Supplementary Table 2. Full list of peptides identified by mass spectrometry from SILAC experiment with WT (light) 3xMBT pulldown as compared to D355N mutant (heavy) pulldown assay.

ProteinId	GeneSymbol	Description	PeptideSequence	max_sn_heavy	max_sn_light	Ratio H_L	Ratio L_H
Q3TTN6_Q3TTN6_MOUSE	1700010I14Rik	Protein 1700010I14Rik (	R.KVQQAYLEALEHNDK.L	2.87	7.95	0.36	2.77
G5E8E3_G5E8E3_MOUSE	2310022A10Rik	Protein 2310022A10Rik	K.AAVVSEAQDSQVTSTK#.S	55.91	318.42	0.18	5.70
G5E8E3_G5E8E3_MOUSE	2310022A10Rik	Protein 2310022A10Rik	K.ASAQPALTVK#.A	19.00	1.51	12.56	0.08
G5E8E3_G5E8E3_MOUSE	2310022A10Rik	Protein 2310022A10Rik	K.ATSSATTTATTPK#.L	21.37	6.89	3.10	0.32
G3UYI6_G3UYI6_MOUSE	A930009A15Rik	Protein A930009A15Rik	R.NSQHLCLSSK#.R	3.16	3.09	1.02	0.98
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	K.AGQTQPNPGILPIQPALTPR@.K	9.57	3.29	2.90	0.34
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	R.ATVQPLPQAAGPSNQPGLLPSVSQPK#.A	9.80	2.74	3.58	0.28
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	R.DLK#VENILLHDR@.G	11.22	2.56	4.38	0.23
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	R.LTDPIPTTETSIAPR.Q	20.96	6.24	3.36	0.30
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	K.AGQTQPNPGILPIQPALTPR@.K	10.24	2.77	3.70	0.27
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	K.AQATPSQPLQSSQPK#.Q	20.97	4.03	5.20	0.19
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	R.ATVQPLPQAAGPSNQPGLLPSVSQPK#.A	13.60	2.95	4.61	0.22
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	R.DLK#VENILLHDR@.G	19.13	3.90	4.91	0.20
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	R.LTDPIPTTETSIAPR.Q	24.00	8.24	2.91	0.34
Q3UHJ0_AAK1_MOUSE	Aak1	AP2-associated protein k	R.R@EQGSSGLGSGSSGGGGSSSGLGSGYIGR@.V	7.27	3.31	2.19	0.46
Q9JKX4_AATF_MOUSE	Aatf	Protein AATF OS=Mus mu	K.ALLTTNQLPQPDVFPVFK#.D	17.25	9.58	1.80	0.56
Q9JKX4_AATF_MOUSE	Aatf	Protein AATF OS=Mus mu	R.EADPEADPEEATR@.A	15.82	8.02	1.97	0.51
Q9JKX4_AATF_MOUSE	Aatf	Protein AATF OS=Mus mu	R.FADFTIYR@.N	15.50	4.69	3.30	0.30
Q9JKX4_AATF_MOUSE	Aatf	Protein AATF OS=Mus mu	K.NQIALWDQLLEGR@.I	14.78	11.12	1.33	0.75
Q9JKX4_AATF_MOUSE	Aatf	Protein AATF OS=Mus mu	R.SLVDLQEELLFQYPDTR@.H	9.91	4.37	2.26	0.44
Q9JKX4_AATF_MOUSE	Aatf	Protein AATF OS=Mus mu	R.VLGKPEPVPEPVAETLPGEPETLPQGPANAHLR.D	15.58	5.54	2.81	0.36
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.STLLLLLTGK#.L	9.62	1.52	6.33	0.16
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.AANAAENDFSVSQAEVSSR@.Q	21.47	8.02	2.68	0.37
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.ANDPYANLSK#.K	8.64	4.52	1.91	0.52
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.AVAEEPPGLR@.S	49.86	13.07	3.82	0.26
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.GAVIVVSHDAR@.L	21.18	6.39	3.31	0.30
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.IGFFNQQYAEQLHM*EETPTEYLQR@.S	34.12	8.08	4.22	0.24
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	R.LQGQLEQGDDTAAEKLEK.V	51.89	14.80	3.51	0.29
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.NLDFGIDM*DSR@.I	10.96	3.30	3.32	0.30
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.NQDEESQEPPELLK#.R	5.98	6.53	0.92	1.09
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	R.QAM*LENASDIK#LEK#.F	15.63	5.37	2.91	0.34
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.QLSVPASDEEDEVPAPIPR@.G	4.82	1.72	2.80	0.36
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	R.SFNLPYQDAR@.K	33.21	11.47	2.90	0.35
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.STLLLLLTGK#.L	42.06	13.86	3.03	0.33
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.TFFEELAVEDK#.Q	13.65	5.83	2.34	0.43
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.AVAEEPPGLR@.S	26.58	6.97	3.81	0.26
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.GAVIVVSHDAR@.L	9.90	2.34	4.23	0.24
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.IGFFNQQYAEQLHM*EETPTEYLQR@.S	21.54	4.13	5.21	0.19
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.NLDFGIDM*DSR@.I	7.11	1.64	4.33	0.23
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.QLSVPASDEEDEVPAPIPR@.G	4.75	2.03	2.34	0.43
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	R.R@LQGQLEQGDDTAAEK#LEK#.V	5.87	2.71	2.17	0.46
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	R.SFNLPYQDAR@.K	13.33	4.78	2.79	0.36
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.SK#PAAADSEGEEEEEDTAK#.E	6.82	1.36	5.01	0.20
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.STLLLLLTGK#.L	25.17	4.61	5.46	0.18
Q6P542_ABCF1_MOUSE	Abcf1	ATP-binding cassette sub	K.TFFEELAVEDK#.Q	6.68	2.77	2.41	0.41
Q99LE6_ABCF2_MOUSE	Abcf2	ATP-binding cassette sub	K.IPPPVIM*VQNVSFK#.Y	5.89	3.88	1.52	0.66
Q99LE6_ABCF2_MOUSE	Abcf2	ATP-binding cassette sub	K.LLTGELLPTDGM*IR.K	14.66	11.03	1.33	0.75
Q99LE6_ABCF2_MOUSE	Abcf2	ATP-binding cassette sub	K.M*M*ASGLTER@.V	13.15	9.77	1.35	0.74
Q99LE6_ABCF2_MOUSE	Abcf2	ATP-binding cassette sub	K.SM*LLSAIGK#.R	13.97	4.12	3.39	0.30
Q99LE6_ABCF2_MOUSE	Abcf2	ATP-binding cassette sub	K.YYTGNYDQYVK#.T	14.26	9.68	1.47	0.68
Q99LE6_ABCF2_MOUSE	Abcf2	ATP-binding cassette sub	K.YYTGNYDQYVK#.T	3.94	1.49	2.64	0.38
Q8K268_ABCF3_MOUSE	Abcf3	ATP-binding cassette sub	R.ALFAR@PDLLLLDEPTNM*LDVR@.A	13.33	5.83	2.29	0.44
Q8K268_ABCF3_MOUSE	Abcf3	ATP-binding cassette sub	R.ALFAR@PDLLLLDEPTNMLDVR@.A	5.35	1.64	3.26	0.31
Q8K268_ABCF3_MOUSE	Abcf3	ATP-binding cassette sub	R.ASVILAGLGFTPK#.M	12.88	3.79	3.40	0.29
Q8K268_ABCF3_MOUSE	Abcf3	ATP-binding cassette sub	K.FSPPILQLDEVDFYYDPK#.H	4.25	2.09	2.03	0.49
Q8K268_ABCF3_MOUSE	Abcf3	ATP-binding cassette sub	R.LAEPQNQGNSQVLLDAPIQLSK#.I	7.29	6.91	1.06	0.95
Q8K268_ABCF3_MOUSE	Abcf3	ATP-binding cassette sub	K.TSNPLVLEEASASQAGSR@.K	7.32	2.88	2.54	0.39
Q8K268_ABCF3_MOUSE	Abcf3	ATP-binding cassette sub	R.VEGGFDQYR@.A	10.00	2.14	4.68	0.21
Q8K268_ABCF3_MOUSE	Abcf3	ATP-binding cassette sub	R.VPAHISLLHVEQEVAGDDTPALQSVLESDTVR@EDLLR@.Q	5.15	1.52	3.38	0.30
Q8VCR7_ABHEB_MOUSE	Abhd14b	Alpha/beta hydrolase do	R.AVAIDLPGLGR@.S	38.02	9.19	4.14	0.24
Q8VCR7_ABHEB_MOUSE	Abhd14b	Alpha/beta hydrolase do	R.FSSETWQNLGTLQR@.L	8.73	2.94	2.97	0.34
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	K.AIYDIER@PDLITYEPFYTSGYEDK#QER@.Q	12.13	7.79	1.56	0.64
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.QLQEEQLM*K#.L	4.93	3.69	1.33	0.75
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.STSQGSINSPVYSR@.H	19.01	4.64	4.09	0.24
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.TLSPTPSAEGYQDVR@.D	21.87	12.63	1.73	0.58
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.TSSESIYSR@PGSSIPGSPGHTIYAK#.V	3.12	1.22	2.55	0.39
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	K.VDNEILDYK#DLAAIPK#.V	33.51	17.71	1.89	0.53
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.GVSM*PNM*LEPK#.I	8.95	3.82	2.34	0.43
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	K.LNSGLGQLILK#.E	10.69	6.16	1.73	0.58
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	K.NGLHR@PVSTDFAQYNSYGDISGGVR@.D	4.25	2.61	1.63	0.61
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.QLQEEQLM*K#.L	22.87	9.16	2.50	0.40
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.SSGR@EEDEEELLR@.R	10.97	3.38	3.25	0.31
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.SSGREEDEEELLR.R	36.91	15.70	2.35	0.43
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.STSQGSINSPVYSR@.H	32.63	15.43	2.11	0.47
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	R.TLSPTPSAEGYQDVR@.D	24.23	10.86	2.23	0.45
Q8K4G5_ABLM1_MOUSE	Ablim1	Actin-binding LIM protei	K.VDNEILDYK#DLAAIPK#.V	45.84	18.67	2.45	0.41
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.AAEEVGYPVM*IK#.A	43.76	2.92	15.00	0.07
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.DFTVASPAEFVTR@.F	22.39	7.24	3.09	0.32
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.DIIVIGNDITYR@.I	18.12	3.67	4.93	0.20
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.EASFEYLQNEGER@.L	14.25	3.26	4.38	0.23
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.EVFFM*NTQSIVQLVQR@.Y	15.18	3.34	4.55	0.22
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.FGAYIVDGLR@.E	12.38	2.59	4.78	0.21
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.FIIGSVSEDNSEDEISNLVK#.L	8.30	2.30	3.61	0.28
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.FVVM*VTPEDLK#.A	155.99	1.12	138.67	0.01
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.GGSWVVIDPTINPR@.H	15.46	11.26	1.37	0.73
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.GQVLPAHTLLNTVDVELIYEGIK#.Y	5.75	7.61	0.76	1.32
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.GSVLEPEGTVEIK#.F	19.59	6.37	3.07	0.33
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.GVINDILDWK#.T	12.59	1.65	7.63	0.13
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.IGLAEEIR@.H	20.36	4.78	4.26	0.23
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.IGSFGPQEDLLFLR@.A	44.39	10.09	4.40	0.23
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.IHNANPELTDGQIQAM*LR@.R	9.59	3.19	3.01	0.33
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.IIQQAGQVWFPDSAFK#.T	8.48	4.83	1.76	0.57
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.ILNVPQDLYEK#.G	12.77	3.23	3.95	0.25
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.ITDIIGK#EEGLGAENLR@.G	18.07	4.77	3.79	0.26
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.ITSENPDEGFK#PSSGTVQELNFR@.S	17.95	5.20	3.45	0.29
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.IYVAANSGAR@.I	12.16	4.40	2.77	0.36
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.LGGIPVGVVAVETR@.T	34.34	11.44	3.00	0.33
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.LGTPELSPTER@.K	18.65	53.82	0.35	2.89
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.LLETESFQLNR@.I	22.92	5.96	3.85	0.26
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.LPELLLK#.N	10.72	2.13	5.02	0.20

Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.LPGGNEIGM*VAWK#.M	6.47	3.57	1.81	0.55
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.M*AALEVYVR@.R	8.33	3.10	2.69	0.37
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.TLR@DPSLPLLELQDIM*TSVSGR@.I	6.66	1.96	3.41	0.29
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.VEVGTEVTDYR@.F	20.64	8.28	2.49	0.40
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	R.VLQAELK#.I	17.93	6.48	2.77	0.36
Q5SWU9_ACACA_MOUSE	Acaca	Acetyl-CoA carboxylase 1	K.VQQAELHTGSLPQIQSTALR@.G	15.57	4.75	3.27	0.31
Q07417_ACADS_MOUSE	Acads	Short-chain specific acyl-	R.ITEIYEGTSEIQR@.L	6.22	2.36	2.63	0.38
P50544_ACADV_MOUSE	Acadvl	Very long-chain specific	K.ELGAFGLQVPSELGGLGLSNTQYAR@.L	8.88	3.10	2.87	0.35
P50544_ACADV_MOUSE	Acadvl	Very long-chain specific	R.SGELAVQALDQFATVVEAK#.L	6.29	1.74	3.62	0.28
Q8BMP6_GCP60_MOUSE	Acbd3	Golgi resident protein G	R.EPGEAAAEGAAEEAR.R	13.90	6.12	2.27	0.44
Q8BMP6_GCP60_MOUSE	Acbd3	Golgi resident protein G	K.IR@QDADSVITVR@.R	17.02	6.34	2.68	0.37
Q8BMP6_GCP60_MOUSE	Acbd3	Golgi resident protein G	K.NANK#PLLDEIVPVYR@.R	12.95	6.91	1.87	0.53
Q8BMP6_GCP60_MOUSE	Acbd3	Golgi resident protein G	K.QQEVVM*AGASLPASSK#.V	7.57	2.75	2.76	0.36
Q8BMP6_GCP60_MOUSE	Acbd3	Golgi resident protein G	K.VLEPEAAEEALENGPK#.D	6.21	2.65	2.34	0.43
Q5EE38_ACD_MOUSE	Acd	Adrenocortical dysplasia	R.VQVAQDHAPAEFYLQVDR@.F	5.37	2.83	1.90	0.53
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.LLDDLFR@.K	31.96	21.34	1.50	0.67
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.SGVSITIDDPVR@.T	26.16	17.01	1.54	0.65
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.TGTLVEEAFWIDK#.I	13.45	5.11	2.63	0.38
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.VTLGDTLTR@.R	10.40	7.16	1.45	0.69
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.GVQAGNSDTEGGQPGR@.K	82.46	34.44	2.39	0.42
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.GVQAGNSDTEGGQPGR@K#.R	4.15	1.37	3.02	0.33
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.K#ISVVSATK#.G	63.15	23.70	2.66	0.38
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.K#VTLGDTLTR@.R	45.67	16.96	2.69	0.37
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.LLDDLFR@.K	278.42	136.20	2.04	0.49
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.SGVSITIDDPVR@.T	133.68	60.46	2.21	0.45
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.SLIPDIKPLAGQEAVVDLHADDSR.I	28.00	7.89	3.55	0.28
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.TALHGVK#.W	18.96	12.23	1.55	0.64
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.TAQVPSPPR@.G	9.24	9.35	0.99	1.01
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.TGTLVEEAFWIDK#.I	81.72	31.06	2.63	0.38
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.TGTLVEEAFWIDK#IK#.S	70.43	29.01	2.43	0.41
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.VSDESVLPLAQK#.S	8.72	4.43	1.97	0.51
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.VTLGDTLTR@.R	141.22	59.01	2.39	0.42
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.WGASTAATQK#.K	41.41	21.32	1.94	0.51
Q52KR6_Q52KR6_MOUSE	Acin1	Acin1 protein OS=Mus m	K.EAVVDLHADDSR@.I	8.29	2.34	3.54	0.28
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.AEEQGAPR@PLHPPPPPPVQPPPHPR@.A	14.91	6.54	2.28	0.44
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.APVVLQPEQIVSEEETPPPLLTK#.E	39.59	14.63	2.71	0.37
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.APVVLQPEQIVSEEETPPPLLTK#.E	3.04	1.69	1.80	0.56
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.ETQIVSLPQEENEVK#.S	43.15	15.08	2.86	0.35
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.GALM*LENLQK#.H	11.85	3.60	3.29	0.30
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.GVQAGNSDTEGGQPGR@.K	66.53	22.10	3.01	0.33
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.HLSHPEPEQQHVIQR@.L	61.62	16.82	3.66	0.27
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.HSTPHAAFQPNSQIGEEM*SQNSFIK#.Q	21.74	8.17	2.66	0.38
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.ISEDETER@.N	10.23	2.99	3.42	0.29
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.LLDDLFR@.K	100.24	27.40	3.66	0.27
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.QFEDEEGEER@.T	21.59	7.55	2.86	0.35
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.SAPLPLTVEEFAPAK#.G	122.56	35.16	3.49	0.29
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.SGVSITIDDPVR@.T	28.28	9.71	2.91	0.34
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.SK#LPEYSQTAEEEEDQETPSR@.N	27.80	7.66	3.63	0.28
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.SQSPSPPPLPEDLEK#.A	8.57	4.38	1.96	0.51
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.TGTLVEEAFWIDK#.I	49.60	17.26	2.87	0.35
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.TGTLVEEAFWIDK#IK#.S	18.46	5.70	3.24	0.31
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.TVTQVVPAEGQENGQR@.E	7.29	3.60	2.03	0.49
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.VSDESVLPLAQK#.S	74.58	20.19	3.69	0.27
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	K.VTLGDTLTR@.R	41.00	13.86	2.96	0.34
Q9JIX8_ACINU_MOUSE	Acin1	Apoptotic chromatin co	R.WGASTAATQK#.K	108.11	9.65	11.20	0.09
Q99KI0_ACON_MOUSE	Aco2	Aconitate hydratase, mit	K.SQFTITPGSEQIR.A	2.40	4.44	0.54	1.85
Q32MW3_ACO10_MOUSE	Acot10	Acyl-coenzyme A thioest	R.DSYIEVLLPLGTDPELR@.D	4.55	3.77	1.21	0.83
Q9CZW4_ACSL3_MOUSE	Acsl3	Long-chain-fatty-acid--C	R.LSPDPWTPETGLVTDAFK#.L	4.31	2.59	1.66	0.60
Q9QUJ7_ACSL4_MOUSE	Acsl4	Long-chain-fatty-acid--C	R.LSPEPWTPETGLVTDAFK#.L	5.47	3.31	1.65	0.61
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.AGFAGDDAPR.A	4366.71	4214.43	1.04	0.97
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.AVFPSIVGRPR@.H	351.14	337.12	1.04	0.96
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.DLTDYLM*K#.I	2939.93	2703.79	1.09	0.92
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.DLTDYLMK#.I	722.19	696.49	1.04	0.96
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.DLTDYLM*K#ILTER@.G	12.57	8.99	1.40	0.72
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DLYANNVLSGGTTM*YPGIADR.M	14.10	23.08	0.61	1.64
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DSYVGDEAQSK#.R	3905.78	3778.19	1.03	0.97
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DSYVGDEAQSK#R@.G	1333.24	1022.19	1.30	0.77
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.EITALAPSTM*K#.I	2658.19	2641.03	1.01	0.99
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.EITALAPSTMK#.I	1565.89	1361.25	1.15	0.87
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVMVGMGQK#.D	58.67	60.10	0.98	1.02
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGM*GQK#.D	1309.98	1253.55	1.05	0.96
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGM*GQK#.D	1367.09	1310.16	1.04	0.96
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVMVGM*GQK#.D	300.67	268.42	1.12	0.89
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGMGQK#.D	274.23	269.09	1.02	0.98
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGMGQK.D	336.59	356.29	0.94	1.06
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IIAPPER@.K	2781.12	3356.90	0.83	1.21
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IIAPPER@K#.Y	692.89	598.96	1.16	0.86
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IK#IIAPPER@.K	37.22	40.32	0.92	1.08
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IWHHSFYNELR.V	46.97	93.11	0.50	1.98
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.KDLYANNVLSGGTTM*YPGIADR.M	7.67	11.37	0.67	1.48
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.QEYDEAGPSIVHR.K	36.45	77.15	0.47	2.12
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.RGILTLK.Y	2579.24	1761.26	1.46	0.68
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.SYELPDGQVITIGNER@.F	3022.77	2822.63	1.07	0.93
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.YPIEHGIITNWDDM*EK#.I	1018.74	970.20	1.05	0.95
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.YPIEHGIITNWDDMEK#.I	1056.08	925.48	1.14	0.88
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.YPIEHGIITNWDDMEK.I	61.32	55.67	1.10	0.91
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.AGFAGDDAPR.A	53.95	368.14	0.15	6.82
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.DLTDYLM*K.I	17.75	26.40	0.67	1.49
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DSYVGDEAQSK.R	5.44	4.03	1.35	0.74
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.EITALAPSTM*K#.I	37.47	44.42	0.84	1.19
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.SYELPDGQVITIGNER.F	44.12	110.25	0.40	2.50
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.AGFAGDDAPR@.A	2684.49	1628.45	1.65	0.61
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.DLTDYLM*K#.I	2010.93	1226.24	1.64	0.61
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.DLTDYLMK#.I	341.08	207.91	1.64	0.61
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DSYVGDEAQSK#.R	2264.95	1369.06	1.65	0.60
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DSYVGDEAQSK#R@.G	679.70	369.59	1.84	0.54
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.EITALAPSTM*K#.I	1814.34	1109.53	1.64	0.61
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.EITALAPSTMK#.I	526.61	303.82	1.73	0.58
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGM*GQK#.D	881.09	491.55	1.79	0.56
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGM*GQK#.D	1005.28	605.74	1.66	0.60
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVMVGM*GQK#.D	104.58	64.44	1.62	0.62
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGMGQK#.D	79.27	43.74	1.81	0.55
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGMGQK#.D	76.25	41.52	1.84	0.54

P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IIAPPER@.K	2094.43	1416.75	1.48	0.68
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IIAPPERK.Y	410.65	230.48	1.78	0.56
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IK#IIAPPER@K#.Y	38.93	15.27	2.55	0.39
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.RGILTLK.Y	1227.65	500.47	2.45	0.41
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.SYELPDGQVITIGNER@.F	2016.19	1167.84	1.73	0.58
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.YPIEHGIITNWDDM*EK#.I	685.72	367.78	1.86	0.54
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.YPIEHGIITNWDDMEK#.I	324.52	216.26	1.50	0.67
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.AGFAGDDAPR@.A	3666.58	1675.39	2.19	0.46
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.DLTDYLM*K#.I	2838.55	1230.23	2.31	0.43
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.DLTDYLMK#.I	351.37	179.68	1.96	0.51
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DLYANNVLSGGTTM*YPGIADR.M	16.16	12.91	1.25	0.80
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DLYANNVLSGGTTM*YPGIADR@.M	8.48	7.67	1.10	0.91
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DSYVGDEAQSK#.R	2732.28	1054.56	2.59	0.39
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.DSYVGDEAQSKR.G	926.39	359.21	2.58	0.39
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.EITALAPSTM*K#.I	2753.90	1280.22	2.15	0.46
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.EITALAPSTMK#.I	708.09	285.89	2.48	0.40
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.GYSFVTTAER.E	40.06	36.04	1.11	0.90
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGM*GQK#.D	1348.23	544.00	2.48	0.40
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGM*GQK#.D	1733.72	793.80	2.18	0.46
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVMVGM*GQK#.D	124.72	58.41	2.14	0.47
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.HQGVM*VGMGQK#.D	111.48	51.94	2.15	0.47
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IIAPPER@.K	2841.04	1394.01	2.04	0.49
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IIAPPER@K#.Y	536.55	316.43	1.70	0.59
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.IK#IIAPPER@.K	16.47	8.51	1.94	0.52
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.QEYDEAGPSIVHR@.K	30.39	24.76	1.23	0.81
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.SYELPDGQVITIGNER@.F	3382.13	1424.53	2.37	0.42
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.SYELPDGQVITIGNER@.F	356.56	151.07	2.36	0.42
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	R.VAPEEHPTLLTEAPLNPK#.A	84.85	94.68	0.90	1.12
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.YPIEHGIITNWDDM*EK#.I	1087.03	479.32	2.27	0.44
P62737_ACTA_MOUSE	Acta2	Actin, aortic smooth mu	K.YPIEHGIITNWDDMEK#.I	601.56	245.41	2.45	0.41
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTM*YPGIADR@.M	990.52	882.85	1.12	0.89
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTM*YPGIADR.M	1315.54	1236.64	1.06	0.94
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTMYPGIADR.M	159.67	134.77	1.18	0.84
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTMYPGIADR@.M	209.81	195.40	1.07	0.93
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.GYSFTTTAER@.E	4486.73	3863.18	1.16	0.86
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.IWHHTFYNELR@.V	1800.35	1676.32	1.07	0.93
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.IWHHTFYNELR.V	105.02	101.73	1.03	0.97
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.K#DLYANTVLSGGTTM*YPGIADR@.M	1036.79	961.77	1.08	0.93
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.KDLYANTVLSGGTTMYPGIADR.M	138.88	138.20	1.00	1.00
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.QEYDESGPSIVHR@.K	2226.11	2175.81	1.02	0.98
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.QEYDESGPSIVHR.K	243.16	209.46	1.16	0.86
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.VAPEEHPVLLTEAPLNPK.A	2900.94	2600.76	1.12	0.90
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.VAPEEHPVLLTEAPLNPK.A	136.75	153.71	0.89	1.12
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.YPIEHGIVTNWDDM*EK#.I	68.79	51.24	1.34	0.74
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.YPIEHGIVTNWDDM*EK.I	5.99	4.15	1.44	0.69
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.YPIEHGIVTNWDDMEK#.I	34.40	27.90	1.23	0.81
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTM*YPGIADR.M	9.43	12.63	0.75	1.34
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.GYSFTTTAER.E	19.23	22.51	0.85	1.17
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.K#DLYANTVLSGGTTM*YPGIADR@.M	6.02	7.50	0.80	1.25
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTM*YPGIADR.M	631.15	347.89	1.81	0.55
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTM*YPGIADR@.M	967.53	505.91	1.91	0.52
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTMYPGIADR@.M	107.82	67.07	1.61	0.62
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTMYPGIADR.M	92.39	55.47	1.67	0.60
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.GYSFTTTAER@.E	2776.94	1518.13	1.83	0.55
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.IWHHTFYNELR@.V	896.74	472.94	1.90	0.53
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.IWHHTFYNELR.V	26.23	10.74	2.44	0.41
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.K#DLYANTVLSGGTTM*YPGIADR@.M	516.89	302.91	1.71	0.59
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.KDLYANTVLSGGTTMYPGIADR.M	42.21	21.35	1.98	0.51
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.QEYDESGPSIVHR@.K	1455.55	864.66	1.68	0.59
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.QEYDESGPSIVHR.K	199.75	113.44	1.76	0.57
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.QEYDESGPSIVHRK.C	75.25	34.18	2.20	0.45
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.VAPEEHPVLLTEAPLNPK#.A	2371.65	1617.88	1.47	0.68
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.VAPEEHPVLLTEAPLNPK.A	68.72	48.88	1.41	0.71
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTM*YPGIADR@.M	1451.24	563.62	2.57	0.39
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTM*YPGIADR.M	911.05	363.17	2.51	0.40
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.DLYANTVLSGGTTMYPGIADR@.M	143.49	63.11	2.27	0.44
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.GYSFTTTAER@.E	2544.13	1029.25	2.47	0.40
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.IWHHTFYNELR@.V	224.44	100.55	2.23	0.45
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.K#DLYANTVLSGGTTM*YPGIADR@.M	663.67	282.46	2.35	0.43
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.K#DLYANTVLSGGTTMYPGIADR@.M	53.32	23.55	2.26	0.44
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.QEYDESGPSIVHR@.K	1909.24	843.43	2.26	0.44
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.QEYDESGPSIVHR.K	280.75	128.03	2.19	0.46
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	R.VAPEEHPVLLTEAPLNPK#.A	106.47	45.91	2.32	0.43
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.YPIEHGIVTNWDDM*EK#.I	67.18	22.74	2.95	0.34
P60710_ACTB_MOUSE	Actb	Actin, cytoplasmic 1 OS=	K.YPIEHGIVTNWDDMEK#.I	11.56	4.80	2.41	0.41
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR@.L	39.70	25.80	1.54	0.65
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	1504.97	1303.97	1.15	0.87
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR@.L	247.21	187.36	1.32	0.76
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	157.58	126.29	1.25	0.80
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR@.L	977.39	847.03	1.15	0.87
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	26.17	34.69	0.75	1.33
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3.49	2.93	1.19	0.84
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.VAPDEHPILLTEAPLNPK.I	44.15	113.48	0.39	2.57
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR@.L	1405.20	750.99	1.87	0.53
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR@.L	203.59	114.03	1.79	0.56
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR@.L	591.39	325.85	1.81	0.55
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR@.L	2137.93	873.63	2.45	0.41
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR@.L	43.00	12.05	3.57	0.28
Q8BFZ3_ACTBL_MOUSE	Actbl2	Beta-actin-like protein 2	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR@.L	13.92	6.50	2.14	0.47
P68033_ACTC_MOUSE	Actc1	Actin, alpha cardiac mus	K.YPIEHGIITNWDDM*EKIWHHTFYNELR.V	30.33	27.33	1.11	0.90
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	R.DDGSTM*M*EIDGDK#.G	1.57	1.87	0.84	1.19
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	R.EGSPANWK#.R	49.97	19.13	2.61	0.38
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	R.ELFQEM*NIELIPPYMIASK#.E	5.37	3.16	1.70	0.59
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	K.IPEGLFDPSNVK#.G	29.19	9.00	3.24	0.31
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	K.LIANNTTVER@.R	340.49	108.49	3.14	0.32
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	R.LK#IPEGLFDPSNVK#.G	78.26	28.57	2.74	0.37
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	K.NGM*VEDWDSFQAILDHTYK#.M	27.22	28.83	0.94	1.06
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	K.QGGPTYYIDTNALR@.V	114.50	41.53	2.76	0.36
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	K.SEASLHPVLM*SEAPWNTR@.A	77.55	26.28	2.95	0.34
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	K.SEASLHPVLMSEAPWNTR@.A	19.63	5.35	3.67	0.27
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	R.STGLILDSGATHTTAIPVHDGYVLQQGIVK#.S	22.41	9.45	2.37	0.42
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	K.VDFPTAIGVVLER@.D	87.24	27.16	3.21	0.31
Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	K.LIANNTTVER@.R	20.89	5.87	3.56	0.28

