEKPERPFLAILGGAK.V	0.9918		2	1811.1777
						K.SVVLMSHLGRPDGIPMPDK.Y	0.9958		2	2050.4419
						R.IKAAIPSIK.H	0.9958		1	941.2022
2794	PGM1_MOUSE	562	68.15	25	593	K.VFQSNANYAENFIQSIVSTVEPALR.Q	0.9958		2	2799.1125
						K.INQDPQVMLAPLISIALK.V	0.9958		2	1965.4021
						R.LVIGQNGILSTPAVSCIIR.K	0.9958		2	2012.3666
						R.NIFDFNALK.E	0.9944		1	1082.2444
						K.LSLCGEESFGTGSDHIR.E	0.9958		2	1865.9605

						K.TQAYPDQKPGTSGLR.K	0.9958	1,2		1619.7746
						K.AIGGIILTASHNPGGPNGDFGIK.F	0.9958		2	2207.4942
						K.SGEHDFGAAFDGDGDR.N	0.9958		2	1653.6183
						R.IDAMHGVVGPYVK.K	0.9958		2	1386.6519
						K.FNISNGGPAPEAITDK.I	0.9958		1	1631.7826
						K.DLEALMLDR.S	0.9958		1	1076.2531
						K.FKPFTVEIVDSVEAYATMLR.N	0.9958		2	2317.7052
						K.TIEEYAICPDLK.V	0.9958		1	1452.6105
						R.NMILGK.H	0.9944		1	675.8645
						K.ADNFEYSDPVDGSISK.N	0.9958	1,2		1744.8089
						K.IFQISK.T	0.9944		1	735.9017
						K.IALYETPTGWK.F	0.9958		1	1279.4784
						K.KILCEELGAPANSAVNCVPLEDFGGHHPDF	0.9958		3	4696.1746
						R.YDYEEVEAEGANK.M	0.9958		1	1517.5457
						R.LYIDSYEK.D	0.9944		1	1031.1504
						R.LIFADGSR.I	0.9924		1	879.0037
						R.FYMTEAIQLIVR.I	0.9944		2	1484.7967
						K.VFQSNANYAENFIQSIVSTVEPALRQEATL\	0.9958		3	3982.3989
						K.FFGNLMDASK.L	0.9924		1	1130.3038
						K.ILCEELGAPANSAVNCVPLEDFGGHHPDPN	0.9958		3	4568.0005
2795	PGM2_MOUSE	620	5.97	2	7	K.ELDELVGAIEEHFFQPQK.Y	0.9958		2	2130.3617
						K.VYWDNGAQIISPHDR.G	0.9958		2	1771.9297
2796	PGM2L_MOUSE	621	3.54	1	2	K.CPNPEEGESVLELSLRLAEK.E	0.9937		2	2271.4956
2797	PGM5_MOUSE	567	28.04	10	47	R.NIFDFNAIK.S	0.9958		1	1082.2444
						R.VEIVDPVDIYLNLLR.N	0.9956		2	1772.0947
						K.VPVYETPAGWR.F	0.9958		2	1275.4496
						R.RPTGLFEGQR.N	0.9944		2	1161.306
						K.TDSFEYVDPVDGTVTK.K	0.9958		2	1773.8908
						R.NYLPNFIQSVLSSIDLR.D	0.9958		2	1980.2713
						K.SFIGQQFAVGSHIYSIAK.T	0.9944		2	1954.2358
						R.LIIGQNGILSTPAVSCIIR.K	0.9958		2	2026.3935
						R.DLEALVTDK.S	0.9944		1	1004.1253
						K.AAGGIILTASHCPGGPGGEFGVK.F	0.9944		2	2154.3966
2798	PGP_MOUSE	321	27.1	5	17	R.YLQQPDCLLVGTNMDNR.L	0.9958		2	2038.2489
						R.AVVVGFDPHFSYMK.L	0.9958		2	1597.8719
						R.FIFDCVSQEYGINPER.T	0.9958		2	1975.1309
						K.LLLAEVDTLLFDCDGVLWR.G	0.9958		2	2249.5781

						K.RLGFITNNSSK.T	0.9958		2	1237.4013
2799	PGRC2_MOUSE	217	12.44	1	14	K.LSTLGSGGESGGDGSPGGAGATAAR.S	0.9958		2	2091.1558
2800	PGS1_MOUSE	369	18.16	4	10	K.EISPDTTLLDLQNNDISELR.K	0.9923		2	2287.4857
						K.NHLVEIPPNLPSSLVELR.I	0.9958		2	2028.3592
						K.LSRVPAGLPDLK.L	0.9955		1	1266.5265
						R.LGLGHNQIR.M	0.9943		2	1008.1685
2801	PGS2_MOUSE	354	25.14	7	93	K.VPWDFPPDTTLLDLQNNK.I	0.9958		2	2114.3623
						R.KSDFNGLNNVLVIELGGNPLK.N	0.9904		2	2242.5803
						K.GLINLSK.L	0.9924		1	744.9096
						K.DLHTLILVNNK.I	0.9958	1,2		1280.5101
						K.ISPEAFKPLVK.L	0.9958		2	1229.5052
						K.SDFNGLNNVLVIELGGNPLK.N	0.9929		2	2114.4063
						R.VPAGLAQHK.Y	0.9958		1	921.0873
2802	PGTA_MOUSE	567	17.28	5	11	R.FVAAQAAVAPAEELAFTDSLITR.N	0.9958		2	2392.7142
						K.ETLEYFSTLKAVDPMR.A	0.9924		2	1901.1847
						R.SCLLPQLHPQPDSGPQGR.L	0.9958		2	1988.1766
						R.LVFLNLQGNSLCQEEGIR.E	0.9958		2	2091.3379
						R.LQQSAALQTLASCPR.L	0.9958		2	1644.8345
2803	PGTB_MOUSE	339	4.42	1	2	K.KDDYEYCMSEYLR.M	0.9958		2	1772.8898
2804	PHAR4_MOUSE	694	9.37	2	2	K.SFVGPTPAPAPAPRTLPAAPASANTAATTT	0.9958		3	3173.5962
						K.TFQIVPEVEFSSSSDLFQDISQQEDQK.T	0.993		2	3133.349
2805	PHB_MOUSE	272	64.71	11	249	R.KLEAAEDIAYQLSR.S	0.9944		2	1607.8039
						R.NITYLPAGQSVLLQLPQ.-	0.993	1,2		1856.1723
						K.AAELIANSLATAGDGLIELR.K	0.9958		2	1999.2719
						R.AATFGLILDDVSLTHLTFGK.E	0.9924		2	2120.4533
						K.FGLALAVAGGVVNSALYNVDAGHR.A	0.9944		2	2372.689
						K.AAIISAEGDSKAAELIANSLATAGDGLIELR.I	0.9958		3	3042.4136
						R.ILFRPVASQLPR.I	0.9958		2	1397.7067
						K.VFESIGKFGLALAVAGGVVNSALYNVDAGH	0.9958		3	3133.5773
						R.VLPSITTEILK.S	0.9924		1	1214.4881
						R.GVQDIVVGEGTHFLIPWVQKPIIFDCR.S	0.9958		3	3125.6067
						K.AAIISAEGDSK.A	0.9924		1	1062.165
2806	PHB2_MOUSE	299	26.76	5	44	R.IYLTADNLVLNLQDESFTR.G	0.9958		2	2226.4912
						K.MLGEALSK.N	0.9924		1	849.0331
						R.VLSRPNAQELPSMYQR.L	0.9958		2	1890.1675
						R.IGGVQQDTILAEGLHFR.I	0.9958	2,3		1855.1038
						K.IVQAEGEAEAAK.M	0.9958		1	1216.3336

2807	PHC1_MOUSE	1012	8.1	4	14	R.KAESEEER.D	0.9958	1	978.0037
						K.MSATQQPPPHIPVQVVGTR.Q	0.9937	2	2044.3794
						K.EEHLMSAMNIK.L	0.9924	1	1303.5342
						R.TATPAPSQTLISSATYTQIQPHSLIQQQQQI	0.9958	3	4016.5033
2808	PHEX_MOUSE	749	3.6	2	3	R.LEIKIAEIMIPHENR.T	0.9944	2	1807.1614
						R.LYVSPDDK.A	0.9958	1	937.0373
2809	PHF8_MOUSE	1023	5.57	2	2	K.LGNGSGAGGILDLLK.A	0.9958	1	1385.6035
						K.FNMSGTSLNDSDDDSADMDLDGSENPLAL	0.9958	3	4007.2755
2810	PHIP_MOUSE	1821	3.95	3	3	R.FSSLMWEVRYIEHNTR.T	0.9936	2	2069.3453
						R.SELYFLIARFLEDGPCQQAAQVLIR.E	0.9924	3	2939.3502
						R.ADVLPSSTCNFLSETNAVKEDLLQK.K	0.9958	3	2781.0552
2811	PHLB1_MOUSE	1371	6.2	4	7	R.ADGGPETGELPSIGEATAALALAGR.R	0.9944	2	2325.5376
						K.QFSQARPLTRYLPNR.K	0.9958	2	1848.1178
						R.WAAHGTSPEDFSLTLGAR.G	0.9946	2	1917.088
						K.NSITEISDNEDELLEYHRR.Q	0.9946	2	2334.4613
2812	PHOP1_MOUSE	267	9.74	1	3	R.DLRAVYETIPLSPGMGDLLQFIAK.Q	0.9944	2	2649.1205
2813	PHP14_MOUSE	124	45.97	5	23	K.WAEYHADIYDK.V	0.9958	2	1411.5132
						R.VHLAEPSGDPAK.E	0.9958	1	1221.3555
						K.AKYPDYEVTWADDGY.-	0.9958	2	1793.8835
						R.NGYDCECLGGGR.I	0.9958	1	1358.3393
						K.YPDYEVTWADDGY.-	0.9958	1	1594.6306
2814	PHS2_MOUSE	103	29.13	2	6	K.VQITLTSHDCGGLTK.R	0.9937	2	1630.8047
						K.MNHHPEWFNVYNK.V	0.9958	2	1716.914
2815	PHYD1_MOUSE	291	30.24	4	10	R.APSDSGPGTSFLGSDPAWASNLFVPLPVR	0.9958	2	2944.2731
						R.IGEIVAEMDVPLHCR.T	0.9958	2	1739.9935
						R.GGLVLIHGEVVHK.S	0.9958	2	1358.6267
						K.QPHFGGEVSPHQDATFLYTEPLGR.V	0.9958	2	2684.9273
2816	PI3R5_MOUSE	871	5.97	2	2	K.AGFPGILDTASPGKLHTIPIPVAR.C	0.9924	2	2429.868
						K.ACQKPEELDSSMEALTLTLTEVVK.R	0.9924	3	2694.0328
2817	PI42A_MOUSE	405	4.69	1	3	K.HGAGAEISTVNPEQYSK.R	0.9958	2	1788.9115
2818	PI42C_MOUSE	421	6.41	2	2	K.KVFLEK.L	0.9958	1	763.9554
						K.HGAGAEISTVHPEQYAK.R	0.9958	2	1795.9493
2819	PIAS2_MOUSE	621	2.58	1	2	-.MADFEELRNMVSSFR.V	0.9911	2	1833.087
2820	PICA_MOUSE	660	23.64	6	26	R.ITAAQHSVTGSAVSK.T	0.9958	2	1457.6267
						K.LVSDDLDSSLANLVGNLGIGNGTTK.N	0.9958	2	2474.7276
						R.ATTLSNAVSSLASTGLSLTK.V	0.9958	2	1923.1711
						R.LFAAYNEGIINLLEKYFDMK.K	0.9958	3	2393.8029

						R.GDIPDLSQAPSSLLDALEQHLASLEGK.K	0.9958		2	2806.0991
						K.HLDYLIQCTNEMNVNIPQLADSLFERTTNS	0.9958		3	4384.9167
2821	PIGA_MOUSE	485	1.86	1	3	R.IILEEVR.E	0.9958		1	872.0525
2822	PIGB_MOUSE	542	6.64	2	2	R.QYVSAQEK.R	0.9944		1	953.0397
						R.KAALSFLLLSNVPLAFYTGLVHQR.G	0.9958		3	2660.1777
2823	PIMT_MOUSE	227	48.02	6	157	K.SGGASHSELIHNLR.K	0.9958		2	1478.6077
						R.MGYAEEAPYDAIHVGAAAPVVPQALIDQLK	0.9958		3	3507.0014
						R.LILPVGPAGGNQMLEQYDK.L	0.9958		2	2044.3734
						K.MKPLMGVIYVPLTDK.E	0.9909		2	1706.1549
						K.ALDVGSGSGILTACFAR.M	0.9958		2	1695.8792
						K.MKPLMGVIYVPLTDKEK.Q	0.9958		2	1963.4444
2824	PIN1_MOUSE	165	45.45	4	13	K.SGEEDFESLASQFSDCSSAK.A	0.9958		2	2182.1817
						R.GQMQKPFEDASFALR.T	0.9958		2	1725.9598
						R.TGEMSGPVFTDSGIHIILR.T	0.9958		2	2031.3343
						R.SKEEALELINGYIQK.I	0.9958		2	1735.975
2825	PININ_MOUSE	725	4.69	2	3	K.KPALQSSVVATSK.E	0.9943		2	1316.5406
						K.LPEVSVEPVLTVHSENK.S	0.9958		2	1878.1326
2826	PIPNA_MOUSE	271	26.94	4	12	K.HVEAIYIDIADR.S	0.9958		2	1415.5889
						K.IETWHKPDLGTQENVHK.L	0.9958		2	2033.2511
						R.MLAPEGALNIHEK.A	0.9958		2	1423.6703
						R.VILPVSVDEYQVGQLYSVAEASK.N	0.9944		2	2495.8321
2827	PIPNB_MOUSE	271	8.86	2	2	K.IYHLKSK.V	0.9958		1	889.0855
						R.MIAPEGSLVFHEK.A	0.9958		2	1458.7155
2828	PIT1_MOUSE	291	15.46	2	2	R.VKTSLNQSLFSISK.E	0.9921		1	1552.8113
						K.LGYTQTNVGEALAAVHGSEFSQTTICR.F	0.9944		3	2912.1517
2829	PITM2_MOUSE	1335	4.42	2	2	K.WNSNDLMDKMESPEPEESQDEIYQQSGSI	0.9944		3	3707.8893
						K.IHVLLLVLHGGTILDTGAGDPSSK.Q	0.9944		3	2414.8076
2830	PIWL1_MOUSE	862	1.86	1	2	K.ELIGLIVLTKYNNK.T	0.9924		1	1618.9573
2831	PIWL2_MOUSE	971	4.22	2	2	R.NDSVLDVMHAIYQQNKEHFQDECSK.L	0.9958		3	3037.2532
						K.GTPQSLGLNLIK.I	0.9958		1	1241.4734
2832	PJA2_MOUSE	707	5.09	2	2	R.EALEVEECSSDDPIIK.C	0.9958		2	1834.938
						K.AAWPKPAGGYQTITGR.R	0.9958		2	1674.8998
2833	PK1IP_MOUSE	382	9.16	2	2	K.YIVVVQNK.V	0.9944		1	963.1649
						K.FHGNQHLISGAEDGHICIWDVKR.W	0.9958		2	2690.9469
2834	PK2L2_MOUSE	621	2.25	1	3	K.FVDLRLNNWISR.G	0.9958	1,2		1533.7733
2835	PK3CA_MOUSE	1068	3.84	3	3	R.ALCTRDPLSEITEQEK.D	0.9944		2	1891.0515
						R.IMSSAK.R	0.9944		1	636.7845

						R.EATLVTIKHELFR.E	0.9944		1	1557.8332
2836	PKDRE_MOUSE	2126	2.82	3	3	K.QPVYEEPSDEAEAVTYLCNR.L	0.9924		2	2371.4853
						R.GAPGLGQGAESSVRGGDTGGLSPR.A	0.9958		2	2184.3304
						R.NDSLCPNCLR.A	0.9958		1	1249.2983
2837	PKHA1_MOUSE	383	4.7	1	2	K.EEVNECGESLDRNNLK.R	0.993	1,2		1906.9672
2838	PKHF1_MOUSE	279	13.98	2	2	R.SQHIIPLEEVTLEPLPETLQAK.N	0.9958		2	2486.8681
						K.KSFVVSAASTTER.Q	0.9958		1	1383.5443
2839	PKHG2_MOUSE	1340	4.4	2	3	K.HWAEGPDSGGREMVEEAIVSMTAVAWYIN	0.9958		3	3582.0145
						R.QGPGGEGTVASQGHWSSSAPTSR.A	0.9958		3	2242.3262
2840	PKHG3_MOUSE	1341	2.16	1	13	K.VPGPELPGSEEEEEEEESLAVAEQGKR.H	0.9944		2	2926.0741
2841	PKHG6_MOUSE	787	3.43	2	2	K.RSPEPR.A	0.9944		1	741.8252
						R.LHTFSMFGMPRLPPEDR.R	0.9907		2	2032.3857
2842	PKHH1_MOUSE	1356	5.97	2	2	K.ELALEMAALMAQVEYGDLEKPTLPGPGGT	0.9944		3	4729.464
						K.RGVSMSSLSSEGDYAIPPDACSLDSDYSEI	0.9944		3	3588.7579
2843	PKHH2_MOUSE	1491	2.75	2	7	R.EGCSEEQLRQLYQR.L	0.9943		2	1796.9005
						R.VQAANPLCLQPEGKPAVKGLLTK.V	0.9958		2	2433.8633
2844	PKHL1_MOUSE	4249	1.69	2	2	R.SAFPVHYLALVSSLSVVAQPVAAQPGQPFI	0.9958		3	3747.3317
						R.VDSRPFSLSAQSVPGGSGSSPGSGSSSSC	0.9958		2	2979.1033
2845	PKHM2_MOUSE	1018	3.14	2	4	K.TKLDEDASPLHPTSSQQK.C	0.9958		2	1983.1424
						R.STASDLTSSK.T	0.9944		1	997.0471
2846	PKHO2_MOUSE	495	13.33	4	6	R.ALMPPVKPSPGPETSAVEDSK.E	0.9958		2	2138.4407
						K.LLNQVLGSEPPPVCAESLLSQAVEQLR.Q	0.9958		2	2949.3404
						K.QTEKLLNQVLGSEPPPVCAESLLSQAVEQL	0.9958		3	3435.8658
						K.KPPAPPPK.I	0.9958		1	832.0336
2847	PKN2_MOUSE	983	7.83	2	2	R.AIPTVNHSGTFSPQTPVPATVPVVDARIPDI	0.9958		3	4253.7991
						K.EGMGYGDRTSTFCGTPEFLAPEVLTETSY	0.9958		3	3474.7433
2848	PKN3_MOUSE	878	3.76	2	2	R.RHLGHVQQLLR.A	0.9924		1	1357.6046
						R.SPMAVLAGSPSESWLRTR.S	0.9934		2	1946.2316
2849	PKNX2_MOUSE	474	4.01	1	3	R.RILQPMLDASNPDPAPK.A	0.9958		2	1864.1699
2850	PLAK_MOUSE	745	12.75	4	7	K.SAIVHLINYQDDAELATR.A	0.9958		2	2030.245
						R.LADGLQKMVPLLNK.N	0.9947		2	1540.9048
						R.NLALCPANHAPLQEAAVIPR.L	0.9907		2	2156.4588
						R.VAAGVLCELAQDKEAADAIDAEGASAPLMI	0.9957		3	3624.0235
2851	PLAP_MOUSE	794	16.5	6	19	K.GDQFSSHLINLLNPK.G	0.9958		2	1683.9047
						R.YVPGTSGPSNTVQTADPFTGAGR.Y	0.9958		2	2281.4435
						K.DHNIEGKAQCLSVISTILEVVQDLEATFR.L	0.9958		3	3287.6605
						K.GQTLGLGNTSFSDPFTGGGR.Y	0.9958		2	1970.1057

						K.KEALTFDQANPTQILGK.L	0.9909		2	1875.132
						K.AINWPEDIVFPALDILR.L	0.9958		2	1983.3177
2852	PLBL1_MOUSE	550	3.64	1	5	R.HTGYVVTQLDGLYLGAQK.R	0.9924		2	1964.2285
2853	PLCB1_MOUSE	1216	4.44	3	4	R.QEQYYSEKYQK.R	0.9943		2	1494.6006
						K.LRELLDVGNIGHLEQR.M	0.9958		1	1863.127
						K.TEDLIQSVLTEVEAQTIEELK.Q	0.9958		2	2389.6593
2854	PLCB2_MOUSE	1181	3.98	2	2	K.KPGGVAEGSLPSSVPVEEDTGWTAEDR.T	0.9958		3	2771.9543
						K.REINNSHIQEVVQAVK.Q	0.9929		2	1865.0995
2855	PLCB3_MOUSE	1234	4.05	3	4	R.LVAGQQQVLQQLEEEEPK.L	0.9958		2	2067.3037
						R.SGYLLKPEFMRRPDK.S	0.9958		2	1838.1779
						R.EPNVPMPDRDR.E	0.9958		1	1326.4699
2856	PLCC_MOUSE	376	9.31	2	3	K.GSSYGNQELKK.K	0.9958		1	1211.3171
						R.RFPLEDIPADETSAAQWLHK.L	0.9958	2,3		2325.5859
2857	PLCD1_MOUSE	756	13.89	5	19	R.NTLDLIAPSPADVQHWVQGLR.K	0.9958		2	2331.6365
						R.SPESQLFSIEDIQEVR.M	0.9958		2	1878.0459
						R.VYQDMNQPLSHYLVSSSHNTYLLEDQLTG	0.9958		3	4359.7675
						K.NSIVDPK.V	0.9958		1	772.8766
						K.VIVEIHGVGQDVASR.Q	0.9957		2	1579.7965
2858	PLCD4_MOUSE	807	6.82	2	2	K.DVLATLAQYAFQSSDYPLILSLENHCTWEQ	0.9944		3	3799.1542
						R.TIEVDKEEEEEEEEEELEK.D	0.9958		2	2366.4023
2859	PLCE1_MOUSE	2282	2.5	3	3	K.QQLSDNQR.Q	0.9958		1	989.0329
						K.FPSPGNAGVSGLAEGILDLFSVK.A	0.9958		2	2276.5945
						R.IVLKPQQETLEEKSIVFDDK.E	0.9944		3	2360.7099
2860	PLCG1_MOUSE	1302	1	1	2	K.IKFSDVLHTIK.E	0.9944		1	1301.5718
2861	PLCL1_MOUSE	1096	1.19	1	5	K.NAKNEAVENIK.Q	0.9956		1	1230.3635
2862	PLD1_MOUSE	1074	1.58	1	3	K.EVELALGINSEYSKR.T	0.9958		2	1708.909
2863	PLD2_MOUSE	933	4.18	2	19	K.HCFSVILGANTWPDLDLR.D	0.9958		2	2115.3624
						R.TVIIGSANINDRSLLGK.R	0.9944		2	1772.0549
2864	PLD4_MOUSE	503	3.58	1	2	K.TSTDLQVLAAHGAQIR.Q	0.9958		2	1681.8894
2865	PLEC1_MOUSE	4691	3.52	10	27	K.QVEVTVHK.G	0.9944		1	940.0873
						R.YSELTTLTSQYIKFISETLR.R	0.9931		2	2394.7271
						R.LLDAQLSTGGIVDPSKSHR.V	0.9944		2	1995.2431
						R.QAEAELALRVK.A	0.9924		1	1228.4343
						R.DGHNLISLLEVLSGDSLPR.E	0.9958		2	2036.2926
						R.ELEMKEK.K	0.9958		1	907.0698
						K.QKQAADAEMEK.H	0.9944		1	1249.3813
						K.VTLVQTLEIQR.Q	0.9958		1	1300.5412

						K.RGLFDEEMNEILTDPSDDTK.G	0.9948	2	2326.4939
						R.VYHDPSTQEPVTYSQLQQR.C	0.9958	2	2277.4551
2866	PLF4_MOUSE	105	23.81	2	22	R.HCAVPQLIATLK.N	0.9958	2	1351.5981
						K.HITSLEVIK.A	0.9958	1	1040.248
2867	PLIN_MOUSE	517	16.63	5	18	K.GVTDNVVDTVVHYVPLPR.L	0.9958	2	1981.259
						R.VLQLPVVSGTCECFQK.T	0.9958	2	1866.0968
						R.VSDSFFRPSVMEPILGR.A	0.9924	2	1938.2518
						K.GPTLLDGDLPEQENVLQR.V	0.9958	2	1995.1967
						K.GVTDNVVDTVVHYVPLPRLSLMEPESEFR.	0.9944	3	3300.754
2868	PLMN_MOUSE	812	34.98	13	55	R.HSIFTPQTNPR.A	0.9958	2	1298.4441
						K.RCSETGGSVVELPTVSQEPSGPSDSETDC	0.9911	3	3719.8558
						K.TPENFPDAGLEMNYCR.N	0.9958	2	1915.0504
						K.TAVTAAGTPCQGWAAQEPHR.H	0.9958	2	2110.2597
						R.CTTPPPPPSPTYQCLK.G	0.9924	2	1845.0345
						K.VILGAHEEYIR.G	0.9958	1	1300.5003
						K.TMSGLDCQAWDSQSPHAHGYIPAK.F	0.9958	3	2658.8708
						R.VVGGCVANPHSWPWQISLR.T	0.9944	2	2164.4405
						R.FTGQHFCGGTLIAPEWVLTAAHCLEK.S	0.9958	2	2945.2795
						R.NPDGEPRPWCFTTDPTK.R	0.9958	2	2019.1437
						R.KLYDYCDIPLCASASSFECGKPQVEPK.K	0.9958	2	3164.4343
						K.CQSWAAMFPHR.H	0.9907	2	1391.5561
						K.WGATFPHVPNYSPSTHPNEGLEENYCR.N	0.9958	2	3161.3392
2869	PLOD1_MOUSE	728	5.22	2	3	R.FLGSGGFIGYAPSLSK.L	0.9958	2	1601.8425
						K.LQVEQFLAEHGSEYQSVK.L	0.9958	2	2093.3006
2870	PLPL5_MOUSE	432	3.47	1	2	R.GTAPSGNRPLNHR.W	0.9924	1	1377.5057
2871	PLPL6_MOUSE	1355	3.54	2	3	R.QLEVVK.S	0.9924	1	715.8681
						R.GCSHIGVLKALEEAGVPVDLVGGTSIGSFIC	0.9958	3	3874.349
2872	PLPL7_MOUSE	1352	2.88	2	2	R.LARMLTGNAIALVLGGGGAR.G	0.9958	2	1912.3042
						K.YPETLVRVVQIIMVR.L	0.9958	2	1817.2432
2873	PLPL8_MOUSE	776	11.98	5	8	R.FGESFSVLANHINSYFK.S	0.9954	2	1961.1839
						K.CIWPDTPLECIVSLGTGR.Y	0.9958	2	2075.3015
						K.LSSPTQMPEAHPVSAK.Q	0.9958	2	1680.9165
						R.GIRILTIDGGGTR.G	0.9958	1	1329.5424
						R.NYGHFPGTNSHYLGGCQYK.M	0.9958	2	2201.3282
2874	PLS4_MOUSE	326	6.13	1	2	R.KWNGFLSTMVNADHFEIR.F	0.9958	2	2166.4619
2875	PLSBL_MOUSE	801	6.12	2	2	K.LLWKPSGDFTDSESDDFEEPGGR.C	0.9958	2	2585.6996
						R.VPPEGPWELQGIELLSQNELYR.Q	0.9958	2	2568.8889

2876	PLSL_MOUSE	627	38.76	12	33	K.ISTSLPVLDLIDAIQPGSINYDLLK.T	0.9958	2	2700.1449
						K.FSLVGIAGQDLNEGNR.T	0.9958	2	1690.8534
						K.AYYHLLEQVAPK.G	0.9958	2	1432.6622
						R.VNHLYSDLSDALVIFQLYEK.I	0.9958	2	2368.6916
						K.VNDDIIVNWVNTTLK.E	0.9958	2	1744.9854
						R.HVIPMNPNTDDLFNAVGDGIVLCK.M	0.9958	2	2640.9801
						K.YAFVNWINK.A	0.9958	2	1155.3415
						K.KLENCNYAVDLGK.N	0.9958	2	1524.6801
						K.LNLAFIANLFNK.Y	0.9958	2	1378.6573
						R.EGESLEDLMKLSPEELLLR.W	0.9958	2	2202.525
						K.KLTPFTIQENLNLALNSASAIGCHVVNIGAE	0.9958	3	3653.1364
						K.YPALHKPENQDIDWGALEGETR.E	0.9958	2	2540.7514
2877	PLST_MOUSE	627	23.13	8	34	K.AYFHLLNQIAPK.G	0.9958	2	1415.6781
						K.YPALTKPENQDIDWTLLEGETR.E	0.9958	2	2590.8492
						R.WANFHLENSGWQK.I	0.9937	2	1617.7636
						R.IDINMSGFNETDDLK.R	0.993	2	1712.8689
						K.TISSSLAVVDLIDAIQPGCINYDLVK.S	0.9924	2	2806.1921
						K.LNLAFVANLFNK.Y	0.9958	2	1364.6304
						R.DGETLEELMKLSPEELLLR.W	0.9958	2	2216.5519
						K.ISFNEFVYIFQEVK.S	0.9924	2	1764.0307
2878	PLUCL_MOUSE	270	27.04	2	2	R.SLHVGQTLPYYGVTPVVSTYPSDHLDR.N	0.9958	2	3003.3409
						R.VIPGLVQGVVCPLVNGVLSLLDVTLAHDVA	0.9958	3	4410.253
2879	PLVAP_MOUSE	438	10.05	2	8	R.TLETLPYHYQLMPEYASLR.R	0.9958	2	2326.6722
						R.VSGPPPNPPPIDPASLEEFKK.R	0.9958	2	2217.5267
2880	PLXA2_MOUSE	1884	4.25	3	3	K.APVPIDDNFCGLDINQPLGGSTPVEGLTLY	0.9958	3	3619.9734
						R.NLCTHDPTTCSFQEGR.I	0.9911	2	1923.9661
						K.QYHHPPDDSALCAFPIRAINLQIK.E	0.9924	2	2806.1626
2881	PLXB1_MOUSE	2119	3.92	3	3	R.YYADIRQTVPASDQEMNSVLAELSR.N	0.9958	3	2858.1523
						R.NHLYCEPPVEQPLPHPHALREAPDALPEF	0.9958	3	4275.7974
						R.VTVVPRQHGQGLAQK.Q	0.9958	1	1618.8795
2882	PLXC1_MOUSE	1574	5.08	4	5	R.ETVGEPFYLLVTTLNQK.I	0.9924	1,2	1953.2426
						K.NGSPYGLQLNEIGLELQVGTR.Q	0.9958	2	2259.5241
						K.YFFDFLDAQAENKK.I	0.99	2	1736.9213
						R.GADEPVWRSEQAIGAIAASR.A	0.9958	3	2085.284
2883	PMFBP_MOUSE	1022	1.86	2	4	K.LLSLQLDIK.N	0.9924	1	1043.292
						R.QLQQLK.K	0.9924	1	757.9083
2884	PMGE_MOUSE	259	44.4	6	127	R.AVGPHQFLGNQEAIQAAIK.K	0.9958	2	1993.273

						R.SYNVTPPPIEESHPYFHEIYSDR.R	0.9958		2	2778.994
						K.SILISAHGNSSR.A	0.9944		2	1242.3775
						R.HYGALIGLNR.E	0.9944	1,2		1114.2925
						K.MALNHGEEQVR.L	0.9958	1,2		1284.4326
						K.HLEGISDEDIINITLPTGVPILLELDENLR.A	0.9958		2	3343.7991
2885	PML_MOUSE	885	3.62	2	2	R.CKGLADFWCFECEQLICSK.C	0.991		2	2452.6304
						K.ISQLAAVNR.E	0.9958		1	972.1325
2886	PMM2_MOUSE	242	10.74	2	2	R.HLEHAGYK.T	0.994		2	955.0611
						K.YDYVFPENGLVAYK.D	0.9958		2	1678.8816
2887	PMS2_MOUSE	859	2.21	1	2	R.TAPGGVQQTGSFSSSIR.G	0.9944		2	1680.8149
2888	PMYT1_MOUSE	490	5.31	1	2	K.LGDFGLLVELGSTGAGEAQEGDPR.Y	0.9958		2	2389.581
2889	PNCB_MOUSE	538	18.77	5	33	R.FLGPDGSLLLDLLQLAEEPPPK.A	0.9958		2	2363.7564
						R.SGLPNFLAVALALGELGYR.A	0.9958		2	1962.2993
						K.QLQSPAVYPVALSEK.L	0.9958		2	1630.8815
						R.GTQEPCTVKPAQVEPLLR.L	0.9955		2	2024.2909
						R.LYLQQGQLCEPLPSLDESR.R	0.9958		2	2247.4761
2890	PNKD_MOUSE	385	21.56	4	4	K.VLPIPVLSDNYSYLIIDTQAGLAVAVDPSDPI	0.9958		3	3413.8926
						R.LFNGVKVLPIPVLSDNYSYLIIDTQAGLAVA\	0.9944		3	4072.691
						K.EEPEPLSPELEYIPR.K	0.9958		2	1798.9873
						R.THCLELQEALGPGPGPTSDDGCSR.A	0.9958		2	2555.6497
2891	PNMA3_MOUSE	466	4.08	2	11	R.DDSQGTRK.Q	0.9924		1	906.9279
						R.RLMECLR.G	0.9944		1	978.1639
2892	PNPH_MOUSE	289	35.99	5	47	R.DHINLPGFCGQNPLR.G	0.9958		2	1738.9097
						R.KLQEGTYVMLAGPNFETVAESR.L	0.9958		2	2441.7613
						K.MLGADAVGMSTVPEVIVAR.H	0.9958		2	1917.2892
						K.EAQIFDYNEIPNFPQSTVQGHAGR.L	0.9958	2,3		2719.9298
						R.FVSILMESIPLPDR.G	0.9958		2	1617.944
2893	PNPT1_MOUSE	783	13.92	7	28	K.EVFRSIILNEYK.R	0.9958		1	1511.7612
						K.YTKIIAMEK.L	0.9924		1	1097.3581
						K.NFMLHYEFPPYATNETGK.V	0.9958		2	2160.4083
						K.YTQQIIQGIQQLVK.E	0.9958		2	1660.9542
						K.ASPSQFMPLVVDYR.Q	0.9958		2	1610.8682
						K.HPTALGLEVGQEIQVK.Y	0.9924		2	1719.9786
						R.KVLQSPATTALK.T	0.9958		2	1257.5162
2894	PO5F1_MOUSE	352	3.41	1	3	K.ELEQFAKLLK.Q	0.9958		1	1219.4667
2895	PO6F1_MOUSE	301	6.98	1	3	R.NQEGQQNLMEFVGGEPSKK.R	0.9931		2	2121.3294
2896	PODXL_MOUSE	503	10.34	3	9	K.VVNLNGELGDSWIVPLDNLTK.D	0.9958		2	2297.6134

						K.ASFKPAEDLCTLHVAPILDNQAVAVK.R	0.9958		2	2809.2011
						K.KVVNLNGELGDSWIVPLDNLTK.D	0.9958		2	2425.7875
2897	POF1B_MOUSE	593	4.22	2	2	R.YILQMRGMSDK.S	0.9958		1	1342.6142
						K.EYEELLASVR.A	0.9924		1	1209.3415
2898	PON1_MOUSE	355	17.75	2	6	K.GIETGAEDLEILPNGLTFFSTGLK.Y	0.9958		2	2523.8425
						K.TITHELLPSINDIAAIGPESFYATNDHYFADP	0.9944		3	3967.3832
2899	PONL1_MOUSE	568	3.17	1	2	R.NQLRTLEPEQLAGLNK.L	0.9924		1	1825.0751
2900	POPD1_MOUSE	358	10.61	2	5	R.NSITSSSDGEDGLHHFLR.G	0.9958		2	1973.066
						K.KLEPQMSLCTQISMLEMR.N	0.9944		2	2196.6096
2901	PP14B_MOUSE	147	25.85	2	2	K.RLNLEEWILEQLTR.L	0.9958		2	1814.0947
						K.ELLVDCYKPTEAFISGLLDK.I	0.9958		2	2312.6313
2902	PP14C_MOUSE	164	25	2	8	R.EDSAPVTTVAAAGQVQQQQR.R	0.9958		2	2085.2382
						K.LQEALVDCYKPTEEFIR.E	0.9958		2	2112.3533
2903	PP16A_MOUSE	524	4.58	1	2	R.LDRSVSYHLSPEENSAPDALVR.D	0.9958		2	2456.6744
2904	PP1A_MOUSE	330	41.21	8	66	K.TFTDCFNCLPIAAIVDEK.I	0.9958		2	2115.3199
						R.AHQVVEDGYEFFAK.R	0.9958	1,2		1640.7924
						K.IFCCHGGLSPDLQSMEQIR.R	0.9958		2	2249.4787
						R.EIFLSQPILLELEAPLK.I	0.9958		2	1954.3575
						K.ICGDIHGQYYDLLR.L	0.9958		2	1723.892
						R.YPENFFLLR.G	0.9958		2	1199.3947
						R.LLEVQGSRPGK.N	0.9936		2	1184.3811
						R.IMRPTDVPDQGLLCDLLWSDPDK.D	0.9958		2	2686.0181
2905	PP1B_MOUSE	327	19.57	3	7	K.IKYPENFFLLR.G	0.9958		2	1440.7282
						K.ICGDIHGQYTDLLR.L	0.9945		2	1661.8211
						R.IMRPTDVPDTGLLCDLLWSDPDKDVQGWC	0.9958		3	3816.1567
2906	PP1R7_MOUSE	361	31.3	6	78	K.LQNLDALTNLTVLSVQSNR.L	0.9958		2	2100.3799
						R.ELYLSNNGIEVIEGLENNNK.L	0.9958		2	2263.4662
						K.IENISNLHQLQMLELGSNR.I	0.9958		2	2210.5132
						R.AIENIDTLTNLESLFLGK.N	0.9958		2	1992.2768
						K.HGGGGIVANLSEQSLK.D	0.9958		2	1567.7422
						K.IEGLQSLVNLR.E	0.9958		2	1242.4612
2907	PP1R8_MOUSE	351	18.52	4	4	K.GLLGLPEEETELDNLTEFNTAHNK.R	0.9958		3	2685.9042
						K.GLLGLPEEETELDNLTEFNTAHNKR.I	0.9944		3	2842.0917
						K.MGGEDDELKGLLGLPEEETELDNLTEFNTA	0.9958		3	3660.9423
						R.LEPHKPQQIPIDSTVSFGASTRAYTLR.E	0.9958		3	3014.4111
2908	PP2AA_MOUSE	309	52.75	8	74	K.YSFLQFDPAPR.R	0.9958		2	1341.5089
						R.GAGYTFGQDISETFNHANGLTLVSR.A	0.9958		2	2656.8711

						K.ELDQWIEQLNECK.Q	0.9958	2	1705.8279
						R.AHQLVMEGYNWCHDR.N	0.9957	2	1917.0747
						K.YFTDLFDYLPLTALVDGQIFCLHGGLSPSID	0.9958	3	4225.7535
						R.NVVTIFSAPNYCYR.C	0.9958	2	1704.889
						R.LQEVPHEGPMCDLLWSDPDDR.G	0.9954	2	2510.7035
						K.SPDTNYLFMGDYVDR.G	0.9958	2	1793.9453
2909	PP2BA_MOUSE	521	6.14	2	4	K.GLTPTGMLPSGVLSGGK.Q	0.9937	2	1572.8603
						K.TQEHFTHNTVR.G	0.9924	2	1370.4673
2910	PPA6_MOUSE	418	39.71	7	96	K.NYVEDIPFLSPVYNPQEVFIR.S	0.9949	2	2540.8779
						R.SPLKPLPLEEQVEWNPK.L	0.9958	2	2005.3214
						R.ESIQMAVGPFLHILEGNLLK.T	0.9958	2	2210.6397
						R.FDYTVTNLAGGPKPHSHYDTEYR.K	0.9958	2	2669.8693
						K.TGVGINNGDDVDFFVLLDNVAAEQVHSLLN	0.9958	3	3914.2867
						K.GSAVIHTDEASSEVLYPNYQSCWVLK.E	0.9958	2	2955.2165
						R.CLLAGLFQHQK.G	0.9958	2	1315.5242
2911	PPAC_MOUSE	158	48.1	5	20	R.SPIAEAVFR.K	0.9944	1	990.1472
						K.SVLFVCLGNICR.S	0.9952	2	1438.6423
						K.IELLGSYDPQK.Q	0.9958	2	1263.4332
						K.EDFATFDYILCMDESNLR.D	0.9934	2	2240.4121
						R.IDSAATSTYEVGNPPDYR.G	0.9929	2	1957.0606
2912	PPBT_MOUSE	524	12.21	3	24	R.NNLTDPSLSEMVEVALRILTK.N	0.9945	2	2344.7289
						K.DTLTVVTADHSHVFTFGGYTPR.G	0.9921	2	2422.6592
						K.KPFTAILYGNGPGYK.V	0.9958	2	1626.8956
2913	PPC1A_MOUSE	271	16.97	2	2	R.ELAIEIGVR.A	0.9924	1	1000.1833
						K.SFPSIHSSFAFSGLGFTTFYLAGKLHCFTES	0.9958	3	3659.0607
2914	PPCE_MOUSE	710	39.44	15	65	K.NILQLHDLTTGALLK.T	0.9958	2	1650.9591
						R.VFLDPNTLSDDGTVALR.G	0.9958	2	1834.0361
						R.VLYVQDSLEGEAR.V	0.9958	2	1479.6299
						K.ITVPFLEQCPIR.G	0.9944	2	1473.7216
						R.SNFLVLCYLHDVK.N	0.9952	2	1608.8438
						K.RLTINGGSNGGLLVAACANQRPDLFGCVIA	0.9958	3	4118.7347
						K.ICDPYSWLEDPDSEQTK.A	0.9958	2	2084.1665
						K.LPEADDIQYPSMLLLTADHDDR.V	0.9958	2	2529.7809
						R.LWYCDLQQEPNGITGILK.W	0.9958	2	2149.4174
						K.FTIGHAWTTDYGCSDTK.Q	0.9958	2	1961.0607
						K.VIEEVSDMFAFIAR.C	0.9955	2	1627.8957
						R.HMGGVLAVANIR.G	0.9958	2	1238.4936

						R.NSPNYRLINIDFTDPDESK.W	0.9954		2	2239.4033
						K.NILQLHDLTTGALLKTFPLDVGSVVGYSGR.	0.9958		3	3186.6787
						R.KQSNPLLIHVDTK.A	0.9958		2	1493.7465
2915	PPCEL_MOUSE	725	2.48	1	4	K.LDQPFIDCIRVAPDEK.Y	0.9945		2	1917.1352
2916	PPCKC_MOUSE	622	3.22	1	4	R.EIISFGSGYGGNSLLGKK.C	0.9958		2	1828.0752
2917	PPCKM_MOUSE	640	8.28	2	3	R.RPKGVPLVYEAFNWR.H	0.9924		1	1833.1459
						R.SAHLCQPEGIHICDGTEAENTAILALLEEQG	0.9958		3	3761.1127
2918	PPGB_MOUSE	474	16.24	4	9	R.RPWLVDYGESGEQVAGFVK.E	0.9958		2	2138.3873
						K.MYVTNDTEVAENNYEALKDFFR.L	0.9958		2	2670.9099
						R.YEDTLVVQDFGNIFTR.L	0.9924		2	1918.1131
						K.GAGHMVPTDKPR.A	0.9958		2	1266.4607
2919	PPIC_MOUSE	212	3.77	1	12	K.HVVFGK.V	0.9944		1	686.832
2920	PPID_MOUSE	370	11.89	3	4	K.HVVFGQVIK.G	0.9924		1	1027.2547
						R.LQPIALSCVLNIGACK.L	0.9958		2	1758.0436
						K.GTGSTTGKPLHFK.G	0.9958		2	1331.5143
2921	PPIF_MOUSE	206	62.62	9	301	R.GANSSSGNPLVYLDVGADGQPLGR.V	0.9958		2	2345.5309
						R.VIPAFMCQAGDFTNHNGTGGR.S	0.9958		2	2251.4474
						K.KIVITDCGQLS.-	0.9958		1	1234.4015
						K.KIESFGSK.S	0.9958		1	896.0312
						K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	0.9958		2	2819.1737
						R.VVLELK.A	0.9958		1	700.8968
						R.SIYGSRFPDENFTLK.H	0.9958		2	1774.9707
						R.FPDENFTLK.H	0.9944		1	1111.2395
						K.HVVFGHVK.E	0.9958	1,2		923.1056
2922	PPM1A_MOUSE	382	25.13	7	12	R.IQNAGGSVMIQR.V	0.9958		2	1274.4808
						K.QVEGVPDLVHVMR.T	0.9944		2	1479.7374
						K.RNVIEAVYNR.L	0.9958		2	1234.4007
						K.QVEGVPDLVHVMRTLASENIPSLPPGGELA	0.9958		3	3342.8352
						K.VHFFTQDHKPSNPLEK.E	0.9958		2	1925.1539
						K.YCCEHLLDHITNNQDFR.G	0.9944		2	2236.3375
						K.KQVEGVPDLVHVMR.T	0.9958		2	1607.9115
2923	PPM1B_MOUSE	390	27.95	5	17	R.ILSAENIPNLPPGGGLAGK.R	0.9924		2	1819.1112
						R.VANYCSTHLLEHITTNEDFR.A	0.9944		2	2421.5945
						R.VEMEDAHTAVVGIPHGLDNWSFFAVYDGH	0.9958		3	3586.9195
						K.GPTEQLVSPEPEVYEIVR.A	0.9958		2	2043.2811
						K.HNAHGAGNGLR.Y	0.9958		2	1104.1733
2924	PPM1F_MOUSE	452	16.15	3	5	R.NAPPSFAVAVTHEAISQLLQTDLSEFK.R	0.9958	2,3		2915.2725

						R.AYFAVFDGHGGVDAAR.Y	0.9958	2	1653.7941
						K.VPGTVLSQEEVEAELIELALGFLGSR.N	0.9958	2	2758.1412
2925	PPM1G_MOUSE	542	8.49	3	3	K.QLIVANAGDSR.C	0.9924	1	1144.273
						K.YLPDIIKDQK.A	0.9944	1	1233.4503
						R.KLEEALSTEGAEDTGNSDK.K	0.9958	2	1995.0612
2926	PPM1J_MOUSE	507	9.47	2	2	R.GHQVEGGCCALVVLYLLGKMYVANAGDSI	0.9958	3	3139.5288
						K.SSREKPGNQVGAPQK.T	0.9944	1	1583.7446
2927	PPME1_MOUSE	386	9.07	2	3	R.GLSNLFLSCPIPK.L	0.9958	2	1446.6959
						R.LPSRPPLPGSGGSQSGAK.M	0.9958	2	1693.9004
2928	PPN_MOUSE	1280	3.05	2	2	R.DICVDGVCRVVGCDHK.L	0.9958	2	1890.0016
						R.GPGGQQEPDWHRAGATIPR.L	0.9958	2	2031.1978
2929	PPOX_MOUSE	477	11.95	2	2	R.SCFPSLFQAEQTHRSILLGLLLGAGQSPQP	0.9958	3	3926.4308
						R.GGLEVLPQALHNHLASK.G	0.9958	2	1785.0561
2930	PPP5_MOUSE	499	14.03	4	6	K.RGVSCQFGPDVTK.A	0.9958	2	1451.5884
						K.FYSQAIELNPGNAIYYGNR.S	0.9958	2	2191.4075
						R.GNHETDNMNQIYGFEGEVK.A	0.9958	2	2183.3136
						K.AEGYEVAHGGR.C	0.9943	2	1146.2046
2931	PPP6_MOUSE	305	3.93	1	2	R.AHQLVHEGYK.F	0.9958	2	1182.3243
2932	PPR3A_MOUSE	1089	12.21	7	18	K.HGIGSVTSIDEPSQVITGNQK.A	0.9958	2	2168.3684
						K.ATFKPGFSPQPSR.R	0.9958	2	1420.6109
						K.EDLDDNANPANGSGR.V	0.9958	1	1545.5193
						K.NFQSVFQTQEGHMGYPK.I	0.9958	2	1999.2079
						R.NFSPLTDDHLFQADR.E	0.9958	2	1776.9029
						K.LPQETAGNDRPIEVK.E	0.9958	2	1667.8595
						R.SSSPGNEYGHPHSEEIISDMGEK.G	0.9958	2	2488.6013
2933	PPR3B_MOUSE	284	7.75	2	2	K.NYRITR.A	0.9958	1	822.9425
						R.DTFSFDISLPEK.I	0.9944	3	1399.5401
2934	PPT2_MOUSE	302	14.24	2	3	R.ESLRPLWEQVQGFR.E	0.9909	2	1745.9786
						R.EAVVPIMEKAPEGVHLICYSQGGLVCR.A	0.9924	3	3014.4421
2935	PQBP1_MOUSE	263	11.03	2	2	R.EELAPYPK.N	0.9958	1	947.0758
						K.DEELDPMDPSSYSDAPR.G	0.9915	2	1924.9875
2936	PR3D1_MOUSE	224	4.91	1	3	R.EFDLDFFDK.T	0.9958	1	1176.2677
2937	PRAF3_MOUSE	188	11.7	2	12	K.TPMGIILDALEQQEDNINK.F	0.9958	2	2143.4168
						K.KTPMGIILDALEQQEDNINK.F	0.9958	2	2271.5909
2938	PRAX_MOUSE	1391	2.66	2	2	R.VSPGEKLEAIAGQLK.I	0.9958	2	1540.8003
						K.VPEMAVPDVRLPEVQLPK.V	0.9952	2	2018.4223
2939	PRC1_MOUSE	603	7.13	3	4	K.ASDPGRFTNR.G	0.9924	1	1121.1979

						K.MQNIKQVIEK.I	0.9944	1	1231.4961
						R.LPPSGSKSVVTSLCSGK.K	0.9924	2	1704.9275
2940	PRCM_MOUSE	354	10.17	2	17	R.TPALSVVDMHTGGEPLR.I	0.9958	2	1781.0368
						R.IVHAGCPEVAGPTLLAK.R	0.9958	2	1734.0148
2941	PRDX1_MOUSE	199	68.84	11	333	R.QITINDLPVGR.S	0.9958	2	1226.4184
						R.SVDEIIR.L	0.9924	1	831.9444
						K.QGGLGPMNIPLISDPK.R	0.9958	2	1637.9348
						K.HGEVCPAGWKPGSDTIKPDVNK.S	0.9958	2,3	2393.6275
						R.LVQAFQFTDK.H	0.9958	1	1197.3763
						K.KQGGLGPMNIPLISDPK.R	0.9958	2	1766.1089
						K.ATAVMPDGQFK.D	0.9958	1	1165.3496
						K.RTIAQDYGVLK.A	0.9958	2	1264.4673
						R.GLFIIDDK.G	0.9958	1	921.0813
						K.LNCQVIGASVDSHFCHLAWINTPK.K	0.9958	2	2769.0644
						K.DISLSEYK.G	0.9958	1	955.0526
2942	PRDX2_MOUSE	198	87.37	10	790	R.QITVNDLPVGR.S	0.9958	1,2	1212.3915
						K.SLSQNYGVLKNDEGIAYR.G	0.9958	2	2028.2291
						R.LVQAFQYTDEHGEVCPAGWKPGSDTIKPN	0.9958	3	3791.0882
						R.KEGGLGPLNIPLLADVTK.S	0.9958	1,2	1836.1821
						K.SAPDFTATAVVDGAFK.E	0.9958	1	1597.7649
						K.LGCEVLGVSVDSQFTHLAWINTPR.K	0.9958	2	2701.0203
						K.EGGLGPLNIPLLADVTK.S	0.9958	1,2	1708.008
						K.YVVLFFYPLDFTFVCPTEIIAFSDHAEDFR.K	0.9958	3	3661.1134
						R.GLFIIDAK.G	0.9924	1	877.0715
						R.QITVNDLPVGRSVDEALR.L	0.9958	2	1983.2321
2943	PRDX3_MOUSE	257	61.09	9	829	K.HLSVNDLPVGR.S	0.9958	1	1207.375
						R.KNGGLGHMNITLLSDITK.Q	0.9958	2,3	1913.2426
						K.AFQFVETHGEVCPANWTPESPTIKPSPTAS	0.9958	2,3	3415.7498
						R.DYGVLLESAGIALR.G	0.9958	2	1477.7007
						R.GLFIIDPNGVVK.H	0.9958	1	1272.5303
						K.NGGLGHMNITLLSDITK.Q	0.9958	1,2	1785.0685
						K.ELSLDDFK.G	0.9958	1	967.0636
						K.ANEFHDVNCEVVAVSVDSHFSHLAWINTPI	0.9958	3	3452.7332
						K.YLVLFFYPLDFTFVCPTEIVAFSDK.A	0.9958	2	3033.4995
2944	PRDX4_MOUSE	274	27.01	4	9	R.QITLNDLPVGR.S	0.9958	1,2	1226.4184
						R.IPLLSDLNHQISK.D	0.9958	2	1478.7318
						R.ENECHFYAGGQVYPGEASR.V	0.9958	2	2172.2409

						K.HGEVCPAGWKPGSETIIPDPAGK.L	0.9958		2	2404.6507
2945	PRDX5_MOUSE	210	71.43	13	979	K.ATDLLLDDSLVSLFGNR.R	0.9944		3	1850.0789
						K.ALNVEPDGTGLTCSLAPNILSQL.-	0.9958		2	2384.6551
						R.LLADPTGAFGK.A	0.9958		1	1090.2645
						K.GVLFGVPGAFTPGCSK.T	0.9958		2	1594.8169
						K.RFSMVIDNGIVK.A	0.993		2	1379.6605
						K.THLPGFVEQAGALK.A	0.9958		2	1468.6958
						K.KVNLAELFK.G	0.994		2	1062.2975
						K.VGDAIPSVEVFEGEPGK.K	0.9958		2	1730.9121
						K.VGDAIPSVEVFEGEPGKK.V	0.9958		2	1859.0862
						K.KGVLFGVPGAFTPGCSK.T	0.9958		2	1722.991
						R.FSMVIDNGIVK.A	0.9958		1	1223.473
						K.VNLAELFK.G	0.9958	1,2		934.1234
						K.GAQVVACLSVNDVFVIEEWGR.A	0.9958		2	2349.6147
2946	PRDX6_MOUSE	224	65.63	12	298	R.DLAILLGMLDPVEK.D	0.9923		2	1527.8597
						R.NFDEILR.V	0.9958		1	907.0141
						R.VVDSLQLTGTKPVATPVDWK.K	0.9958		2	2155.4991
						R.DFTPVCTTELGR.A	0.9958	1,2		1396.506
						K.LPFPIIDDK.G	0.9958		1	1058.2627
						R.VVFIFGPDK.K	0.9924		1	1022.2322
						K.LSILYPATTGR.N	0.9958		1	1192.4007
						K.KGESVMVVPTLSEEEAK.Q	0.9958		2	1834.0919
						R.FHDFLGDSWGILFSHPR.D	0.9958		2	2032.2682
						K.DINAYNGETPTEK.L	0.9946		2	1452.5175
						K.DINAYNGETPTEKLPFPIIDDK.G	0.9958		3	2491.757
						R.DLAILLGMLDPVEKDDNNMPVTAR.V	0.9958		2	2642.0577
2947	PREP_MOUSE	1036	23.07	14	46	K.STHGLAILGPENSK.I	0.9958	1,2		1424.5968
						K.ALIESGLGTDFSPDVGYNGYTR.E	0.9958		2	2333.5163
						R.AFSSLNTLPEDLRPIVPLFCSVLTK.L	0.9958		2	2819.28
						K.LSVFSTVDSPVAPSDK.G	0.9937		2	1649.8382
						K.LVTDPTFKPCQMK.T	0.9958		2	1565.8341
						K.ENPKFLQEK.V	0.9958		1	1133.2896
						K.IHGFTVNQVTPVPELFLTAVK.L	0.9944		2	2311.7294
						R.FFTYGNFQLEGHLK.Q	0.9958		2	1701.9219
						R.LEQSTAVPAQPHWDKPR.E	0.9958		2	1961.1875
						R.KLVTDPTFKPCQMK.T	0.9958		2	1694.0082
						R.NLPDMMHLWSEIFNNPCFEEEEHFK.V	0.9958	2,3		3195.5137

						K.THFVLPFPVNYIGECVR.T	0.9958		2	2049.3459
						K.HQDASCLPALK.V	0.9958		2	1240.3679
						K.KYLLNCDNMR.C	0.9958		2	1327.5073
2948	PREY_MOUSE	112	50.89	2	4	R.YEASTNELVNEELGIAYPIIDGIPNMIPQAAF	0.9958		3	3503.9489
						R.AEQPHTFHPALLQFLVCPLSK.K	0.9958		2	2434.8095
2949	PRGR_MOUSE	923	6.07	3	6	K.TGDQQSLSDVEGAFSGVEATHR.E	0.9932		2	2292.3806
						R.QLLEGESYDGGATAGPFCPPR.S	0.9958		2	2223.3698
						R.QLLSVVK.W	0.9926		1	786.9902
2950	PRI2_MOUSE	505	4.95	1	2	R.DAASALASLDSSLEMDLEGLEEYF.-	0.9958		2	2577.7731
2951	PRKDC_MOUSE	4128	3.13	6	7	R.YAVPLAGLRLLTLHASQFTACLLDNYITLFE	0.9901		3	3953.6233
						K.ELEYCSTVNIVSENSLDLSK.M	0.9958		2	2301.4755
						K.SMEEDPQTSK.E	0.9958		1	1152.2183
						R.AFLGELKTQMTSTVR.E	0.9958		2	1682.9757
						K.ELQKTVLELQYSQELSLLYILQDDIDR.A	0.9958		3	3267.7008
						K.SDEFPPDSLK.Y	0.9924		1	1135.2157
2952	PRKRA_MOUSE	313	10.54	2	6	R.EDSGTFSLGK.M	0.9944		1	1041.1027
						K.NQLNPIGSLQELAIHHGWR.L	0.9958		2	2184.4654
2953	PRKX_MOUSE	355	7.04	1	15	K.LVDRTWTLCGTPEYLAPEVIQSK.G	0.993		2	2678.0234
2954	PRLD2_MOUSE	177	5.08	1	3	K.YPNPMDK.N	0.9958		1	864.9916
2955	PROF1_MOUSE	140	70.71	8	166	R.SSFFVNGLTLGGQK.C	0.9957		2	1455.6537
						R.DSLLQDGEFTMDLR.T	0.9958		2	1640.8053
						K.TFVSITPAEVGVLVGK.D	0.9958	1,2		1617.9261
						K.STGGAPTFNVTVTMTAK.T	0.9958		2	1683.9171
						K.TLVLLMGK.E	0.9924		1	875.1577
						K.EGVHGGLINK.K	0.9958		1	1024.1649
						K.DSPSVWAAVPGK.T	0.9958		1	1214.3635
						K.DRSSFFVNGLTLGGQK.C	0.9943		2	1726.9297
2956	PROF2_MOUSE	140	19.29	1	2	K.YVWAATAGGVFQSITPVEIDMIVGK.D	0.9911		2	2654.0961
2957	PROSC_MOUSE	274	47.81	8	75	R.TFGENYVQELLEK.A	0.9958		2	1570.7393
						K.TKPADMVIEAYGHGQR.T	0.9958		2	1774.0044
						K.HGLLPSETIAVVEHIK.A	0.9958	2,3		1744.044
						K.ASCPSLEFVGLMTIGSFGHDLSQGPNPDF(	0.9958		3	3366.6955
						K.LMAVPNLSMLETVDSVK.L	0.9958		2	1848.2233
						K.KGPTEPLK.V	0.9958		1	870.0367
						K.VMVQINTSGEDSK.H	0.9924		1	1408.5665
						K.WHFIGHLQK.Q	0.9958		1	1166.3707
2958	PRP19_MOUSE	504	5.16	2	3	K.VTSVVFHPSQELVFSASPDATIR.I	0.9958		2	2488.8027

						K.KVTSVVFHPSQELVFSASPDATIR.I	0.9923		2	2616.9768
2959	PRP39_MOUSE	625	7.84	2	2	K.VEFLEDFGSDVNK.L	0.9958		2	1499.6171
						K.FWKTVEMNPQDFTGWVYLLQYVEQENHLI	0.9924		3	3946.4897
2960	PRP6_MOUSE	941	2.66	1	3	K.SVKLEWVLGNISAAQELCEEALR.H	0.9958		3	2616.9403
2961	PRP8_MOUSE	2335	1.63	2	2	K.EQSQLTATQTRTVNK.H	0.9944		2	1705.8656
						R.TVNKHGDEIITSTTSNYETQTFSSK.T	0.9958		3	2789.9696
2962	PRPF3_MOUSE	683	3.22	1	3	K.RVLGFSEPTVVTAALNCVGK.G	0.9958		2	2119.4351
2963	PRPS1_MOUSE	318	16.35	3	31	R.VYAILTHGIFSGPAISR.I	0.9958		2	1803.1142
						K.IFSGSSHQDLSQK.I	0.9958		2	1434.5486
						K.KFSNQETCVEIGESVR.G	0.9919		2	1884.0191
2964	PRR18_MOUSE	307	14.98	2	2	R.VACSHIPAGSTASGTSAGAGAGPDDATRF	0.9958		3	4239.655
						R.FSLNLTPEAILVIQRR.H	0.9958		2	1871.2333
2965	PRR6_MOUSE	252	8.33	1	4	R.SNPGGFGIAPHCLDEGTVR.S	0.9958		2	1985.1296
2966	PRS10_MOUSE	389	29.05	7	51	R.TLMELLNQMDGFDTLHR.V	0.9958		2	2035.3405
						K.ALQSVGQIVGEVLK.Q	0.9958	1,2		1441.7111
						R.KIHIDLPNEQAR.L	0.9958		2	1434.6383
						K.MIMATNRPDTLDPALLRPGRLDR.K	0.9958		3	2624.0948
						K.IHAGPITK.H	0.9958		1	837.0097
						R.EVIELPLTNPELFQR.V	0.9958		2	1799.077
						R.NVCTEAGMFAIR.A	0.9958		2	1369.5445
2967	PRS4_MOUSE	440	60.23	15	147	R.TMLELLNQLDGFDSR.G	0.9958		2	1752.98
						R.VAEEHAPSIVFIDEIDAIGTK.R	0.9958		2	2255.5297
						K.DLLEPGCSVLLNHK.V	0.9958		2	1595.8022
						R.IETLDPALIRPGR.I	0.9932		2	1451.7092
						K.LPLVTPHTQCR.L	0.9944		2	1322.5163
						K.AVANQTSATFLR.V	0.9958		2	1279.4386
						K.APQETYADIGGLDNQIQEIK.E	0.9958		2	2204.3984
						R.GTPMSVGTLEEIIDDNHAIVSTSVGSEHYVS	0.9958		3	4049.4957
						R.MTLADDVTLDDLIMAK.D	0.9958		2	1766.0749
						R.IKDYLLMEEEFIR.N	0.9958		2	1700.0027
						K.VHAVIGVLMDDTDPLVTVMK.V	0.9958		2	2154.588
						K.ESVELPLTHPEYYEEMGIKPPK.G	0.99		2	2587.9471
						R.IFQIHTSR.M	0.9934	1,2		1002.1612
						K.KQEGTPEGLYL.-	0.9958		1	1235.3794
						R.KIEFPLPDEK.T	0.9958		2	1216.4197
2968	PRS6A_MOUSE	442	52.71	13	114	R.TMLELLNQLDGFQPNTQVK.V	0.9958		2	2190.5194
						K.APSIIFIDELDAIGTK.R	0.9958		2	1703.9732

						R.KIEFPMPNEEAR.A	0.9958	2	1461.6758
						K.QIQELVEAIVLPMNHK.E	0.9958	2	1863.2255
						K.EKFENLGIQPPK.G	0.9958	2	1400.6176
						R.QTYFLPVIGLVDAEK.L	0.9958	2	1693.9805
						K.LAGPQLVQMFIGDGAK.L	0.9958	2	1645.9574
						K.AMEVDERPTEQYSDIGGLDK.Q	0.9958	2	2254.4303
						R.VTHELQAMK.D	0.9924	1	1057.253
						K.MATVWDEAEQDGIGEEVLK.M	0.9958	2	2121.3234
						K.TLPYLVSNVIELLDVDPNDQEEDGANIDLD	0.9958	3	3701.977
						R.KMNVSPDVNYEELAR.C	0.9958	2	1765.9788
						K.LKPGDLVGVNK.D	0.9944	1	1140.3683
2969	PRS6B_MOUSE	418	41.39	9	85	K.IQDEIPALSVSRPQTGLSFLGPEPEDLEDL	0.9958	3	3674.0557
						R.ILLELLNQMDGFDQNVNVK.V	0.9958	2	2204.5463
						R.ELLKPNASVALHK.H	0.9958	2	1420.6951
						K.RLIFSTITSK.M	0.9958	2	1166.4062
						K.ENAPAIIFIDEIDAIATK.R	0.9958	2	1945.22
						R.EAVELPLTHFELYK.Q	0.9958	2	1689.9488
						K.LQQELEFLEVQEEYIKDEQK.N	0.9958	2	2539.7986
						K.MNLSEEVDLEDYVARPDK.I	0.9958	2	2124.3271
						K.AVAHHTTAAFIR.V	0.9958	1	1295.4868
2970	PRS8_MOUSE	406	50.99	16	113	R.IDILDSALLRPGR.I	0.9937	2	1439.6982
						K.HPELFEALGIAQPK.G	0.9958	2	1550.7978
						R.TMLELLNQLDGFEATK.N	0.9958	2	1824.0992
						R.EHAPSIIFMDEIDSIGSSR.L	0.9944	2	2105.327
						R.AVAHHTDCTFIR.V	0.9958	1,2	1428.5566
						R.EELQLLQEQGSYVGEVVR.A	0.9958	2	2077.2988
						R.KIEFPPPNEEAR.L	0.9958	2	1427.5999
						K.VDPLVSLMMVEKVPDSTYEMIGGLDK.Q	0.9958	3	2868.3885
						K.EVIELPVK.H	0.9937	1	927.1289
						R.KIAELMPGASGAEVK.G	0.9958	2	1501.7815
						K.VPDSTYEMIGGLDK.Q	0.9958	1,2	1525.7137
						K.GVLLYGPPGTGK.T	0.9958	1	1159.3708
						R.LLREELQLLQEQGSYVGEVVR.A	0.9958	2	2459.8051
						K.ILPNKVDPLVSLMMVEK.V	0.9958	2	1927.4114
						K.IAELMPGASGAEVKGVCTEAGMYALR.E	0.9944	3	2683.0762
						K.QIKEIK.E	0.9958	1	758.9365
2971	PSA_MOUSE	920	27.93	14	36	K.VTLSFPSTLQTGTGTLK.I	0.9958	2	1752.0178

						K.NAATEDLWESLESASGKPIAAVMNTWTK.Q	0.9958		3	3022.3564
						K.ILMDKPEMSVVLK.N	0.9958		2	1503.8989
						R.LPAEVSPINYSLCLKPDLLDFTFEGK.L	0.9958		3	2968.3827
						K.IDFVGELNDK.M	0.9958		1	1150.2737
						R.VLGATLSPELIQK.V	0.9958		2	1369.6445
						R.TIQQCCENILLNAAWLK.R	0.9944		2	2076.3326
						R.VALSNMNVIDR.K	0.9929		2	1232.4405
						R.SPVYLTVLK.H	0.9952		2	1020.2572
						K.VLTFALSEEVRPQDTVSVIGGVAGGSK.H	0.9958		2	2718.0795
						R.TQYSSAMLESLLPGIR.D	0.9924		2	1767.0503
						R.TPVMSTYLVAFVVGEYDFVETRSK.D	0.9958		3	2740.1432
						R.KPYPDDENLVEVK.F	0.9926		2	1546.7173
						K.AFFESHPAPSAER.T	0.9958		2	1446.562
2972	PSA1_MOUSE	263	68.82	11	202	K.THAVLVALK.R	0.9958	1,2		952.1851
						R.IHQIEYAMEAVK.Q	0.9958		2	1432.6776
						K.RAQSELAAHQK.K	0.9944	1,2		1239.3768
						R.HMSEFMECNLDELVK.H	0.9958		2	1883.1074
						K.ILHVDNHIGISIAGLTADAR.L	0.9958		2	2087.3866
						R.NQYDNDVTVWSPQGR.I	0.9958		2	1779.8632
						K.DLEFTIYDDDDVSPFLDGLEERPQR.K	0.9945	2,3		2986.1749
						R.LVSLIGSK.T	0.9944		1	817.0165
						R.ETLPAEQDLTTK.N	0.9958	1,2		1346.4772
						K.NVSIGIVGK.D	0.9958		1	887.0672
						R.RPYGVGLLIAGYDDMGPHIFQTCPSANYFD	0.9958		3	3693.0597
2973	PSA3_MOUSE	255	27.45	5	45	R.HVGMAVAGLLADAR.S	0.9958		2	1381.636
						K.IIYIVHDEVK.D	0.9958	1,2		1229.4619
						K.AFELELSWVGELTK.G	0.9958		2	1622.8584
						R.SNFGYNIPLK.H	0.9924		1	1153.3232
						K.AVENSSTAIGIR.C	0.9924		1	1218.3525
2974	PSA4_MOUSE	261	53.64	7	78	K.HYGFQLYQSDPSGNYGGWK.A	0.9958		2	2205.3501
						K.LNEDMACSVAGITSDANVLTNELR.L	0.9958		2	2594.8195
						R.LYQVEYAMEAIGHAGTCLGILANDGVLLAA	0.9958		3	3420.8714
						R.YLLQYQEPIPCEQLVTALCDIK.Q	0.9958		2	2696.045
						K.ATCIGNNSAAAVSMLK.Q	0.9958		2	1608.8164
						K.QDYKEGEMTLK.S	0.9944		1	1342.5066
						K.EGEMTLKSALALAVK.V	0.9958		2	1561.8774
2975	PSA5_MOUSE	241	58.09	9	185	K.GPQLFHMDPSGTFVQCDAR.A	0.9958		2	2164.3662

						K.RITSPLMEPSSIEK.I	0.993	2	1588.8597
						K.LNATNIELATVQPGQNFHMFTK.E	0.9958	2	2475.8248
						K.LGSTAIGIQTSEGVCLAVEK.R	0.9958	2	2034.2806
						R.AIGSASEGAQSSLQEVYHK.S	0.9958	2	1963.1112
						K.IVEIDAHIGCAMSGLIADAK.T	0.9958	2	2085.3894
						K.LNATNIELATVQPGQNFHMFTKEELEEVIK.	0.9958	3	3445.9123
						R.LFQVEYAIEAIK.L	0.9958	2	1424.68
						K.LGSTAIGIQTSEGVCLAVEKR.I	0.9931	3	2190.4681
2976	PSA6_MOUSE	246	35.77	7	222	R.ILTEAEIDAHLVALAERD.-	0.9944	2	1980.2255
						K.LLDSSTVTHLFK.I	0.9958	2	1361.581
						R.HITIFSPEGR.L	0.9958	2	1157.3146
						K.DCAVIVTQK.K	0.9944	1	1034.1639
						K.AINQGGLTSVAVR.G	0.9958	2	1286.474
						R.ILTEAEIDAHLVALAER.D	0.9958	2	1865.1369
						K.ITESIGCVMTGMTADSR.S	0.9958	2	1830.0444
2977	PSA7_MOUSE	248	37.5	7	36	K.NYTDDAIETDDLTIK.L	0.9958	2	1727.8193
						K.KGSTAVGVR.G	0.9958	1	875.0158
						R.KICALDDNVCMAFAGLTADAR.I	0.9958	2	2313.563
						K.DIVVLGVEK.K	0.9958	1	972.1699
						K.ICALDDNVCMAFAGLTADAR.I	0.9958	2	2185.3889
						R.RPFGISALIVGFDFDGTPR.L	0.9958	2	2066.3671
						K.NIELAVMR.R	0.9958	1	946.1528
2978	PSA7L_MOUSE	250	31.2	6	141	R.AITVFSPDGHLFQVEYAQEAVK.K	0.9958	2	2450.7533
						R.LYQTDPSGTYHAWK.A	0.9958	2	1667.818
						K.LTVEDPVTVEYITR.F	0.9958	2	1635.8547
						K.ALLEVVQSGGK.N	0.9958	1	1101.2883
						K.EAIKLAIK.A	0.9944	1	886.1228
						R.AITVFSPDGHLFQVEYAQEAVKK.G	0.9958	2	2578.9274
2979	PSB1_MOUSE	240	61.67	8	62	K.AGGSASAMLQPLLDNQVGFK.N	0.9958	2	2005.2964
						K.NMQNVEHVPLTLDR.A	0.9958	2	1666.8926
						R.FSPYAFNGGTVLAIAGEDFSIVASDTR.L	0.9958	2	2807.0887
						K.GAVYSFDPVGSYQR.D	0.9958	2	1546.6793
						K.TVIGCSGFHGDCLTLTK.I	0.9952	2	1867.0412
						R.RFFPYYVYNIIGGLDEEGK.G	0.9958	2	2281.5725
						K.AMTTGAIAAMLSTILYSR.R	0.9958	2	1872.2483
						K.DVFISAAER.D	0.9924	1	1008.1191
2980	PSB10_MOUSE	273	8.06	1	7	R.LPFTALGSGQGAAVALLEDR.F	0.9958	2	1987.2633

2981	PSB2_MOUSE	201	35.82	6	35	R.NGYELSPTAAANFTR.R	0.9924	2	1612.7392
						K.MRNGYELSPTAAANFTR.R	0.9958	2	1900.1192
						K.ILLLCVGEAGDTVQFAEYIQK.N	0.993	2	2368.6985
						K.DGIHNLENIAFPK.R	0.9958	2	1468.6524
						R.VIDKDGIHNLENIAFPK.R	0.9919	2	1924.2071
						R.FILNLPTFSVR.V	0.9943	2	1307.5785
2982	PSB3_MOUSE	205	35.12	4	24	R.LYIGLAGLATDVQTVAQR.L	0.9958	2	1890.19
						R.DAVSGMGVIVHVIEK.D	0.9958	2	1554.845
						K.RFGPYYTEPVIAGLDPK.T	0.9958	2	1924.2065
						R.FGIQAQMVTTDFQK.I	0.9958	2	1614.8566
2983	PSB4_MOUSE	264	43.56	6	72	R.VNDSTMLGASGDYADFQYLK.Q	0.9958	2	2196.3931
						K.FDGGVVIAADMLGSYGSLAR.F	0.9958	2	2000.2769
						K.GVEIEGPLSAQTNWDIAHMISGFE.-	0.9958	2	2602.8781
						K.QVLGQMVIDEELLGDGHSYSPR.A	0.9958	2	2444.7216
						R.TQNPMVTGTSVLGVK.F	0.9958	2	1532.7955
						R.FQIATVTEK.G	0.9944	1	1037.201
2984	PSB6_MOUSE	238	45.8	5	209	R.SGSAADTQAVADAVTYQLGFHSIELNEPPL	0.9958	3	4058.4937
						R.QSFAIGGSGSSYIYGYVDATYR.E	0.9958	2	2363.545
						K.DECLQFTANALALAMER.D	0.9958	2	1954.1713
						R.LAAIQESGVER.Q	0.9958	1	1173.3115
						K.LTPIHDHIFCCR.S	0.9944	2	1569.7357
2985	PSB7_MOUSE	277	37.55	5	35	K.VTPLEIEVLEETVQTMDTS.-	0.9958	2	2135.3882
						K.LPYVTMGSGSLAAMAVFEDK.F	0.9958	2	2088.4414
						K.LVSEAIAAGIFNDLGSGSNIDLCVISK.S	0.9958	2	2765.0992
						R.YQGYIGAALVLGGVDVTGPHLYSIYPHGST	0.9958	3	3350.7551
						K.KLVSEAIAAGIFNDLGSGSNIDLCVISK.S	0.9958	2	2893.2733
2986	PSB8_MOUSE	276	10.87	2	3	K.FQHGVIVAVDSR.A	0.9958	2	1328.5137
						K.KGPGLYYVDDNGTR.L	0.9958	2	1555.6873
2987	PSB9_MOUSE	219	40.18	3	7	K.YREDLLAHLIVAGWDQR.E	0.9958	2	2056.3317
						R.IFCALSGSAADAQAIADMAAYQLELHGLELI	0.9958	3	4583.2197
						R.DGSSGGVIYLVTITAAGVDHR.V	0.9958	2	2089.3128
2988	PSD11_MOUSE	422	34.36	9	44	R.YQEALHLGSQLLR.E	0.9958	2	1528.7513
						R.EASIDILHSIVK.R	0.9958	2	1325.548
						R.VQIEHISSLIK.L	0.9958	2	1267.5113
						K.TYEAALETIQNMSK.V	0.9958	2	1599.7962
						K.IMLNTPEDVQALVSGK.L	0.9958	2	1716.0026
						K.LYDNLLEQNLIR.V	0.9958	2	1504.7263

						K.TYHALSNLPK.A	0.9958	2	1144.3158
						K.KFHGILDQGEGVLIIFDEPPVDK.T	0.9958	2	2567.9445
						K.LQATLDMQSGIIHAAEEK.D	0.9958	2	1956.2213
2989	PSD12_MOUSE	456	6.14	2	2	R.LAGVINFQRPK.D	0.9944	2	1243.4947
						R.LQEVIETLLSLEK.Q	0.9958	2	1515.7875
2990	PSD13_MOUSE	376	32.45	7	16	K.ETIEDVEEMLNNLPGVTSVHSR.F	0.9958	2	2470.7137
						K.YYQTIGNHASYYK.D	0.9958	2	1608.7502
						R.QWLIDTLYAFNSGAVDR.F	0.9958	2	1970.1919
						K.DRLELWCTDVK.S	0.9958	2	1435.586
						R.QMTDPNVALTFLEK.T	0.9958	2	1607.8621
						R.VNPLSLVEIILHVVR.Q	0.9958	2	1702.0934
						R.FLGCVDIKDLPVSEQQER.A	0.9921	2	2134.36
2991	PSD7_MOUSE	321	54.83	8	54	K.TFEHVTSEIGAEEAEEVGVEHLLR.D	0.9958	2	2682.9036
						R.SVVALHNLINNK.I	0.9958	2	1322.5503
						K.VLDVSNSFAVPFDEDDKDDSVWFLDHDYL	0.9958	3	4405.8069
						R.IVGWYHTGPK.L	0.9958	1	1158.3451
						K.LPINHQIIYQLQDVFNLLPDASLQEFVK.A	0.9958	3	3297.8217
						R.VVGVLLGSWQK.K	0.9958	2	1186.4398
						K.DLGLPTEAYISVEEVHDDGTPTSK.T	0.9958	2	2574.7577
						K.VVVHPLVLLSVVDHFNR.I	0.9958	2	1944.3304
2992	PSDE_MOUSE	310	14.84	2	2	R.VIDVFAMPQSGTGVSVEAVDPVFQAK.M	0.9958	2	2693.087
						K.SWMEGLTLQDYSEHCK.H	0.9958	2	1985.1415
2993	PSIP1_MOUSE	528	3.6	1	4	K.LPIFFFGTHETAFLGPK.D	0.9958	2	1923.2646
2994	PSMD1_MOUSE	953	29.49	13	62	R.TVGTPIASVPGSTNTGTVPGSEK.D	0.9958	2	2158.3703
						R.LLHVAVSDVNDDVR.R	0.9952	2	1552.7275
						R.TPEQCPSVVSLLSESYNPHVR.Y	0.9958	2,3	2400.6165
						K.SNCKPSTFAYPAPLEVPK.E	0.9958	2	2007.2598
						K.DTSPGSAYQEGGGLYALGLIHANHGGDIID	0.9958	3	3873.2707
						K.LVKEDNLLMAYQICFDLYESASQQFLSSVIC	0.9958	3	4038.5709
						K.DTSEDVEELVEPVAAHGPK.I	0.9958	2	2023.1608
						K.TASAVAGKTPDASPEPK.D	0.9911	2	1627.7917
						K.FGAILAQGILDAGGHNVTISLQSR.T	0.9944	2	2439.777
						K.KEPEPNFQLLDNPAR.V	0.9958	2	1768.967
						R.HGGSLGLGLAAMGTAR.Q	0.9958	2	1469.7019
						R.YQPFKPLSIGGIIILK.D	0.9958	2	1788.2267
						K.EPEPNFQLLDNPARVMPAQLK.V	0.9958	2	2408.7778
2995	PSMD2_MOUSE	908	28.08	14	167	R.MNLASSFVNGFVNAAFGQDK.L	0.9958	2	2118.3716

						R.EDVLTLLLPVMGDSK.S	0.9912	2	1630.9373
						R.AELATEEFLPVTPILEGFVILR.K	0.9947	2	2458.9005
						R.LVGSQEELASWGHEYVR.H	0.9958	2	1961.1411
						K.TITGFQTHTTPVLLAHGER.A	0.9958	2	2080.3512
						K.TPVQSQQPSATTPSGADEK.S	0.9958	2	1930.0355
						K.DTSLYRPALEELR.R	0.9946	2	1563.7508
						R.NECDPALALLSDYVLHNSNTMR.L	0.9958	2	2534.7694
						R.MLVTFDEELRPLPVSVR.V	0.9924	2	2002.3795
						R.VGQAVDVVGQAGKPK.T	0.9958	2	1453.6817
						K.VQQLLHICSEHFDSK.E	0.9958	2	1842.0276
						R.SSTTSMTSVPKPLK.F	0.9958	2	1464.7173
						R.HLAGEVAK.E	0.9924	1	824.9554
						K.GEAIEAILAALEVVSEPFR.S	0.9958	2	2015.3141
2996	PSMD3_MOUSE	530	14.72	5	17	R.ELDTVTLEDIK.E	0.9958	1	1276.4265
						K.AVHGFFTSNNATR.D	0.9929	2	1422.543
						R.FPPKSYNK.D	0.9924	1	981.1393
						K.AKPPPGGEQEPPPPAPQDVEMK.E	0.9958	2	2297.5879
						K.AKPPPGGEQEPPPPAPQDVEMKEEAAAG	0.9944	3	3701.9545
2997	PSMD4_MOUSE	376	28.46	5	24	K.VNVDIINFGEEEVNTEK.L	0.9958	2	1950.1095
						R.LQAQQDAVNIVCHSK.T	0.9958	2	1711.8816
						R.SVMGALASQATK.D	0.9958	1	1164.3624
						R.AAAASAAEAGIATPGTEDSDDALLK.M	0.9958	2	2317.4687
						R.SNPENNVGLITLANDCEVLTTLTPDTGR.I	0.9958	2	3016.2549
2998	PSMD5_MOUSE	504	14.88	4	9	R.ALQSVVQAVPLHELR.E	0.9958	2	1660.9572
						R.IVENSEAVTEILNNAELLK.Q	0.9958	2	2100.3739
						R.AYLSEGPYYVKPVATTAVEGAD.-	0.9958	2	2302.5426
						R.LLQAVEPIHLAR.N	0.9958	2	1360.6426
2999	PSMD6_MOUSE	389	17.74	5	16	K.GAEILEVLHSLPAVR.Q	0.9958	2	1604.89
						R.FLLSLPEHR.G	0.9958	2	1112.317
						K.KGDLLLNR.V	0.9924	1	929.1075
						R.IGLFYMDNDLITR.N	0.9958	2	1571.8316
						K.VYQGLYCVAIRDFK.Q	0.9958	2	1732.9861
3000	PSMD8_MOUSE	257	29.18	4	5	K.HPVSLEQYLMEGSYNK.V	0.9958	2	1896.1248
						K.LVLLELNFLPTTGTK.L	0.9958	2	1660.0068
						K.DIQTNVYIK.H	0.9944	1	1094.2529
						K.GNIPAESYTFFIDILLDTIRDEIAGCIEK.A	0.9958	3	3315.7107
3001	PSMD9_MOUSE	222	12.16	2	11	K.QVEEALHQLHAR.D	0.9958	2	1431.5943

						R.HNIICLQNDHK.A	0.9958	2	1392.5236
3002	PSME1_MOUSE	249	36.55	7	31	K.EPALNEANLSNLK.A	0.9958	1	1413.5706
						R.QLVHELDEAEYQEIR.L	0.9958	2	1873.0294
						K.APLDIPVPDPVKEK.E	0.9944	2	1518.7936
						K.DVTEQLNLVTTWLQLQIPR.I	0.9958	2	2268.6182
						K.APLDIPVPDPVK.E	0.9958	1,2	1261.504
						R.NAYAVLYDIILK.N	0.9909	2	1396.6696
						K.KISELDAFLK.E	0.9944	2	1164.3873
3003	PSME2_MOUSE	239	30.96	5	67	R.QNLFQEADDFLCTFLPR.K	0.9958	2	2115.316
						K.IISLSQLLQEDSLNVADLSSLR.A	0.9958	2	2415.7465
						R.AFYAELYHIISSNLEK.I	0.9958	2	1899.1534
						R.KIISLSQLLQEDSLNVADLSSLR.A	0.9958	2	2543.9206
						K.TKVEAFQTTISK.Y	0.9958	2	1353.5584
3004	PSME3_MOUSE	254	16.14	1	14	K.EPILNIHDLTQIHSDMNLPVPDPILLTNSHDC	0.9958	3	4335.8756
3005	PSME4_MOUSE	1843	2.17	1	2	K.LQCCGDGELEMSRDDILQSLTIVHSCLIGSC	0.9944	3	4241.7422
3006	PSMF1_MOUSE	271	13.65	2	5	R.DPLSPFAVGGDDLDPFGCQR.G	0.9958	2	2164.302
						R.SGIITPIHEQWEK.A	0.9958	2	1538.7435
3007	PSMG1_MOUSE	289	10.73	2	6	R.VTVEAFKPLLSSR.S	0.9958	2	1447.7178
						K.TPESTCSLSSPFLR.A	0.9958	2	1582.7167
3008	PTCD1_MOUSE	695	4.32	2	5	K.NTYLEK.I	0.9924	1	767.8571
						K.KSQVSPNIHIYSTLINAALK.K	0.9944	2	2198.5705
3009	PTEN_MOUSE	403	2.23	1	2	K.EIVSRNK.R	0.9924	1	845.9743
3010	PTER_MOUSE	349	26.65	4	4	R.ENLQLNQEVGAIREELLYFK.A	0.9912	2	2407.7288
						K.VQTVLGLVEPSQLGR.T	0.9958	2	1596.8674
						K.WLAEQTGVHIIAGAGFYVDATHSAATR.A	0.9958	3	2844.1588
						R.AMSVEQLTDVLINEILHGADGTSIK.C	0.9929	2	2656.0234
3011	PTGD2_MOUSE	199	5.53	1	2	R.YIFAYLDIK.Y	0.9944	1	1146.3715
3012	PTH_MOUSE	204	11.76	1	2	R.CAADLALAPLGDAQLVLLRPRR.L	0.9958	2	2390.8009
3013	PTH2_MOUSE	181	40.88	4	23	R.TVLGIGPGPVELIDEVTGHLK.L	0.9958	2	2145.504
						R.SHLGMFPQNSTSEANR.D	0.9958	2	1776.9213
						K.VAAQCSHAAVSAYK.Q	0.9958	2	1463.5994
						K.APDEDTLIQLLTHAK.T	0.9958	2	1665.884
3014	PTHB1_MOUSE	885	7.57	3	3	R.LCVSTDAAAPQAMVVPGGCTPIPESDLEEF	0.9958	3	3172.4635
						R.LLGGAR.V	0.9924	1	586.7122
						K.SPVSLLGLFPDFANPSDDDQVNVMGFR.L	0.9958	3	2939.269
3015	PTN11_MOUSE	597	30.49	11	87	K.IQNTGDYYDLYGGEK.F	0.9958	2	1736.8321
						R.WFHPNITGVEAENLLLTR.G	0.9958	2	2111.4081

						K.NPMVETLGTVLQLK.Q	0.9958		2	1543.8621
						R.ESQSHPGDFVLSVR.T	0.9958		2	1558.6909
						R.TWPDHGVPSDPGGVLDFLEEVHHK.Q	0.9944		2	2669.9127
						K.EKNGDVIELK.Y	0.9958		1	1145.2981
						R.FDSLTDLVEHYK.K	0.9958		2	1467.6183
						R.FIYMAVQHYIETLQR.R	0.9958		2	1913.2445
						K.SYIATQGCLQNTVNDFWR.M	0.9958		2	2174.3435
						K.FATLAELVQYYMEHHGQLK.E	0.9958		2	2279.6184
						R.TVWQYHFRTWPDHGVPSDPGGVLDFLEE	0.9924		3	3788.1753
3016	PTN12_MOUSE	775	6.84	2	2	K.HDAGGIHTEASADSPPAFSDK.K	0.9944		2	2111.1888
						R.TPESFVLADMPVRPEWHELPNQEWSEQR	0.9958		3	3409.7571
3017	PTN13_MOUSE	2453	2.45	3	4	K.ENEYFFVDPDLKLTK.V	0.9958		1	1859.0857
						R.ASTAPEVLQSHSLTSLADVEK.I	0.9946		2	2184.4081
						K.GDRVLAVNGVSLEGATHK.Q	0.9958		2	1824.047
3018	PTN14_MOUSE	1189	3.03	2	3	K.KLEDGMVFTEYEQIPNK.K	0.9952		2	2042.3112
						K.KANGVFSTATLPENAER.S	0.9958		1	1805.9853
3019	PTN2_MOUSE	406	2.22	1	2	K.QLLLNMR.K	0.9958		1	888.1161
3020	PTN20_MOUSE	426	6.1	1	6	R.WNSMDSETAGPSKTVSPVLSGSSR.L	0.9958		2	2481.6966
3021	PTN23_MOUSE	1692	4.08	3	6	K.LQETLGQAGAGPGPSVAKAELAEVR.R	0.9958		2	2450.7544
						K.EAGDFHFQSAVKK.F	0.9943		2	1464.6207
						K.GAPLVKPLPVNPTDPAVTGPDIFAK.L	0.9958	2,3		2515.9555
3022	PTN7_MOUSE	359	24.79	2	2	K.EKVYIATQGPMPNTVADFWEMVWQEDVSI	0.9958		3	4341.0573
						K.HILFSAWPDHQTPESAGPLLRLVAEVETPE	0.9931		3	5090.6733
3023	PTPA_MOUSE	323	27.24	4	16	K.LDQEAENLVATVVPTHLAAAVPEVAVYLK.E	0.9958	2,3		3062.5334
						K.TGPFAEHSNQLWNISAVPSWSK.V	0.9958		2	2457.7074
						R.QPPPDSSEETPPTTQNFIIPK.K	0.9958		2	2324.5493
						K.FPVIQHFK.F	0.9944		2	1016.2309
3024	PTPRD_MOUSE	1894	2.32	2	2	K.FSQEYESIDPGQQFTWEHSNLEVNKPK.N	0.9958		3	3239.4815
						R.KVEVEAVNATAVK.V	0.9958		1	1358.5779
3025	PTPRK_MOUSE	1457	2.33	2	2	K.AAYFDMIRIDSQTNSSHLK.D	0.9944		2	2198.4583
						R.EGVVDIYNCVK.A	0.9958		1	1296.429
3026	PTPRM_MOUSE	1452	4.27	3	3	K.IGHLDPDTEYEISVLLTRPGEGGTGSPGPA	0.9944		3	3306.6567
						R.QVDKWQEEYNGGEGPTVVHCLNGGGR.S	0.9944		3	2888.0484
						K.WQEEYNGGEGPTVVHCLNGGGR.S	0.9958		3	2417.5224
3027	PTPRQ_MOUSE	2300	2.43	2	2	K.VEDLLSGKLPECNENSDSFLWSTTSPSPTL	0.9911		3	3568.839
						R.YSVVITAFVGNVSGAYTDGK.S	0.9958		2	2049.2878
3028	PTPRT_MOUSE	1454	1.51	1	2	R.DQFQPAIRVADLLQHITQMK.R	0.9934		2	2353.7447

3029	PTPRV_MOUSE	1705	5.51	3	4	R.VLAGPYDAWVEGSIWLAESAARPMEVPGA	0.9958		3	3200.6391
						K.IHSCTRPAPPTNLSLGFAHQPATLRASWCH	0.9944		3	3850.2695
						K.SLVPGSCYTVSAWAWSGNLSSDSQK.I	0.9958		3	2688.8762
3030	PTRF_MOUSE	392	25.51	7	86	R.QAEMEGAVQSIQGELSK.L	0.9958		2	1805.9977
						K.SDQVNGVLVLSLLDK.I	0.9958	1,2		1600.8528
						K.IIGAVDQIQLTQAQLEER.Q	0.9958		2	2026.2975
						K.KLEVNEAELLR.R	0.9958	1,2		1314.5247
						K.VMIYQDEVK.L	0.9958		1	1125.3252
						K.SFTPDHVVYAR.S	0.9958		2	1292.4368
						K.VPPFTFHVK.K	0.9958		1	1072.2951
3031	PTRFL_MOUSE	362	34.25	6	37	R.VVIFQEDIPCPASLSVVK.D	0.9958		2	2002.3246
						K.LSQSHSNTGYVVNK.L	0.9958	1,2		1534.6689
						R.GMGVDIISGSLALGPIHEFHSDEFSETEK.E	0.9944		3	3104.4151
						K.GGYSPQEGGDPPTPEPLK.V	0.9958		2	1826.9573
						R.VASVVDSVQASQK.R	0.9958		1	1318.4698
						R.LSSVTEDEDQDAALTIVTVLDR.V	0.9958		2	2391.5915
3032	PUR2_MOUSE	1010	29.6	14	180	R.AFTNPEDACSFITSANFPALVVK.A	0.9958		2	2500.7767
						K.GVEITGFPEAQALGLQVFHAGTALK.D	0.9958		2	2555.9365
						K.IELVVVGPEAPLAAGIVGDLTSAGVR.C	0.9958		2	2504.9298
						R.IYSHSLLPIIR.S	0.9915		2	1312.598
						R.VLTVTAVQENLMSALAEAR.K	0.9958	2,3		2017.3483
						R.HEIPTAQWR.A	0.9958		1	1138.2712
						K.SSSHIVLVISNK.A	0.9958	1,2		1284.4985
						K.ISNAAVSVNDHSALAQFCK.D	0.9958		2	2033.2145
						K.AFAHITGGGLLENIPR.V	0.9958		2	1666.9205
						K.NRVEFDNAVDHVLEEFSVDIVCLAGFMR.I	0.9958		3	3283.6491
						R.FGDPECQVILPLLK.S	0.9958		2	1629.9031
						R.VAVLISGTGSNLQALIDSTR.D	0.9958		2	2016.3024
						K.NLIETIQTNGSLVANGFLKSNFPVQQK.K	0.9911		2	2962.3757
						R.AVDGMQQEGAPYTGILYAGIMLTK.D	0.9958		2	2528.9411
3033	PUR6_MOUSE	425	48.94	11	48	R.IKAEYEGDGIPTVFVSVAGR.S	0.9958		2	2109.3867
						K.RNPGVQEGYK.F	0.9958	1,2		1148.2639
						R.SNGLGPVLSGNTAYPVISCPPITPDWGAQD	0.9958		3	3814.2122
						K.AEYEGDGIPTVFVSVAGR.S	0.9958		2	1868.0532
						K.ITSCIFQLLQEAGIK.T	0.9958		2	1722.0008
						R.VVVLMGSTSDLGHCEK.I	0.9958		2	1732.9557
						R.LPSGIGCSTILSPEGSAQFAAQIFGLNNHLV	0.9958		3	3586.0509

						R.ASILNTWISLK.Q	0.9958	2	1246.4924
						K.NFEWVADRVELLLK.S	0.9958	2	1733.0202
						K.EIVLADVIDNDSWR.L	0.9958	2	1645.8095
						K.KCGETAFIAPQCEMIPIEWVCR.R	0.9944	2	2697.0195
3034	PUR8_MOUSE	484	45.25	11	270	K.GTTGTQASFLQLFEGDHQK.V	0.9958	2	2066.2346
						R.ADAYFSPIHSQLEHLLDPSSFTGR.A	0.9958	2,3	2689.9439
						R.ADLPTLGFTHFQPAQLTTVGK.R	0.9958	2	2243.5675
						K.DRADLPTLGFTHFQPAQLTTVGK.R	0.9958	2	2514.8436
						K.GTTGTQASFLQLFEGDHQKVEQLDK.M	0.9944	3	2779.0355
						R.FLEEEVRPLLKPYGNEMAVK.A	0.9958	2	2363.7772
						R.HLMALTMDPLQTASVQWFER.T	0.9958	2	2375.7657
						K.AAGIIHLGATSCYVGDNTDLIILR.N	0.9958	2	2544.8767
						R.ICLAEAFLTADTILNTLQNISEGLVVYPK.V	0.9944	3	3208.6857
						R.QELPFMATENIIMAMVK.A	0.9958	2	1967.4073
						R.KVDIEVLSVLASLGASVHK.I	0.9958	2	1966.3287
3035	PUR9_MOUSE	592	38.68	13	152	R.EVSDGIVAPGYEEEALK.I	0.9958	2	1806.9641
						K.AFTHTAQYDEAISDYFR.K	0.9958	2	2036.1644
						K.RAEISNAIDQYVTGTIGEGEDLVK.W	0.9958	2	2579.8235
						K.HVSPAGAAVGVPLSEDEAR.V	0.9958	2	1863.0373
						R.AEISNAIDQYVTGTIGEGEDLVK.W	0.9958	2	2423.6361
						K.WEALFEEVPELLTEAEK.K	0.9958	2	2034.2702
						K.WEALFEEVPELLTEAEKK.E	0.9958	2	2162.4443
						R.DVSELTGFPEMLGGR.V	0.9958	1,2	1608.8065
						K.LPITVLNGAPGFINLCDALNAWQLVTELR.G	0.9958	3	3210.71
						K.TVASPDVTVEAAVEQIDIGGVTLLR.A	0.9958	2	2554.9005
						R.SLASLGLSLVASGGTAK.A	0.9958	2	1532.7777
						K.LSGVSVSSDAFFPFR.D	0.9958	2	1616.8137
						K.TLHPAVHAGILAR.N	0.9958	1	1356.6138
3036	PURA_MOUSE	321	38.32	4	69	R.GPGLGSTQGQTIALPAQGLIEFR.D	0.9958	2	2312.631
						R.DSGSEQGGAALGSGGSLGHPGSGSGSGC	0.9958	3	4778.8075
						K.LIDDYGVEEEPAELPEGTSLTVDNK.R	0.9958	2	2734.9275
						K.RFFFDVGSNK.Y	0.9958	2	1217.3696
3037	PURA1_MOUSE	457	65.86	21	465	R.VGIGAFPTEQINEIGDLLQNR.G	0.9958	2	2285.562
						R.ICDLLSDFDEFSAR.F	0.9958	2	1688.7974
						K.EYDFHLLPSGIINTK.A	0.9958	2	1747.9885
						K.RIPYFPANQEILQK.V	0.9958	2	1718.0085
						R.AHLVFDFHQAVDGLQEVQR.Q	0.9958	2	2210.4569

						K.VVDLLATDADIVSR.C	0.9911		2	1487.6934
						K.AVSFIGNGVVIHLPGLFEEAEK.N	0.9958		2	2327.6855
						R.LQQEAAATGSR.V	0.9958		2	1132.2187
						R.CQGGNNAGHTVVVDGK.E	0.9958		2	1613.6934
						R.KWEDLPPQAQSYVR.F	0.9958		2	1717.9218
						R.ASNDRPPGTGGVK.R	0.9958		2	1256.361
						R.GHEWGVTTGR.K	0.9958		2	1100.1789
						K.AVSFIGNGVVIHLPGLFEEAEKNEK.K	0.9958		2	2699.0789
						K.KGIGPTYSSK.A	0.9958		2	1038.1888
						R.DGVYFMYEALHGPPK.K	0.9958		2	1724.9715
						K.NLAHQHQSMFPTLEIDVEGQLK.R	0.9958		2	2536.8651
						R.IPYFPANQEILQK.V	0.9958		2	1561.8211
						R.YAHMVNGFTALALTK.L	0.9958		2	1637.9372
						K.RLIISDR.A	0.9958		2	873.0433
						R.FVENHMGVAVK.W	0.9944		1	1231.4552
						K.LDILDVLSEIK.V	0.9958		1	1258.4979
3038	PURA2_MOUSE	456	9.65	2	14	R.AHIVFDFHQAADGIQEQQR.Q	0.9958		2	2211.4013
						R.VGIGAFPTEQDNEIGELLQTR.G	0.9958		2	2288.5193
3039	PURB_MOUSE	324	20.06	3	9	R.GGGGGGGGGPGGFQPAPR.G	0.9932		2	1440.5179
						R.GGGGFGGGPGPGGLQSGQTIALPAQGLIE	0.9929		2	2855.1826
						K.RFFFDVGCNK.Y	0.994		2	1290.4302
3040	PUS10_MOUSE	527	3.61	1	2	R.VHFTSQEMKELQQTINK.S	0.991		2	2062.3483
3041	PUS7L_MOUSE	702	8.12	2	2	K.EEESAHTYALHQVVLPVLGYNVQYPENQV	0.9944		3	3541.9017
						R.LAAYGPKVVEGDLICSDEDADK.H	0.991		2	2366.5501
3042	PXMP2_MOUSE	194	11.34	1	2	K.AVSSGILSALGNLLAQTIEK.K	0.9958	2,3		1986.3165
3043	PYGB_MOUSE	843	63.82	43	1094	R.IGEGFLTDLSQLK.K	0.9958		1	1421.6335
						R.EIWGVEPSDLQIPPPNLPKD.-	0.9958		2	2245.5371
						R.WLLLCNPGLAEIIVER.I	0.9958		2	1897.2341
						K.DFNVGDYIEAVLDR.N	0.9958		2	1626.7631
						R.VLYPNDNFFEGK.E	0.9944		1	1443.5987
						K.LKDFNVGDYIEAVLDR.N	0.9958		2	1868.0966
						K.TCAYTNHTVLPEALER.W	0.9937		2	1876.0423
						K.KLLSLVDDEAFIR.D	0.9958		2	1519.7813
						K.INPASMFDVHVK.R	0.9958		1	1358.5982
						R.IHSEIVK.Q	0.9958		1	825.9835
						K.VAIQLNDTHPALSIPELMR.I	0.9958		2	2119.487
						R.HLDHVAALFPGDVDR.L	0.9958		2	1662.8454

						R.LKQEYFVVAATLQDIIR.R	0.9958		2	2008.3684
						R.QAVDQISSGFFSPK.D	0.9958		2	1511.6745
						K.LLSLVDDEAFIR.D	0.9958	1,2		1391.6073
						R.GIAGLGDVAEVR.K	0.9958		1	1157.3121
						K.LVTSIGDVVNHDPVVGDR.L	0.9958		2	1893.1069
						K.DVVNMLMYHDR.F	0.9958		2	1393.6185
						R.HLEIIYAINQR.H	0.9958		1	1370.5943
						R.VEHTPDGVLWLDTQVVLAMPYDTPVPGYK	0.9958	2,3		3242.7138
						K.VIPAADLSQQISTAGTEASGTGNMK.F	0.9958		2	2448.7076
						K.VFADYEAYIQCQAQVDR.L	0.9958		2	2077.2238
						R.INMAHLCVIGSHAVNGVAR.I	0.9958		2	2020.3263
						K.ARPEYMLPVHFYGR.V	0.9958		2	1737.0319
						R.NLAENISR.V	0.9958		1	917.0097
						K.QEYFVVAATLQDIIR.R	0.9958		2	1767.0349
						R.YGNPWEK.A	0.9944		1	893.9744
						R.QLLNCLHIITLYNR.I	0.9958		2	1772.0667
						K.DFYELEPEK.F	0.9958	1,2		1170.261
						R.LAACFLDSMATLGLAAYGYGIR.Y	0.9958		2	2335.6894
						R.DYFFALAHTVR.D	0.9958		2	1340.5241
						R.TQQHYYER.D	0.9924		2	1125.1857
						R.IGEGFLTDLSQLKK.L	0.9958		2	1549.8076
						R.EIWGVEPSDLQIPPPNLPK.D	0.9958		2	2130.4485
						K.IVNGWQVEEADDWLR.Y	0.9958		2	1830.9945
						R.VIFLENYR.V	0.9924		1	1054.234
						R.DHLVGR.W	0.9924		1	696.7843
						K.DFYELEPEKFQNK.T	0.9958		2	1687.8462
						R.YEFGIFNQK.I	0.9958		1	1146.2878
						R.WPVSMFEK.L	0.9958		1	1024.2225
						K.KTCAYTNHTVLPEALER.W	0.9958		2	2004.2164
						K.AAPGYHMAK.M	0.9944		1	946.1119
						R.HLHFTLVK.D	0.9924		1	995.2125
3044	PYGL_MOUSE	850	10.47	5	46	R.DYYFALAHTVR.D	0.9958		2	1356.5235
						R.APNDFNLQDFNVGDYIQAVLDR.N	0.9958		2	2525.7368
						K.TFAYTNHTVLPEALER.W	0.994		2	1863.0801
						K.LITSVAEVVNNDPMVGSK.L	0.9945		2	1874.1596
						K.INPSSMFDVHVK.R	0.9958		2	1374.5976
3045	PYGM_MOUSE	842	52.61	32	916	K.DFNVGGYIQAVLDR.N	0.9958		2	1567.7416

						K.WVDTQVVLAMPYDTPVPGYR.N	0.9958		2	2308.6569
						R.QIIEQLSSGFFSPK.Q	0.9958		2	1581.8089
						R.IGEDYISDLDQLR.K	0.9958		2	1537.6665
						R.WLVLCNPGLAEVIAER.I	0.9958		2	1841.1266
						K.VFADYEEYIK.C	0.9958		1	1277.4161
						R.EIWGVEPSR.Q	0.9958		1	1073.1937
						K.LITAIGDVVNHDPAVGDR.L	0.9958		2	1863.0806
						R.GYNAQEYYDRIPELR.Q	0.9958		2	1888.0465
						K.VAIQLNDTHPSLAIPELMR.I	0.9958		2	2119.487
						R.HLQIIYEINQR.F	0.9958		2	1427.6463
						R.GLAGVENVSELK.K	0.9958	1,2		1216.3769
						K.LLSYVDDEAFIR.D	0.9958		2	1441.6238
						R.GLAGVENVSELKK.N	0.9958		2	1344.551
						R.KLLSYVDDEAFIR.D	0.9958		2	1569.7979
						R.IHSEILK.K	0.9924		1	840.0104
						K.VHINPNSLFDVQVK.R	0.9958		2	1610.8534
						K.VIPAADLSEQISTAGTEASGTGNMK.F	0.9958		2	2449.6923
						R.NNVVNTMR.L	0.9958		1	948.085
						R.LPAPDEKI.-	0.9958		1	883.0324
						K.AWDVTVKTCAYTNHTVLPEALER.W	0.9944		3	2675.9672
						K.DIVNMLMHHDR.F	0.9958		2	1381.6105
						R.WPVHLMETLLPR.H	0.9958		2	1492.8223
						R.INMAHLCIAGSHAVNGVAR.I	0.9958		2	1992.2726
						K.ICGGWQMEEADDWLR.Y	0.9958		2	1867.0089
						R.TNFDAFPDK.V	0.9958		1	1055.132
						R.GYNAQEYYDR.I	0.9958		1	1279.3079
						R.RWLVLCNPGLAEVIAER.I	0.9958		2	1997.3141
						R.IGEDYISDLDQLRK.L	0.9958	1,2		1665.8406
						R.TLQNTMVNLALENACDEATYQLGLDMEEL	0.9958		3	4899.2865
						K.ARPEFTLPVHFYGR.V	0.9958		2	1690.945
						R.RMSLVEEGAVK.R	0.9944		1	1219.4418
3046	PYRD_MOUSE	395	28.35	5	17	R.ILGPLADYLVVNVSSPNTAGLR.S	0.9937		2	2270.6341
						R.YGFNSHGLSAVEHR.L	0.9958		2	1574.6957
						K.IAPDLTAQDKEDIASVAR.E	0.9944		2	1914.1228
						R.ELGIDGLIITNTTVSRPVGLQGALRSETGGL	0.9958		3	3778.3445
						K.FRNPVGIAAGFDK.H	0.9958		2	1392.6005
3047	PZRN3_MOUSE	1063	3.95	2	2	R.TDESTRNDESSEQENNGEDATASANPLAG	0.9944		3	3295.2414

						R.GCGRVVK.L	0.9958	1	775.8925
3048	Q000W5_MOUSE	611	5.56	2	2	K.KLVELIGENK.E	0.9943	2	1143.369
						R.LRLPTETLQELLDVHAACEK.E	0.9958	2	2337.6446
3049	Q059P4_MOUSE	1214	3.54	2	2	R.QMHIEQLGLQSQKVQDLTQK.L	0.9958	3	2353.6989
						R.GTQSVSGQDGSSQRPTPTR.I	0.9958	2	1947.0287
3050	Q05AA6_MOUSE	957	1.78	1	4	K.QFNVDICQTCFLTGR.A	0.9958	2	1860.0088
3051	Q05AC5_MOUSE	485	9.69	2	2	K.YSANMEQKNK.D	0.9958	1	1213.3508
						R.NNCDIDAADMNFITPLMKAVQNWTYECVC	0.9958	3	3963.451
3052	Q05C60_MOUSE	120	10.83	1	3	K.FILMKNPTNVK.S	0.9958	1	1305.6214
3053	Q05CJ5_MOUSE	313	19.81	3	3	K.YGDLLPADGILIQGNDLK.I	0.9958	2	1916.1815
						K.DPLLLSGTHVMEGSGR.M	0.9958	2	1669.8932
						K.EANHDGDFGITLTELRALMELR.S	0.994	2	2502.8047
3054	Q05D19_MOUSE	378	4.23	1	3	R.KGLFESNGQNGNGK.W	0.9958	1	1450.551
3055	Q06054_MOUSE	728	1.92	1	2	K.HQKCHTGEKPYK.C	0.9907	2	1513.6623
3056	Q08ED5_MOUSE	561	2.67	1	8	R.FMPAVVDGKFLPR.H	0.9958	2	1477.8077
3057	Q09XV5_MOUSE	2582	2.44	2	2	K.LVELEVECMEEPNHLDLDLETRIPVINK.V	0.9944	3	3349.7872
						K.GSAPAGNPGAAGPPLKPAVTLTSTPTQGE	0.9958	3	2861.1815
3058	Q0GKD5_MOUSE	1196	4.6	2	2	R.MLCEGLRNPVCNLSILWLDLYSLSAQVITEI	0.9958	3	3779.3621
						K.SQTTTALCLKYLSLTIPDK.H	0.9917	2	2154.4749
3059	Q0P557_MOUSE	423	4.73	1	4	K.NGSTISLLAAEEEINQLK.K	0.9912	2	1931.1503
3060	Q0PD08_MOUSE	215	14.88	1	2	R.ESFEHIQAWHQEVVSTQGPDKVVFLLVGH	0.9958	3	3446.8901
3061	Q0VBD0_MOUSE	767	4.04	2	2	K.STTMEHPSLGQLSEK.L	0.9958	2	1645.8249
						R.QVILQWNNNKIK.S	0.9958	1	1498.7684
3062	Q0VBL3_MOUSE	962	3.95	2	2	K.ISELGSQLSDEAVEDGLFHEFK.R	0.9958	2	2451.6489
						R.TAAPTEGKNPLK.K	0.9958	1	1227.4032
3063	Q0VE21_MOUSE	187	18.18	1	2	K.GLYQAAGRTLVTLGGLSIFSGAIAFFPVFSC	0.9944	3	3350.8945
3064	Q0VF76_MOUSE	604	1.32	1	4	K.NLDNIK.N	0.9924	1	716.8125
3065	Q0VGB8_MOUSE	949	6.95	3	16	R.FQIQQTANILRSK.T	0.9924	1	1547.7977
						K.HSTGVASVLNLCEVLLHDCDACATDAECD	0.9944	3	4019.1893
						K.ETLVAVQQLDK.N	0.9924	1	1244.4307
3066	Q0VGY9_MOUSE	1887	2.07	1	4	R.QVDSSGAIDTQQHEEVIVEGPLADPGDLEA	0.9958	3	3972.2801
3067	Q148Q7_MOUSE	538	2.6	1	5	R.SLNLDSIIAEVK.A	0.9958	1	1302.5107
3068	Q148R4_MOUSE	1017	6.1	3	6	K.CAMCASVFLLEEEEK.K	0.9958	1	1816.9932
						R.RNNPIEGLDGK.M	0.9915	2	1213.3359
						K.TATVPMLLTLAFYLTQDAAGEKGNQDPCM	0.9944	3	3286.7488
3069	Q148T8_MOUSE	1336	4.94	2	2	R.NHPEPTPDQITEALGGNLCR.C	0.9925	2	2220.3697
						K.DPVGHPIMHQSGIKHATGEAIFIDDMPPIDQ	0.9958	3	4599.1996

3070	Q149E7_MOUSE	531	2.82	1	13	K.AFIRSSQLLIHER.I	0.9924	1	1570.835
3071	Q149F3_MOUSE	632	2.06	1	3	K.HFTILDAPGHK.S	0.9958	1	1236.416
3072	Q14AK4_MOUSE	347	15.27	2	2	K.NWVLPEAQENNVKK.F	0.9924	2	1669.8778
						K.TPIVLSIAVMALLLAIASFVMLGHLLIFHLYLI	0.9944	3	3837.8739
3073	Q14AS8_MOUSE	509	2.55	1	2	R.SFAGILLDCTK.K	0.9958	1	1225.3936
3074	Q14BH0_MOUSE	1290	2.09	2	2	R.KGGFLTQSNCQEK.S	0.9958	1	1497.6141
						K.SLPSPQAAHK.M	0.9958	1	1036.1759
3075	Q14DN9_MOUSE	464	4.53	1	2	R.EEHRESIQDSAVSSTLTFK.Q	0.9958	2	2165.3214
3076	Q14DT8_MOUSE	756	3.17	2	2	K.FKPDAGVLLNK.Y	0.9958	1	1202.4392
						R.LEYADGAPR.I	0.9921	2	992.0764
3077	Q155P7_MOUSE	2997	1.67	4	10	R.QNAESAK.R	0.9958	1	747.7831
						R.MAQNLQDLQLELISTRSENENLIK.E	0.9956	2	2802.1724
						K.SEIQRMAQNLQDLQLELISTR.S	0.9929	2	2487.8339
						R.KNELEQLK.E	0.9958	1	1002.1558
3078	Q19LI2_MOUSE	512	28.52	8	52	K.VFELIQNGWFLSQVR.L	0.9945	2	1837.1313
						K.STVHLGQEAIFR.C	0.9911	2	1358.54
						K.TPFAVASTR.S	0.9958	1	950.0825
						K.YMHVWSEDSKPVELMWSDETLQAPVLTA	0.9944	3	3821.268
						K.IHGFSPTR.D	0.9924	1	915.0397
						R.CGVEPPVDIHLPALNK.W	0.9958	2	1760.0093
						R.YTALPPFTFESGISDPVEVIVEG.-	0.9958	2	2468.7626
						R.QEGVDGVQKPDVQHK.G	0.9958	2	1664.8155
3079	Q1EQW1_MOUSE	595	5.71	1	4	R.GLPHNQDFPAHENQPLLLTSGCQENPQEV	0.9923	3	3728.9824
3080	Q1JQ89_MOUSE	84	59.52	1	2	R.DIVENSVAVPLLTHPGTAAQNELSINSTTSN	0.9958	3	5009.36
3081	Q1MWP8_MOUSE	544	32.9	9	57	K.DKPVYDELFYTLSPINGK.I	0.9958	2	2100.3758
						K.SISIIDSPGILSGEK.Q	0.9958	2	1516.7319
						R.LPEIYVQLQR.E	0.9958	2	1259.4911
						R.LFEAEAQDLFR.D	0.9958	1	1339.4906
						R.VYIGSFWAQPLQNTDNR.R	0.9958	2	2010.2163
						K.LADCDCDGMLDEEEFALAK.H	0.9958	2	2203.3115
						R.KVLPLEEAYR.F	0.9958	2	1218.4386
						K.LDGYELPNSLPPHLVPPSHR.K	0.9958	2	2239.5388
						K.ISSLMGLISQEEMNMPTQMVQGGAFDGTT	0.9958	3	4410.9042
3082	Q1W5W7_MOUSE	1067	5.72	2	2	K.IEQAFPVFKGAEGGR.V	0.9954	2	1606.8216
						K.AAITHFGQSPYLLIVPYTAAQVQTLAAASND	0.9944	3	4410.0288
3083	Q27YN9_MOUSE	2265	2.3	2	4	R.SSLELDTELSWISGDLLPSSQEEPLSPRDL	0.9958	3	3443.7864
						R.TSSSGSAEPGTAHHEMK.S	0.9958	2	1714.8041

3084	Q2LK61_MOUSE	673	3.71	2	2	R.GSENLIRK.S	0.9958	1	917.0531
						K.SILPGASFLLTAR.T	0.9943	2	1346.6127
3085	Q2LKU8_MOUSE	917	4.25	2	2	K.EEVGDSLDLLK.Q	0.9958	1	1218.3465
						K.LLCEGLRNPACNLSTLWLDVASLR.E	0.9944	3	2773.1371
3086	Q2M4I8_MOUSE	509	11.39	2	2	R.EITQIQDTNDINDITYADLNLPK.E	0.9958	2	2648.8835
						R.LGPLLLCLLLSASCFCTGATGTEVKVTQPE	0.9924	3	3365.8307
3087	Q2TB54_MOUSE	535	5.79	2	4	R.QGTTPETDGPRDETDVR.V	0.9958	2	1874.9157
						K.NSLSGTNALR.G	0.9958	1	1033.1295
3088	Q2TJI9_MOUSE	363	10.74	2	2	R.LLPSYSAFSHSSHDSCK.D	0.9958	2	1924.0429
						K.SPKPVKPVEDEDDTGLQK.S	0.9958	2	1983.1827
3089	Q2TV84_MOUSE	1506	0.73	1	3	R.KGDEENEHK.K	0.9944	1	1086.1033
3090	Q2VEB4_MOUSE	2308	2.3	2	2	K.TKSFDSWSYSEMEK.E	0.9944	2	1725.8671
						K.LLPQKPRGETIQDIDDWELSEMNSDSEIYP	0.9958	3	4163.602
3091	Q2VPA6_MOUSE	1069	0.75	1	7	R.NIGNGK.V	0.9958	1	602.6683
3092	Q2VPC8_MOUSE	1159	17.43	8	28	R.LQPSQLDPEASISAILCDK.N	0.9915	2	2086.313
						K.LHEEDPILSSASDGTGEHFLPQEAIWESSR	0.9958	3	3339.556
						R.TGQLPGISLVPLQEPR.T	0.9958	2	1705.9951
						R.KPWADVSLSTQGGNEQGSELPSK.G	0.9944	2	2416.6067
						R.MEPSPNIPGNILPTSTPEVDGPTQHSMAAF	0.9958	3	3146.5171
						K.NLEFLEGCHPSK.S	0.9958	2	1431.5542
						K.SHSPFHPPFSCDGEGLLMSPGQPCGVEK\	0.9958	3	4616.9516
						K.SQAFHSKPHLETK.K	0.9958	2	1510.6927
3093	Q2XQY6_MOUSE	1464	2.25	2	3	R.VQGTPLLK.H	0.9958	1	856.0531
						R.ADITLIEGSLLVTAIGEPVLR.F	0.9944	3	2181.5779
3094	Q31143_MOUSE	281	2.85	1	2	K.AGPGHVT.-	0.9931	1	638.7013
3095	Q32ME1_MOUSE	1107	2.71	1	5	K.GIIDSTAGEQRQVVAVTGDGTNDGPALK.K	0.9958	3	2771.0135
3096	Q32MX7_MOUSE	661	3.03	1	3	K.DPNTETTEFSDFDLLDALS.-	0.9958	2	2131.211
3097	Q32NY7_MOUSE	118	42.37	2	19	R.LINQVLELQHTLEDLSAR.V	0.9958	2	2093.3879
						K.SENQVLGQYIENLMSASSVFQTTDTKSK.R	0.9958	3	3107.4163
3098	Q3B7Z2_MOUSE	748	14.57	6	18	R.SLSELESLKLPAESNEK.I	0.9958	2	1875.0832
						K.VHFALLGTWDEK.M	0.9958	2	1416.6195
						K.RTGSNISGASSDVSLDEQYK.H	0.9958	2	2115.2181
						R.ELTHIYSGEYWECK.E	0.9958	2	1815.9428
						K.AVKMLAESDDSGDEESVSQTDK.T	0.9958	3	2342.4475
						R.IRLEETLEQLAK.Q	0.99	2	1443.6836
3099	Q3KNY8_MOUSE	790	2.91	1	6	R.EDARINTTIGSVAAQDPDAAR.N	0.9958	2	2172.3164
3100	Q3KPA8_MOUSE	317	21.77	2	2	R.LYGLCIIMLAMGSDVLFILLSYAVILRTVLAIA	0.9958	3	4129.0145

						K.ALNTCVSHILAVLCFYVPVLGLSIVHR.F	0.9944		3	3053.5934
3101	Q3T4H2_MOUSE	1640	2.87	2	3	K.MKQVCNR.S	0.9958		1	936.0833
						R.EVDIHIMELPNNSWGKLSVHLYFDGMSLSH	0.9958		3	4222.8465
3102	Q3T984_MOUSE	530	23.02	7	29	R.KLPSDVTEGEVISLGLPFGK.V	0.9958		2	2087.421
						K.NNQFQALLQYADPVSAQHAK.L	0.9958		2	2244.4716
						K.SLFSSNGGVVKGFK.F	0.9924		1	1427.6433
						R.IAIPGLAGAGNSVLLVSNLNPER.V	0.9958		2	2276.6414
						R.IIVENLFYPVTLDVLHQIFSK.F	0.9958		2	2489.9604
						K.LPSDVTEGEVISLGLPFGK.V	0.9958		2	1959.2469
						R.GQPIYIQFSNHK.E	0.9958		2	1432.6219
3103	Q3T9A7_MOUSE	559	13.06	4	21	K.SPVASIVYELNPNFKPPK.R	0.9958		2	2001.333
						R.EGIDPAPYYWYTDQR.K	0.9958		2	1875.0038
						K.EDGTFYEFGDDIPEAPER.L	0.9958		2	2088.148
						K.YGTCPHGGYGLGLER.F	0.9958		2	1637.7582
3104	Q3T9C9_MOUSE	453	2.21	1	2	R.LAQAVHER.H	0.9944		2	924.0476
3105	Q3T9D4_MOUSE	502	2.19	1	3	K.VSMFVEVHK.A	0.9958		1	1076.2989
3106	Q3T9E4_MOUSE	415	5.3	1	4	R.GVGHEEKGAAPTGAIETTMK.R	0.9958		2	1985.2195
3107	Q3T9S7_MOUSE	1179	21.71	12	56	R.SVVEFLQGYIGIPHGGFPEPFR.S	0.9958		2	2447.7985
						R.GLAPVQAYLHIPDIIK.V	0.9958		2	1749.1063
						R.HIEVQILGDQYGNILHLYER.D	0.9911		2	2411.7227
						R.LDNASAFQGAVISPHYDSLLVK.V	0.9958		2	2346.6451
						K.TNIPFLQNVLNNQQFLAGTVDTQFIDENPEI	0.9958		3	4646.1759
						K.DFTATFGPLDSLNTR.L	0.9958		2	1655.8046
						R.AYSEALAAFGNGALFVEK.F	0.9958		2	1859.0887
						R.VVHSYEELEENYTR.A	0.9958		2	1768.8773
						K.VVEIAPATHLDPQLR.S	0.9958		2	1659.9261
						R.AEAEAQAEELSFPR.S	0.9924		1	1548.6494
						R.NHQGLLLMDTTFR.D	0.9934		2	1546.7845
						R.LQVEHTVTEEITDVDLVHAQIHVSEGR.S	0.9958	2,3		3056.3592
3108	Q3T9V8_MOUSE	1239	4.84	2	14	R.GPPPSGIATLVSGIAGGGAPGQAPGALPGI	0.9958	2,3		2920.3818
						K.SPSAQLMEQVAQLKSLSDTIEK.L	0.991		2	2404.7381
3109	Q3T9X0_MOUSE	538	10.22	2	2	K.STLLVNNGFAISAALLMACSLR.A	0.9958		2	2323.7223
						K.SLDSYCFLVFATICIAGATYFYFVLPETK.N	0.9958		3	3398.8521
3110	Q3T9Y0_MOUSE	1047	1.62	1	11	R.ITEEEQLQLREILER.R	0.9924		2	1900.1393
3111	Q3T9Y2_MOUSE	527	5.88	2	2	K.YDDISLPKSAAICYTAALLK.T	0.9932		2	2214.5299
						R.AGEIIYR.R	0.9958		1	821.9517
3112	Q3TA68_MOUSE	883	5.44	2	2	K.LHLRTLPSEPALLEELVK.L	0.993		2	2059.4569

						R.EPLLVTNGADNALRIWIFDGPAGEGR.L	0.9958		3	2783.1161
3113	Q3TA69_MOUSE	607	9.23	3	7	R.IPCVDAGLISPLVQLLNSK.D	0.9958		2	2038.4015
						R.HVEDGNVTVQHAALSALR.N	0.9958		2	1918.1197
						K.DLASAQLVQILHR.L	0.9958		2	1464.7079
3114	Q3TA75_MOUSE	655	2.14	1	3	R.LRPVNPSPLATK.G	0.9958		2	1293.5522
3115	Q3TAP4_MOUSE	876	0.68	1	2	R.GLAAH.-	0.9958		1	468.5333
3116	Q3TBD2_MOUSE	1116	5.56	2	2	R.YPLLNTVETLTAAGTLIAKVK.A	0.9907		2	2217.6543
						K.MTPGNLGIVFGPTLLRPRPTDATVSLSSLVI	0.9958		3	3979.5896
3117	Q3TBN4_MOUSE	738	8.4	3	10	K.VTGDEWGDNYYLVGPYTEQGVR.T	0.9958		2	2519.6861
						R.YLCAGAVDFYNNLENFNVDK.E	0.9958		2	2367.5427
						R.LPVATIFTTHATLLGR.Y	0.9952		2	1712.0452
3118	Q3TBZ8_MOUSE	656	11.13	2	3	K.ELPGAKPSDDSAVPLTSLAGEAVGASEGTS	0.9958		3	3447.6971
						K.GVQWMELVKIVASWFISPLLSGFMSGVLFII	0.9958		3	3739.6014
3119	Q3TCD4_MOUSE	378	39.95	8	34	R.ASQQDFENALNQVK.L	0.9958		1	1592.7056
						K.WDAWNALGSLPK.E	0.9958		2	1358.5394
						R.EAWAQGLVTEVFPESTFETEVWTR.L	0.9958		2	2814.0802
						R.LYALYK.Q	0.9924		1	770.9469
						R.WLSEECMNAIMSFVSR.K	0.9958		2	1961.224
						R.QNYVDLVSSLSSSSEAPSQGK.R	0.9958		2	2184.3214
						R.ATFHTPFSQLGQSPEACSSYTFPK.M	0.9958	2,3		2689.9068
						K.QATEGPCNMPKPGMLDFVNK.A	0.9958		2	2235.5441
3120	Q3TCF1_MOUSE	2296	1.13	1	2	K.FSQVTPTSFTAQWIAPSVQLTGYR.V	0.9958		2	2687.0269
3121	Q3TCJ8_MOUSE	202	13.86	2	3	K.VEETQTELLEALDKEGR.I	0.9958		2	1961.1333
						K.NLILALK.N	0.9924		1	785.0177
3122	Q3TCR9_MOUSE	564	3.19	1	3	K.FSPGAPSGPGPQPNQK.M	0.9929		2	1566.7135
3123	Q3TDM8_MOUSE	315	6.98	1	2	R.NYGSYSTQASAAAATAELLK.K	0.9958		2	2018.1876
3124	Q3TDN8_MOUSE	299	38.8	7	91	R.KPLEALYGYDYLAK.T	0.9958		2	1644.9079
						K.QVSLLGWSDGGITALIAAAK.Y	0.9958		2	1972.292
						K.VAVNGVHLHYQR.V	0.9958		2	1393.5912
						R.VGEGEHAILLLPGMLGSGK.T	0.9958		2	1879.2249
						R.FHADFLLQHVK.G	0.9958	2,3		1355.5821
						R.HLLPLVQCPTLIVHGEK.D	0.9958	2,3		1955.3171
						K.TCEDWVDGISQFK.Q	0.9958		1	1585.6765
3125	Q3TDT7_MOUSE	167	13.77	1	2	K.IVVIILLVMLPLLCICGLVRR.F	0.9958		3	2465.1616
3126	Q3TEL0_MOUSE	302	21.85	4	18	R.LVQAQYWHDPIK.E	0.9958		2	1498.7245
						K.LQQGYNAIGFSQGGQFLR.A	0.9958		2	1985.2095
						K.ETIPLQESTLYTEDR.L	0.9958		2	1795.9409

						R.CPGESSHICDFIR.K	0.9958		2	1578.6539
3127	Q3TEQ5_MOUSE	243	16.87	2	3	R.SDVTHHVVTSQLPQVPSGAGSRPVGEQEE	0.9958		3	3809.0514
						R.AGSRSDVTHHVVTSQLPQVPSGAGSRPVC	0.9958		3	4180.4478
3128	Q3TET3_MOUSE	180	14.44	1	10	K.GDLSGHFEHVMVALVTAPALFDAK.Q	0.9958		2	2526.9128
3129	Q3TEY8_MOUSE	518	11.2	2	2	K.TFLSKHCADHPNSWDEHLPALSFAFNVTHI	0.9958		3	3962.3386
						K.EIVISRASGSVNPAENTPSTIK.T	0.9958		2	2271.5327
3130	Q3TF18_MOUSE	1014	6.41	2	2	K.QDRIFPPESSAPAPLALPLSVTSAPTAVNS	0.9958		3	4275.864
						K.SLQELLSAHSLSSWGAEVK.A	0.9958		2	2043.2841
3131	Q3TFA5_MOUSE	418	8.37	1	28	R.IQSIPLVIGQFLEAVDQNTAIVGSTTGSNYY	0.9958		3	3556.0099
3132	Q3TFC7_MOUSE	539	30.43	8	18	R.VNLLSFTGSTQVGK.E	0.9958		2	1451.6628
						R.LFLHESIHNEVVDR.L	0.9937		2	1708.9145
						K.FQDEEEVFEWNNEVK.Q	0.9958		2	1943.0331
						R.VGNPWDPNILYGPLHTK.Q	0.9958		2	1922.1937
						K.VMDHPGNYVEPTIVTGLAHDAPIVHQETFA	0.9958		3	4121.7431
						R.EDNEGVYNGSWGGR.G	0.9958		2	1540.5455
						K.GSDCGIVNVNIPTSGAEIGGAFGGEK.H	0.9958		2	2507.6825
						K.KAWNIWADIPAPK.R	0.9958		2	1510.7789
3133	Q3TFS0_MOUSE	658	2.13	1	18	R.TETIRPASIFTK.R	0.9958		2	1364.5846
3134	Q3TFU8_MOUSE	269	5.2	1	4	R.VVGSSPGLLLGR.G	0.9958		1	1155.383
3135	Q3TG36_MOUSE	351	15.1	2	44	R.VEEFSLPDALNEGQVQVR.T	0.9952		2	2031.2297
						K.MNEDTGTDYLAPWQLAQVADGGGIGVVE	0.9909	2,3		3252.5336
3136	Q3TG68_MOUSE	462	4.11	1	4	K.LQEVLDYLTNSASLQMK.S	0.9941		2	1954.2458
3137	Q3TGQ4_MOUSE	858	3.85	1	2	R.GGPLGPAASNMPLLGDVGKPVADMVEGK	0.9915		2	3037.6211
3138	Q3THH1_MOUSE	445	33.26	7	70	R.GSTAPVGGGSFPTITPR.E	0.9958		2	1602.7874
						K.HQSLGGQYGVQGFPTIK.I	0.9958		2	1818.0421
						K.LAAVDATVNQVLASR.Y	0.9957		2	1528.7489
						R.ALDLFSDNAPPPELLEIINEDIAK.K	0.9958		2	2638.9745
						R.TGEAIVDAALSALR.Q	0.9958		2	1387.5761
						K.DGELPVEDDIDLSDVELDDLEKDEL.-	0.9944		2	2831.9521
						K.TCEEHQLCVVAVLPHILDTGAAGR.N	0.9958	2,3		2647.9233
3139	Q3THM1_MOUSE	480	12.92	2	9	R.HRDDALPLAHVAIAVEGPGWANPDNVTLK	0.994	2,3		3078.4575
						K.VANAIIGHYDCTYGGGVHLSSPLASVAVAN	0.9958		3	3143.4925
3140	Q3THX5_MOUSE	870	51.61	23	304	R.DAQSSVLFDVTGQVR.L	0.9958		2	1622.7752
						K.STLITDGSSPINLFNTAFGLLGLGSDGQPPV	0.9958		3	3346.7619
						R.SVQLAIEITTNSQEAAAK.H	0.9958		2	1875.0862
						K.DITPLQVVLPNTALHLK.A	0.9958		2	1873.2462
						R.VPHNAAVQVYDYR.A	0.9958	1,2		1532.6988

						R.HYCIVANPVSR.D	0.9946		1	1316.4686
						R.QAIPLDQNEGIYVQDVK.T	0.9958		2	1931.1528
						R.AVIGSTYMLTQDEVLWEK.E	0.9958		2	2084.3918
						R.GIQDVYVLSEQQGLLLK.A	0.9944		2	1904.2139
						K.VMAGDEWLFEGPGTYIPQK.E	0.9958		2	2139.4303
						K.ELPSGVEELLNLGHDPLADR.G	0.9958		2	2175.4032
						R.LAQDPFPLYPGELLEK.D	0.9958		2	1831.1186
						R.MAVFGFEMSEDAGPDGALLPR.A	0.9958		2	2211.5123
						R.TGEEWLVTVQDTEAHVPDVYEEVLGVVPI	0.9958		3	3851.3019
						R.VVFGPELVSLDPEEQFTVLSLSAGRPK.R	0.9958	2,3		2916.344
						R.SVGAYLPAVFEEVLDLVDAVILTEK.T	0.9944		2	2692.1217
						R.HYCVILDPMGPDGK.N	0.9958		2	1602.8115
						R.IPPYHYIHVLDQNSNVSR.V	0.9958		2	2153.405
						R.AVFPQNGLVVSSVDVQSVEPVDQRTR.D	0.9958		3	2828.1545
						R.DLAVAGPEMQVK.L	0.9958		1	1258.4754
						R.AVFPQNGLVVSSVDVQSVEPVDQR.T	0.9958		2	2570.862
						R.GPLEYVPSAK.V	0.9944		2	1061.223
						K.EVEVVEIIQATVIK.Q	0.9958		1	1570.8669
3141	Q3TIN2_MOUSE	775	13.42	5	16	R.LGYFSVDPDSHQGQIVFNR.T	0.9958		2	2180.3843
						R.VGVTVAQTTMEPHLLEACVR.D	0.9958		2	2212.5354
						K.AFIHWVSQPLVCEIR.L	0.9924		2	1856.1437
						K.DFEQECGVGVVVTPEQIEEAVESTINK.H	0.9958		3	3008.2288
						R.HTGYVIELQNIVR.G	0.9958		2	1542.7782
3142	Q3TIT9_MOUSE	397	5.79	1	6	K.YAVGSACIGGGQGIALIIQNTA.-	0.9958		2	2135.3911
3143	Q3TIY5_MOUSE	795	1.89	1	2	R.AHYGHSEYQYAWR.S	0.9958		2	1668.7679
3144	Q3TJM2_MOUSE	476	27.31	8	59	R.HNTALLAATDLLK.R	0.9958		1	1381.6151
						R.VSSISPGSTTLLSSFGAWDHICNMR.C	0.9932		2	2725.0143
						R.TWGLQATNAVSPLK.E	0.9958		2	1486.7111
						K.DLGSMSHLTGYETDR.Q	0.9958		2	1682.8023
						R.QAAGIQNVSWK.Y	0.9958		2	1202.3555
						R.HAVALLKPTK.V	0.9958	1,2		1078.3433
						R.VALIGDAAHR.I	0.9956		2	1023.1801
						R.MQVWDSCSEALIMFDR.D	0.993		2	1989.2344
3145	Q3TKZ2_MOUSE	245	3.67	1	2	K.EINSLIK.Q	0.9958		1	816.9731
3146	Q3TLL4_MOUSE	771	4.41	1	2	R.SITNDSAVLSLFQSINTMHPQLLELLNQLDE	0.9958		3	3642.1187
3147	Q3TLT4_MOUSE	687	6.7	2	2	K.MEDILAVLAK.D	0.9924		1	1103.3624
						R.QNVLLSATLTEGVTRLVDISLHNPVSISVLD	0.9958		3	3433.9707

3148	Q3TLY0_MOUSE	265	11.32	1	2	R.TYVLQNSMLPSIWGMGLELFRNHIISDR.M	0.9958	3	3292.8414
3149	Q3TM26_MOUSE	241	9.96	1	4	K.GELHSGSLTPTESIMSLGTHSR.F	0.9958	2	2298.5328
3150	Q3TME6_MOUSE	277	9.03	1	7	K.TVFTEQPTWVIDPIDGTTNFVHR.F	0.9958	2	2674.9726
3151	Q3TMI5_MOUSE	263	6.46	1	2	R.EAPELITQQLAHLLR.G	0.9946	2	1733.0207
3152	Q3TMV7_MOUSE	498	12.45	2	2	K.DNAIGNTFFDAGAAEFLTSKLMSEK.S	0.9944	3	2678.9734
						R.QMGYYAAKCMAAASMGHPIDMDFSFELFA	0.9958	3	3728.2738
3153	Q3TN85_MOUSE	322	27.64	2	3	R.AVEYLLTGIPGSPEPEHGSVQESQAPEQPA	0.9958	3	4547.933
						K.AGQGIPAPPEASPTAVPEPSTPFPPVLASG	0.9944	3	4204.7009
3154	Q3TNG1_MOUSE	81	20.99	1	2	K.GLTRTLLIFFDLAWR.L	0.9958	1	1823.1912
3155	Q3TNH0_MOUSE	412	7.77	1	3	R.TEHNQVETSQHFRIDGAVISESTPIAETIK.A	0.9924	2	3339.6433
3156	Q3TNR7_MOUSE	434	10.6	1	3	K.SENNSSNSDIVHVEKEEVPEEAFPGAAAPL	0.9958	3	4752.2356
3157	Q3TNW3_MOUSE	347	3.17	1	4	K.ENEKLQELK.K	0.9958	1	1131.2713
3158	Q3TPJ5_MOUSE	650	2.31	1	10	K.EFQAPIGSEEGLR.L	0.9958	2	1433.5608
3159	Q3TPN0_MOUSE	1403	1	1	3	R.ETESASLDPQTK.Q	0.9958	1	1306.3691
3160	Q3TQ15_MOUSE	889	29.92	16	162	R.SNLVGMGVIPLEYLPGETADSLGLTGR.E	0.9907	2	2761.1627
						R.VILQDFTGVPAVVDFAAMR.D	0.9958	2	2050.4235
						R.YQQAGLPLIVLAGK.E	0.9958	2	1471.7831
						R.YTINIPEDLKPR.M	0.9958	2	1459.6854
						K.NPFAHLAEPLDAAQPGK.R	0.9958	2	1776.9896
						K.QAPQTVHLPSGETLDVFDAAER.Y	0.9958	2	2382.592
						R.IDFEKEPLGVNAQGR.Q	0.9958	2	1673.8662
						K.INPVCPADLVIDHSIQVDFNR.R	0.9912	2	2423.6971
						R.IIPPGSGIIHQVNLEYLAR.V	0.9958	2	2091.4612
						K.NIEVPFKPAR.V	0.9958	1,2	1171.3848
						K.INPVCPADLVIDHSIQVDFNRR.A	0.9958	2	2579.8846
						R.DFNDTSQDPDFTQVVELDLK.T	0.9958	2	2327.4632
						K.SPPFFESLTLDLQPPK.S	0.9958	2	1817.0917
						R.FFNLNK.L	0.9958	1	782.9175
						K.GPFLLGIK.A	0.9958	1	845.0727
						K.KNDIENILNWNVMQHK.N	0.9958	2	1997.2793
3161	Q3TQ67_MOUSE	242	11.16	1	2	K.AILGFTPREGDWLDIEYSVEQGSPK.I	0.9958	3	2809.1046
3162	Q3TR73_MOUSE	120	6.67	1	2	K.YKGELK.Q	0.9958	1	737.8742
3163	Q3TRB1_MOUSE	149	24.83	2	2	R.EEAQVLSSSR.R	0.9944	1	1106.1778
						K.DPGGLVGTKSAVLHPSILIPQGR.A	0.9915	2	2313.7055
3164	Q3TS19_MOUSE	261	10.34	1	6	R.GLLSSAEGEPAVPVLSNHRPPQPLK.G	0.9958	2	2594.9737
3165	Q3TS53_MOUSE	207	19.32	2	22	R.FVPSNPVGILTTSYCELLQNK.V	0.9958	2	2381.6972
						R.LHTANLGDSGFLVVR.G	0.9958	2	1599.8301

3166	Q3TS85_MOUSE	583	2.92	1	2	K.NQEQLAAELAEFTAK.I	0.9958	2	1663.8247
3167	Q3TSX8_MOUSE	611	4.26	1	4	R.ASPALGSGHHDGSGDSLEMSSLDR.A	0.9958	2	2384.4962
3168	Q3TT33_MOUSE	463	8.42	2	11	K.GFGTDEQAIVDVVSNR.S	0.9958	2	1707.8375
						R.DLLSSVSREFSGYVESGLK.T	0.9944	2	2074.2951
3169	Q3TT79_MOUSE	641	16.38	5	9	K.QVQEFLKDGDDVVIIGLFQGDGDPAYLQYC	0.9931	3	4127.5133
						K.DFPEYTFAIADEEDYATEVK.D	0.9958	2	2354.4853
						K.FHHTFSPEIAK.F	0.9958	1	1314.4863
						R.FHVMDVQGSTEASAIK.D	0.9958	1	1720.9379
						K.RFDVSGYPTLK.I	0.9958	2	1283.4698
3170	Q3TTB7_MOUSE	778	19.67	8	20	R.DSWVFGGIDPTTGTAVLQEIAR.S	0.9958	2	2334.5908
						R.RLTQVDLNNPIAVR.I	0.9958	2	1609.8692
						R.NHAVSFDPLFSAVK.N	0.9958	2	1532.7392
						K.LPHLAGTEQNLLLAK.K	0.9958	2	1618.9169
						R.GNVLNLNGAGDPLTPGYPAK.E	0.9958	2	1969.2047
						R.EMNINCTGKIVIAR.Y	0.9958	1	1619.886
						R.GLGMCITAVLASFIAGFNGGWFIKPLK.E	0.9958	3	2870.4346
						R.HIIFAPSSHNK.Y	0.9958	1	1251.4306
3171	Q3TVE4_MOUSE	174	10.92	2	3	R.HRQWVER.R	0.9944	1	1011.1312
						R.IPTLFCPR.I	0.9945	2	1004.1834
3172	Q3TVI3_MOUSE	965	4.56	2	4	R.ILGLCTTINGLSAK.T	0.9924	2	1461.7081
						K.VRSILNIVNEGQISLLPHLAADNLDK.I	0.9944	3	2844.284
3173	Q3TVK3_MOUSE	475	45.47	10	96	R.NINENFGPNTEIHLVPILATAVQEELEK.G	0.9958	3	3134.5132
						R.SPSPFHVVAECR.S	0.9958	2	1386.5163
						R.LDNLHSCFCALQALIDSCASPASLAR.D	0.9958	2	2892.1366
						R.SQVGYHQVGVETYGGGIWSTWFDR.D	0.9958	2	2730.9555
						R.EVAGQVGVPLQDLMVR.N	0.9958	2	1712.0172
						R.ETACTTGVLQTLTLFK.G	0.9958	2	1784.0259
						R.MVTLYDNEEVGSESAQGAQSLLTELILR.R	0.9958	2	3068.423
						R.VLDLGSPQLAMHSIR.E	0.9958	2	1637.9378
						K.SFMISADMAHAVHPNYSDK.H	0.9937	2	2122.3778
						R.NDSPCGTTIGPILASR.L	0.9958	2	1659.8028
3174	Q3TVQ0_MOUSE	977	7.47	3	54	K.MHGGGPSVTAGVPLKK.E	0.994	2	1536.8327
						K.EIGLLADEIEIYGK.S	0.9944	2	1563.7881
						K.DAIKPNLMQTLEGTPVFVHAGPFANIAHGN	0.9958	3	3862.3954
3175	Q3TVV6_MOUSE	800	17.13	7	19	K.RNFILDQTNVSAAAQR.R	0.9958	2	1805.0036
						K.QMADTGKLNTLLQR.A	0.9952	2	1589.8504
						K.NGQDLGVAFKISK.E	0.9944	1	1377.5834

						K.SSGPTSLFAVTVAPPGAR.Q	0.9958	2	1715.9469
						R.LQAALDNEAGGRPAMEPGNGSLDLGGDA	0.9958	3	2982.2115
						K.EKPYFPIPEDCTFIQNVPLEDR.V	0.9958	2	2708.9935
						K.VSELKEELK.K	0.9958	1	1075.2475
3176	Q3TW36_MOUSE	1244	2.01	2	2	K.DVAVVEGGLR.A	0.9924	1	1015.1545
						R.HPTTGHILGYK.E	0.9958	1	1224.405
3177	Q3TW77_MOUSE	602	8.97	3	7	K.AVCCEDHIHCCPAGFQCHTEK.G	0.9958	2	2617.6647
						R.LNTGAWGCCPFAK.A	0.9958	2	1482.6111
						R.VHCCPHGASCDLVHTR.C	0.9958	2	1906.9942
3178	Q3TW93_MOUSE	679	1.18	1	2	R.ALLAGK.D	0.9944	1	572.7257
3179	Q3TWT2_MOUSE	302	41.06	5	25	R.HPIGVLLNAITELQK.N	0.9956	2	1646.9707
						R.MSLQTDEDEHSIEMHLPYTAK.A	0.9958	2	2476.7353
						R.EASHAGSWYTASGPQLNAQLEGWLSQVQ	0.9958	3	3333.5981
						R.SIEHLDKMGMSIIEQLDPVSFSNYLK.K	0.9958	3	2996.4634
						K.AMESHKDEFTIIPVLVGALSESK.E	0.9958	2	2502.8854
3180	Q3TWY7_MOUSE	858	6.53	2	2	R.GNSDIVRLVIECGADCNILSK.H	0.9958	2	2334.5641
						K.ERYIESPLESESPNDSLILEDDSEDFISDNR	0.9944	3	3615.7535
3181	Q3TXG4_MOUSE	943	16.01	6	12	R.APEVSQHVYQAYETILK.N	0.9958	2	1977.2243
						K.LHDINAQLVEDQGFLDTLK.D	0.9958	2	2170.4271
						R.APEVSQHVYQAYETILKN.-	0.9958	2	2091.3281
						R.NSFGLAPAAPLQVHVPLSPNQTVEISLPLN	0.9958	3	3810.4289
						K.DLISDSNPMVVANAVAALSEIAESHPSSNLI	0.9958	3	4176.6423
						R.LGAPISSGLSDLFDLTSGVGTLSGSYVAPK	0.9958	2	2911.2787
3182	Q3TYV2_MOUSE	514	7.2	1	2	R.HCYCLSNRTNDLSDFTALLVDIVGNSTSYL	0.9958	3	4069.4463
3183	Q3TZB7_MOUSE	137	11.68	2	2	K.FLNLIHHAAQGPKK.K	0.9932	2	1574.8692
						K.FLNLIHHAAQGPK.K	0.9909	2	1446.6951
3184	Q3TZN9_MOUSE	1325	2.34	2	3	K.KDLQLLEDGDLTVIGDR.G	0.9958	2	1901.1241
						K.IMVLDSGRLK.E	0.9958	1	1132.4069
3185	Q3TZT4_MOUSE	420	5	1	2	K.SQEHFTALGSFYFLHESLK.N	0.9958	2	2242.4955
3186	Q3U095_MOUSE	558	8.42	2	10	R.HGAGPFKTHILLDTER.H	0.9924	2	1793.0354
						K.EFLHSEELKNTPASVEAELAVTAILEK.L	0.9958	3	2970.3465
3187	Q3U0A6_MOUSE	142	39.44	4	6	K.MGSNVGIYATEALERTFVAFPSTK.T	0.9958	3	2590.9538
						K.FLGHVTSALVSK.Y	0.9958	2	1259.4911
						K.MGSNVGIYATEALER.T	0.9958	1	1611.8102
						K.TYFPHLDLRPGSSQVK.A	0.9958	2	1846.0959
3188	Q3U0G0_MOUSE	232	16.38	2	2	K.KGGTQLQLLK.W	0.9944	1	1086.3201
						R.CIYYFKSSTSASPQGAFSLSGYNR.V	0.9915	2	2692.9104

3189	Q3U0L2_MOUSE	486	10.91	2	2	R.CLSPQSPTPPRSEQTGEDPADYEEYEDFS	0.9958	3	4003.1146
						K.APAPTFQPERAASK.G	0.9958	1	1471.6561
3190	Q3U0M1_MOUSE	1139	4.04	3	5	K.DWPQTFEKFHVQK.E	0.9943	2	1690.8986
						R.IEDFIESLFIVLESKR.L	0.9944	2	1939.2591
						R.GLEISSKLDIR.W	0.9958	1	1231.4349
3191	Q3U179_MOUSE	722	3.74	2	2	K.SQSISKGLDIAQEGR.F	0.9958	1	1589.7459
						K.VTVTVFQK.E	0.9958	1	922.1124
3192	Q3U1D9_MOUSE	316	7.59	2	2	K.NYKNASSTTLGK.Q	0.9924	1	1284.4117
						R.YMLAESKK.N	0.9958	1	970.1718
3193	Q3U2A8_MOUSE	1060	2.64	2	2	K.EVVLYEIPTGPGEK.K	0.9924	1	1531.746
						R.ISSLHLELSK.L	0.9958	2	1127.3262
3194	Q3U2N8_MOUSE	809	3.96	1	2	R.IDLGSITDPLIKSTILGFISNFGQVPK.Q	0.9958	2	2875.3782
3195	Q3U2P5_MOUSE	349	11.46	2	11	K.NPELVPQNYISDSPAQSIVQHLR.W	0.9958	2,3	2606.898
						R.NVLPVLNNLLENR.E	0.9958	2	1508.7611
3196	Q3U365_MOUSE	562	5.87	2	25	R.KEPPVYAAGSMEEK.W	0.9904	2	1536.74
						R.IKPAATSQVEGAGEK.E	0.9958	2	1486.6653
3197	Q3U3J1_MOUSE	446	41.03	11	334	K.LKPNPSLLFSDVYQEMPAQLR.R	0.9958	2,3	2447.8548
						R.HFVTISSPLATQIPQAVGAAYAAK.R	0.9958	2	2442.8204
						R.HLQTYGEHYPLDHFDK.-	0.9958	2	2001.165
						R.VDGNDVFAVYNATK.E	0.9958	1,2	1513.647
						R.QYLLNQGWWDEEQEK.A	0.9958	2	1967.1015
						R.QGQIINPSEDPHLPQEEVLK.F	0.9958	2	2272.5199
						R.IGHHSTSDDSSAYR.S	0.9958	2	1533.5541
						R.KLKPNPSLLFSDVYQEMPAQLR.R	0.9958	2	2576.0289
						R.ISFYMTNYGEEGTHVGSAAALERTDLVFG(	0.9958	3	3584.9416
						R.ISFYMTNYGEEGTHVGSAAALER.T	0.9958	2	2504.7333
						K.KVMEAFEQAER.K	0.9958	1	1338.5212
3198	Q3U4K5_MOUSE	650	7.85	2	3	K.REPITLTLAAFMGIGMAVGVGTGVSALIEGF	0.9958	3	3089.682
						R.LLILLSCACFVGAIPK.D	0.9958	2	1776.1451
3199	Q3U4M6_MOUSE	936	3.85	2	2	R.SKVDGGSGPPTPGPTTTLGPK.K	0.9958	3	1952.1717
						R.YLILDEAQNIK.N	0.9908	1	1320.5285
3200	Q3U4P9_MOUSE	1038	15.99	10	14	K.QYGPDVPEPVLQKLVAAFGELR.N	0.9958	2	2427.8058
						K.DFVLGEHLLLVGNQGVGK.N	0.9958	2	1896.1967
						K.YPSENLHDAITK.A	0.9958	2	1388.5199
						K.CEVVAGSLKIGAVSVPVHNAHEK.M	0.9958	3	2402.7221
						K.IGAVSVPVHNAHEK.M	0.9958	2	1458.6603
						K.LGHILVVDEADK.A	0.9958	1	1309.5052

						K.VPDVLFYDNVQHMVVMEDMLK.D	0.9958		2	2523.9828
						R.AVNQPCAPDHFIQTVSHK.Q	0.9958		2	2050.2475
						R.SIFPIHPSFR.I	0.9958		2	1201.4135
						K.RFELQGSGHSLLPK.E	0.9924		2	1569.8039
3201	Q3U4X8_MOUSE	932	10.19	3	3	K.LGTGFSDEELEEHHQSLQALVLPTPRPYVF	0.9958		3	3420.8064
						R.LRLGLAEQSVLAALAQAVSLTPPGQEFPTA	0.9958		3	3620.1839
						K.DYLDGVGDTLDLVVIGAYLGRGK.R	0.9929		2	2410.7295
3202	Q3U5E1_MOUSE	763	8.65	3	10	R.GQVKPSTSSQPILSAPGPTK.L	0.9958		2	1981.2566
						R.GHSEVVAILQSPGDWMCPVNK.G	0.9958		2	2325.6105
						R.MAAAGGTVSGPSSACKPGR.S	0.9924		2	1762.9446
3203	Q3U5Q7_MOUSE	420	5.24	1	5	K.LLGYGPGDQAGEAQHGFLLR.D	0.9958		2	2100.3415
3204	Q3U7X9_MOUSE	938	3.2	1	17	K.IIGFGSALLEEVDPNPANFVGAGIIHTK.T	0.9929		2	2881.3012
3205	Q3U898_MOUSE	57	36.84	1	16	K.AVHADFFNDFEDLFDDDDVQ.-	0.9958		2	2375.4229
3206	Q3U8M3_MOUSE	97	52.58	4	16	K.TVAGGAWTYNTTSAVTVK.S	0.9958		2	1828.0318
						K.YTCSFCGK.T	0.9944		1	1023.0626
						R.AVGIWHCGSCMK.T	0.9958	1,2		1406.5746
						K.KVGIVGK.Y	0.9944		1	700.8998
3207	Q3U944_MOUSE	547	19.93	5	30	K.GHPDLQGQPADDIFESIGDR.E	0.9958		2	2168.2841
						R.LVSGIQHPGSAGVYETTQHFMDIK.E	0.9958		2	2616.9513
						K.YQEEFEHFQQELDK.K	0.9958		2	1870.9696
						K.SQQEILRQVNEVK.N	0.9944		1	1571.7739
						K.GPHLVQSDGTVPFWAHAGNAIPSADQIR.I	0.9958		2	2943.251
3208	Q3UAV7_MOUSE	414	46.38	14	119	K.LILPYVELDLHSYDLGIENR.D	0.9958		2	2373.7111
						R.SDYLNTFEFMDK.L	0.9958		2	1510.6582
						K.SIEDFAHSSFQMALSK.G	0.9952		2	1799.0081
						R.LVTGWVKPIIIGR.H	0.9958		2	1452.8265
						K.GWPLYLSTK.N	0.9924		1	1065.2572
						R.KIQGGSVVEMQGDEMTR.I	0.9931		2	1866.1145
						K.LDNNTELSFFAK.A	0.9936		2	1399.5431
						R.HAYGDQYR.A	0.9958		2	1010.0537
						K.DIFQEIYDK.K	0.9958		1	1171.2921
						K.TVEAEAAHGTVTR.H	0.9958		1	1342.4514
						K.GQETSTNPIASIFAWSR.G	0.9958		2	1866.0403
						K.KYNVGVK.C	0.9944		1	807.9682
						R.AKLDNNTELSFFAK.A	0.9952		2	1598.796
						K.ALEDVCIETIEAGFMTK.D	0.9944		2	1928.1708
3209	Q3UC49_MOUSE	422	17.3	4	23	K.ALADLVHSHIQSNK.L	0.9958		2	1533.7275

						K.TGILMLNMGGPETLGEVQDFLQR.L	0.9958	2	2520.9215
						K.LLDELSPATAPHK.Y	0.9958	2	1392.595
						R.YVHPLTEEAIEEMER.D	0.9958	2	1847.0497
3210	Q3UDK4_MOUSE	673	7.43	2	14	K.SLENALSSDTSGHFR.R	0.9958	2	1621.7037
						K.LCGGDDDAAGQFFPEAAQVAYQMWELSA	0.9944	3	3391.6589
3211	Q3UDQ8_MOUSE	1087	5.98	2	2	K.NSEGDENYMEFLEVLTEGLER.V	0.9958	2	2475.6429
						R.FKYYHWTLSFLGMSPCLALMFVSSWYYAL	0.9924	3	4775.7516
3212	Q3UE18_MOUSE	142	16.2	1	2	R.YIQYGGPPGDSLPCPQEAHSK.L	0.9921	2	2302.4712
3213	Q3UER0_MOUSE	669	3.89	2	3	R.CPPPPVPLNSK.I	0.9958	1	1206.3935
						R.GSSTITCNRGR.W	0.9958	1	1209.2707
3214	Q3UER8_MOUSE	443	40.18	9	96	K.AIQVYYNPDQPPKPGMIDSATQK.S	0.9958	2	2562.9
						K.EGFGHLSPTGTTEFWLGNEK.I	0.9958	2	2208.3917
						R.LSIGEGQQHHMGGSK.Q	0.9958	2	1566.7319
						K.SSTTNGFDDGIIWATWK.S	0.9958	2	1900.0545
						K.QQFLVYCEIDGSGNGWTVLQK.R	0.9958	2	2443.6844
						K.YEALLLTHETSIR.Y	0.9958	2	1546.7636
						K.ESGLYFIRPLKAK.Q	0.9958	2	1522.8308
						K.CHAGHLNGVYHQGGTYSK.S	0.9958	2	1987.1076
						K.VAQLEAQCQEPCKDSVQIHDTTGK.D	0.9924	2	2743.9197
3215	Q3UFL2_MOUSE	368	19.29	4	6	R.ELTERFEDVWIVSGPLTLPHTR.N	0.9944	3	2596.9457
						R.RSPESTEPLALGAFVVPNK.A	0.9958	2	2013.3012
						R.QPHESAEEAVLEQFGFPLAGTETR.R	0.9958	2,3	2644.8571
						R.FEDVWIVSGPLTLPHTR.N	0.9958	2	1968.2627
3216	Q3UFT4_MOUSE	1057	2.27	1	5	R.LILSHAVQMVQSAALDEMFQHR.E	0.991	2	2525.9465
3217	Q3UFU7_MOUSE	595	13.11	2	2	K.VYEMQNTIQILQMEKVESTK.Q	0.9937	2	2413.8067
						R.LQSAAQSAHSGSGSAPAASASSSFSYGVS	0.9944	3	5573.8573
3218	Q3UFX9_MOUSE	856	11.1	4	4	K.NLPPLSNNLATPVSLHDVPPR.I	0.9912	2	2252.5785
						R.TNSFLCNAGNQLAVLYNDTAVLESHHVALA	0.9944	3	4996.4768
						R.HPRQMDAEALCR.S	0.9944	1	1484.6391
						K.ELAQVPINEK.K	0.9958	1	1141.3097
3219	Q3UFZ6_MOUSE	337	12.46	1	7	K.SSGPPPPSGSSGSEAAAGAAAPASQHPAT	0.9958	3	3577.8181
3220	Q3UGA8_MOUSE	558	5.38	2	4	K.GMGLVNHVFTEDNLK.K	0.9912	2	1674.9122
						K.KLYDSNLGIGHTR.Y	0.9958	2	1474.6597
3221	Q3UGX2_MOUSE	2329	29.45	38	162	K.VLDTPLSEGDEPTTLPAQR.D	0.994	2	2040.2347
						R.AQSLLSAGHPEGEQIIR.L	0.9958	2	1807.0165
						K.NQTLQNEILGHAPR.V	0.9958	2	1591.7672
						R.VSHLEQCFSELSNMAAGR.K	0.9945	2,3	2037.2208

						R.GNTLTQCLGFQEFQK.D	0.9958		2	1771.9336
						R.FAALEKPTTLELK.E	0.9955		2	1461.7417
						K.TLMAQIDGVNLAANNLVESGHPR.S	0.9958		2	2421.7337
						K.DLQDAENFFQFQGDADDLK.A	0.9958		2	2217.3099
						R.LPLAQSADYGTNLQTVQLFMK.K	0.9958		2	2339.7119
						K.GLQDALQGQELSLGEASK.L	0.9958		2	1845.0165
						K.LQAFLQDLDDFK.A	0.994		2	1453.6348
						R.LGHLQSSWDTLR.E	0.9958	1,2		1413.576
						R.LVTQDNFGYDLAAVEAAK.K	0.9958		2	1926.1333
						K.LYQQVLTQAELR.G	0.9958		2	1462.6891
						K.WLDQMDIPNTLEDLEVVQHR.F	0.9958		2	2452.7442
						K.TAGYPHVNVTNFTSSWK.D	0.9958		2	1910.0959
						K.VIEGQTDPDYQLLGQR.L	0.9958		2	1833.008
						R.LIDAGHSEAATIAEWK.D	0.9958		2	1712.8999
						R.ELHLLGVQVQQFQDVATR.L	0.9958		2	2082.3671
						R.QLGIIPLLDPEDVFTENPDEK.S	0.9958		2	2383.6575
						K.QAEAILSNQEYTLAHLEPPDSLAAAEAGIR.I	0.9958		3	3180.4985
						K.RVEEQVNLR.K	0.99		2	1143.2883
						R.LQTHADLNK.W	0.9944		1	1040.1643
						R.GVMEHLEHQAQGFPEEFR.D	0.9958		2	2142.3532
						R.HNLEHAFDVAER.Q	0.9958		2	1438.5424
						R.ELPEDVGLDASTAESFHR.V	0.9958		2	1974.0911
						R.DAHEAQQYYLDAGEAEAWISEQELYVFSD	0.9958		3	4917.3218
						R.FLDLLEPLGR.R	0.9958		1	1173.3977
						R.LENMYHLFQLK.R	0.9958		2	1436.7118
						K.RFLDLLEPLGR.R	0.9947		2	1329.5852
						R.DLEDETLWVEERLPLAQSADYGTNLQTVQ	0.9958		3	3855.3082
						K.LLEVLSGEMLPRPTK.G	0.9943		2	1684.0472
						K.HQAFMAELASHQGWLENIDAEGR.Q	0.9958		3	2611.8511
						K.HKEFLEELEESR.G	0.9958		2	1546.6769
						R.KEELEELFADAPSLGAEAGDTDMSIEK.R	0.9958		2	2897.1341
						R.KFEDFLVSMENNR.D	0.9958		2	1629.8279
						K.HLLEVEDLLQK.H	0.9958		2	1337.559
						K.KHEAIETDTAAYEER.V	0.9958		2	1763.8583
3222	Q3UGZ4_MOUSE	2388	2.01	2	2	R.LEEALRAQQFYR.D	0.9958		1	1524.7196
						K.MDWLQLVLEVLVFGRDAGMAEAWLCSQE	0.9944		3	3734.3321
3223	Q3UGZ7_MOUSE	1998	4.3	4	14	R.IVLFNESLVLLNTTVGK.E	0.9932		2	1861.2322

						K.GPPDWTDYNDFELQWFPGDALTIFNPYSS	0.9944	3	3550.8212
						K.SLSKDAK.E	0.9958	1	748.8546
						R.HFHYTVWPDHGVPETTQSLIQFVR.T	0.9924	3	2896.237
3224	Q3UH74_MOUSE	1495	4.88	4	4	R.YITELLR.K	0.9958	1	908.0855
						K.FTTILSSLQGFLER.V	0.9924	1	1612.8663
						K.IEEDLLTYNIK.G	0.9958	1	1351.5395
						K.IMSDYPQQFHSNLQDFSDQLSSYYEKFVGI	0.9958	3	3949.2532
3225	Q3UH76_MOUSE	1842	9.28	7	11	R.LSVSPLPTLTEDDELLCLFGDSPPHPAR.V	0.9958	3	3078.412
						K.SGSVFLTSHQYPFYDCR.E	0.9958	2	2065.2152
						R.VPSPGISFTYCENPMIR.A	0.9958	2	1969.2288
						K.YYDEIINALEEDPAAQKMQLAFR.L	0.9944	3	2730.0644
						R.VTLNDVPCEVTKFGAQLQCVTGQQLAPGQ	0.9944	3	4399.8769
						R.AHTDSLNTLVALHQLYQYTQK.Y	0.9958	2	2445.7373
						R.VWHLVRPTDEVDEGK.S	0.9958	2	1780.978
3226	Q3UH89_MOUSE	801	2.5	1	4	R.LSVVEEMLSGALVGNLVK.D	0.9958	2	1859.2317
3227	Q3UH93_MOUSE	1925	4.52	4	4	R.RAAGGAPPSAR.A	0.9958	1	1011.1288
						R.TACFVEPAPDVVAVLDSVVQGTGPACESK	0.9924	3	3161.4683
						R.ENIEAKPRNLNVSFQGCGMDSLSVR.A	0.9958	3	2823.1193
						K.ELLVDLIDASAAK.N	0.9924	1	1358.5749
3228	Q3UHH3_MOUSE	2672	1.57	2	4	R.NHGANLAYPPGSTSPIR.I	0.9958	2	1752.9273
						R.AELLVAEAPSKPITVTVEEQR.S	0.9958	2	2281.6115
3229	Q3UHJ6_MOUSE	766	1.83	1	4	R.LTILPISRDTIK.S	0.9958	1	1370.6756
3230	Q3UHK8_MOUSE	1896	4.11	3	3	K.IKVPEQIKPSVSQPQPANSDNGTSTATSTN	0.9958	3	3525.8113
						K.EEVVKAQK.S	0.9958	1	931.077
						K.EAWPSAPGSDPELAPECIDADSASNSESEI	0.9958	3	3176.2105
3231	Q3UHL7_MOUSE	1834	3.98	4	7	R.VETLSQVEVILQQSAADIAR.A	0.9958	2	2171.4557
						R.KAAQNSGEAEYIEK.V	0.9958	2	1538.6543
						K.TLDGELDEK.Y	0.9924	1	1020.0813
						R.NFLTEDSADLDSIEAVANEVLK.M	0.9958	2	2394.5945
3232	Q3UHQ5_MOUSE	2671	9.47	11	14	K.LANGLLDELKTVLNSHK.V	0.9958	2	1866.168
						R.VLQEALCVISGVPGLK.G	0.9958	2	1683.9953
						R.VLPQLISTITASVQNPALCLVTR.E	0.9937	2	2495.9317
						R.KMAAQIIGNMYSLTDQK.D	0.9924	1	1913.2575
						R.RLQELDGELEAALGLLDAIMAR.N	0.9958	2	2398.7802
						K.NLLHSLQSSGVGSK.A	0.9958	2	1427.6005
						R.VAMLRLLTWVIGTGSPR.L	0.9958	2	1871.2945
						R.AGQRVISMYAETAIALLLPQLEQGLFDDLW	0.9944	3	3520.0839

						K.FVHFIDAPSLALIMPIVQR.A	0.9929	2	2168.6483
						R.LQVLASDTLTALCASSSGEDGCAFAEQEE\	0.9958	3	4742.1001
						R.QGVCIGLSEIMK.S	0.9924	1	1335.5678
3233	Q3UHU4_MOUSE	1960	1.17	1	17	R.IAQLEEELEEEQGNTELINDR.L	0.9958	2	2473.6098
3234	Q3UI33_MOUSE	488	27.46	8	19	K.GSYTAQFEHTILLRPTCK.E	0.9958	2	2123.3825
						K.NFDVGHVPIR.L	0.9945	2	1154.3139
						K.NLCDLGIVDPYPPLCDIK.G	0.9958	2	2103.3522
						K.IDFGTHISGR.I	0.9958	2	1103.2229
						K.GAVSAVQQELDKESGALVDEVAK.Q	0.9921	2	2344.581
						K.VQTDPPSVPICDLYPNGVFPK.G	0.9958	2	2344.6355
						K.GAVSAVQQELDK.E	0.9924	1	1245.3751
						R.LCDVGEAIQEVMESYEVEIDGK.T	0.9958	2	2514.7268
3235	Q3UIK0_MOUSE	1278	38.03	28	385	R.AHNVAGPGGPIVTK.E	0.9958	1,2	1318.5186
						K.VGQHLQLHDSYDR.A	0.9958	2	1568.689
						R.VAGASLLKPPVVK.W	0.9958	1,2	1279.609
						K.KLEVYQSIADLAVGAK.D	0.9958	2	1705.9921
						K.LEAPAEEDVWEILR.Q	0.9958	2	1670.8596
						R.LDVPISGDPAPTVVWQK.T	0.9958	2	1823.099
						K.ALDFSEAPSFTQPLANR.S	0.9958	2	1865.0526
						K.LTIDDVTPADEADYSFVPEGFACNLSAK.L	0.9949	2	3047.2649
						K.IHLDCPGSTPDTIVVVAGNK.L	0.9958	2	2094.3386
						R.IAFQHGVTDLR.G	0.9958	2	1257.4349
						K.EPVFIPRPGITYEPPK.Y	0.9958	2	1841.1601
						R.DASPDDQGSYAVIAGSSK.V	0.9958	2	1768.8315
						R.SVFTVEGAEKEDEGVYTVTVK.N	0.9958	2	2288.5133
						K.LRLDVPISGDPAPTVVWQK.T	0.9958	2	2092.4459
						K.VYLFELHITDAQTTSAGGYR.C	0.9929	2	2243.4808
						R.TSGGQSLAELIVQEK.K	0.9958	2	1560.7447
						R.TSDSHEDAGTLDFSSLLK.K	0.9958	1,2	1924.0282
						K.KPVSAFNK.K	0.9958	1	891.058
						R.VFSHNMVGSSDK.A	0.9957	2	1308.4516
						K.KLEPAYQVNK.G	0.9958	1	1190.3849
						K.HHLIINEATLEDAGHYAVR.T	0.9958	2	2160.397
						K.VTEPAPPEKAESEVAPGAPK.E	0.9958	2	2005.2322
						K.ATLILQIVDKPSPPQDIR.I	0.9944	2	2005.3653
						R.KHHLIINEATLEDAGHYAVR.T	0.9958	2	2288.5711
						K.RTLTISQCSLADDAAYQCVVGGEK.C	0.9958	2	2643.8427

						K.DKFDSCNFNLTVHEAIGSGDLDLR.S	0.9958		2	2724.9098
						K.KASTGPHPDAPEDAGADEEWVFDK.K	0.9958		2	2570.688
						K.KLLCETEGR.V	0.9958	1,2		1106.2304
3236	Q3UJ04_MOUSE	998	5.11	2	3	K.NDQQAKIPLK.K	0.9958		1	1155.3396
						R.LEEPGLLNMDMPLEPSEKATDLSLKPTLSA	0.9958		3	4045.5699
3237	Q3UJK3_MOUSE	289	26.99	5	11	K.DVPPVPTLADIAWIAADEEETYAR.V	0.9958		2	2643.9097
						R.SLLKEEDPAVLISEVLR.R	0.9958		2	1912.234
						R.TTELQDELSHLR.S	0.9924		1	1442.5687
						R.IGTNLPLK.L	0.9958		1	856.0531
						K.KPALPALSR.T	0.9958		1	953.1728
3238	Q3UJN1_MOUSE	913	4.93	2	3	R.AIFTTGQGASAVGLTAYVQR.H	0.9952		2	2012.2731
						R.FDVLCVVRDTVDPVQDEMLAR.F	0.9958		2	2478.7889
3239	Q3UJU1_MOUSE	748	9.63	4	26	R.EVAQQAVDADVHAVGVSTLAAGHK.T	0.9958		3	2374.6157
						R.NTQIIIQEESGIPK.V	0.9958		2	1570.7832
						R.EVAQQAVDADVHAVGVSTLAAGHKTLVPE	0.9958		3	3268.7379
						K.YQLEKEDSVEVLAIDNTSVR.K	0.9958		2	2309.5352
3240	Q3UK51_MOUSE	687	13.1	4	7	K.DIAEPHIPCLMPEYFEPQIEDVSEAALEER.I	0.9958		3	3529.863
						K.LASAFSLPIGESLAQR.V	0.9958		2	1660.9108
						R.KLVGHDPLCK.I	0.9944		1	1167.3599
						K.DLIPSVFLPHYQIFIGLLQALDVASR.L	0.9958		3	2927.4594
3241	Q3UKK2_MOUSE	947	6.65	2	2	R.GIEVIFTNGSMVMIDVTEDDAGFYMLEILR.I	0.9958		3	3380.9108
						K.GVIAEEKSELIQHIIATSSSLPGPAHSGR.E	0.9958		3	2986.3549
3242	Q3UKT2_MOUSE	129	11.63	1	2	K.SVVGPYQRGGACR.R	0.9958		1	1407.5382
3243	Q3UM39_MOUSE	771	12.45	5	12	R.IPGMLIIDTPGHESFSNLR.N	0.9937		2	2098.4247
						R.APIICVLGHVDTGK.T	0.9958		2	1480.7136
						R.HTHVQDGEAGGITQQIGATNVPLEAINEQT	0.9958		3	3258.529
						K.RPEEEVLTLR.G	0.9944		2	1242.4178
						R.HLQAQGVEVPSK.D	0.9958		2	1293.4655
3244	Q3UMB3_MOUSE	385	5.19	1	5	R.ARLVSQEHLLLSSPEALR.Q	0.9943		2	2020.3396
3245	Q3UMD3_MOUSE	980	2.76	2	3	R.EKIFLTLENVQSQK.I	0.9944		2	1677.9383
						K.SASDALRAK.R	0.9958		1	919.0256
3246	Q3UMK4_MOUSE	759	4.08	2	2	K.VMLNDPLPGQK.A	0.9958		1	1212.4497
						R.LGSLMQYETPGFLPNK.R	0.9924		1	1796.0912
3247	Q3UML7_MOUSE	1148	1.22	1	2	R.FFSTNSNLSKHK.K	0.9958		1	1410.5724
3248	Q3UMP2_MOUSE	325	7.69	1	17	R.LIDMLSEAGLPVIEATSFVSPK.W	0.9958		2	2318.7309
3249	Q3UMR3_MOUSE	615	1.3	1	2	R.QVLDGK.E	0.9958		1	659.7605
3250	Q3UMT7_MOUSE	592	10.81	4	27	K.SDALETLGFLNHYQMK.N	0.9958		2	1868.1144

						R.AITHLNNNFMFGQK.M	0.9957	2	1635.881
						K.SKPGAAMVEMADGYAVDR.A	0.9958	2	1869.1176
						K.TPASPVVHIR.G	0.9958	2	1077.2718
3251	Q3UMV5_MOUSE	314	5.1	1	3	R.WLIKEELEEMLVEK.L	0.9958	2	1790.1249
3252	Q3UNW7_MOUSE	1180	4.83	3	6	K.EITGLK.K	0.9944	1	660.7887
						R.VLLAFYASTIVSALVAAENLSDNVVAKLFPY	0.9958	3	3670.3269
						K.YNEYSASLLQK.D	0.9958	1	1316.4533
3253	Q3UP90_MOUSE	106	14.15	1	3	K.QFSFDIMLVLNLK.S	0.9958	2	1568.9147
3254	Q3UPC7_MOUSE	1243	1.77	1	2	K.EQLFAMNGSEEKPLLIRPLK.V	0.9949	2	2314.7485
3255	Q3UPF5_MOUSE	946	6.03	2	3	K.DPLEDVSADVTQKFK.Y	0.9924	2	1692.8633
						K.SSTHASVSPASEPSRMMMMMSDPAEYSL(	0.9944	3	4205.7614
3256	Q3UPQ6_MOUSE	1255	1.59	1	24	K.DELKEICSSESSDLGLVK.H	0.9958	2	2010.1689
3257	Q3UPY8_MOUSE	141	12.06	1	2	R.GQRGWLPLELCAATR.L	0.9958	2	1728.9579
3258	Q3UPZ4_MOUSE	1259	8.82	4	4	R.GDVGGEKPVKVLEVPALSLGGAIGSAHLK.	0.9958	3	2800.2712
						R.VTQGPVSATVEVTSPTGFVQSHVLEDVSQ	0.9958	3	3342.6873
						R.DERVASTGSGASPGDAHQAPGEK.G	0.991	2	2225.2932
						R.GHQGHVAAGAVSSTPSNER.T	0.9958	2	1862.9565
3259	Q3UQ40_MOUSE	253	18.18	2	2	K.SCNRSYGVCVIMGVAPTGSQLSFDPLVLLF	0.9958	3	3452.9259
						K.INIDPLITHR.L	0.9944	1	1192.4037
3260	Q3UQC9_MOUSE	108	25	1	3	R.SQPVGAAAWNGASVPGKAESLAYAK.L	0.9958	3	2431.7105
3261	Q3UQD6_MOUSE	204	11.27	1	2	R.AQKLEVQMETESETPAPALGR.D	0.9958	2	2286.5622
3262	Q3UQP1_MOUSE	734	3.95	2	24	R.HHSLMAHSLLSLSEK.Q	0.9943	2	1690.9579
						R.EAYLLLQLFR.T	0.9958	1	1266.526
3263	Q3UQR1_MOUSE	902	2.99	2	5	R.ELETLSDMTGGLR.F	0.9958	1	1422.5933
						K.KPEIILQDPK.G	0.9924	1	1181.4179
3264	Q3UQS8_MOUSE	809	5.93	2	2	R.TKEGQAVLSVRPLQGHQLNDFR.G	0.9931	2	2494.816
						R.AFAQSNPVFPSASSGTSFAAQR.K	0.9909	2	2229.4136
3265	Q3UQT0_MOUSE	1265	3.95	2	2	R.QKPVDLLRYNQK.G	0.993	2	1502.7568
						K.FDDVVQAIRDHAFVTSSFPVILSIEEHCSVE	0.9958	3	3961.3459
3266	Q3UQU9_MOUSE	137	21.9	1	2	K.EPAGLSPASLCNLGGDWHPLGTPECWGR	0.9944	3	3036.2623
3267	Q3UR97_MOUSE	363	11.85	2	2	R.AFEQFLGHLQAVPELR.Q	0.9958	2	1856.1344
						K.YVLYTLAVMGPGPPDRQPAQISR.R	0.9958	3	2530.9476
3268	Q3URQ0_MOUSE	928	5.71	2	2	K.FLQALADGSSRLR.E	0.9958	1	1434.6383
						K.QSALLGLKDLLSQYPFIIDAHLSNILSEVTAV	0.9958	3	3990.589
3269	Q3URU1_MOUSE	512	3.91	1	2	K.LAAAVLESQAMAPLDAFR.M	0.991	2	1875.1932
3270	Q3US09_MOUSE	921	2.93	2	2	K.DDEKVEKPPDNQK.L	0.9958	1	1542.6427
						K.LTMVVLSSEK.L	0.9929	2	1107.3508