Q9Z2N8_ACL6A_MOUSE	Actl6a	Actin-like protein 6A OS=	K.LIANNTTVER@.R	14.85	4.87	3.05	0.33
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.AIM*TYVSSFYHAFSGAQK#.A	17.02	13.50	1.26	0.79
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.ALDFIASK#.G	49.54	47.51	1.04	0.96
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.ATLPDADK#ER@.L	6.69	11.50	0.58	1.72
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.DDPLTNLNTAFDVAER.F	6.01	6.77	0.89	1.13
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	R.ETADTDTADQVM*ASFK#.I	10.62	9.06	1.17	0.85
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	R.FAIQDISVEETSAK#.E	51.05	43.63	1.17	0.85
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.GISQEQM*NEFR.A	12.10	12.27	0.99	1.01
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.GYEEWLLNEIR.R	14.58	14.92	0.98	1.02
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	R.HRPELIDYGK.L	18.85	15.09	1.25	0.80
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.ILAGDK#NYITEDELR@.R	17.17	16.86	1.02	0.98
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.LASDLLEWIR@.R	49.36	36.50	1.35	0.74
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.LLETIDQLYLEYAK#.R	16.92	20.47	0.83	1.21
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.LM*LLLEVISGER.L	18.58	14.58	1.27	0.78
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.LVSIGAEEIVDGNVK#.M	18.75	19.37	0.97	1.03
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.M*LDAEDIVGTARPDEK.A	15.13	14.83	1.02	0.98
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.M*TLGM*IWTIILR.F	7.91	8.77	0.90	1.11
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	R.TINEVENQILTR@.D	34.19	28.78	1.19	0.84
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	R.VGWEQLLTTIAR.T	102.40	109.93	0.93	1.07
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.VLAVNQENEQLM*EDYEK#.L	5.35	7.05	0.76	1.32
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.ALDFIASK#.G	18.53	16.08	1.15	0.87
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	R.FAIQDISVEETSAK.E	24.91	19.27	1.29	0.77
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.GISQEQM*NEFR.A	4.58	4.06	1.13	0.89
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	K.LASDLLEWIR@.R	14.82	8.79	1.69	0.59
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	R.TINEVENQILTR@.D	7.57	8.21	0.92	1.08
Q7TPR4_ACTN1_MOUSE	Actn1	Alpha-actinin-1 OS=Mus	R.VGWEQLLTTIAR@.T	35.06	34.91	1.00	1.00
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	K.DDPVTNLNNAFEVAEK#.Y	5.37	5.25	1.02	0.98
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	R.DYETATLSDIK#.A	22.40	23.14	0.97	1.03
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	R.ETTDTDTADQVIASFK#.V	19.82	16.50	1.20	0.83
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	K.GISQEQM*QEFR@.A	20.87	20.78	1.00	1.00
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	R.HR@PELIEYDK#.L	13.14	14.80	0.89	1.13
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	R.K#DDPVTNLNNAFEVAEK#.Y	17.48	19.09	0.92	1.09
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	K.LSGSNPYTTVTPQIINSK.W	11.11	10.53	1.06	0.95
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	K.LVSIGAEEIVDGNAK#.M	31.30	26.40	1.19	0.84
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	R.M*APYQGPDAAPGALDYK#.S	13.84	13.78	1.00	1.00
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	K.M*LDAEDIVNTAR@PDEK#.A	14.12	15.25	0.93	1.08
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	R.SIVDYK#PSLDLLEQQHQLIQEALIFDNK#.H	28.35	22.54	1.26	0.80
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	R.VEQIAAIAQELNELDYYDSHNVNTR.C	8.45	5.68	1.49	0.67
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	K.VLAGDKNFITAEELR.R	26.47	24.87	1.06	0.94
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	K.VQQLVPK.R	23.62	28.10	0.84	1.19
P57780_ACTN4_MOUSE	Actn4	Alpha-actinin-4 OS=Mus	K.LVSIGAEEIVDGNAK#.M	11.27	9.09	1.24	0.81
Q9QZB7_ARP10_MOUSE	Actr10	Actin-related protein 10	K.TAVVIDLGEAFTK#.C	9.85	3.50	2.82	0.36
Q9QZB7_ARP10_MOUSE	Actr10	Actin-related protein 10	K.FNIDGNNERPTPPPNVDYPLDGEK.I	7.46	3.00	2.48	0.40
P61164_ACTZ_MOUSE	Actr1a	Alpha-centractin OS=Mu	K.AQYYLPDGSTIEIGPSR@.F	49.74	20.85	2.39	0.42
P61164_ACTZ_MOUSE	Actr1a	Alpha-centractin OS=Mu	K.DQLQTFSEEHPVLLTEAPLNPR@.K	106.28	41.90	2.54	0.39
P61164_ACTZ_MOUSE	Actr1a	Alpha-centractin OS=Mu	R.KEGYDFHSSSEFEIVK.A	12.58	4.09	3.08	0.32
P61164_ACTZ_MOUSE	Actr1a	Alpha-centractin OS=Mu	K.AQYYLPDGSTIEIGPSR@.F	15.20	4.77	3.18	0.31
P61164_ACTZ_MOUSE	Actr1a	Alpha-centractin OS=Mu	K.DQLQTFSEEHPVLLTEAPLNPR@.K	31.24	6.40	4.88	0.20
P61164_ACTZ_MOUSE	Actr1a	Alpha-centractin OS=Mu	K.AQYYLPDGSTIEIGPSR@.F	23.11	6.10	3.79	0.26
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	K.AGFAGDQIPK#.Y	98.73	46.03	2.14	0.47
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	K.DQLQTFSEEHPVLLTEAPLNPSK#.N	58.32	30.21	1.93	0.52
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	K.ISAPQER@.L	110.25	84.87	1.30	0.77
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	R.IWQYVYSK#.D	69.49	35.72	1.95	0.51
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	R.TLFSNIVLSGGSTLFK#.G	71.21	28.56	2.49	0.40
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	R.TTGVVLDSGDGVTHAVPIYEGFAM*PHSIM*R@.V	8.70	4.20	2.07	0.48
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	K.VQYTLPDGSTLDVGPAR@.F	14.44	12.04	1.20	0.83
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	K.AGFAGDQIPK#.Y	22.03	5.68	3.88	0.26
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	K.DQLQTFSEEHPVLLTEAPLNPSK#.N	9.09	2.40	3.79	0.26
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	R.TLFSNIVLSGGSTLFK#.G	23.17	5.05	4.59	0.22
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	K.AGFAGDQIPK#.Y	24.86	4.90	5.07	0.20
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	K.DQLQTFSEEHPVLLTEAPLNPSK#.N	16.01	6.12	2.62	0.38
Q8R5C5_ACTY_MOUSE	Actr1b	Beta-centractin OS=Mus	R.TLFSNIVLSGGSTLFK#.G	41.91	9.39	4.47	0.22
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	K.DLM*VGDEASELR.S	20.20	21.11	0.96	1.05
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	R.GYAFNHSADFETVR.M	26.20	22.91	1.14	0.87
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	K.ILLTEPPM*NPTK.N	22.15	22.69	0.98	1.02
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	K.QLYLER@.V	9.29	11.64	0.80	1.25
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	K.DLM*VGDEASELR.S	12.34	9.03	1.37	0.73
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	K.ILLTEPPM*NPTK#.N	12.05	8.89	1.36	0.74
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	K.QLYLER@.V	11.36	7.94	1.43	0.70
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	K.DLM*VGDEASELR@.S	24.12	18.33	1.32	0.76
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	K.HLWDYTFGPEK#.L	5.19	4.73	1.10	0.91
P61161_ARP2_MOUSE	Actr2	Actin-related protein 2 O	K.ILLTEPPM*NPTK#.N	21.82	13.84	1.58	0.63
Q99JY9_ARP3_MOUSE	Actr3	Actin-related protein 3 O	R.AEPEDHYFLLTEPPLNTPENR.E	12.73	29.18	0.44	2.29
Q99JY9_ARP3_MOUSE	Actr3	Actin-related protein 3 O	K.EFSIDVGYER@.F	16.44	18.89	0.87	1.15
Q99JY9_ARP3_MOUSE	Actr3	Actin-related protein 3 O	R.FM*EQVIFK.Y	19.61	24.16	0.81	1.23
Q99JY9_ARP3_MOUSE	Actr3	Actin-related protein 3 O	R.FMEQVIFK.Y	6.03	9.71	0.62	1.61
Q99JY9_ARP3_MOUSE	Actr3	Actin-related protein 3 O	K.GVDDLDFFIGDEAIEK#PTYATK#.W	28.84	35.23	0.82	1.22
Q99JY9_ARP3_MOUSE	Actr3	Actin-related protein 3 O	R.HNPVFGVM*S.-	22.36	22.36	1.00	1.00
Q99JY9_ARP3_MOUSE	Actr3	Actin-related protein 3 O	R.FM*EQVIFK#.Y	21.29	9.34	2.28	0.44
Q99JY9_ARP3_MOUSE	Actr3	Actin-related protein 3 O	K.GVDDLDFFIGDEAIEK#PTYATK#.W	21.17	15.18	1.39	0.72
Q99JY9_ARP3_MOUSE	Actr3	Actin-related protein 3 O	K.NIVLSGGSTM*FR@.D	8.88	4.84	1.83	0.55
Q80US4_ARP5_MOUSE	Actr5	Actin-related protein 5 O	R.INLGGSQAAGYLQR@.L	8.06	2.25	3.58	0.28
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	K.ALQEEAASSADDQSGGANTDSLDESM*APNK#.I	6.40	1.97	3.25	0.31
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.DVTSVLIDLER@.Q	14.16	15.07	0.94	1.06
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.ELSISQSPEQK.V	14.63	20.00	0.73	1.37
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.VLIGESEK#AEQLGFAEVTPVTGASLR@.R	6.50	3.87	1.68	0.60
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	K.AEQLGFAEVTPVTGASLR@.R	9.83	3.63	2.71	0.37
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.AIM*EM*PSFYSPTLPR@.C	6.95	6.23	1.12	0.90
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	K.ARDVTSVLIDLER.Q	16.06	12.20	1.32	0.76
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.DLLQLSYGEAK.K	7.34	34.35	0.21	4.68
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.DVTSVLIDLER.Q	25.23	17.86	1.41	0.71
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.ELSISQSPEQK#.V	21.04	8.88	2.37	0.42
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	K.NSIFELAR.G	10.08	10.83	0.93	1.07
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.QGATPPIWYLTDK#.K	16.22	14.24	1.14	0.88
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.SFQLQQIEFLK#.G	29.46	15.66	1.88	0.53
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.STHSAPAPTPTAVPEATR@.S	46.61	33.50	1.39	0.72
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	K.VLNR@LEELGEGK#.A	20.38	9.35	2.18	0.46
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.YLNTNPVGGLLEYAR@.S	31.48	21.16	1.49	0.67
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.AIM*EM*PSFYSPTLPR@.C	4.53	1.73	2.61	0.38
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.DLLQLSYGEAK#.K	16.58	13.71	1.21	0.83
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.DVTSVLIDLER@.Q	16.74	9.13	1.83	0.55
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	K.NSIFELAR@.G	17.23	10.69	1.61	0.62
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.SFQLQQIEFLK#.G	15.98	9.39	1.70	0.59

Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.STHSAPAPTPTAVPEATR@.S	17.02	7.31	2.33	0.43
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.VLIGESEKAEQLGFAEVTPVTGASLR.R	8.39	4.93	1.70	0.59
Q99MU3_DSRAD_MOUSE	Adar	Double-stranded RNA-sp	R.YLNTNPVGGLLEYAR@.S	34.04	18.19	1.87	0.53
Q9QYC0_ADDA_MOUSE	Add1	Alpha-adducin OS=Mus n	R.M*LDNLGYR@.T	18.42	3.72	4.96	0.20
Q9QYC0_ADDA_MOUSE	Add1	Alpha-adducin OS=Mus n	R.SLVQGELVTASK#.A	17.15	9.15	1.88	0.53
Q9QYC0_ADDA_MOUSE	Add1	Alpha-adducin OS=Mus n	R.TLASAGGPDNLVLLDPGK#.Y	12.77	7.49	1.71	0.59
Q9QYC0_ADDA_MOUSE	Add1	Alpha-adducin OS=Mus n	K.VNLQGDIVDR@.G	21.04	7.42	2.84	0.35
Q9QYC0_ADDA_MOUSE	Add1	Alpha-adducin OS=Mus n	R.YFDR@VDENNPEYLR@.E	16.49	4.57	3.61	0.28
Q9QYC0_ADDA_MOUSE	Add1	Alpha-adducin OS=Mus n	R.SPGTPAGEGSGSPPK#.W	10.25	3.72	2.76	0.36
Q9QYC0_ADDA_MOUSE	Add1	Alpha-adducin OS=Mus n	R.TLASAGGPDNLVLLDPGK#.Y	10.06	3.02	3.33	0.30
Q9QYC0_ADDA_MOUSE	Add1	Alpha-adducin OS=Mus n	R.TSTSAVPNLFVPLNTNPK#.E	8.30	3.83	2.16	0.46
Q9QYC0_ADDA_MOUSE	Add1	Alpha-adducin OS=Mus n	K.VNLQGDIVDR@.G	17.52	4.51	3.88	0.26
Q9QYB5_ADDG_MOUSE	Add3	Gamma-adducin OS=Mus	K.VSSGTPIK#IEDPNQFVPLNTNPTEVLEK#.R	1.83	1.50	1.22	0.82
Q9QYB5_ADDG_MOUSE	Add3	Gamma-adducin OS=Mus	R.GLSFSEATASTLVK#.V	15.20	7.03	2.16	0.46
Q9QYB5_ADDG_MOUSE	Add3	Gamma-adducin OS=Mus	K.VNIIGEVVDQGSTDLK#.I	9.74	3.48	2.80	0.36
Q9QYB5_ADDG_MOUSE	Add3	Gamma-adducin OS=Mus	R.GLSFSEATASTLVK#.V	10.31	4.48	2.30	0.43
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	R.DPLYEIVR@.K	10.91	6.58	1.66	0.60
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.NTTWEDVGLWDPSLTK#.N	7.36	3.46	2.13	0.47
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.SPSVSQSQASR.V	5.86	7.94	0.74	1.35
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.SVGQSYGVGQSVR@.L	14.65	9.75	1.50	0.67
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.SYEALVQHVIEDHER@.I	14.65	9.48	1.55	0.65
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.NTTWEDVGLWDPSLTK#.N	5.20	2.59	2.01	0.50
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.IPSDNLEEPVPK.V	11.44	22.74	0.50	1.99
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	R.LGLGGNAPVSIPQQSQSVK#.Q	7.32	4.84	1.51	0.66
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.SPSVSQSQASR.V	11.33	12.65	0.90	1.12
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.SVGQSYGVGQSVR.L	8.07	3.16	2.56	0.39
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	R.TYEQM*EFPLLK.K	7.89	10.95	0.72	1.39
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.SPSVSQSQASR@.V	6.65	6.64	1.00	1.00
A2BDX0_A2BDX0_MOUSE	Adnp	Activity-dependent neur	K.SVGQSYGVGQSVR@.L	8.59	2.55	3.37	0.30
Q9JKV1_ADRM1_MOUSE	Adrm1	Proteasomal ubiquitin re	K.YLVEFR@.A	5.32	3.76	1.42	0.71
Q640N1_AEBP1_MOUSE	Aebp1	Adipocyte enhancer-binc	R.YLSPDATVSTEVR.A	5.71	7.98	0.72	1.40
Q640N1_AEBP1_MOUSE	Aebp1	Adipocyte enhancer-binc	R.GEDDDGVSEAQETPDHAIFR@.W	13.11	5.70	2.30	0.43
Q640N1_AEBP1_MOUSE	Aebp1	Adipocyte enhancer-binc	R.YLSPDATVSTEVR.A	15.23	9.79	1.55	0.64
Q80YS6_AFAP1_MOUSE	Afap1	Actin filament-associatec	K.AVLTNILLR@.L	23.89	11.50	2.08	0.48
Q80YS6_AFAP1_MOUSE	Afap1	Actin filament-associatec	K.ITQQGTDPLVLAVQSK#.E	14.67	6.78	2.16	0.46
Q80YS6_AFAP1_MOUSE	Afap1	Actin filament-associatec	R.VSLELELTEVK#.E	10.60	3.41	3.11	0.32
Q80YS6_AFAP1_MOUSE	Afap1	Actin filament-associatec	K.AVLTNILLR@.L	13.76	3.71	3.71	0.27
Q80YS6_AFAP1_MOUSE	Afap1	Actin filament-associatec	K.ITQQGTDPLVLAVQSK#.E	9.09	2.95	3.08	0.32
O55112_AFF2_MOUSE	Aff2	AF4/FMR2 family membe	K.ETASKPK#.R	3.30	15.72	0.21	4.77
Q80WT5_AFTIN_MOUSE	Aftph	Aftiphilin OS=Mus muscu	K.EVTLDGSFEDTGNTER@.E	4.39	1.67	2.62	0.38
Q80WT5_AFTIN_MOUSE	Aftph	Aftiphilin OS=Mus muscu	K.GAVASGHLQEPGTSVQTALLNR@.L	15.25	4.46	3.42	0.29
Q80WT5_AFTIN_MOUSE	Aftph	Aftiphilin OS=Mus muscu	K.SQSDVVLSTTSK#.E	7.87	6.45	1.22	0.82
Q8VHH5_AGAP3_MOUSE	Agap3	Arf-GAP with GTPase, AN	R.FESVHPNIYAIYDLIER@.I	4.31	3.95	1.09	0.92
Q8VHH5_AGAP3_MOUSE	Agap3	Arf-GAP with GTPase, AN	K.LFLAPLPSSDVPLGQQLLR@.A	1.79	1.79	1.00	1.00
Q8K2K6_AGFG1_MOUSE	Agfg1	Arf-GAP domain and FG r	K.SSSADFGTFSTSQSHQTASTVSK#.V	6.65	4.46	1.49	0.67
Q80WC7_AGFG2_MOUSE	Agfg2	Arf-GAP domain and FG r	K.IWLGLFDAR@.T	11.82	5.59	2.11	0.47
Q80WC7_AGFG2_MOUSE	Agfg2	Arf-GAP domain and FG r	K.SISM*TTFTEPEVLFLQSR@.G	5.51	5.17	1.07	0.94
A2ASQ1_AGRIN_MOUSE	Agrn	Agrin OS=Mus musculus (	R.STAATPSDVASLATAIFR.E	3.50	5.08	0.69	1.45
Q6PAL7_AHDC1_MOUSE	Ahdc1	AT-hook DNA-binding mc	R.AFASTGLESGASGR@.G	5.87	3.84	1.53	0.65
Q6PAL7_AHDC1_MOUSE	Ahdc1	AT-hook DNA-binding mc	K.VGSGLLADFLGR@.T	7.79	5.51	1.41	0.71
Q6PAL7_AHDC1_MOUSE	Ahdc1	AT-hook DNA-binding mc	R.AFASTGLESGASGR@.G	12.59	8.70	1.45	0.69
Q6PAL7_AHDC1_MOUSE	Ahdc1	AT-hook DNA-binding mc	R.GSYYAGAPSGQTELSQER@.Q	4.77	2.93	1.63	0.61
Q6PAL7_AHDC1_MOUSE	Ahdc1	AT-hook DNA-binding mc	K.SGFLGPM*AEPHPEDTFTVTSL.-	3.80	3.80	1.00	1.00
Q6PAL7_AHDC1_MOUSE	Ahdc1	AT-hook DNA-binding mc	K.VGSGLLADFLGR@.T	20.05	11.50	1.74	0.57
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ASLGSLEGEVEAEASSPK#.G	5.74	2.80	2.05	0.49
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.DDGVFVQEVM*QNSPAAR@.T	9.24	2.43	3.81	0.26
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.EGDQIVGATIYFDNLQSGEVTQLLNTM*GHHTVGLK#.L	18.81	3.25	5.79	0.17
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FQVTVPGAK#.V	37.84	10.40	3.64	0.27
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.HEVTEISNTDVETQPGK#.T	86.04	20.56	4.19	0.24
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.IEGSITGPSVEIGTPDVDVHGLGGK#.L	13.08	2.00	6.55	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LK#GPQITGPSLEGDLGLK#.G	25.19	3.88	6.50	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.LPSGSGPASPTTGSAVDIR@.A	44.10	13.12	3.36	0.30
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.LR@SEDGVEGDLGETQSR@.T	24.15	6.51	3.71	0.27
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.R@VTAYTVDVTGR@.E	9.54	5.58	1.71	0.58
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.SSEVVLSGDDEDYQR@.I	65.89	14.93	4.41	0.23
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VGSLDVNVK#.A	61.74	12.73	4.85	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.VPGVDVSSSLGAGSVEVQAPSLQSGDIGK#.I	7.89	3.07	2.57	0.39
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.LR@SEDGVEGDLGETQSR@.T	16.99	3.41	4.98	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.SSEVVLSGDDEDYQR@.I	18.96	4.19	4.53	0.22
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.VTAYTVDVTGR@.E	8.04	2.63	3.06	0.33
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ADVDISVPK#.L	22.87	4.93	4.64	0.22
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.AEGEIK#VPDVELK#.S	57.98	8.34	6.95	0.14
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.AEGPEVDVNLPK#.A	74.22	21.74	3.41	0.29
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.AESPEM*EVNLPK#.S	12.46	1.85	6.72	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.DDGVFVQEVM*QNSPAAR@.T	14.36	2.64	5.44	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.DDGVFVQEVMQNSPAAR@.T	6.47	1.61	4.02	0.25
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.DIDITSPEFM*IK#.I	13.44	2.04	6.59	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.EGDQIVGATIYFDNLQSGEVTQLLNTM*GHHTVGLK#.L	47.77	7.04	6.78	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.EGVK#DIDITSPEFM*IK#.I	105.39	14.91	7.07	0.14
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.EGVK#DIDITSPEFMIK#.I	22.58	4.50	5.02	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FGVSAGLDGQIPEVGLSVSAPESSVGHK#.G	31.48	8.69	3.62	0.28
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FQVTVPGAK#.V	78.47	12.56	6.25	0.16
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FSVPGFK#.A	38.59	9.11	4.24	0.24
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FSVPGVK#.G	43.56	12.64	3.45	0.29
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GEGLDVNVTLPEGDISISGPK#.V	12.46	3.90	3.19	0.31
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GEYDVTVPR@.A	22.28	5.67	3.93	0.25
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GGVDVILPNVEGK#.A	23.94	8.53	2.81	0.36
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GK#GGVDVILPNVEGK#.A	42.19	8.09	5.22	0.19
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GLEVDVK#.G	41.59	7.59	5.48	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GPSFNVASPESDFGVSLK#.G	6.32	2.99	2.11	0.47
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.HEVTEISNTDVETQPGK#.T	115.62	23.40	4.94	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.IEGSITGPSVEIGTPDVDVHGLGGK#.L	57.15	11.21	5.10	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.IK#GDVPSVGLEGPNIDLQGPEGK#.I	7.51	2.61	2.87	0.35
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.ISM*ADVDLNVAAPK#.G	41.86	9.00	4.65	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.ISMADVDLNVAAPK#.G	13.04	3.63	3.59	0.28
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LDIETSDVSLEGPEGK#.L	12.60	2.17	5.80	0.17
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LDISAPDLNLEGPEGK#.L	15.00	2.99	5.02	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LK#GPDINLPEVSVK#.T	78.00	19.01	4.10	0.24
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LK#GPQITGPSLEGDLGLK#.G	83.32	15.23	5.47	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.LPSGSGPASPTTGSAVDIR@.A	62.67	14.74	4.25	0.24
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.R@VTAYTVDVTGR@.E	16.35	3.61	4.53	0.22
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.SDIDVSGPNVDVK#.V	17.86	2.00	8.92	0.11
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.SEDGVEGDLGETQSR@.T	24.03	3.18	7.55	0.13

E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.SSEVVLSGDDEDYQR@.I	109.72	20.32	5.40	0.19
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VDIDTPQVDVHGPDLK#.I	54.24	11.11	4.88	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.VDIETPNLEGTLTGPK#.I	81.68	14.33	5.70	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VGSLDVNVK#.A	98.84	20.40	4.85	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VNVEAPNVNM*EGLGGK#.L	30.35	5.63	5.39	0.19
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VNVEAPNVNMEGLGGK#.L	14.16	10.62	1.33	0.75
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VPDVNIEGPEGK#.L	16.88	31.09	0.54	1.84
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.VPGVDVSSSLGAGSVEVQAPSLQSGDIGK#.I	29.90	6.35	4.71	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VQANLDTPDINIEGPEAK#.I	3.92	2.26	1.73	0.58
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.VTAYTVDVTGR@.E	55.94	9.93	5.63	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ADLDISGTK#.V	28.25	7.27	3.88	0.26
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ADVDASLPEVEGGVK#.V	25.16	3.79	6.63	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ADVDASLPEVEGGVK#VPDVDIK#GPK#.V	13.10	2.03	6.46	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ADVDISVPK#.L	117.73	17.70	6.65	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.AEGEIK#VPDVELK#.S	144.02	29.09	4.95	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.AEGPEVDVNLPK#.A	226.27	59.07	3.83	0.26
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.AEGPEVSLPK#.A	58.30	12.20	4.78	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.AESPEM*EVNLPK#.S	41.49	5.97	6.95	0.14
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.AESPEMEVNLPK#.S	20.61	4.08	5.05	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.APAVDIK#.G	40.59	19.41	2.09	0.48
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.APDVQLNAPDVDVHGPEWNLK#.M	9.59	4.07	2.36	0.42
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.APEVDVQGPEWSLK#.M	31.46	7.09	4.43	0.23
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ASLGSLEGEVEAEASSPK#.G	9.00	4.57	1.97	0.51
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ATIDVSGPK#LDIETSDVSLEGPEGK#.L	16.56	7.84	2.11	0.47
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.DDGVFVQEVM*QNSPAAR@.T	17.00	4.01	4.24	0.24
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.DDGVFVQEVM*QNSPAAR@.T	18.51	3.02	6.12	0.16
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.DDGVFVQEVMQNSPAAR@.T	7.04	2.78	2.53	0.40
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.EGDQIVGATIYFDNLQSGEVTQLLNTM*GHHTVGLK#.L	53.60	6.42	8.34	0.12
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.EGVK#DIDITSPEFM*IK#.I	91.69	19.59	4.68	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FGM*PGFK#.A	46.27	8.37	5.53	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FGMPGFK#.A	13.81	1.51	9.15	0.11
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FGVSAGLDGQIPEVGLSVSAPESSVGHK#.G	57.82	8.46	6.83	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FK#MPEMNIK#.A	10.06	2.38	4.24	0.24
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FSM*PGFK#.A	179.44	36.51	4.91	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FSMPGFK#.A	42.15	10.19	4.14	0.24
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FSM*PGFK#GEGAEVDVNLQK#.A	16.89	3.41	4.96	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FSM*PSLK#.G	7.30	3.43	2.13	0.47
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FSM*PTLK#.G	14.15	3.59	3.95	0.25
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.FSVPGFK#.A	99.70	17.33	5.75	0.17
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GDVDVSLPK#.V	19.60	6.73	2.91	0.34
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GEGAEVDVNLQK#.A	27.13	5.49	4.94	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GEGLDVNVTLPEGDISISGPK#.V	10.24	1.51	6.78	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GEGPDVDVSLPK#.A	57.33	12.66	4.53	0.22
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GEGPELDVNM*PK#.A	29.53	7.28	4.05	0.25
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GEGPELDVNMPK#.A	5.81	2.26	2.57	0.39
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GEGPEVDIPK#.A	39.66	10.95	3.62	0.28
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GEYDVTVPR@.A	58.21	10.20	5.71	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GGQTGLQGPGLSVSGPQGHLESESGK#.V	6.61	2.28	2.89	0.35
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GGVDVILPNVEGK#.A	57.76	11.81	4.89	0.20
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GGVTGSPEASISGSK#.G	9.75	6.40	1.52	0.66
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GLEVDVK#.G	44.09	11.69	3.77	0.27
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GNLDM*SAPK#.I	22.33	4.78	4.67	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GPAIGGALPGISIQGPEGNLQM*PGIK#.A	4.03	1.88	2.14	0.47
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GPDINLPEVSVK#.T	17.06	2.50	6.83	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GPGLDFEGPDAK#.L	6.14	3.88	1.58	0.63
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GPQISAPSM*DFNLEGPK#.V	7.75	3.47	2.23	0.45
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GPQITGPSLEGDLGLK#.G	29.83	7.31	4.08	0.25
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GPQVSSSLNLDTSK#.L	9.35	3.12	2.99	0.33
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GPSFNVASPESDFGVSLK#.G	8.93	3.54	2.52	0.40
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GSGLGLHGAVPDIGVK#.G	16.21	4.13	3.92	0.25
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.GSR@VDIETPNLEGTLTGPK#.I	23.04	5.64	4.08	0.24
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.HEVTEISNTDVETQPGK#.T	165.95	22.25	7.46	0.13
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.HEVTEISNTDVETQPGK#.T	25.79	4.79	5.38	0.19
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.IEGEM*K#VPDVDIK#.G	58.73	9.26	6.34	0.16
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.IEGSITGPSVEIGTPDVDVHGLGGK#.L	75.96	13.33	5.70	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.IK#GDIDVSVPK#.I	25.44	24.09	1.06	0.95
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.IK#GDVPSVGLEGPNIDLQGPEGK#.I	16.40	8.53	1.92	0.52
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.ISM*ADVDLNVAAPK#.G	107.12	19.27	5.56	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.ISMADVDLNVAAPK#.G	16.79	7.22	2.32	0.43
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ISM*PDIDLHLK#.S	13.56	5.69	2.38	0.42
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ISM*PDLHLK#.G	56.69	13.98	4.06	0.25
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ISM*PDVDLNIK#.G	27.30	6.35	4.30	0.23
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ISM*PDVGLNLK#.G	24.24	37.32	0.65	1.54
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ISMPDVGLNLK#.G	13.66	2.28	6.00	0.17
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ISM*PDVSLNLK#.G	32.57	5.64	5.77	0.17
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ISMPDVSLNLK#.G	11.01	3.03	3.63	0.28
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ISM*PEIDLNLK#.G	19.96	7.61	2.62	0.38
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.ISM*PEVDLNLK#.G	20.94	7.95	2.63	0.38
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LDANIPEVAVEGPEGK#.W	23.67	8.08	2.93	0.34
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LDIETSDVSLEGPEGK#.L	90.09	18.77	4.80	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LDISAPDLNLEGPEGK#.L	178.70	30.22	5.91	0.17
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LK#GPDINLPEVSVK#.T	126.48	26.22	4.82	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LK#GPQITGPSLEGDLGLK#.G	67.89	8.37	8.11	0.12
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.LPSGSGPASPTTGSAVDIR@.A	65.34	14.35	4.55	0.22
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.LSSGQISGPEIK#.G	11.09	5.83	1.90	0.53
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.M*DINAPDM*DVQGPDWHLK#.M	30.34	8.16	3.72	0.27
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.M*DISAPDVEVHGPEWNLK#.M	54.22	9.73	5.57	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.R@VTAYTVDVTGR@.E	32.32	5.84	5.53	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.SDIDVSGPNVDVK#.V	61.52	9.85	6.25	0.16
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.SDIDVSGPNVDVK#VPDVNIEGPEGK#.L	29.34	3.61	8.14	0.12
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.SEDGVEGDLGETQSR@.T	36.08	5.70	6.33	0.16
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.SSEVVLSGDDEDYQR@.I	142.27	22.47	6.33	0.16
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.TPQISM*SDIDLNVK#.G	6.88	3.89	1.77	0.57
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.TSAPEVK#.G	96.78	18.86	5.13	0.19
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VDIDTPQVDVHGPDLK#.I	104.55	17.17	6.09	0.16
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VDIDVPDLDIEGPEGK#.L	46.07	11.88	3.88	0.26
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VDIDVPDVNIEGPDTK#.L	56.19	10.17	5.53	0.18
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VDIDVPDVNVEGPDM*K#.V	4.16	2.55	1.63	0.61
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.VDIETPNLEGTLTGPK#.I	131.16	20.62	6.36	0.16
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.VDIETPNLEGTLTGPK#.I	21.72	3.31	6.56	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VDINAPDVDVR@.G	72.70	19.63	3.70	0.27
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VDVSVPDVDVHGPDWNLK#.M	78.71	19.10	4.12	0.24
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VEGDLK#GPDIDIK#.G	89.96	15.97	5.63	0.18

E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VEVSAPDVSIEGSEGK#.L	54.38	13.38	4.06	0.25
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VGIDAPDVEVHGPDWHLK#.M	116.97	19.79	5.91	0.17
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VGSLDVNVK#.A	130.11	17.82	7.30	0.14
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VK#GDM*DVTVPK#.I	119.64	18.34	6.52	0.15
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VK#GDVDVSLPK#.V	184.83	35.69	5.18	0.19
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VNVEAPNVNM*EGLGGK#.L	56.77	14.98	3.79	0.26
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VNVEAPNVNMEGLGGK#.L	24.54	7.95	3.09	0.32
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VPDVDIK#.G	87.39	11.00	7.94	0.13
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VPDVNIEGPEGK#.L	43.03	70.25	0.61	1.63
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.VPGVDVSSSLGAGSVEVQAPSLQSGDIGK#.I	47.06	8.83	5.33	0.19
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VQANLDTPDINIEGPEAK#.I	12.59	5.79	2.17	0.46
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VSLPDVDLDLK#.G	48.44	10.08	4.81	0.21
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	K.VSVATPDVSLEASEGAVK#.L	8.14	1.80	4.51	0.22
E9Q616_E9Q616_MOUSE	Ahnak	Protein Ahnak OS=Mus m	R.VTAYTVDVTGR@.E	85.44	13.28	6.43	0.16
F7DBB3_F7DBB3_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	R.FSFPAPSSEADVFFPVVR@.E	15.15	7.04	2.15	0.46
F7DBB3_F7DBB3_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	R.SPSTTAELVR@.S	14.59	7.15	2.04	0.49
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.VEADVAPPQVQGDLK#.T	6.23	2.75	2.26	0.44
F7DBB3_F7DBB3_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	R.GESQEVALPSR@.M	14.05	4.08	3.44	0.29
F7DBB3_F7DBB3_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	R.TEGPLQPSGR@.Q	16.40	4.77	3.44	0.29
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.GEVSAPDLEVSLPGVEVDIQAPGAK#.L	9.22	3.12	2.95	0.34
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.LEGELALADKDVAAK.D	171.92	52.87	3.25	0.31
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.LPEGQLPEAELPAAQAAAGAGLK#.G	10.11	3.91	2.59	0.39
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.M*PSFGVSAPGK#PSLEASLEVGAPK#.V	14.55	8.00	1.82	0.55
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.MPSFGVSAPGK#PSLEASLEVGAPK#.V	3.97	2.43	1.63	0.61
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.TPDLSVQLPSADLELK#.A	54.46	18.41	2.96	0.34
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.TPDLSVQLR@.S	19.92	5.80	3.43	0.29
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.VDLK#GPHVDLK#.G	34.92	11.20	3.12	0.32
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.VEADVAPPQVQGDLK#.T	67.95	23.95	2.84	0.35
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.VEADVAPPQVQGDLK#TPDLSVQLPSADLELK#.A	6.54	2.91	2.25	0.44
E9PYB0_E9PYB0_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.VQM*PSLK#.M	46.83	15.45	3.03	0.33
F7CVJ5_F7CVJ5_MOUSE	Ahnak2	Protein Ahnak2 (Fragmen	K.LPEGQLPEAELPAAQAAAAGAGLK#.G	20.34	8.51	2.39	0.42
Q8BK64_AHSA1_MOUSE	Ahsa1	Activator of 90 kDa heat	K.ETFLTSPEELYR@.V	16.38	6.06	2.70	0.37
Q8BK64_AHSA1_MOUSE	Ahsa1	Activator of 90 kDa heat	K.TLFLAVR@.V	20.31	5.62	3.61	0.28
Q8BK64_AHSA1_MOUSE	Ahsa1	Activator of 90 kDa heat	R.VFTTQELVQAFTHAPAALEADR@.G	38.34	19.62	1.95	0.51
Q8BK64_AHSA1_MOUSE	Ahsa1	Activator of 90 kDa heat	R.VFTTQELVQAFTHAPAALEADR@.G	9.54	3.56	2.68	0.37
Q9EQX4_AIF1L_MOUSE	Aif1l	Allograft inflammatory fa	K.M*ISEVTGGVSDTISYR.D	5.97	5.35	1.12	0.90
E9PVP1_E9PVP1_MOUSE	Aim1	Aurora kinase B OS=Mus	K.SNLPNVGSVDADFLGLFK#.A	16.56	3.15	5.26	0.19
E9PVP1_E9PVP1_MOUSE	Aim1	Aurora kinase B OS=Mus	K.VFDPNVFTIGLGK#.K	13.90	5.58	2.49	0.40
P31230_AIMP1_MOUSE	Aimp1	Aminoacyl tRNA synthas	K.GAEADQIIEYLK#.Q	14.43	4.79	3.01	0.33
Q8R010_AIMP2_MOUSE	Aimp2	Aminoacyl tRNA synthas	R.FLFSLFGQK#.H	11.66	4.03	2.89	0.35
O08915_AIP_MOUSE	Aip	AH receptor-interacting	R.NIAEGK#DPLEGQR@.H	12.49	6.65	1.88	0.53
O08915_AIP_MOUSE	Aip	AH receptor-interacting	R.TLHSDNEGSVIDDSR@.T	16.71	7.25	2.30	0.43
O08915_AIP_MOUSE	Aip	AH receptor-interacting	K.VLELDPALAPVVSR@.E	37.29	38.56	0.97	1.03
Q9R0Y5_KAD1_MOUSE	Ak1	Adenylate kinase isoenzy	K.IIFVVGGPGSGK#.G	11.05	3.68	3.00	0.33
Q9WTP7_KAD3_MOUSE	Ak3	GTP:AMP phosphotransf	R.QNM*LQGTEIGVLAK#.T	3.42	2.55	1.34	0.75
O88845_AKA10_MOUSE	Akap10	A-kinase anchor protein	K.SIEQDAVNTFTK#.Y	6.21	2.17	2.87	0.35
O88845_AKA10_MOUSE	Akap10	A-kinase anchor protein	K.SIEQDAVNTFTK#.Y	7.20	3.17	2.27	0.44
O88845_AKA10_MOUSE	Akap10	A-kinase anchor protein	K.VFLPGFLSSNLYYK#.Y	7.19	1.97	3.66	0.27
Q9WTQ5_AKA12_MOUSE	Akap12	A-kinase anchor protein	R.AQENVELPQLK#.G	9.73	30.30	0.32	3.11
Q9WTQ5_AKA12_MOUSE	Akap12	A-kinase anchor protein	R.DVLEPTQALAAGAVPILAK#.A	11.09	3.59	3.09	0.32
Q9WTQ5_AKA12_MOUSE	Akap12	A-kinase anchor protein	K.GAVYVSEELSK#.T	14.09	5.16	2.73	0.37
Q9WTQ5_AKA12_MOUSE	Akap12	A-kinase anchor protein	K.SDTVQLLTVK#.K	9.42	6.47	1.46	0.69
Q9WTQ5_AKA12_MOUSE	Akap12	A-kinase anchor protein	K.TLVHTVSVAVIDGTR@.A	19.77	6.16	3.21	0.31
E9PVD4_E9PVD4_MOUSE	Akap13	Protein Akap13 (Fragmen	R.IGDVLVSQFSGESAER@.L	15.32	2.01	7.63	0.13
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	R.AVLTVVK#DEDHGILDQFSR@.S	28.84	14.76	1.95	0.51
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	K.HLDGIEHTK#EDVVTEQIDFSAAR@.K	3.15	1.97	1.60	0.63
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	K.LWAEDGEFTSAR@.A	22.55	8.23	2.74	0.36
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	R.SVNVSLTQEELDSGLDELSVR@.S	7.82	3.75	2.09	0.48
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	R.TLSM*IEEEIR@.A	9.71	3.98	2.44	0.41
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	K.YSEAAELR.S	22.18	8.47	2.62	0.38
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	K.LWAEDGEFTSAR@.A	12.84	4.21	3.05	0.33
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	R.SVNVSLTQEELDSGLDELSVR@.S	19.57	9.80	2.00	0.50
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	R.TLSM*IEEEIR@.A	8.22	4.01	2.05	0.49
O54931_AKAP2_MOUSE	Akap2	A-kinase anchor protein	K.YSEAAELR@.S	14.99	5.13	2.92	0.34
Q9DBR0_AKAP8_MOUSE	Akap8	A-kinase anchor protein	R.GGISSGGEGVQDR@.D	5.35	5.82	0.92	1.09
Q9DBR0_AKAP8_MOUSE	Akap8	A-kinase anchor protein	K.AVEGEGEPAAAHSDVLTEVEGPVDTAEASSDPHTEK#.L	35.79	14.29	2.50	0.40
Q9DBR0_AKAP8_MOUSE	Akap8	A-kinase anchor protein	R.FGPDNM*GR@.K	39.71	18.98	2.09	0.48
Q9DBR0_AKAP8_MOUSE	Akap8	A-kinase anchor protein	R.GGISSGGEGVQDR.D	45.78	26.32	1.74	0.57
Q9DBR0_AKAP8_MOUSE	Akap8	A-kinase anchor protein	K.LPDK#TVEFLQEYIINR@.N	46.85	16.96	2.76	0.36
Q9DBR0_AKAP8_MOUSE	Akap8	A-kinase anchor protein	R.NEAAM*PTADAGSTLPVIAIPGIM*EDELEQTGAEAK#.D	10.85	6.58	1.65	0.61
Q9DBR0_AKAP8_MOUSE	Akap8	A-kinase anchor protein	R.SFEDEEIQK#.H	42.21	18.29	2.31	0.43
Q9DBR0_AKAP8_MOUSE	Akap8	A-kinase anchor protein	R.SNSSTFIR@.S	41.95	23.71	1.77	0.57
Q9DBR0_AKAP8_MOUSE	Akap8	A-kinase anchor protein	K.TVEFLQEYIINR@.N	32.49	16.88	1.92	0.52
Q9R0L7_AKP8L_MOUSE	Akap8l	A-kinase anchor protein	K.GALTAQDESSQAK#.R	15.04	7.82	1.92	0.52
Q9R0L7_AKP8L_MOUSE	Akap8l	A-kinase anchor protein	R.GIPGLDM*EDDEEGGGGP.-	6.92	6.92	1.00	1.00
Q9R0L7_AKP8L_MOUSE	Akap8l	A-kinase anchor protein	K.TVEDLDGLIQQIYR@.D	14.11	6.25	2.26	0.44
Q9R0L7_AKP8L_MOUSE	Akap8l	A-kinase anchor protein	K.TWTTADFR@.T	13.33	4.66	2.86	0.35
Q70FJ1_AKAP9_MOUSE	Akap9	A-kinase anchor protein	K.LQIQFQHLQANETLQNSTLSR@.T	4.26	2.42	1.76	0.57
Q70FJ1_AKAP9_MOUSE	Akap9	A-kinase anchor protein	K.TTSAAEETIGR@.H	5.03	6.80	0.74	1.35
Q70FJ1_AKAP9_MOUSE	Akap9	A-kinase anchor protein	R.VLLEELEALK#.Q	13.20	4.91	2.69	0.37
Q70FJ1_AKAP9_MOUSE	Akap9	A-kinase anchor protein	K.VTEEGAELSQR@.L	5.44	2.85	1.91	0.52
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.QIAASSQESVGR@.V	5.18	2.64	1.96	0.51
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.LASIVEQVSVLQNQGR@.E	6.90	4.76	1.45	0.69
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.AEIINHLADLLTDQR@EEILLANK#K#.D	34.77	17.31	2.01	0.50
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.DLEEAEGR@.L	14.80	9.68	1.53	0.65
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.FASYLTFSPSEVK#.S	18.93	13.78	1.37	0.73
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.GPVGLEGLLTTK#.W	50.27	19.74	2.55	0.39
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.IIDLIIPR@.G	20.12	8.31	2.42	0.41
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.LASIVEQVSVLQNQGR@.E	11.16	7.62	1.46	0.68
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.LGSAVVTR@.G	24.72	12.76	1.94	0.52
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.LIDIFYPGDQQSVTFGTK#.S	23.75	11.61	2.05	0.49
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.LNSLAIGLR@.Q	47.67	27.13	1.76	0.57
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.LR@HEILLSQSVR@.Q	11.63	11.53	1.01	0.99
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.M*LATLEPEQR@.A	16.02	7.93	2.02	0.49
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.QIAASSQESVGR@.V	24.53	13.53	1.81	0.55
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.TPLFDQIIDM*LR@.V	36.10	17.13	2.11	0.47
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.VGTFFSEVK#PAGPTVEQQGEM*AR@.S	26.28	11.95	2.20	0.45
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.VSGHVITDIVEGK#.K	24.85	13.57	1.83	0.55
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.AEIINHLADLLTDQR@EEILLANK#K#.D	15.49	3.46	4.48	0.22
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.FASYLTFSPSEVK#.S	16.63	4.51	3.69	0.27
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.GQDHVVSDFSEHGSLK#.Y	14.22	3.90	3.65	0.27
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.IIDLIIPR@.G	6.61	2.51	2.64	0.38
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.LASIVEQVSVLQNQGR@.E	9.21	2.86	3.22	0.31

Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.LIDIFYPGDQQSVTFGTK#.S	18.14	5.25	3.46	0.29
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.LNSLAIGLR@.Q	15.02	4.05	3.71	0.27
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.M*LATLEPEQR@.A	31.82	1.42	22.37	0.04
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.QIAASSQESVGR@.V	13.55	3.66	3.70	0.27
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.TPLFDQIIDM*LR@.V	24.30	9.79	2.48	0.40
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	R.VGLGGM*EAK#.V	18.15	5.14	3.53	0.28
Q9Z110_P5CS_MOUSE	Aldh18a1	Delta-1-pyrroline-5-carb	K.VSGHVITDIVEGK#.K	16.71	4.08	4.09	0.24
P47738_ALDH2_MOUSE	Aldh2	Aldehyde dehydrogenase	R.GYFIQPTVFGDVK#.D	6.47	5.62	1.15	0.87
P47738_ALDH2_MOUSE	Aldh2	Aldehyde dehydrogenase	K.VAEQTPLTALYVANLIK.E	11.84	15.53	0.76	1.31
P47738_ALDH2_MOUSE	Aldh2	Aldehyde dehydrogenase	R.VVGNPFDSR.T	4.26	5.98	0.71	1.40
P47740_AL3A2_MOUSE	Aldh3a2	Fatty aldehyde dehydrog	K.IAFGGEM*DEATR@.Y	6.12	1.40	4.37	0.23
Q9DBT5_AMPD2_MOUSE	Ampd2	AMP deaminase 2 OS=Mu	R.NPLPEYLSR@.G	7.59	2.89	2.63	0.38
P53995_APC1_MOUSE	Anapc1	Anaphase-promoting cor	R.AGQLSYK#EDPM*GWQSLLAQTVANR@.N	4.32	2.28	1.89	0.53
P53995_APC1_MOUSE	Anapc1	Anaphase-promoting cor	R.GLFINSEFLPVVK#.C	16.71	6.43	2.60	0.39
P53995_APC1_MOUSE	Anapc1	Anaphase-promoting cor	R.GM*FTLFSYHPVPTEPLPVPK#.L	15.14	5.94	2.55	0.39
P53995_APC1_MOUSE	Anapc1	Anaphase-promoting cor	K.LILEFFSSR@.S	11.70	4.89	2.40	0.42
P53995_APC1_MOUSE	Anapc1	Anaphase-promoting cor	K.LLGSM*DEVVLLSPVPELR@.D	12.03	2.56	4.70	0.21
P53995_APC1_MOUSE	Anapc1	Anaphase-promoting cor	R.QLQPASELWSSDGAAGLVGSLQEVTIHEK#.Q	4.68	2.65	1.76	0.57
P53995_APC1_MOUSE	Anapc1	Anaphase-promoting cor	R.SFDFEGSLSPVIAPK#.K	9.37	3.44	2.72	0.37
P53995_APC1_MOUSE	Anapc1	Anaphase-promoting cor	R.VNVVQYPELSDHEFIEEK#.E	8.23	4.01	2.05	0.49
P53995_APC1_MOUSE	Anapc1	Anaphase-promoting cor	K.WVDSNVPQIIR@.E	6.93	2.97	2.33	0.43
Q9CPV2_APC16_MOUSE	Anapc16	Anaphase-promoting cor	R.FK#PIEQLLGFTPSSG.-	8.54	3.83	2.23	0.45
Q9CPV2_APC16_MOUSE	Anapc16	Anaphase-promoting cor	K.GAGEM*LEDGSER@.F	2.95	1.45	2.03	0.49
Q8BZQ7_ANC2_MOUSE	Anapc2	Anaphase-promoting cor	R.AAVEVLR@.G	11.74	3.52	3.34	0.30
Q8BZQ7_ANC2_MOUSE	Anapc2	Anaphase-promoting cor	R.GVLFFSTPR@.T	8.79	3.33	2.64	0.38
Q8BZQ7_ANC2_MOUSE	Anapc2	Anaphase-promoting cor	R.LGLLM*GAGAQGLR@.E	8.58	2.73	3.15	0.32
Q91W96_APC4_MOUSE	Anapc4	Anaphase-promoting cor	K.ANELLQVIDSSM*K#.N	9.88	4.04	2.45	0.41
Q91W96_APC4_MOUSE	Anapc4	Anaphase-promoting cor	K.FVQEK#PTTTSVQDEFM*HLLLWGK#.A	7.27	3.85	1.89	0.53
Q91W96_APC4_MOUSE	Anapc4	Anaphase-promoting cor	R.LDEQGSIIPTR@.T	12.88	5.56	2.31	0.43
Q91W96_APC4_MOUSE	Anapc4	Anaphase-promoting cor	K.LGQSIESSYSSIQK#.L	7.68	1.63	4.73	0.21
Q91W96_APC4_MOUSE	Anapc4	Anaphase-promoting cor	K.ANELLQVIDSSM*K#.N	6.96	4.82	1.44	0.69
Q91W96_APC4_MOUSE	Anapc4	Anaphase-promoting cor	R.LDEQGSIIPTR@.T	8.69	3.85	2.26	0.44
Q91W96_APC4_MOUSE	Anapc4	Anaphase-promoting cor	K.LLAFALADTK#.K	15.45	4.80	3.22	0.31
Q8BTZ4_APC5_MOUSE	Anapc5	Anaphase-promoting cor	R.SSSPTIAM*PVLLEALALSK#.E	8.11	2.52	3.21	0.31
Q8BTZ4_APC5_MOUSE	Anapc5	Anaphase-promoting cor	K.TSVVGLFLR@.H	11.68	2.12	5.52	0.18
G5E8K5_ANK3_MOUSE	Ank3	Ankyrin-3 OS=Mus muscu	K.AAALLLQNDTNADVESK#.S	5.24	4.58	1.14	0.87
G5E8K5_ANK3_MOUSE	Ank3	Ankyrin-3 OS=Mus muscu	R.DFPQYFAVVSR@.I	10.77	6.69	1.61	0.62
G5E8K5_ANK3_MOUSE	Ank3	Ankyrin-3 OS=Mus muscu	R.IK#QESNQIGPEGGILSSTTVPLVQASFPEGALTK#.R	3.79	2.44	1.55	0.64
G5E8K5_ANK3_MOUSE	Ank3	Ankyrin-3 OS=Mus muscu	R.SSYARDSM*M*IEELLVPSK.E	2.09	3.77	0.56	1.80
G5E8K5_ANK3_MOUSE	Ank3	Ankyrin-3 OS=Mus muscu	K.TLEQQENFEEVAR@.S	6.05	5.54	1.09	0.91
G5E8K5_ANK3_MOUSE	Ank3	Ankyrin-3 OS=Mus muscu	R.YLVQDGAQVEAK#.A	5.92	4.57	1.30	0.77
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.AAGAGNEAAALFLATSGAHANHR@.N	9.95	4.07	2.44	0.41
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.FQLQLLR@.E	12.98	4.38	2.96	0.34
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.HGLANLTAELLQQGANPNLQTEEALPVPK#.E	9.82	4.99	1.97	0.51
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.LLAIVAGLYEQEQYSDLK#.I	5.14	2.79	1.84	0.54
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.AAGAGNEAAALFLATSGAHANHR@.N	20.29	5.66	3.58	0.28
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	K.EDFSSLSAQLLYK#.M	7.51	1.65	4.54	0.22
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.ESGAAEQVDNK#.G	7.55	2.91	2.59	0.39
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.FQLQLLR@.E	24.37	9.02	2.70	0.37
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.GDLFASTFLIK#.N	39.75	8.59	4.63	0.22
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	K.GVM*SLVNVR@.N	15.44	2.80	5.50	0.18
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.HGLANLTAELLQQGANPNLQTEEALPVPK#.E	6.16	6.32	0.98	1.03
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	R.LLAIVAGLYEQEQYSDLK#.I	7.07	1.59	4.44	0.23
Q810B6_ANFY1_MOUSE	Ankfy1	Rabankyrin-5 OS=Mus mu	K.SALFLLEHQADINVR@.T	15.64	4.95	3.16	0.32
E9Q1M6_E9Q1M6_MOUSE	Ankhd1	Protein Ankhd1 OS=Mus	R.QEVVDLLLAR@.G	9.75	2.70	3.61	0.28
E9Q1M6_E9Q1M6_MOUSE	Ankhd1	Protein Ankhd1 OS=Mus	K.TSEIFLSSTAEGADLR@.T	4.72	0.00	#DIV/0!	0.00
E9Q1M6_E9Q1M6_MOUSE	Ankhd1	Protein Ankhd1 OS=Mus	R.LDGEVNSM*STSYK#.S	8.07	2.24	3.60	0.28
E9Q1M6_E9Q1M6_MOUSE	Ankhd1	Protein Ankhd1 OS=Mus	R.QEVVDLLLAR@.G	7.84	3.72	2.11	0.47
E9Q4F8_E9Q4F8_MOUSE	Ankrd11	Protein Ankrd11 OS=Mus	K.AILLESDLSTENK#.L	13.44	5.14	2.61	0.38
E9Q4F8_E9Q4F8_MOUSE	Ankrd11	Protein Ankrd11 OS=Mus	R.FSVASSVVSENAAGQTPTR@PISTNLYR@.S	12.24	3.51	3.48	0.29
E9Q4F8_E9Q4F8_MOUSE	Ankrd11	Protein Ankrd11 OS=Mus	K.VFSSIISEDFSER@.K	19.43	3.19	6.09	0.16
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.APSPAPSSVPLGSEKPSSVSQDR.K	4.96	8.86	0.56	1.79
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.GADVNAPPVPSSR@.D	13.80	6.37	2.17	0.46
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.GASLEEVNDEGYTPLM*EAAR@.E	5.99	2.33	2.57	0.39
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.ILLNAGAEINSR@.T	14.14	6.74	2.10	0.48
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.ITPENVQIIFDDPLPISYSQPEK#.V	6.04	2.05	2.95	0.34
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.LEALLEAAGIGK#.L	18.84	7.18	2.63	0.38
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.LLLSGTADGADLR@.T	12.22	6.01	2.03	0.49
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.NASILLEELDLEK#.L	7.44	6.01	1.24	0.81
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.NVSDYTPLSLAASGGYVNIIK#.I	11.98	3.76	3.19	0.31
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.TEVVSLLLDR@.K	12.03	4.89	2.46	0.41
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.TGLTPLM*EAASGGYAEVGR@.V	7.49	3.65	2.05	0.49
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.AFADPEVLR@.R	15.68	2.41	6.51	0.15
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.DTALTIAADK#.G	12.46	4.33	2.88	0.35
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.GADVNAPPVPSSR@.D	30.33	10.12	3.00	0.33
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.GASLEEVNDEGYTPLM*EAAR@.E	14.80	3.60	4.11	0.24
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.ILLNAGAEINSR@.T	28.96	4.45	6.51	0.15
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.LEALLEAAGIGK#.L	44.88	14.32	3.13	0.32
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.LLLDM*GSDINAQIETNR@.N	7.03	2.97	2.37	0.42
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.LLLSGTADGADLR@.T	24.56	6.89	3.56	0.28
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.NASILLEELDLEK#.L	23.92	8.12	2.94	0.34
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.NVSDYTPLSLAASGGYVNIIK#.I	34.11	8.01	4.26	0.23
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.SNSHLPANSQDVQGYITNQSPESIVEEAQGK#.L	4.58	1.88	2.43	0.41
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.TEVVSLLLDR@.K	44.14	9.85	4.48	0.22
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	K.TGLTPLM*EAASGGYAEVGR.V	19.80	8.10	2.45	0.41
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.VPVQALPM*VVPPQEPDK#PPANLAATLPVR@.S	9.83	3.21	3.06	0.33
Q99NH0_ANR17_MOUSE	Ankrd17	Ankyrin repeat domain-c	R.YIATITDK#.E	8.74	15.47	0.56	1.77
Q8K298_ANLN_MOUSE	Anln	Actin-binding protein an	K.TSVISQSEFAPSK#.G	12.36	4.39	2.82	0.35
P97449_AMPN_MOUSE	Anpep	Aminopeptidase N OS=M	R.M*LSSFLTEDLFK#.K	5.37	2.97	1.81	0.55
P97449_AMPN_MOUSE	Anpep	Aminopeptidase N OS=M	K.VVATTQMQAADAR@K#SFPCFDEPAMK.A	4.83	2.03	2.39	0.42
P97449_AMPN_MOUSE	Anpep	Aminopeptidase N OS=M	R.M*LSSFLTEDLFK#.K	8.23	2.33	3.54	0.28
P97449_AMPN_MOUSE	Anpep	Aminopeptidase N OS=M	K.VVATTQM*QAADAR@.K	5.47	2.32	2.36	0.42
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	K.ALTGHLEEVVLAM*LK#.T	10.42	7.66	1.36	0.74
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	R.ALYEAGER.R	52.18	26.80	1.95	0.51
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	K.DITSDTSGDFR@K#.A	16.01	7.06	2.27	0.44
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	R.FLENQEQEYVQAVK#.S	50.32	20.53	2.45	0.41
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	K.GLGTDEDTLIEILTTR@.S	61.46	30.84	1.99	0.50
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	K.GVDEATIIDILTK.R	43.85	21.11	2.08	0.48
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	R.R@VFQNYGK#.Y	13.25	5.56	2.38	0.42
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	R.SEIDM*NEIK#.V	24.33	11.38	2.14	0.47
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	K.TPAQFDADELR@.G	60.58	50.83	1.19	0.84
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	K.TPAQFDADELR@GAM*K#.G	21.78	11.79	1.85	0.54
P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	K.GLGTDEDTLIEILTTR@.S	6.07	3.13	1.94	0.52