3271	Q3US68_MOUSE	952	2.42	1	2	R.EQNIGDIQVLNGYFVHYFAPK.N	0.9958	2	2453.7594
3272	Q3USC6_MOUSE	623	20.71	7	49	K.APHYPGIGPVDESGIPTAIR.T	0.9958	2	2048.3061
						R.SLERPSSSASMAGDFR.K	0.9917	2	1698.848
						K.SSILQHERPVSIYQSSIDRSLERPSSSASMA	0.9958	3	3896.2835
						R.TSPGRADLPGSSSTFTK.S	0.9945	2	1709.8534
						K.AQPARPPPPVQPGEIGEAIAK.Y	0.9958	2	2124.4477
						R.KIDQNWYEGEHHGR.V	0.9958	2	1769.8735
						K.RVDQNWYEGK.I	0.9958	2	1295.3971
3273	Q3USI4_MOUSE	620	7.9	2	2	R.SAFSPPGQNFSPIVDMDCLAAQGHVLTK.L	0.991	3	2989.3387
						R.GLHLPSLTSLSKGLLTR.E	0.9904	2	1794.1478
3274	Q3USW6_MOUSE	959	3.75	1	2	K.TTEECGTHRNASLEYSTDSDLLSSSGSVTV	0.9958	3	3657.8469
3275	Q3UT28_MOUSE	485	12.58	2	2	K.VTSTLQILELER.C	0.9958	1	1402.6311
						K.LVDLNCILELQLSQWWPEVLEELDPYLEGM	0.9944	3	5412.2467
3276	Q3UT76_MOUSE	567	6.53	2	2	K.GCTFRYHYPCAIDADCLLNEENFSVR.C	0.9958	3	3209.3969
						R.KPGARPR.K	0.9958	1	781.9363
3277	Q3UT86_MOUSE	313	6.71	1	2	R.AFHVPTSTSVAVKILQNTK.E	0.9958	3	2042.3861
3278	Q3UTB4_MOUSE	544	10.29	3	10	K.GRALIAK.E	0.9958	1	728.9132
						K.ELNEFANSFMQKSGEYVWEWILR.V	0.9958	3	2878.2311
						R.VGDAVAQLDELNSMGLTGPR.G	0.9907	2	2044.2873
3279	Q3UTF9_MOUSE	874	3.55	2	2	R.EGLPPSNGILRIQLGSEDPIK.F	0.9929	2	2234.5577
						K.LVIVVK.D	0.9924	1	670.9139
3280	Q3UTG9_MOUSE	908	3.96	2	2	R.WLLLLAAWEAGSGQLHYSIPEEAK.H	0.9944	3	2684.0667
						R.QTLLVLVK.D	0.9944	1	914.1765
3281	Q3UTM9_MOUSE	175	23.43	2	3	K.NMLDFLAVTSLLVCWKDIK.C	0.9958	2	2267.6979
						R.KDTIVSPIGLLQNFHDER.F	0.9958	2	2083.3519
3282	Q3UUC4_MOUSE	149	36.91	2	3	R.CQLAIGLLSFVTR.T	0.9944	2	1478.7411
						K.MNSSFGCSTLSCHQGNTSIQVVNASSWKV	0.9958	3	4301.5771
3283	Q3UUE0_MOUSE	409	2.69	1	2	R.EVAVEGQRK.D	0.9958	1	1016.1423
3284	Q3UUI6_MOUSE	182	41.21	4	19	K.NQLLEQFPGIEPWLNQIMPK.K	0.9958	2	2396.8096
						K.LYPAAVDTIVAIMAEGK.Q	0.9958	1,2	1763.1022
						K.GIGIENIHYLNDGLWHMK.T	0.9958	2	2111.4259
						K.YPFILPHQQVDK.G	0.9917	2	1485.7257
3285	Q3UVK9_MOUSE	332	5.12	2	2	R.VYCLQTEAQLILKNK.K	0.9931	2	1822.1211
						R.VYCLQTEAQLILK.N	0.9924	1	1579.8432
3286	Q3UVW1_MOUSE	170	11.18	1	6	K.QPRSPGSPPAAALEPPR.R	0.9958	3	1728.9486
3287	Q3UVY5_MOUSE	1177	8.41	5	5	R.DWYIGLVSEEQWKR.A	0.9958	2	1810.019
						R.FPQTVLGGPR.L	0.9944	1	1072.2523

						K.DLPCTKLPIPGSVDSQNPDDHSAGTGPK.N	0.9958		3	2905.1138
						R.LLLIGIMRDR.L	0.9958		1	1200.5285
						K.LNAEAVRGQWANLSWELLYATNDDEER.Y	0.9944		3	3165.4026
3288	Q3UW53_MOUSE	926	5.29	2	2	R.RVSAILPGAPDNELPSNEVFQEPEEK.K	0.9958		3	2867.1418
						K.IHPEASHPAAIQQDSCEER.E	0.9958		2	2176.2732
3289	Q3UW54_MOUSE	103	8.74	1	2	K.EMPMNIK.E	0.9958		1	863.0779
3290	Q3UWJ1_MOUSE	430	11.4	2	2	R.DIYGGDYERFGMPGWAVASSFGNMIYK.E	0.9958		3	3033.4023
						K.NFSTLQTVLSATGGGAYK.F	0.9958		2	1816.0208
3291	Q3UWK8_MOUSE	375	1.87	1	3	R.LFVEK.T	0.9958		1	635.7813
3292	Q3UWT6_MOUSE	247	52.63	10	250	R.YNEDLELEDAIHTAILTLK.E	0.9945		2	2202.4662
						K.RYNEDLELEDAIHTAILTLK.E	0.9958		2	2358.6537
						K.LAQQYYLVYQEPIPTAQLVQR.V	0.9958		2	2522.9066
						K.HIGLVYSGMGPDYR.V	0.9958		2	1565.7869
						R.GYSFSLTTFSPSGK.L	0.9958		2	1479.6293
						K.LVQIEYALAAVAGGAPSVGIK.A	0.9907		2	2028.3995
						K.ESFEGQMTEDNIEVGICNEAGFR.R	0.9958		2	2633.7689
						R.RLTPTEVR.D	0.9958		2	972.1325
						R.KLAQQYYLVYQEPIPTAQLVQR.V	0.9958		2	2651.0807
						K.ESFEGQMTEDNIEVGICNEAGFRR.L	0.9913		2	2789.9563
3293	Q3UX37_MOUSE	1390	3.31	2	3	K.LELVPARPFSSSELQRDKPAGPQNMNGVS	0.9944		3	3383.804
						R.SPWTDHHIRQR.T	0.9958		1	1433.5723
3294	Q3UXF8_MOUSE	105	18.1	1	3	R.QQQHKPLNTLPGKCYDR.A	0.9958		2	2084.3085
3295	Q3UXM1_MOUSE	331	3.93	1	2	R.MPKGELSNHIK.N	0.9944		1	1254.49
3296	Q3UYW5_MOUSE	749	6.28	2	2	K.TITISESGVIGSTLNSTTQTPNKIAISPLK.S	0.9958		3	3073.5114
						K.CIGCKNFEESPER.K	0.9958		1	1626.6955
3297	Q3UZ58_MOUSE	521	13.63	3	4	R.AVPTGDVEDLPCGLLLSSVGYK.S	0.9958		2	2291.5696
						R.FGVAPDHPEVK.N	0.9924		2	1196.3482
						R.EAYHAVVLSYGAEDHQPLGIPGEELPGVVS	0.9958		2	3362.7233
3298	Q3UZ78_MOUSE	121	44.63	2	2	R.AQRPCQVPGLHVLLLQGLALALAR.Q	0.9958		2	2596.1038
						R.SYVTMLHTWSTHHAWWIVYASQCFPK.K	0.9958		3	3238.6588
3299	Q3UZG4_MOUSE	319	47.65	9	52	R.TVVSGLVNHVPLEQMQNR.M	0.9958		2	2022.3299
						K.HPDADSLYVEEVDVGEAAPR.T	0.9958		2	2170.297
						K.GAEADQIIEYLK.Q	0.9907	1,2		1350.5114
						K.IWEQIQPDLHTNAECVATYK.G	0.9958		2	2417.6465
						R.ITFDAFPGEPDKELNPK.K	0.9944		2	1919.1412
						R.LSTPLQTNCTASESVVQSPSVATTASPATK	0.9958		3	3035.2983
						K.GAPFEVK.G	0.9924		1	747.8693

						K.QELILAEIHNGVEQVR.V	0.9958		2	1849.0971
						K.KIWEQIQPDLHTNAECVATYK.G	0.993		2	2545.8206
3300	Q3UZI1_MOUSE	264	40.91	6	54	K.RGPGLYYVDSEGNR.I	0.9958		2	1583.7007
						R.DAYSGGAVNLYHVR.E	0.9958		2	1522.6603
						K.FLHGVIVAADSR.A	0.9958	1,2		1285.4887
						K.GMGLSMGTMICGWDK.R	0.9958		2	1644.9254
						K.VIEINPYLLGTMAGGAADCSFWER.L	0.9958		2	2671.9936
						R.GPGLYYVDSEGNRISGTAFSVGSGSVYAY	0.9958		3	3533.8506
3301	Q3UZK5_MOUSE	607	5.6	2	15	K.QLEAESWSRTVDSK.F	0.9912		2	1636.7587
						R.IGDVLVSQFSGESAER.L	0.9958		2	1694.8388
3302	Q3UZY0_MOUSE	1216	3.54	3	3	K.LAQQLRDTTLLHR.F	0.993		2	1565.816
						K.KPCSPKTLPLK.K	0.9937		1	1269.5365
						K.FLQRQAAQLLAQR.L	0.9958		1	1543.8123
3303	Q3V046_MOUSE	102	26.47	1	9	K.TGITTSLPYFIILISYFNLSKSFDK.F	0.9958		3	2870.3581
3304	Q3V061_MOUSE	624	3.37	1	2	K.EEAAALGKLGNSIQQSHNR.L	0.9958		2	2024.2009
3305	Q3V085_MOUSE	411	4.62	1	3	K.VHNPAGIRNSTAVVGSK.D	0.9958		1	1707.9303
3306	Q3V087_MOUSE	258	9.69	2	2	K.GSVETVQKDVDTIK.F	0.9954		2	1519.6922
						K.RIEGNEK.A	0.9958		1	845.9309
3307	Q3V0C6_MOUSE	1014	3.45	2	2	K.LFLEEMSPGHHLNSLGNIFNSSSAK.Q	0.9944		3	2731.0551
						K.KPSLAK.Q	0.9958		1	643.8045
3308	Q3V0G6_MOUSE	1381	7.39	4	4	R.LERPLFEHSPQETQKAPPTAANHGPLTFHI	0.9944		3	4021.444
						K.LPIDPVTQGQEDK.V	0.9943		2	1440.5932
						K.SIIHLWKIPCSMSIVVDISFAIMCGVGLFYLLI	0.9958		3	4284.2224
						K.DFESLDAKR.S	0.9944		1	1081.1705
3309	Q3V0H8_MOUSE	335	14.93	2	5	K.SPGIQRLLLDLLLTEEPQSQEFISK.E	0.9958		2	2856.289
						R.DILTDVHSSINNQTLALMFQK.D	0.9944		3	2389.7289
3310	Q3V0I7_MOUSE	536	3.73	2	2	R.NPIKNIK.W	0.9958		1	827.0146
						R.VQLLDPKEK.V	0.9944		2	1070.2743
3311	Q3V0K9_MOUSE	630	3.65	2	2	R.NEALIALLK.D	0.9958		1	985.212
						R.AGFMLQEADK.L	0.9944		1	1110.2702
3312	Q3V0P3_MOUSE	650	6.77	2	2	K.FSVHEVAWILKEFLGHIK.G	0.9958		2	2154.5626
						K.ETEPELSSCPSGRTHTPGHYAR.Q	0.9944		2	2470.5835
3313	Q3V0T6_MOUSE	679	3.68	1	2	K.EAGLNIFPAVYSHFYVVINNKVR.E	0.9952		3	2652.0709
3314	Q3V0V7_MOUSE	225	8	2	2	K.QLQTRVDYLLK.L	0.9924		2	1377.6267
						K.KPQGKQLQTR.V	0.9958		1	1184.3841
3315	Q3V175_MOUSE	64	39.06	1	4	R.VFSEVELVSNNMQSPEEVPITLK.E	0.9958		2	2590.9483
3316	Q3V1C1_MOUSE	1740	5.46	3	3	R.EPSEEASTPLPGQESAEEEDAEEEESVTQI	0.9958		3	3721.7425

						R.GCSLLFGSQQGMELHR.Q	0.9958	2	1821.0271
						R.GRPQTHAVVLPLNNGDSTLLNTGSTESSP	0.9958	3	3965.2798
3317	Q3V1F1_MOUSE	546	11.72	2	2	K.GNICVISIFGIHHNPSVWPDPEVYDPFRFDF	0.9944	3	4206.6318
						R.NCIGQTFAMNEMMVALALTLLRFR.I	0.9944	3	2802.3499
3318	Q3V1Q3_MOUSE	1095	2.83	2	2	R.LLLSLLPAHIAMEMK.A	0.99	2	1681.1481
						R.MIQAIDGINAQK.Q	0.9944	1	1302.5316
3319	Q3V1Y6_MOUSE	530	2.83	1	5	K.SFQQTQIQNKPEK.K	0.9958	2	1576.7495
3320	Q3V2E0_MOUSE	255	22.35	2	7	R.TLNNDIMLIK.L	0.9958	2	1175.429
						K.IVGGYTCRENSIPYQVSLNSGYHFCGGSLI	0.9944	3	4910.3114
3321	Q3V2G3_MOUSE	246	4.88	1	5	K.TLNNDIMLLK.L	0.9958	2	1175.429
3322	Q3V2X2_MOUSE	1181	3.39	1	2	R.RTSHSELPHTELSSQTPYTLNFSFEELNTL	0.9944	3	4276.6195
3323	Q3V3K0_MOUSE	449	2	1	2	R.YISSLKK.K	0.9958	1	839.0226
3324	Q3V3S0_MOUSE	413	20.58	3	4	K.SSAVSLAENGVMAEEKPVPQLNGSTGDPF	0.9944	3	2942.2274
						R.VPSHSESALNNDSKPCNTNPHLNALSTDS	0.9958	3	3495.6331
						K.SQGAIQGRPPYAASAEEVAK.E	0.9958	2	2031.2327
3325	Q3ZK22_MOUSE	780	1.28	1	2	R.DTLQLSIK.Q	0.9944	1	918.0782
3326	Q497H5_MOUSE	1309	5.5	2	2	R.FNLNQYLPNFYPADMSEPQKQGAGENSP	0.9924	3	3474.7517
						K.AVAVCSVAPNLPPPPPSNSPSDSDSIQKPS	0.9958	3	4058.3699
3327	Q497N3_MOUSE	171	16.37	1	2	K.AGGGAGGGGGAASGPAAGTPSAPGPR.T	0.9958	2	1964.0616
3328	Q497P2_MOUSE	205	19.02	2	4	K.LHYNEGLNIK.L	0.9937	2	1201.3677
						K.TSAASPPVVPSAEQPRPIVEEELSK.K	0.9958	2	2619.9317
3329	Q499E4_MOUSE	774	4.78	2	4	K.QKQEQPLGEVLEELR.A	0.9958	2	1797.0183
						K.LKALQSYSMTESHLGSLR.D	0.9924	2	2022.3269
3330	Q499X2_MOUSE	586	3.41	1	3	R.AGAMVKMAAAGGGGGGGR.Y	0.9958	2	1476.7118
3331	Q4G0C7_MOUSE	502	7.17	2	2	K.AMLEGVDILLAQNDRSSR.C	0.99	2	1989.2542
						R.EMNNLLTFMLSSIR.E	0.9958	2	1669.9948
3332	Q4G0F8_MOUSE	1135	2.2	2	4	K.KYSGSLSVR.E	0.9944	1	997.1393
						K.KDVLDPFNDEEK.E	0.9924	1	1449.5572
3333	Q4H4D7_MOUSE	1733	5.89	4	4	K.KPVPEIPPLLNIGDPEKPSK.G	0.9944	3	2169.5694
						K.EGECFGLLGLNGAGK.T	0.9924	2	1522.6642
						K.GQVTVLLGHNGAGKTTVCSVLTGLITPSK.	0.9958	3	2910.3501
						K.SFYILVGIIFHHDFNSSNEPLPLVVKYDLR.F	0.9958	3	3535.0825
3334	Q4KML4_MOUSE	81	18.52	1	11	R.CANLFEALVGTLK.A	0.9958	2	1436.6575
3335	Q4KML5_MOUSE	617	20.26	7	20	K.LVESGFTTDPVTIENK.G	0.9958	2	1750.9433
						K.DLHVPIPAVAEMNPNVNVFVPPR.D	0.9958	2	2526.9592
						K.VISTLTISEIDWLNLNVYTCR.V	0.9943	2	2511.8438
						K.LICEATNFTPKPITVSWLK.D	0.9958	2	2219.5952

						K.YLATSQVLLSPK.S	0.9952		2	1320.5718
						K.FISKPNEVHK.H	0.9909		2	1199.3952
						K.HPPAVYLLPPAR.E	0.9944		1	1331.6035
3336	Q4KWH5_MOUSE	1682	4.58	4	5	R.SKPPAPALAVNRHSTGSYIASYLR.N	0.9944		3	2557.915
						K.MSNVTLDYCLDIIMK.F	0.9958	1,2		1817.1318
						K.EDPDSFTVRALLK.A	0.9958		1	1491.6842
						K.GTFNPFSGDPLPANPKK.Q	0.9958		1	1788.0129
3337	Q4PLL5_MOUSE	7354	1.07	4	7	R.SVVGIECSPAESPER.E	0.9958		1	1617.7192
						R.EAAVYLLTKQVLDGGIIHHISGLR.L	0.9958		3	2605.0555
						K.GIEGVNPEPCRATQNVFTR.R	0.9915		2	2146.3336
						K.ISVEMEGQRQDEK.A	0.9958		1	1549.6959
3338	Q4QRK2_MOUSE	399	5.26	1	5	K.LCSTQLSLNCPLCVNPVCR.K	0.9958		2	2292.502
3339	Q4U105_MOUSE	900	7.56	2	2	R.AGAAAPELLQALLRSGAHAVPQILHMPDFE	0.9958		3	4440.1717
						R.ASDGSFSLPLKPVISQPIHDSK.S	0.9919		2	2324.639
3340	Q4U205_MOUSE	1117	3.85	2	2	R.IDIVTLLEGPIFDYGNISGTR.S	0.9944		2	2294.6097
						K.GLPQTAVCNLNITLPAHK.K	0.9958		2	1948.2389
3341	Q4V9Z7_MOUSE	389	4.88	1	4	R.TAHMDHSIPEMQTFLQK.H	0.9943		2	2015.3094
3342	Q4VAD3_MOUSE	695	6.19	2	2	K.VEEGRIPTPGANPLDK.A	0.9958		1	1693.8974
						R.TNSVGGNWGVFPPGESPTIVPDK.L	0.9958		3	2356.5969
3343	Q4VC42_MOUSE	1001	5	2	2	R.DWNAWGGYNGELQSLRPILSDFSNAHMIM	0.9924		3	3832.2563
						K.VFDPNVFTIGLGK.K	0.9924		2	1407.6525
3344	Q4ZGD9_MOUSE	553	5.24	2	2	K.WNQTDVNMEGGSKPPER.K	0.9958		2	1946.1015
						K.TMVLQFLK.Q	0.9958		1	980.2537
3345	Q501L8_MOUSE	863	3.48	2	2	R.HVIQSPSTDRMNVTSTAR.R	0.9958		2	2001.2249
						R.DEAVQERK.R	0.9958		1	975.0464
3346	Q53VQ1_MOUSE	115	12.17	1	2	R.YDGSNNYNPSLK.T	0.9958		1	1372.4338
3347	Q53VR3_MOUSE	119	11.76	1	2	K.YDGNNSYNPSLK.N	0.9958		1	1372.4338
3348	Q54AH9_MOUSE	146	6.16	1	160	-.VHLTDAEK.S	0.9958		1	913.0183
3349	Q56A03_MOUSE	415	3.61	1	29	K.SDPDGYEFLEILK.Q	0.9958		1	1526.6831
3350	Q570Z6_MOUSE	1510	3.84	4	4	R.KADSFSSPGK.T	0.9924		1	1024.1185
						R.RMAFDYYPFHR.A	0.9944		1	1503.7209
						K.EVLEGLQEQLTK.D	0.9958		1	1387.5731
						R.EPKSDASSDQGAVSPEK.V	0.9958		1	1732.7985
3351	Q571K1_MOUSE	1916	5.22	4	4	K.EWQDSSREGDVLSQAAFPLSTSENVLSR.I	0.9958		3	3110.3208
						K.EVQKLQAGPLNTDVAPGAPQEK.N	0.9958		3	2291.5663
						R.LRAEAQPVGGTGESMEALLSSNSSLK.E	0.9915		2	2633.9336
						R.ENQHHYSNLFNHCAILEK.E	0.9944		2	2255.4204

3352	Q59IW5_MOUSE	1115	3.68	2	3	K.IQSTYDQVHSVPVPR.K	0.9958	2	1726.9297
						R.GSWASSEEPWVVPGAKTSEDSR.V	0.9924	2	2363.5022
3353	Q5BKP2_MOUSE	858	9.09	3	4	R.GLQPGEEELPDISPPIVIPDDSK.D	0.9958	2	2446.7137
						R.NQAVQALQATNHNLER.A	0.9958	2	1807.9639
						K.NECAFSYDSPNSEGGLYVCMNTFLAFGRE	0.9958	3	3859.1068
3354	Q5BKS5_MOUSE	720	2.64	1	2	R.HLQLQTQLEQLQEETFR.L	0.9958	2	2142.3763
3355	Q5BL10_MOUSE	963	1.97	1	4	R.QLEESVDSLGEELVQLR.A	0.9958	2	1945.1339
3356	Q5DTP0_MOUSE	1285	3.04	2	3	R.TTRPTGVLLGVSSQK.M	0.9957	2	1544.7917
						R.FTAIYDAGIPGHMCNGQWHK.V	0.9945	2	2304.5537
3357	Q5DTP4_MOUSE	615	9.11	3	3	R.NRNLSGGVLMGFMLNR.T	0.9944	2	1780.1162
						R.NLAEEIEMYMNNMSSPLTSR.T	0.9958	2	2331.6358
						K.LGADAKILSNVISK.S	0.9958	1	1429.7001
3358	Q5DTZ4_MOUSE	747	5.49	2	2	R.KPCSIRPCVQQAIDPGNQCPGRCMGHATF	0.9958	3	3353.648
						K.AVATSGLR.L	0.9944	1	774.8955
3359	Q5DU18_MOUSE	889	3.82	2	2	R.IPPKMPSVNSGAMAPEIGLVIDGK.T	0.9944	2	2422.9038
						R.FSHLKK.L	0.9944	1	759.9267
3360	Q5EBQ0_MOUSE	284	7.75	1	9	K.SCSGVMEFSTSGHAYTDTGK.A	0.9958	2	2123.2215
3361	Q5F226_MOUSE	4351	1.49	2	2	K.DEYVLEVTVQDNGDPPLR.S	0.9923	2	2060.2249
						K.SSYNLTVEVTDGFHTIATQVHILMIANINHHI	0.9958	3	5047.6623
3362	Q5FW75_MOUSE	894	4.36	2	8	R.ISNRPAFMPSEGK.M	0.9958	2	1434.6531
						K.NNIDKLEGDHQLIQEALVFDNK.H	0.9958	2	2554.8192
3363	Q5FW83_MOUSE	291	2.75	1	2	K.EKPVEK.S	0.9924	1	729.8516
3364	Q5FW89_MOUSE	302	15.23	2	2	R.TTQEDFFLLLELASPSQTSLYFCASSDR.G	0.9958	3	3228.5025
						R.LTVLEDLRNVTPPK.V	0.9958	1	1595.8797
3365	Q5G5D5_MOUSE	617	11.51	2	3	K.RALPLLPLLAGLGIASALGLGIAGITTSTVYF	0.9958	3	3726.4814
						K.ALSDSLDEIATSIISLQDQIDSLAGVVLQNRF	0.9958	3	3442.8485
3366	Q5HZJ0_MOUSE	1373	3.86	2	2	R.ESDLRHAMANCFEALIGAVYLEGSLEEAK.(	0.9924	3	3225.5636
						R.EVWLNYPLHPLQLQEPNTDR.Q	0.9958	3	2463.7551
3367	Q5HZJ5_MOUSE	669	12.26	2	3	R.VASIVDVSMDSGSLVLSAIGDLPGGSSPSE	0.9958	3	4206.629
						K.RPFTLVISFFSLLSVLCVMLSMAGSVLSCKN	0.9958	3	4018.7843
3368	Q5M9K5_MOUSE	149	59.73	6	107	R.WLHCMTDDPPTTNPPTAR.K	0.9958	2	2111.3027
						R.GVQQVTGHGGLR.G	0.9958	1	1209.3505
						K.FNVSATPEQYVPYSTTRK.E	0.9958	2	2089.3122
						K.EIHEWVPPSTPYK.-	0.9958 1,2		1583.7838
						R.KFIWTNHK.F	0.9958	1	1074.2706
						K.NTFWDVDGSMVPPEWHR.W	0.9958 2,3		2074.2775
3369	Q5NC72_MOUSE	706	2.83	1	6	R.SHTSLKDELSDISQGGSK.A	0.9958	2	1890.0141

3370	Q5NCE6_MOUSE	117	14.53	1	4	R.HDLVISSPFAPGGGK.Q	0.9958	2	1482.6793
3371	Q5PPQ4_MOUSE	887	7.1	3	5	R.QTHHECSECGKTFNQK.S	0.9958	2	1992.0442
						K.TEFASHQETHPEKPYECPDCGK.S	0.9931	3	2648.734
						K.EHLRIHTGETPYACSECGK.A	0.9944	3	2246.3735
3372	Q5PRE9_MOUSE	2387	0.38	1	7	R.SSADAKK.D	0.9944	1	706.774
3373	Q5QGU0_MOUSE	189	12.17	2	8	K.KATVNLLGDEK.K	0.9957	2	1188.3665
						R.IIRPIFLK.H	0.9952	2	1000.3158
3374	Q5R1G5_MOUSE	114	16.67	1	2	R.SNGDSVTQTEGLVTLTK.G	0.9958	2	1750.9005
3375	Q5RJH5_MOUSE	1300	2	2	2	K.EKLALAHYTALNMK.S	0.9958	1	1603.9201
						R.EEAALLMK.Q	0.9958	1	905.0973
3376	Q5RL20_MOUSE	159	13.84	1	2	R.KPFHTDNPSIQGQWHPFTNK.R	0.9958	2	2380.6273
3377	Q5S003_MOUSE	2175	1.89	2	2	R.CVDSYYHTQDNSLLLVFHNPMNLQR.L	0.9958	2	3066.3839
						K.SKDQPEATVTVR.K	0.9958	1	1331.4685
3378	Q5SGK3_MOUSE	1345	3.2	2	2	R.GVQTYQR.V	0.9958	1	851.9377
						K.YPEAPLISGNTALGPAMKSQGHFYPVLLSP	0.9958	3	3384.9207
3379	Q5SPX8_MOUSE	534	8.99	2	2	K.AILDAEPGPRPALQPSPSIR.L	0.9958	2	2086.3989
						R.SLSPKIMQEAFLVQEVIELPVTER.Q	0.9958	3	2758.2458
3380	Q5SUC9_MOUSE	284	13.38	2	5	R.SIGKPLLGGPFSLTTHNGEPK.T	0.9958	2	2151.4704
						K.KAEIAGSIAAHMR.S	0.9958	2	1355.5981
3381	Q5SX22_MOUSE	229	16.59	3	115	K.TITLEVEPSDTIENVK.A	0.9958	1	1788.9897
						K.ESTLHLVLR.L	0.9958	2	1068.2614
						R.TLSDYNIQK.E	0.9958 1,2		1082.1986
3382	Q5SX32_MOUSE	384	19.53	2	2	K.CTALELLEQEHTQGFIITFCSALDNILGGGIF	0.9958	3	5077.7404
						R.RQPYMKPVCGISSAAARPQVGISK.E	0.9958	2	2603.024
3383	Q5SX41_MOUSE	1912	0.52	1	5	K.MVSLLKEK.N	0.9958	1	948.2091
3384	Q5U477_MOUSE	612	1.96	1	3	K.EKHDRPQSEK.E	0.9958	1	1254.3451
3385	Q5U4C7_MOUSE	681	9.1	3	3	K.FQLVLDVAQKAQNLFGK.M	0.9958	2	1920.2621
						K.GNFHEIFNLTENERPLAVCENGWRCCLINF	0.9958	3	3721.0247
						K.YDTPYIIWR.S	0.9958	1	1227.4051
3386	Q5U5V8_MOUSE	1268	4.57	2	2	R.DHFGFPPEKPWGPRDFDER.E	0.9958	3	2330.5235
						K.EMPTPQLSHVSESVNNSIFHQIAEQLQQQN	0.9958	3	4075.5023
3387	Q5XJF6_MOUSE	217	8.29	1	4	K.FSVCVLGDQQHCDEAK.A	0.9958	2	1893.9801
3388	Q60638_MOUSE	1060	5	3	16	R.AAALQVPHAVGAVK.E	0.9958	2	1332.5888
						R.QGTSLLASKELK.D	0.9958	1	1275.4881
						K.IHAPLFSHISGIATEEGADLK.S	0.9958	2	2207.4912
3389	Q60709_MOUSE	751	6.66	3	3	K.VPYVAQEIQEEIDELLQEQR.A	0.9958	2	2430.6739
						R.HYQHVLAVDPEK.A	0.9958	2	1436.6103

						K.MQNHGYENPTYK.Y	0.9958	2	1482.6104
3390	Q61227_MOUSE	703	10.1	2	3	K.LSRPDLPFLIAAFFFLVVAVWGETLIPRYSG	0.9944	3	3653.3507
						K.STVAALLQNLYQPTGGQLLLDGEPLTEYDH	0.9958	3	3965.4142
3391	Q61287_MOUSE	142	21.83	3	1044	K.IGGHGAEYVAEALER.M	0.9958	1	1572.7178
						K.AAWGKIGGHGAEYVAEALER.M	0.9958	2	2086.3146
						K.IGGHGAEYVAEALERMFASFPTTK.T	0.9958	2	2583.9214
3392	Q61484_MOUSE	1231	30.71	22	92	K.VDIDVPDVNIEGPDAK.L	0.9958	1	1696.8517
						K.LDIETSDVSLEGPEGK.L	0.9944	2	1689.8138
						K.GPEVDVDVGDIDIECPEGK.L	0.9958	2	2044.1426
						K.VEAPDVEVHGPDWHLK.M	0.9958	2	1829.022
						K.MDINAPDMDVQGPDWHLK.M	0.9958	2	2083.3412
						K.LDIDVPNVDVQGPELHMK.M	0.9958	2	2020.3081
						K.ISMPDVDLHLK.G	0.9944	2	1268.5139
						K.ISMPDVDLHIK.G	0.9958	2	1268.5139
						K.LKGPDINLPEVSVK.T	0.9958	2	1509.7862
						K.AEGPEVDVNLPK.A	0.9958	1	1268.4093
						K.VKGDVDVSLPK.V	0.9958	1	1157.3525
						K.FSMPGFKGEGPEVDIPK.A	0.9931	2	1836.1126
						K.VGIDAPDVEVHGPDWHLK.M	0.9958	2	1985.2065
						K.VDISAPDVDVQGPDWHLK.M	0.9958	2	1992.1955
						K.MDISAPDVEVHGPEWNLK.M	0.9958	2	2038.2824
						K.VDIDVPDVNIEGPEGK.L	0.9958	2	1696.8517
						K.ISMPDLHLK.G	0.9909	2	1054.2927
						K.VDIDVPDVNIEGPDTK.L	0.9944	1	1726.8779
						K.SDIDVSGPNVDVK.V	0.9958	1	1345.4491
						R.ISMADVDLNVAAPK.G	0.9958	1	1444.6862
						K.LDISAPDLNLEGPEGK.L	0.9958	1	1668.8413
						K.GKADVDASLPEVEGGVK.V	0.9958	2	1671.8449
3393	Q61650_MOUSE	52	23.08	1	9	R.YFDSFGDLSSA.-	0.9958	1	1209.2543
3394	Q61769_MOUSE	2938	4.15	5	6	K.EPVGDSINVEEVKK.S	0.9958	2	1543.7142
						K.MSLESSQAEPVKTPASTK.R	0.9958	2	1892.1315
						R.NQTPVEAGDVGSPADTPEHSSSPQR.S	0.9958	3	2564.6415
						R.SQHGILQMICSK.R	0.9958	1	1402.6178
						R.AQPLEDLDGFQELFQTPAGASDPVSVEES	0.9958	3	4516.9165
3395	Q61785_MOUSE	1300	2.38	1	2	R.LIFNDNINNGKPTFTWKLNNTLFNDTLVK.E	0.9958	3	3396.8705
3396	Q61911_MOUSE	315	4.76	1	3	K.NYIFTNETNPIGR.L	0.9952	2	1539.6879
3397	Q62467_MOUSE	1681	3.09	2	2	K.TPVTESESQSLIASPSASETVPIASGESDIEI	0.9958	3	4091.3399

						K.RNTFMVLNR.S	0.9924		2	1151.3721
3398	Q63ZW6_MOUSE	1691	11.24	5	5	K.GNIGDMGFPGPQGVDGPPGPPGFPGQPG	0.9958		3	3369.7357
						K.GEPGLPGIPGLSGPKGYQGLPGDPGQPGL	0.9944		3	3874.3452
						K.GDQGPPGLPGNPGRPGLNGMK.G	0.9958		2	2017.2701
						K.GEPGQPGFGIPGPPGLPGLSGQKGDGGSI	0.9958		3	3691.0947
						K.GDTCFNCIGTGISGPPGQPGLPGLPGPPGS	0.9944		3	3861.2325
3399	Q63ZX6_MOUSE	578	3.46	1	2	K.EETPLFANPTSKVVSDVK.G	0.9958		2	1962.2072
3400	Q640M5_MOUSE	1874	2.35	3	3	K.VLQTADVSIEEMIEKLQK.D	0.9958		3	2075.4254
						K.LQLKQMGDQLIK.A	0.9958		1	1415.7344
						R.LEKELVAR.Q	0.9924		1	958.146
3401	Q642L7_MOUSE	156	20.51	2	3	K.YYKVDENGK.I	0.9944		1	1116.2157
						R.ECPSDECGAGVFMGSHFDR.H	0.9958		2	2159.2234
3402	Q68FG5_MOUSE	660	2.58	1	2	K.FEEHVQSVDIAAFNK.I	0.9958		2	1734.906
3403	Q68FM3_MOUSE	1146	6.02	3	3	R.LHLGTVSYGTDTMDEIQSHVLNSYLQVHSC	0.9958		3	4576.0136
						R.WTESVGLTLISR.D	0.9958		1	1362.5687
						R.KLSPPSYSK.L	0.9958		1	1007.1747
3404	Q68G59_MOUSE	1209	4.22	3	9	R.KLDEDLQLYQTPLELK.L	0.9958		2	1947.2359
						R.IFALLAGKPVWQLSEQK.Q	0.9943		2	1929.3128
						K.SRSIVGGLLQSK.F	0.9943		2	1245.4648
3405	Q68SA9_MOUSE	1641	2.86	2	3	K.GDDHPQHHDTAILLTR.K	0.9958		2	1826.9663
						R.EILIEEVAEAANFLALRSEDPDK.Y	0.9958		3	2573.8596
3406	Q69Z47_MOUSE	536	9.89	2	2	R.AKITTITPGSTPIIGVLLSTQNNR.C	0.9958		3	2496.9102
						R.SREFSLETCHSSEHGGASSGPSLER.E	0.9929		2	2705.7802
3407	Q69Z54_MOUSE	507	12.62	2	2	R.SEASDSGSESVSFTDGSVRSGSGTDGSDE	0.9958		3	2925.8579
						R.LSSESHHGGSPIHWVLPAGMSAKMLGGVF	0.9944		3	3119.6294
3408	Q69ZB2_MOUSE	1565	1.98	2	3	R.MSAQLVAAESRQK.K	0.9958		1	1419.6391
						K.FRGQLPAPCDPVCK.I	0.9958		2	1645.831
3409	Q69ZC1_MOUSE	976	5.12	2	2	R.DWDVLSSK.G	0.9944		1	950.0361
						R.VLNSSEDAHIIEATCDTPVSIPCSEAQLAGT	0.9944		3	4161.5657
3410	Q69ZJ2_MOUSE	1753	2.62	2	2	R.TDPLGSPDVFTRNNPGFHGAPNSSPIHLNF	0.9958		3	3216.4996
						K.MNGGKECDGGDK.E	0.9924		1	1268.3069
3411	Q69ZX9_MOUSE	609	15.27	3	5	K.GGTPPQQQQQQQQQPGASPPAAPGPK.D	0.9958	2,3		2609.8179
						K.LFLNEDDKPHNPMVNAGAIVVTSLIK.Q	0.9958		3	2837.3068
						R.VLSPEAVRNTLSLMHSCGMYDFSGQFAFH	0.9944		3	3869.414
3412	Q69ZY3_MOUSE	1641	4.2	4	4	K.LELELEQAKAQLAVSLSVQQETANLGPGS\	0.9958		3	3436.8846
						K.NLVATFICVFEK.V	0.9924		2	1441.6764
						R.LSVDANLQIPKELTLASK.R	0.9924		3	1941.2755

						K.ELTLASK.R	0.9924	1	761.8937
3413	Q6A029_MOUSE	810	5.19	2	2	R.RSATISGSATNLASLTAALAK.G	0.9958	2	2005.2791
						R.APLLSEPASAVPTSPFR.I	0.9957	2	1740.997
3414	Q6A0B1_MOUSE	1269	10.72	5	9	K.FSFLLNPQCTHVIVDSADVLSR.C	0.9958	2	2519.8261
						R.AEPSSVPEAGDFQLPDIKPFTNIK.A	0.9958	2	2601.9158
						K.AVVSTVEGSSLDSGGFSLHIGLRDAYLPR.M	0.9958	3	3005.3574
						R.NILGILSRGLLLPK.V	0.9937	2	1507.9034
						K.NEVIICLDCSSSMEGVTFTQAKQVALYALSI	0.9958	3	4134.6175
3415	Q6DD96_MOUSE	935	5.03	3	4	R.GWGSHYRGFVLLSILLGMR.W	0.9958	2	2163.5914
						K.ATDGGIPPLSTETR.M	0.9958	1	1415.5431
						K.YPELVLEK.A	0.9944	1	991.1723
3416	Q6DFX1_MOUSE	754	2.79	1	5	R.HSCIFPGQYNPSFISDESR.R	0.9958	2	2242.3753
3417	Q6DIC7_MOUSE	2044	4.31	4	5	R.SMSLNIGGAR.G	0.9944	1	1006.165
						K.VQPGCYLPSNPEAIVLDIDYK.S	0.9958	2	2392.6771
						K.TNIYLDEEGHQKDPDIGDLLEQLVEEITGSL	0.9958	3	3926.28
						K.ITNVSAIIKPYPK.G	0.9958	1	1444.7575
3418	Q6GQT9_MOUSE	1214	3.62	2	3	K.IQSTVTQPGGK.F	0.9944	1	1116.2596
						K.LYKSESLDNPIQTVSLGQSLFFHFPPLLR.D	0.9958	3	3348.8693
3419	Q6GQX8_MOUSE	1014	3.45	2	14	R.LGTGANMEK.V	0.9958	1	921.0563
						R.HVTSHRSSSFTLLQSLAIEDSR.D	0.9952	2	2472.7202
3420	Q6GT24_MOUSE	224	5.36	1	2	K.DANNMPVTAR.V	0.9924	1	1089.2115
3421	Q6IE04_MOUSE	247	12.55	1	2	K.QSIAYFDSIGQTGKSICETIFQYLQNESK.T	0.9958	3	3357.6643
3422	Q6IEF7_MOUSE	494	12.55	2	3	R.HYVIPKGTAVFPFLSSILLDQK.E	0.9958	3	2474.9487
						K.SDFNLENLAICGSNLFTAGTETTSTTLRFGL	0.9958	3	3919.4303
3423	Q6IFT3_MOUSE	800	4.88	2	6	R.SLNNQFASFIDK.V	0.9958	2	1384.5315
						R.GECGGQVTMPGREYGGQVTMPGR.E	0.9944	3	2425.6625
3424	Q6JIZ0_MOUSE	2448	8.74	10	25	K.GTWQSGFFDHGSFK.E	0.9944	2	1601.7178
						R.LLYGESPWGVTPIPFETPLSPPIAR.G	0.9958	2	2739.1864
						K.HEIAFLGPPSEAMWALGDK.I	0.9958	2	2070.3704
						R.HLEVQVLADQYGNAVSLFGR.D	0.9929	2	2217.4893
						K.TIQSLVQEHPEVIMDCVAYLSQHLTPAER.I	0.9958	3	3366.7798
						K.IWGKMTDSKPLTNSK.V	0.9901	2	1706.9977
						R.EIEFTPTK.A	0.9958	1	965.0911
						K.EEVDSYRITIGNK.T	0.9944	1	1524.6708
						R.VIQVENSHIILTGAGALNK.V	0.9958	2	1978.2993
						R.LGGIPVGVIAVETRTVEVAVPADPANLDSE/	0.9958	3	3189.6335
3425	Q6KAP1_MOUSE	1454	0.96	1	16	K.GHYKFCELLINR.G	0.9958	2	1550.7667

3426	Q6KAU2_MOUSE	1204	1.08	1	11	K.EREWQMESLIR.Y	0.9958	2	1477.6782
3427	Q6NS46_MOUSE	1862	2.95	3	3	R.HILLCRKPALVSTVEGGQDPK.S	0.9935	3	2319.6757
						K.NRIEDPEINSIEDVK.E	0.9932	2	1771.9219
						R.MPVQRDSETVDDK.G	0.9924	1	1520.6544
3428	Q6NS86_MOUSE	746	3.49	1	2	R.LVLVQSAGVLRNLEQEEPFDLSQK.R	0.9958	3	2714.0911
3429	Q6NV66_MOUSE	1788	3.3	2	2	R.GPQAGMAEVGPPGPGK.A	0.9958	1	1450.6525
						K.GSEPQMGPISEAGGCSEPQNAAEAGQEQ,	0.9944	3	4027.2857
3430	Q6NV99_MOUSE	933	3.32	2	3	K.YEHCKAGQAGLTINLHYLEK.E	0.9944	2	2346.6141
						R.FLQILQR.E	0.9958	1	918.127
3431	Q6NVE4_MOUSE	1535	1.24	1	3	K.WGEGNKMTSGVSQGEWK.Q	0.9944	3	1882.0576
3432	Q6NX83_MOUSE	505	3.76	1	2	K.SDSSLETMENPGVMGNK.V	0.9958	2	1796.9619
3433	Q6NXL1_MOUSE	1032	5.62	3	10	R.KLDPDSIPSPIQVIENDR.A	0.9958	2	2037.2774
						K.LFIFHSSLPTAEAPGK.L	0.9958	2	1715.9897
						K.AIREILVNQTAHMLACYR.K	0.9909	2	2160.5084
3434	Q6NXY6_MOUSE	931	3.65	2	2	R.VSAEKLHFSVDSESGDLLVK.D	0.9958	2	2161.4167
						R.YTIGVEAKDR.G	0.9924	1	1152.2926
3435	Q6NZD8_MOUSE	792	10.48	3	40	K.TESYHVEIEATDGGGLSGK.G	0.9958	2	1951.0539
						R.VVSDHDKQQLILDPETGDLLLR.E	0.9958	3	2505.8308
						R.DPAQDDTDVLTLYLVIALASVSSLFLLSVLM	0.9958	3	3883.5757
3436	Q6NZD9_MOUSE	786	2.29	1	6	K.FLSPIASNFLTESTGR.E	0.9958	1,2	1740.9536
3437	Q6NZJ3_MOUSE	561	2.85	1	2	K.FTQEEWAVLDPSQK.K	0.9944	2	1678.8388
3438	Q6NZK1_MOUSE	1749	4.12	3	3	R.AGELQESQGDGLAAISLYLKAGLPAK.A	0.993	2	2601.9597
						K.EVGWENMAFIFLNR.F	0.9944	2	1726.9904
						R.LEEAWGDHLVQQKQLDAAINHYIEAR.C	0.9958	3	3049.3726
3439	Q6NZL1_MOUSE	1150	4.43	2	3	K.TPASAPPPPVAKPAVFIPVNRTPEMQEER.I	0.9958	3	3128.6165
						K.TPLLDDPVFIHPSSVLFK.E	0.9958	2	2026.3831
3440	Q6P0A6_MOUSE	896	1.56	1	2	R.GNEMNLFRLDWR.T	0.9944	1	1551.7631
3441	Q6P1D7_MOUSE	1565	6.45	4	4	K.REAGLQHGEEGQLGNQSALGCR.D	0.9911	2	2368.4942
						R.EQHVNRCLDEAEK.A	0.9956	2	1628.7051
						K.LSDILDAQCITFTTAAARK.E	0.9944	2	2096.3545
						R.ESQERSSLAGSPEALWDDWNEEEGQSPE	0.9958	3	4316.5696
3442	Q6P287_MOUSE	337	13.65	2	2	R.SADAPMFVMGVNHEK.Y	0.9958	1	1633.8775
						K.WDEASAEYVVESTGVFTTMEKAGAHLK.G	0.9958	3	2958.2691
3443	Q6P290_MOUSE	348	22.13	2	2	R.FHQPIYYLLGNLAAADLFAGMAYLFLMFHT	0.9958	3	4089.8109
						K.TVVIILGAFVVCWTPGQVVLLLDGLDCKSCI	0.9944	3	4088.7592
3444	Q6P4T2_MOUSE	2136	4.78	3	8	K.NLELKDLLPYGFAIHHAGMTR.V	0.9941	2	2397.8003
						K.AIRLIQACVDVLSSNGWLSPALAAMELAQM	0.9944	3	4162.8796

						R.MTQNPNYYNLQGISHRHLSDHLSELVEQTI	0.9958		3	4327.7289
3445	Q6P5E8_MOUSE	934	4.82	2	2	K.QVKTPCTSIAPSLVR.V	0.9937		2	1657.917
						R.IPETMVLELGDGDDGVDGSAAIGTGR.E	0.9958		3	2546.7657
3446	Q6P6L5_MOUSE	1124	5.78	3	3	R.IMFINNCSLTDDSEYYVTAGDEKCSTELFVI	0.9944		3	3679.9633
						K.QQEEEPEIDVWELLK.N	0.9958		2	1886.0655
						K.DGEEIDKNQINIR.N	0.9958		2	1544.6616
3447	Q6P8K3_MOUSE	481	6.65	2	2	R.HDETQAYFLK.W	0.9958		1	1252.369
						K.GVVLQVLDVMPLRGLLEK.V	0.9944		1	1980.4601
3448	Q6P8S2_MOUSE	187	12.3	1	2	R.GLPGFPAYLDEELQTALYEIK.H	0.9943		2	2368.6886
3449	Q6P9K9_MOUSE	1587	2.08	2	2	K.TWQRNGLILHTGK.S	0.9944		1	1524.7659
						R.QLTIFNTQAQIAIGGK.D	0.9958		1	1703.9792
3450	Q6P9L1_MOUSE	1442	7.42	3	3	R.AAFALGGLGSGFASTKEELSALVAPAFAHT	0.9958		3	3677.1919
						R.LAGADVVLGVEMTSTGEVAGFGESRCEAY	0.9958		3	3218.5691
						K.SELLPTVRLLESLGYSLYASLGTADFYTEH(	0.9958		3	3632.1046
3451	Q6P9Q3_MOUSE	440	3.64	1	2	K.QLHGKNSFDNANER.S	0.9958		1	1630.7171
3452	Q6P9Q7_MOUSE	359	14.48	2	9	K.VTNEPILAFSQGSPER.D	0.9958		1	1745.9298
						K.GQMEAIPCVVGDEEVWTSDIQYQLSPFNH.	0.9958		3	3688.0285
3453	Q6PAC0_MOUSE	1569	1.59	1	2	R.SLLSGEETGSLPGNYLVPIYSGR.Q	0.9958		2	2410.6861
3454	Q6PAC4_MOUSE	1279	3.6	2	2	R.LQSLPSSHGPSQPGLPAVLSSPSPPLSPR.	0.9958		3	2892.2847
						R.IAKVQPAVQDEAR.S	0.9958		1	1425.6279
3455	Q6PAM4_MOUSE	718	5.29	2	4	R.DSSDALLQRTSPTR.I	0.9958		1	1547.6652
						R.TELEPSLSSPVSFASPEVLR.V	0.9958		3	2146.4021
3456	Q6PB36_MOUSE	1128	1.6	2	3	K.ELQPAK.T	0.9958		1	685.7984
						K.AVYIAPLK.A	0.9958		1	875.099
3457	Q6PB82_MOUSE	1057	4.07	1	2	K.KSPPVPVPSYPSSGSGSSSSSSSASHLASI	0.9958		3	4026.4211
3458	Q6PCN2_MOUSE	1050	3.43	2	10	R.LPLFVK.V	0.9944		1	716.942
						R.LIEVGPSGAQFLGPVIVEIPHFAALR.G	0.9958		2	2732.2413
3459	Q6PD31_MOUSE	939	8.63	3	4	R.ADTIYGYDHDDWLHTPLISPDANIDLTTEQI	0.9958		3	4145.4792
						R.YHSLGLFPMDSLAAEIEGTMR.K	0.9958	2,3		2339.6863
						K.KPGTPGTPGSHDLETALR.R	0.9958		2	1835.0269
3460	Q6PDC0_MOUSE	408	2.7	1	2	R.GGGGGGGGK.K	0.9944		1	603.6127
3461	Q6PDI6_MOUSE	601	10.48	2	2	R.VFEYTPECIVFDLLDIPLYHGWLVDPQIDDI\	0.9944		3	3964.5129
						K.VTASPELAEAAAGRGSGPVGDTGTCR.V	0.9924		3	2488.6397
3462	Q6PEE0_MOUSE	1246	3.69	2	3	K.LAHSVSGQGDAAPHFVGVSMDAAGITQGK	0.9958		3	2810.1137
						K.ERMSEYLGQLAER.R	0.9949		2	1582.7717
3463	Q6PER5_MOUSE	223	25.56	2	6	K.FHTPISFPQIPLAALAVEK.V	0.9948		2	2080.4777
						K.LAQFDTLACTTGSSVHVFVNPATNKPENLF	0.9958		3	3778.1358

3464	Q6PFC6_MOUSE	849	6.24	2	2	K.ALQYSLHGDTPHASNLSFALK.Y	0.9958	3	2271.5376
						K.VDWPLNIVITESCLNKYSGIFSFLLQLK.L	0.9958	3	3299.8439
3465	Q6PFE1_MOUSE	708	7.34	2	2	K.TWSVMPPMSTHRHGLGVAVLEGPMYAVG	0.9958	3	4498.1109
						K.GATSIEK.Y	0.9924	1	705.7862
3466	Q6PFX9_MOUSE	1320	3.86	3	3	K.SALDLADPSAKAVLTGEYK.K	0.9943	2	1950.1962
						K.GANVNEK.N	0.9958	1	731.7837
						K.LMALLTPLNVNCHASDGRK.S	0.9911	3	2111.4333
3467	Q6PGI2_MOUSE	365	7.12	2	3	R.FRSFDALLADLTR.S	0.9958	1	1525.7477
						R.TLQALSNEK.K	0.9944	1	1004.1283
3468	Q6PKB0_MOUSE	369	16.26	3	3	R.SSVPVVGIVLGLLLVVVAIAGGVLLWGR.M	0.9944	3	2758.4502
						K.EQLFLEALKTLEK.I	0.9958	2	1562.8467
						R.KESEFLLNSCPER.L	0.9958	2	1609.7424
3469	Q6R5F1_MOUSE	128	8.59	1	6	K.EWQNPVPFK.E	0.9958	1	1145.303
3470	Q6RT24_MOUSE	2474	1.54	2	7	K.EKNELEEFELLEQK.E	0.9958	2	1778.9537
						R.KIDSLMQENSGLQQTLESVR.A	0.9958	2	2277.5548
3471	Q6T3A5_MOUSE	4060	2.91	3	3	K.VDSNVFYKIVGHALLLGLPTWTEGLALVR.L	0.9958	3	3183.7642
						R.SQGVDLYIQYLTEVFSVEPCSGSLLGGTLL	0.9958	3	4795.4535
						R.LVNQVITAQQTGALENVLGMTVGALLVTQS	0.9958	3	3832.4509
3472	Q6TNG5_MOUSE	436	5.96	1	2	K.ATATYPMDLALDPLSNCTTFPEPR.D	0.9958	2	2682.9711
3473	Q6UY52_MOUSE	187	10.7	1	13	K.EFMEDNNSYSFRHTYLLK.E	0.9958	2	2295.5311
3474	Q6V5K9_MOUSE	347	11.82	2	3	K.GENPGPPSMGSSNVPTGLK.K	0.9958	2	1827.0191
						R.SSRIMSETQPRPPVIPSR.R	0.9909	2	2039.3605
3475	Q6W8Q3_MOUSE	68	30.88	1	2	K.KAEEEEEIDIDLTAPETEK.A	0.9944	2	2190.3197
3476	Q6WG34_MOUSE	429	16.78	2	2	R.STLALSGALCVVVSFFCLLLIHNEPADVGLF	0.9958	3	4196.8091
						K.AGLSLYGNPRHGLLLLMMAGMAASMFLFR	0.9958	3	3140.8545
3477	Q6XBG2_MOUSE	1668	3.24	2	2	R.RLSTAIATMGKPSVIFLDEPSTGMDPR.A	0.9944	3	2892.3583
						K.KYLNSLDLESHANSLISTYSEGNK.R	0.9958	3	2684.9195
3478	Q6XBG3_MOUSE	1683	1.49	2	4	R.AYVDNLLK.M	0.9937	2	936.0959
						R.KLSIIIALIGDTK.V	0.9958	1	1385.7306
3479	Q6XPS7_MOUSE	400	20.25	4	4	R.VLLFPWTEQSVR.A	0.9958	2	1475.7306
						R.AMAEAVVGDDDYGEDPTVHELQEK.A	0.9958	2	2619.7731
						R.GSGSPYHPVCELVYLENTHSSAGGR.V	0.9958	2	2675.8401
						R.QVCLLAHAHGAR.V	0.9958	2	1333.5021
3480	Q6YJU1_MOUSE	308	24.35	5	10	K.THTTCPDCPSPIDLSNPSALEAATESLAK.F	0.9958	3	3085.2808
						K.LVVLPFPGK.E	0.9958	1	970.2431
						R.HVPLIQPVEK.S	0.9944	1	1160.4019
						R.GSIQHLPELDDEKPEESK.G	0.9958	2	2052.2023

						K.KLVVLPFPGK.E	0.9958		2	1098.4172
3481	Q6YK32_MOUSE	536	13.62	4	38	K.DSPVLLDFFEDSELYR.K	0.9958		2	1946.1205
						R.SLQPEIQPFPQTASR.S	0.9958		2	1699.9041
						R.LPPLNIGEVLTLPEANFPSFSLPNCNR.S	0.9958	2,3		3011.4137
						R.SGYVFELLR.V	0.9958		1	1084.2603
3482	Q6ZPK1_MOUSE	1205	8.3	4	4	K.QSTLPRHGCLSSPK.A	0.9958		1	1568.7392
						K.SPTPESSTIASYVTLRK.T	0.9958		2	1838.0679
						R.HGCLSSPKAMVQVSDQTMHSIPTSPSHGS	0.9944		3	4242.6534
						R.ENDVKPDYETPAAQCAHLEDAEPQNADIG	0.9958		3	3483.6526
3483	Q6ZQ98_MOUSE	937	4.38	2	4	K.AHIFCVNALAAKDPIWAAR.L	0.9958		2	2125.4472
						R.QVLRDVTAALDELEVSFR.K	0.9958		2	2062.3305
3484	Q6ZQL8_MOUSE	611	5.73	2	13	R.LSLPTETLQELLDVHVACEK.E	0.9941		2	2296.5891
						R.AKSSPNLAGIK.N	0.9958		1	1086.2767
3485	Q6ZWQ9_MOUSE	172	41.86	3	21	R.DGFIDKEDLHDMLASMGK.N	0.9958		2	2023.2832
						K.NPTDEYLDAMMNEAPGPINFTMFLTMFGEI	0.9958		2	3426.9134
						R.NAFACFDEEAIGTIQEDYLR.E	0.9944		2	2363.5085
3486	Q6ZWZ6_MOUSE	132	12.88	1	27	K.LVEALCAEHQINLIK.V	0.9934		2	1752.0301
3487	Q70FJ1_MOUSE	3779	2.99	5	46	R.LQGLMQEFQKQELEPEXKPGSR.G	0.991		2	2586.9659
						R.DDLEATQTKQALEYESK.L	0.9924		2	1970.0973
						K.SSGIFPSETLEIGEVVEK.D	0.9958		2	1922.1394
						R.VIELQKLLEEAEERPEEGGEQSSR.D	0.9931		3	2756.9836
						R.DLQECLVNSK.S	0.9958		1	1206.3044
3488	Q70KF4_MOUSE	3739	5.24	8	17	R.KLPVPASAPLETASFDLPIEQK.E	0.9958		2	2352.7331
						K.AVNPELLEEPPALSFFYK.D	0.9927		2	2065.3734
						R.SLGIEPVKPIGTEPGPSILEK.G	0.9958		2	2162.5315
						K.LPFKPSVSQNATR.E	0.9958		2	1445.6615
						R.NSLESQDVLTNQEDGPSISESPVLNIENEK	0.9944		3	4139.3839
						K.TYADSYLNVPSSTEHAFPSSAR.N	0.9958		2	2401.5511
						K.GTVPAEVNIAEKPAVHSLPEVTVK.L	0.9944		2	2486.8711
						K.EPILPTQMTFTPERITLSEEER.E	0.9958		3	2618.9617
3489	Q70X91_MOUSE	3604	1.36	2	3	R.DQQRGSFSSTPELGHTSPLLLK.G	0.9958		3	2399.6659
						R.DEVLTDPSLASPVEHPGLKGVGK.S	0.9958		2	2346.6427
3490	Q71LX8_MOUSE	724	1.24	1	11	R.ALLFIPR.R	0.9958		1	830.0611
3491	Q71RI2_MOUSE	499	6.21	2	10	R.KPADGGKGHK.R	0.9958		1	995.1264
						K.GGESGDSHGSETTQRDR.E	0.9958		1	1776.7306
3492	Q78H50_MOUSE	37	32.43	1	8	R.ELINERNMLK.T	0.9944		1	1260.4943
3493	Q78HG1_MOUSE	197	11.68	1	6	K.LVGTPNPSTPLPNTVPQFIAR.E	0.9958		2	2220.5767

3494	Q78J03_MOUSE	175	41.71	5	35	K.ETGMYHCVCCDSPLFSSEK.K	0.9958	2	2308.4197
						K.KYCSGTGWPSFSEAYGSK.G	0.9958	2	2013.1365
						K.KLTPEQFYVTR.E	0.9958	1,2	1382.6023
						R.RLDTSLGCPR.M	0.9958	1,2	1175.2963
						K.GSDESHTGILR.R	0.9958	1	1172.2401
3495	Q78JN3_MOUSE	317	7.26	1	3	R.KNYVDLVSSLSSSSEAPSQGK.R	0.9958	2	2184.3648
3496	Q78Y72_MOUSE	263	8.75	1	2	K.SVPPIAVEGENVLLFVHNLPK.N	0.9958	2	2273.6805
3497	Q7M6U4_MOUSE	576	12.85	2	2	K.NHSDRGAAHYLNENWSSCESPAPPVVPTS	0.9958	3	3760.9439
						K.AAVVQYGPSAPFTQALLDTVVESHLTPLDV	0.9958	3	3785.3318
3498	Q7M6X7_MOUSE	644	4.81	2	2	K.AFHYPLLLSQHKIVHTGK.K	0.9958	3	2090.4789
						R.YIREFILEK.N	0.9958	1	1211.4466
3499	Q7M739_MOUSE	2357	3.44	4	5	K.AEIARSNASLTNNQNLIQSLR.E	0.9943	2	2314.5637
						R.GLQLTPGIGGMQQHFFDDEDR.T	0.993	2	2362.5787
						R.LSQEVEYLTEDVK.R	0.9958	1	1553.7063
						R.GQNLLLTNLQTIQGILER.S	0.9958	2	2025.3561
3500	Q7TME8_MOUSE	910	1.54	1	2	R.LLFSEATSIEFK.R	0.9958	1	1385.6
3501	Q7TMF4_MOUSE	541	6.84	3	31	R.ISLLLDPGSFVESDMFVEHR.C	0.9947	2	2292.6117
						R.ERISLLLDPGSFVESDMFVEHR.C	0.9944	3	2577.9147
						R.EFFEIMPSYAK.N	0.9958	1	1362.583
3502	Q7TMQ1_MOUSE	434	24.42	6	94	K.VAAGHELQPLAIVDQRPSSR.A	0.9958	2	2145.4263
						K.QASEQNWANYSAEQNR.M	0.9958	2	1896.9273
						K.YAYFNGCSSPTAPLSPMSPPGYK.L	0.9958	2	2493.7591
						R.MGQAGSTISNSHAQPFDFPDDSQNAK.K	0.9958	2,3	2751.9006
						K.VAQTDGVNVEMHLK.Q	0.9958	1,2	1541.7625
						K.KVAAGHELQPLAIVDQRPSSR.A	0.9958	2	2273.6004
3503	Q7TMW5_MOUSE	662	5.14	1	2	R.GFLEGIEYADSSTFNPSKWMMVHFDCTGF	0.9958	3	3789.237
3504	Q7TNL5_MOUSE	595	4.2	2	3	R.EELFIQK.L	0.9958	1	907.0544
						K.RPSNSTPPPTQLSK.I	0.9958	2	1510.6903
3505	Q7TNL9_MOUSE	138	25.36	2	8	K.QFLDCSTTQSDLTLCEGFSEALK.Q	0.9909	2	2651.8159
						K.YNHGLSSLP.-	0.9958	1	988.088
3506	Q7TNZ4_MOUSE	842	11.76	4	9	R.VYIIYGNDLGLPPIDLDLDKEAHGILEGFQPS	0.9958	3	3727.2084
						R.MTPCPEEKAQYVLTSPEASSR.F	0.9958	3	2382.6137
						R.FGSVLHLTDLDDDGLDEIIMAAPLR.I	0.9958	2	2728.0894
						R.SLLLIGSPTWK.N	0.9958	2	1215.4783
3507	Q7TPL5_MOUSE	576	18.75	4	4	R.CAPATFAGLVLVGLGVATVK.A	0.9944	2	1945.319
						K.ALVKIVPVFLALIPYWTVYFQMQTTYALQNL	0.9958	3	4024.886
						R.RAACGAVLLAELLER.A	0.9958	3	1642.9054

						R.SFLCGDPRPELVRNCSAPFPNGSASCPEN	0.9958		3	3535.7529
3508	Q7TPM8_MOUSE	624	3.04	1	13	R.HLGGSGSVVPGSPSLDR.H	0.9958		2	1622.7782
3509	Q7TPQ8_MOUSE	401	14.71	2	3	R.GKVFAVSALSVVIFVVFYHSQLSLPNLYQQ	0.9958		3	4129.7484
						K.EAVRQLLSCFPNAFLASK.V	0.9949		2	2052.3471
3510	Q7TQC0_MOUSE	2587	4.37	3	3	K.GNEHSVTDSQLNSFLQGFETQEIVKPIIPLA	0.9958		3	3926.4363
						K.QVSLPQEATVEDAGFPVRGCDGAVVVGLA	0.9924		3	3645.0388
						K.GNEALTENGGESQLQDTYPVSQYLEYHSE	0.9958		3	4259.4254
3511	Q7TQQ3_MOUSE	311	12.54	1	52	R.YVAVCQPLLYVTIMTQKALLSFVAGAYIAGL	0.9958		3	4015.8397
3512	Q7TR02_MOUSE	311	7.4	1	2	K.NTLIFASVLTPLFNPMVYTFR.N	0.9958		2	2445.9251
3513	Q7TRR9_MOUSE	316	21.52	2	2	K.VVHTMMANVYLLLPPVLNPIIYSVKTK.Q	0.9958		3	3055.7938
						K.LACSDTRANNICGLVDLILTTGLDIPCIVLSY	0.9958		3	4161.8111
3514	Q7TSI4_MOUSE	649	2.16	1	3	K.TCCHIMLSQEEK.Q	0.9924		2	1536.6724
3515	Q7TSQ8_MOUSE	878	11.39	6	8	R.MPALETLEILKLVNCPETFTPDMK.C	0.9944		3	2792.2846
						K.LYHQLEQETGIQTGYLR.T	0.9958		2	2050.2786
						R.RMPALETLEILK.L	0.9958		2	1414.7466
						K.LYPVTSFFTHK.R	0.9958		2	1340.5645
						K.NPKPIFTEGK.N	0.9924		2	1131.3171
						R.HVCLGYVHNFSEDSGEEQVVTTDFINR.G	0.9958	2,3		3154.3423
3516	Q7TSY7_MOUSE	1226	5.71	2	2	R.FVNLNKNNWEEPSGSFPEDSFIKPPQDSIG	0.9958		3	3550.8657
						R.KYVVEMFYFNPTTMTSEWTTYYEIAATVSL	0.9944		3	4102.6627
3517	Q7TSZ9_MOUSE	665	4.96	1	3	K.DLMTQNGISYVLNASNSCPKPDFICESRFM	0.9958		3	3653.0513
3518	Q80TH9_MOUSE	284	6.69	1	3	R.SKSSQLDSGAPLSPSSR.S	0.9945		2	1704.8345
3519	Q80TK3_MOUSE	1153	2.86	2	2	K.VAAPAVLNDISK.K	0.9924		1	1198.405
						K.SMPTSQSHGSLTAELWDSK.V	0.9958		2	2063.2464
3520	Q80TR9_MOUSE	1450	2.14	2	2	K.FEKLAATSEAGDAPWK.F	0.9958		2	1721.9072
						R.KVLCGVVTIQK.N	0.9924		1	1245.5145
3521	Q80TS1_MOUSE	1134	2.65	2	6	R.KPLSVSPSTDGLR.S	0.9958		2	1357.5498
						K.FFSELEFGHPPPK.K	0.9958		2	1532.7386
3522	Q80TV0_MOUSE	837	2.87	2	2	R.DKEEGLDGAPAK.Y	0.9958		1	1230.3171
						R.RHPLPSMR.G	0.9958		1	994.2028
3523	Q80U83_MOUSE	1028	1.75	1	2	K.LFLFHTSLPIAEAPGK.L	0.9958		2	1742.0709
3524	Q80UL3_MOUSE	392	13.01	2	2	R.RAFMEEFGAEPELAVSAPGR.V	0.9956		2	2165.4284
						R.DDYEVSCPELDQLVEAALSVPGVYGSR.M	0.9958		2	2970.1823
3525	Q80UU8_MOUSE	130	63.85	2	2	R.QAWAGLEAENGPTPSPGRSPLDSQASPG	0.9958		3	4016.3941
						R.IPEPCAAAFPEAVAEDDAFLPGPPTVSAFL	0.9958		3	4122.6016
3526	Q80UY2_MOUSE	381	21.78	3	14	R.TNTSSVTTTITQATATANTANTENSPQALH	0.9958		3	4008.3049
						R.SNMHFTSSSTGGLSSSQSSYSPSSR.E	0.9958		2	2567.6599

						R.SLFVQELLLSTLVR.E	0.9954	2	1618.9573
3527	Q80VI2_MOUSE	764	4.71	1	3	K.QVIQKTPLPFFAMSLSLSPGSQLMVVGFAE	0.9958	3	3803.5554
3528	Q80VP0_MOUSE	1166	4.63	2	2	K.ELPDPFNDLSVGGWEITEEPVGRLSVWAV	0.9958	3	3727.1651
						R.AVYFRQGVTPSELSGK.T	0.9958	2	1739.9689
3529	Q80VU0_MOUSE	454	17.62	3	10	K.LTPIPSTSPNLQAYHQGNTQVSR.K	0.9958	2	2510.7691
						K.LLPVLQEALSAYLDSAK.M	0.9958	2	1832.1473
						R.ILQGAPETLDRQTAALLHGTIILDCVNMDTN	0.9958	3	3694.2043
3530	Q80WQ3_MOUSE	560	10.36	2	2	R.KVVLAWGLLNVSMAGMIYTEMTGK.L	0.9958	3	2614.1947
						K.LGSPDSTSPSTSPTFWNYSRSVGDYAQTL	0.9958	3	3251.4901
3531	Q80WQ4_MOUSE	447	5.15	1	2	R.QFLQDQKPGSLVADIGCGTGK.Y	0.9944	3	2220.4534
3532	Q80X16_MOUSE	5035	2.32	5	9	K.CAPLFAGTEHR.A	0.9926	2	1259.3733
						R.DIEIGDGFLPVCSLGPGQVGHLNLGQDVSS	0.9944	3	3351.7069
						K.MLPIGLNMCAPTDQDLIVLAK.A	0.9958	2	2314.7701
						R.SLVPLDDLVGIISLPLQIPTLGKDGALVQPK.	0.9958	3	3211.8535
						K.DMELDTSSIEKR.F	0.9958	1	1424.5659
3533	Q80X36_MOUSE	1107	6.23	3	3	R.QVQFHQGFGDLAILKPSNKVLQVSIGPGLP	0.9958	3	3317.9022
						K.SESIHVTLNVEQACYTRDALAK.A	0.9924	3	2506.7411
						R.EEASDLLLNK.K	0.9958	1	1132.256
3534	Q80X68_MOUSE	466	2.79	1	9	K.NYIWNTLNSGR.V	0.9924	1	1338.4655
3535	Q80XL8_MOUSE	866	7.97	2	3	K.GEIGREMYIIQAGQVQVLGGPDGK.A	0.9958	3	2516.8749
						K.ALSPAESPVVAWSDPTTPQEADGQDRAAS	0.9958	3	4226.4735
3536	Q80XP1_MOUSE	1663	1.56	1	4	K.TELTNIELLDDFDEYTMTIQQVIK.S	0.9958	2	2874.2294
3537	Q80Y35_MOUSE	2094	1.62	2	2	K.SSLISSLEEEVSILNR.Q	0.9958	2	1776.9817
						R.SLEAQVAHADQQLR.D	0.9958	2	1566.7141
3538	Q80Y42_MOUSE	577	7.8	2	2	K.LDSGVAAGDVVEVMEGNTVNFR.V	0.9958	2	2280.5145
						R.EHEGMYRCLVSNPVTNLSR.L	0.9917	2	2263.4993
3539	Q80YQ1_MOUSE	1171	9.39	5	10	R.IPESGGDNGVFDIFELIGGAR.R	0.9958	2	2164.3794
						R.NALWHTGNTPGQVR.T	0.9958	2	1551.7049
						K.RPPLCFHNGVQYK.N	0.9958	2	1616.829
						K.GCSSSATNVLLTLDNNVVNGSSPAIRTNYI(	0.9958	3	3461.7796
						R.LCNSPSPQMNGKPCEGEAR.E	0.9958	2	2133.2728
3540	Q810R5_MOUSE	202	9.9	1	17	R.VALEEHPTLLTEAPLNPK.A	0.9946	2	1973.2768
3541	Q811T7_MOUSE	621	9.66	2	2	K.AFVGTLVVLPLSLIVLTMLALR.Y	0.9958	2	2341.0001
						R.CLSIFFTYLLFLQLWEVNSDKVWVLGPEES	0.9958	3	4088.7449
3542	Q85ZW7_MOUSE	330	15.45	2	2	R.FVHIGYVDSIEYQR.Y	0.9924	1	1726.9292
						K.WEPPHTIPIIAILIGLVLGTLVVGTVVIFLVWK	0.9958	3	3609.5059
3543	Q8BFX2_MOUSE	798	3.26	2	2	R.LQEMILPGSR.S	0.9958	1	1144.3746

						R.CQITAQSFAEIK.F	0.9944		1	1396.5493
3544	Q8BFX6_MOUSE	328	7.32	1	2	R.DLKPQNLLISDTGELKLADFGR.K	0.9904		2	2444.7905
3545	Q8BFX7_MOUSE	135	35.56	2	2	K.NYWLVTVLHDR.Q	0.9947		2	1416.6225
						K.VGQGCATPLSLFCDDGDVKFVLDSAFLEG	0.9958		3	3570.8666
3546	Q8BFX8_MOUSE	397	9.82	1	3	K.FQRGSSEPDIEIQSGGGTELSVFAKPSSPM	0.9958		3	3779.1731
3547	Q8BG11_MOUSE	714	2.66	1	8	R.MTAFDADDPATDNALLR.Y	0.9958		2	1837.999
3548	Q8BG37_MOUSE	224	5.8	1	2	K.LPFPIIDDKDR.D	0.993		2	1329.5388
3549	Q8BG77_MOUSE	132	14.39	2	2	R.KWTPVNTGDSSAIAINK.I	0.9958		2	1803.0251
						K.WTPVNTGDSSAIAINK.I	0.9917		2	1674.851
3550	Q8BG87_MOUSE	719	3.89	1	4	R.LEDAHDLVAFSAVAEAVSSYGALSTR.L	0.9958		3	2680.9311
3551	Q8BGB4_MOUSE	413	29.78	6	45	R.EGDAVQLLCQGDGSPSPEYSFFR.Q	0.9958		2	2560.7021
						R.LASVEPQGSEFLGTVHSLGR.V	0.9958		2	2085.3244
						R.GRLVIAK.V	0.9958		1	756.9669
						R.EHPEHYVLEWFLVDGTGAR.H	0.9958		2	2256.482
						R.DANFHCAAHYDLPSGQHGR.L	0.9958		2	2154.2316
						R.LTLHYPTEHVEFWVGSPSTTEGWVR.E	0.9958		2	2930.2487
3552	Q8BGD4_MOUSE	722	15.1	4	5	K.CENEPFAGVSESYNGTGEMGNLTAPCNAN	0.9931		3	3795.8914
						K.TSQTHQNNSTSFQHTDENFGKSIK.D	0.9944		3	2737.8589
						K.GACWIYDNIK.M	0.9958		1	1240.3673
						K.STEPSPPSSNPPASDEPPGSQLSELEEGP	0.9958		3	3480.6026
3553	Q8BH99_MOUSE	313	19.49	2	4	K.LAAVVNNLNTGQVLHVVQALYPFSSSNDE	0.9944		3	3862.2878
						K.RKPSVPDTASPADDSFVDPGER.L	0.9911		2	2344.4997
3554	Q8BI41_MOUSE	618	5.99	2	2	R.FFESAQRPLWGPLFTETVLR.S	0.9945		2	2395.7661
						R.HVDSILQNFQYKK.L	0.9915		2	1620.8485
3555	Q8BIA1_MOUSE	869	5.98	2	2	R.ALAFNTLQALMLDFPDWR.E	0.9958		2	2123.4773
						R.SLQRGEDLQFDQLVSSMSSVAEHCLPSLL	0.9958		3	3404.7859
3556	Q8BIR5_MOUSE	505	6.73	2	2	K.EVSSLQQTVTLLQK.D	0.9958		2	1574.8149
						K.EILHNIQLLKIELSQK.N	0.9958		2	1920.303
3557	Q8BIV6_MOUSE	316	30.7	4	43	K.YTFLDAWEAMEELVDQGLVK.A	0.9958		2	2358.668
						K.GITITAYSPLGSPDRPSAKPEDPLLLEIPK.I	0.9958	2,3		3177.6653
						R.ACGLFAASHNEDFPFHAEY.-	0.9958		2	2184.2947
						R.HIDCAYVYQNESEVGEAIQEK.I	0.9958		2	2483.6166
3558	Q8BIW9_MOUSE	969	4.44	2	2	R.LRDSSLSTVCCALDWLAFDDLLEQAAHR.G	0.9958		3	3264.5513
						K.QLIAREIEMEK.M	0.9935		1	1360.6116
3559	Q8BJS7_MOUSE	891	5.39	3	7	K.TPSARVEITIEPQR.N	0.9958		2	1597.8118
						R.SLPAPDSSTGVEHVQK.G	0.9924		2	1652.8015
						R.NEPEDLDDIFPETK.L	0.9943		2	1662.7473

3560	Q8BK86_MOUSE	218	25.69	3	4	R.VSYTQGQSPEPR.T	0.9958	1,2	1349.4429
						R.EYFYYVDHQGQLFLDDSK.M	0.9958	2	2268.4437
						R.CEDRPVVFTHLLASDSESPR.L	0.9958	2	2316.4986
3561	Q8BKB2_MOUSE	644	8.23	3	3	R.ILQRELQNVQVNQK.V	0.9923	2	1710.9743
						K.SWGEQCTETPDTNSGR.R	0.9958	2	1825.809
						R.GIHSVGGQGSWTPEVIK.R	0.9958	2	1752.9676
3562	Q8BLH5_MOUSE	439	11.85	2	3	K.SEAPPIFLQVSYYRPWIWDRLSGEPLALPA	0.9944	3	3814.3812
						R.YWSWVGRAHDIGLLK.L	0.9937	2	1802.0885
3563	Q8BLK2_MOUSE	205	11.71	2	2	R.TAAAAAASSAPR.R	0.9958	1	1045.1405
						R.QGRAQAPK.A	0.9958	1	855.9724
3564	Q8BLV6_MOUSE	499	4.41	1	3	K.LVYQAASKHMTPVVLELGGK.S	0.9945	2	2142.5646
3565	Q8BN84_MOUSE	532	4.32	1	2	K.LDSASAALISNGPGGSVCFWK.L	0.9944	2	2138.3508
3566	Q8BNC0_MOUSE	163	17.18	1	2	K.VESLISQPMTSGKNELQDHLIFISEK.A	0.9931	3	2945.3576
3567	Q8BP77_MOUSE	482	12.45	3	3	K.KGLIDYDTFK.E	0.9909	2	1200.377
						R.SSSLSDPLEESSPIAAIFDTENLEK.I	0.9957	2	2680.8793
						R.LLEAQACTGGIIHPTTGQK.L	0.9956	2	1996.2371
3568	Q8BP96_MOUSE	878	4.9	2	2	K.VPSVSSSALVSSLHLLK.C	0.9958	2	1725.0385
						R.QEIFQEQLAAVPEFQGLGPLFK.S	0.9958	2	2490.8614
3569	Q8BPV9_MOUSE	530	3.02	1	3	R.SRFQAALSTSSSHR.C	0.9958	1	1535.6597
3570	Q8BPY7_MOUSE	132	17.42	2	7	R.DELGLGEGGRVGLK.L	0.9948	2	1400.5748
						K.APSFLSRDELGLGEGGR.V	0.9958	3	1761.9322
3571	Q8BQ66_MOUSE	276	18.12	2	2	R.GRGGGGSGGPGLGAGPPEECLLGGR.G	0.9944	2	2223.3763
						R.AGATGGDGAGRGGGAAATADR.R	0.9944	1	1717.7525
3572	Q8BQA2_MOUSE	288	6.94	1	5	R.VSEFLKVAEVSGPSFVAK.A	0.9925	2	1895.2059
3573	Q8BQH2_MOUSE	121	8.26	1	2	R.QCLPALRR.A	0.9958	1	1014.1821
3574	Q8BRB0_MOUSE	625	2.4	1	2	R.STVVRGFIDALTR.G	0.9958	2	1435.6664
3575	Q8BRB8_MOUSE	520	61.92	14	111	R.LPSGSGPASPTTGSAVDIR.A	0.9958	2	1770.9371
						R.ELLLPNWQGSGSHGLTIAQR.D	0.9958	2	2178.4557
						R.AGAISASGPELEGAGHSK.F	0.9958	2	1639.7624
						K.GEGIGLDVALPTGEVTLPGVSGDVSLPEIA	0.9958	2	3506.9293
						R.SPEPGQTWTHEVFSSR.S	0.9958	2	1845.9658
						K.FGVSAGLDGQIPEVGLSVSAPESSVGHK.G	0.9958	3	2726.0153
						K.GPQITGPSLEGDLGLK.G	0.9958	2	1582.7942
						K.GDKPGLAIGGNIQAPHLEVNPSSVNIEGLE	0.9958	3	3212.5871
						R.VPGVDVSSSLGAGSVEVQAPSLQSGDIGK	0.9949	2	2742.0123
						K.EGDQIVGATIYFDNLQSGEVTQLLNTMGH	0.9958	3	3788.2238
						R.DDGVFVQEVMQNSPAAR.T	0.9944	2	1864.0399

						K.LKGPQITGPSLEGDLGLK.G	0.9958		2	1824.1277
						K.IEGSITGPSVEIGTPDVDVHGLGGK.L	0.9958		2	2435.6934
						K.TPEMIIQKPK.I	0.9958		2	1185.4675
3576	Q8BRN0_MOUSE	930	3.76	2	6	R.SESGLVNPGALKK.L	0.9923		2	1300.4979
						K.EGSSQHPPLNPDCVSHAR.G	0.9958		2	1989.0777
3577	Q8BS04_MOUSE	1291	5.27	2	2	K.LPTRVDDMPPGISLLPDNILQVLR.I	0.9958		3	2674.1742
						K.GGTHEEIQSIIGYIAATNEEEQLFGILDILFSL	0.9944		3	4434.9903
3578	Q8BTF0_MOUSE	1224	4.74	3	8	R.GVNWAAFHPTMPLIVSGADDR.Q	0.9956		2	2255.556
						R.LLELGPKPEVAQQTR.K	0.9958		2	1679.9572
						R.MCTLIDKFDEHDGPVR.G	0.9952		2	1934.1402
3579	Q8BU53_MOUSE	180	6.67	1	7	R.TSDPLVLELR.M	0.9958		2	1143.3256
3580	Q8BU85_MOUSE	186	41.94	4	8	K.SETKFDSGSGWPAFHDVISSEAIEFTDDFS	0.9944		3	3955.2166
						R.VETSCSQCGAHLGHIFDDGPRPTGK.R	0.9958	2,3		2727.8823
						K.GTESAFEGEYTHHK.D	0.9958		2	1593.6494
						K.FDSGSGWPAFHDVISSEAIEFTDDFSYGMH	0.9958		3	3509.7437
3581	Q8BVQ9_MOUSE	475	33.47	11	37	K.ESDTGLAPPALWDLAADK.Q	0.9958		2	1871.0539
						R.KIEFSLPDLEGR.T	0.9958		2	1404.606
						K.FVVDLSDQVAPTDIEEGMR.V	0.9958		2	2122.3545
						K.KINELTGIK.E	0.9958		1	1016.226
						R.EVVETPLLHPER.F	0.9958		2	1419.6207
						K.ACLIFFDEIDAIGGAR.F	0.9958		2	1768.9733
						K.GVLLFGPPGTGK.T	0.9958		2	1143.3714
						R.ALDEGDIALLK.T	0.9958		1	1158.3373
						K.QTLQSEQPLQVAR.C	0.9958		2	1498.6793
						K.QVEDDIQQLLK.K	0.9958		2	1329.493
						K.YQIHIPLPPK.I	0.9958		2	1206.4734
3582	Q8BVZ1_MOUSE	463	15.55	4	17	R.SLTLELQNAVDALAGCVR.G	0.9958		2	1931.1626
						K.LPFLQQPSDMVVTSAK.D	0.993		2	1762.0741
						R.TQEMLAQLQETLELIQHMQR.G	0.9909		2	2441.8231
						R.HLAYEHSLGK.L	0.9958		1	1155.2987
3583	Q8BXG9_MOUSE	115	10.43	1	2	K.IIIIIIIIIR.R	0.9927		1	1193.6457
3584	Q8BXI0_MOUSE	344	5.52	1	3	R.FPSNLEVEASPQAPSKK.E	0.9958		2	1830.0477
3585	Q8BYM1_MOUSE	145	11.72	1	2	K.MGSNVGIYTTEALER.T	0.9924		1	1641.8365
3586	Q8BZG3_MOUSE	219	4.57	1	5	R.LGGDAALR.G	0.9958		1	772.8796
3587	Q8BZY1_MOUSE	578	2.6	1	2	R.QASGEQESSLAKK.K	0.9958		1	1363.4673
3588	Q8C004_MOUSE	222	7.66	1	6	R.FPLKTDESGACIINR.D	0.99		2	1721.9171
3589	Q8C0E5_MOUSE	555	9.73	2	4	K.EHVPTWLQNTHVYSWPK.N	0.9911		2	2123.3781

						R.LPRDQLYRPPSNGVEAPEESLDLPAELRPH	0.9958		3	3680.1148
3590	Q8C0S0_MOUSE	470	2.98	1	2	K.EAKDALTHQGQK.W	0.9958		1	1326.452
3591	Q8C0T4_MOUSE	737	4.07	2	7	R.EDGNVDIWDLLEK.T	0.9925		2	1546.6739
						R.EQEKIDMALELVK.K	0.9924		2	1546.8194
3592	Q8C170_MOUSE	692	3.18	1	4	K.EFRQNIFSSYSSALAMDDGK.S	0.9943		2	2267.4749
3593	Q8C1P4_MOUSE	151	13.91	1	4	R.VGKGEHAILLLPGMLGSGK.N	0.9958		2	1878.2835
3594	Q8C1Q6_MOUSE	129	10.85	1	2	R.RLEDTSETNLHK.L	0.9956		2	1443.5565
3595	Q8C231_MOUSE	326	4.6	1	2	K.LEFMLVAHGPVCK.I	0.9917		2	1501.7932
3596	Q8C2C6_MOUSE	348	18.68	3	18	K.NVMSAFGLTDDQVSGPPSAPTEDR.S	0.9958		2	2492.6765
						R.IPIHNEDITYDELVLMMQR.V	0.9958		2	2331.7071
						R.NRPPFGQGYAQPGPGYR.-	0.9958		2	1863.0451
3597	Q8C346_MOUSE	102	26.47	1	3	R.AGCCSAGTTNTPPCPDLFLSIWSWR.S	0.993		2	2856.0621
3598	Q8C372_MOUSE	230	14.35	1	3	R.WLVPAALASSRLSGLGAAAPAGANPCPSA	0.9915		2	3077.482
3599	Q8C397_MOUSE	418	8.85	1	2	R.GIDAFSTCLWALLLGLHLAEHYLQAASPGW	0.9958		3	3883.448
3600	Q8C3I9_MOUSE	435	14.71	2	6	K.QSLVLVCQQLLPQLLQGKFPSPVQK.E	0.9911		3	2850.3837
						R.VLESLRSNDLNYFFYFTHVDAGMFGIFDNG	0.9944		3	4157.6948
3601	Q8C4P2_MOUSE	131	25.95	1	3	R.KQGWLAVESVDQGGGSEVHCESDEGGGI	0.9944		3	3435.6135
3602	Q8C4S9_MOUSE	385	9.35	2	11	R.HYLSFEGVGFGTPSQR.E	0.9944		2	1782.953
						K.FSGCSYIDPMTHNLNR.I	0.9958		2	1913.0809
3603	Q8C622_MOUSE	145	11.72	1	3	K.ATGIMNSFVNDIFER.I	0.9943		2	1714.9336
3604	Q8C695_MOUSE	717	8.93	3	6	R.GQVIGFISQEPVLFATTIMENIR.F	0.9958		2	2565.0026
						R.ASAGRTVLVIAHR.L	0.9958		1	1351.5949
						R.EANAHEFISSFPDGYSTVVGER.G	0.9958		2	2413.5621
3605	Q8C6Y1_MOUSE	197	8.63	1	2	K.DCQVAPLTHVFQRQK.S	0.9958		2	1828.0471
3606	Q8C7C3_MOUSE	248	13.31	3	7	K.IQVLQQQADDAEER.A	0.9958		2	1643.7508
						R.AREQAEAEVASLNR.R	0.9958		1	1544.6646
						R.KIQVLQQQADDAEER.A	0.9958		2	1771.9249
3607	Q8C7P0_MOUSE	207	9.18	1	9	R.HSAGVAEVQEQLQHVGR.H	0.9944		2	1846.0127
3608	Q8C7X4_MOUSE	226	9.29	1	2	K.DSKLGGDVNGPGQTNAGIR.S	0.9958		2	1856.9902
3609	Q8C815_MOUSE	640	3.91	1	4	K.NYPHSQHLPSSAAPNLTHLVHRR.H	0.9915		2	2633.9351
3610	Q8C845_MOUSE	240	7.92	1	3	K.AAAGELQEDSGLHVLAR.L	0.9958		2	1737.9102
3611	Q8C8M3_MOUSE	755	4.77	2	3	R.FSLENNFLLQHNIR.K	0.9958		2	1745.9786
						K.FLEQVHQLYDDSFPMEIR.Q	0.9958		2	2268.5488
3612	Q8C8P7_MOUSE	189	16.93	1	97	R.LAAPGTIGLLRSGLLGLAPCPSQAPGPPPK	0.9945	2,3		2908.4234
3613	Q8C8R0_MOUSE	568	2.82	1	3	R.SVRPSLFLSLRSAR.S	0.9958		1	1589.8814
3614	Q8C8Y2_MOUSE	1290	2.87	2	6	K.GPLLIWTISGPDSGVSVHK.E	0.9958		2	1964.2719
						R.QVGLLAAGCQPWNK.D	0.9958		2	1542.7441