P10107_ANXA1_MOUSE	Anxa1	Annexin A1 OS=Mus mus	K.ALLALAK#.G	20.24	8.24	2.46	0.41
P97384_ANX11_MOUSE	Anxa11	Annexin A11 OS=Mus mu	K.TPVLFDVYEIK#.E	6.92	3.94	1.76	0.57
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.AEDGSVIDYELIDQDAR@.E	27.98	11.14	2.51	0.40
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.DALNIETAVK#.T	83.94	48.97	1.71	0.58
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.GVDEVTIVNILTNR.S	121.68	46.63	2.61	0.38
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.LM*VALAK#.G	79.22	32.94	2.41	0.42
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.LMVALAK#.G	17.20	11.09	1.55	0.64
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.LSLEGDHSTPPSAYGSVK#PYTNFDAER@.D	4.36	1.91	2.28	0.44
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.QDIAFAYQR@.R	89.60	38.48	2.33	0.43
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.RAEDGSVIDYELIDQDAR.E	132.56	51.00	2.60	0.38
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.R@AEDGSVIDYELIDQDAR@.E	4.78	2.95	1.62	0.62
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.SALSGHLETVILGLLK#.T	86.51	35.89	2.41	0.41
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.SLYYYIQQDTK#.G	85.57	36.80	2.33	0.43
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.TDLEK#DIISDTSGDFR@.K	48.53	19.92	2.44	0.41
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.TDLEK#DIISDTSGDFR@K#.L	97.80	43.16	2.27	0.44
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.TK#GVDEVTIVNILTNR@.S	68.43	28.77	2.38	0.42
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.TNQELQEINR@.V	203.54	95.90	2.12	0.47
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.TPAQYDASELK#.A	171.19	88.45	1.94	0.52
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.GVDEVTIVNILTNR@.S	8.55	9.80	0.87	1.15
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.RAEDGSVIDYELIDQDAR.E	9.70	9.71	1.00	1.00
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.SALSGHLETVILGLLK#.T	19.23	14.54	1.32	0.76
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.TPAQYDASELK#.A	9.96	9.73	1.02	0.98
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.DALNIETAVK.T	5.45	6.97	0.78	1.28
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.RAEDGSVIDYELIDQDAR.E	10.67	10.40	1.03	0.97
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.SALSGHLETVILGLLK#.T	17.14	16.23	1.06	0.95
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.SLYYYIQQDTK#.G	5.73	5.75	1.00	1.00
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	K.TKGVDEVTIVNILTNR.S	6.58	8.09	0.81	1.23
P07356_ANXA2_MOUSE	Anxa2	Annexin A2 OS=Mus mus	R.TNQELQEINR.V	10.40	19.98	0.52	1.92
P97429_ANXA4_MOUSE	Anxa4	Annexin A4 OS=Mus mus	K.AASGFNATEDAQTLR@.K	15.06	5.28	2.85	0.35
P97429_ANXA4_MOUSE	Anxa4	Annexin A4 OS=Mus mus	R.AEIDM*LDIR@.A	5.49	3.08	1.78	0.56
P97429_ANXA4_MOUSE	Anxa4	Annexin A4 OS=Mus mus	K.GLGTDEDAIIGILAYR@.N	12.07	5.72	2.11	0.47
P97429_ANXA4_MOUSE	Anxa4	Annexin A4 OS=Mus mus	R.INQTYQQQYGR.S	14.52	7.51	1.93	0.52
P48036_ANXA5_MOUSE	Anxa5	Annexin A5 OS=Mus mus	R.DLVDDLK#SELTGK#FEK#.L	32.02	9.98	3.21	0.31
P48036_ANXA5_MOUSE	Anxa5	Annexin A5 OS=Mus mus	K.FITIFGTR@.S	27.12	10.56	2.57	0.39
P48036_ANXA5_MOUSE	Anxa5	Annexin A5 OS=Mus mus	K.GLGTDEDSILNLLTSR@.S	75.55	31.94	2.37	0.42
P48036_ANXA5_MOUSE	Anxa5	Annexin A5 OS=Mus mus	R.GTVTDFPGFDGR@.A	44.36	17.17	2.58	0.39
P48036_ANXA5_MOUSE	Anxa5	Annexin A5 OS=Mus mus	K.QVYEEEYGSNLEDDVVGDTSGYYQR@.M	4.65	3.81	1.22	0.82
P48036_ANXA5_MOUSE	Anxa5	Annexin A5 OS=Mus mus	R.SEIDLFNIR@.K	44.00	20.52	2.14	0.47
P48036_ANXA5_MOUSE	Anxa5	Annexin A5 OS=Mus mus	R.SIPAYLAETLYYAM*K#.G	5.44	6.37	0.86	1.17
P48036_ANXA5_MOUSE	Anxa5	Annexin A5 OS=Mus mus	R.TPEELSAIK#.Q	51.15	20.79	2.46	0.41
P48036_ANXA5_MOUSE	Anxa5	Annexin A5 OS=Mus mus	K.VLTEIIASR@.T	76.44	30.35	2.52	0.40
P14824_ANXA6_MOUSE	Anxa6	Annexin A6 OS=Mus mus	K.GFGSDK#ESILELITSR@.S	20.78	7.87	2.64	0.38
P14824_ANXA6_MOUSE	Anxa6	Annexin A6 OS=Mus mus	R.GSVHDFPEFDANQDAEALYTAM*K#.G	7.08	3.13	2.26	0.44
P14824_ANXA6_MOUSE	Anxa6	Annexin A6 OS=Mus mus	K.M*LVVLLQGTR@.E	9.87	5.27	1.87	0.53
P14824_ANXA6_MOUSE	Anxa6	Annexin A6 OS=Mus mus	R.SEIDLLNIR@.R	18.52	11.05	1.68	0.60
P14824_ANXA6_MOUSE	Anxa6	Annexin A6 OS=Mus mus	K.TLIEILATR@.T	21.16	8.48	2.49	0.40
P14824_ANXA6_MOUSE	Anxa6	Annexin A6 OS=Mus mus	K.WGTDEAQFIYILGNR@.S	8.46	5.08	1.66	0.60
P14824_ANXA6_MOUSE	Anxa6	Annexin A6 OS=Mus mus	K.GFGSDK#ESILELITSR@.S	9.45	3.85	2.45	0.41
P14824_ANXA6_MOUSE	Anxa6	Annexin A6 OS=Mus mus	R.GSVHDFPEFDANQDAEALYTAM*K#.G	6.48	3.62	1.79	0.56
P14824_ANXA6_MOUSE	Anxa6	Annexin A6 OS=Mus mus	R.SEIDLLNIR@.R	10.52	4.37	2.41	0.42
O35643_AP1B1_MOUSE	Ap1b1	AP-1 complex subunit be	K.DIANENEAQFQIR@.D	5.50	2.31	2.38	0.42
O35643_AP1B1_MOUSE	Ap1b1	AP-1 complex subunit be	R.LASQANIAQVLAELK#.E	24.54	8.93	2.75	0.36
O35643_AP1B1_MOUSE	Ap1b1	AP-1 complex subunit be	R.NINLIVQK#.R	30.17	16.33	1.85	0.54
O35643_AP1B1_MOUSE	Ap1b1	AP-1 complex subunit be	R.NVEGQDM*LYQSLK#.L	9.04	4.87	1.86	0.54
O35643_AP1B1_MOUSE	Ap1b1	AP-1 complex subunit be	K.YNDPIYVK#.L	14.60	8.96	1.63	0.61
O35643_AP1B1_MOUSE	Ap1b1	AP-1 complex subunit be	R.LASQANIAQVLAELK#.E	15.23	6.70	2.28	0.44
O35643_AP1B1_MOUSE	Ap1b1	AP-1 complex subunit be	R.NINLIVQK#.R	19.13	7.24	2.64	0.38
O35643_AP1B1_MOUSE	Ap1b1	AP-1 complex subunit be	R.NVEGQDM*LYQSLK#.L	6.74	2.57	2.62	0.38
P22892_AP1G1_MOUSE	Ap1g1	AP-1 complex subunit ga	R.VLAINILGR@.F	13.96	5.99	2.33	0.43
P22892_AP1G1_MOUSE	Ap1g1	AP-1 complex subunit ga	R.YVALTSLLK#.T	10.21	4.69	2.18	0.46
P61967_AP1S1_MOUSE	Ap1s1	AP-1 complex subunit sig	K.AIEQADLLQEEDESPR@.S	10.67	6.89	1.55	0.65
P61967_AP1S1_MOUSE	Ap1s1	AP-1 complex subunit sig	R.FM*LLFSR@.Q	10.58	2.12	4.98	0.20
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	R.ALLLSTYIK#.F	13.66	6.65	2.05	0.49
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	R.IAGDYVSEEVWYR@.V	11.62	7.70	1.51	0.66
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	R.ILVAGDSM*DSVK#.Q	7.95	4.22	1.88	0.53
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	R.NADVELQQR.A	200.75	145.63	1.38	0.73
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	K.NSGVLFENQLLQIGVK#.S	9.28	2.56	3.62	0.28
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	K.VGGYILGEFGNLIAGDPR@.S	12.44	5.14	2.42	0.41
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	R.ALLLSTYIK#.F	15.59	8.22	1.90	0.53
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	R.GLAVFISDIR@.N	9.47	3.22	2.94	0.34
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	K.NSGVLFENQLLQIGVK#.S	8.04	2.29	3.51	0.29
P17426_AP2A1_MOUSE	Ap2a1	AP-2 complex subunit al	K.VGGYILGEFGNLIAGDPR@.S	11.19	3.03	3.70	0.27
P17427_AP2A2_MOUSE	Ap2a2	AP-2 complex subunit al	K.ILVAGDTM*DSVK#.Q	9.16	4.94	1.85	0.54
P17427_AP2A2_MOUSE	Ap2a2	AP-2 complex subunit al	R.LSTVASTDILATVLEEM*PPFPER@.E	25.87	7.11	3.64	0.27
Q9DBG3_AP2B1_MOUSE	Ap2b1	AP-2 complex subunit be	K.ALQHM*TDFAIQFNK#.N	8.37	3.00	2.79	0.36
Q9DBG3_AP2B1_MOUSE	Ap2b1	AP-2 complex subunit be	R.APEVSQYIYQVYDSILK#N.-	5.98	3.18	1.88	0.53
Q9DBG3_AP2B1_MOUSE	Ap2b1	AP-2 complex subunit be	K.LQNNNVYTIAK#.R	14.12	5.05	2.80	0.36
Q9DBG3_AP2B1_MOUSE	Ap2b1	AP-2 complex subunit be	K.VNYVVQEAIVVIR@.D	12.22	5.12	2.39	0.42
Q9DBG3_AP2B1_MOUSE	Ap2b1	AP-2 complex subunit be	K.DIPNENELQFQIK#.E	10.17	6.16	1.65	0.61
Q9DBG3_AP2B1_MOUSE	Ap2b1	AP-2 complex subunit be	K.K#PSETQELVQQVLSLATQDSDNPDLR@.D	7.83	3.01	2.61	0.38
P84091_AP2M1_MOUSE	Ap2m1	AP-2 complex subunit m	K.ASENAIVWK#.I	29.12	11.37	2.56	0.39
P84091_AP2M1_MOUSE	Ap2m1	AP-2 complex subunit m	K.ESQISAEIELLPTNDK#.K	10.09	2.91	3.47	0.29
P84091_AP2M1_MOUSE	Ap2m1	AP-2 complex subunit m	K.QNVNAAM*VFEFLYK#.M	11.44	4.60	2.49	0.40
P84091_AP2M1_MOUSE	Ap2m1	AP-2 complex subunit m	R.SISFIPPDGEFELM*R@.Y	16.96	7.91	2.14	0.47
P84091_AP2M1_MOUSE	Ap2m1	AP-2 complex subunit m	K.SNFK#PSLLAQK#.I	9.86	4.58	2.15	0.46
P84091_AP2M1_MOUSE	Ap2m1	AP-2 complex subunit m	R.SNIWLAAVTK#.Q	28.03	11.84	2.37	0.42
P84091_AP2M1_MOUSE	Ap2m1	AP-2 complex subunit m	R.SPVTNIAR@.T	97.20	37.41	2.60	0.38
P84091_AP2M1_MOUSE	Ap2m1	AP-2 complex subunit m	K.WAR@PPISM*NFEVPFAPSGLK#.V	23.26	11.23	2.07	0.48
P84091_AP2M1_MOUSE	Ap2m1	AP-2 complex subunit m	K.WAR@PPISMNFEVPFAPSGLK#.V	2.96	1.11	2.66	0.38
P62743_AP2S1_MOUSE	Ap2s1	AP-2 complex subunit sig	R.FILIQNR.A	38.43	16.78	2.29	0.44
P62743_AP2S1_MOUSE	Ap2s1	AP-2 complex subunit sig	K.VYTVVDEM*FLAGEIR@.E	10.16	3.24	3.13	0.32
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.EGSTAQLIINTEK#.T	6.79	3.81	1.78	0.56
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.EGSTAQLIINTEK#.T	7.88	4.71	1.67	0.60
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.LLDSITVPVAR@.A	18.86	5.61	3.36	0.30
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.LQILNLAAK#.L	22.13	4.38	5.05	0.20
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.NASELFPAVVK#.N	13.98	3.28	4.26	0.23
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.QFAAATIQTIGR@.C	6.76	1.40	4.82	0.21
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.VVNVANLGAVPSSQDNVHR@.F	13.02	3.12	4.18	0.24
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.ASGYLELSNWPEVAPDPSVR@.N	9.91	1.60	6.20	0.16
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.LLDSITVPVAR@.A	36.06	3.12	11.56	0.09
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.LLQM*QPAQHGEIIR@.H	16.73	3.58	4.67	0.21
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.LLTQYILNLGK#.Y	31.14	5.49	5.67	0.18
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.LQILNLAAK#.L	14.84	2.50	5.95	0.17

Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.LYSLDPEQK#EM*LIEVIEK#.L	5.11	2.11	2.42	0.41
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.NASELFPAVVK#.N	11.91	3.40	3.50	0.29
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.QFAAATIQTIGR@.C	9.25	4.37	2.12	0.47
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.VVNVANLGAVPSSQDNVHR@.F	18.44	4.56	4.04	0.25
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	R.YAEEQQDLALLSISTFQR@.A	6.45	2.06	3.12	0.32
Q9Z1T1_AP3B1_MOUSE	Ap3b1	AP-3 complex subunit be	K.YDQNYDIR@.D	11.15	1.42	7.84	0.13
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	R.ILIEDSDQNLK#.Y	9.02	20.20	0.45	2.24
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	R.ALDLLYGM*VSK#.K	13.00	6.57	1.98	0.51
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	K.EQAADTEAAQEVTQLLVER@.L	18.60	2.42	7.70	0.13
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	R.ILIEDSDQNLK#.Y	62.62	11.45	5.47	0.18
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	K.LFGALTPLEPR@.L	18.18	56.05	0.32	3.08
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	R.LPQFVQSADLEVQER@.A	10.17	2.00	5.09	0.20
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	K.LYASILQQK#.E	15.96	7.46	2.14	0.47
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	K.VTYDIQASLQK#.D	7.18	2.24	3.21	0.31
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	K.YLGLLAM*SK#.I	13.29	5.16	2.57	0.39
O54774_AP3D1_MOUSE	Ap3d1	AP-3 complex subunit de	R.YQDAPGVEHIPVVQIDLSVPLK#.V	6.64	3.08	2.16	0.46
Q9JKC8_AP3M1_MOUSE	Ap3m1	AP-3 complex subunit m	R.VSSQNLVAIPVYVK#.H	16.10	4.79	3.36	0.30
Q9DCR2_AP3S1_MOUSE	Ap3s1	AP-3 complex subunit sig	K.FYQPYSEDTQQQIIR@.E	5.77	1.68	3.43	0.29
Q9DCR2_AP3S1_MOUSE	Ap3s1	AP-3 complex subunit sig	K.FYQPYSEDTQQQIIR@.E	9.66	2.20	4.38	0.23
Q9DCR2_AP3S1_MOUSE	Ap3s1	AP-3 complex subunit sig	R.NINIGDISIK#.V	11.07	1.42	7.77	0.13
Q9JKC7_AP4M1_MOUSE	Ap4m1	AP-4 complex subunit m	R.GVISLSQELSSPDQK#.A	8.04	3.21	2.50	0.40
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.ELPQFATGENLPR.V	35.55	17.46	2.04	0.49
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.EVEELILTESK#.K	12.89	6.81	1.89	0.53
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	R.GLQVYIR@.Q	18.58	8.67	2.14	0.47
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.ITNNINVLIK#.D	16.56	7.37	2.25	0.44
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	R.LAAQFIPK#.F	43.07	18.16	2.37	0.42
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.R@LAAQFIPK#.F	7.46	5.02	1.49	0.67
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.VLEDVTGEEFVLFM*K#.I	11.39	4.34	2.62	0.38
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.ITNNINVLIK#.D	10.87	5.52	1.97	0.51
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.ELPQFATGENLPR.V	27.10	9.83	2.76	0.36
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.EVEELILTESK#.K	16.10	4.86	3.32	0.30
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.ITNNINVLIK#.D	19.75	7.10	2.78	0.36
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	R.K#LPDFLTAK#.L	18.33	10.34	1.77	0.56
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	R.LAAQFIPK#.F	24.73	9.78	2.53	0.40
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.TGEALK#TEENK#IK#.V	8.36	2.26	3.70	0.27
O35841_API5_MOUSE	Api5	Apoptosis inhibitor 5 OS	K.VLEDVTGEEFVLFM*K#.I	12.21	4.24	2.88	0.35
Q99J72_ABEC3_MOUSE	Apobec3	DNA dC->dU-editing enzy	K.GLEIISR.R	16.61	12.21	1.36	0.74
Q99J72_ABEC3_MOUSE	Apobec3	DNA dC->dU-editing enzy	R.NLISQETFK#.F	25.25	23.98	1.05	0.95
Q8VDU3_Q8VDU3_MOUSE	Apol9a	Apol9a protein OS=Mus	K.GTPLAM*SNEAR.I	442.75	175.51	2.52	0.40
Q8VDU3_Q8VDU3_MOUSE	Apol9a	Apol9a protein OS=Mus	R.VLDEVEAAPTGTHVLGEAGTSVDR@.I	54.72	31.16	1.76	0.57
Q8C7I4_Q8C7I4_MOUSE	Apol9b	Protein Apol9b OS=Mus	R.ELTALLAIADR@.G	79.92	40.29	1.98	0.50
Q8C7I4_Q8C7I4_MOUSE	Apol9b	Protein Apol9b OS=Mus	K.HLYEGSASESAEALR@K#.L	100.42	58.78	1.71	0.59
Q8C7I4_Q8C7I4_MOUSE	Apol9b	Protein Apol9b OS=Mus	R.ILATTGSISAQR@.A	150.40	77.85	1.93	0.52
Q8C7I4_Q8C7I4_MOUSE	Apol9b	Protein Apol9b OS=Mus	R.LEGTPLAM*SNEAR@.I	6.44	4.35	1.48	0.68
Q8C7I4_Q8C7I4_MOUSE	Apol9b	Protein Apol9b OS=Mus	R.ILATTGSISAQR@.A	5.53	2.58	2.14	0.47
P12023_A4_MOUSE	App	Amyloid beta A4 protein	K.VESLEQEAANER@.Q	4.75	3.79	1.25	0.80
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.AAFAHFPELYDFALSNVAEVDAR@.D	41.79	24.66	1.69	0.59
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.AGM*QPGLTM*VVGPPGTGK#.T	11.15	6.01	1.86	0.54
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.DADGEEDDTEEAK#.T	5.25	2.84	1.85	0.54
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.EEDGHLFSQLLDM*LK#.F	8.97	5.56	1.62	0.62
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.FWNLIK#.K	9.75	4.48	2.18	0.46
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.FYTGFEINDQTGNALTENEM*TTIHYDR@.I	6.53	2.20	2.97	0.34
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.IFTQLEEFR@.A	49.87	24.81	2.01	0.50
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.IM*ALDIDER@.H	23.60	11.61	2.03	0.49
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.ISILTTYNGQK#.H	10.47	6.12	1.71	0.58
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.ISQIQQLNQM*PLYPTEK#.I	6.46	3.57	1.81	0.55
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.LNLQFLTLHDYLLR@.N	26.29	13.21	1.99	0.50
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.M*AQPIVAFTVVEVAKPNIGENWPTR.V	11.55	8.51	1.36	0.74
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.M*PNQIATLDFNDTFLSIEHLK#.A	61.06	25.99	2.35	0.43
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.QDIEDSVSR@.M	38.01	25.30	1.50	0.67
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.RISQIQQLNQM*PLYPTEK.I	6.71	5.33	1.26	0.79
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.R@NTIQFTHTQIEAIR@.A	16.19	8.01	2.02	0.49
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.SIPLSEPVTM*DK#.V	20.49	12.90	1.59	0.63
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.SQVQQLISLPM*WM*GLQPAR@.L	12.68	7.85	1.62	0.62
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.TDVAVQIISNIYHNFPEQR@.T	45.41	31.67	1.43	0.70
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.TLIVTHSNQALNQLFEK#.I	51.05	39.08	1.31	0.77
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	R.VNYVLAR@.R	23.87	15.22	1.57	0.64
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.VTVSDPALQIPPFR.I	6.59	7.29	0.91	1.10
Q8CFQ3_AQR_MOUSE	Aqr	Intron-binding protein a	K.YSNM*EQSLFTR@.F	20.09	9.90	2.03	0.49
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.APGFGGFGSSAVSGGSTAAM*ITETIIETDK#PK#.V	3.92	5.31	0.74	1.36
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.FSTETTFLVDK#YEIL.-	57.50	20.25	2.84	0.35
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.GK#EVDNFVDK#LK#.S	24.93	11.95	2.09	0.48
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.IEGLLAAFPK#.L	32.24	14.50	2.22	0.45
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.ISDDK#FGR@.I	13.71	8.13	1.69	0.59
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.LFTAESLIGLK#.N	102.16	79.92	1.28	0.78
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.LYM*VLITTK#.N	14.90	43.93	0.34	2.95
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.LYMVLITTK#.N	19.65	8.49	2.32	0.43
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.NSNILEDLETLR.L	212.34	86.81	2.45	0.41
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.QHTFVETESVR@.Y	51.90	18.49	2.81	0.36
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.SEGETIM*SSNM*GK#.R	15.63	7.00	2.23	0.45
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.SFPVNSDVGVLK#.W	41.44	19.00	2.18	0.46
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.TFTEM*DSHEEK#.V	12.13	6.13	1.98	0.50
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.TR@IEGLLAAFPK#.L	34.98	23.11	1.51	0.66
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.VTQVDGNSPVR@.F	139.77	58.25	2.40	0.42
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.YVYQPM*EK#.L	47.84	19.95	2.40	0.42
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.ENVNLAQIR@.T	35.15	11.24	3.13	0.32
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.IEGLLAAFPK#.L	39.47	10.66	3.70	0.27
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.LYM*VLITTK#.N	9.47	4.51	2.10	0.48
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.NSNILEDLETLR@.L	100.70	33.11	3.04	0.33
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.TR@IEGLLAAFPK#.L	33.47	11.83	2.83	0.35
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.ENVNLAQIR@.T	68.32	24.75	2.76	0.36
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.FSTETTFLVDK#YEIL.-	66.08	25.20	2.62	0.38
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.GK#EVDNFVDK#LK#.S	19.97	4.66	4.29	0.23
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.IEGLLAAFPK#.L	27.63	9.36	2.95	0.34
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.LFTAESLIGLK#.N	78.29	29.41	2.66	0.38
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.LYMVLITTK#.N	20.93	7.22	2.90	0.34
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.NSNILEDLETLR@.L	91.36	30.69	2.98	0.34
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.QHTFVETESVR@.Y	9.34	3.47	2.69	0.37
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.SEGETIM*SSNM*GK#.R	16.10	7.80	2.06	0.48
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.SFPVNSDVGVLK#.W	60.67	15.79	3.84	0.26
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.TFTEM*DSHEEK#.V	8.20	2.61	3.15	0.32
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	R.TR@IEGLLAAFPK#.L	31.28	11.66	2.68	0.37
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta (	K.VTQVDGNSPVR@.F	73.57	27.65	2.66	0.38

Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta	R.YVYQPM*EK#.L	21.76	8.52	2.55	0.39
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta	R.FSTETTFLVDK#YEIL.-	16.84	3.11	5.42	0.18
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta	R.IEGLLAAFPK#.L	12.57	2.77	4.54	0.22
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta	K.LFTAESLIGLK#.N	16.90	5.17	3.27	0.31
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta	K.NSNILEDLETLR@.L	46.05	11.39	4.04	0.25
Q5XJY5_COPD_MOUSE	Arcn1	Coatomer subunit delta	K.VTQVDGNSPVR@.F	33.65	8.17	4.12	0.24
P84078_ARF1_MOUSE	Arf1	ADP-ribosylation factor 1	R.DAVLLVFANK#.Q	126.31	78.51	1.61	0.62
P84078_ARF1_MOUSE	Arf1	ADP-ribosylation factor 1	R.ILMVGLDAAGK#.T	24.03	10.00	2.40	0.42
P84078_ARF1_MOUSE	Arf1	ADP-ribosylation factor 1	K.LGEIVTTIPTIGFNVETVEYK#.N	17.12	8.43	2.03	0.49
P84078_ARF1_MOUSE	Arf1	ADP-ribosylation factor 1	R.M*LAEDELR@.D	37.49	15.02	2.50	0.40
P84078_ARF1_MOUSE	Arf1	ADP-ribosylation factor 1	K.NISFTVWDVGGQDK#.I	49.58	15.53	3.19	0.31
P84078_ARF1_MOUSE	Arf1	ADP-ribosylation factor 1	K.QDLPNAM*NAAEITDK#.L	12.00	6.71	1.79	0.56
P84078_ARF1_MOUSE	Arf1	ADP-ribosylation factor 1	K.LGEIVTTIPTIGFNVETVEYK#.N	13.17	5.04	2.61	0.38
P84078_ARF1_MOUSE	Arf1	ADP-ribosylation factor 1	K.LGEIVTTIPTIGFNVETVEYK#.N	11.91	4.94	2.41	0.42
P61750_ARF4_MOUSE	Arf4	ADP-ribosylation factor 4	R.IQEGAAVLQK#.M	15.95	6.06	2.63	0.38
P61750_ARF4_MOUSE	Arf4	ADP-ribosylation factor 4	R.IQEGAAVLQK#.M	12.86	5.51	2.33	0.43
P61750_ARF4_MOUSE	Arf4	ADP-ribosylation factor 4	R.IQEGAAVLQK#.M	15.95	9.27	1.72	0.58
P84084_ARF5_MOUSE	Arf5	ADP-ribosylation factor 5	R.VQESADELQK#.M	6.25	5.05	1.24	0.81
P84084_ARF5_MOUSE	Arf5	ADP-ribosylation factor 5	K.M*LQEDELR@.D	11.79	2.83	4.17	0.24
P84084_ARF5_MOUSE	Arf5	ADP-ribosylation factor 5	R.VQESADELQK#.M	35.21	12.90	2.73	0.37
P62331_ARF6_MOUSE	Arf6	ADP-ribosylation factor 6	R.DAIILIFANK#.Q	52.66	13.74	3.83	0.26
P62331_ARF6_MOUSE	Arf6	ADP-ribosylation factor 6	K.FNVWDVGGQDK#.I	47.43	9.72	4.88	0.20
P62331_ARF6_MOUSE	Arf6	ADP-ribosylation factor 6	R.ILM*LGLDAAGK#.T	28.94	42.36	0.68	1.46
P62331_ARF6_MOUSE	Arf6	ADP-ribosylation factor 6	R.ILMLGLDAAGK#.T	14.76	3.44	4.29	0.23
P62331_ARF6_MOUSE	Arf6	ADP-ribosylation factor 6	K.LGQSVTTIPTVGFNVETVTYK#.N	14.44	8.03	1.80	0.56
Q9EPJ9_ARFG1_MOUSE	Arfgap1	ADP-ribosylation factor	R.DVTTFFSGK#.A	16.07	9.96	1.61	0.62
Q9EPJ9_ARFG1_MOUSE	Arfgap1	ADP-ribosylation factor	K.FR@EFLETQDDYEPSWSLQDK#.Y	11.62	6.64	1.75	0.57
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	R.LAYQELQIDR@.K	19.11	17.64	1.08	0.92
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	R.SQLDLFDDVGTFASGPPK#.Y	8.83	4.66	1.90	0.53
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	K.VSNQSFTEIER.Q	12.49	10.62	1.18	0.85
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	K.YK#DNPFSLGETFGSR@.W	10.58	10.65	0.99	1.01
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	K.AISSDM*FFGR@.E	8.78	2.63	3.34	0.30
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	R.LAYQELQIDR@.K	25.87	11.71	2.21	0.45
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	R.LGM*GLVSR@.S	20.67	10.28	2.01	0.50
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	K.QAEESM*VASM*R@.L	6.10	2.29	2.67	0.38
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	R.SQLDLFDDVGTFASGPPK#.Y	16.72	16.04	1.04	0.96
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	R.SQLDLFDDVGTFASGPPK#.Y	13.36	6.78	1.97	0.51
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	R.SSISHSVLSEM*QM*IEQETPLSAK#.S	3.83	3.32	1.15	0.87
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	R.STELDSNWSWLQLR@.C	12.42	7.69	1.62	0.62
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	K.TEIQTIFK#.R	14.05	5.78	2.43	0.41
Q99K28_ARFG2_MOUSE	Arfgap2	ADP-ribosylation factor	K.VSNQSFTEIER@.Q	30.42	15.91	1.91	0.52
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	R.LSTSSSISSADLFDEQR.K	6.92	6.06	1.14	0.88
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	K.LTNTSFTEIEK#.Q	12.63	7.74	1.63	0.61
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	R.YFDDPM*ELR.S	7.78	5.55	1.40	0.71
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	K.YQEDPEDSYFSSSSK#.W	4.73	4.43	1.07	0.94
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	R.LSTSSSISSADLFDEQR@.K	5.58	3.04	1.84	0.54
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	R.YFDDPM*ELR@.S	5.36	3.04	1.76	0.57
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	R.LSTSSSISSADLFDEQR@.K	14.82	3.46	4.28	0.23
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	K.LTNTSFTEIEK#.Q	25.57	10.03	2.55	0.39
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	R.STELDSNWSWFQLR@.C	11.86	3.68	3.23	0.31
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	R.YFDDPM*ELR@.S	15.19	6.91	2.20	0.45
Q9D8S3_ARFG3_MOUSE	Arfgap3	ADP-ribosylation factor	K.YQEDPEDSYFSSSSK#.W	7.49	8.80	0.85	1.17
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	R.DANTLPK#.I	26.31	10.10	2.60	0.38
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	K.GGPVILADEIK#.N	9.23	4.42	2.09	0.48
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	K.IEQSQHLFQIHK#.E	51.50	13.66	3.77	0.27
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	K.LAQTLSTQLFQM*VHTQK#.Q	35.05	12.15	2.88	0.35
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	R.LK#TPGVDAPSWLEEQ.-	10.08	4.81	2.10	0.48
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	K.LTQQAGDLTVPAGGQR@.T	20.00	7.54	2.65	0.38
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	R.NQLVLFHSAVAAYFAGNQK#.Q	6.64	2.77	2.40	0.42
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	K.QLGDAFADLSLK#.S	23.54	7.95	2.96	0.34
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	K.SLELHEEFGYNADTQK#.L	34.80	10.49	3.32	0.30
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	R.TDLEELNLGPR@.D	47.83	19.96	2.40	0.42
G5E8V9_G5E8V9_MOUSE	Arfip1	MCG18094 OS=Mus mus	R.VEYDAYR@.T	49.16	19.88	2.47	0.40
A2RSX9_A2RSX9_MOUSE	Arfip1	Arfip1 protein OS=Mus m	K.EGVTEAGAPQGGQR@.T	30.38	7.83	3.88	0.26
Q8K221_ARFP2_MOUSE	Arfip2	Arfaptin-2 OS=Mus musc	K.QLEQTLQQFNIK#.L	8.92	4.65	1.92	0.52
Q3UL36_ARGL1_MOUSE	Arglu1	Arginine and glutamate-r	R.IDIFGR@.T	13.85	11.88	1.17	0.86
Q3UL36_ARGL1_MOUSE	Arglu1	Arginine and glutamate-r	R.RVEELVAK.R	126.08	77.91	1.62	0.62
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.FLLDHQGELFPSTDAQGV.-	27.34	27.34	1.00	1.00
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	R.HQIVEVAGDDK#YGR@.K	33.29	11.96	2.78	0.36
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	R.K#IFYVNYLSELSEHVK#.L	12.22	3.30	3.70	0.27
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.LEQLGIPR.Q	37.70	10.84	3.48	0.29
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.SPGQDPIPIVLR@.E	30.52	12.13	2.52	0.40
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.YDDFLK#.S	20.13	5.94	3.39	0.30
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.FLLDHQGELFPSTDAQGV.-	13.65	13.65	1.00	1.00
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	R.HQIVEVAGDDK#YGR@.K	12.57	4.80	2.62	0.38
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.LEQLGIPR@.Q	10.47	4.01	2.61	0.38
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.SPGQDPIPIVLR@.E	15.68	7.33	2.14	0.47
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.FLLDHQGELFPSTDAQGV.-	20.72	20.72	1.00	1.00
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.LEQLGIPR@.Q	9.45	5.24	1.80	0.55
Q5FWK3_RHG01_MOUSE	Arhgap1	Rho GTPase-activating pr	K.SPGQDPIPIVLR@.E	14.01	6.72	2.09	0.48
Q69ZH9_RHG23_MOUSE	Arhgap23	Rho GTPase-activating pr	R.TPVDDK#EPQSVPNIEYLLPNIGR@.T	5.92	2.87	2.06	0.48
Q69ZH9_RHG23_MOUSE	Arhgap23	Rho GTPase-activating pr	R.TPVDDK#EPQSVPNIEYLLPNIGR@.T	5.04	2.91	1.73	0.58
Q8BYW1_RHG25_MOUSE	Arhgap25	Rho GTPase-activating pr	K.SMEKPKTKTDP.-	3.61	14.93	0.24	4.14
Q811P8_RHG32_MOUSE	Arhgap32	Rho GTPase-activating pr	R.FSQLTELPRSDVLK#.D	1.54	3.81	0.40	2.48
P97393_RHG05_MOUSE	Arhgap5	Rho GTPase-activating pr	R.IPFDLLSTLEAEK#.V	6.38	3.30	1.93	0.52
P97393_RHG05_MOUSE	Arhgap5	Rho GTPase-activating pr	R.TQSTDDEYALDGK#.I	7.17	2.51	2.86	0.35
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	R.FIQEVVQSQQAAVSR@.Q	14.15	4.88	2.90	0.34
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	K.K#AFLDFYHSFLEK#.T	12.71	4.44	2.87	0.35
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	R.APGPVHTQEIEENLLSLEVAIR@.Q	5.48	3.05	1.80	0.56
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	R.FIQEVVQSQQAAVSR@.Q	6.09	2.24	2.71	0.37
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	R.LR@PLLSQLGGTLSPNLAAPER@.S	10.14	3.17	3.20	0.31
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	R.R@QESGYLIEEIGDVLLAR@.F	9.48	2.67	3.56	0.28
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	K.R@QEVISELLVTEAAHVR@.M	16.71	4.07	4.11	0.24
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	R.ELVPPDTLLSLPK#.S	18.38	5.33	3.45	0.29
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	R.LLSHLEETQHTISTDEEK#.S	6.54	2.40	2.72	0.37
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	R.LR@PLLSQLGGTLSPNLAAPER@.S	14.06	2.61	5.38	0.19
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	K.QILLSTEEDSGAGPPR@.D	4.40	5.07	0.87	1.15
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	K.R@QEVISELLVTEAAHVR@.M	10.30	2.82	3.66	0.27
Q61210_ARHG1_MOUSE	Arhgef1	Rho guanine nucleotide	R.VPVPPSVAFELDR@.T	8.96	2.60	3.45	0.29
Q68FM7_Q68FM7_MOUSE	Arhgef11	Protein Arhgef11 OS=Mu	K.DIWNIFLEK#.N	15.15	4.10	3.69	0.27
Q68FM7_Q68FM7_MOUSE	Arhgef11	Protein Arhgef11 OS=Mu	R.ELLNSLGGESSGGTTPVGSFHTEAAR@.W	7.62	1.40	5.42	0.18
Q68FM7_Q68FM7_MOUSE	Arhgef11	Protein Arhgef11 OS=Mu	R.LSVDSQEADSGLDSGTER@FPSISESLVNR@.N	3.45	3.29	1.05	0.95
Q68FM7_Q68FM7_MOUSE	Arhgef11	Protein Arhgef11 OS=Mu	R.TLGLGSLYGENDLLDLDGDPLR@ER@.Q	14.25	5.59	2.55	0.39

Q68FM7_Q68FM7_MOUSE	Arhgef11	Protein Arhgef11 OS=Mu	K.YPLLLENIIK#.H	13.61	3.52	3.87	0.26
Q8R4H2_ARHGC_MOUSE	Arhgef12	Rho guanine nucleotide	K.LSEYPNVDELR@.N	7.11	3.17	2.24	0.45
Q80U35_ARHGH_MOUSE	Arhgef17	Rho guanine nucleotide	K.LPLEDTDIIK#.G	11.38	9.71	1.17	0.85
Q80U35_ARHGH_MOUSE	Arhgef17	Rho guanine nucleotide	R.HASVPATFTPIVVPEPAM*SVGPPVAAPEPVGFPVR@.G	5.17	1.89	2.74	0.37
Q80U35_ARHGH_MOUSE	Arhgef17	Rho guanine nucleotide	R.HASVPATFTPIVVPEPAM*SVGPPVAAPEPVGFPVR.G	4.00	2.24	1.79	0.56
Q80U35_ARHGH_MOUSE	Arhgef17	Rho guanine nucleotide	R.LGFEQAFDEAK#.R	14.85	6.20	2.40	0.42
Q80U35_ARHGH_MOUSE	Arhgef17	Rho guanine nucleotide	K.LPLEDTDIIK#.G	16.72	7.23	2.31	0.43
Q80U35_ARHGH_MOUSE	Arhgef17	Rho guanine nucleotide	K.LSESLGFPHQSLDDALR@.D	15.77	5.40	2.92	0.34
Q80U35_ARHGH_MOUSE	Arhgef17	Rho guanine nucleotide	R.LSSGGGGSSETVGR@.D	7.67	4.32	1.78	0.56
Q80U35_ARHGH_MOUSE	Arhgef17	Rho guanine nucleotide	R.R@EEGNQDQTGSLTQTR@.S	10.62	4.08	2.60	0.38
Q80U35_ARHGH_MOUSE	Arhgef17	Rho guanine nucleotide	K.SM*TLGSQGSPITK#.M	7.51	4.32	1.74	0.57
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.ATEAGSLEAR@.L	12.41	5.53	2.25	0.45
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.M*QDIPEETESR@.D	11.23	5.80	1.94	0.52
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.ATEAGSLEAR@.L	7.46	3.25	2.29	0.44
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.FLNQLLER.R	42.51	23.55	1.81	0.55
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.GHDR@LDLPVTVR@.S	21.79	11.91	1.83	0.55
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.GLSSLSLAK#.S	15.66	6.09	2.57	0.39
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.ILQNSHGVEEEYQDLASALGLVK#.E	30.58	37.61	0.81	1.23
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.LGDLLISQFSGSNAEQM*R@.K	8.57	4.79	1.79	0.56
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.M*QDIPEETESR@.D	8.33	4.85	1.72	0.58
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.NNTALQSVSLR@.S	25.03	11.59	2.16	0.46
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.NQALVELLQK#.N	44.03	18.53	2.38	0.42
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.QATELALLQR@.Q	22.06	8.75	2.52	0.40
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.QDVIYELIQTELHHVR@.T	22.43	8.50	2.64	0.38
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.SLHR@PFDDR@EAQELGSPEDR@.L	16.23	7.07	2.30	0.44
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.YIFTSLDK#PSVVSLQNLIVR@.D	37.72	28.53	1.32	0.76
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.YPVLINR@.I	22.03	11.77	1.87	0.53
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.AAVASVTPEK#.Q	62.42	21.60	2.89	0.35
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.AGFVGM*PPPALPR@.G	27.07	25.60	1.06	0.95
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.ATEAGSLEAR@.L	63.77	20.33	3.14	0.32
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.EAQELGSPEDR@.L	17.73	7.91	2.24	0.45
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.EDFPLIETEDK#.A	16.31	7.90	2.06	0.48
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.FLNQLLER@.R	120.13	42.02	2.86	0.35
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.GHDR@LDLPVTVR@.S	50.77	17.83	2.85	0.35
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.GLSSLSLAK#.S	30.72	9.34	3.29	0.30
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.GM*FLISSGPPEM*YEVHAASR@.D	18.06	7.19	2.51	0.40
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.ILQNSHGVEEEYQDLASALGLVK#.E	112.78	39.33	2.87	0.35
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.LESFESLR@.G	36.59	14.39	2.54	0.39
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.LGDLLISQFSGSNAEQM*R@.K	20.23	5.53	3.66	0.27
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.LGDLLISQFSGSNAEQM*R@K#.T	39.47	10.84	3.64	0.27
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.LM*EALFPEGPER@.W	37.26	12.26	3.04	0.33
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.LQDSSDPDTGSEEEVSSR@.L	9.76	3.89	2.51	0.40
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.NNTALQSVSLR@.S	58.40	19.16	3.05	0.33
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.NQALVELLQK#.N	71.01	24.49	2.90	0.34
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.QATELALLQR@.Q	41.11	15.67	2.62	0.38
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.QDVIYELIQTELHHVR@.T	21.74	7.45	2.92	0.34
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.QLAALGQNEPLPAEAPWAR@.R	13.94	4.24	3.29	0.30
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.QLAALGQNEPLPAEAPWAR.R	15.12	3.65	4.14	0.24
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	R.SLHR@PFDDR@EAQELGSPEDR@.L	24.71	9.86	2.51	0.40
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.YIFTSLDK#PSVVSLQNLIVR@.D	89.60	28.28	3.17	0.32
Q60875_ARHG2_MOUSE	Arhgef2	Rho guanine nucleotide	K.YPVLINR@.I	38.69	15.91	2.43	0.41
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.YGQLLEELLR@.E	7.15	2.44	2.93	0.34
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.AAVQLLQEQEAR@.G	26.79	15.28	1.75	0.57
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.EALALEEDLTSQK#.V	25.33	13.31	1.90	0.53
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.EALLAALALR@.R	23.39	9.38	2.49	0.40
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.EAYTLQATSPETK#.L	11.05	6.11	1.81	0.55
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.FFQQAHEWVDEGSAR@.L	14.08	7.70	1.83	0.55
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.GSPVDAEASGLSR@.T	17.89	8.02	2.23	0.45
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.K#APPLPPALLPALSQLQDSGEPPLIQR@.L	13.73	6.83	2.01	0.50
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.NSPSLQPPSPGSSTPALTSGGILGLSR@.Q	5.40	3.96	1.37	0.73
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.SPGDGHNAPAEGPEGEYVELLEVTLPVR@.G	8.58	5.63	1.52	0.66
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.TLSALLTGR@.A	18.29	12.77	1.43	0.70
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	K.VLDIFEQR@.L	25.45	20.28	1.25	0.80
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.YGQLLEELLR@.E	35.89	17.46	2.06	0.49
Q3UPH7_ARH40_MOUSE	Arhgef40	Rho guanine nucleotide	R.YTLDFLVPAK#.H	17.07	9.99	1.71	0.59
Q9ES28_ARHG7_MOUSE	Arhgef7	Rho guanine nucleotide	K.ELELQILTEPIR@.S	9.18	4.70	1.95	0.51
Q9ES28_ARHG7_MOUSE	Arhgef7	Rho guanine nucleotide	K.FNFQQTNEDELSFSK#.G	9.36	3.17	2.95	0.34
Q9ES28_ARHG7_MOUSE	Arhgef7	Rho guanine nucleotide	R.LDK#YPTLLK#.E	18.85	8.76	2.15	0.46
Q9ES28_ARHG7_MOUSE	Arhgef7	Rho guanine nucleotide	K.LPTTGM*TITK#.L	12.88	4.75	2.71	0.37
Q9ES28_ARHG7_MOUSE	Arhgef7	Rho guanine nucleotide	R.NAFEISGSM*IER@.I	10.22	7.41	1.38	0.72
Q9ES28_ARHG7_MOUSE	Arhgef7	Rho guanine nucleotide	K.SLVDTVYALK#DEVQELR@.Q	56.07	17.16	3.27	0.31
Q9ES28_ARHG7_MOUSE	Arhgef7	Rho guanine nucleotide	K.STAALEEDAQILK#.V	13.48	4.75	2.84	0.35
Q9ES28_ARHG7_MOUSE	Arhgef7	Rho guanine nucleotide	K.SYYNVVLQNILETEHEYSK#.E	20.49	6.65	3.08	0.32
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	K.AGPPVPASHIAPTPVQPPM*IR@.R	9.18	2.94	3.12	0.32
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	K.DIGTPEAWR@.V	10.41	4.27	2.44	0.41
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	R.EM*AVVLLANLAQGDSLAAR@.A	16.76	6.60	2.54	0.39
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	K.HPGLLLILGK#.L	12.17	4.04	3.01	0.33
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	R.IGGGDTTEHIQTHFESK#.I	12.08	3.93	3.08	0.33
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	R.ITATM*DDM*LSTR@.S	10.23	4.23	2.42	0.41
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	K.LSIQDNNVDLILATPPFSR@.L	19.35	8.14	2.38	0.42
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	R.LVLETLSK#.L	33.07	15.09	2.19	0.46
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	K.AGPPVPASHIAPTPVQPPM*IR@.R	12.81	6.34	2.02	0.49
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	K.AM*GM*TNLPAVGR@.K	11.27	2.14	5.25	0.19
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	K.EIGGLTQVNK#.N	13.96	4.25	3.28	0.30
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	R.ELATNLNVGTSSSAASSLK#.K	7.62	1.58	4.83	0.21
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	R.EM*AVVLLANLAQGDSLAAR@.A	13.98	3.67	3.81	0.26
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	R.ITATM*DDM*LSTR@.S	9.73	2.79	3.49	0.29
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	K.LSIQDNNVDLILATPPFSR@.L	34.31	10.31	3.33	0.30
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	R.LVLETLSK#.L	31.32	5.91	5.30	0.19
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	R.SNSVGIQDAFPDGSDPTFQK#.R	5.24	1.65	3.17	0.32
A2BH40_ARI1A_MOUSE	Arid1a	AT-rich interactive doma	K.VDENHSEFTLYESR@.L	21.68	4.87	4.45	0.22
E9Q6R4_E9Q6R4_MOUSE	Arid1b	Protein Arid1b OS=Mus	R.GSPVSSLPAVGK#.K	9.22	2.04	4.53	0.22
E9Q6R4_E9Q6R4_MOUSE	Arid1b	Protein Arid1b OS=Mus	R.NDM*PYPYQSR@.Q	5.02	1.18	4.27	0.23
E9Q6R4_E9Q6R4_MOUSE	Arid1b	Protein Arid1b OS=Mus	K.SIIATIDDVLSAR@PGALPEDTNPGPQTDSGK#.F	3.36	1.19	2.83	0.35
E9Q6R4_E9Q6R4_MOUSE	Arid1b	Protein Arid1b OS=Mus	R.SLSFVPGNDAEM*SK#.H	7.73	2.17	3.56	0.28
E9Q6R4_E9Q6R4_MOUSE	Arid1b	Protein Arid1b OS=Mus	K.SSPALAAPDASVDPK#.E	15.66	3.77	4.15	0.24
E9Q6R4_E9Q6R4_MOUSE	Arid1b	Protein Arid1b OS=Mus	R.TDDM*M*VPEQR@.I	9.35	4.18	2.24	0.45
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	R.DFTDEK#EGPITK#.H	3.73	2.98	1.25	0.80
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	R.ALPLPIQM*YYQQQPISTPVVR@.V	10.39	2.61	3.98	0.25
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	K.DALLAGLK#QDEPGQVANQK#.S	6.80	2.27	3.00	0.33
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	R.DFTDEK#EGPITK#.H	5.50	1.90	2.90	0.35
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	K.DIVDDNEVR@.D	14.57	4.41	3.31	0.30
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	K.GLAFLDELR@.Q	25.00	6.55	3.81	0.26