3615	Q8C8Y3_MOUSE	163	6.75	1	2	R.VSPAALPER.R	0.9958		1	940.0873
3616	Q8C9M4_MOUSE	190	12.11	1	2	R.EVQDVTSGKDHIEFHNVVELK.R	0.9937		2	2424.6726
3617	Q8C9P2_MOUSE	377	9.28	2	3	K.SIEELLEQTTHPDGLPLLR.H	0.9958		2	2162.4478
						K.QFSLVRPERGTK.I	0.9958		1	1418.6389
3618	Q8CA16_MOUSE	114	15.79	1	4	R.GATSATQGVQNQEDLK.L	0.9958		2	1647.7392
3619	Q8CB35_MOUSE	509	9.04	2	2	K.IIQTSNSSLSGQPLKPSVR.N	0.9924		2	2013.3017
						K.CLTPALQIPVTVALPTPVTTSPK.I	0.9958		3	2405.8469
3620	Q8CBJ7_MOUSE	214	7.48	1	2	K.GQLGQAGSFLWARK.Y	0.9958	1,2		1519.7464
3621	Q8CC72_MOUSE	171	4.68	1	2	R.ESYIKK.S	0.9924		1	767.9005
3622	Q8CDH8_MOUSE	345	21.74	3	5	R.LDAGHPVYQVSEVEK.D	0.9958		1	1671.8473
						K.TMHEHSQFCMSGDHTLEGTEHAIK.D	0.9958		2	2785.001
						R.FAQILTSDPQVNAFAIFIGSLGDQAARLQR.	0.9958		3	3249.697
3623	Q8CDI4_MOUSE	311	20.9	3	4	R.RMGFIPLPLAVLLIR.V	0.9958		1	1710.2206
						K.SQSKGKPSQGLSTEENLSASVTSQPGHQK	0.9958		3	2999.2211
						K.FEKNNLFQMSNSDIK.E	0.9958		1	1816.0387
3624	Q8CDI7_MOUSE	1110	4.68	3	4	K.KNAAVIEEELK.T	0.9924		1	1244.4307
						K.ELLESTIARLQGELK.A	0.9958		2	1700.9731
						K.LKEASVESEQITANLEEAHR.W	0.9952		2	2255.4466
3625	Q8CDQ7_MOUSE	368	2.99	1	2	K.GCVASGYMK.Q	0.9958		1	973.098
3626	Q8CDS5_MOUSE	1154	3.99	3	4	K.YLLCTSENYKDK.I	0.9958		2	1534.6722
						K.KYFNALAEIFITHQVPSR.I	0.9958		2	2135.4734
						K.YSDAVPAQLK.V	0.9944		1	1092.2371
3627	Q8CDW0_MOUSE	644	4.66	1	5	K.IQHWDLVEGEGAVGVAGASDRAIDNMAK.I	0.991		3	2911.2188
3628	Q8CE68_MOUSE	320	17.81	4	13	K.LFHVSEDPSDPNEK.H	0.9958		2	1614.7087
						K.LLGPLGMK.T	0.9958		1	829.0887
						K.DEGFNITAGIDEETGFVYGGNR.F	0.9958		2	2362.4711
						K.HPNLVHK.R	0.9944		1	844.992
3629	Q8CEQ3_MOUSE	186	12.37	2	2	R.AEEQLGNQLVALQVLGR.G	0.9927		2	1839.102
						R.AEEQLGNQLVALQVLGRGCGR.S	0.9944		2	2269.5321
3630	Q8CER0_MOUSE	246	4.07	1	3	R.MPSLPPLK.L	0.9958		1	883.137
3631	Q8CET2_MOUSE	560	1.79	1	2	K.YFEIEDEK.A	0.9958		1	1073.1443
3632	Q8CEW7_MOUSE	583	7.2	2	2	R.YINDGDFK.D	0.9958		1	972.0422
						K.SICGVCTDGAPATLGCQSGFQRLVLNESPI	0.9958		3	3224.4934
3633	Q8CEY2_MOUSE	272	18.01	2	4	R.KDSPTTATLWWQPSSSTTQK.T	0.9944		2	2251.4576
						R.KDTEPLQVEYYPPMAPSVSTISPTMAR.K	0.9911		3	3010.4469
3634	Q8CFS0_MOUSE	556	5.58	2	2	R.GISHASSSIVSLAR.S	0.9958		2	1385.5632
						R.ADSVANKLGSFGK.T	0.9924		1	1294.4502

3635	Q8CFX3_MOUSE	1038	4.24	3	8	K.YFLQTTTPLDYEK.V	0.9958	2	1619.8114
						R.GNILFGVVAGVVAVALLIALAVLVR.Y	0.9958	3	2449.0849
						K.QRGNILFGVVAGVVAVALLIALAVLVR.Y	0.9958	2	2733.4031
3636	Q8CGG8_MOUSE	1477	1.35	2	2	K.YILNIK.R	0.9924	1	763.9554
						K.QGFFPDSVNK.A	0.9944	2	1139.2529
3637	Q8CGI6_MOUSE	523	11.09	3	5	K.EKVNEFLAFEGPILLDMR.I	0.9944	2	2122.4871
						R.QLSLLTK.T	0.9924	1	802.9896
						K.LIEEISEVDCKDALEMICNLESEGDEK.S	0.9944	3	3170.3959
3638	Q8CGY9_MOUSE	1356	1.25	1	6	R.KMPASPSXESVLESR.V	0.9958	2	1631.8847
3639	Q8CHD0_MOUSE	1481	1.69	2	2	R.YSSSSGGSYEEEK.S	0.9944	1	1410.3905
						R.DKEFNEPR.V	0.9958	1	1035.1014
3640	Q8CHD7_MOUSE	966	2.28	1	3	K.EQSELVAQALKAELVPYLLK.L	0.9958	2	2243.6488
3641	Q8CHT6_MOUSE	337	6.23	1	6	K.ILGLVNPQDTKTVVAVYLK.E	0.9958	2	2072.4961
3642	Q8CHU6_MOUSE	493	2.23	1	2	K.QEKENIINK.L	0.9958	1	1116.2596
3643	Q8CIF8_MOUSE	198	11.11	1	8	R.HRDDTTPSAAPAPQGLEHGK.R	0.9958	2	2086.2284
3644	Q8CIJ3_MOUSE	970	8.35	4	29	K.GYIFLEYASPAHAVDAVK.N	0.9958	2	1952.2169
						R.FSHQGVQLIDFSPCER.Y	0.9958	2	1921.0857
						K.DRPQEADGIDSVIVVDNVPQVGPDR.L	0.9958	2	2691.9145
						R.GFHCESSAHWPIFK.W	0.9958	2	1703.8633
3645	Q8JZY9_MOUSE	80	27.5	1	2	R.HCLLKPFVQLGTLVYPVFLK.E	0.9929	2	2373.8963
3646	Q8K0A8_MOUSE	860	3.02	2	2	R.YSVGLLDMTKQK.E	0.9944	1	1383.6459
						K.FLDSNIGFAK.Q	0.9958	1	1112.2707
3647	Q8K0Y2_MOUSE	404	3.47	1	10	R.QNQEYQVLLDIR.S	0.9958	2	1519.6976
3648	Q8K119_MOUSE	917	3.93	2	11	R.TQFLTENPKTGLEDATEQIK.A	0.9958	2	2264.4943
						K.ITEIPFSMENLK.A	0.9958	2	1422.6795
3649	Q8K159_MOUSE	911	13.06	6	40	R.FAHYVITSQVVNNADK.A	0.9958	2	1807.0159
						K.LCDLLVANNYFTHFFAPK.N	0.9958	2	2171.4693
						K.AQGSHPELSSPASILIMLTDGEPTEGETDR.	0.9958	2,3	3140.4028
						K.GSLVPVSNANLQAAQDFVR.R	0.9958	2	1987.2229
						R.FSLAGATNLNGGLLR.G	0.9958	2	1504.7293
						R.GHVLENHVER.L	0.9958	2	1190.3041
3650	Q8K205_MOUSE	1045	5.07	2	2	R.AGVLFAEDQAKDLLEK.Y	0.9924	1	1747.986
						R.SLHQRQEAVFELLGGISSPAEIPAGTILGLT	0.9958	3	3461.9865
3651	Q8K2E1_MOUSE	587	10.73	3	5	K.HNVEVLGILSDDVETDSVAPGENLK.I	0.9958	2	2651.8871
						K.GIEEEEILPGFILCDLNNLCHSGR.T	0.9943	2	2787.0309
						K.HLIVLINK.M	0.9958	1	950.2125
3652	Q8K2J1_MOUSE	344	10.47	2	2	R.LVYISFRQGIILSVALAGVLGISIVLAVSIWLF	0.9958	2	3661.5388

						R.QGIILSVALAGVLGISIVLAVSIWLFK.R	0.9958		3	2782.4692
3653	Q8K2R3_MOUSE	995	1.81	1	4	K.ALNALNNISVAAENHR.T	0.9952		2	1707.8869
3654	Q8K354_MOUSE	277	11.19	2	3	R.FHQLDIDDPQSIR.A	0.9949		2	1584.7288
						R.CDTLTEVDLVDLMK.K	0.991		2	1652.8635
3655	Q8K486_MOUSE	956	0.94	1	6	K.YPELILK.R	0.9942		1	876.0837
3656	Q8K4A2_MOUSE	871	5.86	2	2	R.TARALLEDDSDTQQVVVLVR.D	0.9926		2	2229.4954
						R.SCPVHLRGVCSCTLFLFVPSWHTCWMR.L	0.9911		3	3395.8137
3657	Q8QZV3_MOUSE	289	5.88	1	157	R.ALQLGTLFSPAEALK.V	0.9958	1,2		1559.8461
3658	Q8R0S9_MOUSE	554	3.43	2	4	R.IASINGK.K	0.9958		1	702.8289
						R.TIIFILGK.G	0.9958		1	905.1686
3659	Q8R142_MOUSE	330	16.36	2	2	K.EDWLLLQASR.R	0.9958		1	1231.394
						K.LELQVLGPQSSAPVWFHILFYLSVGIMFLVN	0.9931		3	4630.5805
3660	Q8R172_MOUSE	380	2.63	1	3	K.LLLQNILK.R	0.9958		1	955.2291
3661	Q8R1A5_MOUSE	1150	3.04	1	3	R.VYFEEALGALEGSFVDLSLVAAVYSSLTTV	0.9958		3	3557.0748
3662	Q8R256_MOUSE	316	12.66	1	2	K.HFGNHNSGSFFSLLLTHDLFYVAVMVWAS	0.9944		3	4498.2649
3663	Q8R287_MOUSE	306	4.9	1	4	R.QVKHIHSAQQLLK.V	0.9924		1	1530.8136
3664	Q8R291_MOUSE	324	7.1	1	13	K.GIPQTLSDYGLKDFLDDFGCK.L	0.9958		2	2390.6179
3665	Q8R2A8_MOUSE	298	14.77	2	6	K.IDMILIHVFTSNFLTILSK.G	0.9929		2	2206.6917
						R.SMSISTTCFLSVFQAITISPR.N	0.9958		2	2347.6979
3666	Q8R2C1_MOUSE	303	10.23	1	3	R.CLSICTTCLLSVFQAVTISPSTSCLAKFK.Q	0.9958		3	3294.7178
3667	Q8R2K3_MOUSE	148	13.51	1	24	R.QATTIIADNIIFLSDQTK.E	0.9958		2	1993.2646
3668	Q8R2U2_MOUSE	564	1.6	1	2	K.YSQSKLK.T	0.9944		1	853.9939
3669	Q8R3A5_MOUSE	364	5.49	1	2	K.LVGDTNIHNSEPPLLGFK.D	0.9958		2	1952.2175
3670	Q8R4B3_MOUSE	915	7.43	2	4	R.YAIATKDNGDEVVSTLK.L	0.9958		2	1825.0257
						R.ITGLTISDLRTEDSGTYICEVTNTFGSAEAN	0.9944		3	5036.6081
3671	Q8R5L0_MOUSE	155	8.39	1	2	K.SLKDIQENAIK.M	0.9924		1	1259.4453
3672	Q8R5L1_MOUSE	279	7.89	1	17	K.AEEQEPELTSTPNFVVEVTK.T	0.9958		2	2248.4485
3673	Q8VC96_MOUSE	700	24.57	9	54	K.SSPFQLFGSPHGEDLLFTDAAHGLLR.V	0.9958		2	2814.1295
						R.RPVEEYEQCYLAR.V	0.9958		2	1713.8535
						R.ILFNQQELFGR.N	0.9958		2	1365.5748
						K.HPTVLQNTDGK.N	0.9958		2	1210.3323
						K.CVNAPLEGYYVVAVVK.K	0.9958		2	1782.0558
						K.HEDFELLCLDGTR.K	0.9958		2	1605.7106
						R.KPVTEAQSCHLAR.V	0.9958		2	1497.6604
						K.HLTVFEAMPTK.A	0.9958		2	1274.5206
						R.SCAPGSDPDSPLCALCVGGNNPAHMCAAI	0.9958		3	4302.4563
3674	Q8VCG1_MOUSE	200	32.5	3	4	R.IAQLICERISYPDLEEVQTLDDTER.G	0.9958		3	3008.2751

						R.AAGYDLFSAYDYTISPMEK.A	0.9957		2	2143.3723
						K.HFIDVGAGVIDEDYR.G	0.9958		2	1706.8522
3675	Q8VCL2_MOUSE	255	25.49	3	3	R.VYYSAGPKDEDQDYIVDHSIAIYLLNPDGLF	0.9944		3	4288.6698
						R.LLGLTGSTEQVAHASR.N	0.9958		2	1640.8369
						R.YVQEFHPR.L	0.9958		1	1076.1997
3676	Q8VCQ8_MOUSE	530	6.42	2	2	K.ASKPMKPAASDLPVPAEGVR.N	0.9958		2	2022.3703
						R.STHQAAVVSK.I	0.9958		2	1028.1533
3677	Q8VCX0_MOUSE	500	7.8	2	8	R.NLGLGK.K	0.9924		1	601.7239
						K.ENMGENTGLFPEVLNTFPILLHIPGLADK.V	0.9944		3	3181.674
3678	Q8VD75_MOUSE	906	4.86	3	3	K.FEELMVCSR.E	0.9924		1	1171.3198
						R.LIQIPQLPENPPNFLR.A	0.9958		2	1890.2358
						R.AGDTGVKLEVNER.I	0.9958		1	1388.5205
3679	Q8VES6_MOUSE	316	10.13	1	2	K.SSHTPDTDKVTALMYTVVTPALNPVIYTLR.	0.9958		3	3305.8139
3680	Q8VF07_MOUSE	330	11.82	1	2	K.LSCTDTRINSAVGLTALISTAGVDSVFIILSY'	0.9958		3	3954.6062
3681	Q8VFC7_MOUSE	318	10.06	2	3	K.ILSVFYTIFTPIMNPVIYTLRNHEVNSAMR.K	0.9944		3	3542.1945
						R.NHEVNSAMR.K	0.9944		1	1058.1571
3682	Q8VFS5_MOUSE	310	21.29	2	2	R.TISFIPCIMQTFLYLAFASIECLILVVMSYDR.	0.9958		3	3817.5089
						K.SQHPEMQQKILSLFYSLFNPMLNPLIYCLR.	0.9958		3	3683.3303
3683	Q8VG54_MOUSE	310	14.19	2	2	K.MLMSFISEKNIISYR.G	0.9944		2	1833.2141
						R.GCMAQLFFFSFFCISECYVLTVMAYDR.Y	0.9958		3	3364.7962
3684	Q8VG95_MOUSE	312	2.24	1	6	K.NIFMSK.-	0.9958		1	739.9079
3685	Q8VGT3_MOUSE	311	11.58	1	3	K.VFSTCGSHLTVVSLFYGTIIGLYLCPSANNF	0.9944		3	3740.2227
3686	Q8VGU3_MOUSE	323	7.43	1	2	R.NGSLSAVSLQGFVLVGFGGGAK.T	0.991		2	2066.3647
3687	Q8VGZ5_MOUSE	316	6.33	1	3	R.FVAICDPLRYTTILTNAR.I	0.9958		2	2125.4418
3688	Q8VHQ0_MOUSE	385	3.38	1	4	K.QGLFLSNVIHK.S	0.9931		2	1256.4905
3689	Q8VIC1_MOUSE	319	10.66	2	2	R.SISIGSTCLLSIFQAIIISHR.E	0.9958		3	2317.7002
						K.LSLTWIRNK.T	0.9945		2	1131.3634
3690	Q8VIE5_MOUSE	2561	3.08	4	5	R.QLFEASK.A	0.9958		1	822.9365
						K.WVNSHLARVGCHIGDLYADLR.D	0.9929		2	2453.7319
						K.LELLAQRFDHK.V	0.9952		2	1370.5943
						R.LLEATSGSGGAAGTAGGAHDLSSTARLLA(	0.9958		3	3007.2901
3691	Q91VA7_MOUSE	384	50.78	17	759	R.HNNLDLVIIR.E	0.9911		2	1207.4184
						R.HLNLEYHSSMIADAVK.K	0.9958		2	1829.0808
						R.KLDLFANVVHVK.S	0.9958		2	1383.6768
						R.NIANPTAMLLSATNMLR.H	0.9958	1,2		1832.1865
						R.VEGAFPVTMLPGDGVGPELMHAVK.E	0.9958		3	2452.8891
						R.HPFAQAVGR.N	0.9958		1	983.1178

						K.GELASYDMQLR.R	0.9958		2	1283.4418
						K.EHHLSEVQNMASEEK.L	0.9958		2	1768.8957
						K.EHHLSEVQNMASEEKLEQVLSSMK.E	0.9958		2	2785.1164
						K.LEQVLSSMK.E	0.9958		1	1035.2439
						R.EQTEGEYSSLEHESAK.G	0.9958	1,2		1824.8523
						K.LDLFANVVHVK.S	0.9958	1,2		1255.5027
						K.LGDGLFLQCCEEVAELYPK.I	0.9958		2	2242.4628
						K.AAAVPVEFK.E	0.9924		1	932.1075
						K.SVIGHLHPHGG.-	0.9958		1	1111.2485
						K.TRHNNLDLVIIR.E	0.9924	2,3		1464.7109
						R.HLNLEYHSSMIADAVKK.V	0.9958		2	1957.2549
3692	Q91VJ2_MOUSE	260	20.38	2	3	K.VPELLGPEDQLVLGPDQPEDEVGESSEEE	0.9958		3	3705.919
						R.SHDTTSNTLTQLLAK.A	0.9958		2	1630.7954
3693	Q91VK2_MOUSE	276	14.13	1	11	K.VMLPNSPEALGQATPGTSSGPGASSGPG(	0.9958		3	3532.8639
3694	Q91VU7_MOUSE	660	1.97	1	2	K.DTMDAINVLSK.Y	0.9958		1	1207.3844
3695	Q91W85_MOUSE	412	16.99	3	65	K.LAASEAATAISHQAIQILGGMGYVTEMPAEI	0.9958		2	3188.6411
						K.MGELGLLAMDVPEELSGAGLDYLAYSIALE	0.9958		2	3628.144
						K.KMGELGLLAMDVPEELSGAGLDYLAYSIAL	0.9944		3	3756.3181
3696	Q91W94_MOUSE	390	11.28	2	2	K.QIHSEEKPYKCEVCGMAFHFPSLLLVHK.R	0.9958		3	3386.8685
						K.RGGAPFMLPGGK.C	0.9958		2	1188.4332
3697	Q91WP8_MOUSE	469	21.75	4	43	K.NSPPPSSYPSVENTGGAVAGPHPGGSLLP	0.9924		3	3485.7887
						R.VPTQPTSGPVPTTQIQEASAEHPPAVAPR.	0.9958		3	2965.2926
						R.SKPVTSRPQSSEMLEQNVK.E	0.9958		2	2146.4235
						K.LLTAHTAAALSK.N	0.9958		2	1197.4203
3698	Q91X22_MOUSE	413	4.6	1	6	K.EPFDPENTEEAEFHVDK.S	0.9958		2	2034.0997
3699	Q91XF8_MOUSE	395	5.06	1	15	K.LVPFVVQLSGHLAQETER.V	0.9958		2	2024.3274
3700	Q91XH4_MOUSE	265	7.17	2	2	K.VSILIGASQDLIPQLK.K	0.9946		2	1696.0403
						K.VSILIGASQDLIPQLKK.K	0.9924		1	1824.2144
3701	Q91XH5_MOUSE	262	53.05	9	67	R.VLSYAPGPLDNDMQQLAR.E	0.9958		2	1989.2537
						R.LLSPGSVMLVSAR.S	0.9958	1,2		1330.6287
						K.LLGLLQK.D	0.9958		1	785.0177
						K.TVVNISSLCALQPYK.G	0.9958		2	1693.947
						R.DMLYQVLAAEEPSVR.V	0.9912		2	1721.966
						K.VVLAAADLGTEAGVQR.L	0.9949		2	1570.7862
						R.LLLINNAATLGDVSK.G	0.9958		2	1542.8161
						K.SDGALVDCGTSAQK.L	0.9958		1	1409.4589
						R.QLKEELGAQQPDLK.V	0.9958		2	1597.8088

3702	Q91XW2_MOUSE	2556	4.3	4	5	R.LVGVLVHSGQANGGHYYSYIIQR.N	0.9944	3	2532.8643
						K.LEGDSVNPQTQLIK.Q	0.9958	1	1542.7294
						R.NSILAIDSIWSDTDDDIFKGEK.Q	0.9921	2	2483.6911
						R.MQSSINGNPPLPNPFGDPNLSQPIMPIQQN	0.9958	3	4818.5962
3703	Q91XX2_MOUSE	931	2.26	1	4	R.IESSASNYYKLVTDGILDR.E	0.9954	2	2145.3739
3704	Q91XY7_MOUSE	932	8.91	2	2	R.VSVRENVAVGTQLLLVNATDPDEGANAEV	0.9944	3	3649.052
						R.DSGDPPLSSNVSLSLFVLDQNDNVPEILYP	0.9958	3	4742.2043
3705	Q91XY9_MOUSE	930	4.09	1	6	K.HTGEIKISENLDYEEMSFYEIEIQAEDGGAY	0.9958	3	4067.4237
3706	Q91Y11_MOUSE	979	6.23	2	3	R.CSAVPMQAGCGLGKPTLVCSSAVGTWSY	0.9958	3	3445.7702
						K.MYENQENKTLVIWLNATDSDEGINK.E	0.9958	3	2927.2122
3707	Q91Y18_MOUSE	950	7.37	2	2	R.LLVLVKDHGEPALTATATVLVSLVENGQAP	0.9958	3	3185.7319
						K.GNIPMTGHCTLLVELLDVNDNAPEVTITSLS	0.9944	3	3791.318
3708	Q91YU9_MOUSE	89	16.85	1	57	-.LSVNDVFVIEEWGR.A	0.9958	2	1663.8705
3709	Q91Z25_MOUSE	376	12.77	2	7	K.EHNGQVTGIDWAPESNRIVTCGTDR.N	0.9944	3	2813.9665
						K.KASSEGGAATGAGLDSLHK.N	0.9958	2	1757.898
3710	Q91Z40_MOUSE	638	5.8	2	9	R.LAGQNHGFNLGTTVR.S	0.9958	2	1585.7629
						R.LPTDTLQELLTVHTACEK.E	0.9958	2	2070.3136
3711	Q921S3_MOUSE	572	6.99	2	7	K.DMAAFNERPIIFALSNPTSK.A	0.9958	2	2223.5518
						K.VFLTTAEVISQQVSDK.H	0.9958	2	1766.0013
3712	Q99K47_MOUSE	557	28.9	9	43	K.THSDSDILTNIEDPSSHVPEFSSSSKTSTVK	0.9944	3	3334.5316
						R.HPDLSGFFDNHFGLISPNFK.E	0.9958	2	2290.5425
						K.THSDSDILTNIEDPSSHVPEFSSSSK.T	0.9958	2	2817.9366
						R.GDFANANNFDNTYGQVSEDLR.R	0.9958	2	2348.4039
						K.AQQIQALQSNVR.A	0.9958	2	1356.5247
						R.NIMEYLR.G	0.9958	1	939.1174
						K.MSPVPDLVPGSFK.S	0.9958	2	1374.6379
						K.EVITSDDGSDCGDATELDISHSFSGSLDELS	0.9958	3	3545.5825
						R.EINLQDYEGHQK.Q	0.9946	2	1474.57
3713	Q99K86_MOUSE	650	3.69	1	13	R.TQSFQLIVQGAPELKPNEIMPK.S	0.9949	2	2469.9018
3714	Q99LC4_MOUSE	463	4.1	1	4	K.NTQPIMDTDGSYFIYSK.L	0.9958	2	1981.1841
3715	Q99LF7_MOUSE	519	3.66	1	4	R.QSYRINSDVLAQQFAVK.T	0.9958	2	1968.2199
3716	Q99LV0_MOUSE	300	29	5	31	K.SSFATPGVNVGLFCSTPAVALGR.A	0.9958	2	2309.5933
						K.VALEMLFTGEPISAQEALR.H	0.9958	2	2076.4156
						R.KVALEMLFTGEPISAQEALR.H	0.9958	2	2204.5897
						R.KPIWSH.-	0.9958	1	767.9059
						R.NHPVPILAMVNGLATAAGCQLVASCDIAVA	0.9958	3	3365.8019
3717	Q99LZ4_MOUSE	210	11.43	1	6	R.AEFLAGHDPPGISLGDAVAGVR.A	0.9958	2	2150.3989

3718	Q99ML6_MOUSE	265	24.15	2	2	K.ATLIRAIPSNAALFLVYEYSR.K	0.993	2	2369.7691
						R.SFFASGGSKDELGPVPLMLSGGFAGICLW	0.9958	3	4201.8857
3719	Q99MR3_MOUSE	914	1.64	1	2	R.GALPLLRLANQLK.K	0.9958	2	1407.7427
3720	Q99MV3_MOUSE	2785	1.01	2	4	K.QFFLLLK.N	0.9958	1	909.1595
						K.NSTVDTIALKDIPNQLK.E	0.9958	2	1871.1411
3721	Q99PA7_MOUSE	320	12.19	2	2	R.ISNEEGIPKTGLLVLVLGIIFMEGNR.A	0.9958	3	2814.3563
						K.MKVLQFFCK.V	0.9924	1	1201.4786
3722	Q9CQ09_MOUSE	240	33.33	5	43	K.SITPLGGFPHYGEVNNDFIMLK.G	0.9958	2	2450.8145
						K.AHIMEIQLNGGTVAEK.V	0.9958	2	1711.9739
						K.QVPVHSVFSQSEVIDVIAVTK.G	0.9958	2	2283.6299
						K.FGHGCFQTAQEK.R	0.9958	1	1410.4949
						K.KAHIMEIQLNGGTVAEK.V	0.9958	2	1840.1479
3723	Q9CQ16_MOUSE	148	16.89	2	43	K.RNQSFCPTVNLDK.L	0.9958	2	1579.7191
						K.LWTLVSEQTR.V	0.9958	1	1233.4099
3724	Q9CQW9_MOUSE	137	16.06	1	4	R.IKEEYEVAEMGAPHGSASVR.T	0.9958	2	2161.3942
3725	Q9CR55_MOUSE	154	8.44	1	5	R.SRSNSHSDHIR.R	0.9958	1	1296.345
3726	Q9CRA2_MOUSE	214	5.14	1	4	K.IPLHVFSPK.Y	0.9944	1	1038.2779
3727	Q9CRJ8_MOUSE	259	7.72	1	2	R.APRVGASLTPELAPVQIK.V	0.9958	2	1848.1961
3728	Q9CSV9_MOUSE	373	5.09	1	4	K.DIHEKQDTLIAFGNSWK.K	0.9958	2	2003.2218
3729	Q9CTX9_MOUSE	187	5.88	1	2	R.ESFHLILTK.R	0.9958	1	1088.292
3730	Q9CUJ9_MOUSE	185	27.03	2	9	K.CPGRAGTRPGSPHSLPGTGSTLPRPPTR.I	0.9943	3	2869.182
						R.LRTAGPPLPASGPPGLSR.R	0.9958	2	1745.0347
3731	Q9CUL6_MOUSE	383	2.35	1	3	R.KVAILLK.Q	0.9958	1	785.0611
3732	Q9CV76_MOUSE	234	16.24	1	2	R.AVRPVALPSSCVTTGAMCHVSGWGTTNKI	0.9958	3	3957.3877
3733	Q9CV95_MOUSE	474	3.8	2	2	R.NEHFQKAIEDK.S	0.9958	1	1359.4814
						K.QAHLRNEHFQK.A	0.9924	1	1408.5625
3734	Q9CVJ2_MOUSE	109	15.6	1	7	R.GARGPGGSDAPVNPK.L	0.9958	2	1380.5033
3735	Q9CWK0_MOUSE	227	3.96	1	2	R.RQHLLLK.V	0.9956	1	908.1349
3736	Q9CX22_MOUSE	229	24.02	4	270	K.KEDLVFIFWAPENAPLK.S	0.9958	2	2018.3629
						K.EILVGDVGQTVDDPYTTFVK.M	0.9958	2	2197.4467
						K.EDLVFIFWAPENAPLK.S	0.9924	2	1890.1889
						K.HELQANCYEKVK.D	0.9958	2	1519.6635
3737	Q9CX86_MOUSE	305	33.44	6	9	K.GDVAEGDLIEHFSQFGAVEK.A	0.9904	2	2149.3214
						K.LFIGGLNVQTSESGLR.G	0.994	2	1691.9249
						R.SRCFGFVTYSNVEEADAAMAASPHAVDGN	0.9944	3	3645.9454
						K.KLFVGGLK.G	0.9958	1	862.1032
						K.RGFGFVYFQSHDAADK.A	0.9958	2	1846.0116

						R.GFGFVYFQSHDAADK.A	0.9958		2	1689.8241
3738	Q9CY10_MOUSE	142	23.94	3	3257	K.VADALANAAGHLDDLPGALSALSDLHAHK.	0.9958		3	2865.1753
						K.KVADALANAAGHLDDLPGALSALSDLHAHK	0.9958		3	2993.3494
						K.VADALANAAGHLDDLPGALSALSDLHAHKL	0.9958		3	3134.5222
3739	Q9CY75_MOUSE	170	18.82	2	2	K.SCYEDGWLIKMTLSDPSEMDELMSEEAYE	0.9958		3	3588.9147
						K.MTLSDPSEMDELMSEEAYEK.Y	0.9958		2	2336.5596
3740	Q9CZ42_MOUSE	343	42.27	8	40	K.SYSPELIVHPVLDSSNAVEEVEK.W	0.9958		2	2542.8022
						R.IGIVGGCQEYTGAPYFAGISALK.V	0.9958		2	2373.6771
						R.LHALVVGPGLGRDDLLLNNVR.G	0.9926		2	2242.6297
						R.STTTTDMITEVGTAFSR.L	0.9958		2	1818.9935
						R.ALSLHTAHATK.D	0.9958		2	1150.3231
						R.DIPVVIDADGLWLVAQQPALIHSYHK.A	0.9958		2	2900.3501
						R.LHALVVGPGLGR.D	0.9958		2	1189.4465
						K.VGADLTHVFCAR.E	0.9943		2	1346.4949
3741	Q9CZ49_MOUSE	574	14.46	2	2	R.YDPFSNTWAAIAPLPEAVSSAAVAPCAGQI	0.9958		3	5426.9345
						R.EEEPGTEAPCAASCHAQRILQTLNAYR.R	0.9958		3	3074.266
3742	Q9CZK9_MOUSE	167	50.3	6	174	K.FEDENFILK.H	0.9909		1	1155.2927
						R.SIYGEKFEDENFILK.H	0.9958		2	1833.0478
						K.HTGPGILSMANAGPNTNGSQFFICTAK.T	0.9958		2	2793.0925
						R.IIPGFMCQGGDFTR.H	0.9958		2	1599.8109
						K.EGMNIVEAMER.F	0.9944		2	1279.4688
						K.KITISDCGQL.-	0.9958		1	1135.2689
3743	Q9CZN0_MOUSE	630	13.02	2	2	R.IISGLFPLQQQARLDASVSVSEASEPSASDI	0.9944		3	4245.6903
						R.AVVMSVANEEPESVDFSAQPAPPEPAPSA	0.9958		3	3648.0327
3744	Q9CZV2_MOUSE	255	17.25	2	2	K.SQSYDCTVDLLECQPSSK.L	0.9958		3	2118.191
						R.ARWTLEYSVCNNQTLEDIWTK.L	0.9958		3	2628.867
3745	Q9D0B5_MOUSE	157	36.31	3	18	K.IPGSINIPLDEVGEALQMNPVDFK.E	0.9944	2,3		2597.9862
						K.SLLNSK.D	0.9958		1	661.7764
						K.AMDTAISLGFNSAQHYAGGWK.E	0.9958		2	2226.4711
3746	Q9D1N2_MOUSE	228	10.09	2	2	K.AAHPQSDGANLPK.S	0.9958		2	1306.4209
						K.FSHPQVVK.A	0.9944		1	942.1057
3747	Q9D3H5_MOUSE	123	33.33	2	2	R.AAGTSSSAGAMASSAEPEEKAGSGFPR.L	0.9958		3	2512.6673
						R.SRLLGGAGGK.A	0.9944		1	916.0683
3748	Q9D3H9_MOUSE	131	12.98	1	3	K.RWTCGNCQLQLELGR.G	0.9943		2	1892.057
3749	Q9D3R5_MOUSE	417	12.47	3	15	K.GVLAIYSYVSKLGSRPWVPQVPIQFHQQR.	0.9958		3	3355.9132
						R.TTVLTDFDGRLLTEAAHVR.V	0.9941		2	2116.3818
						R.LLTEAAHVR.V	0.9958		1	1010.1814

3750	Q9D3V6_MOUSE	382	4.97	1	4	R.HILLAVANDQELNQLLK.G	0.9958	2	1933.2584
3751	Q9D3W1_MOUSE	341	4.4	1	2	K.NEAIQRAAEVAIK.V	0.9944	1	1413.6169
3752	Q9D4D2_MOUSE	429	12.35	2	2	K.CLEMTFGIDIKESDLVSSAYVLVNSLNLTYE	0.9958	3	4415.8301
						K.QETEEDNVEK.E	0.9958	1	1221.22
3753	Q9D4E6_MOUSE	643	2.33	1	2	K.AVEEMNGKDLNGK.Q	0.9958	1	1405.5658
3754	Q9D4K1_MOUSE	575	3.83	2	2	R.IQEMGANEQSWK.C	0.9958	1	1421.5677
						K.EKTAAK.T	0.9958	1	647.7495
3755	Q9D576_MOUSE	247	9.72	1	2	K.QIDSLAAVVLQNRQGLDVLSAK.E	0.991	2	2339.6976
3756	Q9D5J8_MOUSE	232	9.05	2	5	K.FKLDLDFPNLPYLIDGSHK.V	0.9958	2	2233.5719
						K.LDLDFPNLPYLIDGSHK.V	0.9958	2	1958.2212
3757	Q9D5P6_MOUSE	216	14.81	2	3	K.QELRDLFHDFDITGDR.L	0.9952	2	1978.1283
						K.EFKLYTIFCTDK.S	0.9958	1	1565.7724
3758	Q9D5R4_MOUSE	444	4.5	1	41	K.NYLIIQITEVQHAIDQLK.R	0.99	2	2140.4875
3759	Q9D669_MOUSE	585	4.44	1	7	R.SRLEYFTLPVMLPEVVPENFSDER.G	0.9958	2	2869.2617
3760	Q9D6T9_MOUSE	100	24	1	70	K.LSEALGSAALPSHSSAISQHSK.G	0.9958	2	2179.3946
3761	Q9D727_MOUSE	114	44.74	2	2	R.GGVSSPSGALASAEPAPASVTLAELLHLVQ	0.9958	3	2959.3696
						R.HITATHGEPTASLLPR.R	0.9944	2	1701.923
3762	Q9D7A3_MOUSE	345	4.93	1	4	K.QKGAYCDLSSEEEEK.A	0.9924	2	1773.8139
3763	Q9D7N7_MOUSE	112	25	1	12	K.LLAEITAGCSLPGQPAPLMFVGWDSR.F	0.9958	2	2788.2001
3764	Q9D820_MOUSE	169	14.79	1	2	R.TEVVEHPEVFTIEEMMPHIQHLK.G	0.9958	3	2775.2099
3765	Q9D828_MOUSE	389	7.97	2	3	R.LLDSLEPPGEPGPSTSIPENDTVDGR.E	0.9958	2	2693.881
						K.VNRLLDSLEPPGEPGPSTSIPENDTVDGR.I	0.9944	3	3063.3049
3766	Q9DA96_MOUSE	983	1.63	1	6	K.IILVIIGLSNLRPR.F	0.9944	1,2	1577.9975
3767	Q9DAQ4_MOUSE	506	8.1	2	2	K.WPSGWEREAEQLGELWAGR.T	0.9958	2	2258.4575
						R.FLPRNPIPPDVASTPTPK.L	0.9927	2	1948.2725
3768	Q9DAT0_MOUSE	116	12.93	1	2	K.CLLMLCMEAGTER.T	0.9926	2	1584.8185
3769	Q9DBK8_MOUSE	902	2.55	1	3	R.MLSLPSVAQYPADPHLVVTEK.S	0.9958	2	2296.6868
3770	Q9DC90_MOUSE	209	18.18	1	4	R.TGQLSPSCYTCCSSLSSDYTACPLSLVLGE	0.9958	3	3956.2109
3771	Q9DCS2_MOUSE	204	38.24	3	12	R.SLDLLLCINMIHISPLNCTEGLFR.A	0.9958	3	2831.2753
						R.VLEVASGSGQHAAHFAQAFPNAEWQPSD'	0.9958	3	3451.6958
						K.TKAVLITYGPYAVNGK.I	0.9958	1	1695.9994
3772	Q9DCW5_MOUSE	112	23.21	2	21	R.MWKALTYFVALPGVGVSMLNVFLK.S	0.9958	3	2686.332
						K.ALTYFVALPGVGVSMLNVFLK.S	0.9958	2	2240.7522
3773	Q9DCY1_MOUSE	216	23.61	5	18	K.HYGPGWVSMANAGK.D	0.9958	1,2	1475.6647
						K.DTNGSQFFITTVK.T	0.9958	2	1458.6109
						K.IEVEKPFAIAKE.-	0.9958	2	1374.6201
						K.IEVEKPFAIAK.E	0.9958	2	1245.5046

						K.DVIIVDSGK.I	0.9958	1	946.0886
3774	Q9EPW8_MOUSE	1354	8.42	4	8	K.TLNLAGNFLESLSGLHK.L	0.9924	2	1815.0794
						K.MADPAKNPALSILLYIQAFQVVTPHLGR.G	0.9909	3	3065.647
						R.GPAPAGGPAPAGGPAPAEALAQAEVPAQ\	0.9958	3	3054.3458
						R.GAFADGHVLELLVGYRFVTAIFVLPHEK.F	0.9958	3	3100.6335
3775	Q9EQC8_MOUSE	491	2.85	1	3	R.ELELKNTWSENK.L	0.9929	2	1491.6409
3776	Q9EQI5_MOUSE	113	36.28	1	2	R.CTNTISGIPFNSISLVNVYRPGVHCADVEVI/	0.9958	3	4274.7962
3777	Q9EQN8_MOUSE	324	10.19	2	8	R.ELEMSEENQELAILDSENLK.A	0.9958	2	2335.5421
						K.QCHILEQLK.E	0.9958	1	1169.3324
3778	Q9ERC8_MOUSE	2013	4.52	3	3	K.AVILNCSAEGYPVPTIVWK.F	0.9958	3	2118.4467
						K.EVDEGEYTCNVLVQPQLSTSQSVHVTVK.V	0.9958	3	3148.4169
						R.GYQIGYREYSTGGNFQFNIISIDTTGDSEVY	0.9958	3	4295.619
3779	Q9ERN6_MOUSE	4967	4.77	13	39	K.ELTEESDLLSDIFGLDLK.R	0.9958	2	2038.2561
						K.NYQLTSGYKPAPMDLSFIK.L	0.9958	2	2174.5195
						R.ISQTSQVSIDAAHGYSPR.A	0.9958	2	1918.0733
						K.GGGNHPLLVPYDTLTAK.E	0.9958	2	1753.9957
						R.LPQFLQVPSNHEHIEVTR.I	0.9931	2	2145.4257
						K.RLPQFLQVPSNHEHIEVTR.I	0.9958	2	2301.6132
						R.ALGMHETVMEVMVNVLGGGESKEITFPK.M	0.991	3	3005.5325
						K.WLKEPNPEAEELFR.M	0.9924	1	1758.9713
						R.LAENIHELWVMNK.I	0.9958	2	1597.8725
						K.TLLALGCHVGIADEHAEEK.V	0.9958	2	2064.2689
						R.TLLGYGYHLEAPDQDHASR.A	0.9958	2	2144.3079
						R.DLHAMAEMMAENYHNIWAK.K	0.9958	2	2276.6076
						K.TAHGHLVPDR.I	0.9955	2	1103.2259
3780	Q9ES94_MOUSE	307	20.52	2	2	K.GAWPSILLSVQNVIDCGNAGSCEGGNDLP'	0.9958	3	3916.2276
						R.NQHIPQYCGSCWAHGSTSAMADR.I	0.9958	2	2635.7621
3781	Q9ESQ1_MOUSE	1691	6.27	3	3	R.GDEGVQGQRGPSGTPGLPSLTGLPGALGI	0.9958	3	3401.8039
						K.GTHGTPGASITGVPGPAGLPGPK.G	0.9958	3	2027.2877
						K.GDPGPQGTPGLAGTPGKDGRPGLPGLPG	0.9958	3	3783.1087
3782	Q9JIA4_MOUSE	318	3.77	1	6	R.GFEPPGAGKR.G	0.9958	1	1016.1447
3783	Q9JJJ0_MOUSE	729	5.9	2	2	R.RYAQAFQQQDGLYSEDLEK.D	0.9912	2	2290.4509
						R.IWESPLLLAAKENDVQALSK.L	0.9958	3	2226.5779
3784	Q9JJY5_MOUSE	2062	1.41	2	2	K.SQRAADLTR.E	0.9958	1	1018.1178
						K.FVQLNICQQGNIQGGR.I	0.9958	2	1833.0233
3785	Q9JLE7_MOUSE	912	1.86	1	2	K.VYQLPTNSRANAHTR.A	0.9924	2	1728.9083
3786	Q9JMF9_MOUSE	105	24.76	1	2	R.LRLPQGSMLPESQAGTHPLSTVSR.A	0.9944	3	2563.9347

3787	Q9QXA3_MOUSE	4587	1.55	2	4	K.DPTYAIITVEDCDQGANGEIASLSIVAGDFL(	0.9944		3	3788.1225
						K.DANDNSPVLESSPYEAFIVENLPGGSRVIQ	0.9958		3	3488.8357
3788	Q9QXJ5_MOUSE	3006	1.36	2	4	K.DSGFPHVADVSTMQAAQEFIPK.N	0.9958		3	2376.6459
						R.AGSKNIDIIALQSIR.S	0.9958		3	1599.8711
3789	Q9QZ83_MOUSE	393	5.85	1	2	K.DLYANTVLSGGTTMYPGLADR.M	0.9958		2	2216.4706
3790	Q9QZH1_MOUSE	4488	2.65	7	23	K.LISQKVVSPHAFTWLSQLR.H	0.9944		3	2211.6151
						K.CIYSQLQAPIVLKMVK.I	0.9945		2	1892.3167
						K.DSAHPLLSGLHPTPETELDFWTMR.H	0.9958		3	2752.0735
						K.LQTTASQVGNLKSR.L	0.9944		1	1503.6988
						K.LVSELESEKIR.W	0.9958		1	1303.4985
						R.VQVATAELECR.V	0.9924		1	1276.3984
						K.QRECEADLLK.A	0.9958		1	1262.3715
3791	Q9QZV4_MOUSE	726	18.73	7	116	R.EPVQGEIAHQPLQPTGPSSR.E	0.9958	2,3		2129.3372
						R.KQGEEEEEEEEEEEEEEILEENLLPFTIIPNPI	0.9958		3	4113.3858
						R.SHSHEDEDGIVSSEYHR.H	0.9958		2	1984.9903
						R.EHDNEDLGDSAENHLPR.Q	0.9958		2	1948.9573
						R.AAVSAPLSHHR.K	0.9929		2	1146.2943
						K.VDRAAVSAPLSHHR.K	0.9958		1	1516.703
						R.QSHQNEEEEDEAVSTEHWHQSPR.H	0.9958		3	2790.7923
3792	Q9R1N4_MOUSE	323	9.6	1	8	K.LAQAGAEILTYPSAFGSVTGPAHWEVLLR./	0.9958		3	3056.4912
3793	Q9WVE4_MOUSE	738	4.61	1	2	R.GAGVGLGNWNNNAGIPGSSEDLSTEFGHI	0.9958		3	3302.5063
3794	Q9Z0I9_MOUSE	1703	2.23	2	2	R.DIIFLLDGSDNVGK.N	0.9944		1	1506.6959
						R.LTLLGGPTPNTGAALEFVLR.N	0.9958		2	2041.3983
3795	Q9Z2U2_MOUSE	2192	2.05	3	7	K.ECNSLPLFTTNDLLLK.T	0.9958		2	1879.1267
						K.DGIYSCPICAKNFNSK.D	0.9918		2	1875.0205
						K.QEQRPIK.K	0.9924		1	899.0378
3796	QCR1_MOUSE	480	60	21	2270	R.MVLAAAGGVEHQQLLDLAQK.H	0.9958		2	2093.4491
						R.NALVSHLDGTTPVCEDIGR.S	0.9958		2	2055.2182
						K.NNGAGYFLEHLAFK.G	0.9958		2	1581.7709
						R.RIPLAEWESR.I	0.9958	1,2		1257.4349
						R.EMQENDASMQNVVFDYLHATAFQGTPLA(	0.9958		3	4296.6864
						R.VASEQSSHATCTVGVWIDAGSR.Y	0.9958		2	2319.4589
						K.HLSSVSR.V	0.9944		1	785.8784
						K.VVELLADIVQNSSLEDSQIEK.E	0.9958		2	2330.5945
						K.YFYDQCPAVAGYGPIEQLPDYNR.I	0.9958		2	2737.9508
						R.TDLTDYLNR.N	0.9909		2	1111.1967
						R.IQEVDAQMLR.D	0.9958	1,2		1203.399

						R.VYEEDAVPGLTPCR.F	0.9958		1	1606.7387
						K.EVESIGAHLNAYSTR.E	0.9958		2	1647.785
						K.VVELLADIVQNSSLEDSQIEKER.D	0.9958		3	2615.8975
						R.IPLAEWESR.I	0.9958		2	1101.2474
						R.GTATFAQALQSVPETQVSILDNGLR.V	0.9958		2	2617.9188
						R.YETEKNNGAGYFLEHLAFK.G	0.9958		2	2232.457
						R.EHTAYLIK.A	0.9924		1	975.1326
						R.VASEQSSHATCTVGVWIDAGSRYETEK.N	0.9958		3	2970.145
						K.NILRNALVSHLDGTTPVCEDIGR.S	0.9958		2	2551.8284
						K.NNGAGYFLEHLAFKGTK.N	0.9958		2	1868.102
3797	QCR10_MOUSE	56	25	1	3	R.LILDWVPYINGK.F	0.9944		1	1431.7178
3798	QCR2_MOUSE	453	76.6	21	1936	R.IIENLHDVAYK.N	0.9958		2	1315.5119
						K.ITSEELHYFVQNHFTSAR.M	0.9958		2	2180.3843
						K.RGNNTTSLLSQSVAK.G	0.9958		2	1576.7501
						K.LPNGLVIASLENYAPLSR.I	0.9958		1	1928.2389
						K.TSAAPGGVPLQPQDLEFTK.L	0.9958		2	1957.1907
						K.TSAAPGGVPLQPQDLEFTKLPNGLVIASLE	0.9958		3	3866.4063
						K.GSHQPFDVSAFNASYSDSGLFGIYTISQAA	0.9958		3	4568.9568
						K.SMAASGNLGHTPFLDEL.-	0.9958		2	1760.9593
						R.MALVGLGVSHSVLK.Q	0.9958		2	1411.746
						R.GNNTTSLLSQSVAK.G	0.9958		1	1420.5626
						K.AVAQGNLSSADVQAAK.N	0.9958		1	1530.6781
						K.NALANPLYCPDYR.M	0.9958		2	1567.7075
						K.AVAFQNSQTR.I	0.9958		1	1122.226
						K.AGYLMSVETSEGFLSEIGSQALAAGSYMPF	0.9958		3	4835.4061
						R.EQNGDNLVHAAIVAESAAIGNAEANAFSVL	0.9958		3	4149.6127
						R.YEDSNNLGTSHLLR.L	0.9958	1,2		1619.7312
						R.RWEVAALR.S	0.9943		2	1001.1765
						K.KSMAASGNLGHTPFLDEL.-	0.9924		2	1889.1333
						K.AGSRYEDSNNLGTSHLLR.L	0.9958		2	1991.1276
						R.SDIEILMEFLLNVTTAPEFR.R	0.9944		2	2339.7089
						K.VKTSAAPGGVPLQPQDLEFTK.L	0.9958		2	2184.4973
3799	QCR6_MOUSE	89	59.55	4	477	R.SQTEEDCTEELFDFLHAR.D	0.9924		2	2228.2996
						K.EEEEEELVDPLTTVR.E	0.9958	1,2		1788.903
						K.MLTGSGDPKEEEEEELVDPLTTVR.E	0.9958		2	2675.9215
						R.DHCVAHK.L	0.9924		1	866.9182
3800	QCR7_MOUSE	111	56.76	8	333	K.WYYNAAGFNK.L	0.9958		1	1234.3562

						K.YEEDKFYLEPYLK.E	0.9958	1,2		1737.9464
						K.FYLEPYLK.E	0.9958		1	1073.2768
						R.RLPEDLYNDR.M	0.9958		2	1291.4062
						R.KWYYNAAGFNK.L	0.9944	1,2		1362.5303
						K.RALDLTMR.H	0.9958		2	976.1821
						R.ALDLTMR.H	0.9944		1	819.9946
						R.DDTLHETEDVK.E	0.9958		1	1302.3373
3801	QCR8_MOUSE	82	60.98	3	19	R.HVISYSLSPFEQR.A	0.9958		2	1563.7532
						R.VAPPFVVVYLIYTWGNQEFEQSK.R	0.9958		2	2716.1083
						R.KNPAMYENDK.-	0.9958		1	1210.3471
3802	QCR9_MOUSE	64	29.69	1	6	R.AFDQGADAIYEHINEGK.L	0.9958	1,2		1878.9927
3803	QIL1_MOUSE	119	47.9	2	27	R.KAEEVVPPAMYQFSQYVCQQTGLEMPQLI	0.9958		3	3794.3383
						R.DSWNSGIISVMSALSVAPSK.A	0.9958		2	2050.3343
3804	QKI_MOUSE	341	11.44	2	4	K.LMSSLPNFCGIFNHLER.L	0.9958		2	2036.3222
						K.RSAELPDAVGPIVQLQEK.L	0.9958		2	1951.2303
3805	QOR_MOUSE	331	47.43	9	101	R.KPALPYTPGSDVAGIIESVGDK.V	0.9958		3	2215.5083
						R.AGESVLVHGASGGVGLATCQIAR.A	0.9958		2	2211.4491
						K.LQSDVVVPVPQSHQVLIK.V	0.9958		2	1987.35
						K.GWVKPVIGSEYPLEK.A	0.9958		2	1702.9909
						K.VHACGVNPVETYIR.S	0.9958		2	1615.7955
						R.VFEFGGPEVLK.L	0.9958		2	1222.4265
						K.LVLQNGAHEVFNHK.E	0.9958		2	1606.8246
						K.EEFQQFAGLLQAGIEK.G	0.9957		2	1809.0288
						K.AAQAHEDIIHGSGK.T	0.9958		2	1434.5516
3806	QORL_MOUSE	348	6.32	1	4	K.LSAGVFRPLLDEPIPLYEAK.V	0.9958		2	2229.6244
3807	QRSL1_MOUSE	525	10.29	2	4	R.SLWSQAADLFESEGAK.V	0.9958		2	1739.8791
						K.QGQSLGDLDGIPVAVKDNFSTTGIETTCAS	0.9944		3	3569.9289
3808	QSK_MOUSE	1311	2.82	2	10	R.ASDGGANIQLHAQQLLK.R	0.9958		2	1764.9792
						R.DLKAENLLLDANLNIK.I	0.9958		2	1798.0898
3809	QSOX1_MOUSE	748	11.9	4	10	K.NGSGATLPGAGANVQTLR.M	0.9921		2	1684.8497
						R.FFQAFTKNGSGATLPGAGANVQTLR.M	0.993		2	2554.868
						R.ELCSACHNELNGQVPLWDLGATLNFLK.A	0.9958		3	3101.4181
						R.CGRLSGPPSLLLLLLLLSPLLFSGPGAYAAF	0.9958		3	3224.8669
3810	RAB10_MOUSE	200	13	3	6	R.FHTITTSYYR.G	0.9934		2	1289.4331
						K.AFLTLAEDILR.K	0.9909		2	1262.4918
						K.AFLTLAEDILRK.T	0.9958		2	1390.6659
3811	RAB14_MOUSE	215	43.26	6	49	K.IYQNIQDGSLDLNAAESGVQHKPSAPQGGI	0.9958		3	3152.4074

						K.KIYQNIQDGSLDLNAAESGVQHKPSAPQG(	0.9958		3	3280.5815
						R.STYNHLSSWLTDAR.N	0.9958		2	1651.7758
						K.KFMADCPHTIGVEFGTR.I	0.9918		2	1967.2159
						R.NLTNPNTVIILIGNK.A	0.9958		2	1624.9212
						K.SCLLHQFTEK.K	0.9958		2	1263.4021
3812	RAB18_MOUSE	206	20.87	3	4	K.IIQTPGLWESENQNK.G	0.9958		2	1757.9408
						K.TCDGVQCAFEELVEK.I	0.9924		2	1785.8776
						K.HSMLFIEASAK.T	0.9958		2	1234.4559
3813	RAB1A_MOUSE	205	38.54	4	24	K.EFADSLGIPFLETSAK.N	0.9958		2	1725.936
						K.NATNVEQSFMTMAAEIK.K	0.9958		2	1886.1451
						R.FADDTYTESYISTIGVDFK.I	0.9958		2	2173.3374
						R.GAHGIIVVYDVTDQESFNNVK.Q	0.9958		2	2306.537
3814	RAB1B_MOUSE	201	37.31	4	28	K.EFADSLGVPFLETSAK.N	0.9958		2	1711.9091
						R.MGPGAASGGERPNLK.I	0.9958		2	1442.6329
						K.NATNVEQAFMTMAAEIK.K	0.9958		2	1870.1457
						R.GAHGIIVVYDVTDQESYANVK.Q	0.9944		2	2279.5114
3815	RAB21_MOUSE	222	13.96	2	11	R.HVSIQEAESYAESVGAK.H	0.9958	1,2		1805.939
						R.FHALGPIYYR.D	0.9954		2	1237.4465
3816	RAB3I_MOUSE	428	15.19	2	4	R.HFNCAEVSNISAHAPDPASSVPSAVASGLT	0.9958		3	3123.3722
						R.EFLQGATITEASAGNDDIFGLSTDSLSRLR.	0.9958		3	3186.4595
3817	RAB6A_MOUSE	208	7.69	1	2	R.TVRLQLWDTAGQER.F	0.9958		2	1673.8692
3818	RAB7A_MOUSE	207	20.29	2	2	R.GADCCVLVFDVTAPNTFK.T	0.9958		2	2015.2025
						R.NALKQETEVELYNEFPEPIK.L	0.9958		2	2392.6678
3819	RAB9A_MOUSE	201	7.96	1	2	R.SEHLIQTDTVNLHR.K	0.9958		2	1663.8307
3820	RAC1_MOUSE	192	17.19	2	31	K.KLTPITYPQGLAMAK.E	0.9958		2	1633.002
						R.HHCPNTPIILVGTK.L	0.9958	1,2		1587.8284
3821	RAD_MOUSE	308	12.34	2	2	R.GSTPWGPAPPLHR.R	0.9958		2	1373.5571
						K.FIETSAALHHNVQALFEGVVR.Q	0.9944		2	2339.6591
3822	RAD18_MOUSE	509	10.02	3	3	K.LNENVMVFTKNQTEK.E	0.9958		2	1796.0484
						K.SAAEIVQEIESMEK.T	0.9919		1	1564.7479
						R.HQEFVHMYNAQCDALHPKSAAEIVQEIESM	0.9958		3	3772.1648
3823	RAD51_MOUSE	339	22.12	3	5	K.KPIGGNIIAHASTTRLYLR.K	0.9958		2	2082.4568
						K.KLEEAGYHTVEAVAYAPK.K	0.9924		2	1977.2243
						R.MLLRLADEFGVAVVITNQVVAQVDGAAMF/	0.9944		3	3562.1799
3824	RAD54_MOUSE	747	2.01	1	2	R.YLYVRLDGTMSIK.K	0.9958		1	1559.8639
3825	RADI_MOUSE	583	15.09	6	28	K.FFPEDVSEELIQEITQR.L	0.9958		2	2081.2866
						K.KQLQALSSELAQAR.D	0.9958		2	1543.7635

						K.KTQNDVLHAENVK.A	0.99	2	1496.6634
						K.QLQALSSELAQAR.D	0.9958	2	1415.5895
						K.GTELWLGVDALGLNIYEHDDKLTPK.I	0.9958	3	2799.1528
						R.EDSMMEYLK.I	0.9944	1	1146.3156
3826	RAE2_MOUSE	621	4.03	1	3	R.RFNIDLVSKPLYSQGSLIDLLIK.S	0.9946	2	2634.1344
3827	RALA_MOUSE	206	10.68	1	5	K.SALTLQFMYDEFVEDYEPTK.A	0.9955	2	2427.6845
3828	RAN_MOUSE	216	21.76	4	19	K.YVATLGVEVHPLVFHTNR.G	0.9958	2	2053.3714
						K.SNYNFEKPFLWLAR.K	0.9958	2	1786.0428
						K.NLQYYDISAK.S	0.9958	1	1215.3483
						K.KYVATLGVEVHPLVFHTNR.G	0.9958	2	2181.5455
3829	RANB3_MOUSE	491	8.35	2	3	K.DTGQLYAALHHR.I	0.9926	2	1382.5216
						R.SAGSSSPEAGEDSDHEDGNYCPPVK.R	0.9958	2	2593.5562
3830	RANB9_MOUSE	653	12.25	4	13	R.EPVCSALNSAILETHNLPK.Q	0.9958	2	2094.3386
						K.RLYPAVDEQETPLPR.S	0.9909	2	1785.0098
						K.HQLSSLTVPELNSLNVSR.S	0.9958	2	1995.2431
						K.MVSSYLVHHGYCATAEAFAR.S	0.9944	2	2271.5213
3831	RANG_MOUSE	203	30.05	2	4	K.DSHEDHDTSTENADESNHDPQFEPIVSLPE	0.9958	3	3891.9648
						R.AWVWNTHADFADECPKPELLAIR.F	0.9958	2	2741.0441
3832	RANT_MOUSE	216	18.06	4	5	R.HLTGEFEK.E	0.9958	1	961.0623
						R.VCENIPIVLCGNK.V	0.9958	2	1516.7101
						K.FNVWDTAGQEK.F	0.9958	1	1295.3941
						K.RHLTGEFEK.E	0.9958	2	1117.2498
3833	RAP1A_MOUSE	184	23.91	3	19	K.INVNEIFYDLVR.Q	0.9958	2	1495.7184
						K.LVVLGSGGVGK.S	0.9958	1	986.1997
						R.VKDTEDVPMILVGNK.C	0.9958	2	1658.9507
3834	RASA3_MOUSE	834	4.56	2	4	K.YADAVKNFLDLISSSGR.R	0.9915	2	1857.0733
						K.QVIAGVGTLEQEHAQYR.R	0.9958	2	1900.1014
3835	RASH_MOUSE	189	14.29	1	3	K.SALTIQLIQNHFVDEYDPTIEDSYR.K	0.9958	2	2969.2341
3836	RAVR1_MOUSE	748	9.76	2	3	K.QSHLNKAVGSSPMGSSEGLLGLGPGPNGI	0.9958	3	3365.7917
						R.SFSHLLPSPEPSPEGSYVGQHSQGLGGHY	0.9958	3	3731.0288
3837	RB11A_MOUSE	216	14.81	2	7	R.DHADSNIVIMLVGNK.S	0.9958	2	1626.8682
						R.GAVGALLVYDIAK.H	0.9958	2	1290.5455
3838	RB11B_MOUSE	218	10.55	1	15	K.NNLSFIETSALDSTNVEEAFK.N	0.9958	2	2330.5102
3839	RB15B_MOUSE	564	7.27	2	3	K.QKQAAGVISLPVGGSK.G	0.9958	2	1540.8033
						K.GDSFAYIQYESLDAAQAACAK.M	0.9909	2	2280.4187
3840	RB22A_MOUSE	194	21.65	2	5	R.FVEDSFDPNINPTIGASFMTKTVQYQNELH	0.9944	3	3572.9709
						K.NWVRELR.Q	0.9944	1	973.1227

3841	RB27B_MOUSE	218	9.17	1	3	K.CVEKTQVPDTVNGGNSGK.L	0.9958	2	1891.0111
3842	RB33A_MOUSE	237	6.75	1	4	R.IFKIIVIGDSNVGK.T	0.9958	1	1503.8253
3843	RB40B_MOUSE	278	20.14	2	2	K.FLLVGDSDVGKGEILASLQDGAAESPYGHF	0.9958	3	3666.0386
						K.SFSMASGLNTRMMHGR.S	0.9924	1	1784.0791
3844	RB6I2_MOUSE	1120	4.38	3	3	R.DNTIMDLQTQLK.E	0.9958	1	1420.6208
						K.KTQEEVAALK.R	0.9958	1	1117.2877
						R.VVQEENQHMQMTIQALQDELR.I	0.9958	2	2541.8567
3845	RBBP6_MOUSE	1790	2.01	2	2	K.LNYDTVTFDGLHISLCDLKK.Q	0.9919	2	2353.6435
						K.SAKEHQEAKPAK.D	0.9958	1	1324.4795
3846	RBBP7_MOUSE	425	18.82	3	5	K.EGYGLSWNSNLSGHLLSASDDHTVCLWDI	0.9958	3	3715.9807
						K.DYALHWLVLGTHTSDEQNHLVVAR.V	0.9941	2	2776.0837
						K.HPAKPDPSGECNPDLR.L	0.9958	2	1790.8963
3847	RBBP9_MOUSE	186	51.08	5	55	R.GHFQNTEFHELISVVK.S	0.9958	2	1886.1173
						K.KGLEQIPGFQCLAK.N	0.9958	2	1589.8413
						K.AVIVPGNGGGDVATHGWYGWVK.K	0.9958	2	2241.5137
						K.ANCPHIVQFGSTDDPFLPWK.E	0.9958	2	2330.5707
						K.TIIIGHSSGAIAAMR.Y	0.9958	2	1498.7838
3848	RBCC1_MOUSE	1588	1.39	2	2	K.NEEMQNVR.T	0.9944	1	1020.1052
						K.QELANNLHVR.L	0.9944	1	1194.3359
3849	RBGP1_MOUSE	1064	3.95	3	4	K.IQDLEHHLGLALSEVQAAK.K	0.9958	2,3	2073.3567
						K.ESPQDSAITR.D	0.9958	1	1104.1619
						K.LQLVEAECKIQDLEHHLGLALSEVQAAK.K	0.9958	3	3144.5615
3850	RBM19_MOUSE	952	10.61	4	4	K.MVRAEVSSEDEDEEDSEDEAVNCEEGSEE	0.9958	3	4518.4259
						R.LVLEWADSEVTVQTLR.R	0.9958	1	1860.1173
						K.ILVRNIPFQANQR.E	0.9958	1	1569.8502
						K.TVILAKNLPAGTLAAEIQETFSR.F	0.9924	3	2444.8339
3851	RBM22_MOUSE	420	3.81	1	2	R.YYGINDPVADKLLK.R	0.9958	2	1609.8626
3852	RBM3_MOUSE	153	35.29	2	35	R.GFGFITFTNPEHASDAMR.A	0.9958	2	1999.2079
						K.LFVGGLNFNTDEQALEDHFSSFGPISEVVV	0.9958	3	3496.8981
3853	RBM38_MOUSE	237	16.88	2	2	R.SLQTGFAVGVQQLHPTLIQR.T	0.9958	2	2194.5418
						K.IFVGGLPYHTTDASLR.K	0.9958	2	1747.9915
3854	RBM41_MOUSE	413	1.69	1	2	R.MMTGR.M	0.9958	1	595.7528
3855	RBM4B_MOUSE	357	5.04	1	2	K.LHVGNISPTCTNQELR.A	0.9958	2	1840.0123
3856	RBP10_MOUSE	648	5.25	2	3	R.LYPAVNQHETPLPR.S	0.9958	2	1635.8631
						K.QPPLMLALGQASECLR.L	0.9944	3	1785.0778
3857	RBP2_MOUSE	3053	3.14	3	3	K.GGEDEDGSDEDVVHNEDIHFEPIVSLPEVE	0.9958	3	4800.0211
						K.AMELKPLNVSNNALVWTASDYADGEAKVE	0.9931	3	3705.1773

						K.YNGTGGQSIYGDK.F	0.9958		1	1360.4228
3858	RBPMS_MOUSE	197	8.12	1	33	R.TLFVSGLPLDIKPR.E	0.9958		2	1556.8888
3859	RC3H2_MOUSE	1187	3.12	2	2	K.EEDPIIPFSDGPIISK.W	0.9932		2	1757.9781
						R.KHSSTGDLLSIELQQAK.S	0.9924		1	1856.0861
3860	RCC2_MOUSE	520	3.65	1	3	R.LIEALSHEAIVLAACGR.N	0.993		2	1824.0966
3861	RCL1_MOUSE	373	9.65	2	2	R.GMPPGGGGEVLFSCPVRK.V	0.9929		2	1846.1206
						R.QRLVLSTLSGRPVK.I	0.9947		2	1554.8765
3862	RCN1_MOUSE	325	11.08	2	5	R.HWILPQDYDHAQAEAR.H	0.9958	2,3		1951.1081
						R.EEFTAFLHPEEFEHMK.E	0.9958		2	2022.2391
3863	RCN2_MOUSE	320	13.75	2	2	K.KLSEEEILENQDLFLTSEATDYGR.Q	0.9958		2	2802.0209
						R.RDPTANEDPEWILVEK.D	0.9958		2	1913.0941
3864	RCN3_MOUSE	328	14.02	3	4	R.EELTAFLHPEEFPHMR.D	0.9954		2	1984.2366
						R.MDLAGDSDGWVSLAELR.A	0.9958		2	1836.0265
						R.AWIAHTQQR.H	0.9944		1	1111.2485
3865	RD23A_MOUSE	363	13.77	2	31	R.QVIQQNPALLPALLQQLGQENPQLLQQISR	0.9958		3	3380.9156
						K.NENLAANFLLSQNFDDE.-	0.9958		2	1955.0447
3866	RD23B_MOUSE	416	19.95	3	75	R.ESQAVVDPPPQAVSTGTPQSPAVAAAAAT	0.9958		3	4593.0178
						R.QIIQQNPSLLPALLQQIGR.E	0.9958		2	2131.5265
						K.NFVVVMVTKPK.A	0.9931		2	1262.5963
3867	RDH13_MOUSE	334	4.49	1	2	R.LVGLAMAHGSPGR.G	0.9958		2	1266.504
3868	RDH14_MOUSE	334	17.07	3	11	R.QELCQAGGAGPDGTDGQLVVK.E	0.9945		2	2101.2439
						K.YGEINFEDLNSEQSYNK.S	0.99		2	2051.1303
						R.KLWDISEVMVGILK.-	0.9958		2	1632.0142
3869	REC8_MOUSE	591	2.2	1	2	K.ETLPEATPDPR.K	0.9924		1	1226.3287
3870	REEP6_MOUSE	201	13.43	1	10	K.HHMALDSAASQLSGRALDLAAGITR.D	0.9958		2	2563.8943
3871	REL1_MOUSE	185	10.27	1	2	R.FLLQLLGFWLLLSQPCR.T	0.9904		2	2105.5401
3872	RELN_MOUSE	3461	1.62	3	8	R.QAITQDLDLRGAK.F	0.9924		1	1429.6163
						R.FLLMSGGKPSRK.C	0.9924		1	1321.6238
						K.WLLHPGGTKMPVCGSTGDALVFIEK.A	0.9958		2	2715.1487
3873	RENT1_MOUSE	1124	8.81	5	16	R.YEDAYQYQNIFGPLVK.L	0.9958		2	1949.1699
						R.EAIDSPVSFLALHNQIR.N	0.9958		2	1911.168
						R.GNTSGSHIVNHLVR.A	0.9958		2	1491.6499
						K.RFTAQGLPDLNHSQVYAVK.T	0.9958		2	2145.4257
						K.ENPSATLEDLEKPGVDEEPQHVLLR.Y	0.9958		2	2817.0819
3874	REST_MOUSE	1082	7.95	3	3	K.AELAAPQLIMLANVALTGEASGSCCDYLVG	0.9958		3	3510.8704
						K.EPPPSMEPPCPEELPQAEPPPMEDCQK.E	0.9944		3	3118.3862
						R.THTGERPYKCELCPYSSSQK.T	0.9909		2	2429.5806

3875	RET_MOUSE	1115	6.55	3	3	R.YTNTLLSGDSWAQQTFRVEHSPIETLVQVN	0.9958	3	4006.3806
						K.QVNHPHVIK.L	0.9958	1	1072.2553
						R.RPSLDSTENQVPVDSFKIPEDPK.W	0.9958	3	2599.8571
3876	REXO4_MOUSE	432	4.4	1	4	K.QKSQAAEKPLVSQMDDK.M	0.9945	2	1904.1455
3877	RFA2_MOUSE	270	10.37	2	5	R.SQLQHMPVPSIK.Q	0.9958	2	1365.6336
						K.ACPRPEGLNFQDLR.S	0.993	2	1673.8351
3878	RFC2_MOUSE	349	8.88	2	2	R.EGNVPNIIIAGPPGTGK.T	0.9924	1	1634.8729
						R.FALACNASDK.I	0.9944	1	1097.1791
3879	RFIP5_MOUSE	645	8.68	3	11	K.YYHLTHDELIGLLLQR.E	0.9958	2	1985.2932
						R.IMETSPTLLQISPGPPK.-	0.9958	2	1810.159
						K.GSPSLGASPHHSSTGEEK.A	0.9958	2	1765.8339
3880	RFTN1_MOUSE	554	12.09	2	14	R.RPETKPGSTGDVPSAQQPGIPSPSAENEA	0.9958	3	3605.8999
						K.VQEAASQGLKFVSVVPQYQPSVSSAGSR.I	0.9958	3	2908.2407
3881	RGL2_MOUSE	778	5.91	2	2	R.HLLDARTAGADMMFTPALLATHR.A	0.9911	3	2510.9348
						R.ELLMQEVKPQPPVEPHSKK.A	0.9937	2	2215.6159
3882	RGL3_MOUSE	709	5.64	2	2	R.ALEKHNVPQPWAR.D	0.9958	1	1546.7721
						R.STPERSGEGQTPIPATDTFLHYR.T	0.9944	2	2561.7703
3883	RGNEF_MOUSE	1693	3.19	3	5	K.DMIAAVDLKVSEYEK.N	0.9958	2	1711.9679
						K.EELQLDHSTVDK.I	0.9958	2	1414.512
						K.ATMPSGAAETEEEVRNLESGR.S	0.9958	2	2235.3875
3884	RGRF2_MOUSE	1189	4.46	2	2	R.CEEEQAGK.E	0.9924	1	950.944
						R.ETLKNCNPPAVPYLGMYLTDLAFIEEGTPN	0.9958	3	4622.1661
3885	RGS11_MOUSE	443	22.57	4	8	R.ELLDDPVGRAHFMDFLQK.E	0.9946	2	2132.4418
						K.GDRMVISCQEQTYWLVNKPPPGAPNILEQ	0.9958	3	3782.2318
						R.LLITVIPHAVAGRDLVEWLVQK.F	0.9958	3	2471.992
						R.QPHRYVLDAAQLHIYMLMK.K	0.9944	3	2328.7986
3886	RGS9_MOUSE	675	4.74	2	6	R.EPSADHSRPQPRAPPK.A	0.9958	1	1770.9455
						R.KEIMYYQQALMR.S	0.9958	1	1574.8964
3887	RHBD3_MOUSE	385	6.49	1	6	R.VEGAVSLLVEGLVDTEALVTEGR.S	0.9944	3	2357.6635
3888	RHG05_MOUSE	1501	4.2	3	5	K.EPRPPSYTVSVVGLSGTEKDK.G	0.993	2	2247.5101
						R.RNWESNYFGMPLQDLVTAEKPIPLFVEK.C	0.9958	3	3323.8341
						K.VNLFILGK.D	0.9944	1	904.1405
3889	RHG12_MOUSE	838	7.4	3	7	R.MTYQSIAIVFGPTLLKPER.E	0.9958	2	2165.5988
						R.LFGHFPGPEFLDIEK.T	0.9943	2	1747.0031
						R.ATTPPNQGRPDSPVYANLQELK.I	0.9958	3	2397.65
3890	RHG17_MOUSE	846	6.86	2	2	K.AALDCSTSHLDEFYSDPHAVAGALKSYLR.I	0.9958	3	3196.4663
						K.KLPLTALAQNMQEASAQLEESLLGK.M	0.9958	3	2685.1083

3891	RHG23_MOUSE	1483	1.21	1	2	R.QMNLGFGDESPEPEAR.G	0.9944	2	1777.9031
3892	RHG25_MOUSE	648	7.87	2	2	K.FVFEVIPASSDQNRIGQDSYVLMASSQVEN	0.9958	3	4021.5056
						K.QVYEEQIKNLEK.E	0.9924	1	1521.7105
3893	RHG30_MOUSE	1101	1.73	1	2	R.LVKILEVLQELPIQNYR.T	0.9958	2	2069.4954
3894	RHOA_MOUSE	193	45.6	6	93	K.HFCPNVPIILVGNK.K	0.9944	2	1608.8901
						K.QVELALWDTAGQEDYDR.L	0.9958	2	2010.1241
						K.DQFPEVYVPTVFENYVADIEVDGK.Q	0.9958	2	2775.0405
						R.IGAFGYMECSAK.T	0.9944	1	1334.4957
						K.HFCPNVPIILVGNKK.D	0.9958	2	1737.0642
						K.MKQEPVKPEEGR.D	0.9956	2	1428.6464
3895	RHOB_MOUSE	196	8.16	1	2	K.HFCPNVPIILVANK.K	0.9958	2	1622.917
3896	RIB1_MOUSE	608	4.93	2	9	K.VTAEVVLVHPGGGSTSR.A	0.9958	2	1666.8747
						R.LAHLGVQIK.G	0.9958	1	979.2107
3897	RIC1_MOUSE	1422	3.38	2	2	K.LLPFCPPVVLAQSVENVWTTCRANK.Q	0.9958	3	2901.3106
						K.APMETLLLSVFRDMVVVFR.A	0.9944	3	2224.7278
3898	RIC8B_MOUSE	560	9.11	4	5	K.KILVPVTTK.E	0.9944	1	999.2822
						R.ALYIVRAGEAGAIER.V	0.9958	1	1589.835
						K.LCNLLRK.C	0.9958	1	917.1057
						K.VSEFPVIVESLK.C	0.9958	2	1347.5945
3899	RIFK_MOUSE	155	30.32	4	4	K.NFDSLESLISAIQGDIEEAK.K	0.9958	2	2180.3734
						K.QLDLPEHLKLK.D	0.9958	2	1334.6017
						K.QLDLPEHLK.L	0.9958	1	1093.2682
						K.SMETHIIHTFK.E	0.9958	2	1344.5713
3900	RILP_MOUSE	369	18.43	3	13	R.LPSQASSSVGAGSAAELVYHLAGALGTEL(	0.9944	3	3283.6659
						R.FGPDAAAGLVPLVVR.A	0.9958	2	1482.766
						R.RSQETEALQEQLQR.L	0.9958	2	1716.8485
3901	RIMB1_MOUSE	1846	2	2	2	R.QALGPGVPPK.A	0.9944	1	964.1527
						K.FNIGFGDRPNLELLRALGELQQR.C	0.9958	3	2658.0353
3902	RIMS1_MOUSE	1463	2.46	2	5	K.ESGALLGLKVVGGK.M	0.9958	2	1328.595
						K.DAPQVLPGQLSVKLWYDK.V	0.9943	2	2058.3849
3903	RIN3_MOUSE	980	4.9	2	2	R.QLASTLLSPLESPIQEASSEK.Q	0.9958	3	2229.4894
						K.ALVEPTLHSEEELEAIVESALYK.C	0.9958	3	2571.8841
3904	RINI_MOUSE	456	72.81	17	109	K.DISSAVQANPALTELSLR.T	0.9958	2	1886.1124
						R.ELDLSNNCMGGPGVLQLLESLK.Q	0.9958	2	2388.7047
						R.ELHLNDNPMGDAGLK.L	0.9958	2	1624.8089
						R.SLLELQMSSNPLGDEGVQELCK.A	0.9958	2	2448.7139
						R.TNELGDGGVGLVLQGLQNPTCK.I	0.9958	2	2271.4986

						R.WTELLPLIQQYEVVR.L	0.9958	2	1888.2169
						K.ELVLSNNDLHEPGVR.I	0.9958	2	1692.8693
						K.LSLQNCGLTEAGCGILPGMLR.S	0.9958	2	2261.574
						R.ALEEERPSLR.I	0.9937	2	1200.3372
						K.LGNAGIAALCPGLLLPSCK.L	0.9958	2	1926.2391
						R.LLCESLLEPGCQLESLWIK.T	0.9958	2	2289.6063
						K.QPSCTLQQLVLYDIYWTNEVEEQLR.A	0.9958	3	3127.4437
						K.DLCDVVASK.A	0.9958	1	1007.0949
						K.TCSLTAASCPYFCSVLTK.S	0.9958	2	2067.2418
						K.LQLEYCNLTATSCEPLASVLR.V	0.9958	2	2439.7004
						R.ELWLGDCDVTNSGCSSLANVLLANR.S	0.9958	3	2765.9691
						K.LLCEGLQDPQCR.L	0.9958	2	1489.6007
3905	RINT1_MOUSE	792	6.19	2	2	K.SDVNTAAPAGSEQLSQGGSDDALLSYVSA	0.9944	3	3329.5555
						R.IQSALKDAEESK.Q	0.9944	2	1319.4545
3906	RIR1_MOUSE	792	2.4	1	2	K.IIDINYYPIPEAHLSNK.R	0.9958	3	2001.2896
3907	RL10_MOUSE	214	35.05	5	26	K.FNADEFEDMVAEK.R	0.9958	2	1545.6606
						R.VHIGQVIMSIR.T	0.9958	2	1253.5486
						K.EHVIEALR.R	0.9958	1	967.113
						R.IFDLGR.K	0.9958	1	720.8467
						K.VDEFPLCGHMVSDEYEQLSSEALEAAR.I	0.9958	2	3084.304
3908	RL10A_MOUSE	217	33.18	7	51	R.ILGPGLNK.A	0.9944	1	812
						K.FPSLLTHNENMVAK.V	0.9958	2	1601.8609
						R.KFLETVELQISLK.N	0.9958	2	1548.8632
						K.AVDIPHMDIEALK.K	0.9958	2	1452.7088
						K.KYDAFLASESLIK.Q	0.9958	1,2	1485.7203
						K.YDAFLASESLIK.Q	0.9958	2	1357.5462
						K.AVDIPHMDIEALKK.L	0.9947	2	1580.8829
3909	RL11_MOUSE	178	31.46	3	30	K.VLEQLTGQTPVFSK.A	0.9958	1,2	1547.7917
						R.KLCLNICVGESGDR.L	0.9958	2	1621.7632
						K.NNFSDTGNFGFGIQEHIDLGIK.Y	0.9958	2	2424.6317
3910	RL12_MOUSE	165	66.06	7	136	K.IGPLGLSPK.K	0.9958	1	882.091
						R.QAQIEVVPSASALIIK.A	0.9958	2	1667.9866
						K.FDPNEVKVVYLR.C	0.9926	2	1479.719
						K.HSGNITFDEIVNIAR.Q	0.9958	2	1686.865
						R.CTGGEVGATSALAPK.I	0.9958	1	1419.5408
						R.HPHDIIDDINSGAVECPAS.-	0.9958	2	2048.1395
						K.EILGTAQSVGCNVDGR.H	0.9958	2	1676.79

3911	RL13_MOUSE	211	25.12	5	20	K.LATQLTGPVMPIR.N	0.9923	2	1397.7191
						K.STESLQANVQR.L	0.9944	1	1233.3237
						K.LILFPR.K	0.9924	1	758.9823
						R.NGMILKPHFHK.D	0.9958	1	1322.614
						K.LATQLTGPVMPIRNVYK.K	0.9932	2	1902.3055
3912	RL13A_MOUSE	203	4.93	1	4	R.LAHEVGWK.Y	0.9958	1	940.0898
3913	RL14_MOUSE	217	18.89	3	10	K.AAIAAAAAAAAAK.A	0.9958	1	1042.2235
						K.LVAIVDVIDQNR.A	0.9958	2	1355.5773
						K.CMQLTDFILK.F	0.993	2	1269.5079
3914	RL15_MOUSE	204	33.33	6	38	R.NPDTQWITKPVHK.H	0.9958	2	1564.7843
						R.RNPDTQWITKPVHK.H	0.9915	2	1720.9718
						K.GATYGKPVHHGVNQLK.F	0.9958	2	1706.9449
						K.FHHTIGGSR.R	0.9958	1	1012.116
						K.FFEVILIDPFHK.A	0.9958	2	1505.7997
						R.NTLQLHR.Y	0.9958	1	882.0103
3915	RL17_MOUSE	184	41.3	5	165	K.GLDVDSLVIEHIQVNK.A	0.9924	2	1780.0312
						K.SAEFLLHMLK.N	0.9958	2	1189.4583
						R.YSLDPENPTK.S	0.9958	1	1164.2573
						R.INPYMSSPCHIEMILTEK.E	0.993	2	2164.5057
						K.EQIVPKPEEEVAQK.K	0.9958	2	1624.8315
3916	RL18_MOUSE	188	14.36	2	8	R.TNRPPLSLSR.M	0.9943	2	1141.3157
						K.ILTFDQLALESPK.G	0.9955	1,2	1475.7252
3917	RL18A_MOUSE	176	12.5	2	15	R.AHSIQIMK.V	0.9958	1	928.1375
						R.IFAPNHVVAK.S	0.9958	1	1096.3176
3918	RL19_MOUSE	196	27.04	5	14	K.VWLDPNETNEIANANSR.Q	0.9958	2	1944.0678
						K.KVWLDPNETNEIANANSR.Q	0.9958	2	2072.2419
						K.KLLADQAEAR.R	0.9958	2	1115.2749
						R.HMYHSLYLK.V	0.9958	1	1192.421
						R.ILMEHIHK.L	0.9915	2	1021.2658
3919	RL21_MOUSE	160	30.63	4	132	R.VYNVTQHAVGIIVNK.Q	0.9958	2	1655.9377
						R.TNGKEPELLEPIPYEFMA.-	0.9958	2	2079.3723
						K.KGDIVDIK.G	0.9958	1	888.0519
						R.VYNVTQHAVGIIVNKQVK.G	0.9958	3	2011.375
3920	RL22_MOUSE	128	45.31	4	25	K.FTLDCTHPVEDGIMDAANFEQFLQER.I	0.9958	2	3085.3376
						K.AGNLGGGVVTIER.S	0.9958	2	1243.4056
						K.ITVTSEVPFSK.R	0.9958	1	1208.3971
						K.SKITVTSEVPFSK.R	0.9958	2	1423.6494

3921	RL23_MOUSE	140	53.57	6	64	R.ISLGLPVGAVINCADNTGAK.N	0.9958	2	1971.2274
						R.LPAAGVGDMVMATVK.K	0.9958	2	1460.7901
						R.LNRLPAAGVGDMVMATVK.K	0.9958	2	1844.2409
						K.DGVFLYFEDNAGVIVNNK.G	0.9958	2	2015.2298
						K.FRISLGLPVGAVINCADNTGAK.N	0.9958	2	2274.5914
						K.KVHPAVVIR.Q	0.9924	1,2	1019.2785
3922	RL23A_MOUSE	156	47.44	7	91	K.VNTLIRPDGEK.K	0.9958	2	1242.4178
						R.LAPDYDALDVANK.I	0.9958	1	1405.5474
						K.KIEDNNTLVFIVDVK.A	0.9958	2	1748.0294
						K.LDHYAIIK.F	0.9958	1	973.1601
						K.FPLTTESAMK.K	0.9958	1	1125.3252
						K.KLYDIDVAK.V	0.9958	1	1065.2548
						R.NKLDHYAIIK.F	0.9958	1	1215.438
3923	RL24_MOUSE	157	15.92	2	14	R.AITGASLADIMAK.R	0.9958	1	1262.5072
						K.VFQFLNAK.C	0.9958	1	967.1558
3924	RL26_MOUSE	145	26.21	3	45	K.ANGTTVHVGIHPSK.V	0.9958	2	1418.5955
						K.FNPFVTSDR.S	0.9958	1,2	1083.1888
						R.HFNAPSHIR.R	0.9944	1	1079.2064
3925	RL27_MOUSE	136	33.82	3	41	K.VYNYNHLMPTR.Y	0.9958	2	1408.6177
						K.NIDDGTSDRPYSHALVAGIDR.Y	0.9958	2	2273.4239
						R.KVTAAMGK.K	0.9958	1	806.0111
3926	RL27A_MOUSE	148	8.78	1	2	K.TGVAPIIDVVR.S	0.9958	1	1140.3683
3927	RL28_MOUSE	137	7.3	1	4	R.KPATSYVR.T	0.9958	1	922.0721
3928	RL29_MOUSE	160	8.13	1	8	K.ALVKPQAIKPK.M	0.9958	2	1193.5186
3929	RL3_MOUSE	403	24.81	7	42	K.SINPLGGFVHYGEVTNDFIMLK.G	0.9958	2	2452.8304
						R.LEQQVPVNQVFGQDEMIDVIGVTK.G	0.9919	2	2688.068
						K.DDASKPVHLTAFLGYK.A	0.9958	2	1763.0031
						K.AHLMEIQVNGGTVAEK.L	0.9958	2	1697.947
						K.KAHLMEIQVNGGTVAEK.L	0.9958	2	1826.1211
						R.ERLEQQVPVNQVFGQDEMIDVIGVTK.G	0.9958	2	2973.371
						R.HGSLGFLPR.K	0.9958	1	984.1459
3930	RL30_MOUSE	115	39.13	3	31	K.LVILANNCPALR.K	0.9958	2	1354.6018
						K.TGVHHYSGNNIELGTACGK.Y	0.9944	2	2016.1437
						R.KSEIEYYAMLAK.T	0.9952	2	1446.7015
3931	RL31_MOUSE	125	27.2	3	44	R.IHGVGFK.K	0.9958	1	757.9108
						K.LYTLVTYVPVTTFK.N	0.9929	2	1645.9793
						R.EYTINIHK.R	0.9958	1	1018.1576

3932	RL32_MOUSE	135	23.7	3	33	K.GQILMPNIGYGSNKK.T	0.9958		2	1620.9073
						K.SYCAEIAHNVSSK.N	0.9958		2	1466.5567
						K.GQILMPNIGYGSNK.K	0.9958		2	1492.7332
3933	RL35_MOUSE	123	30.89	3	11	R.VLTVINQTQK.E	0.9958		1	1144.3567
						K.QLDDLKVELSQLR.V	0.9923		2	1557.7874
						K.YKPLDLRPK.K	0.9958		2	1130.3757
3934	RL35A_MOUSE	110	22.73	2	2	R.DETEFYLGK.R	0.9958		1	1102.1858
						K.NNTVTPGGKPNK.T	0.9944		2	1227.3628
3935	RL36_MOUSE	105	18.1	2	3	R.AMELLK.V	0.9924		1	704.903
						R.YPMAVGLNK.G	0.9924		1	993.2091
3936	RL36A_MOUSE	106	9.43	1	4	K.HFELGGDK.K	0.9958		1	902.9823
3937	RL38_MOUSE	70	30	2	19	K.DFLLTAR.R	0.9958		1	835.9786
						R.YLYTLVITDK.E	0.9958		1	1229.4589
3938	RL4_MOUSE	419	38.66	12	128	K.NVTLPAVFK.A	0.9958		1	989.2028
						R.IEEVPELPLVVEDKVEGYK.K	0.9958		2	2186.5072
						K.KLEAAATALATK.S	0.9958	1,2		1188.4099
						R.YAICSALAASALPALVMSK.G	0.9958		2	1938.299
						R.NIPGITLLNVSK.L	0.9958		1	1269.5272
						R.QPYAVSELAGHQTSAESWGTGR.A	0.9958		2	2333.4789
						R.KLDELYGTWR.K	0.9958		2	1281.4539
						R.RGPCIIYNEDNGIIK.A	0.9958		2	1762.9696
						K.SNYNLPMHK.M	0.9952		2	1104.2689
						R.IEEVPELPLVVEDK.V	0.9958		2	1609.8572
						K.APIRPDIVNFVHTNLR.K	0.9958	2,3		1863.1728
						K.RYAICSALAASALPALVMSK.G	0.9958		2	2094.4865
3939	RL5_MOUSE	297	38.05	8	58	K.HIMGQNVADYMR.Y	0.9958	1,2		1435.6587
						K.GAVDGGLSIPHSTK.R	0.9958	1,2		1339.4911
						K.RFPGYDSESK.E	0.9958		1	1186.2664
						R.IEGDMIVCAAYAHELPK.Y	0.9952		2	1918.1811
						K.VGLTNYAAAYCTGLLLAR.R	0.9958		2	1928.2048
						K.NNVTPDMMEEMYK.K	0.9958		2	1602.8325
						R.YLMEEDEDAYKK.Q	0.9958	1,2		1534.6777
						K.EFNAEVHR.K	0.9958		1	1002.0745
3940	RL6_MOUSE	296	42.57	10	75	R.SQFSLTNGMYPHK.L	0.9958		2	1510.7075
						K.QLDSGLLLVTGPLVINR.V	0.9958		2	1809.1594
						R.SSITPGTVLIILTGR.H	0.9958		2	1528.8326
						K.HLTDAYFK.K	0.9958	1,2		995.1228