E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	R.NLSFEESNVK#.L	12.78	4.81	2.66	0.38
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	K.QPTVGGTGSAPR@.A	9.08	3.15	2.88	0.35
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	R.VTTLGGFAK#.V	16.25	6.05	2.69	0.37
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	R.ALPLPIQM*YYQQQPISTPVVR@.V	18.04	3.24	5.56	0.18
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	K.GLAFLDELR@.Q	27.23	6.76	4.03	0.25
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	R.NLSFEESNVK#.L	21.05	3.07	6.85	0.15
E9Q7E2_E9Q7E2_MOUSE	Arid2	Protein Arid2 OS=Mus m	K.NQWGEIVEEFNFPR@.S	6.43	1.84	3.51	0.29
Q8BM75_ARI5B_MOUSE	Arid5b	AT-rich interactive doma	K.VAAAEASTDDQPTDLSLPK#.N	3.94	3.15	1.25	0.80
Q9Z1K5_ARI1_MOUSE	Arih1	E3 ubiquitin-protein liga	R.DISQDSLQDIK#.Q	11.47	3.99	2.87	0.35
Q9Z1K5_ARI1_MOUSE	Arih1	E3 ubiquitin-protein liga	R.EVNEVIQNPATITR@.I	9.18	24.20	0.38	2.64
Q9Z1K5_ARI1_MOUSE	Arih1	E3 ubiquitin-protein liga	R.EVNEVIQNPATITR@.I	4.01	1.23	3.25	0.31
Q9Z1K5_ARI1_MOUSE	Arih1	E3 ubiquitin-protein liga	R.DISQDSLQDIK#.Q	9.11	3.59	2.54	0.39
Q9Z1K5_ARI1_MOUSE	Arih1	E3 ubiquitin-protein liga	R.DISQDSLQDIK#.Q	8.14	3.64	2.23	0.45
Q9Z1K5_ARI1_MOUSE	Arih1	E3 ubiquitin-protein liga	K.NNQSIIFENNQADLENATEVLSGYLER@.D	5.78	2.03	2.84	0.35
P61211_ARL1_MOUSE	Arl1	ADP-ribosylation factor-l	K.AILVVFANK#.Q	18.54	6.35	2.92	0.34
P61211_ARL1_MOUSE	Arl1	ADP-ribosylation factor-l	K.GTGLDEAM*EWLVETLK#.S	8.04	1.56	5.14	0.19
P61211_ARL1_MOUSE	Arl1	ADP-ribosylation factor-l	R.ILILGLDGAGK#.T	23.28	6.37	3.66	0.27
P61211_ARL1_MOUSE	Arl1	ADP-ribosylation factor-l	R.ILILGLDGAGK#.T	13.26	2.81	4.73	0.21
Q9D0J4_ARL2_MOUSE	Arl2	ADP-ribosylation factor-l	R.LAGATLLIFANK#.Q	5.03	1.17	4.29	0.23
Q9JKW0_AR6P1_MOUSE	Arl6ip1	ADP-ribosylation factor-l	R.AVGWWK#.R	22.03	5.52	3.99	0.25
Q9JKW0_AR6P1_MOUSE	Arl6ip1	ADP-ribosylation factor-l	K.WTTEQQQR@.F	21.10	2.60	8.11	0.12
Q9JM93_AR6P4_MOUSE	Arl6ip4	ADP-ribosylation factor-l	R.SAGEDNDGPVLTDEQK#.S	8.03	4.16	1.93	0.52
Q8R5J9_PRAF3_MOUSE	Arl6ip5	PRA1 family protein 3 OS	R.AWDDFFPGSDR@.F	152.23	54.77	2.78	0.36
Q8R5J9_PRAF3_MOUSE	Arl6ip5	PRA1 family protein 3 OS	K.K#TPM*GIILDALEQQEDNINK#.F	39.16	15.88	2.47	0.41
Q8R5J9_PRAF3_MOUSE	Arl6ip5	PRA1 family protein 3 OS	K.M*EGIGLK#.K	87.60	42.50	2.06	0.49
Q8R5J9_PRAF3_MOUSE	Arl6ip5	PRA1 family protein 3 OS	K.TPM*GIILDALEQQEDNINK#.F	44.93	21.67	2.07	0.48
Q8R5J9_PRAF3_MOUSE	Arl6ip5	PRA1 family protein 3 OS	K.TPM*GIILDALEQQEDNINK#.F	6.51	3.26	2.00	0.50
Q8VEH3_ARL8A_MOUSE	Arl8a	ADP-ribosylation factor-l	R.GVSAIVYM*VDAADQEK#.I	2.53	2.06	1.23	0.81
Q8VEH3_ARL8A_MOUSE	Arl8a	ADP-ribosylation factor-l	K.LWDIGGQPR@.F	16.25	4.39	3.70	0.27
Q8VEH3_ARL8A_MOUSE	Arl8a	ADP-ribosylation factor-l	K.M*NLSAIQDR@.E	11.36	6.58	1.73	0.58
Q8VEH3_ARL8A_MOUSE	Arl8a	ADP-ribosylation factor-l	K.NELHNLLDK#PQLQGIPVLVLGNK#R@.D	23.78	6.41	3.71	0.27
Q9WV32_ARC1B_MOUSE	Arpc1b	Actin-related protein 2/3	K.NSVSQISVLSGGK.A	16.15	28.57	0.57	1.77
Q9WV32_ARC1B_MOUSE	Arpc1b	Actin-related protein 2/3	R.TWKPTLVILR.I	20.89	21.15	0.99	1.01
Q9WV32_ARC1B_MOUSE	Arpc1b	Actin-related protein 2/3	K.NSVSQISVLSGGK#.A	8.21	7.25	1.13	0.88
Q9WV32_ARC1B_MOUSE	Arpc1b	Actin-related protein 2/3	R.TWK#PTLVILR@.I	9.56	4.64	2.06	0.49
Q9WV32_ARC1B_MOUSE	Arpc1b	Actin-related protein 2/3	K.NSVSQISVLSGGK#.A	11.03	9.65	1.14	0.88
Q9CVB6_ARPC2_MOUSE	Arpc2	Actin-related protein 2/3	R.ASHTAPQVLFSHR.E	7.55	15.87	0.48	2.10
Q9CVB6_ARPC2_MOUSE	Arpc2	Actin-related protein 2/3	K.DSIVHQAGM*LK.R	8.15	8.40	0.97	1.03
Q9CVB6_ARPC2_MOUSE	Arpc2	Actin-related protein 2/3	R.IIEETLALK#.F	64.10	85.62	0.75	1.34
Q9CVB6_ARPC2_MOUSE	Arpc2	Actin-related protein 2/3	-.M*ILLEVNNR.I	39.26	29.52	1.33	0.75
Q9CVB6_ARPC2_MOUSE	Arpc2	Actin-related protein 2/3	-.MILLEVNNR.I	11.26	13.65	0.82	1.21
Q9CVB6_ARPC2_MOUSE	Arpc2	Actin-related protein 2/3	K.VFM*QEFK#.E	23.05	24.99	0.92	1.08
Q9CVB6_ARPC2_MOUSE	Arpc2	Actin-related protein 2/3	K.VFMQEFK#.E	11.34	13.77	0.82	1.21
Q9CVB6_ARPC2_MOUSE	Arpc2	Actin-related protein 2/3	K.YFQFQEEGK.E	8.96	11.60	0.77	1.29
Q9CVB6_ARPC2_MOUSE	Arpc2	Actin-related protein 2/3	R.IIEETLALK#.F	12.84	7.90	1.63	0.62
Q9JM76_ARPC3_MOUSE	Arpc3	Actin-related protein 2/3	K.DTDIVDEAIYYFK#.A	5.34	4.48	1.19	0.84
Q9JM76_ARPC3_MOUSE	Arpc3	Actin-related protein 2/3	K.ANVFFK#.N	17.08	11.68	1.46	0.68
Q9JM76_ARPC3_MOUSE	Arpc3	Actin-related protein 2/3	K.DTDIVDEAIYYFK#.A	6.45	7.10	0.91	1.10
Q9JM76_ARPC3_MOUSE	Arpc3	Actin-related protein 2/3	R.ETK#DTDIVDEAIYYFK#.A	24.40	19.07	1.28	0.78
Q9JM76_ARPC3_MOUSE	Arpc3	Actin-related protein 2/3	R.ETK#DTDIVDEAIYYFK#.A	3.98	4.29	0.93	1.08
Q9JM76_ARPC3_MOUSE	Arpc3	Actin-related protein 2/3	K.LIGNM*ALLPLR.S	42.67	41.37	1.03	0.97
Q9JM76_ARPC3_MOUSE	Arpc3	Actin-related protein 2/3	K.DTDIVDEAIYYFK#.A	5.34	6.18	0.86	1.16
Q9JM76_ARPC3_MOUSE	Arpc3	Actin-related protein 2/3	R.ETK#DTDIVDEAIYYFK#.A	9.26	9.73	0.95	1.05
Q9JM76_ARPC3_MOUSE	Arpc3	Actin-related protein 2/3	K.LIGNM*ALLPLR.S	31.47	20.79	1.51	0.66
P59999_ARPC4_MOUSE	Arpc4	Actin-related protein 2/3	R.AENFFILR.R	89.10	61.31	1.45	0.69
P59999_ARPC4_MOUSE	Arpc4	Actin-related protein 2/3	K.ELLLQPVTISR@.N	153.26	119.44	1.28	0.78
P59999_ARPC4_MOUSE	Arpc4	Actin-related protein 2/3	R.IVAEEFLK.N	152.87	62.84	2.43	0.41
P59999_ARPC4_MOUSE	Arpc4	Actin-related protein 2/3	K.VLIEGSINSVR@.V	132.21	104.13	1.27	0.79
P59999_ARPC4_MOUSE	Arpc4	Actin-related protein 2/3	K.ELLLQPVTISR@.N	11.69	10.16	1.15	0.87
P59999_ARPC4_MOUSE	Arpc4	Actin-related protein 2/3	K.ELLLQPVTISR.N	11.28	8.74	1.29	0.77
Q9CPW4_ARPC5_MOUSE	Arpc5	Actin-related protein 2/3	K.ALAAGGVGSIVR.V	36.56	38.88	0.94	1.06
Q9D898_ARP5L_MOUSE	Arpc5l	Actin-related protein 2/3	K.ALAVGGLGSIIR@.V	50.24	36.21	1.39	0.72
Q9D898_ARP5L_MOUSE	Arpc5l	Actin-related protein 2/3	K.GFEK#PTENSSAVLLQWHEK#.A	2.38	3.28	0.72	1.38
Q9D898_ARP5L_MOUSE	Arpc5l	Actin-related protein 2/3	K.SSEIEQAVQSLDR@.N	20.74	19.05	1.09	0.92
Q9D0A3_ARPIN_MOUSE	Arpin	Arpin OS=Mus musculus	K.GNEIEPNFSATR@.K	11.85	4.19	2.83	0.35
P17981_NAR2A_MOUSE	Art2a	T-cell ecto-ADP-ribosyltr	-.MPSNNFK#.F	16.98	2.67	6.36	0.16
Q9WV54_ASAH1_MOUSE	Asah1	Acid ceramidase OS=Mus	K.LPGM*IGSLPDPFGEEM*R@.G	4.95	24.74	0.20	5.00
Q9WV54_ASAH1_MOUSE	Asah1	Acid ceramidase OS=Mus	R.WYVVQTNYDR@.W	4.48	2.40	1.87	0.54
Q9QWY8_ASAP1_MOUSE	Asap1	Arf-GAP with SH3 domai	K.AIYNSGQDHVQNEENYAQVLDK#.F	8.09	3.47	2.33	0.43
Q9QWY8_ASAP1_MOUSE	Asap1	Arf-GAP with SH3 domai	R.GEQSTGENSLEDLTK#.A	7.90	4.33	1.82	0.55
Q9QWY8_ASAP1_MOUSE	Asap1	Arf-GAP with SH3 domai	R.IQSLELDK#LGTSELLLAK#.N	14.59	6.33	2.30	0.43
Q9QWY8_ASAP1_MOUSE	Asap1	Arf-GAP with SH3 domai	R.NTVTLLEEALDQDR@.T	9.45	5.13	1.84	0.54
Q9D8Z1_ASCC1_MOUSE	Ascc1	Activating signal cointeg	K.TFENFYFGSLR@.L	8.53	6.20	1.38	0.73
Q9D8Z1_ASCC1_MOUSE	Ascc1	Activating signal cointeg	K.TFENFYFGSLR@.L	7.04	2.07	3.40	0.29
Q9D8Z1_ASCC1_MOUSE	Ascc1	Activating signal cointeg	K.TFENFYFGSLR@.L	10.68	4.60	2.32	0.43
Q91WR3_ASCC2_MOUSE	Ascc2	Activating signal cointeg	R.LASFYEM*AIPELESAIK#.K	4.76	2.69	1.77	0.57
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	K.FLNEQFQEPYTPELK#PVEK#.T	7.40	9.18	0.81	1.24
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	K.AGEDGEVSGEGVLPFDPK#.E	6.62	3.89	1.70	0.59
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	K.ALAAEM*TNYFSK#.R	8.22	3.59	2.29	0.44
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	R.ALFEIALR@.K	8.85	3.91	2.26	0.44
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	K.FLNEQFQEPYTPELK#PVEK#.T	14.37	6.63	2.17	0.46
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	R.IVGLSTALANAR@.D	27.98	13.06	2.14	0.47
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	K.M*QNINEDLK#DILQAAK#.Q	9.89	4.09	2.42	0.41
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	K.QDNYNEEVADLK#.L	4.48	1.34	3.36	0.30
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	K.R@LEPLGIVVK#.E	12.81	6.98	1.84	0.54
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	K.TEGDIFAIVSK#.A	9.15	10.79	0.85	1.18
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	R.TGYFSSTDLGR@.T	11.79	5.55	2.12	0.47
E9PZJ8_ASCC3_MOUSE	Ascc3	Activating signal cointeg	R.YVDFPITDVLQM*M*GR@.A	9.34	4.97	1.88	0.53
Q9CQE6_ASF1A_MOUSE	Asf1a	Histone chaperone ASF1	R.VGYYVNNEYTETELR@.E	11.23	3.76	2.99	0.33
Q91X20_ASH2L_MOUSE	Ash2l	Set1/Ash2 histone methy	R.DIFEGVYFPAISLYK#.S	22.82	8.38	2.72	0.37
Q91X20_ASH2L_MOUSE	Ash2l	Set1/Ash2 histone methy	K.FGLLDQDLSNIGPAYDNQK#.Q	6.23	2.46	2.53	0.39
Q91X20_ASH2L_MOUSE	Ash2l	Set1/Ash2 histone methy	K.HYSSGYGQGDVLGFYINLPEDTETAK#.S	10.25	3.94	2.60	0.38
O54984_ASNA_MOUSE	Asna1	ATPase Asna1 OS=Mus m	K.LEETLPVIR@.S	22.81	13.32	1.71	0.58
O54984_ASNA_MOUSE	Asna1	ATPase Asna1 OS=Mus m	R.LLNFPTIVER@.G	61.58	23.87	2.58	0.39
O54984_ASNA_MOUSE	Asna1	ATPase Asna1 OS=Mus m	K.YLDQM*EDLYEDFHIVK#.L	14.89	5.06	2.94	0.34
Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	K.ELYLFDVLR@.A	19.20	9.16	2.10	0.48
Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	K.HSTTPFLK#.V	8.18	5.65	1.45	0.69
Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	K.ILQDYVEHQVDDEM*M*SAASQK#.F	7.27	4.43	1.64	0.61
Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	R.LAVVDPLFGM*QPIR@.V	5.39	3.72	1.45	0.69
Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	K.ELYLFDVLR@.A	17.02	9.94	1.71	0.58
Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	K.ILQDYVEHQVDDEM*M*SAASQK#.F	6.45	3.37	1.91	0.52
Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	R.LAVVDPLFGM*QPIR@.V	5.29	2.47	2.15	0.47
Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	K.ELYLFDVLR@.A	26.96	7.00	3.85	0.26

Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	K.ILQDYVEHQVDDEM*M*SAASQK#.F	6.70	1.92	3.49	0.29
Q61024_ASNS_MOUSE	Asns	Asparagine synthetase [gl	R.LAVVDPLFGM*QPIR@.V	18.00	6.50	2.77	0.36
Q8BSY0_ASPH_MOUSE	Asph	Aspartyl/asparaginyl beta	K.LGVYDADGDGDFDVDDAK#.V	5.59	2.62	2.13	0.47
Q8CJ27_ASPM_MOUSE	Aspm	Abnormal spindle-like mi	K.AAVVTLQSAYR@GM*K#.V	13.63	5.67	2.41	0.42
Q8CJ27_ASPM_MOUSE	Aspm	Abnormal spindle-like mi	R.LM*EAERGFQAGCR@.K	3.18	2.46	1.29	0.77
P16460_ASSY_MOUSE	Ass1	Argininosuccinate syntha	R.TTSLELFM*YLNEVAGK#.H	4.70	4.81	0.98	1.02
P16460_ASSY_MOUSE	Ass1	Argininosuccinate syntha	R.TTSLELFM*YLNEVAGK#.H	4.45	2.57	1.73	0.58
Q8QZV7_ASUN_MOUSE	Asun	Protein asunder homolog	R.IM*WNELETLVR.A	21.40	9.22	2.32	0.43
Q8QZV7_ASUN_MOUSE	Asun	Protein asunder homolog	K.K#ELSPVLTSEVHSVR@.A	15.20	9.69	1.57	0.64
Q8QZV7_ASUN_MOUSE	Asun	Protein asunder homolog	R.SVLLEQPR@.K	24.79	8.45	2.93	0.34
Q8QZV7_ASUN_MOUSE	Asun	Protein asunder homolog	R.TLLM*ENAER@.V	14.05	4.72	2.97	0.34
Q8QZV7_ASUN_MOUSE	Asun	Protein asunder homolog	R.TQGIIPLAPISK#.S	31.11	11.08	2.81	0.36
Q8QZV7_ASUN_MOUSE	Asun	Protein asunder homolog	R.TQGIIPLAPISK#.S	8.99	1.15	7.79	0.13
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.LITNTAEAVLQK#.M	8.80	5.73	1.53	0.65
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.EFLFSLPDK.N	11.39	10.79	1.06	0.95
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.FFEDLILK#.Q	13.24	16.38	0.81	1.24
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.GEIVVIGATNR@.L	8.96	10.48	0.85	1.17
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.IGASLADVDPM*QLDTSVR@.F	6.91	5.90	1.17	0.85
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.KLEDLGVFNETEESNLTM*YTR.G	4.52	4.93	0.92	1.09
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.LITNTAEAVLQK.M	23.15	20.65	1.12	0.89
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.VFTKPVDPDEVPDYVTVIK.Q	18.55	13.63	1.36	0.73
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.AAGDGFTVK#.G	36.34	21.34	1.70	0.59
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.AVLQALEVLPVAPPPEPR@PLTAEEVK#.R	6.28	5.98	1.05	0.95
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.DFEAALQK#.I	35.35	20.73	1.71	0.59
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.DNSLNAM*NSSSR@.S	6.69	2.13	3.15	0.32
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.EFLFSLPDK#.N	58.20	34.71	1.68	0.60
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.FDR@EFLFSLPDK#.N	14.17	6.17	2.30	0.44
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.FFEDLILK#.Q	44.27	25.64	1.73	0.58
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.GEIVVIGATNR@.L	35.92	20.88	1.72	0.58
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.GSQVEQQELISM*EQALAILSQPTPSLVLDHK#.Q	14.08	4.94	2.85	0.35
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.IGASLADVDPM*QLDTSVR@.F	18.58	10.60	1.75	0.57
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.K#LEDLGVFNETEESNLTM*YTR@.G	22.02	11.52	1.91	0.52
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.K#TTVYYQSPLESK#PR@.H	6.77	6.83	0.99	1.01
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.LDSIDPALR@.R	61.63	30.72	2.01	0.50
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.LEDLGVFNETEESNLTM*YTR.G	9.69	6.25	1.55	0.64
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.LEEQEEDTFR@.E	18.41	13.12	1.40	0.71
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.LESNIDLK#.N	22.20	15.56	1.43	0.70
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.LITNTAEAVLQK#.M	81.80	44.79	1.83	0.55
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.LQLDLSSITISAK#.D	63.66	33.05	1.93	0.52
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.NNSSSSNIENELEEPK#.E	3.81	1.97	1.93	0.52
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.NNSSSSNIENELEEPK#ETTEGTELR@K#.D	28.06	17.44	1.61	0.62
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.NQAQTSSESSFDK#.N	8.23	4.41	1.86	0.54
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.QDQIHSSIVSTLLALM*DGLDSR@.G	15.40	9.57	1.61	0.62
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.QNSPPVGDK#K#PDQEQNEK#.L	7.72	7.20	1.07	0.93
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	K.QPM*DLSSVISK#.I	15.49	10.93	1.42	0.71
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.SDTEDSQHTHAEHTEPGNTDESSVEESDK#.Q	4.97	3.31	1.50	0.67
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.SSLELHSR.S	126.82	16.91	7.50	0.13
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.STTSSATDSLDLSSEFLSLQDSGGR@.R	22.79	15.40	1.48	0.68
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.TK#FFEDLILK#.Q	26.06	13.13	1.98	0.50
G3X963_G3X963_MOUSE	Atad2	ATPase family AAA domai	R.VFTK#PVDPDEVPDYVTVIK#.Q	59.87	49.46	1.21	0.83
E9Q166_E9Q166_MOUSE	Atad2b	Protein Atad2b OS=Mus r	R.LDLPALYSVSAK#.T	8.81	30.24	0.29	3.43
E9Q166_E9Q166_MOUSE	Atad2b	Protein Atad2b OS=Mus r	K.LSDAFLGELAEK.C	5.49	6.26	0.88	1.14
E9Q166_E9Q166_MOUSE	Atad2b	Protein Atad2b OS=Mus r	R.SFNNILAVLQK#.I	12.54	9.59	1.31	0.76
E9Q166_E9Q166_MOUSE	Atad2b	Protein Atad2b OS=Mus r	K.SPGPGPGPGAGAGAEPGATGGSSHFISSR@.T	3.58	2.04	1.75	0.57
E9Q166_E9Q166_MOUSE	Atad2b	Protein Atad2b OS=Mus r	R.VLEVVPLPDGGEK#.S	7.44	5.10	1.46	0.69
Q4QY64_ATAD5_MOUSE	Atad5	ATPase family AAA domai	K.NIASPSQDLLSLLK#.H	10.93	4.78	2.29	0.44
Q8R0S1_ATF7_MOUSE	Atf7	Cyclic AMP-dependent tr	K.K#AEELTSQNIQLSNEVTLLR@.N	6.32	3.98	1.59	0.63
Q9D8Z6_ATGA1_MOUSE	Atg101	Autophagy-related prote	K.M*PTQSEVDNVFDTGLR@.D	5.21	2.71	1.92	0.52
Q9D8Z6_ATGA1_MOUSE	Atg101	Autophagy-related prote	R.NSGGDGLGQM*SLEFYQK#.K	2.07	2.42	0.86	1.17
Q6P4T0_ATG2A_MOUSE	Atg2a	Autophagy-related prote	R.LELSEPQFR@.S	16.92	7.26	2.33	0.43
Q6P4T0_ATG2A_MOUSE	Atg2a	Autophagy-related prote	R.LNVDQDALFFLK#.D	16.51	5.64	2.93	0.34
Q6P4T0_ATG2A_MOUSE	Atg2a	Autophagy-related prote	R.LSQPLFELR@.C	14.41	3.76	3.83	0.26
Q6P4T0_ATG2A_MOUSE	Atg2a	Autophagy-related prote	R.SELNSGPGPPAPTR@.L	9.78	1.90	5.14	0.19
Q9CPX6_ATG3_MOUSE	Atg3	Ubiquitin-like-conjugatii	K.ALEVAEYLTPVLK#.E	7.32	2.72	2.69	0.37
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.DLDVVVVSVAGAFR@.K	9.78	1.33	7.38	0.14
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.ELGGAIDSGAAYVLEQASSHIGNSTQAAVR@.D	15.57	4.87	3.20	0.31
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.GGSDPETTGIQIWSEVFTVK#.K	8.52	2.75	3.10	0.32
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.GLLEYFK#.A	17.54	2.92	6.00	0.17
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	K.SM*LQATAEANNLAAAASAK#.D	9.83	2.85	3.44	0.29
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.GGSDPETTGIQIWSEVFTVK#.K	8.61	2.54	3.39	0.29
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.GLLEYFK#.A	20.16	7.58	2.66	0.38
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	K.NVFSTFR@.T	20.19	9.51	2.12	0.47
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	K.SM*LQATAEANNLAAAASAK#.D	9.79	2.60	3.76	0.27
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.DLDVVVVSVAGAFR@.K	11.82	4.20	2.81	0.36
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	K.EGGHSDWLGDPEEPLTGFSWR@.G	9.47	0.98	9.61	0.10
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.ELGGAIDSGAAYVLEQASSHIGNSTQAAVR@.D	42.24	10.51	4.02	0.25
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.GGSDPETTGIQIWSEVFTVK#.K	10.63	4.33	2.46	0.41
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	R.GLLEYFK#.A	28.21	8.30	3.40	0.29
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	K.NVFSTFR@.T	31.13	6.95	4.48	0.22
Q91YH5_ATLA3_MOUSE	Atl3	Atlastin-3 OS=Mus muscu	K.SM*LQATAEANNLAAAASAK#.D	14.06	3.85	3.65	0.27
O35126_ATN1_MOUSE	Atn1	Atrophin-1 OS=Mus musc	R.VAALGNDPLAR@.L	10.81	2.67	4.05	0.25
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	R.AVAGDASESALLK#.C	13.42	1.42	9.46	0.11
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	R.AVFQANQENLPILK#.R	93.75	21.93	4.28	0.23
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	R.GIVVYTGDR@.T	14.84	1.89	7.85	0.13
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.GVGIISEGNETVEDIAAR@.L	16.61	3.21	5.18	0.19
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.IVEIPFNSTNK#.Y	18.61	5.02	3.71	0.27
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	R.SPDFTNENPLETR@.N	16.27	4.03	4.04	0.25
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.TSATWFALSR@.I	9.61	2.70	3.56	0.28
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.VDNSSLTGESEPQTR@.S	11.11	3.52	3.15	0.32
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.ADIGVAM*GIVGSDVSK#.Q	9.38	2.32	4.04	0.25
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	R.AVAGDASESALLK#.C	17.76	2.60	6.84	0.15
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	R.AVFQANQENLPILK#.R	73.52	13.22	5.56	0.18
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	R.GIVVYTGDR@.T	15.98	3.14	5.09	0.20
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.GVGIISEGNETVEDIAAR@.L	29.03	7.77	3.74	0.27
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.IVEIPFNSTNK#.Y	42.19	12.83	3.29	0.30
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.M*SINAEDVVVGDLVEVK#.G	12.26	4.10	2.99	0.33
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.NM*VPQQALVIR@.N	16.57	4.35	3.81	0.26
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.QAADM*ILLDDNFASIVTGVEEGR@.L	9.53	2.99	3.18	0.31
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	R.QGAIVAVTGDGVNDSPALK#.K	11.92	3.46	3.44	0.29
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	R.SPDFTNENPLETR@.N	25.52	15.02	1.70	0.59
Q8VDN2_AT1A1_MOUSE	Atp1a1	Sodium/potassium-trans	K.VDNSSLTGESEPQTR@.S	15.98	5.44	2.94	0.34
P14094_AT1B1_MOUSE	Atp1b1	Sodium/potassium-trans	K.SYEAYVLNIIR@.F	31.33	8.35	3.75	0.27
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	K.AM*GVVVATGVNTEIGK#.I	7.51	2.45	3.07	0.33