						K.AVDLQILPK.I	0.9958	1	997.223
						K.FVIATSTK.V	0.9958	1	867.033
						R.NPVLVR.G	0.9958	1	697.8558
						R.HQEGEIFDTEK.E	0.9958	1,2	1333.3971
						K.EKYEITEQR.K	0.9958	1	1196.3024
						K.KAGSDAAASRPR.A	0.9958	2	1187.3011
3941	RL7_MOUSE	270	37.41	9	72	R.GYGKINK.K	0.9944	1	779.9145
						K.FGIICMEDLIHEIYTVGK.R	0.9958	2,3	2139.4805
						R.IALTDNSLIAR.S	0.9958	1	1187.3818
						K.KVPAVPETLK.K	0.9958	1,2	1082.3287
						K.TTHFVEGGDAGNREDQINR.L	0.9958	2	2117.1991
						R.KAGNFYVPAEPK.L	0.9958	2	1321.5187
						K.KVATVPGTLK.K	0.9958	1	1014.2535
						K.VATVPGTLK.K	0.9944	1	886.0794
						K.TTHFVEGGDAGNR.E	0.9958	2	1361.4135
3942	RL7A_MOUSE	266	45.86	10	136	K.VAPAPAVVK.K	0.9924	1	852.0647
						K.VPPAINQFTQALDR.Q	0.9944	1	1570.7886
						K.NFGIGQDIQPK.R	0.9958	1	1217.3671
						K.AQLVVIAHDVDPIELVVFLPALCR.K	0.9944	2	2689.1797
						K.KVVNPLFEK.R	0.9949	2	1074.3085
						K.VVNPLFEK.R	0.9924	1	946.1344
						R.KTCTTVAFTQVNSEDK.G	0.9958	2	1829.9678
						R.AGVNTVTTLVENKK.A	0.9958	2	1474.6976
						K.KVAPAPAVVK.K	0.9944	1	980.2388
						R.HWGGNVLGPK.S	0.9944	1	1065.2199
3943	RL8_MOUSE	257	47.86	10	81	R.ASGNYATVISHNPETK.K	0.9958	1	1689.8223
						R.AVVGVVAGGGR.I	0.9958	1	942.1062
						R.TELFIAAEGIHTGQFVYCGK.K	0.9947	2	2242.5023
						K.KAQLNIGNVLPVGTMPEGTIVCCLEEKPGD	0.9958	3	3397.844
						K.DIIHDPGR.G	0.9958	1	923.0165
						K.AQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	0.9958	2,3	3269.6699
						K.KVISSANR.A	0.9924	1	875.0158
						R.KVGLIAAR.R	0.9924	1	828.0457
						R.GAPLAKVVFR.D	0.9912	2	1058.3121
						K.RTELFIAAEGIHTGQFVYCGK.K	0.9958	2	2398.6898
3944	RL9_MOUSE	192	60.42	7	57	R.DFNHINVELSLLGK.K	0.9958	2	1599.8271
						R.SVYAHFPINVVIQENGSLVEIR.N	0.9958	2	2485.8455

						K.TILSNQTVDIPENVEITLK.G	0.9958		2	2128.4277
						K.DELILEGNDIELVSNSAALIQQATTVK.N	0.9958		3	2886.2261
						R.KFLDGIYVSEK.G	0.9958	1,2		1299.5095
						R.TICSHVQNMIK.G	0.9958		2	1331.539
						K.FLDGIYVSEK.G	0.9958		1	1171.3355
3945	RLA0_MOUSE	317	18.93	3	12	K.TSFFQALGITTK.I	0.9958		2	1314.5242
						K.AFLADPSAFAAAAPAAAATTAAPAAAAAPA	0.9958		2	2698.0507
						R.GHLENNPALEK.L	0.9958		2	1222.3433
3946	RLA1_MOUSE	114	53.51	2	76	K.AAGVSVEPFWPGLFAK.A	0.9958	1,2		1676.9555
						K.ALANVNIGSLICNVGAGGPAPAAGAAPAGC	0.9958		3	3785.1718
3947	RLA2_MOUSE	115	76.52	7	98	R.YVASYLLAALGGNSSPSAK.D	0.9958		2	1870.1125
						K.LASVPAGGAVAVSAAPGSAAPAAGSAPAA	0.9958		2	2776.0758
						K.NIEDVIAQGVGK.L	0.9958		1	1243.4026
						K.ILDSVGIEADDDRLNK.V	0.9958		2	1773.9377
						K.LASVPAGGAVAVSAAPGSAAPAAGSAPAA	0.9958		3	2904.2499
						K.ILDSVGIEADDDR.L	0.9958	1,2		1418.5004
						K.KILDSVGIEADDDR.L	0.9958		2	1546.6745
3948	RM01_MOUSE	314	25.8	4	31	K.TVEPFASVIALPHLFSSEVNK.V	0.9958		2	2286.6329
						K.IAEENGAAFAGGTDLVK.K	0.9958		2	1663.8247
						K.KFQVLDFTNPK.Q	0.9958		2	1337.5614
						K.IATLDMPSDQIAANLQAVINEVCK.H	0.9958		2	2615.9679
3949	RM02_MOUSE	306	15.69	2	11	R.MAVAAQEGDAHPLGALPVGTLINNVESEP(	0.9958		3	3115.4882
						R.KVNGTAIIQLPSK.R	0.9958		2	1369.6475
3950	RM03_MOUSE	348	25.57	5	47	K.HNIIYVNGSVPGHK.N	0.9958		2	1535.7458
						R.RPGAISTGDIAR.V	0.9941		2	1214.3671
						K.SSTWWDEHLSEENLSFVK.Q	0.9958		2	2195.3495
						K.HAVTLLQVQDCHVLK.Y	0.9958		2	1762.0282
						K.LNPLKDEPWPLHPWEPGSFR.V	0.9958		2	2416.7441
3951	RM04_MOUSE	294	17.01	3	7	R.IGLAELHPDVFATAPR.L	0.9958		2	1707.9701
						R.RPVQAWVESLR.G	0.9958		2	1341.5558
						K.HQTLVLTLPSVAFLEDK.L	0.9952		2	1912.2365
3952	RM09_MOUSE	265	30.19	5	8	R.WGEYWCDVTVNGLDTVR.V	0.9958		2	2071.2195
						K.FLRSCHLEVGMK.N	0.9958		1	1477.7308
						K.LLSQGLAVYASPENR.K	0.9924		2	1618.8302
						K.DNLELILTQSVDEIGVR.G	0.9958		2	1915.1509
						K.HWLAQQAAK.S	0.9958		1	1053.2089
3953	RM10_MOUSE	262	33.97	5	31	R.YLLQHQPVQLTSLLDQYVK.E	0.9932		2	2287.6641

						R.NLLPLFVGHNLLLVSEEPK.V	0.9958		2	2133.5388
						K.SVPFLPLLGGCVDDTILSR.Q	0.9952		2	2060.3643
						R.CLPPPPKPPK.E	0.9958		1	1131.3697
						R.YLLQHQPVQLTSLLDQYVKEQNEGDCATS	0.9958		3	3822.1432
3954	RM11_MOUSE	192	32.29	4	11	K.AKDDAFAMQDVPLSSVVR.S	0.9958		2	1950.217
						R.AGQAIPGPPLGPILGQR.G	0.9958		2	1642.9419
						K.DLSAEELEAFQK.E	0.9958		1	1380.4943
						K.HVYEIACVK.A	0.9958		1	1119.272
3955	RM12_MOUSE	201	52.24	7	353	K.IQQLVQDIASLTLLEISDLNELLK.K	0.9958	2,3		2711.1687
						K.NYVQGINLVQAK.K	0.9958	1,2		1347.5571
						K.KLVESLPQEIK.A	0.9958		2	1284.5388
						K.IQDVGLMPMGGMVPGPVSAAAPASEAAEE	0.9958	2,3		3352.8142
						K.IQQLVQDIASLTLLEISDLNELLKK.T	0.9958		2	2839.3428
						R.SEALAGAPLDNAPK.E	0.9958		1	1354.5028
						R.RSEALAGAPLDNAPK.E	0.9958		2	1510.6903
3956	RM13_MOUSE	178	33.15	4	11	K.VYSSHTGYPGGFR.Q	0.9958		2	1428.5467
						R.LHLFPDEDIPEDILK.N	0.9958		2	1795.0423
						K.RLDEYTQEEIEAFPR.V	0.9958		2	1897.0514
						R.HIAFSGNK.W	0.9958		1	873.9871
3957	RM14_MOUSE	145	15.86	2	2	K.FDSNNVVLIEDNGNPVGTRIK.I	0.9958		2	2302.5492
						K.FDSNNVVLIEDNGNPVGTR.I	0.9958		2	2061.2157
3958	RM15_MOUSE	295	10.17	2	3	R.VDPTQPIDLTQLVNGR.G	0.9958		2	1766.9921
						K.YGFNEGHSFR.H	0.9944		2	1214.2822
3959	RM16_MOUSE	251	7.17	1	3	K.TLLPVPTFENVSIPER.S	0.9958		2	1813.1039
3960	RM17_MOUSE	176	21.59	1	3	R.DSNLTLLNQLLLGLQQDLHHNQDASLHSS(	0.9958		3	4041.4332
3961	RM20_MOUSE	149	23.49	2	4	R.QQEGFAAALGDGKEPEGIFSR.V	0.9958	2,3		2208.3922
						K.YPAFIVNLIK.C	0.9958		1	1178.46
3962	RM21_MOUSE	209	31.1	3	4	K.RVNELIATGQYGR.L	0.9958		2	1477.6633
						K.TSLSSPPWQEVVLPDPVEETR.H	0.9958		2	2367.6177
						R.LVSVCSRSILASQGSGSASLWSASR.R	0.9958		3	2567.8278
3963	RM22_MOUSE	206	16.02	2	2	R.GMSIDQALAQLEFNDK.K	0.9958		2	1780.9904
						K.LVEGPPPPPEVPK.T	0.9958		2	1356.6048
3964	RM23_MOUSE	146	55.48	4	18	R.NVLYPLYQLGGPQLR.V	0.9958		2	1732.0354
						K.VAYVQLAHGQTFTFPDLFPEK.D	0.9958		2	2409.7466
						R.TNFFIQLVRPGTAQPEDTVQFR.I	0.9958		2	2565.8913
						R.NYLEQIYNVPVAAVR.T	0.9958		2	1750.0073
3965	RM24_MOUSE	216	26.39	4	18	R.NWVVLEGLNTHYR.Y	0.9958		2	1601.8051

						R.GTMIASEAPLLHHQVK.L	0.9958		2	1733.0386
						R.YGMSRPGSIADK.R	0.9958		2	1282.4571
						R.KPTEIQWR.F	0.9957		2	1058.2254
3966	RM27_MOUSE	148	33.78	3	34	K.MEGHYVHAGNILGTQR.Q	0.9958		2	1784.0025
						K.TFVHVVPAKPEGTFK.L	0.9958		2	1657.953
						K.NTEAVDLVTSLPK.G	0.9924		2	1387.5731
3967	RM28_MOUSE	257	32.3	4	27	R.ERVEDVPIPVHYPPESQQGLWGGEGLILG`	0.9958		3	3492.9157
						R.SFVIPEAEAEWVGLTLEEALEK.Q	0.9958		2	2461.7711
						R.LQEQVLSRPAVVQK.R	0.9958		2	1595.8827
						R.YPVHLWQK.L	0.9958	1,2		1071.2669
3968	RM30_MOUSE	160	13.13	1	5	K.STGELVVQWHLKPVEQEAK.S	0.9958		2	2179.4808
3969	RM32_MOUSE	187	10.7	1	2	R.APSVETMVLYTGEKPSEK.D	0.9958		2	1967.2415
3970	RM33_MOUSE	65	46.15	2	19	K.LSLLHYDPIVNK.K	0.9958	1,2		1412.672
						K.LVSQAGTGFSFNHK.R	0.9924		2	1493.6622
3971	RM37_MOUSE	423	9.69	3	8	K.KVVVEPVGPVDFQPETFR.K	0.9958		2	2044.358
						K.VVVEPVGPVDFQPETFR.K	0.9958		2	1916.1839
						K.KVLSLVDDPANHIENQEQR.V	0.9958		2	2206.4203
3972	RM38_MOUSE	380	10.26	2	7	R.TPPLGPMPNEDIDVSNLER.L	0.9958		2	2095.3319
						R.WDDSVTHTFHQLLDMR.E	0.9958		2	2002.2115
3973	RM39_MOUSE	336	10.12	2	10	K.SILALVDGQPWDMYKPLTK.S	0.9958		2	2176.5787
						R.FQGLSLPTHLR.A	0.9958		2	1269.4893
3974	RM41_MOUSE	135	6.67	1	2	K.LFQLYPK.N	0.9958		1	909.1161
3975	RM43_MOUSE	183	7.65	1	6	R.FLTSVLHNGLGR.Y	0.9958		2	1314.5302
3976	RM45_MOUSE	306	21.24	3	7	R.WGFVESLEPAQVVHVR.C	0.9958		2	1854.1185
						R.LERPIHLACTAGIFDPYVPPEGDAR.M	0.9958		3	2796.1211
						R.LHTLVTEHCFPDMVWDLK.Y	0.9958		2	2242.5635
3977	RM46_MOUSE	283	10.95	2	12	K.ALTPLQEEMAGLLQQIEVER.S	0.9958		2	2269.6184
						R.SLYSDHELR.A	0.9958		1	1120.2071
3978	RM48_MOUSE	211	6.16	1	2	K.ARPELEELLAK.L	0.9958		2	1269.4838
3979	RM49_MOUSE	166	23.49	3	13	K.TPITQVNEVTGTLR.I	0.9958		2	1529.7337
						K.DVEEFLSPLLGK.T	0.9924		1	1347.5511
						R.KVEGDIWALQK.D	0.9958		2	1287.5015
3980	RM50_MOUSE	159	23.27	2	39	K.SKFDELVASNLPPNLK.I	0.9958		2	1773.0391
						R.LLAGLADGLGHAVPNSR.L	0.9958		2	1661.9016
3981	RM51_MOUSE	128	25	2	5	R.ALFGVYDNIGILGNFEK.H	0.9958		2	1871.143
						R.MFIEDLHNLNK.R	0.9958		2	1374.5976
3982	RM52_MOUSE	121	28.93	1	8	R.LQQGLAANPSGYGPLTELPDWSFADGRP/	0.9958		3	3483.9232

3983	RM53_MOUSE	118	16.95	1	13	R.GAHLTTQEMLSALASHIR.D	0.9958	3	1937.2243
3984	RM55_MOUSE	127	22.05	2	3	R.MLAMPLDLDALSPEER.R	0.9944	2	1802.1109
						R.LYPVLLVK.Q	0.9958	1	945.2334
3985	RN123_MOUSE	1314	4.26	3	3	K.ACINQHLMNNK.D	0.9952	2	1343.5097
						R.SICYLLGQPEPLAPGTTLPAPDR.K	0.9924	2	2467.7907
						R.VTGIVQEKLLSDYLYR.I	0.9917	2	1898.2096
3986	RN19B_MOUSE	732	10.38	2	2	K.ILWQLGTLIGAPVGISLIAGIAIPAMVIGIPVY	0.9924	3	3772.7008
						R.SHAAACPSTPQVHGAPSPSAHKNLAAPAE	0.9944	3	3489.8388
3987	RNBP6_MOUSE	1105	2.99	2	2	K.DFEQYLPLVIEPLIK.T	0.9932	2	1818.1632
						K.FMQDASNVMQLLLK.T	0.9958	2	1638.9807
3988	RNF34_MOUSE	376	5.32	1	2	R.ASLSDLSSLEEVEGMSVR.Q	0.9909	2	1910.1035
3989	RNH2A_MOUSE	301	3.32	1	3	R.LADLEALK.V	0.9958	1	873.0373
3990	RNT2_MOUSE	259	5.79	1	3	K.LILTQHWPPTVCK.E	0.9921	2	1593.8755
3991	RNZ2_MOUSE	831	2.77	1	2	R.FGPDTQHLILNENCPSVHNLR.S	0.993	2	2462.6934
3992	ROA1_MOUSE	320	33.44	7	16	R.SSGPYGGGGQYFAKPR.N	0.9958	2	1629.7721
						R.NQGGYGGSSSSSSYGSGR.R	0.9958	1	1695.6561
						R.EDSQRPGAHLTVK.K	0.9958	2	1438.5833
						K.KIFVGGIK.E	0.9944	1	862.1032
						K.LFIGGLSFETTDESLR.S	0.9958	2	1785.9915
						R.SHFEQWGTLTDCVVMR.D	0.9958	2	1967.1725
						K.YHTVNGHNCEVR.K	0.9958	2	1486.5529
3993	ROA2_MOUSE	353	38.24	9	66	R.GFGFVTFDDHDPVDK.I	0.9958	2	1696.8132
						K.YHTINGHNAEVR.K	0.9958	2	1411.5198
						R.NMGGPYGGGNYGPGGSGGSGGYGGR.S	0.9958	2	2191.2555
						R.GGGGNFGPGPGSNFR.G	0.9958	2	1378.4465
						K.LFIGGLSFETTEESLR.N	0.9958	2	1800.0184
						K.RGFGFVTFDDHDPVDK.I	0.9909	2	1853.0007
						R.KLFIGGLSFETTEESLR.N	0.9958	2	1928.1925
						K.KLFVGGIK.E	0.9924	1	862.1032
						R.GFGDGYNGYGGGPGGGNFGGSPGYGGG	0.9958	2	2496.5303
3994	ROA3_MOUSE	379	23.22	7	25	K.LFIGGLSFETTDDSLR.E	0.9958	2	1771.9647
						K.IFVGGIKEDTEEYNLR.D	0.9958	2	1884.096
						R.GGNFGGGGGNFGR.G	0.9958	1	1154.1869
						R.KLFIGGLSFETTDDSLR.E	0.9958	2	1900.1387
						R.EDSVKPGAHLTVK.K	0.9958	2	1381.5718
						R.GFAFVTFDDHDTVDK.I	0.9958	2	1714.8285
						K.LFIGGLSFETTDDSLREHFEK.W	0.9958	3	2442.6873

3995	ROAA_MOUSE	285	18.95	3	14	R.EYFGQFGEIEAIELPIDPK.L	0.9958	2	2196.4614
						K.KIFVGGLNPEATEEK.I	0.9958	2	1632.8541
						R.GFVFITFKEEDPVK.K	0.9958	2	1656.9189
3996	ROCK1_MOUSE	1354	6.72	5	8	K.EQSSPSMVLDIDKLFHVRPVTQGDVYR.A	0.9944	3	3118.5347
						R.ELQDQLEAEQYFSTLYK.T	0.9958	2	2106.2934
						K.ETLSTQLDLAETKAESEQLAR.G	0.9958	2	2334.5425
						K.ILFYNDEQDK.E	0.9958	1	1285.3959
						K.EEEINNLK.A	0.9958	1	989.0703
3997	ROCK2_MOUSE	1388	5.98	4	4	R.SPINVESLLDGLNSLVLDLDFPALR.K	0.9958	2	2712.1155
						K.SNMEIDMTYQLKVIQQSLEQEEAEHK.T	0.9958	3	3123.4769
						K.KLYALEEHLSSEVQAK.E	0.9958	2	1846.0905
						K.EELNNKLK.D	0.9958	1	988.1289
3998	ROP1L_MOUSE	230	8.7	1	3	K.FLALGCSSLGRTLNTAMK.N	0.9924	2	1941.2623
3999	ROS_MOUSE	2340	1.92	2	3	R.TSVSVSEPAKFNQFTIIQTSLKPLPGNFSST	0.9944	3	3553.0496
						R.QGEFPSAK.L	0.9958	1	863.9457
4000	RP1_MOUSE	2095	2.34	3	4	K.IYPFMPQSKK.H	0.9944	1	1239.5182
						R.VSSDNPGMYGNADTTSVDTLIDK.N	0.9934	2	2401.5611
						K.ENGKLIDNGK.W	0.9958	1	1088.2059
4001	RP1L1_MOUSE	1859	3.5	3	3	R.HQDVKEDSPWVSSGESQGR.V	0.9921	2	2129.2071
						R.RQQTVVLSHK.N	0.9944	1	1196.3951
						R.MLSQEDLGTVQGADEKQGLGVAEGEEGE	0.9958	3	3063.2739
4002	RPA49_MOUSE	482	5.39	2	4	R.MIEIAKAMR.L	0.9958	1	1063.3619
						R.ALGPGIPHIINTK.L	0.9924	1	1331.6011
4003	RPAC1_MOUSE	346	4.62	1	3	K.DHAKFSPVATASYR.L	0.9909	2	1550.7141
4004	RPAP1_MOUSE	1409	3.12	2	2	R.LMETIVQEFLPTSWSPIGVGPTPSLYK.V	0.9958	3	2992.5
						R.SHGFHRPNLVTGK.G	0.9958	2	1450.6431
4005	RPB1_MOUSE	1970	1.62	2	2	R.TTSNDIVEIFTVLGIEAVR.K	0.9958	2	2078.3703
						K.QDVIEVIEK.A	0.9924	1	1073.2316
4006	RPC2_MOUSE	1133	4.32	2	3	K.DVPITYK.G	0.9958	1	835.9756
						K.GVCGLIVPQEDMPFCDSGICPDIIMNPHGFI	0.9958	3	4234.7883
4007	RPGP2_MOUSE	712	8.29	3	7	R.GGLDVTHGQTGVESVYTTFR.D	0.9912	2	2125.3024
						R.IPLAGLSKLPSVPQIAK.A	0.9958	2	1733.1478
						K.EFLDLLGDTITLQDFK.G	0.9958	2	1869.1217
4008	RPIA_MOUSE	303	23.76	5	31	K.AGPVVTDNGNFILDWK.F	0.9956	2	1746.9603
						K.NNQVLGIGSGSTIVHAVQR.I	0.9958	2	1951.1929
						R.VKQENLDLICIPTSFQAR.Q	0.9958	2	2133.4186
						K.LASHTAVENHVK.N	0.9958	1,2	1306.4642

						K.KLASHTAVENHVK.N	0.9958	2	1434.6383
4009	RPN2_MOUSE	631	3.01	1	5	R.LQVSNVLSQPLAQAAVK.L	0.9958	2	1767.0788
4010	RPTOR_MOUSE	1335	4.64	2	2	R.VGAISCLAFHPHWPHLAVGSNDYYISVYSV	0.9958	3	3619.0393
						K.NYPLPSPAATEGGSLTPVRDSPCTPR.L	0.9946	2	2741.9837
4011	RRBP1_MOUSE	1605	12.34	10	25	R.LIEILSEKTGVIQDTWHK.A	0.9931	3	2111.446
						K.KPPTLEPSMDIVLK.L	0.9958	2	1568.9122
						K.QVLQLQASHK.E	0.9924	1	1152.339
						K.ETLLALLPGLSISAHQNYAEWLQEFK.E	0.9924	3	2973.3984
						K.VEPAVSSIVNSIQVLASK.S	0.9958	2	1842.143
						R.SHVEDGDVAGSPAVPPAEQDPMK.L	0.9958	2	2334.5195
						K.HMAAASAECQNYAK.E	0.9958	2	1552.6679
						R.VSAVAVAPTSVHSSVGHTPIATVPAMPQEK	0.9958	2	2970.4137
						K.IPEHDLDPNVTIILK.E	0.9958	2	1718.0031
						R.EHTSHLEAELEK.H	0.9958	2	1423.5223
4012	RREB1_MOUSE	1700	3.59	2	2	K.KPEPEAGQAEPLSPRPPPCPTLSVTVEPK.	0.9958	3	3110.5005
						K.DIEKNIEYVSSPTAELVDAFCAPETVCR.L	0.9958	3	3215.4702
4013	RRFM_MOUSE	262	33.97	5	45	R.ESGMNLNPEVEGTLIR.V	0.9958	2	1759.9721
						R.TAPGSLDHITVVTADGK.V	0.9958	2	1682.8711
						R.ALVEDIISLEEVDEDMK.S	0.9958	2	1949.1775
						K.VALNQIGQISMK.S	0.9958	1,2	1302.5749
						K.SPQVILVNMASFPECTAAAIK.A	0.9958	2	2248.6087
4014	RS10_MOUSE	165	27.27	3	35	K.KAEAGAGSATEFQFR.G	0.9958	2	1570.7019
						R.DYLHLPPEIVPATLR.R	0.9912	2	1735.0361
						R.IAIYELLFK.E	0.9944	1	1110.3819
4015	RS11_MOUSE	158	38.61	5	25	R.DVQIGDIVTVGECRPLSK.T	0.9958	2	1987.2268
						K.NIGLGFK.T	0.9944	1	748.9004
						R.ILSGVVTK.M	0.9944	1	817.0165
						K.NMSVHLSPCFR.D	0.9958	2	1348.5286
						K.RVLLGETGK.E	0.9958	1	973.1606
4016	RS12_MOUSE	132	25.76	3	25	K.TALIHDGLAR.G	0.9958	1	1067.2333
						K.DVIEEYFK.C	0.9944	1	1043.1614
						K.KLGEWVGLCK.I	0.9958	2	1190.3941
4017	RS13_MOUSE	151	29.14	4	34	K.GLAPDLPEDLYHLIK.K	0.9958	2	1694.9683
						K.GLSQSALPYR.R	0.9958	1	1092.2401
						K.KGLTPSQIGVILR.D	0.9958	2	1382.6896
						K.GLTPSQIGVILR.D	0.9958	2	1254.5155
4018	RS14_MOUSE	151	62.25	6	58	R.IEDVTPIPSDSTR.R	0.9958	2	1430.5547

						K.TPGPGAQSALR.A	0.9958	2	1055.1789
						R.DESSPYAAMLAAQDVAQR.C	0.9958	2	1924.0924
						K.ADRDESSPYAAMLAAQDVAQR.C	0.9958	2	2266.4473
						K.EEQVISLGPQVAEGENVFGVCHIFASFNDT	0.9958	3	4379.7926
						K.KEEQVISLGPQVAEGENVFGVCHIFASFND	0.9958	3	4507.9667
4019	RS15_MOUSE	145	68.28	5	90	R.DMIILPEMVGSMVGVYNGK.T	0.9958	2	2054.4855
						K.TFNQVEIKPEMIGHYLGEFSITYKPVKHGRF	0.9958	3	4485.1229
						R.GVDLDQLLDMSYEQLMQLYSAR.Q	0.9958	2	2589.9381
						K.TFNQVEIKPEMIGHYLGEFSITYKPVK.H	0.9958	3	3170.6936
						K.EAPPMEKPEVVK.T	0.9924	2	1354.6043
4020	RS15A_MOUSE	130	37.69	5	20	R.MNVLADALK.S	0.9944	1	975.1913
						K.WQNNLLPSR.Q	0.9958	1	1128.2761
						K.ILGFFF.-	0.9958	1	743.9237
						R.QFGFIVLTTSAGIMDHEEAR.R	0.9958	2	2223.5084
						K.WQNNLLPSRQFGFIVLTTSAGIMDHEEAR.I	0.991	3	3332.7613
4021	RS16_MOUSE	146	33.56	4	22	K.GPLQSVQVFGR.K	0.9958 1,2		1188.372
						K.DILIQYDR.T	0.9958	1	1036.1729
						K.LLEPVLLLGK.E	0.9958	1	1095.4111
						K.VNGRPLEMIEPR.T	0.9958	2	1411.6623
4022	RS17_MOUSE	135	55.56	5	87	R.DNYVPEVSALDQEIIEVDPDTK.E	0.9958	2	2490.6801
						K.LLDFGSLSNLQVTQPTVGMNFK.T	0.9958	2	2410.7907
						R.RDNYVPEVSALDQEIIEVDPDTK.E	0.9958	2	2646.8676
						K.IAGYVTHLMK.R	0.9958 1,2		1133.3941
						K.RVCEEIAIIPSK.K	0.9958 1,2		1415.6391
4023	RS18_MOUSE	152	29.61	4	12	K.YSQVLANGLDNK.L	0.9958	1	1322.4606
						R.VITIMQNPR.Q	0.9958 1,2		1072.311
						R.KADIDLTK.R	0.9958	1	904.0513
						K.IPDWFLNR.Q	0.9917 1,2		1061.2285
4024	RS19_MOUSE	145	34.48	5	34	K.ELAPYDENWFYTR.A	0.9958	2	1704.8358
						K.VPEWVDTVK.L	0.9944 1,2		1073.234
						R.IAGQVAAANK.K	0.9924	1	943.091
						R.RVLQALEGLK.M	0.9958	2	1127.3726
						R.VLQALEGLK.M	0.9958	1	971.1851
4025	RS2_MOUSE	293	27.3	5	45	K.SPYQEFTDHLVK.T	0.9952	2	1464.6177
						K.AFVAIGDYNGHVGLGVK.C	0.9943	2	1717.9652
						K.SLEEIYLFSLPIK.E	0.9958 1,2		1552.8511
						K.ESEIIDFFLGASLKDEVLK.I	0.9958	2	2154.465

						K.TYSYLTPDLWK.E	0.9958	1,2		1387.5749
4026	RS20_MOUSE	119	39.5	4	105	K.TPVEPEVAIHR.I	0.9958		2	1248.4245
						K.RLIDLHSPSEIVK.Q	0.9958		2	1507.7733
						R.LIDLHSPSEIVK.Q	0.9958	1,2		1351.5859
						K.QITSISIEPGVEVEVTIADA.-	0.9958		2	2072.3172
4027	RS21_MOUSE	83	32.53	2	6	K.DHASIQMNVAEVDR.T	0.9958		2	1585.7319
						K.TYGICGAIR.R	0.9943		2	1011.1321
4028	RS23_MOUSE	143	53.85	8	65	K.GHAVGDIPGVR.F	0.9958	1,2		1078.2162
						K.VANVSLLALYK.G	0.9924	1,2		1191.4563
						K.ANPFGGASHAK.G	0.9958		1	1057.1539
						K.ITAFVPNDGCLNFIEENDEVLVAGFGR.K	0.9958		3	2998.2849
						K.AHLGTALK.A	0.9944		1	810.9719
						K.KITAFVPNDGCLNFIEENDEVLVAGFGR.K	0.9958		3	3126.459
						R.KGHAVGDIPGVR.F	0.9958	1,2		1206.3903
						K.KAHLGTALK.A	0.9958		1	939.1459
4029	RS24_MOUSE	133	27.82	3	11	K.TTGFGMIYDSLDYAK.K	0.9958		2	1682.8854
						K.QMVIDVLHPGK.A	0.9958		2	1237.5029
						R.THFGGGK.T	0.9924		1	703.7758
4030	RS25_MOUSE	125	18.4	2	12	K.LNNLVLFDK.A	0.9912	1,2		1076.281
						K.LITPAVVSER.L	0.9958	1,2		1085.2889
4031	RS26_MOUSE	115	34.78	3	11	R.DISEASVFDAYVLPK.L	0.9958	1,2		1654.8572
						R.NIVEAAAVR.D	0.9944		1	943.091
						K.LHYCVSCAIHSK.V	0.9958	1,2		1475.6197
4032	RS27_MOUSE	84	15.48	1	3	K.DLLHPSPEEEK.R	0.9958		1	1294.4039
4033	RS28_MOUSE	69	26.09	2	7	R.EGDVLTLLESER.E	0.9958		1	1361.4918
						K.GPVREGDVLTLLESER.E	0.9958		1	1770.9805
4034	RS3_MOUSE	243	53.91	8	109	K.GGKPEPPAMPQPVPTA.-	0.9958	1,2		1574.8352
						K.RFGFPEGSVELYAEK.V	0.9958		2	1729.9298
						K.KPLPDHVSIVEPK.D	0.9958		2	1459.7288
						R.FIMESGAKGCEVVVSGK.L	0.9958		2	1799.0583
						K.FVDGLMIHSGDPVNYYVDTAVR.H	0.9958		2	2469.7742
						R.GLCAIAQAESLR.Y	0.9958		2	1289.4405
						K.DEILPTTPISEQK.G	0.9958		1	1471.6476
						K.IMLPWDPSGKIGPK.K	0.9929		2	1539.8761
4035	RS30_MOUSE	59	22.03	2	28	R.FVNVVPTFGK.K	0.9958		1	1108.3256
						R.RFVNVVPTFGK.K	0.9958		2	1264.5131
4036	RS3A_MOUSE	264	41.67	9	152	K.ACQSIYPLHDVFVR.K	0.9958	1,2		1705.9201

						K.NCLTNFHGMDLTR.D	0.9958		1	1579.7369
						K.TSYAQHQQVR.Q	0.9958		2	1218.3145
						K.LMELHGEGGSSGK.A	0.9958		1	1302.4449
						R.VFEVSLADLQNDEVAFR.K	0.9958		2	1953.1589
						R.ADGYEPPVQESV.-	0.9958		1	1291.3569
						R.LFCVGFTK.K	0.9924		1	972.1382
						K.VVDPFSK.K	0.9958		1	791.9225
						R.KTSYAQHQQVR.Q	0.9958		2	1346.4886
4037	RS4X_MOUSE	263	34.22	8	67	R.TDITYPAGFMDVISIDK.T	0.9958		2	1887.1548
						R.LSNIFVIGK.G	0.9958		1	991.2187
						K.GNKPWISLPR.G	0.9958		2	1168.3842
						R.KIFVGTK.G	0.9958		1	792.9969
						K.VNDTIQIDLETGK.I	0.9945		2	1446.5975
						K.GIPHLVTHDAR.T	0.9958		2	1216.3854
						R.ERHPGSFDVVHVK.D	0.9958		2	1507.6921
						R.HPGSFDVVHVK.D	0.9958		1	1222.3891
4038	RS5_MOUSE	204	18.14	2	29	K.WSTDDVQINDISLQDYIAVK.E	0.9958		2	2324.5493
						R.VNQAIWLLCTGAR.E	0.9958		2	1502.7227
4039	RS6_MOUSE	249	34.14	7	59	K.LNISFPATGCQK.L	0.9958	1,2		1336.4968
						K.LFNLSK.E	0.9958		1	721.8748
						R.GCIVDANLSVLNLVIVK.K	0.9958		2	1828.1687
						K.RMATEVAADALGEEWK.G	0.9958		2	1777.9898
						K.DIPGLTDTTVPR.R	0.9958		1	1285.4399
						R.MATEVAADALGEEWK.G	0.9958		2	1621.8023
						K.NKEEAAEYAK.L	0.9944		1	1153.234
4040	RS7_MOUSE	194	47.94	5	271	R.TLTAVHDAILEDLVFPSEIVGK.R	0.9958		2	2368.7325
						K.DVNFEFPEFQL.-	0.9958	1,2		1385.5157
						K.AIIIFVPVPQLK.S	0.9958		2	1338.7196
						K.IVKPNGEKPDEFESGISQALLELEMNSDLK.	0.9958		3	3332.7474
						K.VETFSGVYK.K	0.9958		1	1030.1656
4041	RS8_MOUSE	208	54.81	9	39	R.QWYESHYALPLGR.K	0.9958		2	1620.8076
						K.ISSLLEEQFQQGK.L	0.9958	1,2		1507.6836
						R.IIDVVYNASNNELVR.T	0.9958		2	1719.9353
						R.KYELGRPAANTK.I	0.9921		2	1348.5449
						R.ADGYVLEGK.E	0.9958		1	952.052
						R.LDVGNFSWGSECCTR.K	0.9958		2	1788.8433
						K.LTPEEEEILNK.K	0.9958		1	1315.4631

						K.YELGRPAANTK.I	0.9931		2	1220.3708
						K.NCIVLIDSTPYR.Q	0.9958		2	1451.6287
4042	RS9_MOUSE	194	11.86	2	4	R.KQVVNIPSFIVR.L	0.9958		2	1400.7073
						K.HIDFSLR.S	0.9944		1	888.014
4043	RSLBB_MOUSE	247	4.45	1	14	R.LPVVLVANK.A	0.9958		1	953.2132
4044	RSPO4_MOUSE	228	8.77	1	4	K.CGATCESCFSQDFCIRCK.R	0.9921		2	2287.3183
4045	RSSA_MOUSE	295	44.75	8	82	R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y	0.9958		2	2998.2855
						R.FTPGTFTNQIQAAFR.E	0.9958		2	1699.9065
						K.FLAAGTHLGGTNLDFQMEQYIYK.R	0.9958		2	2618.9666
						K.FAAATGATPIAGR.F	0.9958		2	1204.3714
						K.LLLAARAIVAIENPADVSVISSR.N	0.9944		3	2379.8057
						R.ADHQPLTEASYVNLPTIALCNTDSPLRYVD	0.9958		3	4286.7175
						R.AIVAIENPADVSVISSR.N	0.9958		2	1741.9823
						R.KSDGIYIINLK.R	0.9944		1	1264.5077
4046	RSU1_MOUSE	277	19.49	2	7	K.NLEVLNFFNNQIEELPTQISSLQK.L	0.9958	2,3		2820.1717
						K.AENNPWVTPIADQFQLGVSHVFEYIR.S	0.9958		2	3032.3849
4047	RT05_MOUSE	432	8.56	2	10	R.EECGPLPIVVASPHGALSK.E	0.9958		2	1962.2195
						R.SGFLWPGLNVPLIK.S	0.9958		2	1541.8766
4048	RT06_MOUSE	125	29.6	2	2	R.GGYFLVDFYAPTSAVENILEHLAR.D	0.9958		2	2684.0233
						R.DIDVVRPNIVK.H	0.9912		1	1268.4991
4049	RT07_MOUSE	242	19.83	3	15	K.LSHELLEAFHNR.G	0.9958		2	1466.6395
						K.NCEPVIGLVPILK.G	0.9958		2	1452.7436
						R.KPVAELTEEEKYDQELK.K	0.9958		2	2050.2701
4050	RT09_MOUSE	390	18.72	4	7	R.ATQWGEDGRPFHFLFYTGK.Q	0.9958		2	2258.5003
						R.HLANMMGEDPETFAEEDIDR.A	0.9958		2	2321.4952
						K.HPEHIFPK.Q	0.9958		1	1005.1643
						K.IHVNGVDYLIYFPITQDR.E	0.9958		2	2164.4686
4051	RT11_MOUSE	191	21.47	2	5	K.KGTGIAAQTAGIAAAAK.A	0.9924	1,2		1500.7385
						R.FSLYPPVPGQESSLQWAGMK.F	0.9958		2	2223.5512
4052	RT12_MOUSE	139	28.06	2	2	R.GKYDCGHVQK.K	0.9958		2	1192.2829
						K.EAVCFIPGEGHTLQEHHVVLVEGGR.T	0.9958		3	2772.0587
4053	RT14_MOUSE	128	11.72	1	2	R.HLADHGLLSGVQR.A	0.9958		2	1403.5839
4054	RT16_MOUSE	135	14.81	1	7	R.FVEQLGSYDPLPNSHGEK.L	0.9958		2	2018.1901
4055	RT17_MOUSE	120	31.67	3	4	R.VIDPVTGKPCAGTAYLESPLSEPR.E	0.9958	2,3		2558.8573
						K.VGRVIDPVTGKPCAGTAYLESPLSEPR.E	0.9958		3	2871.2292
						K.HELAEIIFK.V	0.9958		2	1100.303
4056	RT18B_MOUSE	254	35.43	4	5	R.DADFGTVHGAVSVTPPAPTLLSGEPWYPW	0.9958		3	4241.6648

						R.ECGLLSYYVPQVEPR.D	0.9945	2	1811.0106
						K.LHVDFRNVK.L	0.9929	2	1128.3194
						R.GPPEEDAPSSLPVSPYESEPWK.Y	0.9958	2	2399.5726
4057	RT18C_MOUSE	143	23.78	2	2	K.NLTTAAGCFTDRGTQAVSVIWR.R	0.9912	2	2425.6727
						R.HITGLCGK.K	0.9958	1	886.005
4058	RT22_MOUSE	359	20.61	5	10	K.KIDGLLIDQIQR.D	0.9958	2	1412.6725
						R.HADVLNLCVAQFEPDSAEYIK.V	0.9958	2	2420.6471
						K.VHHQTYEDIDR.H	0.9958	2	1413.4893
						R.KPINDVLAEDK.I	0.9958	1	1242.4148
						K.KPAFMDEEVQR.I	0.9958	1	1350.5322
4059	RT23_MOUSE	177	37.85	4	9	K.LFVETGKALLAEGIILR.R	0.9958	2	1844.248
						R.DLMRAGVLK.E	0.9958	1	1003.2481
						K.ADIQDIFYQEDQIR.A	0.9958	2	1754.8938
						R.LQASSEGHEPQEDDDLAQR.G	0.9958	2	2126.1577
4060	RT24_MOUSE	167	24.55	2	3	K.GWLSLHTGNLDGEDHAAER.T	0.9958	2	2079.193
						K.GNKPVSYEEAHAPHYIAHR.K	0.9958	2	2177.3866
4061	RT27_MOUSE	415	8.92	2	2	K.EKLPACEAEDLATYEQK.L	0.9952	2	1996.1444
						R.EKEEYHLADLASLMDK.A	0.9958	2	1893.1187
4062	RT28_MOUSE	186	30.65	3	7	R.HSPLTQLGPAK.D	0.9924	1	1149.3353
						R.IFHIVEDDLYIDFGGK.F	0.9958	2	1882.1229
						R.FLGGTTDTTILEADAVLLGLQEIR.D	0.9958	2	2547.9085
4063	RT29_MOUSE	391	12.79	3	4	R.TLIAPEELSLVHNLR.K	0.9958	2	1705.9951
						R.KPALELLGYLK.N	0.9958	2	1245.548
						K.HGEQHEGQHYSIPLQDLK.T	0.9958	2	2117.2853
4064	RT30_MOUSE	442	25.34	6	15	R.TLVNLLAPLNPVLSTAALDCK.R	0.9958	2	2224.6123
						K.QLPEFVPLDYSIPTEIPVMK.C	0.9958	2	2317.7455
						R.YQINDKPHNQIR.I	0.9945	2	1526.6951
						R.WQATVHAAPSVDEK.I	0.9958	2	1539.6879
						K.TADPCCYGHTQFHLIPDR.L	0.9958	2	2189.324
						K.KYVVHPQISALNADR.W	0.9955	2	1711.9615
4065	RT31_MOUSE	384	38.8	10	36	R.NEFLSPELVAAASAVADSLPFDK.Q	0.9958	2	2392.6678
						K.RNEFLSPELVAAASAVADSLPFDK.Q	0.9958	2	2548.8553
						K.AFADEPPEPEASPSLWEIEFAK.Q	0.9958	2	2461.6868
						K.KDLLDIIK.D	0.9944	1	958.1863
						K.KVDQSVPANEISQK.A	0.9958	2	1543.7172
						R.ASTRPQHQIQFDEDMDSSLK.Q	0.9944	2	2334.5225
						R.KPSASLEATVDR.L	0.9958	1	1274.4166

						R.ISFTHIISNMK.I	0.9958		2	1291.5511
						K.QLASVADQPFENGFEEMIQWTK.E	0.9911		2	2569.8481
						R.GRKPSASLEATVDR.L	0.9958		2	1487.656
4066	RT34_MOUSE	218	22.48	3	3	R.VRPDYTAQNLDHGR.A	0.9944		2	1642.7715
						K.HEEEAFTAFTAKPEDR.L	0.9958		2	1878.9927
						K.SWLWQHDEPCYWR.L	0.9958		2	1863.9953
4067	RT35_MOUSE	320	33.75	6	29	K.MDTDQDWPSVYPTAAPFKPSAVPLPVR.M	0.9958	2,3		2987.3997
						K.SSSENSVLQTLLQMR.A	0.9958		2	1693.9128
						R.AAESSVAPSREELLGTK.E	0.9958		2	1745.9273
						K.IPNFLHLTPVAIK.R	0.9958		2	1463.8063
						R.LKNEGENEASLAQYK.E	0.9958		2	1694.8388
						K.LSSLNLDNHAK.K	0.9944		1	1212.3482
4068	RT36_MOUSE	102	76.47	5	524	K.GSTSPDLLMHQGPPDTAEIIK.S	0.9958		2	2208.4913
						K.LSASEALGSAALPSHSSAISQHSK.G	0.9958	2,3		2337.5516
						R.RKPMSQEEMEFIQR.G	0.9958		2	1810.0961
						R.KPMSQEEMEFIQR.G	0.9958		2	1653.9087
						R.VVQVVKPHAPLIK.F	0.9944		2	1428.8045
4069	RT4I1_MOUSE	396	40.66	9	45	K.VHAASVNPIDVNMR.S	0.9958		2	1523.7502
						K.SLTHTQAASLPYVALTAWSAINK.V	0.9958		2	2444.7929
						R.FTQNMMLPIIHYPNEVIIK.V	0.9958		2	2302.7981
						K.YFQPGDEVWAAVPPWK.Q	0.9958		2	1891.1357
						R.TFPFSEVPEAFLK.V	0.9958		2	1512.7454
						K.TKGEEFPLTLGR.D	0.9958		2	1348.5419
						K.QGTLSEFVVVSGNEVSHKPK.S	0.9958		2	2143.4044
						R.KLGADEVIDYTLGSVEEQLK.S	0.9958		2	2208.4705
						K.AWGAHVTAVCSK.D	0.9958		2	1287.4271
4070	RT63_MOUSE	102	14.71	1	9	R.YIADQLDHLNISK.K	0.9958	1,2		1530.7209
4071	RTKN_MOUSE	564	11.35	2	2	R.TFSLDAAPADHSLGPSRSVAPLPPQR.S	0.9958		3	2689.003
						R.AGELEQAPEWPFTLSISNKYGDDEVTNTLC	0.9958		3	3840.1486
4072	RTN2_MOUSE	471	15.29	3	21	R.LSQQIASHVVSTATQLR.H	0.9958		2	1840.0897
						K.IPGTGTLAPTASVSGSK.A	0.9958		2	1544.7453
						R.SVSEPRDPPQQSGLGDSLESIPSLSQSPEF	0.9944		3	3335.5657
4073	RTN3_MOUSE	964	6.02	2	3	R.VDAPVSLATGIPCSHPSIPDSFPEQPAFLSK	0.9958		3	3266.6411
						R.YPSSVLLGRQFSHTTAALEEVSR.C	0.9907		2	2549.8461
4074	RTN4_MOUSE	1162	14.46	7	20	R.GPLPAAPPTAPER.Q	0.9958		2	1274.4624
						K.YQFVTEPEDEEDEEDEEEEEDDEDLEELE\	0.9958		3	4106.0384
						K.ESETFSDSSPIEIIDEFPTFVSAK.D	0.9958		2	2676.8903

						R.SPAASAPSLPPAAAVLPSK.L	0.9929	2	1733.0177
						R.KPAAGLSAAPVPPAAAPLLDFSSDSVPPAF	0.9958	2	2969.4105
						R.HQAQIDHYLGLANK.S	0.9945	2	1608.7971
						K.VPLLLPNVSALESQIEMGNIVKPK.V	0.9958	3	2591.1248
4075	RTTN_MOUSE	2226	3.19	3	5	R.FLQVLPACTEDEK.L	0.9958	2	1550.7149
						R.KSAAEQLAVIMQDIK.M	0.9958	1	1645.9549
						R.YHLPVHVTGHHAVSPYSIVLPLPTECLTLKF	0.9958	3	4179.8793
4076	RU17_MOUSE	448	6.92	2	2	R.DPIPYLPPLEKLPHEK.H	0.9958	2	1887.2291
						R.GYAFIEYEHER.D	0.9958	2	1414.5169
4077	RUFY1_MOUSE	712	7.72	3	7	R.VCDSCHTLLLQR.C	0.9958	2	1502.6429
						K.VCEEQEQALQEMGLHLSQSK.L	0.9958	2	2345.5525
						K.DTSCLLQTELQQVEGLK.K	0.9952	2	1963.1584
4078	RUNX2_MOUSE	607	8.4	2	2	K.VVALGEVPDGTVVTVMAGNDENYSAELRN	0.9958	3	3609.0608
						R.GTGLPAITDVPR.R	0.9958	1	1197.3769
4079	RUNX3_MOUSE	409	4.89	1	2	R.RFTPPSTAFPCGGGGGGK.M	0.9958	2	1751.9054
4080	RUSC1_MOUSE	893	4.82	2	3	K.DRSDWLIVFSPDTELPPTGSLGGSLAPPR.I	0.9958	3	3082.4399
						R.GPGLPLVPQAKK.D	0.9958	1	1205.4862
4081	RUSC2_MOUSE	1514	1.98	1	3	R.AAGQGPLAQLMDPGPAFSGSPATSHTQR.	0.9958	3	2752.0337
4082	RUSD3_MOUSE	344	12.5	2	2	R.LLLPGTGSRDPPSELLAPLPPYFSR.T	0.9958	3	2695.1338
						R.TENLGLEELAHVLR.A	0.9954	2	1594.8082
4083	RUVB1_MOUSE	456	12.28	3	6	R.AVLLAGPPGTGK.T	0.9958	1	1081.3005
						R.AQTEGINISEEALNHLGEIGTK.T	0.9958	2	2325.5376
						R.ALESSIAPIVIFASNR.G	0.9917	2	1688.9646
4084	RUVB2_MOUSE	463	8.42	3	4	K.EVVHTVSLHEIDVINSR.T	0.9958	2	1948.1863
						R.GTSYQSPHGIPIDLLDR.L	0.9958	2	1870.0721
						R.KEVVHTVSLHEIDVINSR.T	0.9952	2	2076.3604
4085	RWDD1_MOUSE	243	18.93	2	5	K.LFHGTPVTIENFLSWK.A	0.9958	2	1890.1919
						K.YPDETPLYEIFSQENLEDNDVSDILK.L	0.9958	3	3088.3051
4086	RXFP1_MOUSE	758	4.88	2	24	R.DLELDCDEANLR.A	0.9958	2	1463.5072
						K.LYLSHNRITFLKPGVFEDLHR.L	0.9958	3	2556.9731
4087	S10A1_MOUSE	94	18.09	1	258	K.DLLQTELSGFLDVQK.D	0.9958	2	1706.9335
4088	S10A6_MOUSE	89	29.21	1	22	K.DQEVNFQEYVAFLGALALIYNEALK.-	0.9958	2	2860.2359
4089	S10A8_MOUSE	89	24.72	1	2	K.MVTTECPQFVQNINIENLFR.E	0.9958	2	2454.7694
4090	S10A9_MOUSE	113	14.16	1	2	R.SITTIIDTFHQYSR.K	0.9958	2	1682.8736
4091	S10AB_MOUSE	98	69.39	3	21	K.TEFLSFMNTELAAFTK.N	0.9958	2	1851.1243
						R.CIESLIAVFQK.Y	0.9958	2	1308.5267
						K.LDLNCDGQLDFQEFLNLIGGLAIACHDSFIQ	0.9958	3	3983.3559

4092	S10AD_MOUSE	98	14.29	1	3	K.ELATQQLPHLLK.D	0.9958	2	1391.6536
4093	S12A5_MOUSE	1138	4.22	2	2	R.EDVKGDGNPK.E	0.9958	1	1059.121
						K.SIPTGTILAIATTSAVYISSVVLFGACIEGVVL	0.9958	3	3481.0766
4094	S12A6_MOUSE	1150	5.65	2	2	R.TSNPQDVTEDPSQNSITGEHSQLLDDGHK	0.9958	3	3279.4149
						R.ESVPETSRSEPMSELSGATTSLATVALDPS	0.9958	3	3409.6576
4095	S12A7_MOUSE	1083	7.39	4	7	K.LANYTNLSQGVVEHEEDEDSR.R	0.9958	2	2406.4815
						K.NMALFEEEMDSNPMVSSLLNK.L	0.9958	2	2400.7391
						K.SQDAQLVLLNMPGPPK.S	0.9958	2	1709.0136
						R.IFTVAQVDDNSIQMKK.D	0.9944	2	1838.1291
4096	S23A1_MOUSE	605	6.94	1	2	R.IPYPCQWGLPTVTVAAVLGMFSATLAGIIES	0.9958	3	4334.9492
4097	S23IP_MOUSE	998	3.41	2	5	R.RLEFPSGETIVMHNPK.V	0.9958	2	1856.1498
						R.AHTSTTQLQEELEK.V	0.9958	2	1615.7374
4098	S2542_MOUSE	318	23.27	3	16	R.QVLSSLLSGALAGALAK.T	0.9958	2	1599.9114
						R.MQTAGVTGHQHGSILSTLR.S	0.9958	2	1995.2639
						K.TLYFGFTPTVLGVIPYAGLSFFTYESLKSLH	0.9958	3	3627.2201
4099	S2543_MOUSE	341	6.74	1	2	R.QIVKTQGVLGLWNGLTANLLK.V	0.9925	2	2267.7202
4100	S2546_MOUSE	418	8.85	2	36	R.SFGSGTELGHWVTTPPDIPGSR.N	0.9958	2	2299.5046
						R.RPEGFDGLGYR.G	0.9958	2	1267.3867
4101	S25BP_MOUSE	136	32.35	2	3	R.VVLVNNILQNAQER.L	0.9958	2	1610.8539
						R.DLFAEGLLEFLRPAVQQLDSHVHAVR.E	0.9958	3	2962.3811
4102	S26A4_MOUSE	780	1.92	1	2	K.KCINSTVGFDAIR.V	0.9958	2	1481.658
4103	S26A5_MOUSE	744	4.7	2	3	K.EVGNANVANATVVK.V	0.9958	2	1386.5479
						K.ELLFHSIHDAVLGSQVR.E	0.9957	2	1922.1942
4104	S27A1_MOUSE	646	15.79	4	4	R.LLGQTDVAVYGVAVPGVEGK.A	0.9958	2	1973.2768
						R.QPERLALVDASSGICWTFAQLDTYSNAVAI	0.9958	3	3716.1107
						R.FGVPQIGEFYGATECNCSIANMDGKVGSC	0.9958	3	3731.9707
						R.ILTHVYPIR.L	0.9954	2	1112.3604
4105	S29A3_MOUSE	475	16.21	2	2	K.TASLGFCAVSLYFVTAFIIPAISTNIQSMHK.(	0.9958	3	3389.9435
						K.VDTSSWTRGFFSLTIACMAIISSSSTIFNSS\	0.9958	3	4585.1691
4106	S35C2_MOUSE	364	3.85	1	6	K.ARVVLSWTDYLR.R	0.9937	2	1479.722
4107	S36A4_MOUSE	500	17.4	3	3	R.SLLVSITRAGAILIPR.L	0.9911	2	1681.0751
						K.ILYSFGIFVTYSIQFYVPAEIIIPGVTARLHAK	0.9958	3	3729.443
						R.FPQALNIGMAIVTVLYISLATLGYMCFRDEIH	0.9958	3	3650.3383
4108	S38A3_MOUSE	505	3.76	1	2	K.HLEGLLPVGVPTTDTQR.T	0.9958	2	1834.0825
4109	S38A4_MOUSE	547	1.83	1	2	K.YELPEVIR.A	0.9958	1	1019.1857
4110	S38AA_MOUSE	1090	2.94	2	3	K.ELVPGDLEAVHK.A	0.9944	1	1307.4893
						K.LAVPAGQKPENAKPNR.D	0.9958	2	1690.9431

4111	S6OS1_MOUSE	574	1.57	1	2	R.ANNFTKR.S	0.9944	1	850.9529
4112	S9A10_MOUSE	1175	0.94	1	3	K.SVNHTLAHK.V	0.9924	1	1007.1374
4113	SAA4_MOUSE	130	21.54	2	6	R.SGKNPNHFRPEGLPEK.F	0.9958	2	1808.0067
						K.YFQGLLNR.Y	0.9932	2	1011.1686
4114	SAAL1_MOUSE	474	5.06	1	2	R.NPSPPPPTCGSEDEEDLGGGDR.I	0.9958	2	2284.2776
4115	SACS_MOUSE	4582	1.35	3	16	R.FGNAVILLYIQHSDSKDINFLLALAMTLK.S	0.9958	3	3250.867
						R.ADADTVLLFLK.S	0.9924	1	1206.4246
						R.TQFSDVLDLYLGNHFK.L	0.9943	2	1898.1253
4116	SAE1_MOUSE	350	6.29	1	10	R.NDVFDSLGISPDLLPDDFVR.Y	0.9929	2	2235.4552
4117	SAE2_MOUSE	638	4.39	2	3	K.GTILISSEEGETEANNPKK.L	0.9945	2	2018.1852
						K.QPNPR.K	0.9944	1	611.6786
4118	SAHH_MOUSE	432	49.54	13	98	R.GISEETTTGVHNLYK.M	0.9958	2	1649.7979
						R.WSSCNIFSTQDHAAAAIAK.A	0.9958	2	2079.2427
						K.SKFDNLYGCR.E	0.9958	2	1260.3581
						K.KLDEAVAEAHLGK.L	0.9958	1	1381.5718
						K.GETDEEYLWCIEQTLHFK.D	0.9958	2	2299.4645
						K.DGPLNMILDDGGDLTNLIHTK.Y	0.9958	2	2253.5323
						K.VNIKPQVDR.Y	0.9952	2	1069.2492
						K.QAQYLGMPINGPFKPDHYR.Y	0.9958	2	2233.5523
						K.YPVGVHFLPK.K	0.9958	2	1157.4007
						K.ALDIAENEMPGLMR.M	0.9958	2	1560.8237
						K.YPQLLSGIR.G	0.9958 1,2		1047.2425
						K.VPAINVNDSVTK.S	0.9958	1	1257.4295
						R.VIITEIDPINALQAAMEGYEVTTMDEACK.E	0.9958	3	3227.6322
4119	SAHH3_MOUSE	613	14.19	3	4	K.GCCAALKAMGSIVYVTEIDPICALQACMDG	0.9944	3	3580.0131
						R.HRDGGEALVSPDGTVTEAPR.T	0.9958	3	2065.2071
						R.SISQSSTDSYSSAASYTDSSDDETSPRDK.(	0.9958	3	3076.0351
4120	SAKS1_MOUSE	297	14.14	2	3	R.LPDGTSLTQTFR.A	0.9958	2	1336.4875
						R.AFSEADMERPLQELGLVPSAVLIVAK.K	0.9958	2	2785.2714
4121	SALL4_MOUSE	1067	3.94	2	2	R.GTKVAVNQR.G	0.9944	1	973.1203
						K.VFGTDSSLQIHLRSHTGERPYVCPICGHR.F	0.9958	3	3381.7106
4122	SAM50_MOUSE	469	20.9	5	57	R.TKDDIIICEIGEVFK.A	0.9958	2	1781.0222
						R.SLEPLPSSGTDFGALGEEAEFVEVEPEAK.(	0.9958	2	3036.2727
						K.DVVVQHVHFDGLGR.T	0.9958 1,2		1578.7709
						R.THFFLNAGNLCNLNYGEGPK.A	0.9958	2	2267.4717
						K.SSLSHAMVIDSR.N	0.9958 1,2		1303.476
4123	SAMH1_MOUSE	627	6.06	3	7	R.FIKFAR.I	0.9958	1	781.9761

						R.FEHSLGVGYLAGCLVR.A	0.9958	2	1779.0148
						K.SFLYEIVSNK.R	0.993	2	1200.377
4124	SAMN1_MOUSE	372	13.98	2	2	K.ESVPLSSNPDILSASQLEDCPRDSGCYISSI	0.9958	3	4030.1477
						R.ELTNGSEEQSK.T	0.9958	1	1222.2511
4125	SAP_MOUSE	557	17.06	6	70	K.EVVDSYLPVILDMIK.G	0.9958	2	1735.0888
						K.QCDDFVAEYEPLLLEILVEVMDPGFVCSK.I	0.9958	3	3417.8247
						K.TCEWIHDSSLSASCK.E	0.9944	1	1781.8488
						K.LVLYLEHNLEK.N	0.9958	2	1371.6195
						K.FSELIVNNATEELLVK.G	0.9958	1	1820.0929
						K.KLVLYLEHNLEK.N	0.9958	2	1499.7935
4126	SAPL1_MOUSE	522	7.47	1	2	K.WMVNNHSAAVLSMLSGAQETDLASVCTAL	0.9958	3	4076.5613
4127	SAPS2_MOUSE	923	2.71	1	2	R.IANAVVQNLEQGPVQAHISEVIR.G	0.9958	2	2486.8338
4128	SAR1A_MOUSE	198	23.74	2	4	K.VELNALMTDETISNVPILILGNK.I	0.9958	2	2498.9379
						K.NYLPAINGIVFLVDCADHSR.L	0.9924	2	2275.5353
4129	SAR1B_MOUSE	198	23.74	2	8	K.NYLPAINGIVFLVDCADHER.L	0.9958	2	2317.5725
						K.EELDSLMTDETIANVPILILGNK.I	0.9958	2	2529.9056
4130	SAS6_MOUSE	654	1.68	1	7	K.LEESKQLLK.N	0.9924	1	1088.2896
4131	SASH1_MOUSE	1230	4.31	3	3	K.SEDGDDEEPPYRGPFCGR.A	0.9923	2	2084.0857
						R.TQSRHPSQPPPVPAK.K	0.9958	2	1627.8435
						R.DFEAQPPVKPGLTR.T	0.9958	2	1555.774
4132	SBDS_MOUSE	250	12.4	2	3	K.DIHYSVKPNK.S	0.9911	1	1201.3677
						K.DLDEVLQTHSVFVNVSK.G	0.9958	2	1931.1528
4133	SBNO1_MOUSE	1390	1.94	2	4	R.AGFLIGDGAGVGK.G	0.9924	1	1162.3311
						K.DQVQLKDLLK.N	0.9958	1	1200.4209
4134	SBP1_MOUSE	472	74.36	23	544	R.GGSVQVLEDQELTCQPEPLVVK.G	0.9958	2	2426.6923
						K.DGFNPAHVEAGLYGSR.I	0.9958	2	1690.8125
						K.GTWEKPGDAAPMGYDFWYQPR.H	0.9958	2	2473.7241
						R.HEIIQTLQMTDGLIPLEIR.F	0.9958	2	2221.6202
						K.SPQYSQVIHR.L	0.9958	2	1215.3543
						R.FLHDPSATQGFVGCALSSNIQR.F	0.9958	2	2406.6263
						R.NTGTEAPDYLATVDVDPK.S	0.9958	2	1907.0411
						R.IFVWDWQR.H	0.9958	2	1150.325
						K.GWMLPEMPGLITDILLSLDDR.F	0.9958	2	2386.8269
						K.LILPGLISSR.I	0.9958	1	1069.3329
						K.RLYATTSLYSAWDK.Q	0.9958	2	1675.8815
						R.LAGQIFLGGSIVR.G	0.9958	2	1331.6011
						R.HNVMVSTEWAAPNVFK.D	0.9958	2	1831.0991

						R.FLYFSNWLHGDIR.Q	0.9958	2	1668.8949
						K.RIPGGPQMIQLSLDGK.R	0.9958	2	1711.0325
						K.EPLGPALAHELR.Y	0.9944	2	1303.5039
						R.QYDISNPQKPR.L	0.9958	2	1346.4856
						R.IPGGPQMIQLSLDGK.R	0.9958	2	1554.845
						K.DELHHSGWNTCSSCFGDSTK.S	0.9958	2	2326.3296
						K.LNPNFLVDFGK.E	0.9958	1	1264.4667
						K.CNVSSLHTSHCLASGEVMVSTLGDLQGNG	0.9958	3	3160.4152
						K.GSFVLLDGETFEVK.G	0.9937	2	1541.7411
						K.LNPNFLVDFGKEPLGPALAHELR.Y	0.9958	2	2548.9475
4135	SC22C_MOUSE	303	8.91	1	3	R.MKPVTALGVLSLVLNIMCAALNLIR.G	0.9958	2	2712.3779
4136	SC23A_MOUSE	765	11.63	4	13	R.GPQVQQPPPSNR.F	0.9958	2	1305.4361
						R.HLLQAPVDDAQEILHSR.F	0.9958	2	1943.1698
						R.GAVQFVTQYQHSSGQR.R	0.9958	2	1793.9364
						K.VNPSQTHNNMYAWGQESGAPILTDDVSLQ	0.9958	3	4045.4903
4137	SC31A_MOUSE	1230	14.39	9	15	K.GDVSGVLIAGGENGNIILYDPSK.I	0.9958	2	2289.5474
						K.AQDGSSPLSLQDLIEK.V	0.9958	2	1701.8712
						R.EALAAVLTYAKPDEFSALCDLLGTR.L	0.9931	2	2726.065
						R.SAQLQHAVQSQGFIGYCQK.K	0.9958	2	2151.3526
						R.EQTLSPTIINGLHSIAR.S	0.9958	2	1851.113
						R.RQPVFISQVVTEK.D	0.9958	2	1531.7953
						K.LVTFESVAVPLQQGAEQQR.R	0.9912	2	2101.3671
						K.AQGKPVSGQESSQSPYER.Q	0.9958	2	1936.0452
						K.KPIPEEHLILK.T	0.9917	2	1317.6145
4138	SC5D_MOUSE	299	12.37	1	2	K.LYDDIGDFPNGWIHLMVSVVSFLFFTDMLIY	0.9958	3	4232.9503
4139	SC6A2_MOUSE	617	13.94	3	3	R.MNPQVQPELGGADPLPEQPLRPCK.T	0.9958	2	2673.0253
						R.VAYGITPENEHHLVAQR.D	0.9958	2	1935.1496
						K.FDNNCYRDALLTSTINCVTSFISGFAIFSILG	0.9958	3	4516.0164
4140	SCAM1_MOUSE	338	13.02	2	2	K.VHGLYRTTGASFEK.A	0.9958	2	1566.7569
						K.MPNVPNTQPAIMKPTEEHPAYTQITK.E	0.9958	3	2938.3864
4141	SCEL_MOUSE	652	4.45	2	2	K.RPLENLQAGDSIWIYR.Q	0.9947	2	1932.1893
						K.KSPTGNDLK.S	0.9958	1	960.0751
4142	SCG2_MOUSE	617	11.99	3	21	R.LGAVLLLIHLIFLISGAEAASFQR.N	0.9921	2	2554.0941
						K.YPELLNTNQLK.R	0.9924	1	1333.5272
						R.LLQKPLDSQSIYQLIEISRNLQIPPEDLIEMLI	0.9958	3	3880.5757
4143	SCLY_MOUSE	432	7.87	2	2	R.VLVHTDAAQALGK.R	0.9958	2	1323.5351
						R.NFRPGTENTPMIAGLGK.A	0.9958	2	1804.074

4144	SCN8A_MOUSE	1978	2.22	2	2	K.TNFYMVPGMLEPLLCGNSSDAGQCPEGFC	0.9931		3	3641.018
						R.FVASNPSK.V	0.9924		1	849.9621
4145	SCNAA_MOUSE	1958	2.04	2	2	R.KTSDNPDFNYTSFDSFAWAFLSLFR.L	0.9958		2	2978.2463
						K.QEDISATIIQK.A	0.9958		1	1246.4032
4146	SCNBA_MOUSE	1765	5.33	3	22	K.IGNWVFTGIFIAEMCLKIIALDPYHYFR.H	0.9944		3	3389.9918
						R.DPWNWLDFIVIGTAIAPCFLGNK.V	0.9958		3	2649.0301
						R.TLLFALMMSLPSLFNIGLLLFLVMFIYAIFGM	0.9958		3	4305.3874
4147	SCNNG_MOUSE	655	5.34	2	3	R.FLNLIPLLVFNENEK.G	0.9952		2	1804.1393
						K.YSAVSDLLTDLDSETK.Q	0.9958		2	1757.889
4148	SCOT_MOUSE	520	65	23	2891	R.QFLSGELEVELTPQGTLAER.I	0.9958		2	2218.4686
						K.DIPNGATLLVGGFGLCGIPENLIGALLK.T	0.9946		2	2824.2995
						R.AGGAGVPAFYTSTGYGTLVQEGGSPIK.Y	0.9958		2	2586.8608
						K.DLTAVSNNAGVDNFGLGLLLR.S	0.9958		2	2160.4349
						R.GGHVNLTMLGAMQVSK.Y	0.9944		2	1643.9599
						K.ETVTVLPGASFFSSDESFAMIR.G	0.9958		2	2392.6857
						K.YGDLANWMIPGK.M	0.9958	1,2		1365.5897
						R.EFNGQHFILEEAITGDFALVK.A	0.9958		2	2379.6745
						K.STGCDFAVSPNLMPMQQIST.-	0.9958		2	2185.4379
						K.DGSVAIASKPR.E	0.9958		2	1101.248
						K.NGLTLIELWEGLTVDDIK.K	0.9958		2	2030.3257
						K.NGLTLIELWEGLTVDDIKK.S	0.9958		2	2158.4998
						K.KNGLTLIELWEGLTVDDIK.K	0.9958		2	2158.4998
						K.FYTDPVEAVK.D	0.9958		1	1169.3196
						K.CTLPLTGK.Q	0.9944		1	890.0337
						K.KSTGCDFAVSPNLMPMQQIST.-	0.9958		2	2313.6119
						R.NFNLPMCK.A	0.9944		1	1024.189
						K.AAGTTVVEVEEIVDIGSFAPEDIHIPK.I	0.9958		2	2838.184
						R.MISSYVGENAEFER.Q	0.9958	1,2		1632.7852
						K.GMGGAMDLVSSSK.T	0.9944		1	1240.4322
						K.GVFDVDKK.N	0.9924		1	908.0422
						K.VVVTMEHSAK.G	0.9958		1	1101.3062
						K.FYTDPVEAVKDIPNGATLLVGGFGLCGIPEI	0.9958		3	3974.5959
4149	SCPDH_MOUSE	429	23.78	4	45	R.SVSCLKPVPIVGTK.L	0.9958		2	1485.7735
						K.GVYIIGSSGFDSIPADLGVLYTR.N	0.99		2	2401.7215
						K.GPEAGYVATPIAMVQAAMTFLSDASDLPK.	0.9958		2	2953.395
						K.LGRPSLSSEVGVIICDISNPASLDEMAK.Q	0.9958		2	2960.3357
4150	SCRB2_MOUSE	478	14.02	3	22	K.NGAPIIMSFPHFYQADEK.F	0.9958		2	2066.3386

						R.SVHITFSSFENVEGLPAFR.Y	0.9958	2	2138.3873
						K.GMHPNKEEHESFVDINPLTGIILR.G	0.9958	2	2748.129
4151	SCRN2_MOUSE	425	40.24	7	88	R.GLLTGEQTPPAQGLGSLFQAFVER.E	0.9958	2	2517.8443
						R.NISNQLSIGTDISAEHPELR.S	0.9958	2	2195.394
						R.DEVQEVVFIPAGTHVPGSR.L	0.9958	2	2038.2676
						R.SSTAQEAVHVIAGLLDR.Y	0.9958	2	1767.9798
						R.GHQAALGLMEDEQEQAQQLR.K	0.9958	2	2253.4515
						R.TTASMVSVLPQDPTKPCVHFLTATPDPSR.	0.9944	3	3155.5593
						R.SVFKPFIFEVGVSQSPQVLSPTFGAQDPVF	0.9958	3	3265.7362
4152	SCRN3_MOUSE	418	20.81	5	15	K.AVSEEIESILQSGHLDEEK.T	0.9958	2	2114.2707
						R.LFDEVQEVIYCPAAVHNDLEK.R	0.9958	2	2490.7382
						R.GNITFETMMEILR.D	0.9958	2	1555.8476
						K.HQEALEMISNSK.E	0.9958	2	1387.5505
						K.SPTFEPERPVAK.K	0.9958	2	1358.537
4153	SDCB1_MOUSE	299	8.36	1	5	K.SIDNGIFVQLVQANSPASLVGLR.F	0.9958	2	2399.7526
4154	SDF2_MOUSE	211	31.75	3	4	R.YGSGSGQQSVTGVTSVDDSNSYWR.I	0.9958	2	2538.603
						K.AMEGIFMKPSELLR.A	0.9958	2	1622.9813
						K.HSSTDVLLSVTGEQYGRPISGQK.E	0.9958	2	2460.7062
4155	SDK1_MOUSE	2193	5.88	6	7	K.YIIPSLQK.L	0.9958	1	962.1772
						R.LASGSPHTFTTVEVGATVRQFTATELAPES	0.9944	3	3757.1943
						R.HLNVKSTFSK.K	0.9958	1	1161.3463
						R.VVYEPLAPVQGVSKVVTVDVK.G	0.9958	2	2227.6494
						K.LLAWPADAPETVTVVTIAPDFHGIHHGYITN	0.9958	3	3599.1265
						R.EGHKIIPSSR.I	0.9958	1	1124.2852
4156	SDPR_MOUSE	418	31.82	6	39	R.DNSQVNAVTVHTLLDK.L	0.9958	2	1754.9377
						K.VLIFQEESEIPASVFVK.E	0.9958	2	1936.2555
						K.RLENNHAQLLR.R	0.9958	2	1364.5503
						K.VLIFQEESEIPASVFVKEPVPSAAEGK.E	0.9958	3	2902.3141
						R.RGNNSAVGSNADLTIEEDEEEEPVALQQA(	0.9958	3	3598.7759
						K.FQHPNTDMLQEKPSSPSPMPSSTPSPSLN	0.9958	3	4097.5178
4157	SDSL_MOUSE	329	20.97	3	7	R.DGWVNVSPFDHPLIWEGHASLVR.E	0.9958	2	2632.9407
						K.LGIPVTIVLPEGTSVQVVR.R	0.9958	2	1978.383
						R.VTPLLESWALSQVAGMPVFLK.Y	0.9958	2	2287.7656
4158	SELB_MOUSE	583	4.63	2	2	R.LAFHGVLLQGLEDKNYIESFLPALR.V	0.9958	3	2845.314
						R.LAFHGVLLQGLEDK.N	0.9925	2	1540.8027
4159	SELM_MOUSE	145	12.41	1	2	K.AFVTEDIQLYHNLVMK.H	0.991	2	1922.2494
4160	SEM3C_MOUSE	751	2	1	2	K.NHVPITTMEISSK.K	0.9958	1	1457.6849

4161	SEM3D_MOUSE	777	7.21	2	2	K.ARLICSIPGSDGADTHFDELQDIYLLPTR.D	0.9958	3	3275.6086
						K.DYIQILSSPNFSLDQYCEQMWYK.E	0.9944	3	2930.224
4162	SEM3F_MOUSE	785	3.06	2	2	R.EAPGALRPPELQDQK.K	0.9958	2	1649.8442
						R.HVPPSPREAPGALRPPELQDQK.K	0.9958	3	2420.7336
4163	SEM7A_MOUSE	664	8.89	2	2	R.LLLVFWVAAASAQGHSRSGPR.I	0.9944	2	2224.5735
						R.HEENVEQSCEPGHQSPSCILFIENLTARQY	0.9958	3	4088.3307
4164	SENP3_MOUSE	568	7.75	2	5	K.SLVLQLIQSYQRMPGNAMVR.G	0.9924	2	2305.7619
						R.LKSGGGFGPDPGSGTTVPTR.R	0.9958	2	1889.0751
4165	SENP6_MOUSE	1132	2.3	2	20	R.SYEESIK.G	0.9958	1	855.9201
						K.SGGSAGALFLKALDR.S	0.9945	2	1463.6768
4166	SENP8_MOUSE	221	8.6	1	15	R.RQPESPLQLLTPTYITK.K	0.9958	2	1986.3189
4167	SEP11_MOUSE	431	19.49	4	20	R.NLSLSGHVGFDSLPDQLVNK.S	0.9958	2	2141.3885
						K.AAAQLLQSQAQQSGAQQTK.K	0.9958	2	1958.1386
						R.SLFNYHDTRIHACLYFIAPTGHSLK.S	0.9958	3	2963.3343
						R.EMLIRVNMEDLR.E	0.9958	2	1519.8176
4168	SEPP1_MOUSE	380	13.42	2	3	K.APEWYIGDQNPMLNSEGK.V	0.9958	2	2050.2501
						K.LESQGYFNISYIVVNHQGSPSQLKHSHLK.K	0.9958	3	3312.7123
4169	SEPT2_MOUSE	361	25.76	4	25	K.ASIPFSVVGSNQLIEAK.G	0.9958	2	1761.0281
						R.LYPWGVVEVENPEHNDFLK.L	0.9943	2	2286.5487
						K.QQPTQFINPETPGYVGFANLPNQVHR.K	0.9958	3	2954.2743
						R.TMLITHMQDLQEVTQDLHYENFR.S	0.9958	3	2864.2202
4170	SEPT7_MOUSE	436	16.51	4	58	K.STLINSLFLTDLYSPEYPGPSHR.I	0.9958	2	2608.9103
						R.KLAAVTYNGVDNNK.N	0.9958	2	1507.6866
						K.IYEFPETDDEEENK.L	0.9958	1	1758.7895
						K.KMEMEMEQVFEMK.V	0.9926	2	1691.0434
4171	SEPT8_MOUSE	429	14.45	3	25	R.SLSLGGHVGFDSLPDQLVSK.S	0.9958	2	2057.311
						R.LRPQTYDLQESNVHLK.L	0.9958	2	1942.182
						K.AAMEALQSQALHATSQQPLR.K	0.9958	2	2152.4332
4172	SEPT9_MOUSE	583	6.17	2	7	R.SFEVEEIEPPNSTPPRR.V	0.9944	2	1985.1607
						R.RTEITIVKPQESVLR.R	0.9958	2	1770.0824
4173	SERA_MOUSE	533	3.94	1	2	R.ALVDHENVISCPHLGASTK.E	0.9958	2	2049.2573
4174	SERHL_MOUSE	311	7.07	1	2	R.AVSPEEMLQGFLNNNSHLDK.D	0.9958	2	2244.484
4175	SERPH_MOUSE	417	41.25	10	100	K.DQAVENILLSPLVVASSLGLVSLGGK.A	0.9958	2	2581.0251
						R.LYGPSSVSFADDFVR.S	0.9958	2	1660.8235
						K.LRDEEVHTGLGELLR.S	0.9958	2	1737.9535
						R.SALQSINEWASQTTDGKLPEVTK.D	0.9958	2	2504.7563
						K.HLAGLGLTEAIDK.N	0.9958	2	1338.5467

						R.STGLAFSLYQAMAK.D	0.9958	2	1488.7418
						K.LFYADHPFIFLVR.D	0.9958	2	1638.9524
						K.LQMVEMPLAHK.L	0.9958	2	1297.6166
						K.LSSLIILMPHHVEPLER.L	0.9909	2	1985.3953
						K.GVVEVTHDLQK.H	0.9958	2	1225.3873
4176	SET_MOUSE	289	18.69	2	2	K.EQQEAIEHIDEVQNEIDR.L	0.9958	2	2196.2921
						K.IPNFWVTTFVNHPQVSALLGEEDEEALHYL	0.9958	3	3728.1553
4177	SET1B_MOUSE	1985	2.37	2	2	K.ESLSASSSSSASSSSGSSTTSPSSSASDK.I	0.9958	2	2641.5836
						K.FKIDEFYVGPVPPK.Q	0.9949	2	1636.9311
4178	SETB2_MOUSE	713	3.65	2	2	K.EPAVEMNHR.N	0.9958	1	1083.2072
						K.GTFVCIYSGRLLR.R	0.9958	1	1542.7875
4179	SETBP_MOUSE	1535	2.48	2	8	R.QSNTGNNFVKK.R	0.9958	1	1237.3579
						R.YSFDFCSLDNPEAIPSDTSTKNR.H	0.9915	2	2665.7956
4180	SETD5_MOUSE	1441	0.62	1	3	R.NCPIQKR.N	0.9944	1	916.0343
4181	SETX_MOUSE	2646	2.72	3	3	R.GAAIMSSLALHSVQSNSVQLACVQLIRGLLI	0.9958	3	3266.8365
						R.ADDDLVSFTEVTDTLVKAPCEGHVK.M	0.9944	3	2747.9819
						K.LVMEIIKLIK.E	0.9944	1	1200.6092
4182	SF01_MOUSE	653	4.75	2	4	R.ILRPWQSSETR.S	0.9931	2	1373.5546
						K.TVIPGMPTVIPPGLTR.E	0.993	2	1650.0325
4183	SF3A1_MOUSE	791	5.94	2	5	K.ASKPLPPAPAPDEYLVSPITGEK.I	0.9958	2	2378.7277
						R.TQQAAQANITLQEQIEAIHK.A	0.9958	2	2236.4899
4184	SF3A3_MOUSE	501	4.19	1	2	R.KEELNAISGPNEFAEFYNR.L	0.9958	2	2229.4106
4185	SF3B1_MOUSE	1304	3.07	2	2	K.IWDPTPSHTPAGAATPGR.G	0.9958	2	1833.0134
						R.NRPLSDEELDAMFPEGYK.V	0.9958	2	2112.3185
4186	SFPQ_MOUSE	699	17.31	7	26	R.NLSPYVSNELLEEAFSQFGPIER.A	0.9958	2	2640.9091
						R.FAQHGTFEYEYSQR.W	0.9944	2	1763.8632
						R.FGQGGAGPVGGQGPR.G	0.9958	2	1342.4569
						K.DKLESEMEDAYHEHQANLLR.Q	0.9958	2	2429.6233
						R.RMEELHSQEMQK.R	0.9958	2	1546.7565
						K.MPGGPKPGGGPGMGAPGGHPKPPHR.G	0.9904	2	2329.7057
						R.MEELHSQEMQK.R	0.9924	1	1390.569
4187	SFR18_MOUSE	805	1.49	1	2	R.QRSPIALPVK.Q	0.9949	1	1109.3573
4188	SFR19_MOUSE	1256	4.62	2	2	R.SPFLKPDERAPAEVAK.V	0.9958	2	1756.0116
						R.SQESGAADTATVLDTAADSFLVELVSILDPI	0.9958	3	3976.3399
4189	SFRS1_MOUSE	248	13.71	2	4	R.GGPPFAFVEFEDPR.D	0.9958	2	1565.7252
						R.GTGRGGGGGGGGGAPR.G	0.9958	1	1228.2699
4190	SFRS3_MOUSE	164	22.56	3	9	R.DAADAVR.E	0.9958	1	717.7569

						R.NPPGFAFVEFEDPR.D	0.9958	2	1622.7771
						K.VYVGNLGNNGNK.T	0.9958	1	1249.3689
4191	SG269_MOUSE	1735	2.36	2	2	K.SFLGTSGELSVK.E	0.9958	1	1225.3843
						R.SETASSLSQKVCNGGISPGNPGNSK.D	0.9958	3	2477.6135
4192	SGCA_MOUSE	387	29.97	6	9	R.SPYNPGFLYGSPTPEDR.G	0.9956	2	1898.0386
						R.CAQGQPPLLSCYDTLAPHFR.V	0.9958	2	2332.5531
						R.VFVHPLEHATFLR.L	0.9958	2	1566.846
						R.LTYHAHLQGHPDLPR.W	0.9958	2	1755.9767
						R.EVPRPLSTLPMFNVR.T	0.9924	2	1757.1039
						K.RDMATSDIQMFHHCSIHGNTEELR.Q	0.9958	3	2887.1402
4193	SGCB_MOUSE	320	15	2	31	R.RNENLVITGNNQPIVFQQGTTK.L	0.9958	2	2472.7635
						R.THNILFSTDYETHEFHLPSGVK.S	0.9958	2	2573.8241
4194	SGCG_MOUSE	291	7.22	1	10	R.VTGPEGALFEHSVETPLVR.A	0.9958	2	2039.2957
4195	SGOL2_MOUSE	1164	2.66	2	2	K.ENYDPIQDPCTLVKK.T	0.9958	2	1821.0033
						K.FLQDGKFDLCQK.T	0.9944	1	1499.6727
4196	SGT1_MOUSE	641	1.72	1	4	R.DPIDLRACR.V	0.9924	1	1116.2285
4197	SGTA_MOUSE	315	12.06	2	4	K.ALELDPDNDTYKSNLK.I	0.9958	2	1836.9934
						R.MGLALSSLNKHAEAVAYYK.K	0.9958	2	2067.4107
4198	SH3BG_MOUSE	214	49.07	5	71	K.EENIIYSFLGLAPPPGSK.V	0.9958	2	1933.2115
						K.VFVATSSGSIAIR.K	0.9958	2	1308.5205
						K.KQQEVVGFLEANK.I	0.9958	2	1490.6995
						K.KPQNGIPLPPQIFNEEQYCGDFDSFFSAK.E	0.9958	3	3375.6845
						K.SEEASSLPNGDVAGEAEGAAEGTEK.A	0.9958	2	2406.4327
4199	SH3L1_MOUSE	114	42.11	2	3	R.ENNAVYAFLGLTAPPGSK.E	0.9958	2	1850.0813
						R.ENVPEDSRPSTGYPLPPQIFNECQYR.G	0.9958	3	3095.3179
4200	SH3L3_MOUSE	93	37.63	1	12	K.ATPPQIVNGNHYCGDYELFVEAVEQDTLQE	0.9958	3	3827.1616
4201	SHAN2_MOUSE	1476	3.93	2	2	K.KPAGISNCLPSSFLPPPESFDAVTDSGIEEV	0.9958	3	3620.9148
						R.EDGDTKPDHSPSTVPEGVPK.T	0.9958	2	2093.2115
4202	SHAN3_MOUSE	1805	5.87	4	4	R.NYNSQTAFQVAIIAGNFELAEVIKTHK.D	0.9958	3	3008.4038
						R.SPTPVHSPDADRPGPLFVDVQTRDSER.G	0.9944	3	2977.2199
						R.RAESPCAPLSAGNSPGPGASTGMDGPGA	0.9958	3	3182.4584
						R.SLPHQLLLQR.L	0.9958	2	1205.4459
4203	SHB_MOUSE	503	3.78	1	7	R.LDYCGGGGGGDPGGGQR.A	0.9958	1	1580.5768
4204	SHBG_MOUSE	403	12.16	2	5	R.DSVALHWRLLLLLLLLMPPPTHQGR.A	0.9958	3	2891.537
						K.YLSNGPGQEPVMVMTIDLTK.I	0.9958	2	2194.566
4205	SHIP2_MOUSE	1257	2.7	2	3	K.SMIGSTAQQFLTFLSHR.G	0.9924	2	1925.2127
						R.KPASTETSCPLSK.L	0.9958	2	1406.542

4206	SHLB1_MOUSE	365	12.05	3	6	R.ELIQTSALNFLTPLR.N	0.9958	2	1717.0183
						K.KLAADAGTFLSR.A	0.9958	2	1250.4404
						K.GKVPITYLELLN.-	0.9958	2	1360.6366
4207	SHLB2_MOUSE	400	12.25	3	24	R.DFIHTASLSFLTPLR.N	0.9958	2	1718.9933
						R.LLLEGISSTHVNHLR.C	0.9958	2	1689.9553
						K.TELDAHFENLLAR.A	0.9917	2	1529.6927
4208	SHOT1_MOUSE	631	5.71	2	3	R.VSMLAVEEYEELQVNLELEK.D	0.9945	2	2366.6857
						R.ESAEALATKLNK.E	0.9958	1	1275.4447
4209	SHPRH_MOUSE	1674	4.18	3	6	R.DFPHAGPQLLGGILADEMGLGKTVEVLALI	0.9958	3	3685.3196
						R.RSETVSVLEATEEETR.L	0.9958	2	1836.9506
						K.KLGQLLYLTNLEK.S	0.9958	2	1533.8516
4210	SHPS1_MOUSE	513	11.5	2	2	R.AQPAPKPEPSFSEYASVQVQR.K	0.9958	2	2317.5633
						K.GPSEPDTEIQSGGGTEVYVLAKPSPPEVS(	0.9943	3	3425.6874
4211	SHRM2_MOUSE	1481	2.63	2	5	K.ESRQSLACPAELPPLPSGLER.D	0.9925	2	2308.5627
						R.ELEDKIHLGEEQLK.C	0.9958	2	1681.8834
4212	SI1L1_MOUSE	1782	2.92	2	4	K.DLAEKNVTNTPIDPSGK.F	0.9924	1	1799.9756
						K.EELHPTASSQLAPSFSSSSSSSSGPRTFYF	0.9958	3	3286.4955
4213	SIA8B_MOUSE	375	6.4	2	10	K.QILKFLDAEK.D	0.9958	1	1205.4399
						R.VEWVNALILK.H	0.9958	1	1185.4521
4214	SIL1_MOUSE	465	3.66	1	179	K.LLVILATNQPLPAKK.K	0.9958	2	1620.0317
4215	SIN3A_MOUSE	1282	3.12	3	3	R.QTGIQK.E	0.9958	1	674.7752
						K.YYLKSLDHQGINFK.Q	0.9958	2	1726.9725
						R.LKVEDALSYLDQVK.L	0.9958	2	1621.8712
4216	SIN3B_MOUSE	1098	4.46	2	2	R.GQEDLLSEFGQFLPEAK.R	0.9958	2	1909.1027
						R.YVEQYVGSEGASSSSTEGFLLKPVFLQR.N	0.9958	3	3080.421
4217	SIPA1_MOUSE	1037	3.28	2	2	R.RSFSELYMLSLK.E	0.9958	1	1474.7583
						R.ARAHSHEDASRPAATPTR.L	0.9958	3	1932.0658
4218	SIRT2_MOUSE	389	18.51	4	10	R.DVAWLGDCDQGCLALADLLGWK.K	0.9958	2	2477.7083
						R.NLFTQTLGLGSQK.E	0.9958	2	1407.6097
						R.KEYTMGWMK.E	0.9944	1	1174.4181
						R.KVICLVGAGISTSAGIPDFR.S	0.9931	2	2062.3831
4219	SIRT3_MOUSE	257	22.18	3	3	R.LVDLLGWTQELLDLMQR.E	0.9958	2	2044.4168
						K.DVVQLGDVVHGVER.L	0.9924	2	1522.7013
						R.CPVCTGVVKPDIVFFGEQLPAR.F	0.9944	2	2490.8372
4220	SIRT5_MOUSE	310	57.74	12	205	R.NPSQVWEFYHYR.R	0.9958	1,2	1626.7709
						K.HIAIISGAGVSAESGVPTFR.G	0.9958	2	1970.2358
						R.RVVVITQNIDELHR.K	0.9958	2	1692.959

						R.VVVITQNIDELHR.K	0.9958		2	1536.7715
						R.SKEPNPGHLAIAQCEAR.L	0.9958		2	1879.0489
						R.GVPVAEFNMETTPATDR.F	0.9958		2	1836.0265
						K.NLLEIHGTLFK.T	0.9958		2	1285.529
						K.EPNPGHLAIAQCEAR.L	0.9958		2	1663.7967
						K.TLPEALAPHETER.T	0.9958	1,2		1464.6182
						K.GAPEPETQDARIPVDK.L	0.9958		1	1723.8803
						R.SPICPALAGK.G	0.9958		1	1014.1761
						R.CEEAGCGGLLRPHVVWFGENLDPAILEEV	0.9958		3	3539.8586
4221	SK2L2_MOUSE	1040	5.96	5	5	R.CSKESLK.N	0.9958		1	851.9415
						K.DLRPVDNRQSVLK.S	0.9958		2	1540.7629
						K.AIGNTELENK.F	0.9958		1	1089.1906
						R.WISSGEYIQMSGR.A	0.9958		1	1514.6959
						R.KAQIALDIK.S	0.9924		1	1000.2266
4222	SKP1_MOUSE	163	33.13	3	8	K.RTDDIPVWDQEFLK.V	0.9929		2	1762.9597
						K.VDQGTLFELILAANYLDIK.G	0.9958		2	2137.4809
						K.LQSSDGEIFEVDVEIAK.Q	0.9944		2	1880.0588
4223	SKT_MOUSE	1946	2.11	2	2	R.SLLVLDEVPPAPEPPTSISPASR.K	0.9944		2	2373.7087
						R.DCGASLPHMAQEVSPRSLLVLDEVPPAPE	0.9944		3	4110.5947
4224	SLAP2_MOUSE	259	16.22	2	2	K.TSSPSPSSSGPDQEPVSMQPER.H	0.9944		2	2288.4046
						R.HKVTAVALGSFPAGEQAR.L	0.9948		2	1840.0922
4225	SLIK1_MOUSE	696	1.44	1	5	K.EWLENIPK.N	0.9958		1	1029.1809
4226	SLIK3_MOUSE	980	6.02	2	2	K.IYRSDFWNFSSLDLLHLGNNR.I	0.9958		3	2568.854
						R.LYTNSFLHLNNAVSINLGNNALQDIQTGAF	0.9958		3	3677.1112
4227	SLIK4_MOUSE	837	6.21	2	21	K.LQNIEGGAFLGLSALKQLHLNNNELK.I	0.9958		3	2836.2639
						K.KPTVKHEGLGNSECGSMQLQLR.K	0.9958		2	2470.7723
4228	SLIRP_MOUSE	112	64.29	6	32	R.GMGWVQFSSQEELQNALQQEHHIIDGVK.I	0.9958		3	3210.5481
						K.IPWTAAASELR.E	0.9958		2	1215.3946
						R.EHFAQFGHVR.R	0.9958	1,2		1228.3555
						R.KIPWTAAASELR.E	0.9944	1,2		1343.5687
						K.IHVQAQR.A	0.9944		1	851.984
						R.SSTGRPIAFVR.K	0.9929		2	1191.3756
4229	SLIT1_MOUSE	1531	1.5	2	3	K.NDFAGLK.Q	0.9958		1	764.8565
						K.SIPPGAFSPYRK.L	0.9944		2	1320.5339
4230	SLIT2_MOUSE	1521	2.17	2	3	K.YSFECTDGSSFVDEVEKVVK.C	0.9946		2	2326.4847
						K.LVSVNFVNK.E	0.9924		1	1020.2169
4231	SLIT3_MOUSE	1523	1.64	2	8	R.DLEILTLNNNNISR.I	0.9958		1	1629.8106

						K.MDFAGLK.N	0.9958	1	781.9452
4232	SLK_MOUSE	1233	11.92	7	16	R.WTTSQLLQHPFVTVDSNKPVR.E	0.9958	2	2454.7911
						R.KLQEQEVFFK.M	0.9958	2	1296.5089
						R.DLNPEEFWEIIGELGDGAFGK.V	0.9958	2	2337.5475
						K.ILNEKPTTDGPEK.A	0.9943	2	1442.6091
						K.RPKLENLPDTQDQQTVDVNSVSEENENNF	0.9924	2	3370.5278
						R.LVVTGAEARALGSEGEAAATEVDLER.K	0.9958	3	2615.8571
						K.LKELDEEHSQELK.E	0.9958	2	1598.7502
4233	SLMAP_MOUSE	845	7.69	5	8	R.LEHLQEKTLK.E	0.9958	1	1239.4575
						K.LLSAQDEILLLR.Q	0.9958	2	1384.6591
						K.LHMDMENLQEEK.D	0.9958	2	1517.712
						K.QEEIQQK.G	0.9958	1	902.9799
						K.YNGAVNEIKDLSDK.L	0.9958	1	1566.7081
4234	SMBP2_MOUSE	993	2.92	2	2	R.ELQSRGVCLLK.L	0.9958	1	1303.5108
						R.TGLYGQRLVTFEPR.K	0.9958	2	1637.879
4235	SMC1A_MOUSE	1233	2.6	2	2	K.GDMDELEKEMLSVEK.A	0.9958	1	1753.9772
						K.SKLESELANFGPR.I	0.9958	2	1448.6188
4236	SMC1B_MOUSE	1248	2.32	3	7	K.HNLLLDCK.V	0.9958	1	1013.1479
						K.KLDLSK.K	0.9958	1	703.8571
						K.QMEEKILQK.G	0.9958	1	1147.3752
4237	SMC3_MOUSE	1217	0.66	1	3	K.LNENLR.R	0.9958	1	758.8527
4238	SMCA5_MOUSE	1051	3.33	2	6	R.FLICMLHKLGFDK.E	0.9918	2	1622.9752
						R.LDSIVIQQGRLVDQNLNK.I	0.9946	2	2054.3543
4239	SMCR7_MOUSE	454	13.22	2	3	K.FPELPFGALVPGGPLYDGLQAGTAEHVR.L	0.9952	3	2910.3018
						R.LLLAWPLEGLASNLWLQDLYPVETARLR.A	0.9958	3	3252.8271
4240	SMD1_MOUSE	119	18.49	1	3	R.YFILPDSLPLDTLLVDVEPK.V	0.9958	2	2288.6862
4241	SMD2_MOUSE	118	17.8	1	6	K.REEEEFNTGPLSVLTQSVK.N	0.9957	2	2164.377
4242	SMD3_MOUSE	126	26.98	2	2	R.FLILPDMLK.N	0.9958	1	1090.4095
						K.VLHEAEGHIVTCETNTGEVYR.G	0.9958	2	2415.5878
4243	SMEK1_MOUSE	820	1.83	1	5	K.FKEVIPISDPELK.Q	0.9912	2	1515.7899
4244	SMG1_MOUSE	3658	2.13	3	3	R.APGSRLSSGGGGTK.Y	0.9958	1	1232.339
						K.LQGKLLEEIEFLEGAEGVDHPSHTLQHR.Y	0.9958	3	3184.5357
						R.VAQDSPHLILYPAIVGTISLSSESQASGNK.Y	0.9958	3	3084.4533
4245	SMG5_MOUSE	1017	5.11	3	3	K.VYYEVIQLIKTNK.K	0.9958	2	1611.9219
						R.SEVPDSLNGPLGPSEASIASNLQAMSTQMI	0.9958	3	3594.0058
						R.KVYYEVIQLIK.T	0.9958	1	1396.7129
4246	SMKW_MOUSE	499	6.01	2	2	K.YCHNQDIVHQDIK.A	0.9958	2	1670.7881

						K.KYNESMGAYLILK.A	0.9944	1	1530.8224
4247	SMKX_MOUSE	640	5.31	1	5	R.ATDVWSLGVVLYFMATGCLPFNGYSYEAI	0.9958	3	3631.1464
4248	SMPX_MOUSE	85	29.41	3	77	K.FPGPVVNLSEIQNVK.S	0.9958	2	1641.9078
						K.KFPGPVVNLSEIQNVK.S	0.9958	2	1770.0819
						K.KPIPGMK.K	0.9944	1	771.0087
4249	SMRC2_MOUSE	1213	3.3	2	2	R.DIGEGNLSTAAAAALAAAAVK.A	0.9958	2	1886.1124
						K.MKEEVPTALVEAHVR.K	0.9944	2	1710.0013
4250	SMTL2_MOUSE	456	17.11	2	2	R.LIEVEDMMVMGRKPDPMCVFTYVQSLYN	0.9944	3	3774.4301
						R.ASNSCILENGHQLDAGPANGSSEVQTSSA	0.9958	3	4516.8516
4251	SMTN_MOUSE	923	7.48	3	26	R.HSQRAADGSTVGTVTK.T	0.9958	2	1615.7434
						R.STSFGVPNANSIKQMLLDWCR.A	0.9924	3	2425.7309
						R.ELAHSLAELQSCPQEEGPGGRGLALR.S	0.9944	3	2777.0325
4252	SMYD1_MOUSE	485	30.93	7	71	R.LLSIASEVLSYLQAYEEASHYAR.R	0.9932	2	2614.9146
						K.ISEGEELTVSYIDFLHLSEER.R	0.9958	2	2467.6917
						R.EAALNNQPMQVMAEPSNEPAPALFHK.K	0.9958	3	2836.2098
						R.AYSAVVFDSLINFVCHTCFK.R	0.9958	2	2379.6497
						R.AGLTNWHAGHIEVGHGMICK.A	0.9958	2	2189.4657
						K.AYAILLVTHGPSHPITK.D	0.9944	2	1819.157
						K.GLKDDLFLAAK.E	0.9958	2	1191.413
4253	SMYD2_MOUSE	433	5.77	2	2	R.LYMGLENK.A	0.9958	1	968.1559
						R.EFESHLDKLDNEK.K	0.9958	2	1604.7136
4254	SMYD5_MOUSE	416	8.41	2	3	K.FKDQLELLLGLFK.E	0.9958	2	1564.9084
						R.LTGKPSQILPHPELCSVR.K	0.9944	2	2033.3446
4255	SNAA_MOUSE	295	11.19	2	2	K.AALCHFCIDMLNAK.L	0.9958	2	1664.8923
						K.HDAATCFVDAGNAFK.K	0.9958	2	1624.7161
4256	SND1_MOUSE	910	10.66	6	9	K.FFTESR.L	0.9958	1	786.8626
						R.LGTLPPAFSTR.V	0.9944	1	1160.3586
						R.AGNLAR.R	0.9924	1	601.6835
						R.SASYKPVFVTEITDDLHFYVQDVETGTQLE	0.9958	3	3561.9239
						K.VWAHYEERPVEEVMPVLEEK.E	0.9958	2	2470.8023
						K.VHVFYIDYGNR.E	0.9958	2	1383.5492
4257	SNP23_MOUSE	210	26.19	3	12	R.EDEMEENLTQVGSILGNLK.N	0.9958	2	2120.3362
						K.NMALDMGNEIDAQNQQIQK.I	0.9958	2	2162.3973
						R.AHQVTDESLESTR.R	0.9958	2	1473.5394
4258	SNPC4_MOUSE	1333	5.93	3	3	K.AIAATHGHLEWHLVAEELGTSRSAFQCLQ	0.9944	3	3362.7386
						R.LQRLLQPK.L	0.9944	1	996.2412
						R.AAPSLTQLSVQPPVSGQPLATKSSLPVNW	0.9958	3	3646.2218

4259	SNRK_MOUSE	748	2.14	1	2	K.YILDPQKALFSSVK.V	0.9958	1	1609.906
4260	SNTA1_MOUSE	503	14.12	3	5	R.HGVDTHLFSVESPQELAAWTR.Q	0.9958	2	2381.6097
						K.QIGWLTEQLPSGGTAPTLALLTEK.E	0.9958	2	2525.9048
						K.NSAGGTSVGWDSPPASPLQR.Q	0.9958	2	1985.1203
4261	SNX1_MOUSE	522	3.07	1	3	K.YLETLLHSQQQLAK.Y	0.9958	2	1672.9218
4262	SNX10_MOUSE	201	8.96	1	2	R.LQSNALLVQLPELPSK.N	0.9958	2	1751.0764
4263	SNX12_MOUSE	165	30.91	2	3	R.LNSKPQDLTDAYGPPSNFLEIDIFNPQTVG	0.9958	3	3604.9983
						R.GDEGIFEESFIEER.R	0.9937	2	1657.7307
4264	SNX15_MOUSE	337	2.67	1	9	K.KDPEDIK.E	0.9924	1	844.9402
4265	SNX2_MOUSE	519	17.15	5	7	K.SAAMLGNSEDHTALSR.A	0.9958	2	1660.7991
						K.YLHVGYIVPPAPEK.S	0.9958	2	1583.8705
						R.ELILSSEPSPAVTPVTPTTLIAPR.I	0.9958	2	2490.8999
						R.AVNTQALSGAGILR.M	0.9958	2	1371.5797
						K.HPTLLQDPDLR.Q	0.9958	2	1305.4765
4266	SNX27_MOUSE	539	4.82	1	2	R.SINGELYAPLQHVSAVLPGGAADR.A	0.9958	2	2436.73
4267	SNX29_MOUSE	476	2.52	1	5	R.ENEVLKVQLK.K	0.9958	1	1200.4209
4268	SNX3_MOUSE	162	25.31	3	5	R.GDDGIFDDNFIEER.K	0.9958	2	1642.6757
						R.KQGLEQFINK.V	0.9958	1,2	1205.3995
						R.CLHMFLQDEIIDK.S	0.9958	2	1662.9075
4269	SO1A6_MOUSE	670	8.81	2	2	K.SVGTGANMVFQNCSCIR.S	0.9944	2	1902.0645
						K.EFFLMMKNLFCNPIYMLCVLTSVLQVNGVA	0.9958	3	4510.4296
4270	SO1B2_MOUSE	689	2.61	1	2	K.TPILLLYVALIYVMKR.K	0.9958	2	1907.4516
4271	SOCS1_MOUSE	212	12.74	1	3	R.TSALLDACGFYWGPLSVHGAHERLR.A	0.9931	2	2815.1296
4272	SOCS3_MOUSE	225	29.33	2	2	K.LQESGFYWSAVTGGEANLLLSAEPAGTFLI	0.9944	3	3299.7075
						R.AYYIYSGGEKIPLVLSRPLSSNVATLQHLCF	0.9958	3	3508.0239
4273	SODC_MOUSE	154	38.96	5	472	K.GDGPVQGTIHFEQK.A	0.9958	1,2	1513.65
						R.HVGDLGNVTAGK.D	0.9958	1,2	1168.295
						R.VISLSGEHSIIGR.T	0.9924	2	1368.576
						K.DGVANVSIEDR.V	0.9958	1	1175.2407
						K.AVCVLKGDGPVQGTIHFEQK.A	0.9943	2	2184.4662
4274	SODM_MOUSE	222	83.33	13	2283	K.GDVTTQVALQPALK.F	0.9924	1	1441.6677
						K.AIWNVINWENVTER.Y	0.9958	1	1744.9475
						K.LTAVSVGVQGSGWGWLGFNK.E	0.9958	2	2064.3513
						K.HHAAYVNNLNATEEK.Y	0.9958	2	1711.8314
						R.LQIAACSNQDPLQGTTGLIPLLGIDVWEHA	0.9958	3	4091.6191
						K.YHEALAK.G	0.9944	1	831.9469
						K.FNGGGHINHTIFWTNLSPK.G	0.9958	2	2141.3964

						K.GELLEAIK.R	0.9958		1	873.0373
						R.DFGSFEK.F	0.9958		1	829.8846
						K.NVRPDYLK.A	0.9924		2	1005.1619
						K.GELLEAIKR.D	0.9958		1	1029.2248
						K.HSLPDLPYDYGALEPHINAQIMQLHHSK.H	0.9958		3	3226.6367
						K.RDFGSFEK.F	0.9947		2	986.0721
4275	SORC1_MOUSE	1167	1.29	1	2	R.DWRLLQAPDADLR.G	0.9958		1	1569.7605
4276	SORCN_MOUSE	198	11.11	1	14	R.CLTQSGIAGGYKPFNLETCR.L	0.9958		2	2273.4829
4277	SORL_MOUSE	2215	1.9	2	3	K.IITENDHVLLFWKSLALK.E	0.9934		2	2141.5614
						K.HSRSQVEILASQLTGLMDMK.V	0.9944		2	2245.6172
4278	SOX1_MOUSE	391	9.97	1	4	K.DKYSLAGGLLAAGAGGGGAAVAMGVGVG	0.9958		3	3158.603
4279	SOX10_MOUSE	466	3.86	1	2	R.KLADQYPHLHNAELSK.T	0.9958		2	1865.0989
4280	SOX12_MOUSE	314	5.41	1	2	K.IMDQWPDMHNAEISK.R	0.9932		2	1816.0565
4281	SOX3_MOUSE	375	16.53	2	2	K.NPVGPPTPAAGTGVPAAPGAAGKSGANP/	0.9958		3	4667.7995
						K.SGANPAGGANAGNGGSGGANGGGGGG	0.9958		3	2957.9205
4282	SP130_MOUSE	1057	3.6	2	6	R.LTNLQEGIIPK.K	0.9931		2	1226.4588
						R.KQQHVISTEEGDMMETNSTDDEK.S	0.9958		3	2653.8061
4283	SPA3A_MOUSE	422	9.95	2	2	K.LALENPHKNIVFSPLSISAALALMSLGAK.G	0.9944		3	3007.6049
						R.YNFQSAKIK.A	0.9958		1	1099.2749
4284	SPA3C_MOUSE	417	13.91	4	100	R.MQQVEASLQPETLR.K	0.9929	1,2		1630.8566
						K.NPDTNIVFSPLSISAALAIVSLGAK.G	0.9958		2	2499.9103
						R.DEELSCTVVELK.Y	0.9926		2	1422.5384
						R.MQQVEASLQPETLRK.W	0.9958		2	1759.0307
4285	SPA3F_MOUSE	445	9.89	2	4	R.TLMVLVNYIYFK.G	0.9958		2	1504.8707
						K.VTNPESDENFLNVEYAFPQVLEIMPEYR.S	0.9958		3	3345.7047
4286	SPA3K_MOUSE	418	49.76	17	702	K.AVLDVAETGTEAAAATGVIGGIR.K	0.9944		2	2143.402
						K.ISFDPQDTFESEFYLDEK.R	0.9958		2	2211.3429
						K.NPDTNIVFSPLSISAALALVSLGAK.G	0.9958		2	2499.9103
						K.EVFTEQADLSGITETK.K	0.9958		2	1768.9152
						K.TLFPSQIEELNLPK.F	0.9958		2	1629.8938
						R.LEEDVLPEMGIK.E	0.9958	1,2		1373.6044
						R.HFRDEELSCSVLELK.Y	0.9958	2,3		1863.0435
						K.KLSVSQVVHK.A	0.9958	1,2		1125.3567
						R.ALYQTEAFTADFQQPTEAK.N	0.9958		2	2160.3447
						R.DEELSCSVLELK.Y	0.9958	1,2		1422.5384
						K.FSIASNYR.L	0.9958	1,2		958.0617
						K.DLQILAEFHEK.T	0.9958		2	1343.5223

						K.LSVSQVVHK.A	0.9958	2	997.1826
						R.KTLFPSQIEELNLPK.F	0.9958	2	1758.0679
						K.ELISELDER.T	0.9958	1	1104.2023
						K.TMEEILEGLK.F	0.9958	2	1163.3716
						K.AVLDVAETGTEAAAATGVIGGIRK.A	0.9958	2	2271.5761
4287	SPA3M_MOUSE	418	10.53	2	41	R.ALYQTEAFTADFQKPTEAK.N	0.9958	2	2160.388
						K.NIVFSPLSISAALALVSLGAK.G	0.9958	2	2072.4961
4288	SPAG1_MOUSE	901	3.55	2	2	K.YIENCSDVKHLEK.I	0.9958	2	1635.7803
						R.EDGGSDEAAMGNIQK.K	0.9944	2	1522.5836
4289	SPAS2_MOUSE	545	1.65	1	3	K.HFVSERK.Y	0.9958	1	903.0287
4290	SPB6_MOUSE	378	33.86	8	25	K.LEENYNMNDALYK.L	0.9958	2	1617.7705
						K.FKLEENYNMNDALYK.L	0.9958	2	1893.1212
						K.FYEAELEELDFQGATEESR.Q	0.9958	2	2264.3637
						K.CSGNGGGDVHQGFQSLLTEVNK.T	0.9958	2	2305.432
						R.LDKMDEEEVEVFLPK.F	0.9958	2	1822.0803
						K.AFVEVNEEGTEAAAATAGMMTVR.C	0.9918	2	2356.6277
						K.GTTASQMAQALALDK.C	0.9958	2	1506.7143
						K.EHTREMPFK.V	0.9958	1	1175.3477
4291	SPCS_MOUSE	504	6.55	2	2	K.AAGSSLLNKITNSLVLNVIK.L	0.9958	2	2056.4539
						K.MQDVDLFIK.R	0.9958	1	1109.3258
4292	SPEC1_MOUSE	1067	7.5	4	17	K.ELADLEEENRALK.E	0.9958	1	1530.6751
						K.ERWALSTEDANASDPSAEGTASPESDAQF	0.9958	3	3373.5279
						K.HVSSLLAKMEK.D	0.9958	1	1243.5071
						K.KLGSSPTSSCNPTPTK.H	0.9958	1	1662.8035
4293	SPEE_MOUSE	302	15.23	2	2	R.YQDILVFRSK.T	0.9944	1	1269.4863
						R.HFCKSLFPVVDYAYCSIPTYPSGQIGFMLC	0.9958	3	3775.2517
4294	SPEF2_MOUSE	1734	1.79	2	2	K.EEHLAALQTEEQAAQFR.L	0.9958	2	1972.1216
						R.RIAVQLMHVR.H	0.9918	2	1223.5253
4295	SPEG_MOUSE	3262	5.33	8	14	R.GLLATQQAEPSPPSIVVTPSEPR.S	0.9958	2	2375.6842
						R.LQESPSLSALSETQPPSPARPSVPK.L	0.9958	2	2604.92
						R.GVLVTGDGAGAPVFLRPLK.N	0.9943	2	1868.2297
						K.RALPGPSTQPPATPTSPHR.R	0.993	2	1969.2107
						R.ALPGPSTQPPATPTSPHR.R	0.9958	2	1813.0232
						K.IVDFGSAQPYNPQALKPLGHR.T	0.9958	2	2309.6328
						K.ISGTPPPSVTWTHFGHPVNEGDNLR.L	0.9944	2	2716.9725
						R.VPTVPPRPGSSLSGSIENLESEAVFEAK.F	0.9958	3	2899.2273
4296	SPG20_MOUSE	671	10.73	3	18	R.GISIAAAEPGHTGPAWEAAR.Q	0.9958	2	1963.16

						R.IQPEEKPVEVSPAVTR.G	0.9945	2	1780.0312
						R.FLDNSLDTVLNRPPGFLQVCDWLYPLVPDI	0.9958	3	3562.0283
4297	SPG7_MOUSE	781	7.17	2	2	R.STSMSGFSNTEEEQTLNQLLVEMDGMGTT	0.9958	3	4345.769
						R.HVFIDLPTLQER.R	0.9958	2	1468.6958
4298	SPKAP_MOUSE	1687	1.9	2	2	R.NELAHTLSNVILK.H	0.9924	1	1452.6939
						R.STELGKEAIAEALLR.E	0.9958	1	1601.8406
4299	SPON1_MOUSE	807	6.94	2	2	K.IRPLTSLDHPQSPFYDPEGGSITQVARVVIE	0.9958	3	3580.0379
						R.MLKSLAELGDCNEDLEQAEK.C	0.9958	2	2294.5019
4300	SPOPL_MOUSE	392	3.32	1	3	K.MADNLLAAADK.Y	0.9958	1	1133.305
4301	SPRL1_MOUSE	650	4.77	2	2	K.SIPACTDFEVAQFPLR.M	0.9924	2	1852.0631
						K.GHQLQLDYFGACKSIPACTDFEVAQFPLR.I	0.9944	3	3370.7211
4302	SPRY4_MOUSE	207	28.5	3	23	R.GPVAPAFALWDGELLTHSGLEVPK.G	0.9958	2	2505.8761
						R.ISVIHTLQTDFR.G	0.9958	2	1430.6469
						R.IGVADVDMSRDSCVGADDR.S	0.9952	2	2039.1475
4303	SPS1_MOUSE	392	20.41	3	12	R.NEVSFVIHNLPVLAK.M	0.9958	2	1680.9878
						K.LLESLQENHFQEDEQFLGAVMPR.L	0.9958	2	2732.0399
						R.LGIGMDTCVIPLRHGGLSLVQTTDYIYPIVD	0.9958	3	4269.945
4304	SPS2_MOUSE	452	8.63	2	10	K.NEVSFVIHNLPIIAK.M	0.9958	2	1695.0147
						R.SFSNYRPFEPQTLGFSPSWR.L	0.9911	2	2404.6463
4305	SPS2L_MOUSE	558	3.76	1	5	R.TPCSSLLPLLNTHAVASGK.Q	0.9958	3	1967.239
4306	SPSY_MOUSE	366	26.78	4	37	R.LVEYDIDEVVYDEDSPYQNIK.I	0.9943	2	2547.7315
						R.IYPHGLVLLDLQSYDSDVQGK.Q	0.9958	2	2361.6568
						K.GLQSIFQEQGMTESVHTWQDHGYLATYTN	0.9958	3	3471.7821
						K.DVLILGGGDGGILCEIVK.L	0.9923	2	1829.1101
4307	SPT2_MOUSE	682	7.18	2	2	R.QPGSNSGSAPGQPNPGTARPTLSSGPVPI	0.993	3	2929.1819
						R.RQNGSSSSGPEQSAGGIR.K	0.9958	2	1775.8325
4308	SPT20_MOUSE	790	2.28	1	2	R.SGGFYSAEDADSPPER.G	0.9927	2	1685.7008
4309	SPT5H_MOUSE	1082	3.88	2	3	K.DATESTARVELHSTCQTISVDR.Q	0.9917	2	2477.6135
						K.VVSISSEHLEPITPTK.N	0.9958	2	1737.9909
4310	SPTA1_MOUSE	2415	40.04	55	221	K.ALNVPSSPYTWLTVDVLGR.I	0.9958	2	2089.3989
						K.SQLDDVHAFQQFNWK.A	0.9958	2	1864.0269
						K.LLVDSQLLQQLYQDSDDLK.T	0.9958	2	2235.4961
						K.ANVQLQQYLADLHEAEAWIK.E	0.9958	2	2341.6286
						K.TIGGVISSPELAEDLTGTEILLER.H	0.9958	2	2514.8327
						R.AEQVDGVINLGNSLIER.R	0.9958	2	1828.0324
						K.VADELLFEELLTPEGAHIR.Q	0.9958	2	2153.4399
						K.DLNDLAQELISSGTFNIDQIEEK.M	0.9958	2	2593.8041

K.TALINADELPTDVASGEALLAR.H	0.9958	2	2241.5034
R.QEAFLENEDLGNSVGSVEALLQK.H	0.9958	2	2491.7142
K.LAPDELPGFPQHQR.E	0.9958	2	1605.7935
R.EIDNTLQNINSK.R	0.9958	2	1389.5052
R.ALNAADPGSDLLSVQALQR.Q	0.9958	2	1940.1637
K.GTQLYEANQLLQFENNAEDLK.R	0.9958	2	2439.6409
R.GDSGDTLAATQSLLK.K	0.9958	2	1477.6115
K.KTENTGVELDDVWELQK.K	0.9958	2	2005.1889
K.YSTIGLAQQWDQLHQLGMR.M	0.9958	2	2246.5487
R.RAEVLNQYQR.F	0.9958	2	1277.4257
R.LAQFVQHWEK.L	0.9958	2	1286.4759
R.TELNEAWDTLQGLTSDR.K	0.9958	2	1950.0691
K.SNGADLTAFLTLLAK.H	0.9958	2	1535.7807
R.MQHNLEQQIQAK.D	0.9958	2	1468.6708
R.IWNHLPDIIK.E	0.9958	2	1249.4985
K.KHEAFLVDLNAFENSIK.A	0.9958	2	1976.2395
K.CRALNAADPGSDLLSVQALQR.Q	0.9958	2	2256.49
K.RLEGELVAHEPAVQNVLDTAESLR.D	0.9944	2,3	2647.9481
R.GVNLEESLEYLQFMENAEEEEAWLGEK.C	0.9958	3	3188.4433
R.DQAEVCQQQQAAPVDEAGR.E	0.9958	2	2101.1602
K.HDTLDASLQSFQQER.L	0.9958	2	1775.8723
K.LIDNDHYDSENIAAIR.D	0.9958	2	1859.9903
R.TELNEAWDTLQGLTSDRK.E	0.9958	2	2078.2432
K.EHEAFLASLAGAQEDFNYLLELDK.Q	0.9947	2	2724.9837
R.FENVQSLAAAHHEK.L	0.9958	2	1581.7281
K.TSDDIESAFQALAEGK.A	0.9958	2	1682.7814
K.IEDLGDSMEEALILDIK.Y	0.9957	2	1905.1677
R.FQSADATGQELLDGNHEASEEIR.E	0.9958	2	2518.6128
K.TGQEMIEDGHYASEAVAAR.L	0.991	2	2036.1804
R.YNEFLLAYEAGDMLEWIQEK.K	0.9958	2	2463.7639
R.HEVILADIASHEPR.I	0.9958	2	1587.7758
R.LLWDLLLELTQEK.S	0.9958	2	1614.9225
K.KNDVLTLLSSINK.D	0.9958	2	1445.6995
R.QEAFLENEDLGNSVGSVEALLQKHDDFEE.	0.9958	3	4169.415
R.KLAPDELPGFPQHQR.E	0.9958	2	1733.9676
K.KHEALENDFAVHK.N	0.9958	2	1538.7031
K.EPQLTSEDYGKDLVSSEALFHNHK.R	0.9958	3	2745.9622

						K.KFEEFQEELTAR.K	0.9958		2	1527.6739
						K.HGLLESDVTAR.Q	0.9958	1,2		1198.3213
						K.GYVSLEDYTSFLIDKESENIK.T	0.9958		2	2451.6893
						K.ETYALFQFFQDLDDEEAWIEEK.L	0.9944		2	2767.9618
						K.VLETAEEIQHR.R	0.9958		2	1325.4643
						R.EEPVNIPQLQQQVETLYHSLLDR.A	0.9958		2	2751.0685
						R.KLLVDSQLLQQLYQDSDDLK.T	0.9958		3	2363.6702
						K.HESFVSEVQAK.S	0.9958	1,2		1261.3769
						R.LADEQYQLLSSAHAVEMFHR.E	0.9929	2,3		2346.6226
						K.RWLEEVEWQVTSEDYGK.V	0.9958		2	2155.3281
4311	SPTA2_MOUSE	2472	37.1	52	333	K.IAALQAFADQLIAVDHYAK.G	0.9958		2	2059.3727
						R.LQQSHPLSASQIQVK.R	0.9958		2	1664.9022
						K.DLASVNNLLKK.H	0.9958		1	1215.4355
						K.LIQEQHPEEELIK.T	0.9958		1	1606.8162
						K.KGDILTLLNSTNK.D	0.9958		2	1417.6457
						K.QEAFLLNEDLGDSLDSVEALLK.K	0.9958		2	2420.6758
						K.YTEHSTVGLAQQWDQLDQLGMR.M	0.9958		2	2577.8309
						K.REELITNWEQIR.T	0.9958		2	1587.7758
						R.AQLADSFHLQQFFR.D	0.9958		2	1708.9169
						R.MQHNLEQQIQAR.N	0.9958		2	1496.6842
						K.ALINADELANDVAGAEALLDR.H	0.9958		2	2155.3696
						K.KIEDLGAAMEEALILDNK.Y	0.9958		2	1974.2769
						K.RLEAELAAHEPAIQGVLDTGK.K	0.9958		2	2219.5027
						R.AGTFQAFEQFGQQLLAHGHYASPEIK.E	0.9958	2,3		2877.1882
						K.ASAFNSWFENAEEDLTDPVR.C	0.991		2	2299.4149
						K.LIQNNHYAMEDVATR.R	0.9958		2	1775.9769
						R.SLGYDLPMVEEGEPDPEFEAILDTVDPNR.I	0.9944		3	3249.5269
						K.DLNSQADSLMTSSAFDTSQVK.E	0.9958		2	2246.4077
						K.MTLVASEDYGDTLAAIQGLLK.K	0.9958		2	2210.5476
						K.KHEALMSDLSAYGSSIQALR.E	0.9958		2	2178.4681
						R.SSLSSAQADFNQLAELDR.Q	0.9944		2	1953.0727
						K.SADESGQALLAASHYASDEVR.E	0.9958		2	2178.2768
						K.HQALQAEIAGHEPR.I	0.9958		2	1557.7091
						R.DLAALEDKVK.A	0.9944		1	1102.2731
						K.NQALNTDNYGHDLASVQALQR.K	0.9958		2	2329.4911
						R.SQLLGSAHEVQR.F	0.9958		2	1325.4673
						K.EAALTNEEVGADLEQVEVLQK.K	0.9958		2	2286.498

						R.LEESLEYQQFVANVEEEEAWINEK.M	0.9944	2,3	2928.1352
						R.EAFLNTEDKGDSLDSVEALIK.K	0.9958	2	2295.5053
						K.DFDFWLSEVEALLASEDYGK.D	0.9958	2	2335.5286
						R.LIQSHPESAEDLK.E	0.9957	2	1467.6189
						R.MMLDHCLELQLFHR.D	0.9958	2	1844.1659
						K.HEAFETDFTVHK.D	0.9958	2	1461.5737
						K.KFEEFQTDLAAHEER.V	0.9958	2	1850.9823
						R.NVEDIELWLYEVEGHLASDDYGK.D	0.9958	2	2695.8988
						K.HQLLEADISAHEDR.L	0.9952	2	1634.7459
						K.HQAFEAELHANADR.I	0.9958	2	1609.6982
						K.HALLEADVAAHQDR.I	0.9958	2	1546.6829
						K.EAIVTSEELGQDLEHVEVLQK.K	0.9958	2	2367.6153
						K.EPIVGSTDYGKDEDSAEALLK.K	0.9958	2	2238.4101
						K.KHEAFETDFTVHK.D	0.9958	2	1589.7477
						K.KHQLLEADISAHEDR.L	0.9958	2	1762.9199
						K.HQAFEAELSANQSR.I	0.9958	2	1588.6768
						R.ALSSEGKPYVTK.E	0.9958	1	1280.4637
						R.ECEDVMDWINDKEAIVTSEELGQDLEHVE\	0.9958	3	3903.2265
						R.VASNPYTWFTMEALEETWR.N	0.9958	2	2332.5922
						K.KLSDDNTIGQEEIQQR.L	0.9958	2	1875.0025
						R.RQDLEDSLQAQQYFADANEAESWMR.E	0.9958	2,3	3003.1859
						R.QFQDAGHFDAENIK.K	0.9912	2	1620.7184
						K.KLLVSSEDYGR.D	0.9924	1	1267.4246
						R.LAQFVEHWK.E	0.9958	2	1158.3451
						R.LIQSHPESAEDLKEK.C	0.9958	2	1724.9084
4312	SPTB2_MOUSE	2363	29.83	36	225	K.EGEDMIAEEHFGSEKIR.E	0.991	2	1978.1407
						R.MHTTFEHDIQALGTQVR.Q	0.9958	2	1985.2249
						K.DLTSVMRLLSK.H	0.9944	1	1263.5383
						R.LQALDTGWNELHK.M	0.9958	2	1525.7043
						R.DVSSVELLMNNHQGIK.A	0.9958	2	1785.0252
						K.DVAEEITNYRPTIDTLHEQASALPQAHAESI	0.9958	3	3748.0545
						R.QNLLSQSHAYQQFLR.D	0.9958	2	1834.0445
						K.EGMQLISEKPETEAVVK.E	0.9958	2	1889.1713
						K.TAGYPNVNIHNFTTSWR.D	0.9958	2	1979.1619
						K.DDEEMNTWIQAISSAISSDK.H	0.9958	2	2241.3882
						K.HQILEQAVEDYAETVHQLSK.T	0.9958	2	2339.5669
						R.TLETPAAQMEGFLNR.K	0.9958	2	1678.9006

						R.FQIQDISVETEDNKEK.K	0.9904		2	1924.0716
						K.WLHGLESQIQSDDYGK.D	0.9958	1,2		1877.0202
						R.DMGEMVTQGQTDAQYMFLR.Q	0.9958		2	2222.5105
						R.AQTLPTSVVTITSESSPGKR.E	0.9958		2	2060.3122
						K.EIEELQSQAQALSQEGK.S	0.9958		2	1889.0263
						R.LVSQDNFGFDLPAVEAATK.K	0.9958		2	2023.2499
						K.VIESTQDLGNDLAGVMALQR.K	0.9958		2	2131.4088
						R.EVVAGSHELGQDYEHVTMLQER.F	0.9958	2,3		2528.7558
						R.DASVAEAWLLGQEPYLSSR.E	0.9958		2	2093.3006
						K.DALLSALSIQNYHLECNETK.S	0.9958		2	2320.5274
						K.QAEAFLNNQEYVLAHTEMPTTLEGAEAAIK	0.9958		3	3291.6569
						K.SAASGIPYHSEVPVSLK.E	0.9958		2	1742.9695
						K.KHEAIETDIAAYEER.V	0.9958		2	1775.9127
						R.MPLATSTDHGHNLQTVQLLIK.K	0.9958		2	2318.6965
						R.SQNIITDSSSLNAEAIR.Q	0.9958		2	1819.9664
						K.SNAHYNLQNAFNLAEQHLGLTK.L	0.9958		2	2484.7336
						R.KHNLLASK.E	0.9958		1	911.0922
						K.EAEKLESEHPDQAQAILSR.L	0.9958		2	2152.3256
						K.EQWLNNMQIPEKLEDLEVIQHR.F	0.9958	2,3		2764.1284
						K.LLTQHENIKNEIDNYEEDYQK.M	0.9958		2	2637.8193
						R.IHCLENVDK.A	0.9944		2	1128.2365
						K.HQAFMAELASNK.E	0.9952		2	1347.5316
						K.HRPDLIDFDK.L	0.9958		2	1256.4038
						K.KQQMLENQMEVR.K	0.9958		2	1534.7889
4313	SPTC2_MOUSE	560	5.36	2	2	K.HNNMQSLEKLLK.D	0.9924		2	1455.7154
						R.QEIGNLDKHEELEK.L	0.9958		2	1682.8278
4314	SPYA_MOUSE	413	12.59	2	3	R.YQCLLLVDSVASLGGVPIYMDQQGIDIMYS	0.9958		3	3781.2938
						K.VLNAPPGISLISFNDK.A	0.9958		2	1685.9609
4315	SQRD_MOUSE	450	18.44	5	10	K.KYPNVFGIGDCTNLPTSK.T	0.9958		2	2012.236
						K.HNLIEVRPDK.Q	0.9958		2	1221.4019
						K.ANIIFNTALGTIFGVK.K	0.9958		2	1680
						K.KYADALQEIIR.E	0.9958		2	1320.5315
						K.NHYEVLVLGGGAGGITMATR.M	0.9958		2	2017.3104
4316	SQSTM_MOUSE	442	8.37	2	4	K.NYDIGAALDTIQYSK.H	0.9958		2	1672.8321
						K.LIFPNPFGHLSDSFSHSR.W	0.9958		2	2059.2914
4317	SR140_MOUSE	1029	1.46	1	3	R.LKNPNAPMLPPPK.N	0.9914		1	1417.7527
4318	SRA1_MOUSE	220	9.09	1	8	R.APETSGPPPVDHPPPSSK.A	0.9958		2	1797.9622

4319	SRBD1_MOUSE	1015	3.25	2	19	K.SSQQVDDESKDVAVK.E	0.9958	2	1635.7252
						R.VQDPLAELVKFDPK.H	0.9924	1	1599.8675
4320	SRBP2_MOUSE	1130	8.14	3	3	K.GIDLGSLVDSDVDLK.I	0.9944	2	1546.7148
						R.SVLSLESGAGGWFDWMVPTLLLWLVNGVI	0.9958	3	3934.715
						R.LHQLHITGKLPAGSACSDVHMALCAVNLAE	0.9958	3	3833.2497
4321	SRBS1_MOUSE	1290	4.26	3	4	K.SVLEGGDIPLQGLSGLK.R	0.9958	2	1683.9426
						R.HFIPADYLESTEEFIR.R	0.9958	2	1968.173
						R.KLAPVQVLEYGEAIAK.F	0.9958	2	1730.0575
4322	SRC8_MOUSE	546	3.11	1	2	K.TVQGSGHQEHINIHK.L	0.9958	2	1685.8399
4323	SRCA_MOUSE	910	38.02	21	383	R.VYVSSFWPQDYKPDTHR.E	0.9958	2	2126.3354
						R.AITQELPSLLGSIGLGK.N	0.9958	2	1698.0129
						R.YQLYTGAEPTTSEFTVLMHGPK.L	0.9958	2	2471.7871
						K.IYHTSIKPLEQSYK.Y	0.9958	2,3	1707.9671
						K.STMINYLLGLEDTR.Y	0.9958	2	1626.8652
						R.GNPVIAQWEEVEDASEEAPLR.D	0.9958	2	2340.5083
						K.EEISLLEDLNQVIENR.L	0.9958	2	1915.1076
						K.TLMLNEDKPADDYSAVLQR.L	0.9958	2	2180.4376
						K.LLSQQCSYMGGCFLEK.I	0.9958	2	1922.1355
						R.VTFVDTPGIIENR.K	0.9958	2	1461.6579
						K.LIGIEVPHK.L	0.9958	1,2	1006.2333
						K.DFFGINPISNFK.L	0.9958	1	1399.5889
						K.NLLLHYPDGR.E	0.9958	2	1198.3671
						K.AEVDTESGEKVEDQGEPRPSLDAGSAIEAI	0.9958	3	3230.3801
						K.TPGATGHEEEGPQLDVEDLNTGFEGSK.T	0.9958	2	2815.9207
						R.ELFLKEEISLLEDLNQVIENR.L	0.9958	2	2545.8926
						R.KIYHTSIKPLEQSYK.Y	0.9958	2	1836.1411
						R.ADLIFVVFDPTK.L	0.9958	1	1365.6122
						R.QHEITDGEITSKPMVLFLGPWSVGK.S	0.9958	2	2771.2036
						K.DIVEDPDKFYIFK.T	0.9952	2	1629.8499
						R.EAYKDFFGINPISNFK.L	0.9958	2	1891.1333
4324	SRFB1_MOUSE	441	2.04	1	3	R.IRVLVIR.K	0.9944	1	869.1416
4325	SRP68_MOUSE	625	5.76	2	4	R.KTLNFK.M	0.9958	1	750.9163
						R.LYDIILQNLVELLQLPGLEEDRTFQK.E	0.9958	3	3102.5981
4326	SRPR_MOUSE	636	3.62	1	3	K.NVAADIAVQLCESVANKLEGK.V	0.9944	2	2230.4895
4327	SRRM1_MOUSE	946	3.38	2	5	K.MMQINLTGFLNGKNAR.E	0.9944	2	1809.1547
						K.VNLEVIKPWITK.R	0.9958	2	1440.7691
4328	SSB_MOUSE	152	19.08	2	5	R.SLNRVQLLGR.V	0.9944	1	1156.3737

						K.NPVTIFSLATNEMWR.S	0.9958		2	1780.0515
4329	SSDH_MOUSE	523	50.29	14	100	R.HQSGGNFFEPTLLSNVTR.D	0.9958		2	2005.1973
						R.WLPAPATFPVYDPASGAK.L	0.9924		1	1889.1607
						K.EAQGEILYSALFLEWFSEEAR.R	0.9958		2	2489.7436
						R.DMLCITEETFGPLAPVIK.F	0.9958		2	2035.3693
						R.VGNGFEEGTTQGPLINEK.A	0.9958		2	1891.0447
						K.IITAESGKPLK.E	0.9937		2	1157.3959
						R.VAEQLEVGMVGVNEGLISSVECPFGGVK.(	0.9958		2	2906.2869
						K.FDKEEEAVAIANAAEVGLAGYFYSQDPAQI'	0.9944	2,3		3560.9012
						K.ILLHHAANSVK.R	0.9958	1,2		1203.43
						K.QPVGVAAIITPWNFPSAMITR.K	0.9929		2	2270.6977
						R.GIHDSFVTK.F	0.9958		2	1004.1307
						K.RVSMELGGLAPFIVFDSANVDQAVAGAMA	0.9958		2	3153.6387
						R.RIYGDIIYTSAK.D	0.9958		2	1400.6176
						K.RHQSGGNFFEPTLLSNVTR.D	0.9944		2	2161.3848
4330	SSFA2_MOUSE	1252	9.19	5	5	R.GPDLAAAPYSTQNSSVLPLYENTFQELQV\	0.9958		3	3409.7771
						R.FFNSSSFARGIDIK.V	0.9944		2	1589.7911
						R.AKVEIVAEK.R	0.9958		1	987.1845
						K.IFRASVALTPTAPSR.T	0.9958		1	1587.8625
						R.NGGSFEDDLSLGAEANHLHEPDAQVENCN	0.9958		3	3966.1492
4331	SSH1_MOUSE	1042	2.5	2	2	R.HNKLWR.Q	0.9958		1	854.0023
						K.LRSIMMSQDLENVTSK.E	0.9944		2	1853.1591
4332	SSH3_MOUSE	649	6.16	2	2	R.SPPASGHSTPVGPTQDR.V	0.9958		2	1691.7978
						R.DFIDNQMLLLMAQQDRASR.I	0.9958		2	2266.5952
4333	SSNA1_MOUSE	119	10.08	1	3	K.LARVNENLAR.K	0.9958		1	1156.3304
4334	SSPO_MOUSE	4998	1.18	3	9	R.QCPCLVDGAHYWPGQRIK.M	0.9944		2	2186.4101
						K.VYTGPGLSLHHAGLFLLLTTR.L	0.9944		2	2267.6793
						R.ADPVEAPMAGPGPR.E	0.9958		1	1365.5469
4335	ST14_MOUSE	855	14.04	4	8	K.VFNGHLRITNEIFLDAYENSTSTEFISLASQ\	0.9958		3	3746.1681
						K.EGGTGALILQKGEIR.V	0.993		2	1542.7758
						K.SVEYSTVVRPICLPDATHVFPAGKAIWVTG'	0.9944		3	3882.4229
						R.SFDVAPCDEHGSDLVTVYDSLSPMEPHAV	0.9944		3	3431.7212
4336	ST1C1_MOUSE	304	3.95	1	2	R.ILYLFYEDMK.E	0.9944		1	1335.6007
4337	ST38L_MOUSE	464	7.54	2	10	K.GHPFFEGVDWGHIR.E	0.9924		2	1654.8277
						K.LTLENFYSNLILQHEER.E	0.9958		2	2120.3696
4338	ST5_MOUSE	1134	4.5	2	3	K.STLEENAYEDIVGGLPK.E	0.9915		2	1836.0056
						R.EGPGSEWSVSEGCPSVGCPSVVPSPCSS	0.9958		3	3137.2357

4339	STA5A_MOUSE	793	10.09	5	8	R.LGDLNYLIYVFPDRPK.D	0.9958	2	1924.2499
						R.IQAQFAQLGQLNPQER.M	0.9958	2	1842.0647
						R.GQATQLLEGLVQELQK.K	0.9958	2	1756.0092
						K.LGHYATQLQNTYDR.C	0.9958	2	1680.8173
						R.HILYNEQR.L	0.9958	1	1073.1967
4340	STA5B_MOUSE	786	6.74	3	3	K.LGHYATQLQSTYDR.C	0.9958	2	1653.7917
						K.DEVYSKYYTPVPCEPATAK.A	0.9958	2	2219.4187
						K.ATQLLEGLVQELQK.K	0.9958	2	1570.8265
4341	STAB1_MOUSE	2571	2.49	3	6	K.GFVDNMTLSGPDLELHASNATFLSINASR.(	0.9909	2	3079.4113
						R.ICVAIDECGLDTR.G	0.9958	2	1522.6277
						R.GGCHADALCSYVGPGQSR.C	0.9958	2	1892.955
4342	STABP_MOUSE	424	3.3	1	2	R.NEFTITHVLIPR.Q	0.9958	2	1440.6854
4343	STAM2_MOUSE	523	7.07	2	2	K.LNVIDDDVEEIKK.S	0.9958	1	1530.7154
						K.HSELSELNVKVLEALDLYNK.L	0.9944	2	2315.6287
4344	STAR3_MOUSE	446	9.87	2	3	R.QGKEATAVVDQILAQEENWK.F	0.9944	2	2258.493
						R.DRYLSSGIATTHCSKPPTHK.Y	0.9944	3	2257.4772
4345	STAR7_MOUSE	295	14.24	2	2	K.SFDENGFDYLLTYSDNPQTVFPR.Y	0.9958	2	2726.9153
						R.AVEHPSVPESPEFVR.V	0.9958	2	1680.8577
4346	STAT3_MOUSE	770	26.23	10	34	R.LENWITSLAESQLQTR.Q	0.9958	2	1890.1033
						K.IMDATNILVSPLVYLYPDIPK.E	0.9958	2	2376.8567
						R.FLQESNVLYQHNLR.R	0.9958	2	1761.978
						K.ESHATLVFHNLLGEIDQQYSR.F	0.9958	2	2458.6927
						R.LLQTAATAAQQGGQANHPTAAVVTEK.Q	0.9958	2,3	2577.857
						K.MQQLEQMLTALDQMR.R	0.9958	2	1837.1775
						R.SIVSELAGLLSAMEYVQK.T	0.9958	2	1939.2745
						R.YLEQLHQLYSDSFPMELR.Q	0.9958	2	2270.5647
						K.VVENLQDDFDFNYK.T	0.9958	2	1746.8706
						K.YCRPESQEHPEADPGSAAPYLK.T	0.9958	2	2503.6532
4347	STAT4_MOUSE	749	4.27	2	2	K.AMSSEESSNGSLSVEFR.H	0.9944	2	1817.922
						R.LSALAFADILR.D	0.9958	1	1190.4282
4348	STAU1_MOUSE	487	5.75	2	2	R.NAAENMLEILGFKVPQAQPAKPALK.S	0.9958	2	2680.1809
						K.RNAAENMLEILGFK.V	0.9958	2	1606.8804
4349	STEA3_MOUSE	488	2.87	1	2	K.FMLPGDHTQGEK.T	0.9958	2	1360.5273
4350	STIL_MOUSE	1262	3.96	2	2	K.QMNSMDSVGTFLDVK.R	0.9944	2	1672.9087
						K.RYGLLQSSDNSEDEEEPPSHADSESDHVL	0.9958	3	3514.5707
4351	STIM2_MOUSE	746	2.68	1	8	R.IAVHETSFMISQLKISDR.S	0.9932	2	2076.4186
4352	STIP1_MOUSE	543	23.39	8	27	R.ELIEQLQNKPSDLGTK.L	0.9958	2	1814.0459

						K.HYTEAIK.R	0.9958		1	861.9731
						K.ELDPTNMTYITNQAAVHFEK.G	0.9958		2	2323.5824
						K.LDPQNHVLYSNR.S	0.9958		2	1456.6011
						R.AMADPEVQQIMSDPAMR.L	0.9958		2	1891.1825
						K.AAALEFLNR.F	0.9958		1	1005.1619
						K.ALSAGNIDDALQCYSEAIK.L	0.9958		2	2040.2006
						K.FMNPFNLPNLYQK.L	0.9958		2	1626.9134
4353	STK10_MOUSE	966	10.56	4	4	K.ANQSRPNSSALETLGGEALTNGGLELPSS\	0.9944		3	3608.9011
						K.ETGALAAAKVIETK.S	0.9924		2	1402.6311
						R.IQMDEEKQIPDQDENPSPAASK.S	0.9923		2	2471.6551
						K.LWIMIEFCPGGAVDAIMLELDR.G	0.9944		3	2550.9999
4354	STK24_MOUSE	431	16.01	3	3	K.NNPPTLEGNYSKPLK.E	0.9958		2	1672.8785
						K.AANVLLSEHGEVKLADFGVAGQLTDTQIK.I	0.9931		3	3026.4167
						K.RPFSQCLSTIISPLFAELK.E	0.9958		2	2208.5719
4355	STK38_MOUSE	465	8.39	2	3	R.NLNHSLPSDFTFQNMNSK.R	0.9944		2	2095.294
						K.VTLENFYSNLIAQHEER.E	0.9958		2	2064.2621
4356	STK39_MOUSE	556	11.15	2	3	K.VLMLTLQNDPPTLETGVEDK.E	0.9958		2	2214.536
						R.VKEENSEISVNAGGIPEQIQSLSVHDSQAQ	0.9958		3	4155.3947
4357	STML2_MOUSE	353	15.58	2	5	K.DSNTVLLPSNPSDVTSMVAQAMGVYGALT	0.9958	2,3		3068.4842
						R.ESLNANIVDAINQAADCWGIR.C	0.9958		2	2331.5133
4358	STOM_MOUSE	284	19.01	2	6	K.NSTIVFPLPVDMLQGIMGSNH.-	0.9958		2	2271.6545
						K.NLSQILSDREEIAHHMQSTLDDATDDWGIK	0.9958		3	3440.7229
4359	STON1_MOUSE	730	4.25	2	5	R.KDFSLETQGVCRPNGLK.L	0.9948		2	1950.1681
						K.DFPGFPGIPK.A	0.9958		1	1075.2523
4360	STRAP_MOUSE	350	26.86	6	17	R.QGDTGDWIGTFLGHK.G	0.9952		2	1632.7728
						R.IYDLNKPEAEPK.E	0.9958		2	1417.6018
						R.SIAFHSAVSLEPIK.S	0.994		2	1499.7502
						R.FSPDGELYASGSEDGTLR.L	0.9958		2	1901.9812
						K.EISGHTSGIK.K	0.9958		1	1029.1381
						K.SFEAPATINSASLHPEK.E	0.9958		2	1799.9781
4361	STRN_MOUSE	780	5.38	2	4	R.ALAFHPIEPVLITASEDHTLK.M	0.9958		2	2303.6635
						R.VISHPTLPISITAHEDR.H	0.9958		2	1887.146
4362	STRN3_MOUSE	796	5.28	2	6	R.ALAFHPVEPVLVTASEDHTLK.L	0.9958		2	2275.6097
						R.VVSHPTLPVTITAHEDR.H	0.9934		2	1873.1191
4363	STRN4_MOUSE	760	11.05	3	3	R.GSSGPAQINQVVSHPSQPLTITAHDDR.G	0.9958		3	2814.0439
						K.HEEAIHAVACHPSK.A	0.9958		2	1586.7136
						R.TGKSVHSMVAHLDAVTCLAVDPNGVFLMS	0.9944		3	3971.4275

4364	STRUM_MOUSE	1159	3.02	2	3	K.AAKTALNNTLDLANVK.E	0.9924		2	1657.9077
						K.ELQNFLSMFQKIILK.E	0.9958	1,2		1853.2732
4365	STUB1_MOUSE	304	10.86	2	9	R.IHQESELHSYLTR.L	0.9909		2	1613.7703
						K.EGGARLGTGGGGSPDK.S	0.9958		1	1416.4905
4366	STX12_MOUSE	274	19.34	3	35	R.DFNSIIQTCSGNIQR.I	0.9958		2	1753.8755
						K.ELGSLPLPLSASEQR.Q	0.9958		2	1597.8088
						K.LQENLQQLQHSTNQLAK.E	0.9958		2	1994.215
4367	STX16_MOUSE	326	20.25	2	2	R.SIAADVDELADDRMALVSGISLDPEAAIGVT	0.9944		3	3244.6386
						K.HLNRPTLDDSSEEEHAIEITTQEVTQLFHR.(	0.9958		3	3547.8198
4368	STX17_MOUSE	301	9.3	1	4	K.LAALPVAGALIGGVVGGPIGLLAGFK.V	0.9958		2	2332.8784
4369	STX4_MOUSE	298	13.42	3	13	K.KTQHGVLSQQFVELINK.C	0.9958		2	1970.2791
						K.TQHGVLSQQFVELINK.C	0.9958		2	1842.1051
						K.AIEPQKEEADENYNSVNTR.M	0.9958		2	2208.3031
4370	STX7_MOUSE	261	24.52	3	4	K.DLGMMIHEQGDMIDSIEANVESAEVHVQQ/	0.9958		3	4025.4293
						K.ETDKYIK.E	0.9924		1	897.0159
						R.TLNQLGTPQDSPELR.Q	0.9958		2	1669.832
4371	STXB1_MOUSE	594	3.7	1	3	R.AAHVFFTDSCPDALFNELVK.S	0.9958		2	2282.5237
4372	STXB2_MOUSE	593	3.54	2	2	R.FLDDLKTLDQK.L	0.9946		2	1336.5279
						K.AGVEAR.A	0.9944		1	602.6683
4373	STXB3_MOUSE	592	5.07	2	2	R.HIAVVLEEIPK.L	0.994		2	1248.5083
						K.SCEVIIGSTHILTPR.K	0.9958		2	1683.9115
4374	SUCA_MOUSE	333	52.25	12	1079	K.ISALQSAGVVVSMSPAQLGTTIYK.E	0.9932		2	2422.8426
						K.HLGLPVFNTVK.E	0.9958		2	1225.4765
						K.AKPVVSFIAGITAPPGR.R	0.9944		2	1682.0189
						K.QGTFHSQQALEYGTK.L	0.9958		2	1695.829
						R.MGHAGAIIAGGK.G	0.9958	1,2		1083.2939
						R.LIGPNCPGVINPGECK.I	0.9924		1	1725.9147
						K.IICQGFTGK.Q	0.9958		1	1024.1712
						K.TGATASVIYVPPPFAAAAINEAIDAEIPLVVC	0.9958		3	4611.2735
						K.ISALQSAGVVVSMSPAQLGTTIYKEFEK.R	0.9958		3	2956.4242
						K.HIYIDK.N	0.9958		1	788.9218
						R.KHIYIDK.N	0.9958		1	917.0959
						R.RMGHAGAIIAGGK.G	0.9958		2	1239.4814
4375	SUCB1_MOUSE	463	62.85	26	837	K.YDATMVEINPMVEDSDGK.V	0.9958		2	2015.2142
						R.SFQGPVLIGSAQGGVNIEDVAAENPEAIVK	0.9958		3	4105.6318
						K.LHGGTPANFLDVGGGATVQQVTEAFK.L	0.9958		2	2615.9053
						K.IFDLQDWSQEDER.D	0.9937		2	1681.7557

						K.MGFPSNIVDSAAENMIK.L	0.9958		2	1825.1048
						R.SFQGPVLIGSAQGGVNIEDVAAENPEAIVK.	0.9958		2	3011.3587
						K.INFDSNSAYR.Q	0.9958		1	1187.2541
						K.KIFDLQDWSQEDER.D	0.9958	1,2		1809.9298
						K.VQAILVNIFGGIMR.C	0.9958		2	1531.8999
						K.KEQAVTLAQK.M	0.9958		1	1116.303
						R.REYYFAITMER.S	0.9915		2	1479.6935
						K.EQAVTLAQKMGFPSNIVDSAAENMIK.L	0.9958		3	2794.2105
						R.ICNQVLVCER.K	0.9924		2	1291.4223
						K.LYNLFLK.Y	0.9958		1	911.132
						K.SSDEAYAIAK.K	0.9958		1	1055.1296
						K.IFDLQDWSQEDERDK.E	0.9958		2	1925.0184
						K.ALIADSGLK.I	0.9958		1	888.0519
						K.AQVLAGGR.G	0.9958		1	771.8949
						K.AVSSQMIGQK.L	0.9958		1	1049.2304
						K.EAANADINYIGLDGSIGCLVNGAGLAMATM	0.9958		2	3453.9137
						K.KVQAILVNIFGGIMR.C	0.9958	2,3		1660.074
						K.EPIDIVEGIK.K	0.9958		1	1113.2963
						K.IVFSPEEAK.A	0.9924		1	1020.1705
						R.CDVIAQGIVMAVK.D	0.9958	1,2		1404.6741
						R.DKEAANADINYIGLDGSIGCLVNGAGLAMA	0.9958		3	3697.1764
						R.EYYFAITMER.S	0.9958		2	1323.506
4376	SUCB2_MOUSE	433	40.65	10	81	R.LEGTNVQEAQNILK.S	0.9947		2	1557.7441
						K.VVGELAQQMIGYNLATK.Q	0.9924	1,2		1836.1565
						K.SSGLPITSAVDLEDAAKK.A	0.9958		2	1803.0196
						R.SHNGPVIVGSPQGGVDIEEVAASSPELIFK.	0.9958		3	3035.3807
						K.IDATQVEVNPFGETPEGQVVCFDAK.I	0.994		2	2751.9728
						K.SSGLPITSAVDLEDAAK.K	0.9958	1,2		1674.8455
						R.MAENLGFLGSLK.N	0.9958		1	1280.5249
						R.FFVANTAK.E	0.9958		1	898.0495
						K.EQIDIFEGIKDSQAQR.M	0.9944		2	1878.0489
						K.VEAILVNIFGGIVNCAIIANGITK.A	0.9958		2	2500.9507
4377	SUGT1_MOUSE	336	21.13	4	22	R.LFQSFSDALIDGDPQAALEELTK.A	0.9958		2	2509.7723
						K.DYASALETFAEGQK.L	0.9958		2	1530.6311
						R.LLHPIIPEQSTFK.V	0.9957		2	1523.8155
						R.KVEINPPDDMEWK.Q	0.994		2	1601.8145
4378	SULF1_MOUSE	870	5.17	2	2	R.MYPHRPIMMVISHAAPHGPEDSAPQFSK.L	0.9911		3	3133.6308

						K.GPSDLLTVRQNAR.N	0.9924	1	1427.6035
4379	SUOX_MOUSE	546	34.98	11	104	R.LHVVGAPGGQSLSLSLDDLHK.F	0.9958	3	2144.4355
						R.NHLPVPNLDPHTYR.L	0.9958	2	1673.8717
						R.VSVESEESYSHWQR.R	0.9958	2	1723.796
						K.AVDDSYNVQPDTVAPIWNLR.G	0.9958	2	2274.4949
						K.TGVWVTLGSEVFDVTK.F	0.9958	2	1738.9781
						K.HEVTVTLQCAGNR.R	0.9958	2	1485.6061
						K.FVDLHPGGPSK.L	0.9958	1,2	1154.3109
						R.LHVVGAPGGQSLSLSLDDLHKFPK.H	0.9958	2	2516.9029
						R.INSQRPFNAEPPPELLTEGYITPNPIFFTR.N	0.9958	3	3460.9139
						K.IGELNPEDSMSPSVEASDPYADDPIR.H	0.9958	2	2805.9838
						R.LCDVLAQAGHR.L	0.9945	2	1240.3709
4380	SURF6_MOUSE	355	6.48	2	2	R.QLLDRLQAR.Q	0.9924	1	1113.3053
						K.DTYLQDLAKK.I	0.9958	1	1195.358
4381	SUV3_MOUSE	779	6.03	2	2	K.WPLLPPKNIK.D	0.9958	1	1206.5168
						K.APNTSLFVPLTVKPQGPSADGDVGAELTRI	0.9958	3	3392.8339
4382	SUV91_MOUSE	412	4.13	1	2	R.MDSNFGLAGLPGSPK.K	0.9944	2	1491.7021
4383	SVEP1_MOUSE	3567	1.49	2	2	R.MASCKCGTHTGQFECICEK.G	0.9911	2	2305.4289
						R.TCQENRDWDGHEPMCIPVDCGSPPVPTN	0.9958	3	3483.6487
4384	SVIL_MOUSE	2170	2.03	2	2	K.EEEDTPGSSLEK.Q	0.9958	1	1321.3373
						R.GTTPVSKPLEDIEARPDMQLESDLKLDR.L	0.9944	3	3155.5475
4385	SWP70_MOUSE	585	10.26	3	3	K.EQALQEAMAQLEQLELER.K	0.9958	2	2130.3777
						R.QQMEEQVAQKSSELEQYLQR.V	0.9958	3	2453.6862
						K.WHLEQQQAIQTTEAEK.Q	0.993	2	1941.1075
4386	SYAC_MOUSE	968	18.29	10	28	R.EIADLGEALATAVIPQWQK.D	0.9958	2	2054.3507
						K.NVGCLQEALQLATSFAQLR.L	0.9958	2	2120.3795
						R.LYVTYFGGDEAAGLEPDLECR.Q	0.9958	2	2376.5476
						K.THSPQTSAMLFTVDNEAGK.I	0.9958	2	2035.236
						R.NSSHAGAFVIVTEEAIAK.G	0.9958	2	1845.0623
						K.KDPEMVK.D	0.9944	1	847.0173
						R.GGYVLHIGTIYGNLK.V	0.9915	2	1605.8772
						K.VGDQVRLFIDEPR.R	0.9958	2	1544.7507
						K.MSNYDTDLFMPYFEAIQK.G	0.9958	2	2214.5123
						R.QIWQNLGLDEAR.I	0.9924	1	1443.6023
4387	SYAM_MOUSE	980	7.04	2	2	R.TVESYVQEVVGQDKPVFMEEVPLAHTAR.I	0.9958	2	3160.5689
						R.YSTEVLQAPPGFLGSLVPVVVETLGSAYPE	0.9958	3	3920.4919
4388	SYAP1_MOUSE	365	4.66	1	2	K.GLGNYLYNFASAATK.K	0.9958	2	1590.7759

4389	SYCE1_MOUSE	329	8.51	2	3	K.EMCVLDSSKEQLLK.E	0.9958	2	1680.9203
						R.ISFLNSQIDK.E	0.9958	1	1165.3317
4390	SYCM_MOUSE	551	16.33	7	23	R.AVNTILDLVHHANR.Q	0.9958	2	1573.7953
						R.ANEMNVTPASLASLFEEEFK.Q	0.9958	2	2228.4786
						R.SWQRPQGQDTGVQVHNSLTGR.K	0.9958	2	2352.5313
						R.HSSDFALWK.A	0.9958	1	1091.2114
						K.RANEMNVTPASLASLFEEEFK.Q	0.9958	2	2384.6661
						K.HLLLGLASFVEDAR.A	0.9945	2	1541.7905
						K.RHSSDFALWK.A	0.9958	2	1247.3989
4391	SYCP2_MOUSE	1500	2.33	2	2	R.FTGASESLINQISR.R	0.9952	2	1523.686
						K.AVSKTSESGMDYAASPK.S	0.9924	1	1729.8994
4392	SYDC_MOUSE	501	21.36	7	13	R.LPLQLDDAIRPEVEGEEDGR.A	0.9958	2	2252.4429
						K.IISAASEGGANVFTVSYFK.N	0.9958	2	1962.2096
						R.YGISSMIQSQEKPDR.V	0.9917	2	1739.9409
						R.FGAPPHAGGGIGLER.V	0.9958	2	1436.6133
						R.LQSGICHLFR.E	0.9952	2	1231.4063
						R.VTMLFLGLHNVR.Q	0.9958	2	1400.7252
						R.ETLINK.G	0.9924	1	717.8406
4393	SYDM_MOUSE	653	14.4	4	4	R.YILETLLK.E	0.9958	1	993.2316
						R.VSGTVISRPPGQENPK.M	0.9958	2	1666.8747
						R.GQDLMSNAPDSVSPEELKPYHIHVLWPAD	0.9958	3	4451.8189
						K.MREYLCNLHGFVDIETPTLFK.R	0.993	2	2584.9588
4394	SYEM_MOUSE	523	7.27	2	2	K.RLLLAEPHVVALGHR.V	0.9958	2	1682.0249
						R.LLGLLERPGLSLTQDVLNR.E	0.9958	2	2108.4893
4395	SYEP_MOUSE	1512	17	14	84	K.THMVVSNTLEDFQK.V	0.9958	1,2	1649.8591
						K.TGQEYKPGNPSAAAVQTVSTK.S	0.9952	2	2135.3385
						K.NPDVGLKPVWYSPK.V	0.9944	2	1600.8577
						K.SLTGIEYKPVSATGAEDKDK.K	0.9958	2	2110.3257
						R.AIQGATSHHLGQNFSK.M	0.9958	2	1696.8631
						K.DQVDSAVQELLQLK.A	0.9958	2	1586.7826
						K.NHIEDFAPEVAWVTR.S	0.994	2	1784.9689
						K.AALLNQHYQVNFK.G	0.9958	2	1546.7691
						K.SLTGIEYKPVSATGAEDK.D	0.9958	2	1867.063
						K.KLGVENCYFPIFVSQAALEK.E	0.9958	2	2314.6526
						K.DYVPGQPPASQNSHSNPVSNAQPAGAEKI	0.9958	3	3274.4875
						K.YNVYPTYDFACPIVDSIEGVTHALR.T	0.9958	2	2902.1988
						R.FPPEASGYLHIGHAK.A	0.9958	2	1624.8393

						K.WDVSGNRATVAPDK.K	0.9944	1	1516.6536
4396	SYFA_MOUSE	508	23.43	5	23	R.SIPLEGLVQSELMHLPSGK.V	0.9926	2	2036.3942
						R.RLEVADGGLDSAELATQLGVEHQAVVGAV	0.9958	3	3034.3965
						K.RLQLVQAGQAEK.L	0.9958	2	1341.5534
						R.GVLPDSGHLHPLLK.V	0.9924	1	1483.7538
						R.NETLDATHLAEFHQIEGVIADHGLTLGHLM(	0.9958	3	3710.2023
4397	SYFB_MOUSE	589	19.02	6	13	K.TPGFEIIHGLLDR.I	0.9958	2	1468.6958
						R.ALVAIGTHDLDTLSGPFTYTAK.R	0.9958	2	2292.5939
						K.QIISKEQGHGK.A	0.9958	1	1225.3903
						K.DSGKDVGAK.N	0.9924	1	876.942
						R.LDMAAAGFTEALTFALCSQEDIADKLGLDIS	0.9958	3	3589.0151
						K.VRPFAVAAVLR.N	0.9958	2	1199.4849
4398	SYG_MOUSE	729	22.22	9	38	K.TLHVEEVVPSVIEPSFGLGR.I	0.9958	2	2166.482
						R.TFFSFPAVVAPFK.C	0.9956	2	1458.7429
						R.YPLFEGQETGKK.E	0.9958	2	1397.5706
						R.LGDAVEQGVINNSVLGYFIGR.I	0.993	2	2222.5058
						K.TVNVVQFEPNK.G	0.9958	2	1275.4472
						K.LPFAAAQIGNSFR.N	0.9958	2	1392.6005
						K.VPLVAEKPLKEPK.T	0.9958	2	1448.7893
						K.APQVDVDRAVAELK.A	0.9958	2	1511.7184
						K.KSEMESVLAQLDNYGQQELADLFVNYNVK	0.9958	3	3347.7211
4399	SYHC_MOUSE	509	4.72	1	13	R.IGDYVQQHGGVSLVEQLLQDPK.L	0.9958	2	2424.716
4400	SYIC_MOUSE	1262	7.29	4	23	K.APLKPYPVPTSDNILIQEQTQLK.G	0.9958	2	2595.0111
						K.LSVFHGETEIQNQTDLLSLSGR.T	0.9958	2	2445.6915
						R.LMAPYTPFLTELMYQNLK.L	0.9958	2	2174.621
						R.FGWDCHGLPVEYEIDKTLGIK.G	0.9958	3	2478.773
4401	SYIM_MOUSE	1012	31.92	14	67	K.FIPGAALNSMTDMLDRRPYWCISR.Q	0.9958	3	2872.2985
						K.VSPLLPATHVTMAK.G	0.9958	2	1465.7943
						R.TVMVHGFTLGEK.G	0.9958	2	1319.5615
						K.VLSELGVDAQSLSAMEIR.E	0.9958	2	1919.2005
						R.FLLGNLTGFNPETDSVPVK.N	0.9958	2	2049.3312
						K.VHFVPGWDCHGLPIETK.V	0.9958	2,3	1993.2384
						K.IAPVASALETTFDVVAAFSGVDLEGGTCSH	0.9958	3	3675.0498
						R.AFAPILPHLAEEVFQHIPYVTEPK.S	0.9958	2	2748.1968
						R.TAGDIELTGTFVINLEGGDIR.E	0.9958	2	2192.4307
						K.TKDEYLINSQTTEHIIK.L	0.9958	2	2034.2737
						R.SCQTALAEILDVLVR.A	0.9958	2	1688.9281

						K.KPGLEEAVESACAMR.D	0.9958	2	1648.8378
						K.TEFCLHDGPPYANGDPHVGHALNK.I	0.9958	2	2647.8321
						K.GTGLVHTAPAHGMEDYSVASQHSLPMDCI	0.9944	3	4944.3965
4402	SYK_MOUSE	595	9.08	3	5	K.LPETSLFETEETR.K	0.9958	2	1552.6782
						K.ITYHPDGPEGQAYEVDFTPPFR.R	0.9944	2	2537.7472
						K.EVLLFPAMKPEDK.K	0.9958	2	1517.8237
4403	SYLC_MOUSE	1178	10.44	5	33	R.TEPGVPVSLVNPQPSSGHFSTK.I	0.9958	2	2266.5156
						K.FSEAEHWLDYFPPLAVQDLK.T	0.9958	2	2406.6996
						K.NYPVWQHITLTTLR.S	0.9958	2	1743.0183
						R.DDMVLPFEPVPVLEIPGIGNLPAVTVCDELI	0.9958	3	3378.9119
						R.LALADAGDTVEDANFVEAMADAGILR.L	0.9958	2	2649.9324
4404	SYLM_MOUSE	902	6.1	5	5	R.NLHPESWTQSNIK.H	0.9958	2	1554.7025
						R.QDAFVALTRK.A	0.9958	1	1149.3353
						K.VHELVLQSELGMK.L	0.9958	2	1483.7662
						K.IPVPQHVAQDQDK.V	0.9958	2	1475.6445
						K.IPVPQHVAQDQDKVHELVLQSELGMK.L	0.9958	3	2940.3874
4405	SYMC_MOUSE	902	12.64	7	18	K.QLALAEGKPIETPK.G	0.9958	2	1495.7593
						R.LFVSEGSPGSLPVLAAAAR.A	0.9958	2	1843.1332
						R.HGNQYIQVNEPWK.R	0.9958	2	1613.7727
						R.GIGVFGDMAKDTGIPADIWR.F	0.9958	2	2120.4308
						R.AELLISTVGPEECVVPFLTRPK.V	0.9958	2	2456.8511
						K.LQQHPVLPVPGER.N	0.9958	2	1470.7147
						K.KQLALAEGKPIETPK.G	0.9958	2	1623.9334
4406	SYN1_MOUSE	706	10.48	2	2	R.ASTAAPVASPAAPSPGSSGGGGFFSSLSN	0.9944	3	2836.0874
						R.SLVIGLQYAGIPSVNSLHSVYNFCDKPWVF	0.9924	3	4377.0754
4407	SYNC1_MOUSE	470	4.47	1	2	R.EPALQEVQQVHQDILAAYK.L	0.9958	2	2181.4533
4408	SYNE3_MOUSE	975	2.87	1	2	R.VALPLQLLLLLFLLLLFLLPAGEEER.S	0.9944	3	2948.6891
4409	SYNJ1_MOUSE	1574	8.7	4	4	K.DNIGRNQPSPQAGLAGPGPAGYGAARPTI	0.9958	3	3129.4653
						K.RPPPPRPVAPPARPAPPQRPPPPSGARSF	0.9958	3	3394.9594
						R.DNKYVLLASEQLVGVCLFVFIRPQHAPFIR.	0.9958	3	3532.1351
						K.VLDAYGLLGVLRLNLGDTMLHYLVLVTGCM	0.9958	3	3693.4073
4410	SYNPO_MOUSE	929	4.52	2	3	R.SPPSYSTLYPSSDPKPSHLK.G	0.9958	2	2189.4295
						R.AASPAKPSSLDLVPNLPR.A	0.9958	2	1834.1258
4411	SYP2L_MOUSE	975	6.87	3	3	R.RFSTPAPQPTAEPLAPTVLVPR.A	0.9943	2	2346.7349
						R.APPPIAYNPLLSPFFPQAAR.T	0.9958	2	2168.5461
						R.NSARPEAPGPAVPEPASVR.E	0.9958	2	1903.105
4412	SYRC_MOUSE	660	13.64	6	24	K.SDGGYTYDTSDLAAIK.Q	0.9958	2	1677.7619

						K.YIDKVEIAGPGFINVHLR.K	0.9958		2	2042.3885
						K.VEIAGPGFINVHLR.K	0.9958		2	1522.7904
						R.LNHVGDWGTQFGMLIAHLQDK.F	0.9944		2	2381.7142
						K.IVFVPGCSVPLTIVK.S	0.9929		2	1629.9898
						K.GFDILGIKPVQR.M	0.9958		2	1343.6121
4413	SYSC_MOUSE	512	21.48	5	48	K.EAVGDDESVPENVLNFDDLTADALAALK.V	0.9958	2,3		2933.1523
						K.YLIATSEQPIAALHR.D	0.9958		2	1683.9481
						K.EVMQEVAQLSQFDEELYK.V	0.9958		2	2187.4261
						K.KLDLEAWFPGSGAFR.E	0.9958		2	1694.9304
						R.EIGNLLHPSVPISNDEDADNKVER.I	0.9958		3	2662.873
4414	SYSM_MOUSE	518	6.76	2	2	R.KFDIEAWMPGR.G	0.9958		2	1350.578
						R.KGELRPADLPAIISTWQELR.Q	0.9958		3	2294.6591
4415	SYT1_MOUSE	421	3.56	1	3	K.KMDVGGLSDPYVK.I	0.9924		1	1409.6404
4416	SYT5_MOUSE	386	9.84	2	5	K.MDVGGLSDPYVKVHLLQGGK.K	0.9944		2	2114.4675
						R.QTLNPHFGETFAFK.V	0.993		2	1637.8351
4417	SYTC_MOUSE	722	4.02	2	2	K.VVWDLDRPLETDCTLELLK.F	0.9958		2	2316.6227
						K.DSKPIK.V	0.9929		1	687.8143
4418	SYTL1_MOUSE	567	4.06	1	3	K.ATSKILENGEEAPGLGPSLDR.M	0.9958		2	2155.3696
4419	SYTL2_MOUSE	950	5.47	3	4	K.LPEDHSLQQTKPEQSKTGK.A	0.9931		2	2152.369
						K.QTVSTEPENASHTK.A	0.9944		2	1529.6036
						K.SSHFTKLPSELSK.S	0.9945		2	1461.6579
4420	SYTM_MOUSE	723	9.13	5	5	K.FGEPWDLNPGDGAFYGPK.I	0.9924		2	1968.1321
						R.EAAELR.D	0.9958		1	688.7587
						K.TPTLFSTKLWEQSGHWEHYR.A	0.9958		3	2504.7667
						K.LWEQSGHWEHYR.A	0.9944		2	1628.7465
						R.EASAPTPPHWLAER.F	0.9958		2	1562.7251
4421	SYUA_MOUSE	140	27.14	2	3	K.EQVTNVGGAVVTGVTAVAQKTVEGAGNIA	0.9958		3	3416.8565
						K.EQVTNVGGAVVTGVTAVAQK.T	0.9958		2	1929.1808
4422	SYV_MOUSE	1263	7.92	4	8	K.SLGNVIDPLDVIHGVSLQGLYDQLLNSNLDI	0.9958		3	3893.3398
						R.IPAYFITVHDPAVPPGEDPDGR.Y	0.9958		2	2364.6195
						R.YGEAGDGPGWGGPHPR.I	0.9958		2	1610.6854
						R.CGEMAQAASAAVTRGDLR.I	0.9958		2	1865.0375
4423	SYWC_MOUSE	481	11.85	3	29	K.TLIDVLQPLIAEHQAR.R	0.9958		2	1818.1264
						K.MSASDPNSSIFLTDTAK.Q	0.9958		2	1785.9636
						K.ISFPAVQAAPSFSNSFPK.I	0.9958		2	1896.1528
4424	SYWM_MOUSE	360	16.11	2	3	R.AGVSNMVAIHAAVSGLSVEEVVRSSAGLD	0.9944		3	3155.5535
						K.HDGTVGLLTYPVLQAADILCYK.S	0.9958		2	2448.7876

4425	SYYM_MOUSE	472	10.38	3	3	K.NGLSLLKIGK.R	0.9958	1	1043.295
						R.GLEALAANHAR.L	0.9958	1	1123.2571
						R.AGHNVIALVGGSTALLGDPSGR.T	0.9958	2	2063.3213
4426	T10_MOUSE	276	65.94	10	62	R.GELVSHFLTSDMDSLSYLK.K	0.9958	2	2143.4163
						K.KVSTEGHLYNGFNIIAADLSTSK.G	0.9958	2	2466.7533
						K.LADFWGNNSEILSGLDMEEGK.A	0.9958	2	2326.5397
						K.VSTEGHLYNGFNIIAADLSTSK.G	0.9958	2	2338.5792
						K.DVLVTQLLDVLNNEEAQLPDPAIEDQGQEY	0.9958	3	4163.6251
						K.AGGTWLGISTR.G	0.9958	2	1119.2657
						R.TNTIILVDANGHVTFTER.S	0.9958	2	2002.2346
						R.GRGELVSHFLTSDMDSLSYLK.K	0.9958	2	2356.6557
						R.LILAANRDEFYNRPSK.L	0.9958	2	1908.1673
						R.GEPEPIVLTPGTYGLSNALLETPWK.K	0.9958	2	2684.0612
4427	T132C_MOUSE	1107	7.5	3	6	R.FSSLPPYLPVSFHVLRAETAFFLK.E	0.9958	2	2768.2737
						R.KSVLAVGIGHVGVK.F	0.9924	3	1364.6743
						K.DFSLTAISLDEAVVSIPQPLSPWWPTVVAE(	0.9924	3	4177.7436
4428	T132D_MOUSE	1097	5.83	2	3	K.FKWPIIAAENEGQGALVK.V	0.9945	2	1972.2945
						K.VTITDLGVQLVTGLSLSLQLSPGSNRAIFAT	0.9958	3	4440.2017
4429	T161A_MOUSE	480	2.92	1	2	K.KQDWDWTLPVIK.L	0.9958	1	1529.7789
4430	T22D4_MOUSE	387	5.17	1	8	R.ALASPEQLAQLPSSGLPR.L	0.9958	2	1836.0983
4431	T2EB_MOUSE	292	7.53	1	4	K.QWLMTEALVNNPKIEVVDGK.Y	0.9958	2	2285.6636
4432	TA2R4_MOUSE	297	14.14	2	2	K.FLDANSLWLVTILNSLYCVKITNFQHPVFLL	0.9944	3	3922.6551
						K.IFCFYK.-	0.9944	1	878.0246
4433	TAAR6_MOUSE	345	11.3	1	3	K.TPYSPGSRVILYAVFGFGAVLAVFGNLMVM	0.9944	3	4017.869
4434	TAB2_MOUSE	693	11.11	2	2	R.STPTSLHIHGVPPPVLNSPQGNSIYIRPYIT	0.9944	3	4028.5601
						K.EIDLFQARGPHFNPSAIHNFYDNIGFVGPVF	0.9958	3	3921.4527
4435	TACC2_MOUSE	1149	11.75	5	35	R.GLPSSQEPLLQVPEKPSQK.E	0.9958	2	2063.3586
						K.GTYTFDIDKWDDPNFNPFSSTSK.M	0.9958	2	2683.8469
						R.IGSTEVEKPPGLLFQQPDLDSALQVAR.A	0.9958	3	2910.2969
						K.RSPLSDPPSQDPTPAATPEAPSAISTVVHA	0.9958	3	3600.8749
						R.LAHPASLCGALGYLEPDLAEK.N	0.9958	2	2226.5005
4436	TACC3_MOUSE	631	1.43	1	2	K.SFSDLFK.R	0.9958	1	843.9549
4437	TADBP_MOUSE	414	11.11	2	24	R.FGGNPGGFGNQGGFGNSR.G	0.9958	2	1727.7929
						R.LVEGILHAPDAGWGNLVYVVNYPK.D	0.9958	2	2626.03
4438	TAF1C_MOUSE	836	7.66	2	2	R.AEPPPAPQCSQQDELTERLTEAWEGR.V	0.9958	3	2997.1706
						K.QGPPALLQVMQVEKGATGISLSPHLSGELA	0.9958	3	3547.0735
4439	TAF2_MOUSE	1104	2.9	2	2	K.LTHQVVCINNINFQRK.S	0.9917	2	1985.2627

						K.EELDKIVAYELK.T	0.9958		1	1450.6721
4440	TAF3_MOUSE	932	5.79	2	2	K.ASTSSNNFTKSLATPLPLSSGTSSSDNSWT	0.9958		3	4163.4701
						R.EPLSSINPQK.T	0.9944		1	1113.256
4441	TAF9_MOUSE	264	9.09	1	3	K.NILITTNMVSQNTAESANALKR.K	0.9927		2	2390.7173
4442	TAGL_MOUSE	201	23.88	3	26	K.TDMFQTVDLYEGK.D	0.9958		2	1547.7199
						R.LVEWIVVQCGPDVGRPDR.G	0.9958		2	2096.3599
						K.HVIGLQMGSNR.G	0.9958		2	1212.4124
4443	TAGL2_MOUSE	212	47.17	7	66	R.YGINTTDIFQTVDLWEGK.N	0.9958		2	2101.3202
						R.DDGLFSGDPNWFPK.K	0.9958		2	1595.7081
						K.LINSLYPEGQAPVK.K	0.9958		2	1529.7765
						R.TLMNLGGLAVAR.D	0.9958		2	1216.4845
						K.QYDADLEQILIQWITTQCR.E	0.9958	2,3		2395.6404
						K.QMEQISQFLQAAER.Y	0.9958		2	1679.8883
						K.LINSLYPEGQAPVKK.I	0.9931		2	1657.9505
4444	TAL1_MOUSE	329	11.55	2	2	R.SLHPALLPAADGAGPR.-	0.9944		3	1543.766
						K.YINFLAKLLNDQEEEGTQR.A	0.9958		2	2282.515
4445	TALDO_MOUSE	337	25.82	8	30	R.WLHNEDQMAVEK.L	0.9921		2	1500.6691
						R.WLHNEDQMAVEKLSDGIR.K	0.9915		2	2142.3941
						K.SYEPQEDPGVKSVTK.I	0.9958		2	1664.8095
						R.ILDWHVANTDK.K	0.9958		2	1312.4679
						K.LAPALSVK.A	0.9958		1	799.0012
						R.ILDWHVANTDKK.S	0.9958		2	1440.642
						K.ALAGCDFLTISPK.L	0.9958		2	1393.5891
						K.LFVLFGAEILK.K	0.9958		2	1250.5669
4446	TANC1_MOUSE	1856	2.59	2	2	K.EPQLQSMLSLR.S	0.9958		1	1302.5316
						R.NQHLEGTGPFTAGTGCGHFGDRLGASQSI	0.9924		3	3499.7502
4447	TAOK1_MOUSE	1001	3	2	11	K.QLMTLENKLK.A	0.9958		1	1218.4974
						K.MQLQQELELLNAYQSK.I	0.9958		2	1937.2183
4448	TATD1_MOUSE	295	5.08	1	2	R.YVGGVVHSFDGTK.E	0.9958		2	1366.5162
4449	TAU_MOUSE	733	11.19	6	20	R.QQVSSMSGAPLLPQGLR.E	0.9958		2	1770.0569
						K.HVPGGGSVQIVYKPVDLSK.V	0.9958		2	1981.3024
						K.IGSLDNITHVPGGGNK.K	0.9958		2	1579.7532
						K.SHPASELLR.R	0.9958		1	1010.138
						R.TPSLPTPPTR.E	0.9944		2	1067.2303
						K.IGSLDNITHVPGGGNKK.I	0.9958		1	1707.9273
4450	TAXB1_MOUSE	814	2.58	2	3	K.EQVKIAENVK.L	0.9958		1	1158.3403
						K.LIAVLEK.E	0.9958		1	786.0025