O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	R.IGIFGQDEDVTSK#.A	12.34	28.25	0.44	2.29
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	K.IR@DEM*VATEQER@.T	2.28	0.00	#DIV/0!	0.00
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	K.ISLPVILM*DETLK#.F	7.70	4.09	1.88	0.53
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	K.LDEFGEQLSK#.V	8.71	3.71	2.35	0.43
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	K.M*NVFDTELK#.G	10.90	5.85	1.86	0.54
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	K.NM*LFSGTNIAAGK#.A	8.92	3.82	2.33	0.43
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	K.SEIGIAM*GSGTAVAK#.T	6.70	5.38	1.24	0.80
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	K.TASEM*VLADDNFSTIVAAVEEGR@.A	17.40	9.32	1.87	0.54
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	K.TVEEVLGHFGVNESTGLSLEQVK#.K	6.52	2.46	2.64	0.38
O55143_AT2A2_MOUSE	Atp2a2	Sarcoplasmic/endoplasm	R.VDQSILTGESVSVIK#.H	21.08	11.89	1.77	0.56
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.APGIIPR.I	58.66	50.96	1.15	0.87
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.AVDSLVPIGR@.G	59.88	35.29	1.70	0.59
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.EIVTNFLAGFEP.-	34.18	34.18	1.00	1.00
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.ELIIGDR.Q	47.80	29.31	1.63	0.61
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.EVAAFAQFGSDLDAATQQLLSR@.G	85.59	46.23	1.85	0.54
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.FENAFLSHVISQHQSLLGNIR@.S	35.83	21.55	1.66	0.60
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.GM*SLNLEPDNVGVVVFGNDK.L	10.82	6.94	1.56	0.64
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.GMSLNLEPDNVGVVVFGNDK#.L	5.51	2.15	2.56	0.39
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.HALIIYDDLSK#.Q	50.01	31.74	1.58	0.63
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.ILGADTSVDLEETGR@.V	49.69	25.90	1.92	0.52
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.LK#EIVTNFLAGFEP.-	74.06	51.12	1.45	0.69
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.NVQAEEM*VEFSSGLK.G	9.26	6.34	1.46	0.68
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.QGQYSPM*AIEEQVAVIYAGVR@.G	8.43	12.74	0.66	1.51
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.R@LTDADAM*K#.Y	6.70	6.11	1.10	0.91
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.TGAIVDVPVGEELLGR@.V	96.57	63.18	1.53	0.65
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.TGTAEM*SSILEER.I	42.40	26.85	1.58	0.63
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.TSIAIDTIINQK#.R	61.66	41.46	1.49	0.67
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.VLSIGDGIAR@.V	116.59	58.64	1.99	0.50
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.VVDALGNAIDGK#.G	64.23	41.44	1.55	0.65
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.ILGADTSVDLEETGR.V	1.59	3.85	0.41	2.42
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.LK#EIVTNFLAGFEP.-	17.22	2.37	7.27	0.14
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.LTELLK#.Q	8.61	2.08	4.14	0.24
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.ILGADTSVDLEETGR@.V	7.23	3.65	1.98	0.51
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.LK#EIVTNFLAGFEP.-	10.16	3.79	2.68	0.37
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.VVDALGNAIDGK#.G	8.53	8.66	0.98	1.02
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.AVDSLVPIGR@.G	14.01	3.95	3.54	0.28
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.HALIIYDDLSK#.Q	4.82	3.79	1.27	0.79
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.ILGADTSVDLEETGR@.V	12.04	3.26	3.69	0.27
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	K.LK#EIVTNFLAGFEP.-	9.74	2.80	3.48	0.29
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.VLSIGDGIAR@.V	13.17	2.94	4.48	0.22
Q03265_ATPA_MOUSE	Atp5a1	ATP synthase subunit alp	R.VVDALGNAIDGK#.G	9.92	7.82	1.27	0.79
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.AHGGYSVFAGVGER.T	20.28	24.25	0.84	1.20
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	R.AIAELGIYPAVDPLDSTSR@.I	15.28	33.35	0.46	2.18
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	R.FTQAGSEVSALLGR.I	37.71	44.71	0.84	1.19
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR.A	2.89	2.52	1.15	0.87
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.IGLFGGAGVGK#.T	33.07	38.64	0.86	1.17
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	R.IM*DPNIVGNEHYDVAR.G	28.12	43.81	0.64	1.56
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	R.IM*NVIGEPIDER@.G	15.38	18.26	0.84	1.19
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	R.IPSAVGYQPTLATDM*GTM*QER.I	20.09	21.34	0.94	1.06
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.IPVGPETLGR.I	7.27	15.41	0.47	2.12
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	R.LVLEVAQHLGESTVR@.T	9.97	10.34	0.96	1.04
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.SLQDIIAILGM*DELSEEDKLTVSR.A	31.14	30.32	1.03	0.97
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	R.TIAM*DGTEGLVR@.G	18.60	18.63	1.00	1.00
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.TVLIMELINNVAK#.A	2.26	7.27	0.31	3.22
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	R.VALTGLTVAEYFR@.D	24.03	25.83	0.93	1.07
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.VALVYGQM*NEPPGAR@.A	8.32	10.51	0.79	1.26
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.VLDSGAPIK.I	42.32	22.23	1.90	0.53
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.VLDSGAPIK#IPVGPETLGR@.I	43.41	50.37	0.86	1.16
P56480_ATPB_MOUSE	Atp5b	ATP synthase subunit bet	K.VVDLLAPYAK#.G	16.63	24.45	0.68	1.47
Q91VR2_ATPG_MOUSE	Atp5c1	ATP synthase subunit gam	K.ELIEIISGAAALD.-	15.16	15.16	1.00	1.00
Q9D3D9_ATPD_MOUSE	Atp5d	ATP synthase subunit del	K.AQSELSGAADEAAR@.A	5.19	10.35	0.50	2.00
P56135_ATPK_MOUSE	Atp5j2	ATP synthase subunit f, m	R.DFTPSGIAGAFR@.R	8.04	7.26	1.11	0.90
Q9DB20_ATPO_MOUSE	Atp5o	ATP synthase subunit O, m	K.LVRPPVQVYGIEGR.Y	5.45	5.58	0.98	1.02
Q9CYN9_RENR_MOUSE	Atp6ap2	Renin receptor OS=Mus m	K.ILVDALQK.F	5.66	7.07	0.80	1.25
P51863_VA0D1_MOUSE	Atp6v0d1	V-type proton ATPase sub	K.LLFEGAGSNPGDK#.T	12.88	6.59	1.96	0.51
P51863_VA0D1_MOUSE	Atp6v0d1	V-type proton ATPase sub	R.LYPEGLAQLAR@.A	25.09	10.70	2.34	0.43
P51863_VA0D1_MOUSE	Atp6v0d1	V-type proton ATPase sub	K.NVADYYPEYK#.L	9.12	5.99	1.52	0.66
P51863_VA0D1_MOUSE	Atp6v0d1	V-type proton ATPase sub	R.SIAELVPK#.C	9.30	4.06	2.29	0.44
P62814_VATB2_MOUSE	Atp6v1b2	V-type proton ATPase sub	K.AVVGEEALTSDDLLYLEFLQK#.F	5.25	3.04	1.73	0.58
P62814_VATB2_MOUSE	Atp6v1b2	V-type proton ATPase sub	K.AVVGEEALTSDDLLYLEFLQK#.F	1.96	2.86	0.69	1.46
P57746_VATD_MOUSE	Atp6v1d	V-type proton ATPase sub	K.FTAGDFSTTVIQNVNK#.A	15.38	7.36	2.09	0.48
P57746_VATD_MOUSE	Atp6v1d	V-type proton ATPase sub	R.TLAYIITELDER@.E	6.91	3.16	2.18	0.46
P50518_VATE1_MOUSE	Atp6v1e1	V-type proton ATPase sub	R.AR@DDLITDLLNEAK#.Q	6.80	6.30	1.08	0.93
P50518_VATE1_MOUSE	Atp6v1e1	V-type proton ATPase sub	K.IQM*SNLM*NQAR@.L	11.05	6.19	1.79	0.56
Q9CR51_VATG1_MOUSE	Atp6v1g1	V-type proton ATPase sub	K.EEAQAEIEQYR@.L	3.23	2.48	1.30	0.77
Q8BVE3_VATH_MOUSE	Atp6v1h	V-type proton ATPase sub	K.LGESVQDLSSFDEYSSELK#.S	4.39	1.81	2.42	0.41
Q8BVE3_VATH_MOUSE	Atp6v1h	V-type proton ATPase sub	R.GAVDAAVPTNIIAAK#.A	7.17	3.14	2.28	0.44
Q8BVE3_VATH_MOUSE	Atp6v1h	V-type proton ATPase sub	K.LGESVQDLSSFDEYSSELK#.S	4.11	3.31	1.24	0.80
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.AATENSENDITM*QSLPK#.G	7.31	3.68	1.98	0.50
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.YYM*SDDISR@.D	16.17	7.28	2.22	0.45
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.AATENSENDITM*QSLPK#.G	16.47	5.99	2.75	0.36
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.AATENSENDITMQSLPK#.G	5.07	2.04	2.48	0.40
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.LIETTSNM*NSSYIK#.F	30.43	8.38	3.63	0.28
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.LIETTSNMNSSYIK#.F	9.21	3.32	2.77	0.36
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.STETSIISK#.K	22.09	5.51	4.01	0.25
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.YYM*SDDISR@.D	12.50	3.67	3.41	0.29
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.AATENSENDITM*QSLPK#.G	11.74	2.59	4.53	0.22
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.AGSLGINLVAANR@.V	19.43	2.57	7.55	0.13
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	R.EAIYNDVLTK#.Q	16.42	4.86	3.38	0.30
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	R.FLAQGTM*EDK#.I	6.49	2.76	2.35	0.42
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	R.GGGDGNVDDTGNNPSVSLK#.L	17.48	3.61	4.84	0.21
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	R.LFIISTK#.A	25.24	5.65	4.47	0.22
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.LFQDFQM*LSR@.I	39.99	7.66	5.22	0.19
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.LIETTSNM*NSSYIK#.F	24.78	5.12	4.84	0.21
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.LIETTSNMNSSYIK#.F	7.15	8.76	0.82	1.22
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.LVLDENEETK#EPLVQVHR@.N	10.74	3.24	3.31	0.30
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.LYQYYLDHLTGVGNSTEGGR@.G	16.24	3.92	4.15	0.24
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.M*VLLFEILR@.M	24.07	4.54	5.30	0.19
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.STETSIISK#.K	28.86	4.64	6.22	0.16
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.SVPATVDDDDDDNDPENR@.I	13.42	4.96	2.70	0.37
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	R.VVDQQQVER@.H	47.89	13.54	3.54	0.28
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.VVEATNSM*TAVR@.I	12.31	2.19	5.61	0.18
Q61687_ATRX_MOUSE	Atrx	Transcriptional regulator	K.WAEEFNDETNVR@.G	8.37	2.91	2.87	0.35

Q61687_ATRX_MOUSE	Atrx	Transcriptional regulato	K.YYM*SDDISR@.D	12.48	2.93	4.27	0.23
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	K.HPASEWPFLIISDHFLK#.S	9.56	5.30	1.80	0.55
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.ITLLDIVIAK#.L	25.42	12.47	2.04	0.49
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.LSGIM*VPAPIQDLEALR@.A	7.91	6.77	1.17	0.86
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.LSGIM*VPAPIQDLEALR.A	19.26	12.96	1.49	0.67
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	K.LVGEEQLTK#DDISIFVR@.H	15.58	7.99	1.95	0.51
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.M*K#DLEENLNIAINVIEAHQK#.H	12.76	9.78	1.30	0.77
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.NLTEDNSQNQDVIAK#.M	24.74	14.29	1.73	0.58
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	K.SPELVEAM*YGK#.L	10.34	5.23	1.98	0.51
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.ITLLDIVIAK#.L	13.48	6.36	2.12	0.47
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.LSGIM*VPAPIQDLEALR@.A	8.75	3.34	2.62	0.38
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	K.LVGEEQLTK#DDISIFVR@.H	8.72	4.10	2.13	0.47
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.NLTEDNSQNQDVIAK#.M	7.99	3.81	2.10	0.48
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.ALTALFK#.E	11.91	6.15	1.94	0.52
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.ITLLDIVIAK#.L	26.14	11.09	2.36	0.42
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.LSGIM*VPAPIQDLEALR@.A	6.63	4.20	1.58	0.63
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	K.LVGEEQLTK#DDISIFVR@.H	16.19	4.81	3.36	0.30
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	R.NLTEDNSQNQDVIAK#.M	10.45	6.50	1.61	0.62
P28658_ATX10_MOUSE	Atxn10	Ataxin-10 OS=Mus muscu	K.SPELVEAM*YGK#.L	7.55	94.13	0.08	12.47
Q7TQH0_ATX2L_MOUSE	Atxn2l	Ataxin-2-like protein OS=	R.EIESSPQYR@.L	16.00	11.75	1.36	0.73
Q7TQH0_ATX2L_MOUSE	Atxn2l	Ataxin-2-like protein OS=	R.GPHHLDNSSPGPGSEAR@.G	15.54	3.36	4.62	0.22
Q7TQH0_ATX2L_MOUSE	Atxn2l	Ataxin-2-like protein OS=	K.LQPSSSPETGLDPFPSR@.I	12.36	2.75	4.49	0.22
Q7TQH0_ATX2L_MOUSE	Atxn2l	Ataxin-2-like protein OS=	K.LSLTPTDVK#.E	17.06	3.45	4.94	0.20
Q7TQH0_ATX2L_MOUSE	Atxn2l	Ataxin-2-like protein OS=	K.TTYDSSLSSYTVPLEK#.D	6.12	3.01	2.03	0.49
O70126_AURKB_MOUSE	Aurkb	Aurora kinase B OS=Mus	R.DIK#PENLLLGLQGELK#.I	10.19	8.15	1.25	0.80
P01887_B2MG_MOUSE	B2m	Beta-2-microglobulin OS	K.TPQIQVYSR.H	78.54	73.50	1.07	0.94
P01887_B2MG_MOUSE	B2m	Beta-2-microglobulin OS	K.TVYWDRDM*.-	14.04	12.90	1.09	0.92
P01887_B2MG_MOUSE	B2m	Beta-2-microglobulin OS	K.VEM*SDM*SFSK.D	28.88	29.15	0.99	1.01
Q3UI43_BABA1_MOUSE	Babam1	BRISC and BRCA1-A com	R.ALGAQASVGSR@.S	31.14	8.17	3.81	0.26
Q60739_BAG1_MOUSE	Bag1	BAG family molecular ch	K.ILEEIDTM*VLPEQFK.D	4.29	4.79	0.90	1.12
Q60739_BAG1_MOUSE	Bag1	BAG family molecular ch	K.TEEM*VQTEEM*ETPR.L	3.64	4.42	0.82	1.22
Q91YN9_BAG2_MOUSE	Bag2	BAG family molecular ch	R.LLESLDQLELR@.V	11.89	4.82	2.47	0.41
Q91YN9_BAG2_MOUSE	Bag2	BAG family molecular ch	R.R@LETLLR@.N	17.58	5.58	3.15	0.32
Q91YN9_BAG2_MOUSE	Bag2	BAG family molecular ch	R.DAATAVEQEK#EILLEMIHSIQNSQDM*R@.Q	6.03	2.09	2.88	0.35
Q91YN9_BAG2_MOUSE	Bag2	BAG family molecular ch	K.FLDDLGNAK#.S	26.45	12.55	2.11	0.47
Q91YN9_BAG2_MOUSE	Bag2	BAG family molecular ch	R.LLESLDQLELR@.V	49.01	24.94	1.97	0.51
Q91YN9_BAG2_MOUSE	Bag2	BAG family molecular ch	R.R@LETLLR@.N	29.89	16.20	1.84	0.54
Q91YN9_BAG2_MOUSE	Bag2	BAG family molecular ch	K.SLQNTDGK#FN.-	26.50	14.02	1.89	0.53
Q91YN9_BAG2_MOUSE	Bag2	BAG family molecular ch	R.TLTVEVSVETIR@NPQQEESLK#.H	13.14	6.20	2.12	0.47
Q9JLV1_BAG3_MOUSE	Bag3	BAG family molecular ch	K.AAPSPAPAEPAAPK#.S	9.93	8.21	1.21	0.83
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.APPQTQLPSGASSGTGSASATHGGAPLPGTR@.G	17.76	8.03	2.21	0.45
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.DIQTLLSR@.M	23.03	8.16	2.82	0.35
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.DLEAPEVQESYR@.Q	10.94	4.68	2.34	0.43
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.ENASPAPGTTAEEAM*SR@.G	4.66	2.41	1.93	0.52
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.ESFSLVQVQPGVDIIR@.T	19.43	7.91	2.46	0.41
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.LINLVGESLR@.L	24.28	9.07	2.68	0.37
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.LLGNTFVALSDLR@.C	31.63	12.22	2.59	0.39
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	K.LQEYNVGGK#.V	21.21	7.47	2.84	0.35
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.LQVVLEHMPVGPDAILR@.Y	7.11	1.64	4.32	0.23
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.M*ATHTLITGLEEYVR@.E	11.42	4.44	2.57	0.39
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.TFIVGAQM*NVK#.E	8.44	6.97	1.21	0.83
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.APPQTQLPSGASSGTGSASATHGGAPLPGTR@.G	7.33	6.18	1.19	0.84
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.DIQTLLSR@.M	12.18	4.21	2.90	0.35
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.ESFSLVQVQPGVDIIR@.T	15.35	9.38	1.64	0.61
Q9Z1R2_BAG6_MOUSE	Bag6	Large proline-rich prote	R.M*ATHTLITGLEEYVR@.E	7.21	4.30	1.68	0.60
Q8BKX1_BAIP2_MOUSE	Baiap2	Brain-specific angiogene	K.EGDLITLLVPEAR@.D	4.58	2.92	1.57	0.64
Q8BKX1_BAIP2_MOUSE	Baiap2	Brain-specific angiogene	K.M*GELASESQGSK#.E	9.85	2.53	3.89	0.26
Q8BKX1_BAIP2_MOUSE	Baiap2	Brain-specific angiogene	K.TIM*EQFNPSLR@.N	5.00	1.88	2.67	0.38
O08734_BAK_MOUSE	Bak1	Bcl-2 homologous antag	R.R@YDTEFQNLLEQLQPTAGNAYELFTK#.I	5.13	2.87	1.79	0.56
O08734_BAK_MOUSE	Bak1	Bcl-2 homologous antag	R.QLALIGDDINR@.R	11.43	5.01	2.28	0.44
O54962_BAF_MOUSE	Banf1	Barrier-to-autointegratic	K.AYVVLGQFLVLK.K	6.39	19.20	0.33	3.00
O54962_BAF_MOUSE	Banf1	Barrier-to-autointegratic	R.DFVAEPM*GEKPVGSLAGIGDVLSK.R	40.44	134.70	0.30	3.33
O54962_BAF_MOUSE	Banf1	Barrier-to-autointegratic	R.DFVAEPMGEKPVGSLAGIGDVLSK.R	2.39	9.95	0.24	4.17
Q8VBU8_BANP_MOUSE	Banp	Protein BANP OS=Mus m	R.EVQAVSNLSGQGK#.H	3.84	1.28	3.01	0.33
Q8VBU8_BANP_MOUSE	Banp	Protein BANP OS=Mus m	R.EVQAVSNLSGQGK#.H	5.05	3.01	1.67	0.60
Q8VBU8_BANP_MOUSE	Banp	Protein BANP OS=Mus m	R.EVQAVSNLSGQGK#.H	8.87	1.49	5.95	0.17
Q9DCT6_BAP18_MOUSE	Bap18	Chromatin complexes su	K.VGEIFSAAGAAFTK#.L	8.24	3.52	2.34	0.43
Q9DCT6_BAP18_MOUSE	Bap18	Chromatin complexes su	K.VGEIFSAAGAAFTK#.L	35.17	12.49	2.82	0.35
Q07813_BAX_MOUSE	Bax	Apoptosis regulator BAX	R.IGDELDSNM*ELQR@.M	30.92	9.52	3.25	0.31
Q07813_BAX_MOUSE	Bax	Apoptosis regulator BAX	R.M*AGETPELTLEQPPQDASTK#.K	10.89	16.19	0.67	1.49
Q07813_BAX_MOUSE	Bax	Apoptosis regulator BAX	R.M*AGETPELTLEQPPQDASTK#K#.L	6.77	3.82	1.77	0.57
Q07813_BAX_MOUSE	Bax	Apoptosis regulator BAX	R.M*IADVDTDSPR@.E	44.55	21.40	2.08	0.48
Q07813_BAX_MOUSE	Bax	Apoptosis regulator BAX	K.TGAFLLQGFIQDR@.A	29.53	10.27	2.88	0.35
Q07813_BAX_MOUSE	Bax	Apoptosis regulator BAX	R.VAADM*FADGNFNWGR@.V	7.39	1.70	4.35	0.23
Q07813_BAX_MOUSE	Bax	Apoptosis regulator BAX	R.VVALFYFASK#.L	7.80	1.81	4.31	0.23
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.HSPSALQDVFVELLSPHSK#.R	7.03	4.08	1.72	0.58
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.YFVEETVEVIR.N	3.62	2.58	1.40	0.71
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.DFIEDYVDVLR@.Q	11.79	9.76	1.21	0.83
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.HSPSALQDVFVELLSPHSK#.R	10.74	8.45	1.27	0.79
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.ISFGQEDSIASK#.Q	10.69	7.63	1.40	0.71
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	K.LLTLVSTR@.D	12.98	7.39	1.76	0.57
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.LR@DFLLDIEDR@.I	10.55	8.61	1.23	0.82
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.LSNPSLVK#.K	13.17	8.57	1.54	0.65
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	K.DAIDPLLFR@.Y	11.69	5.13	2.28	0.44
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.DFIEDYVDVLR@.Q	43.76	12.86	3.40	0.29
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	K.EM*YESAVVK#.A	7.51	2.27	3.30	0.30
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.HSPSALQDVFVELLSPHSK#.R	30.96	7.98	3.88	0.26
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.HYDDFFER@.T	9.61	2.07	4.64	0.22
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.IYQGTLGAIK#.V	35.31	12.05	2.93	0.34
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	K.LGLHVSPSTVDQVSTPLAAK#.K	24.65	8.34	2.95	0.34
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.LHILASGADVTSANAK#.Y	25.94	5.74	4.52	0.22
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	K.LLTLVSTR@.D	31.46	9.31	3.38	0.30
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.LR@DFLLDIEDR@.I	31.41	8.14	3.86	0.26
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.LSNPSLVK#.K	32.16	10.05	3.20	0.31
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	K.LSSTSVYDLTPGEK#.M	9.54	2.41	3.96	0.25
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	K.TVNEDVEEM*EM*EQAR@.V	7.47	3.07	2.44	0.41
O88379_BAZ1A_MOUSE	Baz1a	Bromodomain adjacent t	R.YFVEETVEVIR@.N	14.29	5.80	2.47	0.41
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase	R.AGTGENAPWVVEDELVK#.K	18.55	8.83	2.10	0.48
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase	R.DSSSLSSPLNPK#.L	19.08	15.97	1.19	0.84
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase	K.FLQGFM*APK.Q	8.89	19.23	0.46	2.16
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase	K.FSDFLLDPYK#.Y	62.00	30.69	2.02	0.50
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase	K.FSDFLLDPYK#YM*TLNPSTK#.R	16.99	5.83	2.91	0.34
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase	K.GGLGYM*EGTSEFEAR.V	18.98	28.64	0.66	1.51

Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.IISNVPADSLIR@.T	86.49	44.35	1.95	0.51
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.KPFPLVKPLPGEEPLFTIPHTQEAFR.T	57.54	36.59	1.57	0.64
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.LADDEGDSDSESVGQSR.G	6.82	17.86	0.38	2.62
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.LVDSAWLEIM*TK#.Y	20.34	11.69	1.74	0.57
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.LVDSAWLEIMTK#.Y	15.22	6.07	2.51	0.40
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SDLIEVATR.L	23.99	41.49	0.58	1.73
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SRPKDDPEVDDLVLQTK.R	6.57	22.11	0.30	3.37
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SVQEFLTDM*K.Q	9.14	20.16	0.45	2.21
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.YWLFSNEVPGLFIEK.G	4.61	7.62	0.60	1.65
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.FSDFLLDPYK.Y	7.80	15.66	0.50	2.01
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.FSDFLLDPYKYM*TLNPSTK.R	5.46	7.08	0.77	1.29
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.GGLGYM*EGTSEFEAR.V	2.07	2.95	0.70	1.43
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.K#PFPLVK#PLPGEEPLFTIPHTQEAFR@.T	4.54	4.01	1.13	0.88
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SDLIEVATR.L	5.64	11.72	0.48	2.08
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.AGTGENAPWVVEDELVK#.K	8.87	3.76	2.36	0.42
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.DDPEVDDLVLQTK#.R	16.15	25.47	0.63	1.58
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.DEAEDYYDVIEHPM*DFQTIQNK#.C	20.68	10.82	1.91	0.52
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.EAWEEEQEVAELLK#EEFPNWYEK#.L	10.25	1.68	6.11	0.16
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.FEDQELGGR.N	133.40	86.84	1.54	0.65
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.FLQGFM*APK#.Q	76.37	49.91	1.53	0.65
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.FSDFLLDPYK#.Y	32.00	12.15	2.63	0.38
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.FSDFLLDPYK#YM*TLNPSTK#.R	9.47	3.27	2.90	0.35
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.GGFLYLNR@.V	57.39	34.10	1.68	0.59
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.GGLGYM*EGTSEFEAR@.V	92.05	57.87	1.59	0.63
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.GGLGYMEGTSEFEAR@.V	8.46	5.27	1.61	0.62
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.HLPPAALHLIAYYK#.E	17.42	14.80	1.18	0.85
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.IEQQVEVEADDM*ISAVK#.S	17.15	8.67	1.98	0.51
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.IEQQVEVEADDMISAVK#.S	9.09	3.59	2.53	0.40
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.IISNVPADSLIR@.T	46.36	21.16	2.19	0.46
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.K#PNLGLK#.S	22.95	14.37	1.60	0.63
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.LADDEGDSDSESVGQSR@.G	76.24	42.23	1.81	0.55
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.LETSEFFELTSEEK#.L	57.72	30.74	1.88	0.53
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.LLSNEDR.A	101.02	68.73	1.47	0.68
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.LPEELR@.A	122.38	81.32	1.50	0.66
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.LSEIPLTLHSVSELVR@.L	144.18	104.94	1.37	0.73
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.LVDSAWLEIM*TK#.Y	7.11	4.95	1.44	0.70
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.LVDSAWLEIMTK#.Y	9.92	3.74	2.65	0.38
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.QQVSAELWK#.E	56.24	140.65	0.40	2.50
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.R@YELLEHK#.K	28.14	17.27	1.63	0.61
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SDLIEVATR@.L	127.58	76.20	1.67	0.60
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SRPKDDPEVDDLVLQTK.R	67.12	43.42	1.55	0.65
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SVQEFLTDMK#.Q	15.32	13.85	1.11	0.90
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.WDM*SAENAR@.C	19.82	13.17	1.51	0.66
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.YELLEHK#.K	22.64	14.41	1.57	0.64
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.YWLFSNEVPGLFIEK#.G	59.78	34.29	1.74	0.57
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.AGTGENAPWVVEDELVK#.K	17.61	2.11	8.36	0.12
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.DDPEVDDLVLQTK#.R	24.21	8.85	2.74	0.37
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.DEAEDYYDVIEHPM*DFQTIQNK#.C	16.10	5.29	3.04	0.33
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.DSSSLSSPLNPK#.L	14.82	18.33	0.81	1.24
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.FEDQELGGR@.N	84.86	33.79	2.51	0.40
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.FSDFLLDPYK#.Y	70.08	9.05	7.74	0.13
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.FSDFLLDPYK#YM*TLNPSTK#.R	18.61	3.83	4.86	0.21
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.GGFLYLNR@.V	46.59	15.57	2.99	0.33
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.GGLGYM*EGTSEFEAR@.V	72.59	18.45	3.94	0.25
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.GGLGYMEGTSEFEAR@.V	7.29	2.96	2.47	0.41
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.IEQQVEVEADDM*ISAVK#.S	19.21	7.80	2.46	0.41
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.IEQQVEVEADDM*ISAVK#.S	5.55	3.06	1.82	0.55
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.IISNVPADSLIR@.T	88.48	16.58	5.34	0.19
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.ILM*TYSVQDHM*ETR@.Q	4.83	2.03	2.38	0.42
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.K#PFPLVK#PLPGEEPLFTIPHTQEAFR@.T	35.95	4.92	7.31	0.14
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.LADDEGDSDSESVGQSR@.G	30.12	7.20	4.19	0.24
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.LETSEFFELTSEEK#.L	49.38	16.90	2.92	0.34
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.LSEIPLTLHSVSELVR.L	14.66	15.35	0.95	1.05
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.QQVSAELWK#.E	47.94	33.64	1.42	0.70
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.R@DSSSLSSPLNPK#.L	23.69	1.90	12.44	0.08
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.R@FEDQELGGR@.N	17.85	5.72	3.12	0.32
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SDLIEVATR@.L	93.35	26.85	3.48	0.29
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SR@PK#DDPEVDDLVLQTK#.R	42.38	11.40	3.72	0.27
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SVQEFLTDM*K#.Q	48.89	14.30	3.42	0.29
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.SVQEFLTDMK#.Q	10.25	4.14	2.47	0.40
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	K.VDEEAVEK#.K	13.02	2.89	4.51	0.22
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.WASM*SEEQR@.K	7.18	2.00	3.59	0.28
Q9Z277_BAZ1B_MOUSE	Baz1b	Tyrosine-protein kinase E	R.YWLFSNEVPGLFIEK#.G	41.16	15.40	2.67	0.37
Q91YE5_BAZ2A_MOUSE	Baz2a	Bromodomain adjacent t	R.LAVLEQNVER@.R	7.60	4.63	1.64	0.61
Q91YE5_BAZ2A_MOUSE	Baz2a	Bromodomain adjacent t	R.VVLSDLQIR@.G	9.98	6.27	1.59	0.63
Q91YE5_BAZ2A_MOUSE	Baz2a	Bromodomain adjacent t	K.EGEIDVAASSIPELER@.H	5.21	4.04	1.29	0.77
Q91YE5_BAZ2A_MOUSE	Baz2a	Bromodomain adjacent t	R.GESQTPVQGQAR@.N	7.65	4.40	1.74	0.58
Q91YE5_BAZ2A_MOUSE	Baz2a	Bromodomain adjacent t	R.IM*EETSGIEEEEEEENTTAVHGR@.R	5.71	4.05	1.41	0.71
Q91YE5_BAZ2A_MOUSE	Baz2a	Bromodomain adjacent t	K.K#LETQEILSEDDK#AK#.M	11.90	6.98	1.70	0.59
Q8VBW5_BBX_MOUSE	Bbx	HMG box transcription fa	K.IIISGVPSR@.K	11.29	5.05	2.24	0.45
Q61335_BAP31_MOUSE	Bcap31	B-cell receptor-associate	K.AENEALAMQK#.Q	40.60	19.53	2.08	0.48
Q61335_BAP31_MOUSE	Bcap31	B-cell receptor-associate	K.AENEALAM*QK#.Q	85.77	37.33	2.30	0.44
Q61335_BAP31_MOUSE	Bcap31	B-cell receptor-associate	K.GAAEDGDK#LDIGNTEM*K#.L	38.18	15.76	2.42	0.41
Q61335_BAP31_MOUSE	Bcap31	B-cell receptor-associate	K.KYM*EENDQLKK.G	130.28	57.76	2.26	0.44
Q61335_BAP31_MOUSE	Bcap31	B-cell receptor-associate	K.LK#DELASTK#.K	87.08	35.27	2.47	0.41
Q61335_BAP31_MOUSE	Bcap31	B-cell receptor-associate	K.YM*EENDQLK#.K	14.39	6.70	2.15	0.47
Q61335_BAP31_MOUSE	Bcap31	B-cell receptor-associate	K.YM*EENDQLK#K#.G	8.65	4.50	1.93	0.52
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	R.EAAAALVEEETR@.R	6.65	4.21	1.58	0.63
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	K.HIQDLNWQR@.K	8.52	6.12	1.39	0.72
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	K.LR@EM*ESNWVSLVSK#.N	23.01	14.26	1.61	0.62
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	K.NM*QLTAGSK#.L	9.25	6.09	1.52	0.66
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	K.NYLSYLTAPDYSAFETDIM*R@.N	2.92	2.70	1.08	0.93
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	K.R@YELPAPSSGQK#.N	8.92	90.07	0.10	10.10
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	R.TIVQLENEIYQIK#.Q	71.21	41.60	1.71	0.58
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	R.TIVQLENEIYQIK.Q	9.29	8.19	1.13	0.88
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	R.EAAAALVEEETR@.R	5.61	3.21	1.75	0.57
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	R.EM*ESNWVSLVSK#.N	7.22	3.20	2.26	0.44
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	K.NYLSYLTAPDYSAFETDIM*R@.N	1.99	2.92	0.68	1.47
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	K.R@YELPAPSSGQK#.N	5.59	35.25	0.16	6.31
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	R.TIVQLENEIYQIK#.Q	65.80	45.08	1.46	0.69
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	R.TIVQLENEIYQIK#.Q	12.90	6.12	2.11	0.47
Q9D287_SPF27_MOUSE	Bcas2	Pre-mRNA-splicing factor	R.YELPAPSSGQK#.N	13.48	10.28	1.31	0.76
P59017_B2L13_MOUSE	Bcl2l13	Bcl-2-like protein 13 OS=	R.AEGAAQLSEER.A	10.05	4.00	2.51	0.40