4451	TB182_MOUSE	1720	7.44	5	7	R.KPISGVQGNDPGISLPQR.D	0.9958		2	1864.1117
						R.SPALLPSTVEGPPGAPLLQAK.E	0.9958		2	2044.3989
						R.SPPSGSQSLLEGIMTASSSK.G	0.9958		2	1965.1829
						R.AKPPVKPKPRGLPSKPALPAKPSLLVPVGF	0.9958		3	3545.3883
						R.GFGIRSLSSGFSPEEAQQQDEEFEK.K	0.9944		3	2803.9555
4452	TBA1A_MOUSE	451	64.52	15	924	R.FDGALNVDLTEFQTNLVPYPR.I	0.9958		2	2410.6885
						R.AVFVDLEPTVIDEVR.T	0.9958		2	1702.9451
						R.LIGQIVSSITASLR.F	0.9958		2	1458.7416
						R.AFVHWYVGEGMEEGEFSEAR.E	0.9958		2	2331.5207
						R.NLDIERPTYTNLNR.L	0.9956		2	1719.8949
						R.QLFHPEQLITGK.E	0.9958	1,2		1411.6439
						R.IHFPLATYAPVISAEK.A	0.9958		2	1758.0703
						K.TIGGGDDSFNTFFSETGAGK.H	0.9958		2	2009.093
						K.VGINYQPPTVVPGGDLAK.V	0.9958		2	1826.1027
						K.AYHEQLSVAEITNACFEPANQMVK.C	0.9958		2	2752.037
						R.RNLDIERPTYTNLNR.L	0.9952		2	1876.0824
						R.AVCMLSNTTAIAEAWAR.L	0.9958		2	1866.1084
						R.ECISIHVGQAGVQIGNACWELYCLEHGIQP	0.9958		3	4299.6567
						K.LADQCTGLQGFLVFHSFGGGTGSGFTSLL	0.9958		3	3392.7767
						R.TIQFVDWCPTGFK.V	0.9958		2	1599.7925
4453	TBA1B_MOUSE	451	6.87	2	197	R.LISQIVSSITASLR.F	0.9958		2	1488.7679
						R.SIQFVDWCPTGFK.V	0.9924		1	1585.7656
4454	TBA4A_MOUSE	448	27.46	5	107	K.TIGGGDDSFTTFFCETGAGK.H	0.9958		2	2069.1548
						R.AVFVDLEPTVIDEIR.N	0.9958		2	1716.972
						K.DVNAAIAAIK.T	0.9958		1	986.1564
						K.LSDQCTGLQGFLVFHSFGGGTGSGFTSLL	0.9958		3	3408.7761
						R.ECISVHVGQAGVQMGNACWELYCLEHGIQ	0.9926		3	4303.6629
4455	TBA8_MOUSE	449	17.59	4	69	R.IHFPLVTYAPIISAEK.A	0.9958		2	1800.1509
						R.AVMVDLEPTVVDEVR.A	0.9958		2	1672.9342
						K.INDDDSFTTFFSETGNGK.H	0.9958		2	1996.0509
						K.AYHEQLSVAEITSSCFEPNSQMVK.C	0.994		2	2757.0101
4456	TBAL3_MOUSE	446	8.74	2	2	R.SFGGGTGSGFTSLLMER.L	0.9958		2	1704.8951
						K.VGINYQPPAVVPGGDLAR.V	0.9958		1	1824.0898
4457	TBAP_MOUSE	176	14.77	1	3	K.TISPEHVIQALESLGFGSYISEVK.E	0.9958		2	2605.9476
4458	TBB2A_MOUSE	445	61.12	19	1278	K.GHYTEGAELVDSVLDVVR.K	0.9958		2	1960.1509
						K.LTTPTYGDLNHLVSATMSGVTTCLR.F	0.9958		2	2710.0406
						R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	0.9958		2	2800.0647

						K.NSSYFVEWIPNNVK.T	0.9958	1,2		1697.8877
						K.EVDEQMLNVQNK.N	0.9958		2	1447.6031
						R.AILVDLEPGTMDSVR.S	0.9958		2	1616.8701
						K.IREEYPDR.I	0.9952		2	1078.1698
						R.EIVHIQAGQCGNQIGAK.F	0.9958		2	1824.0129
						K.RISEQFTAMFR.R	0.9944		2	1386.6116
						R.FPGQLNADLR.K	0.9924		1	1131.2767
						K.MSATFIGNSTAIQELFK.R	0.9958		2	1859.1474
						R.ISEQFTAMFR.R	0.9958		2	1230.4241
						K.ESESCDCLQGFQLTHSLGGGTGSGMGTLI	0.9958		3	3329.5924
						R.KESESCDCLQGFQLTHSLGGGTGSGMGTI	0.993		3	3457.7665
						K.LAVNMVPFPR.L	0.9926		2	1144.4204
						R.INVYYNEAAGNK.Y	0.9924		1	1356.4777
						R.ALTVPELTQQMFDSK.N	0.9958		2	1708.9672
						R.LHFFMPGFAPLTSR.G	0.9958		2	1621.9403
						R.KLAVNMVPFPR.L	0.9958		2	1272.5945
4459	TBB2B_MOUSE	445	13.26	3	38	R.INVYYNEATGNKYVPR.A	0.9958		2	1902.1167
						R.INVYYNEATGNK.Y	0.9958	1,2		1386.504
						K.VSDTVVEPYNATLSVHQLVENTDETYCIDN	0.9958		3	4595.9034
4460	TBB2C_MOUSE	445	34.16	9	208	R.AVLVDLEPGTMDSVR.S	0.9958		2	1602.8432
						K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	0.9958		2	3118.2995
						R.EIVHLQAGQCGNQIGAK.F	0.9958		2	1824.0129
						R.ALTVPELTQQMFDAK.N	0.9958		2	1692.9678
						K.EAESCDCLQGFQLTHSLGGGTGSGMGTLI	0.9958		3	3313.593
						R.KEAESCDCLQGFQLTHSLGGGTGSGMGTI	0.9958		3	3441.7671
						R.INVYYNEATGGK.Y	0.9958		1	1329.4521
						R.YLTVAAVFR.G	0.9924		2	1040.2505
						R.IMNTFSVVPSPK.V	0.9958		1	1320.5897
4461	TBB3_MOUSE	450	16.44	3	29	K.MSSTFIGNSTAIQELFK.R	0.9958		2	1875.1468
						K.LATPTYGDLNHLVSATMSGVTTSLR.F	0.9958		2	2606.9537
						R.SGAFGHLFRPDNFIFGQSGAGNNWAK.G	0.9958		3	2797.0641
4462	TBB5_MOUSE	444	19.37	5	25	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	0.9958		3	3104.2726
						R.ALTVPELTQQVFDAKNMMAACDPR.H	0.9958		3	2708.0859
						R.ALTVPELTQQVFDAK.N	0.9958		2	1660.9078
						K.MAVTFIGNSTAIQELFK.R	0.9958		2	1871.2018
						R.ISVYYNEATGGK.Y	0.9958		1	1302.4265
4463	TBB6_MOUSE	447	10.29	2	64	K.MASTFIGNSTAIQELFK.R	0.9958		2	1859.1474

						K.LTTPTYGDLNHLVSATMSGVTTSLR.F	0.9958	2	2636.98
4464	TBC15_MOUSE	671	7.45	2	2	R.EPVSLEEWNK.S	0.9958	1	1231.3477
						K.VTNYIFDSLRGSDPSTHQRPPSEMADFLSI	0.9958	3	3964.3985
4465	TBC17_MOUSE	645	4.5	1	9	R.SKPGLSWAYLVLVTQAGGSLPALHFHR.G	0.9952	3	2907.3909
4466	TBC23_MOUSE	684	2.49	1	7	K.EVVNIQTWINKPDIK.H	0.9958	2	1798.0923
4467	TBC9B_MOUSE	1263	0.63	1	2	R.DFLVQR.I	0.9958	1	777.8986
4468	TBCA_MOUSE	108	27.78	3	48	R.RLEAAYTDLQQILESEK.D	0.9958	2	2008.2359
						R.LEAAYTDLQQILESEK.D	0.9954	2	1852.0484
						K.QAEILQESR.M	0.9924	1	1074.179
4469	TBCB_MOUSE	244	21.31	3	7	R.GTVMYVGLTDFKPGYWVGVR.Y	0.9958	2	2246.6318
						K.LDQEDALLGSYPVDDGCR.I	0.9958	2	2024.1145
						R.IHVIDHSGVR.L	0.9924	1	1133.2956
4470	TBCD4_MOUSE	1307	9.26	6	27	R.ALPSLASLPALASQPALASSR.V	0.9944	2	2022.3525
						K.ESNSSCSLPSLHTSFSAPSFTAPSFLK.S	0.9958	3	2888.1261
						R.SLTSSLENIFSR.G	0.9958	2	1354.5028
						R.THVHIGEGPAIISNSTIPENVTSGGR.F	0.9958	2	2644.9041
						R.QNMDLLEK.L	0.9958	1	991.1474
						R.HASAPSHVQPSDSEK.N	0.9958	2	1577.6506
4471	TBCD5_MOUSE	815	7.36	3	35	K.EWEELFVNNNYLATVR.Q	0.9944	2	1998.2023
						K.QASSEMPGCTGGTTPDDFILVSK.E	0.9958	2	2399.5978
						K.EDQILVSLAGLKQIK.D	0.9958	1	1655.9756
4472	TBCE_MOUSE	524	15.65	4	6	K.TGITWTEVLHCAPSWPVLEELYLK.S	0.9958	2	2844.2458
						K.SNNISISERPVNVLQK.M	0.9958	2	1799.0372
						R.LEHLVLSDIGLSSIHFPDAEIGCK.T	0.9958	2	2651.9855
						K.QVQTIGFEHITK.K	0.9958	1	1401.6054
4473	TBCEL_MOUSE	424	14.15	2	3	K.IVSNVPQLEFLNLSSNPLSLSVLER.T	0.9958	2	2770.1986
						K.LEPLAEVDLRPQSSAKVEVHFNDQVEEMS	0.9944	3	3567.9959
4474	TBRG4_MOUSE	630	13.81	4	17	K.GPFLPASAVAPIPSPSNK.K	0.9958	2	1751.0355
						K.LVHINTTALLEHPEYK.G	0.9958	2	1879.1662
						K.ALLGNTDKGSLEVATQYGWVLDAEVLLDAI	0.9958	3	3999.5126
						R.LSYLLSEKPK.E	0.9944	1	1178.4142
4475	TBX1_MOUSE	479	9.81	2	2	R.VLSPALPGPGGLVPLPGGSGGR.H	0.9958	2	1956.2956
						R.EFDRDSGPAALGDATHPPQLLAR.V	0.9958	3	2435.6585
4476	TCAL5_MOUSE	200	5.5	1	2	K.ENEGKPENK.G	0.9944	1	1045.0941
4477	TCAL8_MOUSE	117	11.11	1	7	R.GEPAEPSPEPK.E	0.9958	1	1138.2194
4478	TCB1_MOUSE	173	20.23	1	2	R.CQVQFHGLSEEDKWPEGSPKPVTQNISAE	0.9944	3	3770.0753
4479	TCOF_MOUSE	1320	8.56	4	4	R.SVPAAGKAGAPATQAQK.G	0.9924	3	1553.7587

						K.SSQVRPVSTVTPGSSGK.G	0.9958		2	1674.8515
						K.SAEPLANTVLASETEEEGNAQALGPTAK.S	0.9958		3	2800.0056
						K.ASGTTAQSSSSESEDGDEDLIPATQPSTYA	0.9958		3	4358.5842
4480	TCPA1_MOUSE	556	21.76	7	24	K.IHPTSVISGYR.L	0.9958		2	1230.4093
						R.SQNVMAAASIANIVK.S	0.9958		2	1517.7839
						K.MLVDDIGDVTITNDGATILK.L	0.9958		2	2105.4083
						R.AFHNEAQVNPER.K	0.9958		2	1412.5045
						R.SLLVIPNTLAVNAAQDSTDLVAK.L	0.9946		2	2354.7062
						K.HGSYENAVHSGALDD.-	0.9958		2	1572.5877
						K.WIGLDLVHGKPR.D	0.9958		2	1391.6591
4481	TCPB_MOUSE	535	32.71	10	93	K.KLGGSLADSYLDEGFLLDK.K	0.9958		2	2042.2933
						K.LGGSLADSYLDEGFLLDK.K	0.9956		2	1914.1193
						R.LALVTGGEIASTFDHPELVK.L	0.9958		2	2098.4039
						R.VQDDEVGDGTTSVTVLAAELLR.E	0.9958		2	2289.5016
						R.SLHDALCVLAQTVK.D	0.9958	1,2		1555.7808
						R.TVYGGGCSEMLMAHAVTQLANR.T	0.9944		2	2367.6662
						R.MLPTIIADNAGYDSADLVAQLR.A	0.9923		2	2348.6764
						R.LSSFIGAIAIGDLVK.S	0.9958		2	1504.8101
						K.GSGNLEAIHVIK.K	0.9958		2	1238.4294
						R.AAHSEGHITAGLDMK.E	0.9945		2	1538.7185
4482	TCPD_MOUSE	539	18.37	5	19	K.GIHPTIISESFQK.A	0.9958		2	1457.6695
						R.ETLLNSATTSLNSK.V	0.9958		2	1479.6274
						R.ALIAGGGAPEIELALR.L	0.9958		2	1551.8265
						K.KLGGTIDDCELVEGLVLTQK.V	0.9944		2	2189.4773
						K.AQDIEAGDGTTSVVIIAGSLLDSCTK.L	0.9917		2	2622.8524
4483	TCPE_MOUSE	541	24.77	7	76	K.SQDDEIGDGTTGVVVLAGALLEEAEQLLDR	0.9958		2	3115.3752
						R.WVGGPEIELIAIATGGR.I	0.9952		2	1740.0122
						K.IAILTCPFEPPKPK.T	0.9958		2	1611.9311
						K.LGFAGVVQEISFGTTK.D	0.9958		2	1654.9035
						K.KQQISLATQMVR.M	0.9958		2	1403.683
						K.GSNDMQYQHVIETLIGK.K	0.9958		2	1934.1743
						K.VLVDINNPEPLIQTAK.T	0.9958		2	1765.0599
4484	TCPG_MOUSE	545	28.81	8	38	R.NVLLDPQLVPGGGASEMAVAHALTEK.S	0.9946	2,3		2619.0081
						K.GISDLAQHYLMR.A	0.9958		2	1404.6269
						K.MLLDPMGGIVMTNDGNAILR.E	0.9958		2	2132.5593
						K.KIGDEYFTFITDCK.D	0.9958		2	1737.9129
						R.EIQVQHPAAK.S	0.9958		1	1121.2816

						R.EDDVGTGAGLLEIK.K	0.9958	1	1417.556
						R.TQDEEVGDGTTSVIILAGEMLSVAEHFLEQ	0.9958	3	4604.1605
						R.IVSRPEELREDDVGTGAGLLEIK.K	0.9958	2	2497.8082
4485	TCPH_MOUSE	544	13.42	4	21	K.SQDAEVGDGTTSVTLLAAEFLK.Q	0.9958	2	2253.4681
						K.LPIGDVATQYFADR.D	0.9958	2	1566.7539
						K.KVQGGALEESQLVAGVAFK.K	0.9958	2	1932.2273
						R.SLHDAIMIVR.R	0.9958	2	1155.4008
4486	TCPQ_MOUSE	548	21.17	8	35	K.RLVPGGGATEIELAK.Q	0.9918	2	1511.7617
						K.ILGSGIYSSSVLHGMVFK.K	0.9958	2	1896.2549
						K.GEENLMDAQVK.A	0.9958	1	1234.3667
						K.QITSYGETCPGLEQYAIK.K	0.9958	2	2059.2464
						K.HFSGLEEAVYR.N	0.9958	2	1308.4362
						K.LYSVHQEGNK.N	0.9958	1	1175.2865
						K.KFAEAFEAIPR.A	0.9958	2	1279.4814
						R.ELEVQHPAAK.M	0.9921	2	1122.2663
4487	TCPW_MOUSE	531	8.66	2	6	K.DGNVLLHEMQIQHPTASIIAK.V	0.9958	2	2316.6806
						K.VHAELADILTEAVVDSVLAIR.R	0.9915	2	2235.5859
4488	TCPZ_MOUSE	531	20.53	5	37	K.VATAQDDITGDGTTSNVLIIGELLK.Q	0.9958	2	2545.8468
						K.NAIDDGCVVPGAGAVEVALAEALIK.Y	0.9958	2	2453.7613
						K.ALQFLEQVK.V	0.9958	1	1076.281
						K.DGNVLLHEMQIQHPTASLIAK.V	0.9958	2	2316.6806
						K.VHAELADVLTEAVVDSILAIR.K	0.9958	2	2235.5859
4489	TCRG1_MOUSE	1100	1.91	1	9	K.IKSDFFELLSNHHLDSQSR.W	0.9958	2	2274.4979
4490	TCRGL_MOUSE	590	2.88	1	5	R.KDQEHFFNQFILILK.K	0.9958	2	1921.2493
4491	TCTP_MOUSE	172	79.07	7	83	R.DLISHDELFSDIYK.I	0.9958	1,2	1695.8663
						K.GKLEEQKPER.V	0.9945	2	1214.3641
						R.VKPFMTGAAEQIK.H	0.9944	2	1420.71
						R.TEGAIDDSLIGGNASAEGPEGEGTESTVVT	0.9958	3	4803.1329
						R.EIADGLCLEVEGK.M	0.9944	2	1433.5647
						K.HILANFNNYQFFIGENMNPDGMVALLDYR.I	0.9958	3	3418.869
						R.EIADGLCLEVEGKMVSR.T	0.9958	1	1907.1555
4492	TDIF2_MOUSE	758	1.58	1	6	K.AVITPDFEKK.H	0.9958	1	1148.3446
4493	TDPZ2_MOUSE	364	5.22	1	2	R.FHSLASAQSVFLESSFK.H	0.9958	2	1886.1143
4494	TDRD5_MOUSE	1040	4.13	3	81	R.LNHTEKLNQLESTFK.S	0.9958	2	1803.0251
						K.DLLALSPVLLSDFEK.A	0.9929	2	1660.9482
						K.EDVSNSR.A	0.9924	1	806.8076
4495	TDRD6_MOUSE	2134	4.17	3	3	R.SEFFHLPSEVLGCVLAGLVPAGGGGTGGG	0.9944	3	3753.1315

						K.FQGTWEVILADEHGVIAEDMISR.F	0.9944	3	2617.9361
						K.ANLVPPYQDSVGNKNDGGFPLTR.E	0.9958	3	2460.7086
4496	TEAD2_MOUSE	445	3.15	1	7	K.VETERAQLEDGR.F	0.9912	2	1403.4917
4497	TEBP_MOUSE	160	28.13	3	9	K.HLNEIDLFHCIDPNDSK.H	0.9957	2	2068.2164
						K.LNWLSVDFNNWK.D	0.9958	2	1536.73
						R.KGESGQSWPR.L	0.993	2	1132.2211
4498	TEKT1_MOUSE	418	10.29	2	2	K.EADIIHGVMNLLIRTLEESTEQIR.L	0.9958	3	2782.1846
						R.RQCEVVDEAFINGLK.E	0.9958	2	1778.969
4499	TEN1_MOUSE	2731	1.9	2	2	R.ENVLMSTNLTATSTIYILKQENTQSTYR.V	0.9958	3	3221.6068
						R.ILENGVNVTVSQMTSVLNGR.T	0.9958	3	2132.4399
4500	TEN2_MOUSE	2764	2.89	2	2	R.SQIHAPAPAPNDLATTPESVQLQDSWVLN	0.9958	3	3998.3983
						R.EGWNGEHCTIDGCPDLCNGNGRCTLGQN	0.9958	3	4642.7118
4501	TEN4_MOUSE	2771	0.65	1	8	K.RLSSNSIVPFHLYMFK.N	0.9958	2	1940.3135
4502	TENA_MOUSE	2110	3.27	2	3	K.FTTDLDSPREFTATEVQSETALLTWRPPR.	0.9944	3	3366.7117
						K.DVPGDRTTIDLTHEDNQYSIGNLRPDTEYE	0.9958	3	4121.4204
4503	TENC1_MOUSE	1400	6.36	4	4	R.EVVILEDPGVPALCSCPACEEK.L	0.993	2	2473.678
						R.STNQHVTFASPLPDVTQPPEHPLQENQSN	0.9958	3	3441.7386
						R.DPQCSASSELSGPSTPLHTSSPVQGKESN	0.9952	2	3142.2861
						R.DPQCSASSELSGPSTPLHTSSPVQGK.E	0.9958	2	2655.8011
4504	TENN_MOUSE	1560	3.14	2	2	R.ADLQTFNESAYAVYDFFQVASSKER.Y	0.9944	3	2888.1193
						R.YDITGLQPGTEYKITVVPIR.G	0.9958	2	2264.6268
4505	TENS3_MOUSE	1440	3.4	2	2	R.KQGSATDNVCHLFAEHDPEQPASAIVNFV	0.9944	3	3398.6795
						R.YVQFLSGLLSGAMK.M	0.9958	1	1514.823
4506	TEP1_MOUSE	2629	3.12	4	7	R.IDGHISVHPDILSLENR.C	0.9958	2	1916.1441
						R.FLNAHDSIDKLEAQLR.S	0.9914	2	1871.1032
						R.DPDFLSSVPDAWKPDFISESEEAAHR.V	0.9925	3	2947.1437
						K.LCGHVPGHSDILSLK.N	0.9958	2	1633.8541
4507	TERA_MOUSE	806	54.71	31	648	R.LIVDEAINEDNSVVSLSQPK.M	0.9958	2	2171.4094
						R.QAAPCVLFFDELDSIAK.A	0.9958	2	1925.1548
						R.ETVVEVPQVTWEDIGGLEDVKR.E	0.9958	2	2499.7802
						R.IVSQLLTLMDGLK.Q	0.9958	2	1431.7741
						R.ELQELVQYPVEHPDK.F	0.9958	1	1825.0282
						R.KYEMFAQTLQQSR.G	0.9958	2	1630.859
						R.WALSQSNPSALR.E	0.9958	2	1330.4862
						K.AIGVKPPR.G	0.9944	1	838.0409
						R.ETVVEVPQVTWEDIGGLEDVK.R	0.9952	2	2343.5927
						R.HPALFK.A	0.9958	1	712.8699

						K.MTNGFSGADLTEICQR.A	0.9958		1	1800.9471
						R.QTNPSAMEVEEDDPVPEIR.R	0.9958		2	2157.3136
						R.EVDIGIPDATGR.L	0.9958		1	1243.3592
						K.LADDVDLEQVANETHGHVGADLAALCSEA	0.9958		3	3674.9696
						R.AVANETGAFFFLINGPEIMSK.L	0.9958		2	2257.6093
						R.VINQILTEMDGMSTK.K	0.9944		1	1680.9722
						K.MDELQLFR.G	0.9958		1	1052.2335
						K.NAPAIIFIDELDAIAPK.R	0.9958		2	1812.1161
						K.GVLFYGPPGCGK.T	0.9958		1	1252.4217
						R.LDQLIYIPLPDEK.S	0.9958		1	1557.8272
						R.LGDVISIQPCPDVK.Y	0.9958	1,2		1541.7509
						R.GILLYGPPGTGK.T	0.9958		1	1173.3977
						R.RIVSQLLTLMDGLK.Q	0.9958		2	1587.9616
						K.GDDLSTAILK.Q	0.9958		1	1033.1668
						R.LEILQIHTK.N	0.9958	1,2		1095.3274
						K.DVDLEFLAK.M	0.9958		1	1050.1968
						K.MDLIDLEDETIDAEVMNSLAVTMDDFR.W	0.9958		2	3103.4551
						K.KMDLIDLEDETIDAEVMNSLAVTMDDFR.W	0.9958		2	3231.6292
						K.NVFIIGATNRPDIIDPAILRPGR.L	0.9958		3	2519.9529
						R.RDHFEEAMR.F	0.9952		2	1191.3067
						K.RELQELVQYPVEHPDK.F	0.9958		2	1981.2157
4508	TESC_MOUSE	214	16.36	2	3	R.NVVEELLSGNPHIEK.E	0.9958		2	1678.8827
						R.KENFNNVPDLELNPIR.S	0.9958		2	1913.1405
4509	TF2H3_MOUSE	309	8.41	1	2	K.NGGLGDFFGDPGNALPDCNPSGSK.D	0.9958		2	2394.4822
4510	TF3C4_MOUSE	817	3.06	2	3	K.NYQVQFVTLK.T	0.9958		1	1240.4447
						R.HPVPEDPDWIK.R	0.9924		1	1333.4863
4511	TF65_MOUSE	549	6.19	2	6	R.IQTNNNPFHVPIEEQR.G	0.9911		2	1937.1221
						R.SIHSFQNLGIQCVK.K	0.9958		2	1631.8382
4512	TFAM_MOUSE	243	18.52	3	18	K.YKEQLTPSQLMGMEK.E	0.9958		2	1784.0956
						R.ELILLGKPK.R	0.9958		1	1011.2932
						R.SAYNIYVSESFQEAK.D	0.9958	1,2		1736.8755
4513	TFR1_MOUSE	763	5.11	2	4	R.SAFSNLFGGEPLSYTR.F	0.9958		2	1746.917
						R.HIFWGSGSHTLSALVENLK.L	0.9958		2	2097.3812
4514	TGDS_MOUSE	355	3.38	1	2	K.QPTNPYASSK.A	0.9924		1	1093.1815
4515	TGFR2_MOUSE	592	5.07	2	2	R.SCSQEKIPEDGSLNTTK.-	0.9958		2	1894.9965
						R.DLKSSNILVK.N	0.9958		1	1117.3311
4516	TGM1_MOUSE	815	5.52	2	3	R.LEGSGLQRPKVLNVGDIGGNETVTLR.Q	0.9958		3	2724.0897

						K.AIHSNNREDITHIYK.H	0.9957	2	1811.9951
4517	TGM2_MOUSE	686	31.92	11	85	R.WDNNYGDGISPMAWIGSVDILR.R	0.9958	2	2480.7571
						R.VVTNYNSAHDQNSNLLIEYFR.N	0.9958	2	2498.7141
						K.SVEVSDPVPAGDLVK.A	0.9958	1,2	1512.7001
						R.GYEASVDSLTFGAVTGPDPSEEAGTK.A	0.9958	2	2586.7253
						K.LAEKEETGVAMR.I	0.9944	2	1334.5304
						K.YDAPFVFAEVNADVVDWIR.Q	0.9958	2	2227.4809
						R.GLLIEPAANSYLLAER.D	0.9958	2	1731.0019
						R.DLYLENPEIK.I	0.9958	1	1234.3917
						K.NPLSDPLYDCIFTVEGAGLTK.E	0.9958	2	2311.5598
						R.VDLFPTDIGLHK.L	0.9957	2	1355.5767
						R.VGDSMSMGNDFDVFAHIGNDTSETR.E	0.9915	2	2703.8715
4518	THEM2_MOUSE	140	60.71	5	86	R.GAPGVSVDMNITYMSPAK.I	0.9958	2	1839.1317
						K.VTLVSAAPEK.L	0.9924	1	1015.1949
						K.TLAFASVDLTNK.T	0.9958	1	1280.4637
						K.LGTLHGGLTATLVDSISTMALMCTER.G	0.9958	2	2750.1641
						K.IGEEIVITAHILK.Q	0.9958	2	1436.7349
4519	THIC_MOUSE	397	27.96	5	8	R.TAIGSFNGALSTVPVHEMGTTVIK.E	0.9924	2	2431.8096
						R.ILVTLLHTLER.V	0.9958	2	1308.6072
						R.IVSWSQAGVEPSVMGVGPIPAIK.Q	0.9958	2	2323.7558
						K.VNIDGGAIALGHPLGASGCR.I	0.9958	2	1936.1442
						K.VAPEEVSEVIFGHVLTAGCGQNPTR.Q	0.9958	2	2668.9323
4520	THIKA_MOUSE	424	51.89	15	188	R.IAQFLSGIPETVPLSTVNR.Q	0.9958	2	2043.3708
						K.NTTPDELLSAVLTAVLQDVR.L	0.9958	2	2156.4411
						R.LKPEQLGDISVGNVLEPGAGAVMAR.I	0.9958	2	2522.9225
						R.QCSSGLQAVANIAGGIR.N	0.9958	2	1702.8742
						R.FPQASASDVVVVHGR.R	0.9958	1,2	1569.7605
						R.SKAEELGLPILGVLR.S	0.9958	2	1595.923
						K.TITVSQDEGVRPSTTMQGLAK.L	0.9958	2	2220.5029
						K.DGGSTTAGNSSQVSDGAAAVLLAR.R	0.9958	2	2206.3311
						K.QDDFALASQQK.A	0.9958	1	1251.3385
						K.AEELGLPILGVLR.S	0.9958	2	1380.6707
						K.VNPLGGAIALGHPLGCTGAR.Q	0.9958	2	1932.1992
						R.AEIVPVTTTVLDDK.G	0.9958	1	1501.7173
						R.AEIVPVTTTVLDDKGDK.K	0.9944	2	1802.0319
						R.QKQDDFALASQQK.A	0.9958	2	1507.6433
						K.KTITVSQDEGVRPSTTMQGLAK.L	0.9958	2	2348.677

4521	THIL_MOUSE	424	62.5	18	817	R.IAAFADAAVDPIDFPLAPAYAVPK.V	0.9958		2	2444.8327
						K.FASEITPITISVK.G	0.9958		1	1406.6623
						R.TPIGSFLGSLASQPATK.L	0.9958		1	1675.9225
						R.QATLGAGLPISTPCTTVNK.V	0.9958		1	1930.1749
						K.IHMGNCAENTAK.K	0.9958	1,2		1346.4669
						K.EVYMGNVIQGGEGQAPTR.Q	0.9958		2	1907.1083
						K.ENGTITAANASTLNDGAAALVLMTAEAAQR	0.9958	2,3		2947.2469
						K.EDIAMWEVNEAFSVVVLANIK.M	0.9958		2	2378.7455
						K.KEDIAMWEVNEAFSVVVLANIK.M	0.9958		2	2506.9196
						K.LEDLIVK.D	0.9958		1	830.0123
						R.QEQDTYALSSYTR.S	0.9958		2	1562.6329
						K.LGTAAIQGAIEK.A	0.9958	1,2		1172.3671
						K.VNIHGGAVSLGHPIGMSGAR.I	0.9958		2	1931.223
						K.GKPDVVVKEDEEYK.R	0.9958	1,2		1635.8113
						R.LNVKPLAR.I	0.9958		1	911.1355
						K.DGLTDVYNK.I	0.9958		1	1025.1033
						K.TVFQKENGTITAANASTLNDGAAALVLMTA	0.9958		3	3550.9659
						K.MLEIDPQKVNIHGGAVSLGHPIGMSGAR.I	0.9958		2	2886.36
4522	THIM_MOUSE	397	90.68	28	2783	K.VPPETIDSVIVGNVMQSSSDAAYLAR.H	0.9958	2,3		2721.0546
						K.DMDLIDVNEAFAPQFLSVQK.A	0.9958		2	2281.5855
						K.DFSATDLTEFAAR.A	0.9958		2	1444.5407
						K.LEDTLWAGLTDQHVK.L	0.9958	1,2		1726.9267
						R.TPFGAYGGLLK.D	0.9958		1	1124.325
						K.QTMQVDEHARPQTTLEQLQK.L	0.9929		2	2382.6537
						K.TNVSGGAIALGHPLGGSGSR.I	0.9944		2	1808.992
						R.ITAHLVHELR.R	0.9944		2	1189.4031
						K.DGTVTAGNASGVSDGAGAVIIASEDAVK.K	0.9958		2	2533.7087
						K.YAVGSACIGGGQGIALIIQNTV.-	0.9958		2	2163.4449
						R.VVGYFVSGCDPTIMGIGPVPAINGALK.K	0.9958		2	2734.1921
						R.VGVPTETGALTLNR.L	0.9958		1	1428.6286
						R.YALQSQQR.W	0.9958	1,2		994.0953
						K.LPSVFK.K	0.9944		1	690.8607
						K.LPMGMTAENLAAK.Y	0.9958	1,2		1347.6307
						K.HNFTPLAR.V	0.9924	1,2		956.0922
						K.RTPFGAYGGLLK.D	0.9958		2	1280.5125
						K.ALDLDPSK.T	0.9924		1	858.9671
						R.LCGSGFQSIVSGCQEICSK.D	0.9958		2	2118.2466

						R.GVFIVAAK.R	0.9924	1	805.0079
						R.VVGYFVSGCDPTIMGIGPVPAINGALKK.A	0.9958	2,3	2862.3662
						K.AANEAGYFNEEMAPIEVK.T	0.9958	1	1984.1878
						K.DGTVTAGNASGVSDGAGAVIIASEDAVKK.I	0.9958	3	2661.8828
						K.KAGLSLK.D	0.9958	1	716.8992
						K.ALDLDPSKTNVSGGAIALGHPLGGSGSR.I	0.9944	3	2648.9358
						K.DAEVVLCGGTESMSQSPYCVR.N	0.9958	2	2346.5032
						K.KDGTVTAGNASGVSDGAGAVIIASEDAVK.I	0.9958	2,3	2661.8828
						K.KHNFTPLAR.V	0.9958	1	1084.2663
4523	THIO_MOUSE	105	82.86	6	79	K.EAFQEALAAAGDK.L	0.9958	1	1321.4295
						K.EKLEASITEYA.-	0.9958	1	1254.3795
						K.YSNVVFLEVDVDDCQDVAADCEVK.C	0.9958	2	2790.9265
						K.VGEFSGANK.E	0.9958	1	908.9866
						K.LVVVDFSATWCGPCK.M	0.9958	2	1739.9411
						K.MIKPFFHSLCDK.Y	0.9958	1,2	1523.7993
4524	THIOM_MOUSE	166	40.36	3	84	R.VVNSETPVVVDFHAQWCGPCK.I	0.9958	2	2430.6545
						K.VDIDDHTDLAIEYEVSAVPTVLAIK.N	0.9944	2	2728.0686
						K.FVGIKDEDQLEAFLK.K	0.9958	2	1753.005
4525	THNS1_MOUSE	747	4.55	2	2	K.FICASNQNHVLTDFIK.T	0.9958	2	1908.1303
						K.MDYQVCVADVDVLK.S	0.9944	1	1655.8696
4526	THNS2_MOUSE	483	10.14	2	4	K.FPEAVQAAGLTPETPAEILALEHK.E	0.9958	2,3	2533.884
						K.LSEAVTSESVTDEAITQTMAR.C	0.9958	2	2240.4443
4527	THOC1_MOUSE	657	5.94	2	2	K.MVEHILNTEENWNSWKNEGCPSFVK.E	0.9958	3	3050.3381
						R.QIECDSEDMK.M	0.9958	1	1255.3052
4528	THOP1_MOUSE	687	7.57	3	8	R.QANAGLFNLRQIVLAK.V	0.9957	2	1757.0891
						R.TSILRPGGSEDASAMLK.Q	0.9912	2	1733.9775
						R.NILDFPQHVSPCK.D	0.9958	2	1555.7399
4529	THRB_MOUSE	618	20.39	8	41	R.ETWTTNINEIQPSVLQVVNLPIVERPVCK.A	0.9958	3	3378.8597
						K.TFGLGEADCGLRPLFEK.K	0.9958	2	1911.1309
						K.KPVPFSDYIHPVCLPDK.Q	0.9958	2	2013.3099
						R.LYQGNLAVTTLGSPCLPWNSLPAK.T	0.9958	2	2601.9715
						R.TTDAEFHTFFNEK.T	0.9958	2	1587.6855
						K.SPQELLCGASLISDR.W	0.9958	2	1646.8041
						R.KSPQELLCGASLISDR.W	0.9958	2	1774.9781
						R.TTDAEFHTFFNEKTFGLGEADCGLRPLFEK	0.9958	3	3479.7932
4530	THS7A_MOUSE	1645	4.07	2	2	K.NCYHYDYNVTDWSTCQLSEKAVCGNGIK.T	0.9944	3	3384.5381
						K.TCRCEEGYTEVMSSNSTLEQCTLIPVVVIPT	0.9958	3	4047.4161

4531	THTM_MOUSE	297	39.39	7	34	K.SHSEPAEFSAQLDPSFIK.T	0.9958	1,2	1991.1644
						R.HWLNQNLPISSGK.S	0.9958	1,2	1494.6933
						R.DGIEPGHIPGSVNIPFTEFLTNEGLEK.S	0.9958	2	2912.2255
						K.THEDILENLDAR.R	0.9958	2	1426.526
						R.ALVSAQWVAEALK.A	0.9958	2	1386.6341
						R.AFGHHSVSLLDGGFR.H	0.9958	2	1600.777
						R.AQPEHIISEGR.G	0.9958	1	1237.3579
4532	THTR_MOUSE	297	23.23	4	21	R.YLGTQPEPDIVGLDSGHIR.G	0.9958	2	2068.2939
						K.KVDLSQPLIATCR.K	0.9958	2	1501.7325
						R.GSVNMPFMDFLTK.D	0.9958	2	1487.7719
						K.EGHPVTSEPSRPEPAVFK.A	0.9958	2	1965.1729
4533	THUM2_MOUSE	498	7.83	2	2	K.KQLPIAVSSLHK.G	0.9958	1	1321.6059
						R.ASSVQCLGRMRPCGSLVPVESFK.V	0.9915	2	2566.9105
4534	THY1_MOUSE	162	32.72	4	86	K.DNSIQHEFSLTR.E	0.9958	2	1447.5473
						R.HENNTKDNSIQHEFSLTR.E	0.9958	3	2171.2907
						K.HVLSGTLGIPEHTYR.S	0.9958	2	1680.9041
						K.VTSLTACLVNQNLR.L	0.9912	2	1589.7985
4535	THYG_MOUSE	2766	2.28	2	4	K.CPEGSFSQDGRCTPCPAGTYQEQAGSSA	0.9958	3	3790.8663
						R.ACQRPQLWQTMQTQAHFQLLLPPGK.M	0.9958	3	2979.4388
4536	TI8AB_MOUSE	97	13.4	1	2	R.FIDTSQFILNR.L	0.9958	2	1354.5486
4537	TIAM1_MOUSE	1591	2.7	2	4	K.HKMPPAAAEETPPYSNYNTLPCR.K	0.9958	3	2645.9154
						R.CYLASLQGGELPNPKR.L	0.9958	2	1804.0221
4538	TIAM2_MOUSE	1715	2.51	2	2	K.SLPPSPNQSQLLEEFLDNFR.K	0.9958	3	2332.5749
						R.RHSAAGSPSSQRPSPTDSR.L	0.9931	2	1982.0799
4539	TIE1_MOUSE	1134	2.12	1	2	R.GFSKPSDLVGVFSCVGGAGARR.T	0.9958	2	2225.4784
4540	TIF1B_MOUSE	834	18.11	6	9	R.VLVNDAQK.V	0.9924	1	887.0238
						R.LDLDLTSDSQPPVFKVFPGSTTEDYNLIVIE	0.9958	3	3611.0399
						K.LTEDKADVQSIIGLQR.F	0.9912	2	1787.0232
						K.RPAASSAAAASAAASSPAGGGGEAQELLE	0.9958	3	3326.4962
						K.VFPGSTTEDYNLIVIERGAAAAAAGQAGTV	0.9958	3	4503.1731
						K.IVAERPGTNSTGPGPMAPPR.A	0.9958	2	2006.2872
4541	TIM10_MOUSE	90	41.11	2	28	K.KLTELSMQDEELMK.R	0.9958	2	1695.9839
						R.AQQLAAELEVEMMADMYNR.M	0.9958	2	2214.5313
4542	TIM13_MOUSE	95	34.74	2	27	K.VQIAVANAQELLQR.M	0.9958	2	1553.802
						K.CIGKPGGSLDNSEQK.C	0.9958	2	1590.6965
4543	TIM14_MOUSE	116	14.66	1	4	K.REAALILGVSPTANK.G	0.9949	2	1540.8033
4544	TIM16_MOUSE	125	29.6	2	55	R.AGHQSAAASNLSGLSLQEAQQILNVSK.L	0.9958	2	2724.003

						R.AGHQSAAASNLSGLSLQEAQQILNVSKLSF	0.9944		3	3635.0257
4545	TIM44_MOUSE	452	21.68	8	25	K.KLGELTGTVK.E	0.9944		1	1046.2523
						K.VFEANEEALGVVLHK.D	0.9944		2	1655.8913
						K.QSAESVSKSGEK.L	0.9958		1	1237.3091
						K.KLEESDALQEAR.R	0.9958		2	1389.5052
						R.KGFLSGLLDNIK.Q	0.9958		2	1305.5602
						K.GFLSGLLDNIK.Q	0.9958		1	1177.3861
						K.ELDESVLGQTGPYR.R	0.9958		1	1564.6922
						K.ALGFQFHSR.I	0.9958		2	1063.204
4546	TIM50_MOUSE	353	14.16	2	5	R.LQPFNGVALRPWDGNSDDRVLLDLSAFLK	0.9958		3	3258.7043
						R.TVLEHYALEDDPLEAFK.Q	0.9958		2	1991.2048
4547	TIM8A_MOUSE	97	29.9	2	23	R.FQQLVHQMTELCWEK.C	0.9958		2	1978.2391
						K.SKPVFSESLSD.-	0.9958		1	1196.2994
4548	TIM9_MOUSE	89	53.93	3	25	R.FQEYHIQQNEALAAK.A	0.9958	1,2		1790.9731
						R.EVKPEEVTCSEHCLQK.Y	0.9958	1,2		1974.1072
						K.LTETCFLDCVK.D	0.9958		1	1386.5171
4549	TIM9B_MOUSE	100	24	2	2	R.LMAAYVHLMPALVQR.R	0.9958		2	1714.1401
						K.LIHSNHRLMAAYVHLMPALVQR.R	0.9915		3	2572.1107
4550	TIP_MOUSE	610	3.44	1	8	R.SANFLDHLFVGIPRPPGEK.S	0.9958		2	2095.4087
4551	TIPRL_MOUSE	271	7.38	1	17	R.IQHGSGFGIEFNATDALR.C	0.9958		2	1934.1185
4552	TITIN_MOUSE	35213	5.83	97	209	K.EEMTVVWNAPEYDGGK.S	0.9958		1	1825.9874
						K.DGQKLPAGK.D	0.9958		1	914.0495
						K.DSVSITWEPPLLDGGSK.I	0.9958		2	1801.9909
						R.DGQVISTSTLPGVQISFSDGR.A	0.9958		2	2165.3647
						R.SIATVEMVIDGATGQLPHK.T	0.9958		2	1968.2757
						K.KQEPIAPESISSKPVIVTGLR.D	0.9958		2	2250.6439
						K.SIHEQVSSISETTK.S	0.9945		2	1546.6745
						K.NFHGQCSATASLTVLPLVEEPPR.E	0.9958		2	2524.8022
						R.MEEEKVQVIK.V	0.9924		1	1233.4657
						R.LVINRTHASDEGPYK.L	0.9907		2	1700.8919
						K.ISVAYQQEELVQER.I	0.9958		2	1692.8663
						K.MKPRPIAILQGLSDQKVCEGDIVQLEVK.V	0.9944		3	3166.7131
						R.VGTGEPVETDSPVEAR.S	0.9915		2	1643.7478
						K.NLGSDTRYSIQNTDSSSLLVIPQVTR.N	0.9958		3	2866.1576
						K.APADDGGSPITGYLVEK.R	0.9958		2	1690.8474
						R.SDTGLYSITAVNNLGTASK.E	0.9958		2	1913.0917
						K.LTWFSPEDDGGSPITNYVIQK.R	0.9958		2	2368.6049

K.MTLVENTATLTVLKVAK.G	0.9944	2	1833.2372
R.VLDSPSAPVNLTIR.E	0.9937	2	1482.7202
K.SISGEINVNVIAPPSAPK.E	0.9958	2	1794.0581
R.LFVEEIPVEIIRPPQDILEAPGADVIFLAELNK	0.9958	3	3690.3147
K.IELPATVTGKPEPK.I	0.9958	2	1480.7447
K.APPIEPAPTPIAAPVTAPVVGK.K	0.9958	2	2094.5022
K.LQFEVQKVDRPVDTSETK.E	0.9945	2	2120.3672
K.VNPNCGSTTFVVPDLISEQQYFFR.V	0.9958	2	2820.0967
R.IHAENLYGISDPLVSDSMK.A	0.9944	2	2090.3557
R.IMAENAAGISAPSATSPFYK.A	0.9931	2	2027.2995
R.SSVSLAWNKPIYDGGAPVR.G	0.9958	2	2018.2798
K.GVPFPTLTWFK.A	0.9958	1	1293.5511
K.LTWEPPEFDGGSPILHYVLER.R	0.9958	2	2456.76
K.EATLQFEEPEGVFPGASSAAQVSPVTIKPL	0.9958	3	3955.4944
K.AVNEAGVSKPSATVGPVIVK.D	0.9958	2	1924.248
K.VIGLPGPCK.D	0.9944	1	941.1247
R.GPPPTLNLQAVQAQTTLPK.E	0.9958	2	1975.2957
R.FGVTITVHPEPR.V	0.9958	2	1353.5638
K.VPGPPGTPQVTAVTK.D	0.9958	2	1449.6903
R.LLERPPEFTLPLYNK.T	0.9958	2	1831.165
K.VLDRPGPPEGPVQVTGVTAEK.C	0.9958	2	2147.4362
K.VLDRPGPPEGPVAISGVTAEK.C	0.9958	2	2090.3843
K.TPILAINPIDRPGEPENLHIADK.G	0.9958	2	2524.8797
K.DAGEYTITATNPFGTK.E	0.9958	2	1686.8156
K.APCSVSVLDTPGPPINFVFEDIR.K	0.9958	2	2531.8341
R.AVPPEEIPPAVAPSIPLLLPLPEEK.K	0.9958	2,3	2618.129
R.FSCDTDGEPVPTVTWLR.E	0.9958	2	1981.1352
K.DEYEAPTIVLDPTIK.D	0.9944	1	1704.9146
R.FKVSGLTEGHEYEFR.I	0.9958	2	1799.9805
R.AGGSLRLFVPIK.G	0.9944	1	1258.5497
K.GNYPQSSTAAPDHALLSSVAAETLQLGEK.	0.9958	3	2957.2237
R.TTTTAVHIQPAQEQAR.K	0.9958	2	1752.9248
K.LKDVHETLGFPVAFECR.I	0.9958	2	2019.2738
K.LPPVVLSTPQGTGELPSIDGAVHTQPGR.G	0.9958	3	2825.1943
R.QEGAAPVFIREISDVEISVEDVAK.L	0.9944	3	2602.9011
R.VAAENMYGVGEPVQAAPIIAKYQFDPPGPF	0.9958	3	3385.8621
R.KAYATITNNCTK.N	0.9944	2	1385.5261

K.TFTITVVVIGRPGPVTGPIEVSSVSAESCVL	0.9958	3	3902.4431
R.KSYSTVTTK.C	0.9944	1	1015.1515
R.WDPPEDDGGCEIQNYILEKCESK.R	0.9958	3	2783.8941
R.NVYTLEIRNAAVSDSGK.Y	0.9958	2	1838.0275
K.TQLPTAPEAPREMPPEMNTFEEISVEPEML	0.9958	3	5119.7362
K.DLHHVDVDKTEVSLVWNKPDR.D	0.9944	3	2503.777
K.ANHVNVPDCAFTVTDLVEGGK.Y	0.9958	2	2244.4321
K.DTITFEVTVNYEGISYK.W	0.9934	2	1980.1785
K.RDTTTTVWDVVSATVAR.T	0.9924	2	1879.08
R.FILNVQSKPTAEVK.W	0.9958	2	1574.8607
K.SSISLAWKPPAK.D	0.9954	2	1285.529
K.AGDSIVLSAISILGKPLPK.S	0.9941	2	1880.2786
K.ILVPSTGYPRPK.A	0.9958	2	1328.5974
K.EEFILEILK.T	0.9958	1	1134.3581
K.TSVTLTWEPPLLDGGSK.I	0.9958	2	1802.0343
K.IENYDQSTQVTWYFGVRQLENSEK.Y	0.9958	3	2936.1638
K.MSFSNGVAVLTIPDVQISLGGKYTCLAENE	0.9958	3	4486.0572
K.LRPGSGGEKPPDEAPFTYQLK.A	0.9958	2	2288.5651
R.VREPAISAVEQTAQR.T	0.9937	2	1655.8515
R.IMAEKEEEELLRPVTTTQR.L	0.9958	2	2274.5945
R.GKPFPEVAWTK.D	0.9958	1	1260.4783
K.VHELAAEFISKPQNLEILEGEK.A	0.9958	2	2495.8351
R.QEHIQVTHGQVGVGK.K	0.9958	2	1617.8051
R.NVHVEVYDRPSPPR.N	0.9958	2	1665.8491
R.VTAVNEYGPGVPTDIPKPVLASDPLSEPDP	0.9958	3	3457.9054
K.KDGQVLR.E	0.9944	1	815.948
R.RAPEPKPEFHVHEPGK.L	0.9958	2	1856.094
K.VEKPLYGVEVFVGETAR.F	0.9958	2	1894.1778
R.KTQTTTMATGPEVPPPWK.Q	0.9958	2	1971.2787
K.LVRPLYSVEVMETETAR.F	0.9958	2	1994.3135
K.VLVLDKPGPPR.D	0.9958	2	1191.4593
R.VQILDKPGPPGGPIEFKTVTAEK.I	0.9944	3	2422.8272
K.HLVDTISEEGDTVHLTSSISNAK.E	0.9958	2	2454.6531
R.MSFVNSEAILDITDVKVDDSGTYSCEATND	0.9944	3	4660.9421
K.TFINIIVLDRPGPPTGPVAISDITEESVTLKW	0.9944	3	3932.5493
R.NAAHEDGGIYSLTVENPAGTK.T	0.9958	2	2145.2902
R.VEVFDVPGPVLDLKPVVTNR.K	0.9958	2	2194.5791

						K.GRPEPDITWSK.E	0.9958		2	1286.4301
						K.EDLQKPVLDLKLSGVLTVK.A	0.9927		2	2096.5156
						K.IGTGPPTESKPVIAK.T	0.9958		2	1495.7593
						R.RPDYDGGSPNLSYHVER.R	0.9958		2	1963.0733
						K.GRPTPEITWSK.E	0.9958		2	1272.4465
						K.HLALSNNFR.G	0.9932		2	1072.2119
4553	TKT_MOUSE	623	24.56	7	31	K.ILATPPQEDAPSVDIANIR.M	0.9958		2	2021.278
						R.LGQSDPAPLQHQVDIYQK.R	0.9958		2	2038.2676
						K.NMAEQIIQEIYSQVQSK.K	0.9958		2	2010.2696
						R.KISSDLDGHPVPK.Q	0.9958		2	1393.5828
						K.GHAAPILYAVWAEAGFLPEAELLNLR.K	0.9958		2	2823.267
						K.SKDDQVTVIGAGVTLHEALAAAESLK.K	0.9958		2	2624.9512
						R.TSRPENAIIYSNNEDFQVGQAK.V	0.9958		2	2482.6689
4554	TLN1_MOUSE	2541	28.93	36	266	K.TLSHPQQMALLDQTK.T	0.9944		2	1711.9739
						R.GVGAAATAVTQALNELLQHVK.A	0.9958	2,3		2092.4031
						R.EGISQEALHTQMLTAVQEISHLIEPLASAAR	0.9958		3	3345.7955
						K.EADESLNFEEQILEAAK.S	0.9958		2	1937.0673
						K.LGAASLGAEDPETQVVLINAVK.D	0.9958		2	2196.5059
						R.GVAALTSDPAVQAIVLDTASDVLDK.A	0.9958		2	2470.7796
						K.LLGEIAQGNENYAGIAAR.D	0.9958		2	1861.0647
						K.QAAASATQTIAAAQHAASAPK.A	0.9958		2	1966.1612
						K.RVAGSVTELIQAAEAMK.G	0.9944		2	1775.0734
						K.VSHVLAALQAGNR.G	0.9958	1,2		1336.5369
						K.VSQMAQYFEPLTLAAVGAASK.T	0.9958		2	2183.5274
						K.VVAPTISSPVCQEQLVEAGR.L	0.994		2	2141.3954
						K.LAQAAQSSVATITR.L	0.9958		2	1417.6053
						K.LHTDDELNWLDHGR.T	0.993		2	1721.8265
						K.VEHGSVALPAIMR.S	0.9958		2	1380.6482
						R.SGASGPENFQVGSMPPAQQQITSGQMHR	0.9958		3	2929.2116
						R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	0.9958	2,3		2756.0446
						K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.	0.9958		2	3053.3496
						K.NGNLPEFGDAIATASK.A	0.9936		2	1605.7447
						K.APGQLECETAIAALNSCLR.D	0.9958		2	2075.2587
						K.LLAALLEDEGGNGRPLLQAAK.G	0.9958		2	2150.4832
						K.ASVPTIQDQASAMQLSQCAK.N	0.9958		2	2135.3631
						R.AVTDSINQLITMCTQQAPGQK.E	0.9958		2	2305.5745
						K.MVGGIAQIIAAQEEMLR.K	0.9958		2	1831.1988

						K.RLLSDLLPPSTGTFQEAQSR.L	0.9958		2	2217.4869
						R.LNEAAAGLNQAATELVQASR.G	0.9958		2	2028.2297
						R.IGITNHDEYSLVR.E	0.9919		2	1517.6817
						K.VMVTNVTSLLK.T	0.9958		2	1205.4986
						R.DPVQLNLLYVQAR.D	0.9958		2	1529.7795
						R.VAGSVTELIQAAEAMK.G	0.9958		2	1618.8859
						R.LLSDLLPPSTGTFQEAQSR.L	0.9958		2	2061.2994
						K.VGAIPANALDDGQWSQGLISAAR.M	0.9958		2	2311.5595
						R.VQELGHGCSALVTK.A	0.9958		2	1499.6733
						K.AGFLDLK.D	0.9958		1	763.9121
						R.GHMPPLTSAQQALTGTINSSMQAVQAAQA	0.9958		3	4811.3498
						R.YDQATDTILTVTENIFSSMGDAGEMVR.Q	0.9958		3	2966.2613
4555	TLN2_MOUSE	2375	7.54	7	8	K.LAQAAQSSAATITQLAEVVK.L	0.9941		2	2001.2877
						R.GQSGELAAASGKFSDDFDEFLDAGIEMAG	0.9958		3	3493.737
						K.AHEACGPMEIDSALNTVQTLK.N	0.9958		2	2286.5281
						K.FSDDFDEFLDAGIEMAGQAQTKEDQMQVI(	0.9958		3	3693.0481
						K.MAAAESQLKPLPGETLEK.C	0.9958		2	1914.2244
						K.GVGSSMAQLLTCAAQGNEHYTGVAAR.E	0.9958		2	2650.8921
						K.LLVDSLPPSTKPFQEAQSELNQAAADLNQS	0.9958		3	4134.5492
4556	TLR9_MOUSE	1032	4.94	2	2	K.DVVVLVILRPDAHRSR.Y	0.9909		2	1846.1862
						R.QLPPSLEYLLVSYNLIVKLGPEDLANLTSLR	0.9944		3	3471.0746
4557	TM117_MOUSE	514	8.75	2	4	K.SSHLTSENLSLHLKESTSEVEAEQEPAASQ	0.9958		3	3396.6061
						K.DSESLKDLNR.T	0.9958		1	1177.2566
4558	TM135_MOUSE	458	8.95	2	4	R.IYAPLYLIAAVLR.K	0.9958	1,2		1476.8455
						K.FYSWTPGFGAALPASYVAILIERK.S	0.9958		3	2659.1027
4559	TM143_MOUSE	458	7.42	2	7	K.MATSLLLLLFAAFMGVK.A	0.9944		1	1827.3369
						R.LLIQEFHSSPAER.A	0.9958		1	1527.7202
4560	TM16K_MOUSE	659	4.4	1	2	R.QSLATLLITSQILNQVVESLLPYWLQR.K	0.9958		3	3128.6824
4561	TM170_MOUSE	144	37.5	2	5	R.FMSVSILLMGIVGPITAGILTSAAIAGVYR.A	0.9958		3	3023.7059
						R.EGSGGGGGSAGLLQQILSLK.L	0.9958		2	1830.0483
4562	TM1L2_MOUSE	507	17.95	4	21	R.GIEFPMADLDALSPIHTPQR.S	0.9958		2	2209.5249
						R.VSNEEVTEELLHVNDDLNNVFLR.Y	0.9958		2	2699.9341
						K.VLALIQAWADAFR.S	0.9958		2	1474.7459
						K.VMSEMLTEMVPGQEDSSDLELLQELNR.T	0.9958		2	3095.4789
4563	TM55A_MOUSE	257	15.56	2	5	R.CPCNCLLICK.D	0.9944		1	1338.4513
						R.SPLLSASHSGNVTPTAPPYLQESSPR.A	0.9958		2	2694.9609
4564	TM7S3_MOUSE	565	7.43	2	3	R.IKELFQK.E	0.9924		1	906.113

						R.DPIPGGCNLEFDLDIDPNLYLDYNFFETTIK.	0.9958	3	3650.9833
4565	TM7S4_MOUSE	470	4.89	2	2	K.YENVYITK.Q	0.9944	1	1030.1656
						R.IEYLHAKLLEK.R	0.9944	1	1357.6359
4566	TM9S1_MOUSE	606	6.6	1	2	R.GDDGGFFPRTLEIHWLSIINSMVLVFLLVGF	0.9958	3	4278.1622
4567	TM9S2_MOUSE	662	8.16	3	16	K.RPSENLGQVLFGER.I	0.9958	2	1602.7904
						K.FCNPGFPIGCYITDK.G	0.9924	2	1789.9576
						K.HTHIDKPDCSGPAMDISNK.A	0.9958	2	2124.299
4568	TM9S4_MOUSE	643	5.44	2	2	R.FEVIPQSIRLEDLK.T	0.9958	2	1687.9768
						R.GDRIVNTPFQVLMNSEK.K	0.9944	2	1949.2323
4569	TMC5_MOUSE	967	8.07	2	2	R.TRPDYESSIEPDYNDFRSESYHAGLPMEPI	0.9958	3	5018.3112
						R.LKPSADCGPFRGLPSFIQSIYSWIDTLSR.R	0.9944	3	3313.7467
4570	TMC6_MOUSE	810	8.4	2	2	R.NVLDLIYGQTLTWLGVLFSPLLPAVQILR.L	0.9944	3	3254.9267
						R.VAEEGLELLPLGLGRGDQTLPGLEGAPALS	0.9958	3	3502.9903
4571	TMCO3_MOUSE	678	3.83	2	2	K.FVLAVLVLSLILPR.S	0.9958	2	1554.0153
						K.GATATQRK.Q	0.9944	1	832.9352
4572	TMED4_MOUSE	227	26.43	3	4	R.CFIEEIPDETMVIGNYR.T	0.9958	2	2087.318
						K.EVFLPSTPGLGMHVEVK.D	0.9952	2	1841.1755
						R.VHLDIQVGEHANNYPEIAAK.D	0.9958	2	2219.4618
4573	TMED5_MOUSE	229	23.14	2	4	R.VNFWSVVNLMVMVVVSAIQVYTLKSLFEDI	0.9958	3	3461.158
						R.MWLPFPVLLLSALPAALLR.G	0.9958	2	2122.7063
4574	TMED8_MOUSE	326	16.56	2	2	R.QAAEGPAFWSPAARR.G	0.9944	2	1615.7916
						K.EDLESTNVSSPLASASDPAAESSPYRPQM'	0.9958	3	3607.8818
4575	TMED9_MOUSE	214	5.61	1	2	K.DPEDKVILAR.Q	0.9924	1	1156.3244
4576	TMEDA_MOUSE	219	19.18	2	4	R.RLEDLSESIVNDFAYMK.K	0.9958	2	2031.2879
						K.DLLVTGAYEITDQSGGAGGLR.T	0.9958	2	2094.2859
4577	TMLH_MOUSE	421	20.43	4	5	R.RPENELWVK.L	0.9958	1	1171.3415
						K.TVHLDETMLFFTWPDGHVTR.Y	0.9958	2	2403.7173
						R.ILWNSKLYQQAQVPSVDFQCFLETNEGLK.	0.9958	3	3457.8738
						R.HTDTTYFQEPCGIQVFHCLK.H	0.9958	2	2482.6869
4578	TMM25_MOUSE	365	10.96	2	2	R.LAWYLDGQLQEATTSRLLSVGGDAFSGGT	0.9944	3	4007.4057
						R.LAWYLDGQLQEATTSR.L	0.9915	2	1853.0416
4579	TMM65_MOUSE	234	11.54	2	2	K.LEALPPTPGQLR.Y	0.9958	1	1292.5211
						R.LLPLLGSRTAR.S	0.9958	1	1197.4666
4580	TMOD1_MOUSE	359	25.63	5	29	K.VEMEIVNMLEKNTTLLK.F	0.9944	2	2006.4237
						R.TLENELDELDPDNALLPAGLR.Q	0.9958	2	2309.5352
						R.LVEALPHNTSLVELK.I	0.9958	2	1663.9548
						K.TLNVESNFISGAGILR.L	0.9958	2	1691.9249

						R.DLDEDEILGALTEEELR.T	0.9958	2	1961.0869
4581	TMOD3_MOUSE	352	17.33	3	3	K.DLDEDELLGKLSESELK.Q	0.9929	2	1934.1046
						K.ILPVFDEPPNPTNVEESLK.R	0.9958	2	2139.41
						K.QLETVLDDLDPENALLPAGFR.Q	0.9958	2	2327.5963
4582	TMPS9_MOUSE	1065	1.41	1	2	K.QEADILQKGIQAR.L	0.9958	2	1470.6689
4583	TMTC1_MOUSE	942	5.2	2	2	R.CGATSLMASTVLLLLLFSWK.T	0.9952	2	2212.6619
						R.CGLVPAGAAALLAGASCLCYGRSLR.G	0.9958	3	2565.8739
4584	TNAP3_MOUSE	775	2.58	1	3	K.EINLVDDYFELVQHEYKK.W	0.9956	2	2283.5426
4585	TNF10_MOUSE	291	16.15	2	2	R.MMVICIVLLQVLLQAVSVAVTYMYFTNEMK	0.9958	3	3510.3135
						K.RQLYQLIEEVTLR.T	0.9944	1	1661.9419
4586	TNI3K_MOUSE	834	8.27	3	3	R.DLNSHNILLYEDGHAVVADFGESRFLQSLD	0.9958	3	4095.4431
						R.ILDLQSKLIIAVDVAK.G	0.9958	2	1740.1369
						K.GMEYLHSLTQPIIHR.D	0.9958	2	1796.0972
4587	TNNC1_MOUSE	161	83.85	9	507	K.AAVEQLTEEQKNEFK.A	0.9958	2	1764.9298
						R.IDYDEFLEFMK.G	0.9958	1,2	1450.646
						K.NADGYIDLDELK.M	0.9958	1	1366.4674
						K.GKSEEELSDLFR.M	0.9958	1,2	1410.5236
						K.MMLQATGETITEDDIEELMK.D	0.9958	2	2299.6285
						K.AAFDIFVLGAEDGCISTK.E	0.9958	2	1915.1163
						K.SEEELSDLFR.M	0.9958	2	1225.2976
						R.MLGQNPTPEELQEMIDEVDEDGSGTVDFD	0.9958	3	4218.6807
						K.AAVEQLTEEQK.N	0.9958	1,2	1246.3599
4588	TNNI3_MOUSE	211	35.55	6	165	R.CQPLELDGLGFEELQDLCR.Q	0.9958	2	2293.4677
						K.NIDALSGMEGR.K	0.9958	1	1163.2909
						K.NITEIADLTQK.I	0.9958	1	1246.4032
						R.ISADAMMQALLGTR.A	0.9944	1	1478.7651
						R.KNIDALSGMEGR.K	0.9944	1	1291.465
						R.AYATEPHAK.K	0.9924	1	988.088
4589	TNNT1_MOUSE	262	3.82	1	3	R.VDFDDIHR.K	0.9958	1,2	1017.0861
4590	TNNT2_MOUSE	301	40.53	10	928	K.DLNELQTLIEAHFENR.K	0.9958	2	1943.1234
						K.ALAIDHLNEDQLR.E	0.9946	2	1508.6744
						K.ELWQSIHNLEAEK.F	0.9958	1,2	1597.7679
						K.ELWQSIHNLEAEKFDLQEK.F	0.9958	2	2358.6128
						K.ALSNMMHFGGYIQK.Q	0.9958	2	1597.8903
						K.YEINVLR.N	0.9958	1	907.0574
						R.LFMPNLVPPK.I	0.9958	1	1156.4717
						K.DAEEGPVEDTKPKPSR.L	0.9958	2	1755.8791

						R.KALAIDHLNEDQLR.E	0.9958	2	1636.8485
						K.IPDGERVDFDDIHR.K	0.99	2	1684.8057
4591	TNPO1_MOUSE	890	7.3	3	3	K.LCSLLDSEDYNTCEGAFGALQK.I	0.9958	2	2492.6308
						R.FSDQFPLPLK.E	0.9958	1	1192.4002
						K.DFMIVALDLLSGLAEGLGGNIEQLVAR.S	0.9958	3	2816.2855
4592	TNPO3_MOUSE	923	4.98	2	2	R.DLIHTGVANDHEEDFELR.K	0.9943	2	2111.2322
						R.HCQLEPDHEGVPEETDDFGEFRMR.V	0.9944	3	2932.073
4593	TOIP1_MOUSE	520	6.92	2	8	R.LEQHSQQPQLSPATSGR.G	0.9958	2	1865.0128
						R.ISHLVLPVQPENTLK.A	0.9929	2	1689.0079
4594	TOLIP_MOUSE	274	22.63	3	25	R.IAWTHITIPESLK.Q	0.9958	2	1509.7887
						R.ITPTQQQQQIQLDAQAAQQLQYGGTVGTV	0.9958	3	3328.6664
						R.GPVYIGELPQDFLR.I	0.9958	2	1604.8461
4595	TOM1_MOUSE	492	44.72	12	65	K.YEAPQTTDGLAGALDAR.Q	0.9958	2	1749.8748
						R.GDLSQHATPLPTPAVLPGDSPITPTPEQIGI	0.9958	3	3136.5291
						R.ISNEQLTEELLMINDNLNNVFLR.H	0.9958	2	2734.0967
						K.VLNLIQSWADAFR.S	0.9958	2	1533.7703
						R.AGLQSLETSGHLEDDFDMFALTR.G	0.9958	2	2554.7907
						R.FHVLVANQDFVENVLVR.T	0.9958	2	2000.3079
						K.VLNLIQSWADAFRSSPDLTGVVAVYEDLR.I	0.9958	3	3236.6519
						K.GLEFPMTDLDMLSPIHTPQR.T	0.9924	2	2299.6649
						R.SSPDLTGVVAVYEDLR.R	0.9949	2	1721.9048
						R.VMSEMLTELVPTQVEPADLELLQELNR.T	0.9958	3	3099.5819
						R.ILELIPR.I	0.9958	1	854.0806
						K.NNPPTIVHDK.V	0.9924	1	1135.2651
4596	TOM20_MOUSE	145	21.38	2	70	K.LPTISQR.I	0.9924	1	814.9603
						K.FFLEEIQLGEELLAQGDYEK.G	0.994	2	2372.6337
4597	TOM22_MOUSE	142	26.76	2	16	R.QILLGPNTGLSGGMPGALPPLPGK.M	0.9958	2	2286.7381
						K.LQMEQQQQLQQRQILLGPNTGLSGGMPG	0.9958	3	3826.4675
4598	TOM40_MOUSE	361	32.69	6	14	R.GSERTPGAAASGAAAASEDGSCGCLPNP	0.9958	3	3636.6821
						K.QLSPTEAFPVLVGDMDNSGSLNAQVIHQL	0.9958	3	3593.049
						R.FQVTHTVALGTIGESNYHFGVTYVGTK.Q	0.9909	2	2928.2737
						R.RPGEEGTVMSLAGK.Y	0.993	2	1432.6348
						R.TPGAAASGAAAASEDGSCGCLPNPGTFEE	0.9958	3	3207.2491
						R.TPGAAASGAAAASEDGSCGCLPNPGTFEE	0.9958	3	3335.4231
4599	TOM70_MOUSE	611	17.51	6	31	K.YEQAIQCYTEAISLCPTEK.N	0.9958	2	2305.4757
						K.SEMEMAHLYSLCDAAHAQTEVAK.K	0.9958	2	2593.852
						K.NREPLMPSPQFIK.S	0.9958	2	1557.8511

						K.ECLEDVTAVCILEGFQNEQSMLLADK.V	0.9958		2	3014.3035
						K.SYFSSFTDDIISQPMLK.G	0.9946		2	1980.2397
						K.KECLEDVTAVCILEGFQNEQSMLLADK.V	0.9958		3	3142.4776
4600	TOP2A_MOUSE	1528	4.91	3	6	K.NFKGTIEELASNQYVINGEVAILDSTTIEISEI	0.9958		3	3979.4736
						K.LLGLPEDYLYGQSTSYLTYNDFINK.E	0.9958		3	2929.2525
						K.SSTPNHKK.W	0.9958		1	898.9945
4601	TOP2B_MOUSE	1612	1.49	2	3	K.LIEVVK.K	0.9944		1	700.8968
						K.KLQLEETMPSPYGR.R	0.9946		2	1649.9024
4602	TOP3A_MOUSE	1003	4.79	2	3	K.TVAQALLPPTTAGESNSVTCNCGREAVLLT	0.9958		3	3387.7473
						R.ARFSEITPHAVR.T	0.9958		1	1384.5809
4603	TOPRS_MOUSE	1033	1.94	1	5	R.SPVVITIDSDSDGESEVK.A	0.9958		1	1877.9971
4604	TP4A1_MOUSE	173	14.45	2	11	R.FLITHNPTNATLNK.F	0.9958		2	1584.8155
						K.QLLYLEK.Y	0.9944		1	907.0978
4605	TP4AP_MOUSE	797	4.14	2	2	K.KYPGFLLNNFHNLLR.F	0.9958		3	1847.1728
						K.NDFVIFLFTLMTSK.K	0.9919		2	1677.0112
4606	TP53B_MOUSE	1957	3.12	2	2	K.EECPEAMEVETSVISIDSPQK.L	0.9958		3	2379.5612
						R.ENPFQNLKVLLVSDQQQNFLELWSEILMTC	0.9958		3	4049.6313
4607	TPA_MOUSE	559	8.05	2	2	K.GGLYTDITSHPWQAAIFVKNK.R	0.9944		2	2347.6787
						K.LTWEYCDMSPCSTCGLRQYK.R	0.9924		3	2556.7477
4608	TPD54_MOUSE	220	32.27	4	11	R.TPVVEGLTEGEEEELRAELAK.V	0.9958		2	2300.5249
						K.GVLSDFMTDVPVDPGVVHR.T	0.9958		2	2041.3294
						R.SWHDVQVSTAYVK.T	0.9958		2	1520.6848
						K.KTQETLSQAGQK.T	0.9958		1	1319.4575
4609	TPGS1_MOUSE	303	7.26	1	6	R.TAFNNNVSVAYECLSASGRK.K	0.9943		2	2189.3557
4610	TPIS_MOUSE	249	89.16	17	1917	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	0.9958		2	3031.4326
						K.VVLAYEPVWAIGTGK.T	0.9958		1	1603.9017
						R.IIYGGSVTGATCK.E	0.9958	1,2		1327.4864
						K.VVFEQTK.V	0.9944		1	850.9903
						K.VIADNVK.D	0.9944		1	758.8931
						K.IAVAAQNCYK.V	0.9958		1	1138.275
						R.HVFGESDELIGQK.V	0.9958		2	1459.5987
						K.DLGATWVVLGHSER.R	0.9958		2	1540.719
						K.TATPQQAQEVHEK.L	0.9958		2	1467.5785
						K.VSHALAEGLGVIACIGEK.L	0.9958		2	1825.0814
						R.RHVFGESDELIGQK.V	0.9957		2	1615.7862
						K.VTNGAFTGEISPGMIK.D	0.9958		1	1622.8768
						K.SNVNDGVAQSTR.I	0.9958	1,2		1248.295

						K.FFVGGNWK.M	0.9958		1	955.1039
						K.ELASQPDVDGFLVGGASLKPEFVDIINAKQ.	0.9958		3	3159.5633
						K.CLGELICTLNAANVPAGTEVVCAPPTAYIDF	0.9958		3	3565.9437
						R.KFFVGGNWK.M	0.9958		1	1083.2779
4611	TPM1_MOUSE	284	53.17	16	417	K.SIDDLEDELYAQK.L	0.9958		1	1539.6361
						R.RIQLVEEELDR.A	0.9958		2	1400.5748
						K.KATDAEADVASLNR.R	0.9958		2	1461.5718
						K.MEIQEIQLK.E	0.9958		1	1132.3606
						K.AISEELDHALNDMTSI.-	0.9958		1	1759.9257
						R.IQLVEEELDR.A	0.9958	1,2		1244.3873
						K.LVIIESDLER.A	0.9958		1	1187.3788
						R.KLVIIESDLER.A	0.9958		2	1315.5529
						K.GTEDELDKYSEALK.D	0.9958		2	1598.7039
						K.ATDAEADVASLNR.R	0.9958		1	1333.3977
						K.EDKYEEEIK.V	0.9958		1	1183.2573
						K.QLEDELVSLQK.K	0.9904		2	1302.4674
						R.KYEEVAR.K	0.9958		1	895.0031
						R.SKQLEDELVSLQK.K	0.9912		2	1517.7197
						R.LATALQK.L	0.9958		1	744.9096
						K.SLEAQAEK.Y	0.9958		1	875.9542
4612	TPM3_MOUSE	284	13.73	3	6	K.MELQEIQLK.E	0.9958		1	1132.3606
						R.SKQLEDELATMQK.K	0.9958		1	1521.7259
						R.KLVIIEGDLER.T	0.9958		2	1285.5266
4613	TPM4_MOUSE	248	27.42	4	25	R.RIQLLEEELDR.A	0.9958		2	1414.6017
						K.EENVGLHQTLDQTLNELNCI.-	0.9958		2	2341.5029
						R.AQEQLATALQNLEEAEK.A	0.9958		2	1887.0538
						R.KIQALQQQADDAEDR.A	0.9958		2	1729.8442
4614	TPP1_MOUSE	562	21.89	4	102	K.NPFLITDEVVDYISGGGFSNVFPRPPYQEE.	0.9958		3	4146.6453
						K.FRPSFPASSPYVTTVGGTSFK.N	0.9958		2	2234.5163
						R.LFGGSFTHQASVAK.V	0.9958		2	1450.6371
						R.AYPDVAALSDGYWVVSNMVPIPWVSGTSA	0.9958		3	4776.4205
4615	TPP2_MOUSE	1262	12.76	10	22	K.IIDIIDTTGSGDVNTATEVEPK.D	0.9958		2	2289.4986
						K.DGEIIGLSGRVLK.I	0.9958		2	1357.5931
						K.EELQSQVELLNSFEK.K	0.9958		2	1793.9683
						K.SWVQTLRPVNAK.T	0.9955		2	1399.6359
						K.LIKEELQSQVELLNSFEK.K	0.9958		2	2148.4613
						R.LSNTLSLDIHENHSLALLGK.K	0.9958		2	2176.4777

						K.IPANWTNPLGK.Y	0.9958		2	1211.4062
						K.ADNIEVFAQGHGIIQVDK.A	0.9958		2	1955.1778
						K.VNESSHYDLAFTDVHFKPGQIR.R	0.9958		2	2561.8161
						K.KETGASSFLCR.Y	0.9944		2	1256.3673
4616	TPPP_MOUSE	218	28.9	3	11	K.RLSLESEGANEGATAAPELSALEEAFR.R	0.9925		3	2820.0422
						R.VDLVDESGYVPGYK.H	0.9958		2	1541.6977
						R.TITFEQFQEALEELAK.K	0.9958		2	1898.1199
4617	TPPP3_MOUSE	176	19.32	2	15	K.SKEEAFDAICQLIAGK.E	0.9958		2	1780.9819
						R.QDILDDSGYVSAYK.N	0.9958		2	1574.6843
4618	TPST1_MOUSE	370	16.76	3	3	K.FLHIPWNHSVLHHEEMIGKAGGVSLSK.V	0.9958		3	3025.501
						K.SLTYLARLFPNAK.F	0.9944		1	1494.777
						R.STDQVIKPVNVGALSK.W	0.9958		1	1656.92
4619	TR102_MOUSE	329	5.17	1	2	R.IANCSWQIFLYLKWR.L	0.9943		2	1999.3318
4620	TR103_MOUSE	312	7.05	1	2	K.FTDRLQVNTLQNCSTSNTLK.D	0.9911		2	2341.5493
4621	TR150_MOUSE	951	2.42	2	10	R.SIFQHIQSAQSQR.S	0.9958		2	1530.6835
						K.QTNADK.E	0.9944		1	676.7043
4622	TRA2B_MOUSE	288	9.03	2	2	K.YGPIADVSIVYDQQSRR.S	0.9929		1	1968.1765
						R.HVGNR.A	0.9958		1	582.6401
4623	TRAF5_MOUSE	558	6.99	2	4	R.AYLNGDGSGKGTHLSLYFVVMR.G	0.9958		2	2386.7307
						R.AALQDHMLLVLEK.N	0.9958		2	1481.7937
4624	TRAF7_MOUSE	594	1.68	1	11	K.MNLEAHLK.E	0.9924		1	956.1479
4625	TRAP1_MOUSE	706	18.41	6	32	R.GVVDSEDIPLNLSR.E	0.9958		1	1514.6757
						R.HLAEHSPYYEAMK.Q	0.9958		2	1576.7668
						R.AQLLQPTLEINPR.H	0.9944		2	1493.7465
						R.ESEPELAQLLVDQIYENAMIAAGLVDDPR.A	0.9958		2	3201.5727
						R.LDTHPAMVTVLEMGAAR.H	0.9924		2	1813.1401
						R.SAAPESPGYQWLSDGSGVFEIAEASGVRP	0.9958		3	3252.5212
4626	TRCG1_MOUSE	825	2.42	1	2	R.LICYQLRFIYQEAFPNFR.N	0.9931		2	2379.7326
4627	TRDMT_MOUSE	415	6.99	2	4	K.LSFNMILMSPPCQPFTR.I	0.9943		2	2040.4121
						K.YILLENVK.G	0.9924		1	992.2035
4628	TRFE_MOUSE	697	76.04	43	1185	K.YLGAEYMQSVGNMR.K	0.9958		2	1619.8506
						K.AVSSFFSGSCVPCADPVAFPK.L	0.9958		2	2231.442
						K.QEDFELLCPDGTR.K	0.9958		2	1580.6575
						K.AVLTSQETLFGGSDCTGNFCLFK.S	0.9952		2	2553.7603
						K.DFQLFSSPLGK.D	0.9958	1,2		1239.4136
						K.DSAFGLLR.V	0.9958		1	879.0037
						K.NNGKEDLIWEILK.V	0.9958		2	1572.8015

						R.KPVDQYEDCYLAR.I	0.9958		2	1657.7864
						R.LYLGHNYVTAIR.N	0.9958		1	1420.6542
						K.KGTDFQLNQLEGK.K	0.9958	1,2		1478.6451
						K.SKDFQLFSSPLGK.D	0.9958		2	1454.6659
						K.HTTIFEVLPEK.A	0.9958		2	1314.5242
						K.DFASCHLAQAPNHVVVSR.K	0.9958		2	2009.198
						K.NLKQEDFELLCPDGTR.K	0.9958		2	1936.0949
						K.LCQLCPGCGCSSTQPFFGYVGAFK.C	0.9958		2	2742.9523
						K.ADRDQYELLCLDNTR.K	0.9958		2	1882.991
						K.VAQEHFGK.G	0.9958		2	916.0244
						R.SAGWVIPIGLLFCK.L	0.9958		1	1561.8737
						K.HQTVLDNTEGKNPAEWAK.N	0.9958		2	2039.212
						K.HTTIFEVLPEKADR.D	0.9958		2	1656.8791
						R.LTVGALLACAALGLCLAVPDK.T	0.9958		2	2127.5049
						R.IPSHAVVAR.K	0.9958		2	950.1288
						K.GTDFQLNQLEGK.K	0.9958	1,2		1350.471
						K.FDEFFSQGCAPGYEK.N	0.9958		2	1782.8695
						R.NQQEGVCPEGSIDNSPVK.W	0.9958		2	1959.0429
						K.EDLIWEILK.V	0.9924		1	1159.3678
						K.HQTVLDNTEGK.N	0.9944		1	1242.3311
						K.WCAVSEHENTK.C	0.9958		2	1361.4198
						K.SCHTGLGR.S	0.9944		1	887.9371
						R.LLEACTFHKH.-	0.9958		1	1256.4131
						K.CDEWSIISEGK.I	0.9926	1,2		1324.3961
						K.WCALSHLER.T	0.9948		2	1172.2951
						K.ASDTSITWNNLK.G	0.993		2	1350.471
						K.KTSYPDCIK.A	0.9958	1,2		1112.2341
						K.CAPNNKEEYNGYTGAFR.C	0.9943		2	1992.0777
						R.LYLGHNYVTAIRNQQEGVCPEGSIDNSPVK	0.9958		3	3360.6739
						K.DLLFKDSAFGLLR.V	0.9958		2	1495.7618
						K.IECESAETTEDCIEK.I	0.9958		2	1814.8269
						K.GYYAVAVVK.A	0.9958		1	970.1564
						R.DQYELLCLDNTR.K	0.9958		2	1540.6361
						R.LLEACTFHK.H	0.9924		1	1119.272
						R.TAGWNIPMGMLYNR.I	0.9958		2	1624.9159
						K.IVNGEADAMTLDGGHAYIAGQCGLVPVMAI	0.9958		3	5132.6574
4629	TRHDE_MOUSE	1025	1.66	1	5	K.VPYSLPKLDLLAVPK.H	0.9958		2	1654.0459

4630	TRI30_MOUSE	496	4.84	1	3	R.VPYPFGNLRPNLHVANIVERLK.G	0.9909	2	2548.0091
4631	TRI32_MOUSE	655	6.87	2	13	K.GSTPGMFNLPVSLYVTSQSEVLVADR.G	0.9958	3	2769.1419
						R.EADHQPPGHCTLPVK.E	0.9924	1	1686.8309
4632	TRI35_MOUSE	501	4.99	1	2	K.KMLGSVESVPFSLDPNTAAGWLK.V	0.9958	2	2448.8395
4633	TRI36_MOUSE	729	7.41	2	2	K.SFRPAAQASFEDYVVNISK.Q	0.993	2	2130.3647
						R.YEQDSGHDSGSEDACFDSSQPFTLVTIGM	0.9944	3	3438.6235
4634	TRI47_MOUSE	641	8.11	3	3	R.HNLGQVPEADSVSFLQELLALR.L	0.9958	2	2437.7581
						R.GHELVPLEQER.A	0.9958	2	1307.449
						R.SAGGTGGSGGPAR.C	0.9921	2	1032.058
4635	TRI50_MOUSE	483	3.73	1	2	R.QSVDCSSSPPNVSLAR.V	0.9924	1	1704.8004
4636	TRI54_MOUSE	366	12.3	2	4	K.VELAGRPEPGYESMEQFSVSVEHVAEMLF	0.9958	3	3278.679
						R.NLLVENIIDIYK.Q	0.9955	2	1447.7148
4637	TRI60_MOUSE	466	5.15	1	8	R.DVLCTQCSLSVEHQGHYTCPIK.K	0.9929	2	2633.8159
4638	TRI66_MOUSE	1242	4.99	2	2	R.KVTVTSLTGQQPQEVESTSEEHR.L	0.9958	3	2571.7606
						K.DLAIPSELEEPINLSVKKPFLAPVINTSTALQ	0.9958	3	3897.5041
4639	TRI72_MOUSE	477	64.15	16	818	R.ALMPALEELTFDPSSAHPSLVVSSSGR.R	0.9958	2,3	2800.156
						K.TVAVLEHQLVEVEETVR.Q	0.9958	2	1952.2151
						R.TLVCGVCASLGSHR.G	0.9958	2	1517.6575
						R.LPGPVYPIFDVCWHDK.G	0.9958	2	1944.2061
						R.ELSSLNSYLEQLR.Q	0.9958	1,2	1552.7245
						R.LDIQLPVISDDFK.F	0.9958	1,2	1503.7356
						K.VLEEVADKPQTEFLMK.F	0.9944	2	1878.1908
						R.QELSCPLCLQLFDAPVTAECGHSFCR.A	0.9958	2,3	3097.3158
						R.VAGEPAADGTVACPCCQAPTRPQALSTNL	0.9958	3	3498.7731
						R.RELSSLNSYLEQLR.Q	0.9958	2	1708.912
						R.LVEGLAQVPQGHCEEHLDPLSIYCEQDR.T	0.9958	3	3294.5342
						K.AVAVVAQQLLSQGEHYWEVEVGDKPR.W	0.9958	3	2910.259
						R.MFLAALESSLDR.E	0.9958	2	1353.5762
						K.NAQPLLLVGPEQEQA.-	0.9958	1	1607.8039
						R.LHAVPSQGLWLLGLR.D	0.9958	2	1661.003
						K.ILEAHVEAK.E	0.9931	2	1010.1784
4640	TRIM1_MOUSE	685	1.9	1	2	R.FLQSAKNIAER.V	0.9958	1	1277.4661
4641	TRIM7_MOUSE	510	5.1	1	2	R.TLPCPLPCPQCREPARPSQLRPNR.Q	0.9929	2	2902.2275
4642	TRIO_MOUSE	3043	1.12	2	3	K.SSKSLQLDIIPASIPGSEVK.L	0.9958	2	2070.391
						R.TSQNTLDSDK.L	0.9958	1	1109.1351
4643	TRIP6_MOUSE	480	10.63	2	2	R.GIIRPGSLDAEIDSLTSMLADLDGGR.S	0.9958	3	2673.9983
						R.EPGPGVPEGPSGVHIPAGGGR.G	0.9958	2	1925.1111

4644	TRM11_MOUSE	460	1.74	1	2	R.QYGLEK.F	0.9958	1	737.8308
4645	TRM1L_MOUSE	728	8.52	2	4	R.LADLEKLAFGTEGDVDSASSLNSDNPGTEI	0.9958	3	4140.3468
						K.GIEVLFAVALEHFVLVVVR.V	0.9924	2	2111.5785
4646	TRMU_MOUSE	417	11.51	3	4	R.VAPEASSDSPGLHPTS.-	0.9958	1	1552.6378
						R.VHWIAEEPPAALVR.D	0.9958	2	1588.8497
						K.IAAENSLHHVLQK.R	0.9958	2	1460.6762
4647	TRNT1_MOUSE	434	3.92	1	2	K.LQSPEFQSLFTEGLK.S	0.9958	2	1724.9512
4648	TRPA1_MOUSE	1125	1.69	1	2	K.AVAMLLSYNADILLNKK.Q	0.9944	2	1878.2805
4649	TRPM6_MOUSE	2028	3.01	2	2	K.YGQFLLVPSSGKQVPLSLETPPHLFR.S	0.9944	3	2912.4044
						K.IHTCSRQGVPVVGLVMEGGPNVILWVWET	0.9958	3	3463.0442
4650	TRPM7_MOUSE	1863	6.07	4	7	K.AAVTTGAWILTGGVNTGVAK.H	0.9952	2	1888.1741
						R.SCDMVFGPANLGEDAIK.N	0.9958	2	1825.0095
						K.NHVFVYGQQWLVGSLEQAMLDALVMDRV	0.9944	3	3682.2929
						R.DVVAPYQTLLNPLSKLNVLNNLHSHFILVDI	0.9944	3	3946.5388
4651	TRPM8_MOUSE	1104	6.61	3	3	K.YISERTSQDSNYGGK.I	0.9958	2	1705.7783
						R.DTLIRSCDDEGHFSAQYIMDDFTR.D	0.9958	3	2894.0645
						R.TLYSSVSRSTDVSYSDSDLVNFIQANFK.K	0.9958	3	3145.4064
4652	TRRAP_MOUSE	2565	1.99	2	2	K.IIAALFKALNSTNSELQEAGEACMR.K	0.9924	3	2739.0821
						R.DEALSGSELTAKLEPAFLSGLR.C	0.9958	2	2305.5902
4653	TRXR1_MOUSE	613	34.09	12	89	R.VVGFHVLGPNAGEVTQGFAAALK.C	0.9958	2	2283.6353
						K.IPVTDEEQTNVPYIYAIGDILEGK.L	0.9958	2	2678.9959
						R.WGLGGTCVNVGCIPK.K	0.9958	2	1618.8054
						K.MTESVQSHIGSLNWGYR.V	0.9944	2	1966.1785
						R.FLIATGERPR.Y	0.9958	2	1160.3616
						K.LMHQAALLGQALK.D	0.9958	2	1394.7185
						K.EYCISSDDLFSLPYCPGK.T	0.9958	2	2152.2943
						K.VLVLDFVTPTPLGTR.W	0.9958	2	1628.9524
						K.FGEENIEVYHSFFWPLEWTVPSR.D	0.9958	2	2871.1803
						K.KVLVLDFVTPTPLGTR.W	0.9958	2	1757.1265
						K.CDYDNVPTTVFTPLEYGCCGLSEEK.A	0.9958	2	2956.0843
						R.LYGGSNVKCDYDNVPTTVFTPLEYGCCGL	0.9958	3	3775.0122
4654	TRXR2_MOUSE	524	37.02	9	63	K.IIVDAQEATSVPHIYAIGDVAEGRPELTPTAI	0.9958	2,3	3476.9518
						R.EPPQLVLGLHFLGPNAGEVTQGFALGIK.C	0.993	2	2904.3818
						K.KLPTNQLQVTWEDHASGK.E	0.9958	2	2053.2822
						R.DAHHYGWEVAQPVQHNWK.T	0.9958	2	2203.3836
						K.LMHQAALLGGMIR.D	0.9958	2	1411.7668
						K.KVAVADYVEPSPR.G	0.9909	2	1431.6317

						K.ASFVDEHTVR.G	0.9958		2	1161.2596
						K.CGASYAQVMQTVGIHPTCSEEVVK.L	0.9958	2,3		2652.9113
						R.GFDQQMSSLVTEHMESHGTQFLK.G	0.9958	2,3		2638.9295
4655	TRXR3_MOUSE	697	6.89	2	2	R.KFTPILVQQLEK.G	0.9945		2	1444.7575
						K.YGWEYNQQVKHNWEAMTEAIQSHIGSLNV	0.9958		3	3898.2628
4656	TS1R1_MOUSE	842	5.58	2	2	R.MMLRLAR.A	0.9958		1	891.181
						R.SAGGRLCFLMLGSLVAGSCSLYSFFGKPT	0.9958		3	3895.4935
4657	TSH2_MOUSE	1030	2.33	1	3	K.MTAVYANILSDSYWSGLGLGFK.L	0.9924		2	2394.7473
4658	TSN_MOUSE	228	9.65	1	7	R.EILTLLQGVHQGTGFQDIPK.R	0.9958		2	2195.5235
4659	TSNAX_MOUSE	290	21.03	3	6	R.AVTTGLQEYVEAVSFQHFIK.T	0.9958		2	2268.5743
						K.ILQVAQELSGEDMHQFHR.A	0.9958		2	2139.3935
						K.LTPVDYLLGVADLTGELMR.M	0.9958		2	2077.4437
4660	TSP2_MOUSE	1172	1.11	1	2	K.LPNSGQEDFDK.D	0.9942		2	1250.3073
4661	TT21B_MOUSE	1315	0.91	1	2	K.KMGEVAEAIK.T	0.9958		1	1076.2964
4662	TTBK1_MOUSE	1308	5.2	3	6	R.KCYMLDFGLAR.Q	0.9924		1	1374.6069
						R.LASGASSSSSEEQRR.A	0.9952		2	1552.598
						R.SRIPRPISVSMPVEGQQLPGRPHGAASATI	0.9958		3	3755.2901
4663	TTC1_MOUSE	292	7.53	1	2	K.DLGNLVLRPFGLSTENFQIK.Q	0.9958		2	2262.6139
4664	TTC26_MOUSE	554	9.57	2	2	K.LMNFHQNLQDIKEDQLSLASIHYMR.S	0.9958		3	3046.4889
						R.QCMASCFFLLKQFDDVLIYLNSFK.S	0.9958		3	2989.4312
4665	TTC27_MOUSE	847	1.89	1	7	K.NLELNDDTVLNEIK.L	0.9924		1	1630.7924
4666	TTC28_MOUSE	1691	1.54	2	3	K.EEGGADRLELK.E	0.9958		1	1217.3213
						R.DVLSLLNLSPR.H	0.9958		1	1227.4465
4667	TTC29_MOUSE	471	8.07	2	2	K.EDIDYYLEQNFK.G	0.9927		2	1577.6874
						R.NNLQSLDMIRACTMLGDIYNEK.G	0.9944		3	2600.9308
4668	TTC9B_MOUSE	239	20.5	3	3	R.YIQLTQLK.M	0.9958		1	1007.2181
						K.AAQGARPGGLPTPSPGPTTSPGPAR.L	0.993		2	2299.5515
						K.VLEKQQGNFK.A	0.9958		1	1191.3726
4669	TTF1_MOUSE	859	3.38	2	2	K.RPQKCPSQCLESK.Q	0.9958		1	1618.7626
						R.YPEEKTLITNLK.R	0.9958		1	1449.6873
4670	TTF2_MOUSE	1138	2.28	2	2	K.NRLTYATIDGSVNPK.Q	0.9958		2	1649.8442
						K.KDVVIHR.F	0.9958		1	867.039
4671	TTHY_MOUSE	147	53.74	4	127	K.TLGISPFHEFADVVFTANDSGHR.H	0.9958		2	2518.7477
						R.HYTIAALLSPYSYSTTAVVSNPQN.-	0.9958		2	2598.8718
						K.KTSEGSWEPFASGK.T	0.9958		2	1511.6311
						K.TAESGELHGLTTDEK.F	0.9958		2	1588.6684
4672	TTL11_MOUSE	727	4.68	2	5	K.VWSDIISLVIK.T	0.9924		1	1273.5584

						R.SWILPEEFQLFVSQVQTVK.E	0.9958		3	2279.6409
4673	TTL12_MOUSE	639	7.82	3	14	R.SLDTHVTNNLHSIIR.H	0.9957		2	1720.926
						K.FNQTYQLAHGTAEEK.V	0.9958		2	1737.8663
						R.LLDEFVSLHGPTLR.A	0.9954		2	1597.8546
4674	TTLL4_MOUSE	1193	1.42	2	3	R.SFSLPQK.G	0.9958		1	806.9371
						K.YSPSMK.S	0.9924		1	712.8389
4675	TTLL5_MOUSE	1328	2.48	2	2	R.QASEAELEEVLTFYTQKNK.S	0.9958		2	2229.4485
						K.EDEQMELVVR.F	0.9958		1	1248.3936
4676	TTLL8_MOUSE	832	3.97	2	2	K.QMPPIASVGLSESLLDAPPK.V	0.9924		2	2051.4058
						R.GRDIVCMDR.V	0.9944		1	1122.2507
4677	TULP2_MOUSE	562	8.36	2	2	K.VLQGDDGDASNHNAWNMTCPQPRIPGPR	0.9958		3	3105.3374
						R.VQKGAGHGLLLLQNK.A	0.9958		3	1576.8826
4678	TVB2_MOUSE	133	26.32	2	4	R.LLLYVSLCLVETALMNTKITQSPR.Y	0.9926		2	2765.2905
						R.YLILGRANK.S	0.9924		1	1048.2736
4679	TWF1_MOUSE	350	13.14	3	10	K.HQTLQGVAFPISR.D	0.9958		2	1454.6719
						K.KYLLSQSSPAPLTAAEEELR.Q	0.9958		2	2204.4851
						R.YHFFLYK.H	0.9958		1	1018.2029
4680	TWF2_MOUSE	349	36.39	7	59	K.HQTLQGLAFPLQPEAQR.A	0.9958		2	1935.193
						R.ETIELVHTEPTNVAQLPSR.I	0.9958		2	2135.3818
						K.EFGGGHIKDELFGTVK.D	0.9958		2	1734.9493
						R.AVLPLLDAQEPCYLLFR.L	0.9958		2	2019.3575
						K.DDLSLAGYQK.H	0.9958		1	1110.209
						R.LDSQNAQGFEWLFLAWSPDNSPVR.L	0.9958		2	2779.0404
						K.HLSSCAAPAPLTSAER.E	0.9929		2	1668.8132
4681	TWSG1_MOUSE	222	7.66	1	2	K.STVEELHEPIPSLFR.A	0.9958		2	1754.9805
4682	TXD10_MOUSE	456	17.32	3	4	K.DASDMVQFINSILDGTVPAQGGDSIFQR.L	0.9944		3	2983.2794
						K.GFVEDLNESFKDNR.K	0.9917		2	1670.7759
						K.SEMENQEQIEESKEQESSSGGSLAPTVQE	0.9958		3	3394.5562
4683	TXD12_MOUSE	170	52.35	4	13	K.VRPEIINESGNPSYKYFYVSAEQVVQGMK.I	0.9958		3	3334.7711
						K.VRPEIINESGNPSYK.Y	0.9958		2	1703.8925
						K.FAESTEISELSHNFVMVNLEDEEEPRDEDF	0.9958		3	4502.7768
						K.EAAASGLPLMVIIHK.S	0.9958		2	1550.8999
4684	TXIP1_MOUSE	704	4.4	2	2	R.EKDFFPGLGFGDAIPPFLR.F	0.9958		3	2124.4466
						R.SLAEEYLR.Y	0.9958		1	981.0935
4685	TXLNB_MOUSE	685	18.69	6	19	K.EITSHFQTTLTDIQTQIEQQSER.N	0.9958	2,3		2734.9365
						R.EQPPPEVTDIPVGPSTGLPR.E	0.9958		2	2087.3373
						R.CSTSGQAPEQEGSLHPEK.G	0.9958		2	1943.0002

						K.YDISPSPESEGDSAVVPGCESR.E	0.9958		2	2339.3973
						K.KYTELLDEHR.T	0.9958		2	1304.4453
						K.AVENLATAFTILHHPEFTPDQPTER.Q	0.9958		2	2836.1332
4686	TXN4B_MOUSE	149	9.4	1	2	R.GKLIVQSPIDPK.N	0.9924		1	1295.5651
4687	TXND4_MOUSE	406	22.41	5	9	K.SNPVHEIQSLDEVTNLDR.S	0.9958		2	2067.2199
						R.HPLLHIQK.T	0.9944		1	986.2052
						R.VASILHDDCAFLSAFGDLSKPER.Y	0.9958		3	2549.809
						R.FSQMLHPIFEEASDVIKEEYPDK.N	0.9958		2	2754.0834
						R.HMYVFGDFK.D	0.9958		2	1144.3331
4688	TXND5_MOUSE	417	9.59	2	7	K.ALAPTWEQLALGLEHSETVK.I	0.9958		2	2194.4924
						K.VDCTQHYAVCSEHQVR.G	0.9958		3	1990.0717
4689	TXNL1_MOUSE	289	14.53	2	17	R.SEPTQALELTEDDIKEDGIVPLR.Y	0.9958		2	2569.8254
						R.IDQYQGADAVGLEEK.I	0.9958		2	1636.7557
4690	TYB4_MOUSE	50	30	1	2	K.NPLPSKETIEQEK.Q	0.9958		2	1513.6879
4691	TYSD1_MOUSE	568	9.15	2	2	R.ARARPLQPPRPAQLLLLLSCPAFR.S	0.9929		2	2743.2834
						R.TGSAALTQTGTAFLPGDSCSDDLR.L	0.9958		3	2442.5647
4692	TYY1_MOUSE	414	4.83	2	2	K.KGGGK.K	0.9958		1	446.5271
						K.SGGGASSGGGR.V	0.9958		1	849.8356
4693	U2AF2_MOUSE	475	11.58	2	4	K.SIEIPRPVDGVEVPGCGK.I	0.9958		2	1910.1437
						R.RPHDYQPLPGMSENPSVYVPGVVSTVVPI	0.9958		3	3561.9941
4694	U383_MOUSE	713	6.87	2	2	R.TVNAGSECVLEGLAAERGAGAPAPGLWVF	0.9931		3	3468.8261
						K.RECGGLQTLLK.N	0.9944		1	1275.457
4695	U515_MOUSE	290	10	2	6	R.YEPVPLDKMWGLAEFHCPK.C	0.9958		2	2318.6613
						K.QNHLPK.V	0.9958		1	736.8491
4696	U530_MOUSE	465	22.58	6	19	K.GIYSFGLMETNFYDQAQK.L	0.9958		2	2113.3491
						R.DHILLFNDAHFLMASLGAR.D	0.9958		2	2142.4833
						K.DVGLPLCQALLEAENGNPDR.V	0.9958		2	2182.3612
						R.DVFNQLLIHAAMTCTSSVHK.N	0.9958		2	2273.5781
						R.IVQIGGSNAQR.D	0.9924		1	1143.2883
						R.VLELLLPIR.Y	0.9958		2	1066.3726
4697	U539_MOUSE	99	20.2	1	3	R.LSVVFGEHTLLVTVSGQR.V	0.9958		2	1943.2535
4698	UACA_MOUSE	1411	1.77	1	4	R.MSTVSQSLKEAQEANAAILADHR.Q	0.9909	2,3		2471.7478
4699	UAP1_MOUSE	522	3.64	1	2	K.DVVNVYEPQLQHHVAQK.K	0.9958		2	2005.2407
4700	UAP1L_MOUSE	507	11.44	2	2	R.GVEFVHVYCVDNILVRLADPVFIGFCVLQG	0.9958		3	4040.5496
						K.EHDFFHLDPTNVVLFEQR.M	0.9958		2	2244.471
4701	UAP56_MOUSE	428	7.24	2	4	K.NCPHIVVGTPGR.I	0.9944		2	1307.4613
						K.FMQDPMEIFVDDETK.L	0.9958		2	1846.0768

4702	UB2D1_MOUSE	147	13.61	1	15	K.IYHPNINSNGSICLDILR.S	0.9958	2	2100.3483
4703	UB2G1_MOUSE	170	39.41	4	8	R.WEVLIIGPPDTLYEGGVFK.A	0.9958	2	2134.4797
						K.FITEIWHPNVDK.N	0.9958	2	1499.7093
						R.QLAELNKNPVEGFSAGLIDDNDLYR.W	0.9958	3	2793.0624
						K.AHLTFPK.D	0.9958	1	813.9749
4704	UB2L3_MOUSE	154	61.69	5	361	K.TDQVIQSLIALVNDPQPEHPLR.A	0.9958	2	2484.8149
						K.GQVCLPVISAENWKPATK.T	0.9958	2	1999.2836
						R.IEINFPAEYPFKPPK.I	0.9958	2	1791.0997
						R.NIQVDEANLLTWQGLIVPDNPPYDK.G	0.994	2	2854.1889
						K.IYHPNIDEK.G	0.9958	1	1129.2578
4705	UB2V1_MOUSE	147	34.69	3	8	R.VNMSGVSSSNGVVDPR.A	0.9958	2	1605.7631
						R.WTGMIIGPPR.T	0.9937	2	1128.3776
						K.GVGDGTVSWGLEDDEDMTLTR.W	0.9915	2	2254.3869
4706	UBA1X_MOUSE	1058	59.36	34	502	R.IYDDDFFQNLDGVANALDNIDAR.M	0.9958	2	2615.7723
						K.SLPASLVEPDFVMTDFAK.Y	0.9958	2	1968.2721
						K.GNVQVVIPFLTESYSSSQDPPEK.S	0.9958	2	2522.7711
						K.NIILGGVK.A	0.9958	1	814.0159
						K.AVTLHDQGTTQWADLSSQFYLR.E	0.9958	2	2538.7789
						R.HQYYNQEWTLWDR.F	0.9958	2	1839.964
						R.KPLLESGTLGTK.G	0.9958	1,2	1244.4741
						R.QMNPYIQVTSHQNR.V	0.9958	2	1716.9121
						K.NFPNAIEHTLQWAR.D	0.9958	2	1697.8937
						R.QFLFRPWDVTK.L	0.9958	2	1437.6842
						K.NGSEADIDESLYSR.Q	0.9958	2	1556.5829
						R.NEEDATELVGLAQAVNAR.S	0.9958	2	1901.0403
						K.LAYVAAGDLAPINAFIGGLAAQEVMK.A	0.9958	2	2605.0674
						R.LAGTQPLEVLEAVQR.S	0.9912	2	1624.8778
						R.FEVQGLQPNGEEMTLK.Q	0.9958	2	1821.0552
						K.MLQTSSVLVSGLR.G	0.9958	2	1391.669
						R.AAVASLLQSVQVPEFTPK.S	0.9958	2	1886.1986
						R.YDGQVAVFGSDFQEK.L	0.9958	1,2	1690.8065
						K.IHVSDQELQSANASVDDSR.L	0.9958	2	2072.1527
						K.NGFLNLALPFFGFSEPLAAPR.H	0.9924	2	2279.6463
						K.YFLVGAGAIGCELLK.N	0.9958	2	1611.8878
						K.VLGPYTFSICDTSNFSDYIR.G	0.9958	2	2356.5598
						K.FMPIMQWLYFDALECLPEDK.E	0.9958	2	2547.9523
						K.IIPAIATTTAAVVGLVCLELYK.V	0.9958	2	2317.7809

						R.LAELNSYVPVTAYTGPLVEDFLSSFQVVVL	0.9958		3	4382.9977
						K.DNPGVVTCLDEAR.H	0.9958		2	1446.5231
						K.VVQGHQQLDSYK.N	0.9958		2	1402.5498
						R.QLYVLGHEAMK.M	0.9958		2	1289.5353
						K.ATLPSPDKLPGFK.M	0.9958		2	1371.6195
						K.NFAMIGLGCGEGGEVVVTDMDTIEK.S	0.9958		2	2643.9498
						K.MYPIDFEKDDDSNFHMDFIVAASNLR.A	0.9958		2	3092.4243
						R.VGEFCHSR.G	0.993		2	992.0453
						R.QLLHNFPPDQLTSSGAPFWSGPK.R	0.9958	2,3		2525.8259
						K.IHVSDQELQSANASVDDSRLEELK.A	0.9958		2	2684.8767
4707	UBA3_MOUSE	462	8.23	2	8	K.ELGLVDGQELAVADVTTPQTVLFK.L	0.9958		2	2544.9048
						R.LPEHCIEYVR.M	0.9932		2	1316.4656
4708	UBA6_MOUSE	1053	3.32	2	3	K.FDLNEPLHLSFLQSAAK.L	0.9954		2	1931.1986
						R.NAVFQLEEALSSNK.A	0.9958		2	1550.7087
4709	UBAC1_MOUSE	409	13.2	2	37	R.KPSPEELDQGIDPNSPLFQAILDNPVVQLG	0.9958		3	3786.2738
						R.VNNNQQNAACEWLLGDR.K	0.9958		2	2003.1045
4710	UBC12_MOUSE	183	16.94	2	4	K.VGQGYPHDPPK.V	0.9958		2	1195.3201
						K.TCDISFSDPDDLLNFK.L	0.9958		2	1888.0039
4711	UBCP1_MOUSE	318	8.49	2	2	K.EIAKLDDFLELNHK.Y	0.9924		2	1685.9176
						K.GKPAENDVK.L	0.9958		1	958.0593
4712	UBE2B_MOUSE	152	12.5	1	12	K.LVIEFSEEYPNKPPTVR.F	0.9924		2	2019.3049
4713	UBE2F_MOUSE	185	16.76	2	7	K.LHCFQLTVSPDEGYYQGGK.F	0.9958		2	2200.3783
						R.DKVDEYIK.R	0.9958		1	1010.132
4714	UBE2K_MOUSE	200	16	2	14	R.LWAHVYAGAPVSSPEYTK.K	0.9958		2	1977.2267
						K.KIENLCAMGFDR.N	0.9958		2	1454.6502
4715	UBE2N_MOUSE	152	65.13	6	171	K.LELFLPEEYPMAAPK.V	0.9958	1,2		1749.0748
						R.YFHVVIAGPQDSPFEGGTFK.L	0.9958	2,3		2197.4546
						R.TVLLSIQALLSAPNPDDPLANDVAEQWK.T	0.9958		3	3020.4094
						R.LLAEPVPGIK.A	0.9958		1	1037.2877
						K.IYHPNVDK.L	0.9958		1	986.1155
						K.DKWSPALQIR.T	0.9929		2	1214.4099
4716	UBE2O_MOUSE	1288	8.23	4	4	R.LIHGEDSDSEGDDDGRGSSGCSEAGGAG	0.9958		3	3304.1743
						R.VDVSSKVEVVWADNSK.T	0.9958		2	1762.9573
						K.GPTRTPYEDGLYLFDIQLPNIYPAVPPHFC	0.9958		3	4444.9222
						R.LLFSHDLVSGR.Y	0.9958		2	1244.4361
4717	UBE2Z_MOUSE	356	8.15	2	10	R.LHLQGQTMQDPFGEK.R	0.9958		2	1729.9482
						R.GHFDYQSLLMR.L	0.9958		2	1367.5652

4718	UBE3A_MOUSE	885	5.31	2	6	R.YYHQLTEGCGNEACTNEFCASCPTFLR.M	0.9958	3	3287.3873
						K.YLFRPEEIELLICGSR.N	0.9943	2	1996.2799
4719	UBE4B_MOUSE	1173	4.52	3	4	K.FPTECFFLTLHAHHLSILPSCRR.Y	0.9924	3	2841.2201
						R.DLKVENPEK.Y	0.9958	1	1072.2035
						R.QMLTESMLEPVPELK.E	0.993	2	1746.0871
4720	UBIP1_MOUSE	540	8.33	2	13	K.QNENGEYTDHLHSASCQIKVFKPK.G	0.9909	3	2832.0679
						K.LTKEDLVQICGAADGIR.L	0.9958	2	1860.0838
4721	UBL4A_MOUSE	157	19.75	2	2	R.LVDSPATPIWQLISK.V	0.9958	2	1668.9738
						R.FLHPEVTEAMEK.G	0.9912	2	1431.6465
4722	UBP10_MOUSE	792	2.78	1	3	K.IAELLETVTLIHKPVSLQPR.G	0.9917	2	2258.7098
4723	UBP14_MOUSE	493	21.3	6	27	K.EKFEGVELNTDEPPMVFK.A	0.9952	2	2110.3863
						R.SSSSGHYVSWVR.R	0.9958	2	1352.449
						R.LPAYLTIQMVR.F	0.9958	2	1305.6214
						K.FPLMLDVYELCTPELQEK.M	0.9958	2	2226.5557
						R.LSGGGDWHIAYVLLYGPR.R	0.9944	2	1975.2572
						R.ASGEMASAQYITAALR.D	0.9958	2	1640.8517
4724	UBP15_MOUSE	981	3.98	2	3	K.WYYFDDSSVSTASEDQIVSK.A	0.9958	2	2328.4504
						K.RNDSIIVDIFHGLFK.S	0.9958	2	1775.0605
4725	UBP19_MOUSE	1360	4.41	2	2	R.GAVGGAKVAVPTGPTPLDSTPPGGGPHPL	0.9958	3	3377.7385
						K.GLCRPENIGYPFLVSVPASR.L	0.9958	2	2233.5413
4726	UBP29_MOUSE	869	2.99	2	4	K.VSYDDLIMPLSQLLVLK.D	0.9958	2	1948.3686
						R.DVEIK.G	0.9944	1	603.6934
4727	UBP2L_MOUSE	1107	7.23	5	6	R.RYPSSISSSPQK.D	0.9952	2	1337.4753
						R.AINVLLEGNPDTHSWEMVGK.K	0.9958	2	2211.4974
						K.QRPQATAEQIRLAQMISDHNDADFEEK.V	0.9944	3	3143.4149
						K.SANDSTVHSPFTK.R	0.9915	2	1391.4802
						K.QRPQATAEQIR.L	0.9936	2	1298.4446
4728	UBP34_MOUSE	3393	3.54	6	6	R.DIFNLLFLLPSLK.D	0.9944	1	1533.8944
						K.NYYYVVAKIFQIQFPLYTAYK.H	0.9958	2	2634.0924
						K.MIALVALLVEQSR.S	0.9913	2	1443.7881
						K.QLNPALIPTLQELLNK.C	0.9927	2	1806.1558
						R.EEELEDIKQFK.K	0.9958	1	1408.5481
						R.FVGLTNLGATCYLASTIQQLYMIPEARQAVI	0.9958	3	3778.3675
4729	UBP37_MOUSE	979	2.86	2	3	K.RSLGFLPQPTPLSVK.K	0.9958	2	1640.9664
						K.KIPFNALIR.R	0.9958	1	1072.339
4730	UBP4_MOUSE	962	5.93	2	3	K.SRPSSASSGAVLYGQPLLVSVPK.H	0.9958	2	2301.6481
						R.FAPQFSGYQQQDSQELLAFILDGLHEDLNF	0.9958	3	3481.8028

4731	UBP47_MOUSE	1376	1.38	1	8	K.FLEVDEYPEHIKNLVQK.E	0.9958	2	2102.3947
4732	UBP5_MOUSE	858	35.9	16	123	K.IFQNAPTDPTQDFSTQVAK.L	0.9958	2	2109.3
						R.YFDGSGGNNHAVEHYR.E	0.9958	2	1823.8784
						R.IGEWELIQESGVPLKPLFGPGYTGIR.N	0.9958	2	2858.3098
						K.LDVSIEMPEELDISQLR.G	0.9958	2	1988.2605
						R.KQEVQAWDGEVR.Q	0.991	2	1445.5748
						R.VDYIMQLPVPMDAALNKEELLEYEEK.K	0.9958	3	3082.5509
						R.QQDAQEFFLHLINMVER.N	0.9958	2	2119.4027
						K.LGTITPDGADVYSYDEDDMVLDPSLAEHLS	0.9958	3	4182.6169
						K.KFTFGLDWVPK.K	0.9958	2	1338.592
						K.LGHGLLSGEYSKPALESGDGEQVPEQK.E	0.9958	3	2827.0771
						R.VTSAVEALLSADSASR.K	0.9958	2	1577.7319
						R.GTGLQPGEEELPDIAPPLVTPDEPK.G	0.9958	2	2600.8823
						R.ENLWLNLTDGSILCGR.R	0.9958	2	1862.0588
						K.IVILPDYLEIAR.D	0.9958	1,2	1415.716
						K.KLDVSIEMPEELDISQLR.G	0.9958	2	2116.4345
						K.VPLPELVR.A	0.9944	1	923.1435
4733	UBP7_MOUSE	1103	2.81	2	2	K.INDRFEFPEQLPLDEFLQK.T	0.9958	2	2379.6745
						R.DLLEECKK.A	0.9958	1	1035.1486
4734	UBP8_MOUSE	1080	2.13	2	2	K.YVAVYNLIKK.R	0.9958	1	1211.4899
						R.EDSGAAAKR.S	0.9924	1	904.9554
4735	UBQL1_MOUSE	582	14.95	5	23	R.QLIMANPQMQQLIQR.N	0.9958	2	1813.1865
						R.FQQQLEQLSAMGFLNR.E	0.9958	2	1911.1858
						R.NPEISHMLNNPDIMR.Q	0.9958	2	1782.0424
						K.EKEEFAVPENSSVQQFK.E	0.9926	2	1997.1687
						R.ALSNLESIPGGYNALR.R	0.9943	2	1675.8821
4736	UBQL2_MOUSE	638	8.93	3	29	R.NPEISHLLNNPDIMR.Q	0.9958	2	1764.0093
						R.FQQQLEQLNAMGFLNR.E	0.9958	2	1938.2115
						R.NQDLALSNLESIPGGYNALR.R	0.9958	2	2146.3647
4737	UBQL4_MOUSE	596	18.12	5	35	R.LQLPVFLQQMQNPESLSILTNPR.A	0.9958	2	2668.1266
						R.FQQQLEQLNSMGFINR.E	0.9958	2	1954.2109
						R.AMQALLQIQQGLQTLQTEAPGLVPSLGSFC	0.9924	3	3452.994
						R.NPEISHMLNNPELMR.Q	0.9958	2	1796.0693
						R.HMIMANPQMQQLMER.N	0.9958	2	1859.2479
4738	UBR3_MOUSE	1889	2.22	2	4	K.AATAAHLK.A	0.9958	1	782.9181
						K.RDPLASTSSDALDSLQNSGTAQVFSLVAEF	0.9958	3	3137.3873
4739	UBR4_MOUSE	5180	3.34	8	18	K.LFSYCVKVK.V	0.9958	1	1144.3655

						K.KVQLTPGQTEVK.I	0.9958	2	1328.5516
						K.TFQEEFMPVETFSEFLDAAGLLSEITDPESI	0.9958	3	3770.1959
						K.HAAQELATLLLSLPAPASVQQQSK.S	0.9958	2	2502.8735
						K.YDELYSSLTTLLAAGSQLDTTR.R	0.9958	2	2419.6477
						K.LEQVSSDEGIGTLAENLLEALR.E	0.9958	2	2358.6079
						R.GLAMQHPATQVLIGTDSITSLHK.L	0.9958	2	2419.8016
						K.AGAQGDPDVPECLK.V	0.9944	1	1457.5463
4740	UBR5_MOUSE	2792	1.47	2	5	K.FTCIGALYSELLAVSSK.G	0.9958	1	1860.1236
						K.SSAGISSMPNITVGTQVCLR.N	0.9958	3	2079.3423
4741	UBXD1_MOUSE	442	23.53	5	11	R.INCLEGSHEFFEAIGFK.K	0.9941	2	1999.1963
						K.EEISPHLAVPGVFFICPLTGVTLR.R	0.9958	2	2654.0906
						K.SVLRPELLAAIEQLS.-	0.9958	2	1639.9328
						K.QAILSHFSTDPVAASIMK.I	0.9958	2	1917.2305
						K.KVTLPVPDQEGQEEFYVLGEDAR.A	0.9958	2	2620.8755
4742	UCHL1_MOUSE	223	43.95	4	27	R.MPFPVNHGASSEDSLLQDAAK.V	0.9958	2	2215.4425
						-.MQLKPMEINPEMLNK.V	0.9944	2	1817.2301
						R.FADVLGLEEETLGSVPSPACALLLLFPLTAC	0.9958	3	3957.4816
						K.VNFHFILFNNVDGHLYELDGR.M	0.9958	2	2520.8094
4743	UCHL3_MOUSE	230	50.87	7	35	R.WLPLEANPEVTNQFLK.Q	0.9958	2	1900.1845
						R.VTHETSAHEGQTEAPSIDEK.V	0.9958	2	2167.2505
						K.KFLEESVSMSPEER.A	0.9958	2	1668.8591
						K.TSDETLLEDAIEVCKK.F	0.9958	2	1852.0119
						K.QTISNACGTIGLIHAIANNK.D	0.9958	2	2097.3452
						K.TSDETLLEDAIEVCK.K	0.9958	2	1723.8378
						K.VDLHFIALVHVDGHLYELDGR.K	0.9912	2	2419.7453
4744	UCKL1_MOUSE	548	6.57	2	4	R.TTSQCKSEPPLLR.T	0.9958	2	1517.6886
						K.QITGVSILRAGETMEPALR.A	0.9931	2	2043.3892
4745	UCRI_MOUSE	274	62.04	12	699	K.EIDQEAAVEVSQLR.D	0.9958	1	1587.727
						K.NVVSQFVSSMSASADVLAMSK.I	0.9937	2	2159.4774
						R.GVAGALRPLLQGAVPAASEPPVLDVK.R	0.9958	2	2526.9823
						K.VPDFSDYR.R	0.9958	1	999.0679
						R.SGPFAPVLSATSR.G	0.9924	1	1290.4618
						R.KGPAPLNLEVPAYEFTSDDVVVVG.-	0.9958	2	2517.8383
						R.ESLSGQAAARPLVATVGLNVPASVR.F	0.9944	2	2464.8277
						R.AEVLDSTK.S	0.9944	1	862.9555
						K.EIDQEAAVEVSQLRDPQHDLDR.V	0.9958	2	2564.7282
						K.LSDIPEGK.N	0.9944	1	858.9671

						R.RAEVLDSTK.S	0.9944	1,2		1019.1429
						K.KEIDQEAAVEVSQLR.D	0.9958		2	1715.9011
4746	UCRP_MOUSE	161	12.42	1	12	R.GHSNIYEVFLTQTVDTLK.K	0.9958		2	2066.3183
4747	UD19_MOUSE	528	7.01	2	18	K.TYSISHTLEDLDREFK.Y	0.9932		2	1955.1314
						R.GHEVVVVIPEVSWQLGK.S	0.9958		1	1877.1937
4748	UFD1_MOUSE	307	5.86	2	3	K.KGVEPSPSPIKPGDIK.R	0.9958		2	1649.9279
						K.GVEPSPSPIKPGDIK.R	0.9958		2	1521.7539
4749	UFM1_MOUSE	85	55.29	3	20	K.VPAATSAIITNDGIGINPAQTAGNVFLK.H	0.9958		3	2755.1436
						K.FAAEEFKVPAATSAIITNDGIGINPAQTAGN\	0.9958		3	3578.0593
						K.HGSELRIIPR.D	0.9958		2	1178.3799
4750	UFSP1_MOUSE	217	7.83	1	2	K.DVHLGLPVPCHDPAR.L	0.9958		2	1683.8736
4751	UGDH_MOUSE	493	4.67	1	2	R.VLDGLHSELQTIGFQIETIGK.K	0.9945		2	2299.6293
4752	UGGG1_MOUSE	1527	4.13	2	2	K.VWQLQDLSFQTAARILAASGALSLVVMK.D	0.9924		2	3018.5878
						R.GQYQGLSQDPNSLSNLDQDLPNNMIHQVF	0.9958		3	3465.8193
4753	UGPA_MOUSE	508	71.46	24	1059	K.TLDGGLNVIQLETAVGAAIK.S	0.9958		2	1984.3006
						K.TYNTDVPLVLMNSFNTDEDTK.K	0.9958		2	2418.6344
						K.AMSQDGASQFQEVILQELELSVK.K	0.9958		2	2551.8713
						K.IFNTNNLWISLGAVK.R	0.9958		2	1690.9829
						R.NENTFLDLTVQQIEHLNK.T	0.9958		2	2157.3879
						K.IQRPPEDSIQPYEK.I	0.9958		2	1700.8889
						R.RFESIPDMLELDHLTVSGDVTFGK.N	0.9956		2	2708.0583
						K.ILTTAASHEFEHTK.K	0.9958		2	1585.7569
						K.ILTTAASHEFEHTKK.D	0.9958		2	1713.931
						R.GLPDNISSVLNK.L	0.9958		2	1257.4295
						R.EFPTVPLVK.L	0.9924		1	1030.2523
						K.GTVIIIANHGDR.I	0.9944		2	1266.4428
						K.RCEFVMEVTNK.T	0.9958		2	1413.5977
						K.DVSYSGENTEAWYPPGHGDIYASFYNSGL	0.9958		3	4231.4878
						K.RLQEQNAIDMEIIVNPK.T	0.9929		2	2012.3318
						K.SFENSLGINVPR.S	0.9958		1	1333.4869
						K.TTSDLLLVMSNLYSLNAGSLTMSEK.R	0.9931		2	2690.0963
						R.LQEQNAIDMEIIVNPK.T	0.9943		2	1856.1443
						K.LNGGLGTSMGCK.G	0.9958		1	1195.3423
						R.FESIPDMLELDHLTVSGDVTFGK.N	0.9944		2	2551.8708
						K.EYIFVSNIDNLGATVDLYILNHLMNPPNGK.I	0.9958		3	3376.8518
						R.CEFVMEVTNK.T	0.9958		1	1257.4102
						K.TYNTDVPLVLMNSFNTDEDTKK.I	0.9958		2	2546.8085

						R.LVEIAQVPK.A	0.9958		1	997.223
4754	ULA1_MOUSE	534	24.16	5	14	K.NLVLPGIGSFTIIDGNLVSGEDAGNNFFLQK	0.9958	2,3		3251.6635
						R.LWGDHGQEALESAHVCLINATATGTEILK.N	0.9958		3	3136.4547
						K.NVNTALNTTQIPSSIEDIFNDDR.C	0.9958		2	2578.7521
						R.YGAAEPHTIAAFLGGAAAQEVIK.I	0.9958		2	2286.5926
						R.YPGVSNYQVEEDIGK.L	0.9958		2	1698.8266
4755	ULK4_MOUSE	1303	6.14	2	2	R.DELLPQYEHILMEPDPVPAYALKLLVAMTEI	0.9958		3	4264.9442
						R.LVEESKLVPLIFEVILEHQESILGNTMQSVIA	0.9944		3	4610.4499
4756	UN13A_MOUSE	1712	2.34	2	2	R.VPEYPAWFEPFVIQWLDENEEVSR.D	0.9958		3	2981.2903
						K.QYFHAGGVGLKK.T	0.9958		1	1305.5223
4757	UN13B_MOUSE	1591	5.28	3	8	R.ILSQRSNDEVAR.E	0.9958		2	1388.5235
						K.YMCPGVPAVMSTLMANINAYYAHTTASTN\	0.9958		3	4590.1228
						K.DHVLGPQESLPEETASSPFTQAR.A	0.993		2	2497.6806
4758	UN45B_MOUSE	931	25.03	14	77	R.DGLQNYEALLGLTNLSGR.S	0.9958		2	1935.1442
						K.DDFVQDIPALQAMFELAK.A	0.9958		2	2052.3497
						R.VYEVVRPLVSLLDTQR.D	0.9934		2	1888.2175
						R.RLNTSIQEQLR.V	0.9958		2	1358.5405
						K.ALPDIENYMFENHDQLR.Q	0.9958		2	2106.3172
						K.QITSHLLDMLVSK.K	0.9958		2	1485.7821
						K.NVNAIQTVSGILQGPFDLGNQLLGMK.G	0.9958		2	2729.1669
						R.GLVIAHNLLSADAELAR.K	0.9958		2	1764.0348
						K.EEALVLDTKK.D	0.9958		1	1146.3263
						R.DQALNLLNK.N	0.9944		1	1029.1814
						K.VVGQVPDLPSCLPLTDNTR.M	0.9958		2	2082.3276
						R.MLASILINKLYDDLR.C	0.9944		1	1779.148
						R.LCLHDQLSVQHR.G	0.9958		2	1506.6708
						R.KICEEYITSK.F	0.9958		2	1271.4193
4759	UQCC_MOUSE	295	6.44	1	13	K.NPQSILKPHAPTYNDEGL.-	0.9958		2	1995.1992
4760	UROK_MOUSE	433	9.47	2	3	K.MLCAADPEWK.T	0.9944		1	1221.3797
						R.SIQTICLPPRFTDAPFGSDCEITGFGK.E	0.9958		3	3016.3095
4761	UROL1_MOUSE	1319	3.49	2	3	R.EDPGLRNHTR.L	0.9958		1	1195.2803
						R.DFVALNVTSSSFHVSWSLNSTQNYNFHIQ\	0.9958		3	3735.1064
4762	US6NL_MOUSE	819	8.55	4	7	K.SHSALPALPVAIPGSAETRLPNSR.Q	0.9958		2	2442.7806
						K.YAVEGKSHSALPALPVAIPGSAETR.L	0.9958		3	2522.8638
						R.DAHRSHLSNLPNYAAFQHIPFQAHGLPEVS	0.9958		3	4009.4355
						K.SHSALPALPVAIPGSAETR.L	0.9958		2	1875.135
4763	USH2A_MOUSE	5193	3.16	5	6	R.AQSINGSSVEVAWNEPAVVK.G	0.9958		2	2086.3091

						K.EAPPENMDPPTLHITGPESIEITWTPPR.N	0.9958		3	3127.4957
						R.LELFPIPSASLSYEVTGLQPFTVYEFR.L	0.9958		3	3105.5573
						R.TLHDSVTDSVSSVIQVGQSLNGSEQFVGR	0.9944		3	3726.0692
						R.VNQDGCLSSDSTVNCGGNDSILVYRGSQ	0.9958		3	5066.3486
4764	USMG5_MOUSE	58	22.41	1	2	K.KYFNSYTLTGR.M	0.9958		2	1350.5168
4765	USO1_MOUSE	959	15.22	7	8	K.EQDDLLVLLADQDQK.I	0.9958		2	1743.9085
						R.LEVGIQAMEHLIHVLQTDR.S	0.9958		2	2203.5645
						R.TAIQKQLDSSNSTIAILQTEK.D	0.9945		2	2290.5761
						R.ASQKPQPNFPSPEYMIFDHEFTK.L	0.9958		3	2740.0619
						K.SVPVEGESEHVSAAK.T	0.9924		2	1526.6433
						K.TLEQHDNIVTHYK.N	0.9958		2	1598.7557
						R.LLTSLLKQLGPPVQQIILVSPMGVSR.L	0.9958		3	2789.4363
4766	USP9X_MOUSE	2559	3.83	6	6	R.TGETGVEETILEGHLGVTK.E	0.9958		2	1971.1717
						R.NHQNLLDSLEQYVK.G	0.9958		2	1701.8766
						K.LMGDEPDLDPDINK.D	0.9944		2	1572.7272
						K.WTWAVEWLGDELER.R	0.9958		2	1790.9726
						R.ELDMEPYTVAGVAK.L	0.9958		2	1523.7412
						K.KLPPVLAIQLK.R	0.9944		1	1220.5846
4767	UTP15_MOUSE	528	2.27	1	4	K.FIVLQELVEK.E	0.9958		1	1218.479
4768	UTP20_MOUSE	2788	1.83	2	24	R.EAAEEKAGAGGK.M	0.9958		1	1118.1888
						K.GRGAVAEEEEEEEPAAGEDEELEEEAVPT	0.9958		3	3770.8177
4769	V2R26_MOUSE	855	7.6	4	5	K.YYQHILAMVFAIEK.I	0.9958		2	1727.0741
						K.IITWGK.H	0.9924		1	717.8864
						K.VTEYSSMDTVNWK.H	0.9958		2	1560.7186
						K.EVSAIKLDIFNYQSLQSGTEAHVK.V	0.9958		2	2679.0019
4770	VAMP2_MOUSE	116	16.38	2	8	R.LQQTQAQVDEVVDIMR.V	0.9958		2	1874.1193
						R.RLQQTQAQVDEVVDIMR.V	0.9958		2	2030.3067
4771	VAMP3_MOUSE	103	18.45	2	9	R.LQQTQNQVDEVVDIMR.V	0.9958		2	1917.1443
						R.RLQQTQNQVDEVVDIMR.V	0.9958		2	2073.3318
4772	VAPA_MOUSE	249	28.11	4	29	K.HEQILVLDPPSDLK.F	0.9958		2	1604.8437
						K.FKGPFTDVVTTNLK.L	0.9958		2	1567.8253
						K.FMVQTIFAPPNISDMEAVWK.E	0.9958		2	2325.7456
						K.VAHSDKPGSTSAVSFR.D	0.9958		2	1646.8002
4773	VAPB_MOUSE	243	20.99	3	26	K.FRGPFTDVVTTNLK.L	0.9958		2	1595.8387
						K.VEQVLSLEPQHELK.F	0.9958		2	1649.8846
						R.CVFELPAENAKPHDVEINK.I	0.9958	2,3		2211.4455
4774	VASN_MOUSE	673	5.05	2	2	R.YLQGNTVQLRSLR.L	0.9958		1	1548.7855

						R.HIQPGAFDALDRLLELK.L	0.9958		1	1937.2492
4775	VATA_MOUSE	617	14.26	5	15	K.EILQEEEDLAEIVQLVGK.A	0.9958		2	2056.3178
						R.VGSHITGGDIYGIVNENSLIK.H	0.9958		2	2187.4576
						K.ADYAQLLEDMQNAFR.S	0.9958		2	1785.969
						R.VGHSELVGEIIR.L	0.9958		1	1309.5082
						K.LPANHPLLTGQR.V	0.9958		2	1317.5338
4776	VATB2_MOUSE	511	36.4	9	61	K.TVSGVNGPLVILDHVK.F	0.9958		2	1648.9432
						R.QIYPPINVLPSLSR.L	0.9958		2	1597.898
						K.RIPQSTLSEFYPR.D	0.9958		2	1594.8106
						K.IPIFSAAGLPHNEIAAQICR.Q	0.9929		2	2179.4931
						R.YAEIVHLTLPDGTK.R	0.9958		2	1557.7869
						K.RSGQVLEVSGSK.A	0.9958		2	1247.394
						R.NGSITQIPILTMPNDDITHPIPDLTGYITEGQ	0.9958		3	4113.6289
						R.GIVNGAAPELPVPTGGPMAGAR.E	0.9958		2	2033.3532
						R.GPVVLAEDFLDIMGQPINPQCR.I	0.9958		2	2470.8121
4777	VATC2_MOUSE	427	4.22	1	2	R.TAAYSVLKANLENLEK.R	0.993		2	1765.0165
4778	VATE1_MOUSE	226	13.27	3	3	K.KIQMSNLMNQAR.L	0.9956		2	1434.7149
						R.DDLITDLLNEAK.Q	0.9958		2	1360.5041
						R.ARDDLITDLLNEAK.Q	0.9958		2	1587.7703
4779	VCAM1_MOUSE	739	2.84	1	4	K.DPEIQFSGPLEVGKPVTVK.C	0.9958		2	2041.3519
4780	VCIP1_MOUSE	1220	5.49	4	4	K.HFPGEFGSEILVQK.V	0.9924		2	1588.8033
						K.YIKLEEDGGCVIGGDR.S	0.9958		2	1781.9263
						K.GRAEGGPSTAAHSAHTVK.Q	0.9958		1	1734.8692
						K.ELMPPQAGMEK.E	0.9958		1	1231.4676
4781	VDAC1_MOUSE	296	79.39	20	4597	K.VNNSSLIGLGYTQTLKPGIK.L	0.9958		2	2104.4545
						K.KLETAVNLAWTAGNSNTR.F	0.9958		2	1947.1582
						K.WNTDNTLGTEITVEDQLAR.G	0.9958		2	2177.3324
						K.SENGLEFTSSGSANTETTK.V	0.9958	1,2		1961.0032
						K.YQVDPDACFSAK.V	0.9958		1	1401.4816
						K.LTFDSSFSPNTGK.K	0.9944		1	1401.5157
						R.WTEYGLTFTEK.W	0.9958		1	1375.5206
						K.LETAVNLAWTAGNSNTR.F	0.9958		2	1818.9841
						K.TKSENGLEFTSSGSANTETTK.V	0.9958		2	2190.2823
						R.VTQSNFAVGYK.T	0.9958		1	1214.3635
						R.EHINLGCDVDFDIAGPSIR.G	0.9958		2	2129.3001
						R.GALVLGYEGWLAGYQMNFETSK.S	0.9958		2	2435.7565
						K.REHINLGCDVDFDIAGPSIR.G	0.9958		2	2285.4876

						K.TDEFQLHTNVNDGTEFGGSIYQK.V	0.9958	2	2601.7454
						R.VTQSNFAVGYKTDEFQLHTNVNDGTEFGG	0.9958	3	3797.0857
						K.LTLSALLDGK.N	0.9958	1,2	1031.2377
						K.LTFDSSFSPNTGKK.N	0.9958	2	1529.6897
						K.LGLGLEFQA.-	0.9924	1	948.1069
						K.GYGFGLIK.L	0.9944	1	855.0245
						K.SRVTQSNFAVGYK.T	0.9958	2	1457.6292
4782	VDAC2_MOUSE	295	71.86	11	293	K.VNNSSLIGVGYTQTLRPGVK.L	0.9958	2	2104.4141
						K.WNTDNTLGTEIAIEDQICQGLK.L	0.9958	2	2520.7217
						K.VCEDFDTSVNLAWTSGTNCTR.F	0.9958	2	2434.5104
						R.TGDFQLHTNVNNGTEFGGSIYQK.V	0.9958	2	2528.6971
						K.SCSGVEFSTSGSSNTDTGK.V	0.9958	2	1908.8933
						K.WCEYGLTFTEK.W	0.9924	1,2	1434.5543
						K.LTFDTTFSPNTGK.K	0.9944	1	1429.5694
						K.YQLDPTASISAK.V	0.9944	1	1294.4472
						K.GFGFGLVK.L	0.9944	1	824.9982
						R.ECINLGCDVDFDFAGPAIHGSAVFGYEGWI	0.9958	3	4518.8864
						K.LTLSALVDGK.S	0.9924	1	1017.2108
4783	VDAC3_MOUSE	283	45.23	8	206	K.VNNASLIGLGYTQTLRPGVK.L	0.9958	2	2102.4416
						R.IETSINLAWTAGSNNTR.F	0.9958	2	1849.0104
						K.LSQNNFALGYK.A	0.9958	2	1255.416
						K.AADFQLHTHVNDGTEFGGSIYQK.V	0.9931	2	2536.7197
						K.NFNAGGHK.V	0.9924	1	844.9053
						K.WNTDNTLGTEISWENK.L	0.9958	2	1909.019
						K.LTLDTIFVPNTGK.K	0.9958	1	1419.661
						K.LTLSALIDGK.N	0.9958	1	1031.2377
4784	VGFR2_MOUSE	1367	5.78	4	14	R.GAFGQVIEADAFGIDK.T	0.9958	2	1638.8174
						K.TGYLSIVMDPDELPLDERCER.L	0.9958	2	2509.7566
						R.AASVGLPGDFLHPPKLSTQK.D	0.9943	2	2064.3922
						R.VVGNDTGAYKCSYR.D	0.9924	1	1590.699
4785	VIGLN_MOUSE	1268	17.59	13	24	R.DKFPEVIINFPDPAQK.S	0.9958	2	1859.132
						R.EENPVHSVEPSIQENGDEAGEGREAK.E	0.9958	3	2808.8889
						K.ASVITQVFHVPLEER.K	0.9958	2	1725.9853
						K.IQIPRPDDPSNQIK.I	0.9958	2	1621.8338
						K.FPEVIINFPDPAQK.S	0.9958	2	1615.8693
						K.ANSFTVSSVSAPSWLHR.F	0.9958	2	1847.0403
						K.FLIGKGGGK.I	0.9924	1	877.0745

						K.IVGELEQMVSEDVPLDHR.V	0.9958		2	2067.3215
						K.APDMSSSEEFPSFGAQVAPK.T	0.9958		2	2083.277
						R.SIMEECGGVHIHFPVEGSGSDTVVIR.G	0.9958		2	2814.1084
						R.RCDIIIISGR.K	0.9958		2	1203.3935
						R.IIFPAAEDKDQDLITIIGK.E	0.9958		2	2101.4479
						K.RELLELASR.M	0.9912		2	1087.2645
4786	VIME_MOUSE	466	46.14	15	401	R.KVESLQEEIAFLK.K	0.9937		2	1534.793
						R.LLQDSVDFSLADAINTEFK.N	0.9958		2	2127.3557
						R.ISLPLPTFSSLNLR.E	0.9958		2	1558.8613
						R.LQDEIQNMKEEMAR.H	0.9956	1,2		1735.9679
						R.TYSLGSALRPSTSR.S	0.9924		2	1496.6634
						K.KLHDEEIQELQAQIQEQHVQIDVDVSKPDL	0.9944		3	4039.4918
						R.ETNLESLPLVDTHSK.R	0.9958	1,2		1683.8559
						K.ILLAELEQLK.G	0.9958	1,2		1170.435
						R.FANYIDK.V	0.9924		1	870.9805
						R.EMEENFALEAANYQDTIGR.L	0.9958		2	2202.357
						R.EMEENFALEAANYQDTIGRLQDEIQNMK.E	0.9933		3	3302.6119
						R.QVQSLTCEVDALK.G	0.9958		2	1491.6477
						R.SLYSSSPGGAYVTR.S	0.9915		2	1445.5718
						K.LHDEEIQELQAQIQEQHVQIDVDVSKPDLT	0.9958		3	3911.3177
						K.FADLSEAANR.N	0.9944		1	1094.1692
4787	VINC_MOUSE	1066	48.12	31	184	R.VDQLTAQLADLAAR.G	0.9952		2	1485.6805
						R.VLQLTSWDEDAWASK.D	0.9958		2	1749.9176
						R.ALASIDSK.L	0.9958		1	804.9188
						R.GILSGTSDLLLTFDEAEVR.K	0.9958		2	2037.2744
						K.AIPDLTAPVAAVQAAVSNLVR.V	0.9958		2	2077.4319
						R.NPGNQAAYEHFETMK.N	0.9958		2	1737.8841
						K.AQMQEAMTQEVSDVFSDTTTPIK.L	0.9958		2	2558.8349
						K.AQQVSQGLDVLTAK.V	0.9958	1,2		1458.6549
						R.TNISDEESEQATEMLVHNAQNLMQSVK.E	0.9958		3	3048.3235
						K.SLLDASEEAIKK.D	0.9941		2	1304.4833
						K.KIDAAQNWLADPNGGPEGEEQIR.G	0.9958		2	2509.6946
						R.AANFENHSGR.L	0.9958		2	1103.1392
						R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	0.9958		3	3103.5146
						K.LLAVAATAPPDAPNREEVFDER.A	0.9958		2	2382.6353
						K.CDRVDQLTAQLADLAAR.G	0.9958		2	1917.0954
						K.TISPMVMDAKAVAGNISDPGLQK.S	0.993		2	2344.7468

						K.LVQAAQMLQSDPYSVPAR.D	0.9958	2	1975.2701
						K.MLGQMTDQVADLR.A	0.9932	2	1478.7217
						R.IPTISTQLK.I	0.9924	1	1001.2114
						K.AVAGNISDPGLQK.S	0.9932	2	1270.4282
						R.DPNASPGDAGEQAIR.Q	0.9958	2	1498.5492
						K.GILEYLTVAEVVETMEDLVTYTK.N	0.9958	2	2618.0113
						K.VAMANIQPQMLVAGATSIAR.R	0.9958	2	2043.4504
						K.GWLRDPNASPGDAGEQAIR.Q	0.9958	2	2011.1612
						K.QVATALQNLQTK.T	0.9958	2	1315.5125
						R.EAFQPQEPDFPPPPPDLEQLR.L	0.9957	2	2448.6941
						R.ALASQLQDSLK.D	0.9924	1	1174.3397
						R.ELTPQVISAAR.I	0.9958	1	1185.3659
						R.MALLMAEMSR.L	0.9934	2	1153.4585
						K.ELLPVLISAMK.I	0.9958	1	1214.5493
						K.MSAEINEIIR.V	0.9958	1	1176.3734
4788	VINEX_MOUSE	733	10.23	5	6	R.KMPDLQLDWTLEDPPK.V	0.9958	2	1927.2226
						R.SSVDSPRDWYR.R	0.9924	1	1368.4484
						R.SQTQSLNTPGPTLSHPR.A	0.9958	2	1821.9877
						R.SAFPFPITLQEPR.S	0.9958	2	1503.741
						R.KVNEHWYEGR.I	0.9958	2	1318.4343
4789	VIP2_MOUSE	1129	4.52	3	4	K.AAAGGPSQAMAPHTSSR.M	0.9958	2	1597.7459
						R.FFVGPEDAEINPGNYR.R	0.9924	2	1825.975
						R.YAILNRDPNNPK.E	0.9958	1	1415.5919
4790	VLDLR_MOUSE	873	19.24	8	17	R.EPASIAVDPLSGFVYWSDWGEPAK.I	0.9958	2	2622.8933
						R.HSASVGHTYPAISVVSTDDDLA.-	0.9958	2	2243.3917
						K.SLEFLAHPLALTIFEDR.V	0.9958	2	1973.2792
						R.VYWIDGENEAVYGANK.F	0.9929	2	1828.9757
						R.RPLVTEDIQWPNGITLDLVK.S	0.9958	2	2308.683
						R.CDGDPDCKDGSDEVNCPSR.T	0.9958	2	2184.0897
						R.LYWLDSKLHMLSSVDLNGQDR.R	0.9958	2	2491.8242
						K.CPTSEIQCGSGECIHK.K	0.9958	2	1863.9173
4791	VNN3_MOUSE	500	10	2	2	K.DTQVDSVLLPTAWYNTLPLLSAVPFHSVW/	0.9958	3	3499.0062
						R.GGAPLPILVMALYGR.V	0.9944	2	1528.8963
4792	VNS2_MOUSE	185	4.32	1	3	K.EFIQHK.G	0.9924	1	801.9206
4793	VP13A_MOUSE	3166	3.06	4	8	K.GLVGAVTRPTGGIIDMASSTFQGIK.R	0.9958	2	2477.8816
						R.SVTMDSAPKPFTDVSIVMRSAGHSQISR.I	0.9944	3	3006.4217
						K.GLVSGFVSGITGIVTKPIK.G	0.9958	2	1874.2743

						R.SFQIQASALPVSHISQK.L	0.9958	2	1842.1051
4794	VP13B_MOUSE	4013	1.4	3	9	K.DFLNGPADIYLDVSKPLK.A	0.9958	2	2006.3061
						K.GALTSITNLATSLARNMGR.L	0.9958	2	1948.2481
						R.ISLMTYSSVALPK.F	0.9958	2	1410.7119
4795	VP13C_MOUSE	3748	4.62	8	8	R.QTAAGRVK.M	0.9958	1	830.9627
						K.LSRTAIQPGTSHPDIQLLHPINLEFFVSR.N	0.9958	3	3288.777
						K.KNPIQDK.S	0.9944	1	842.9707
						K.IEFETNPENSPADQTLIVQSQPVEVIYDAK.T	0.9958	3	3376.6984
						R.GVVGGVTGIITKPVEGAK.K	0.9943	2	1683.0012
						R.VAESTEEVSSLRPPR.L	0.9958	2	1657.821
						K.QEMIAIHSVNLLLK.S	0.9958	1	1609.9677
						R.NLSAAWYTQIPGMEIKGELKPMQVALSQDI	0.9958	3	4021.7378
4796	VP33B_MOUSE	617	7.78	4	6	K.LYKVENKPALSANEQLCFLVRPR.I	0.9904	2	2747.1791
						K.LNLIPR.V	0.9944	1	725.9095
						K.NMRYIASLVNADK.L	0.9958	1	1495.7368
						K.VENKPALSANEQLCFLVRPR.I	0.9924	3	2342.6696
4797	VP37B_MOUSE	285	23.51	3	4	R.VGLPSQQGFSAQLVSPYPPALPQRPPPR.M	0.9944	3	2986.4465
						K.FLDGELPLDSFIDVYQSK.R	0.9955	2	2087.3337
						K.YQELQVLFEAYQIKK.T	0.9958	2	1901.2127
4798	VP37C_MOUSE	352	17.61	3	8	K.FSSALQPGTLLDLLQIEGMK.I	0.9958	2	2162.5494
						R.SLAEQNLEFQGPLEISR.S	0.9958	2	1932.1405
						K.DKTLQELEEMQNDPEAIAR.L	0.9931	2	2231.4394
4799	VPS11_MOUSE	941	5.63	4	4	K.LQKQSQQIAQDELR.V	0.9944	1	1685.8778
						K.KNLFEMAINLAK.S	0.9958	1	1392.6996
						K.DYPRVELDTHGCGLR.C	0.9958	2	1788.9237
						K.LEMLFK.K	0.9958	1	781.0008
4800	VPS25_MOUSE	176	20.45	2	3	K.QLAAWCSLVLSFCRLHK.Q	0.9958	2	2090.4083
						R.KLPVESIQIVLEELR.K	0.9958	2	1767.1191
4801	VPS29_MOUSE	182	17.58	3	6	K.TLAGDVHIVR.G	0.9958	2	1081.2602
						K.IQHILCTGNLCTK.E	0.9958	2	1558.7504
						K.ESYDYLKTLAGDVHIVR.G	0.9958	2	1980.2279
4802	VPS35_MOUSE	796	8.79	4	7	K.LNLEHIATSSAVSK.E	0.9958	2	1470.6659
						R.SDDPDQQYLILNTAR.K	0.9958	2	1749.8748
						K.HFHPLFEYFDYESR.K	0.9958	2	1888.0483
						K.IREDLPNLESSEETEQINK.H	0.9958	2	2245.4051
4803	VPS36_MOUSE	386	4.4	1	2	R.RWETVPVSQSLQTNK.G	0.9958	2	1773.9865
4804	VPS41_MOUSE	853	5.04	2	2	R.GFQENECRDYHLEYSEGESLFYVVSPR.D	0.9924	3	3312.4987

						R.NFVEETVYLLSR.M	0.9958	1	1470.6653
4805	VPS4A_MOUSE	437	12.81	3	4	R.LYQHAVEYFLHAIK.Y	0.9958	2	1733.0226
						R.SLATTRPTVNADDLLK.V	0.991	2	1715.9444
						R.LHLGSTPHNLTDANIHELAR.K	0.9958	2	2210.4575
4806	VPS4B_MOUSE	444	13.74	3	7	R.ENKPSIIFIDEIDSLCGSR.S	0.9924	2	2194.4125
						R.SLSSTKPTVNEQDLLK.L	0.9958	2	1760.9823
						R.LHLGSTQNSLTEADFQELGR.K	0.9943	2	2217.4001
4807	VPS53_MOUSE	832	10.7	4	9	K.QNVPIIRDNLASTR.K	0.9944	2	1597.8148
						K.CMVQCSQLSTGEPMIALTTIFQKYLR.E	0.9958	3	3077.5565
						K.LESPPPSTNPFLEDETTPEMEELALEKGEL	0.9958	3	3827.2026
						R.RLDDNIR.T	0.9944	1	901.9981
4808	VRK2_MOUSE	503	5.57	2	2	K.TNLLDELPESVLK.W	0.9958	1	1471.691
						K.TNLLDELPESVLKWAPSGSSCSELVK.Y	0.9931	3	2861.1847
4809	VRK3_MOUSE	453	17	2	2	R.LLDALEYLHENEYVHGNLTAENVFVNPEDL	0.9958	3	4945.4529
						R.VTTSLQALATGTELTDQNGKHWTLGALQIF	0.9944	3	3225.6292
4810	VTDB_MOUSE	476	35.92	10	113	K.DLCGQSTTQAMDQYTFELSR.R	0.9958	2	2352.5007
						K.FSSSTFEQVNQLVK.E	0.9958	2	1614.7954
						R.RTQVPEVFLSK.V	0.9944	2	1304.5321
						K.VPTANLENVLPLAEDFTEILSR.C	0.993	2	2442.7716
						K.HLSLLTTMSNR.V	0.9958	2	1273.4931
						R.KFSSSTFEQVNQLVK.E	0.9943	2	1742.9695
						K.NYLSMVGSCCTSANPTVCFVK.E	0.9958	2	2396.6157
						K.GQEMCADYSENTFTEYK.K	0.9958	2	2074.1458
						R.CCESTSEDCMASELPEHTIK.I	0.9958	2	2385.457
						K.SCESDAPFPVHPGTPECCTK.E	0.9958	2	2277.3475
4811	VTNC_MOUSE	478	22.38	5	45	K.LIQDVWGIEGPIDAAFTR.I	0.9958	2	2002.2774
						R.IYVTGSLSHSAQAK.K	0.9958	2	1462.6457
						R.RVDSVNPPYPR.S	0.9958	2	1300.4599
						R.GQYCYELDETAVRPGYPK.L	0.9958	2	2147.3148
						K.VEQQEEILRPDTTDQGTPEFPEEELCSGKF	0.9958	3	4398.7005
4812	VWA3A_MOUSE	1148	4.44	2	4	K.FEKLTLADLISQGTVELEDCNNAVPK.V	0.99	2	2906.2257
						R.SCPDQPSEFLSDFIQQSTLGR.S	0.9932	2	2413.5689
4813	VWF_MOUSE	2813	3.84	4	5	K.GDDFLTPAGLVEPLVVDFGNAWK.L	0.9958	2	2461.7765
						R.YVTSQIHGARPGASK.A	0.9958	1	1572.7641
						R.TNTGQALQYLSEHSFSPSQGDRVEAPNLV	0.9958	3	4553.9581
						K.VIAPATFHTICQQDSCHQER.V	0.9958	2	2399.5573
4814	WAPL_MOUSE	1200	3.67	2	6	R.SEDCILSLDNESLLEMK.D	0.9958	2	1997.1879

						R.CLRVLESVTVHNPENQSYLIAYK.D	0.9944		3	2735.0783
4815	WASP_MOUSE	520	8.46	1	3	R.QEPLPPPPPPCRGGGGGGGGGGGGGGG	0.9958		3	3686.0073
4816	WD40C_MOUSE	469	11.73	2	5	R.QQNIKPLCSREGGTGVR.S	0.9958		2	1901.099
						K.ASEVEQGAGTSSLPGRAAAAAGTGQADGI	0.9958		3	3124.4349
4817	WDFY3_MOUSE	3508	2	2	2	K.DDLQLLFSAITSWCPPYNLPWRK.S	0.9958		3	2822.2018
						R.QHALMTIQQLVLSPNGEDDMGTLLGLMHS	0.9958		3	4728.4946
4818	WDR1_MOUSE	606	66.34	21	255	K.AHDGGIYAISWSPDSTHLLSASGDK.T	0.9958		2	2586.7771
						R.NIDNPAIADIYTEHAHQVVVAK.Y	0.9958		2	2419.6995
						K.FGAVFLWDTGSSVGEITGHNK.V	0.9958		2	2223.4497
						K.KVFASLPQVER.G	0.9929		2	1274.5058
						R.LATGSDDNCAAFFEGPPFK.F	0.9958		2	2045.1786
						K.SYIYSGSHDGHINYWDSETGENDSFSGK.G	0.9958	2,3		3154.2024
						K.YAPSGFYIASGDISGK.L	0.9958		2	1633.7979
						R.IWDTTQK.E	0.9944		1	891.9994
						K.VFASLPQVER.G	0.9958		2	1146.3317
						K.DHLLSISLSGYINYLDK.N	0.9958		2	1952.2145
						R.DYSGQGVVK.L	0.9958		1	953.0397
						R.VYSILASTLKDEGK.L	0.9958		2	1524.7545
						R.MTVNESEQLVSCSMDDTVR.Y	0.9958		2	2202.3792
						R.FATASADGQIFIYDGK.T	0.9958		2	1704.8767
						K.GPVTDVAYSHDGAFLAVCDASK.V	0.9958		2	2281.4498
						K.SIQCLTVHR.N	0.9948		2	1114.256
						R.FVNCVRFSPDGNR.F	0.9958		2	1568.6983
						K.IWDVNVNSVVSTFPMGSNVLDQQLGCLWC	0.9958		3	3436.8733
						R.LHHVSSLAWLDEHTLVTTSHDASVK.E	0.9958		3	2785.0886
						K.GDHFLYTNGK.C	0.9958		1	1152.2517
						K.IVCLAWSPDNEHFASGGMDMMVYVWTLSI	0.9958		3	4016.5566
4819	WDR13_MOUSE	485	12.99	2	2	R.AVYEDRPPGSVVPTSVAEASR.A	0.9958		2	2188.402
						K.AAVNKLQGHSAPVLDVSFNCDESLLASSD/	0.9958		3	4046.5104
4820	WDR19_MOUSE	1341	1.42	1	2	R.NAHDVLFSMYAELKAQK.I	0.9948		2	1966.2622
4821	WDR23_MOUSE	549	5.1	2	3	R.GSFSLGEQSR.V	0.9958		1	1068.1313
						R.TALQQSFPQMLHQR.E	0.9958		2	1685.9414
4822	WDR26_MOUSE	641	20.75	5	11	R.LALLNVATQGVHLWDLQDR.V	0.9944		2	2163.4844
						K.RSELPIAELTGHTR.T	0.9958		2	1580.7843
						K.RLSQSDEDVIR.L	0.9924		1	1318.4294
						K.TLEGHAYGVSYIAWSPDDSYLVACGPDDC	0.9958		3	4933.287
						K.AENDLNELKPLVHSPHAIVVRGALEISQTLL	0.9958		3	3917.5876

4823	WDR57_MOUSE	358	18.16	2	2	K.RPRHELLLGAAGAGPGAGPQQATPGALLQ	0.9958	3	3284.7518
						K.LPGHAGSINEVAFHPDEPIILSASSDK.R	0.9958	2	2803.1009
4824	WDR59_MOUSE	992	6.15	2	2	K.RKPSTAVEYLAAHLSK.I	0.9958	3	1772.0574
						R.DVQTLAMLCSVFEAQSRPQGLPNPFGPFP	0.9958	3	4543.0827
4825	WDR60_MOUSE	999	2.9	2	2	R.DQEAEKAHSR.G	0.9958	2	1171.2119
						R.VQRQTVVSVHDLPEK.A	0.9958	2	1735.981
4826	WDR61_MOUSE	305	17.05	3	4	R.TCIHTFFDHQDQVWGVK.Y	0.9958	2	2119.3099
						K.ENIETVVTGSLDDLVK.V	0.9958	2	1732.9256
						K.LLHTLEGHAMPIR.S	0.9958	2	1488.7911
4827	WDR93_MOUSE	695	2.88	1	5	K.NWIVPAIYHPVAEIQLDK.M	0.9944	2	2107.46
4828	WFDC1_MOUSE	211	10.43	1	3	R.TLPPGACQATRCQADSECPR.H	0.9956	2	2276.3663
4829	WHRN_MOUSE	918	8.71	3	4	R.LLSANVRQLHQALTALLSEPER.E	0.9944	3	2460.8393
						K.SPSEDLPGIKPPPPPPPLAQGHDRLLGQPF	0.9958	3	3165.6224
						R.EDPAPLSSAAHSGIVFSAPRNR.S	0.9958	3	2280.5051
4830	WIPI1_MOUSE	446	7.85	2	2	K.THSLLSSGTTEENK.E	0.9958	2	1504.5938
						R.LNFSGQKNICTLSTIQK.L	0.9944	1	1953.2121
4831	WNK3_MOUSE	1789	2.07	2	2	R.FCINQTIKNR.E	0.9915	2	1294.4625
						K.SCESTPSTMGYTSNWISSLSQIR.G	0.9958	3	2593.7908
4832	WNK4_MOUSE	1222	3.85	2	3	R.NTETGVPMSQTEADLALRPSPALTSTGPTF	0.9958	3	3100.4278
						K.HLSEVEALQTLQK.K	0.9944	2	1496.7037
4833	WNT11_MOUSE	354	6.5	1	3	R.WNCSSIELAPNYLLDLERGTR.E	0.9958	2	2508.7595
4834	WNT7A_MOUSE	349	4.01	1	5	R.TLMNLHNNEAGR.K	0.994	2	1370.526
4835	WNT9B_MOUSE	359	7.52	1	2	K.VSSATNEALGRLELWAPAKPGGPAK.G	0.9944	3	2521.879
4836	WT1_MOUSE	449	4.45	1	5	R.YGPFGPPPPSQASSGQAR.M	0.9944	1	1801.956
4837	XDH_MOUSE	1335	22.7	12	59	K.DQTIAPSSSLFNPEDFKPLDPTQEPIFPPEL	0.9958	3	3741.1889
						R.NKPEPTVEEIENAFQGNLCR.C	0.9958	2	2346.5249
						R.TVWMDHTFFPGYR.R	0.9958	2	1657.8865
						R.VLFKPGTTEVQELSLCFGGMADR.T	0.9958	2	2556.9026
						K.ITYEDLPAIITIQDAIK.N	0.9958	2	1918.2377
						K.IPAFGSIPIEFR.V	0.9958	2	1347.5999
						K.KVPGFVCFLTSEDVPGSNITGIFNDETVFAK	0.9958	3	3390.7804
						R.VTWIQVSTMEELLDLK.A	0.9958	2	1906.2446
						K.SVASIGGNIITASPISDLNPVLMASR.A	0.9958	2	2584.991
						K.IHITETSTNTVPNTSPTAASASADLNGQAIYI	0.9958	3	4091.4413
						K.DEVTCVGHIIGAVVADTPEHAHR.A	0.9958	2	2484.6971
						K.VGFMKTGTIVALEVAHFSNGGNSEDLSR.S	0.9958	3	2938.2848
4838	XIP_MOUSE	91	83.52	4	36	R.GTLSDEHAGVISVLAQQAAR.L	0.9958	2	2024.2413

						K.NPSIVGVLCTDSQGLNLGCR.G	0.9958		2	2161.3521
						R.LTSDPTDIPVVCLESDNGNIMIQK.H	0.9944		2	2660.9625
						K.HDGITVAVHK.M	0.9958		2	1077.2284
4839	XIRP1_MOUSE	1129	51.11	26	137	R.LATAEAQSLHQQVLSR.H	0.9958		2	1752.9682
						R.HPQGSDPVATSMPVQDVLQASTPATGVTC	0.9958		3	4102.5255
						K.NLFETLPLDSIGQGEPSAYGNINR.G	0.9958		2	2606.8516
						K.VVLPNGKPVAQAPLQEAR.K	0.9958		2	1888.2205
						R.GQLHALTSVSR.E	0.9958		2	1169.3261
						K.LFQTEPLCAIQDAEGTIHEVKAACR.E	0.9958		3	2859.1408
						K.DFQPSPDLIPPGPDVQHQR.H	0.9958		2	2144.3513
						R.STLWLFETKPLDAFR.D	0.9958		2	1825.1173
						K.AASGRPEASPLGSGAPDLQEAMQNLR.L	0.9958		2	2624.8883
						R.VPPTESIIHVTPLDSTMEMGQLR.I	0.9958		2	2552.9637
						R.TEEDLSLPHPSAPEGLPPPPPK.E	0.9958		2	2306.5774
						R.WLFETQPLEMIHQQEQQKPEEEEGK.G	0.9958		3	3113.4254
						R.HVFETESLPASNQSSGR.K	0.9958		2	1846.9511
						R.WLFETYPMSELAEK.R	0.9958		2	1744.9997
						R.ISGSTPCPPPSR.A	0.9909		2	1256.3673
						R.WIFETQPLDAIR.E	0.9958		2	1489.7141
						K.FTWLFENCPMGSLAAESIR.G	0.9958		2	2230.5092
						K.AETQSCTWMFGPQSLNPAEGSGEQHLQT	0.9958		3	3904.139
						K.NLEEAVAEDLAEVLGSEEPTEGDVQCMR.V	0.9958	2,3		3092.2784
						R.GQNTDSAEQSQGSDAPVYAMQDSR.G	0.9958		2	2543.5946
						K.LFQTEPLCAIQDAEGTIHEVK.A	0.9958		2	2400.6569
						R.LGSRPSIQEQSPLELR.S	0.9958		2	1811.0482
						K.WMFETQPLDTLGR.S	0.9958		2	1594.8255
						R.VGHQEGEGLVTECLPSNGTSVLPLSQGVP	0.9958		3	3618.9458
						K.EVPETTINLGSIPTGSVHK.F	0.9958		2	1980.2255
						R.KFEEGSFTNSSDQEPEGLRPSGGDVQAAF	0.9958		3	3097.2383
4840	XIRP2_MOUSE	3784	2.46	4	6	K.GNVKTSTWLFETHR.I	0.9958		2	1676.8723
						K.YKLMNQTTPEIQK.E	0.993		2	1594.8664
						R.GTAGSPLQLVLEPGLQQGFSVKGENLAAS	0.9958		3	3857.3989
						K.LSTLDHTGTETDLSSKHHTK.Q	0.9958		3	2209.3775
4841	XLR_MOUSE	208	5.29	1	2	K.EQQALKLSK.C	0.9958		1	1045.2242
4842	XPOT_MOUSE	963	4.26	2	2	R.EEACDCLFEIVNK.G	0.9958		2	1627.7206
						K.KLTYDEEYNFENEGEDEAMFVEYR.K	0.9958		3	3022.1794
4843	XPP1_MOUSE	623	35.96	11	36	K.DTPTQEDWLVSVLPEGSR.V	0.9958		2	2030.1986

						K.GHIAVSAAVFPTGTK.G	0.9958		2	1456.6848
						R.RQQADFVDLSFPTISSTGPNGAIIHYAPVPE	0.9958		3	3701.0898
						K.GHLLDSFAR.S	0.9958		1	1016.1447
						R.TLSLDEVYLIDSGAQYK.D	0.9958		2	1916.1351
						R.GSLTFEPLTLVPIQTK.M	0.9958		2	1745.0691
						R.QQADFVDLSFPTISSTGPNGAIIHYAPVPET	0.9958		3	3544.9023
						K.TFSDEPLEAGMIVTDEPGYYEDGAFGIR.I	0.9958		3	3081.3339
						K.DAVALCELFNWLEQEVPKGGVTEISAADK..	0.9958		3	3191.5281
						R.SALWDSGLDYLHGTGHGVGSFLNVHEGP(	0.9958		3	3632.9367
						R.TMHFGTPTAYEK.E	0.9958	1,2		1383.5616
4844	XRN1_MOUSE	1719	4.71	3	3	R.EHFSEVFVDLK.W	0.9958		1	1350.5138
						K.MTPQESPPASSSSSQAAQPVSSHVETASQ	0.9924		3	3733.9623
						K.SWQGVTIYFSGHETPGEGEHKIMEFIR.S	0.9944		3	3137.4962
4845	XRN2_MOUSE	951	2.94	2	2	K.NLTVILSDASAPGEGEHK.I	0.9956		2	1839.0123
						R.LNNDPGWKNLTVILSDASAPGEGEHK.I	0.9944		3	2764.0239
4846	YB010_MOUSE	857	3.5	1	2	K.FQHWDLVEGEGAGGVAGASERAIDNMAK.	0.9958		3	2917.1822
4847	YB016_MOUSE	637	9.58	2	4	R.KPLRQAMIENAAAAAAAAAAAAAAAAAAAT	0.9958		3	4217.7417
						K.KTFNTLVLSK.E	0.9958		1	1151.3916
4848	YB022_MOUSE	722	6.79	2	2	K.FPGLLPSIGSTHMQTLQQKIPNGPSSR.W	0.9958		3	2893.3336
						R.RDMLNEGFASSALMPEGENK.F	0.9912		2	2197.4426
4849	YB023_MOUSE	1002	6.39	3	9	R.EHEDQSSLMLNAPLK.G	0.9924		2	1712.9153
						R.LHDSNK.K	0.9958		1	713.7685
						K.VNQWALESLAQMLPILKESIHPMLLSLIIAA	0.9958		3	4187.9893
4850	YBOX1_MOUSE	322	16.46	2	15	K.GAEAANVTGPGGVPVQGSK.Y	0.9958		2	1696.8577
						R.RPQYSNPPVQGEVMEGADNQGAGEQGRI	0.9958		3	3225.4796
4851	YBOX2_MOUSE	360	5.56	1	5	R.TPGNQATAASGTPAPPAR.S	0.9958		2	1665.8033
4852	YD007_MOUSE	1109	4.24	2	2	R.LLQPASVTRSHSNIPSSQSTTSFLSHHSIK.T	0.9944		3	3249.6108
						K.ILRELDTEISFLK.G	0.9958		2	1577.8614
4853	YES_MOUSE	541	11.28	2	2	K.TLKPGTMMPEAFLQEAQIMKK.L	0.9958		2	2393.9235
						K.SPAIKYTPENLTEPVSPSASHYGVEHATVA	0.9944		3	3756.1174
4854	YETS2_MOUSE	1407	4.55	3	9	K.LPVASQASQGTGSPIPK.I	0.9958		2	1638.8613
						R.FYLPPTPGSGFVGDITQK.I	0.9937		2	1925.1913
						K.LDRTYTGLQTLGAETVVDVELHR.H	0.9958		3	2587.8925
4855	YJ005_MOUSE	354	16.95	3	5	R.ASDDLGEPDVFATAPFR.S	0.9958		2	1808.9421
						R.TTELATADPFALAPFPSK.A	0.9958		2	1878.1321
						K.EAFSGPAAGKPFHPQALSK.Y	0.9958		2	1941.1967
4856	YKT6_MOUSE	198	21.72	2	9	K.QVDRIDWPVGSPATIQYTGLDDHLSK.Y	0.9958		3	2913.2163

						K.IILHNTMESLLER.G	0.9958	2	1569.8596
4857	YMEL1_MOUSE	715	5.45	2	2	R.GTVGFSGAELENLVNQAALK.A	0.9958	2	2019.2621
						R.GPTLGHVSLLPENDR.W	0.9958	2	1605.7911
4858	Z280C_MOUSE	742	7.28	2	5	R.NPSSNALVALPSFHPALK.S	0.9945	2	1864.1545
						K.VEESQSKDDDDELIFVGEISSSKPAISNILNF	0.9958	3	3536.8285
4859	ZADH1_MOUSE	351	30.2	6	181	K.VDPQLVDGHLSYFLGAIGMPGLTSLIGVQE	0.9958	3	3256.7846
						K.DKFEPGILQLSQWFK.E	0.9958	2	1837.1283
						K.FEPGILQLSQWFK.E	0.9958	2	1593.8657
						R.VVLNSRPGKNGNPVAENFR.V	0.9958	2	2069.331
						K.GDFVTSFYWPWQTK.A	0.9958	2	1762.9616
						K.CLFLTSELGFDAAVNYK.T	0.9944	2	1949.1768
4860	ZADH2_MOUSE	377	24.67	6	36	R.HFLDFQGSAIPR.T	0.9958	2	1388.5687
						K.LVVELPHPVSSK.L	0.9958	1,2	1305.5602
						R.FVGINASDINYSAGR.Y	0.9958	2	1584.7288
						R.LIVIGFISGYQSPTGLSPIK.A	0.9958	2	2091.4985
						R.LSPNFHEAVTLR.R	0.9958	1	1384.5779
						R.GFFLNHYFSK.Y	0.9958	2	1260.4374
4861	ZAN_MOUSE	5376	2.16	4	4	K.TWTSPGCTQSCACMGGVVQCQSSQCPPC	0.9944	3	3642.7695
						K.DAEGGLVPAGK.T	0.9924	1	1014.1234
						K.TWVSRGCTQSCVCTGGSIQCLSSQCPPGA	0.9958	3	3654.809
						R.SPDIWEQGPLCVHFAFHMFGLSWGAQLRL	0.9958	3	3897.5445
4862	ZC3HF_MOUSE	426	9.39	3	18	K.KHGEAEK.K	0.9944	1	798.8741
						K.ELQELNELFKPVVAAQK.I	0.9958	2	1957.2774
						R.HFLEAIENNK.Y	0.9957	2	1215.3513
4863	ZCHC2_MOUSE	1168	4.2	2	2	R.GPPPPPSPPRGLEPPVASGPTAGAGMPG(	0.9958	3	3337.7838
						K.RSLSSGNK.K	0.9958	1	848.9346
4864	ZCHC6_MOUSE	1491	5.7	4	4	K.EPLLPVYLGSWIEEFSLNKLGNFSLK.D	0.9958	3	2995.4882
						R.YSESKEK.R	0.9958	1	870.9347
						K.FFHLRSGLEVDISLYNTLALHNTR.L	0.9958	3	2818.2077
						K.YIVIEDPFDLNHNLGAGLSR.K	0.9958	3	2244.5119
4865	ZDBF2_MOUSE	2493	3.49	4	9	R.DLSLLEEEVEEEK.Q	0.9958	1	1562.6679
						K.LERGQQQSLELAHK.V	0.9944	2	1637.8362
						K.TKHLEEVNSDDEYGGSQPTFK.F	0.9944	2	2382.5023
						K.LVRPPVICNAPASSLPSGSFERPVAANSVP	0.9958	3	3247.6909
4866	ZDH13_MOUSE	622	3.7	1	3	K.GAVIDQLGGDLNSTPLHWAIR.Q	0.9958	2	2234.5198
4867	ZDH14_MOUSE	489	12.27	2	2	K.DEHGGHQFLTPDEAPSPPRMLGAGSPLAH	0.9931	3	3266.5749
						R.QTGVFYLTLILILVTSGLFFAFDCR.Y	0.9929	2	2896.4083

4868	ZDHC8_MOUSE	762	8.53	2	2	R.SQTDSLFGDSGVYDTPSSYSLQQASVLTE	0.9931	3	3394.5866
						R.APRTSSSSLQADQANNNAPGPRPGSGSHI	0.9944	3	2919.0597
4869	ZEP1_MOUSE	2688	5.99	5	7	R.TDNSECSSPCCSTTPPSYTSTAFDVLLKAM	0.9958	3	4442.7418
						R.QAAVEDSTASESHVPGSGQSVDESCQGC	0.9944	3	4036.0682
						R.SESADQAVSPPTPFAR.T	0.9906	1	1660.7807
						K.VSTSLTPTVGSFPAPSESACVLPLK.S	0.9924	3	2546.8866
						K.ALSVHSDIEDSGESDEEGLADGRQNNPCV	0.9958	3	3230.3057
4870	ZEP2_MOUSE	2430	2.39	3	5	R.MTGSDDVFYPGTVGIPPQRMLR.R	0.9958	2	2438.8219
						R.QPQIDPEQIGNAASAQLFGSGK.L	0.9943	2	2257.4649
						R.QEQSAVLK.M	0.9958	1	903.0232
4871	ZF106_MOUSE	1888	3.65	3	7	R.TLYAGLANGTVVTFDIK.N	0.9958	2	1784.0624
						K.NETEKESGLKPTLR.Q	0.9958	2	1602.785
						K.QEPMSPEQEGNMNALPQGCASNVSKELL	0.9944	3	3559.8709
4872	ZFA_MOUSE	742	3.1	1	2	K.TFMPIAWEAAYGNNSDGIENR.N	0.99	2	2357.5591
4873	ZFAN5_MOUSE	213	10.33	1	5	R.ADAGLNNCEGAAGSTSEKSR.N	0.9944	3	1996.0209
4874	ZFHX4_MOUSE	3550	1.46	3	5	R.EVGLKK.R	0.9958	1	673.8308
						R.EYEVDHEGKASPVESDGSSIPDDLGLEPK.	0.9944	3	3101.2611
						K.EEESEAIKPEK.H	0.9924	1	1289.3819
4875	ZFPL1_MOUSE	310	10.97	2	3	R.LGRAAADSDPNLDPLMNPHIR.V	0.9904	2	2274.5596
						R.KRPLTLLQR.A	0.9958	1	1125.4031
4876	ZFY21_MOUSE	234	8.55	1	6	R.QCADCALVSHREAEFYDK.Q	0.9958	2	2200.3015
4877	ZHX1_MOUSE	873	5.96	2	2	K.VLIPVNSIPTYNAALDNNPLLLNTYNK.F	0.9944	3	2986.4381
						K.EENTEQGESIDVSSSGISISK.T	0.9958	2	2197.2714
4878	ZMY11_MOUSE	562	1.96	1	2	K.YTKIFNDFK.D	0.9958	1	1176.3574
4879	ZMYM2_MOUSE	1376	2.33	2	2	K.TVEQHLRLSFGTVFR.H	0.9958	2	1791.0629
						R.QLDEDLLVLDELK.S	0.9958	1	1543.7545
4880	ZMYM3_MOUSE	1370	4.01	2	2	K.DPGGVLDGATELLGLGGLLYK.A	0.9958	2	2059.3672
						K.TNCCDQCGAYIYARPGGLGPELLFHDGQQ	0.9958	3	3427.6528
4881	ZN313_MOUSE	229	24.02	3	8	R.FSYDTFVDYDVDEDDMINQVLQR.S	0.9958	2	2829.0205
						R.SANFMEHIQR.R	0.9934	2	1233.3874
						K.SVVCPICASMPWGDPSYR.S	0.9958	2	2083.2985
4882	ZN318_MOUSE	2064	3	2	6	K.ITVPAKGSEFLIPVTGFYCQLCEEFLGDPIS	0.9944	3	4168.6651
						R.YISREEGPLSPFLGQLDEDYR.T	0.9958	3	2485.7124
4883	ZN394_MOUSE	521	2.11	1	3	R.KGFCEESTK.D	0.9958	1	1086.1529
4884	ZN423_MOUSE	1292	3.56	3	7	K.TYQCIKCQMTFENER.E	0.994	2	2009.1733
						K.KAEPADLQGMLLK.N	0.9958	2	1414.7033
						R.GSTPDSTLKPLR.G	0.9958	1	1272.4441

4885	ZN473_MOUSE	892	3.03	2	2	K.EQLERHNK.I	0.9958	1	1054.1508
						R.IHTGEKPYTCGTCGK.A	0.9924	1	1709.8286
4886	ZN521_MOUSE	1311	5.57	3	3	K.CIFCGESFGTEVELQCHITTHSK.K	0.9944	2	2741.9125
						K.HNHLENQGKVHK.C	0.9958	3	1441.5924
						K.KRPEDGEELEEDAVHSCDSCLQVFESLSD	0.9958	3	3991.1568
4887	ZN532_MOUSE	1036	1.54	1	2	K.EPVANSREASPLPK.E	0.9958	1	1495.6756
4888	ZN569_MOUSE	679	7.66	2	2	R.NVMLENYNNLITVGPPLTKPEVIFKLEQEEE	0.9958	3	4343.9454
						K.NFITHQKIHTR.E	0.9944	2	1395.6071
4889	ZN580_MOUSE	172	7.56	1	5	R.EATPGEPGPRK.G	0.9924	1	1139.2535
4890	ZN609_MOUSE	1413	4.46	2	2	K.DSPYYQGFESYYSPGYAQSSPGTLTSSSQ	0.9958	3	4068.3272
						R.AGDGASAGGLVAAVAPKGSEK.A	0.9924	2	1814.0055
4891	ZN692_MOUSE	531	2.45	1	5	R.LGFSLHSQLAK.F	0.9958	2	1201.4111
4892	ZN770_MOUSE	705	2.55	1	2	K.NCERSSGKPNIEQTQR.T	0.9954	2	1905.0007
4893	ZNF2_MOUSE	427	3.75	1	12	R.DCGKAFYGVTSLNR.H	0.9958	1	1588.7265
4894	ZNF22_MOUSE	237	11.81	2	6	K.SFFQSSNLIQHR.R	0.9958	2	1464.6237
						K.SFSQSSTLFQHK.K	0.9958	2	1397.5303
4895	ZNFX1_MOUSE	1909	1.68	2	2	R.VQIVTAMGVPR.G	0.9944	1	1171.4436
						K.AEANGIQDVWQLDLSSR.W	0.993	2	1903.0587
4896	ZO1_MOUSE	1745	5.79	5	10	R.EAGFLRPVTIFGPIADVAR.E	0.9958	2	2030.3775
						K.FNHNLLPSETVHKPELSSK.T	0.9958	2	2178.4527
						R.GEGPPLPPHADPAKVYR.K	0.9958	2	1802.0427
						R.LPEPQKPQVKPPEDIVR.S	0.9958	2	1971.3073
						K.STAMEETAIWEQHTVTLHR.A	0.9958	2	2241.4833
4897	ZO2_MOUSE	1167	7.63	4	17	R.EDAVLYLLEIPKGETVTILAQSR.A	0.9958	2	2559.9628
						K.QTLINIPALNDSDSEVEDISEIESNR.S	0.9958	2	2903.0832
						R.LATELPDLFQTAKTEPK.D	0.9958	2	1903.1827
						R.HSSHDMLSHSWEGNR.E	0.9958	2	1780.8718
4898	ZO3_MOUSE	905	5.75	2	2	R.GDVFHVVDTLYPGSGPGHGHSSHGGLWL	0.9958	3	3529.92
						K.WETQADSHYTQDQR.R	0.9958	2	1765.7929
4899	ZRAB3_MOUSE	1069	4.96	2	2	R.IGQCSSVNIHYLIANGTLDSLMWAMLNR.K	0.9958	3	3179.6455
						K.SLLNAAWTAKLPLEQLNEMLR.N	0.9958	3	2412.8529
4900	ZSCA2_MOUSE	614	6.19	2	5	R.SQLVVHQRTHTGEKPYK.C	0.9909	2	2009.2754
						K.GFSNSSNFITHQRTHLK.E	0.9958	1	1975.174
4901	ZSWM4_MOUSE	1101	4.27	2	2	K.NWYSLFTPVEAVTIVAVTGTTHATLLRLQLI	0.9944	3	3817.38
						R.RHQLESYK.Q	0.9958	1	1061.1857
4902	ZXDAB_MOUSE	873	3.78	1	11	R.GGGAGGGGGGSGGGGGGGGGGGGGGC	0.9926	2	1960.8477
4903	ZY11A_MOUSE	627	2.71	1	9	R.AVLPVMLKLVAIGMR.N	0.9937	2	1612.1315

4904	ZY11B_MOUSE	744	4.97	1	2	R.SFNPFFPLLGCFTTPGVQLWAVWAMQHV(	0.9944	3	4082.6467
4905	ZYX_MOUSE	564	14.54	4	36	K.VNPFRPGDSEPPVAAGAQR.A	0.9958	2	1966.1637
						K.FSPGAPSGPGPQPIKK.W	0.9958	2	1565.8125
						R.GPLSQAPTPAPK.F	0.9958	2	1164.347
						R.KPQVQLHVQPQAKPHVQPQPVSSANTQPI	0.9944	3	3226.6687
4906	ZZEF1_MOUSE	2924	2.46	4	6	R.EAAAALRPAPPCESLVSR.H	0.9958	2	1896.1198
						R.CVYMDNANEPHNVIILK.H	0.9944	2	2031.3002
						K.HTNIFTLLVLVGFPQVLCVGTRCVYMDNAN	0.9958	3	4498.2185
						R.ECELLMLNR.S	0.9958	1	1178.3552