P59017_B2L13_MOUSE	Bcl2l13	Bcl-2-like protein 13 OS=	K.QQGPSPPGVQLDVAPQSLNPEVLLK#.L	9.21	3.10	2.97	0.34
P59017_B2L13_MOUSE	Bcl2l13	Bcl-2-like protein 13 OS=	K.YVVLSYLGLLSQEK#.Q	10.62	5.01	2.12	0.47
P59017_B2L13_MOUSE	Bcl2l13	Bcl-2-like protein 13 OS=	R.AEGAAQLSEER@.A	15.45	3.54	4.37	0.23
P59017_B2L13_MOUSE	Bcl2l13	Bcl-2-like protein 13 OS=	R.AEGAAQLSEER@.A	7.87	2.18	3.61	0.28
P59017_B2L13_MOUSE	Bcl2l13	Bcl-2-like protein 13 OS=	K.QQGPSPPGVQLDVAPQSLNPEVLLK#.L	10.30	1.68	6.11	0.16
P59017_B2L13_MOUSE	Bcl2l13	Bcl-2-like protein 13 OS=	K.YVVLSYLGLLSQEK#.Q	10.60	3.87	2.74	0.37
Q921K9_BCL7B_MOUSE	Bcl7b	B-cell CLL/lymphoma 7 p	R.TDDSQPPTLGQEILEEPSLPASEVADEPPTLTK#.E	1.76	2.11	0.83	1.20
O08664_BCL7C_MOUSE	Bcl7c	B-cell CLL/lymphoma 7 p	R.GGGPLILLDLNDENSNQSFHSEGSLQK#.G	11.74	4.86	2.41	0.41
O08664_BCL7C_MOUSE	Bcl7c	B-cell CLL/lymphoma 7 p	K.WVPVVDPQEEER@.R	9.71	4.96	1.96	0.51
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.DR@LLASTLVHSVK#.K	12.56	9.92	1.27	0.79
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.FHDSEGDDTEETEDYR@.Q	18.02	8.87	2.03	0.49
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.K#AEGEPQEESPLK#.S	11.26	4.01	2.81	0.36
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SATSGDIWPGLSAYDNSPR@.S	12.49	4.70	2.66	0.38
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SPAVTLNER.F	50.93	49.32	1.03	0.97
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SQEEPK#DTFEHDPSESIDEFNK#.S	21.43	4.70	4.56	0.22
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.SSFYPEGDQETAK#.T	52.18	30.89	1.69	0.59
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.VFLLDR@.G	82.08	31.57	2.60	0.38
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.DR@LLASTLVHSVK#.K	48.09	14.22	3.38	0.30
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.EEEWDPEYTPK#.S	8.50	2.43	3.50	0.29
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.ETAYIVERPSTAK.D	15.70	5.33	2.95	0.34
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.EVQSPEQVK#.S	55.55	18.53	3.00	0.33
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.FHDSEGDDTEETEDYR@.Q	67.67	15.13	4.47	0.22
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.FTDEESR@.V	44.19	16.74	2.64	0.38
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.GFK#EEIQK#.G	45.87	18.73	2.45	0.41
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.GFKEEIQKGDK.K	73.97	19.56	3.78	0.26
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.GRADGDWDDQEVLDYFSDKESAK.Q	36.94	9.26	3.99	0.25
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.GR@ADGDWDDQEVLDYFSDK#ESAK#.Q	6.88	4.48	1.54	0.65
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.IDISPSALR@.K	19.82	7.65	2.59	0.39
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.K#SVLADQGK#.S	17.59	5.64	3.12	0.32
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.QK#FHDSEGDDTEETEDYR@.Q	11.55	2.80	4.13	0.24
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.R@FTDEESR@.V	21.04	5.80	3.63	0.28
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.R@PK#EEEWDPEYTPK#.S	10.95	4.20	2.61	0.38
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SATSGDIWPGLSAYDNSPR@.S	17.92	4.01	4.46	0.22
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.SIFDHIK#.L	72.88	27.94	2.61	0.38
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SPAVTLNER@.F	205.76	70.36	2.92	0.34
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SQEEPKDTFEHDPSESIDEFNK.S	30.01	9.01	3.33	0.30
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.SSFYPEGDQETAK#.T	154.43	58.79	2.63	0.38
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SVLADQGK#.S	121.34	52.84	2.30	0.44
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.TITPQNAPR@.E	221.93	68.06	3.26	0.31
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.VFLLDR@.G	416.44	112.77	3.69	0.27
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.DR@LLASTLVHSVK#.K	8.90	4.31	2.06	0.48
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.FHDSEGDDTEETEDYR@.Q	18.35	6.19	2.97	0.34
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SATSGDIWPGLSAYDNSPR@.S	5.74	2.18	2.64	0.38
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SPAVTLNER.F	51.17	24.51	2.09	0.48
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	K.SQEEPK#DTFEHDPSESIDEFNK#.S	35.79	14.59	2.45	0.41
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.SSFYPEGDQETAK#.T	39.30	12.55	3.13	0.32
Q8K019_BCLF1_MOUSE	Bclaf1	Bcl-2-associated transcri	R.VFLLDR@.G	68.45	17.09	4.01	0.25
Q6PAJ1_BCR_MOUSE	Bcr	Breakpoint cluster regio	R.STLVLHDLLK#.H	8.12	2.79	2.91	0.34
Q6PAJ1_BCR_MOUSE	Bcr	Breakpoint cluster regio	K.AAATTSQPVLTSQQIETIFFK#.V	6.29	2.10	2.99	0.33
Q6PAL0_BEND3_MOUSE	Bend3	BEN domain-containing	R.LFPELFTTENLR@.L	7.32	2.69	2.72	0.37
O35623_BET1_MOUSE	Bet1	BET1 homolog OS=Mus m	K.LLAEM*DSQFDSTTGFLGK#.T	23.60	9.87	2.39	0.42
P28653_PGS1_MOUSE	Bgn	Biglycan OS=Mus muscul	K.IQAIELEDLLR.Y	16.56	14.82	1.12	0.90
P28653_PGS1_MOUSE	Bgn	Biglycan OS=Mus muscul	K.IQAIELEDLLR@.Y	11.89	10.01	1.19	0.84
Q921C5_BICD2_MOUSE	Bicd2	Protein bicaudal D hom	K.FSDDTVTAEPNNDAEALVNGFEHSGLVK#.S	5.44	1.93	2.82	0.35
Q921C5_BICD2_MOUSE	Bicd2	Protein bicaudal D hom	K.GLLATEVGR@.A	27.95	10.24	2.73	0.37
Q921C5_BICD2_MOUSE	Bicd2	Protein bicaudal D hom	K.GR@YEAEGQALTEK#.I	15.66	6.42	2.44	0.41
Q921C5_BICD2_MOUSE	Bicd2	Protein bicaudal D hom	R.LLQDYSELEEENISLQK#.Q	12.25	5.34	2.29	0.44
Q921C5_BICD2_MOUSE	Bicd2	Protein bicaudal D hom	R.LTENLSALR@.R	16.97	3.93	4.32	0.23
Q921C5_BICD2_MOUSE	Bicd2	Protein bicaudal D hom	R.NVLTNTQSENER.L	21.04	8.00	2.63	0.38
Q921C5_BICD2_MOUSE	Bicd2	Protein bicaudal D hom	K.VAADGESR@EESLIQESASK#.E	8.74	4.17	2.09	0.48
Q921C5_BICD2_MOUSE	Bicd2	Protein bicaudal D hom	K.VGLLATLQDTQK#.Q	30.45	11.97	2.54	0.39
O08539_BIN1_MOUSE	Bin1	Myc box-dependent-inte	R.TYLASVK#.A	9.28	9.23	1.01	0.99
O08539_BIN1_MOUSE	Bin1	Myc box-dependent-inte	R.VNHEPEPASGASPGATIPK#.S	20.52	9.39	2.19	0.46
Q9JI08_BIN3_MOUSE	Bin3	Bridging integrator 3 OS=	K.FSSIFPSLNM*AVK#.R	4.97	2.46	2.02	0.50
Q9JI08_BIN3_MOUSE	Bin3	Bridging integrator 3 OS=	R.LDYFQPSFESLIR@.A	16.04	4.46	3.59	0.28
O88738_BIRC6_MOUSE	Birc6	Baculoviral IAP repeat-c	K.IDVSSTEGYDLFITQLK#.D	5.59	1.81	3.09	0.32
O88738_BIRC6_MOUSE	Birc6	Baculoviral IAP repeat-c	R.TLPVLLLYSIK#.E	10.82	4.30	2.51	0.40
O88738_BIRC6_MOUSE	Birc6	Baculoviral IAP repeat-c	K.VLDLSNFEILAK#.V	5.77	2.69	2.15	0.47
O55102_BL1S1_MOUSE	Bloc1s1	Biogenesis of lysosome-r	R.TIATALEYVYK#.G	31.35	14.48	2.16	0.46
O55102_BL1S1_MOUSE	Bloc1s1	Biogenesis of lysosome-r	K.TLQVQAAQFAK#.Q	15.08	7.09	2.13	0.47
Q6PGF5_Q6PGF5_MOUSE	Bms1	BMS1 homolog, ribosom	K.GK#PGPDTQSEDIEEEEVK#EETDPSEEESAR@.K	8.64	7.15	1.21	0.83
Q6PGF5_Q6PGF5_MOUSE	Bms1	BMS1 homolog, ribosom	R.IAATGVVLDLDK#.S	12.13	8.27	1.47	0.68
Q6PGF5_Q6PGF5_MOUSE	Bms1	BMS1 homolog, ribosom	R.K#VLALLDALSTIHSQK#.M	11.94	5.13	2.33	0.43
Q6PGF5_Q6PGF5_MOUSE	Bms1	BMS1 homolog, ribosom	K.GK#PGPDTQSEDIEEEEVK#EETDPSEEESAR@.K	10.48	8.49	1.23	0.81
Q6PGF5_Q6PGF5_MOUSE	Bms1	BMS1 homolog, ribosom	R.IAATGVVLDLDK#.S	23.69	7.93	2.99	0.33
Q6PGF5_Q6PGF5_MOUSE	Bms1	BMS1 homolog, ribosom	K.ILAEEEELYGDFEDLETGDVHK#.G	16.99	7.44	2.28	0.44
Q6PGF5_Q6PGF5_MOUSE	Bms1	BMS1 homolog, ribosom	R.K#VLALLDALSTIHSQK#.M	10.47	5.72	1.83	0.55
Q6PGF5_Q6PGF5_MOUSE	Bms1	BMS1 homolog, ribosom	K.LIYGTVTEDNEDEDGDPAEELGGLFHVSQPDR@.G	3.78	1.87	2.02	0.50
Q6PGF5_Q6PGF5_MOUSE	Bms1	BMS1 homolog, ribosom	K.VLALLDALSTIHSQK#.M	12.34	7.36	1.68	0.60
P97504_BMX_MOUSE	Bmx	Cytoplasmic tyrosine-pr	K.GKEGAFMVR@.N	7.36	9.50	0.78	1.29
Q8BMQ3_BNC2_MOUSE	Bnc2	Zinc finger protein bason	K.EGQAVAVPSSK.T	2.95	8.66	0.34	2.94
E9Q6J5_E9Q6J5_MOUSE	Bod1l	Protein Bod1l OS=Mus m	K.ETVEDTTISTGLVK#.G	4.36	1.60	2.73	0.37
P97452_BOP1_MOUSE	Bop1	Ribosome biogenesis pro	R.VNVDPEDLIPK#.L	5.19	3.08	1.68	0.59
A2A654_A2A654_MOUSE	Bptf	Protein Bptf OS=Mus mu	K.ESASTQVITPR@.A	6.67	3.58	1.86	0.54
A2A654_A2A654_MOUSE	Bptf	Protein Bptf OS=Mus mu	K.EVLVVNSQGEVSR@.L	8.42	2.81	3.00	0.33
A2A654_A2A654_MOUSE	Bptf	Protein Bptf OS=Mus mu	R.FIAPEQGGESVESTK#.C	4.97	3.59	1.38	0.72
A2A654_A2A654_MOUSE	Bptf	Protein Bptf OS=Mus mu	R.LIIEEDTDNENEK#.K	6.79	3.59	1.89	0.53
A2A654_A2A654_MOUSE	Bptf	Protein Bptf OS=Mus mu	K.LSTPSPDTGVDTISVK#.E	10.83	7.79	1.39	0.72
A2A654_A2A654_MOUSE	Bptf	Protein Bptf OS=Mus mu	K.SFLAAANEEILDSLR@.I	20.35	9.86	2.06	0.48
A2A654_A2A654_MOUSE	Bptf	Protein Bptf OS=Mus mu	R.TETSETEITTTEIIK#.R	3.31	1.89	1.75	0.57
A2A654_A2A654_MOUSE	Bptf	Protein Bptf OS=Mus mu	K.VGSPATVTFQQNK#.N	9.17	4.53	2.02	0.49
G5E8P1_G5E8P1_MOUSE	Brd1	MCG7283 OS=Mus musc	K.ELTGGSATFSVR@.K	10.77	7.60	1.42	0.71
G5E8P1_G5E8P1_MOUSE	Brd1	MCG7283 OS=Mus musc	R.ETLTYAQAQR@.M	8.95	4.81	1.86	0.54
G5E8P1_G5E8P1_MOUSE	Brd1	MCG7283 OS=Mus musc	R.IVEYSPPSAPR@.R	14.50	6.43	2.25	0.44
G5E8P1_G5E8P1_MOUSE	Brd1	MCG7283 OS=Mus musc	R.LETLLQPR@.K	15.78	10.15	1.56	0.64
G5E8P1_G5E8P1_MOUSE	Brd1	MCG7283 OS=Mus musc	R.LTPLTVLLR@.S	65.77	32.08	2.05	0.49
G5E8P1_G5E8P1_MOUSE	Brd1	MCG7283 OS=Mus musc	R.VHGEPASDLSDID.-	8.77	8.77	1.00	1.00
G5E8P1_G5E8P1_MOUSE	Brd1	MCG7283 OS=Mus musc	R.LTPLTVLLR@.S	24.91	10.88	2.29	0.44
Q7JJ13_BRD2_MOUSE	Brd2	Bromodomain-containi	R.AVHEQLAALSQGPISK#PK#.R	11.50	4.00	2.88	0.35
Q7JJ13_BRD2_MOUSE	Brd2	Bromodomain-containi	K.DLPDSQQQHQSSK#.K	3.47	1.67	2.07	0.48
Q7JJ13_BRD2_MOUSE	Brd2	Bromodomain-containi	R.IGIDEDDK#GPR@.A	9.32	4.76	1.96	0.51
Q7JJ13_BRD2_MOUSE	Brd2	Bromodomain-containi	R.K#ADTTTPTPTAILAPGSPASPPGSLEPK#.A	6.08	4.19	1.45	0.69
Q7JJ13_BRD2_MOUSE	Brd2	Bromodomain-containi	R.LAELQEQLR@.A	37.41	12.38	3.02	0.33

Q7JJ13_BRD2_MOUSE	Brd2	Bromodomain-containi	K.SLHSAGPPLLAVSAAPPAQPLAK#.K	43.62	19.37	2.25	0.44
Q7JJ13_BRD2_MOUSE	Brd2	Bromodomain-containi	K.VASM*PQEEQELVVTIPK#.N	11.97	5.13	2.33	0.43
Q7JJ13_BRD2_MOUSE	Brd2	Bromodomain-containi	K.VASMPQEEQELVVTIPK#.N	4.79	1.66	2.88	0.35
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	R.DAQEFGADVR@.L	25.03	8.95	2.80	0.36
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.HQFAWPFQQPVDAVK#.L	14.60	6.07	2.41	0.42
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.INELPTEETEIM*IVQAK#.G	16.78	7.48	2.24	0.45
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.INELPTEETEIMIVQAK#.G	5.86	2.68	2.19	0.46
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.K#EEVEENK#.K	4.74	1.90	2.50	0.40
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	R.LAELQEQLK#.A	59.08	20.93	2.82	0.35
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.M*PDEPEEPVVTVSSPAVPPPTK#.V	8.17	3.25	2.52	0.40
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.AVHEQLAALSQPQQNK#PK#.K	16.01	1.36	11.80	0.08
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	R.DAQEFGADVR@.L	15.83	2.60	6.09	0.16
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.DVPDSQQHPGPEK#.S	8.13	2.79	2.91	0.34
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.HQFAWPFQQPVDAVK#.L	6.73	3.64	1.85	0.54
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.INELPTEETEIM*IVQAK#.G	20.22	4.16	4.87	0.21
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.INELPTEETEIMIVQAK#.G	6.93	2.16	3.20	0.31
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	R.QTNQLQYLLR@.V	10.31	3.11	3.31	0.30
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	R.SR@EDEDALEQAR@.R	10.18	2.03	5.02	0.20
Q9ESU6_BRD4_MOUSE	Brd4	Bromodomain-containi	K.VDVIAGSSK#.M	16.87	4.90	3.44	0.29
O88665_BRD7_MOUSE	Brd7	Bromodomain-containi	K.EAEITQIEPTGR@.L	21.05	6.63	3.18	0.31
O88665_BRD7_MOUSE	Brd7	Bromodomain-containi	R.EM*YLAEQVTNNLK#.E	12.69	1.81	7.01	0.14
O88665_BRD7_MOUSE	Brd7	Bromodomain-containi	R.HFYEEYVEK#PLK#.L	27.48	6.01	4.58	0.22
O88665_BRD7_MOUSE	Brd7	Bromodomain-containi	R.LQSGVNTLQGFK#.E	28.27	4.65	6.09	0.16
O88665_BRD7_MOUSE	Brd7	Bromodomain-containi	R.LTALQAVTTFGAPAEVFDSEEAEVFQR@.K	35.56	10.83	3.28	0.30
O88665_BRD7_MOUSE	Brd7	Bromodomain-containi	K.QEEVEQTPLQEALNQLM*R@.Q	8.99	2.22	4.05	0.25
O88665_BRD7_MOUSE	Brd7	Bromodomain-containi	R.SLQDLDM*SSPEDEGQTR@.A	14.95	3.03	4.93	0.20
Q8R3B7_BRD8_MOUSE	Brd8	Bromodomain-containi	R.LLEAGPTQFTTPLPSFTTVASEPPVK#.L	3.88	2.34	1.66	0.60
Q8R3B7_BRD8_MOUSE	Brd8	Bromodomain-containi	K.GEVVETVEDVIVR@.K	7.33	3.31	2.21	0.45
Q8R3B7_BRD8_MOUSE	Brd8	Bromodomain-containi	K.K#LEEEEAEVK#.R	4.70	1.15	4.08	0.25
Q8R3B7_BRD8_MOUSE	Brd8	Bromodomain-containi	R.SGDQNWVSVSR@.A	5.31	1.91	2.78	0.36
Q8R3B7_BRD8_MOUSE	Brd8	Bromodomain-containi	R.SSAAGDIGEADGSSGK#.G	15.62	4.54	3.44	0.29
Q8R3B7_BRD8_MOUSE	Brd8	Bromodomain-containi	R.LLEAGPTQFTTPLPSFTTVASEPPVK#.L	17.47	7.17	2.44	0.41
Q8R3B7_BRD8_MOUSE	Brd8	Bromodomain-containi	K.LLSTGPTEPWSIR@.E	9.65	3.69	2.61	0.38
Q3UQU0_BRD9_MOUSE	Brd9	Bromodomain-containi	R.GGSR@PSSNLSSLSTASER@.E	5.78	3.12	1.85	0.54
Q3UQU0_BRD9_MOUSE	Brd9	Bromodomain-containi	R.LSVGEQPDVAHDPYEFLQSPEPAAPAK#N.-	5.47	2.99	1.83	0.55
Q3UQU0_BRD9_MOUSE	Brd9	Bromodomain-containi	R.TQPAENESTPIQR@.L	14.38	6.13	2.35	0.43
Q8K3W0_BRE_MOUSE	Bre	BRCA1-A complex subuni	K.LPVDFSNIPTYLLK#.D	22.08	5.82	3.80	0.26
Q8K3W0_BRE_MOUSE	Bre	BRCA1-A complex subuni	K.LPVDFSNIPTYLLK#.D	17.58	6.76	2.60	0.38
Q8BXV2_BRI3B_MOUSE	Bri3bp	BRI3-binding protein OS	R.ATSSFSQSVSSLFGEDNVR@.A	3.26	2.21	1.47	0.68
Q9DCA5_BRX1_MOUSE	Brix1	Ribosome biogenesis pro	R.FVLNLIK#.I	25.84	15.77	1.64	0.61
Q9DCA5_BRX1_MOUSE	Brix1	Ribosome biogenesis pro	R.ILIFSSR@.G	19.24	10.38	1.85	0.54
Q9DCA5_BRX1_MOUSE	Brix1	Ribosome biogenesis pro	R.FVLNLIK#.I	18.77	8.64	2.17	0.46
Q9DCA5_BRX1_MOUSE	Brix1	Ribosome biogenesis pro	K.FLVQNIHTLAELK#.M	24.02	18.13	1.32	0.75
Q9DCA5_BRX1_MOUSE	Brix1	Ribosome biogenesis pro	R.FVLNLIK#.I	20.44	12.85	1.59	0.63
Q9DCA5_BRX1_MOUSE	Brix1	Ribosome biogenesis pro	R.ILIFSSR@.G	14.93	8.65	1.73	0.58
Q3U1T3_BRM1L_MOUSE	Brms1l	Breast cancer metastasis-	K.LLLYDTVQSELEEK#.I	24.98	11.06	2.26	0.44
Q3U1T3_BRM1L_MOUSE	Brms1l	Breast cancer metastasis-	R.LYYDGEWYIR@.G	6.59	3.57	1.85	0.54
P18572_BASI_MOUSE	Bsg	Basigin OS=Mus musculu	R.R@K#PDQTLDEDDPGAAPLK#.G	5.19	4.62	1.12	0.89
P18572_BASI_MOUSE	Bsg	Basigin OS=Mus musculu	K.YIVDADDR@.S	13.94	8.40	1.66	0.60
P18572_BASI_MOUSE	Bsg	Basigin OS=Mus musculu	K.YVVVSTPEK#.S	16.75	9.56	1.75	0.57
Q8R2Q8_BST2_MOUSE	Bst2	Bone marrow stromal an	R.IKELENEVTKLNQELENLR.I	7.51	7.72	0.97	1.03
Q8R2Q8_BST2_MOUSE	Bst2	Bone marrow stromal an	K.K#VSQALEQQAR@.I	19.58	16.67	1.17	0.85
Q8R2Q8_BST2_MOUSE	Bst2	Bone marrow stromal an	K.LNQELENLR@.I	56.09	51.61	1.09	0.92
Q8R2Q8_BST2_MOUSE	Bst2	Bone marrow stromal an	R.IK#ELENEVTK#.L	24.04	9.96	2.41	0.41
Q8R2Q8_BST2_MOUSE	Bst2	Bone marrow stromal an	K.LNQELENLR@.I	46.86	24.67	1.90	0.53
Q8R2Q8_BST2_MOUSE	Bst2	Bone marrow stromal an	K.VSQALEQQAR@.I	58.07	23.45	2.48	0.40
E9QAE3_E9QAE3_MOUSE	Btaf1	Protein Btaf1 OS=Mus m	R.IIEGLQDLDDDVR@.A	6.84	2.11	3.24	0.31
E9QAE3_E9QAE3_MOUSE	Btaf1	Protein Btaf1 OS=Mus m	K.AQIADLPAGSSGTILVELDEGQK#PYLVQR@.R	4.42	5.03	0.88	1.14
E9QAE3_E9QAE3_MOUSE	Btaf1	Protein Btaf1 OS=Mus m	R.IAAGQAVEAIVK#.N	15.74	4.09	3.85	0.26
E9QAE3_E9QAE3_MOUSE	Btaf1	Protein Btaf1 OS=Mus m	K.IATM*ETM*NIFLEK#.V	7.12	2.82	2.53	0.40
E9QAE3_E9QAE3_MOUSE	Btaf1	Protein Btaf1 OS=Mus m	K.QSTLQAAELIDSEFR@.A	4.14	3.93	1.05	0.95
E9QAE3_E9QAE3_MOUSE	Btaf1	Protein Btaf1 OS=Mus m	K.VANVVINQTASDSK#.V	5.08	3.55	1.43	0.70
Q8R149_BUD13_MOUSE	Bud13	BUD13 homolog OS=Mu	K.K#QDQDTTDLGAQFEFTETVFR@.D	12.10	4.01	3.02	0.33
Q8R149_BUD13_MOUSE	Bud13	BUD13 homolog OS=Mu	R.YLSGTDAGLEGGPEAGR@.K	10.65	3.22	3.30	0.30
E0CX20_E0CX20_MOUSE	Bud31	Protein BUD31 homolog	K.APPDGWELIEPTLDELDQK#.M	11.70	11.49	1.02	0.98
E0CX20_E0CX20_MOUSE	Bud31	Protein BUD31 homolog	R.K#APPDGWELIEPTLDELDQK#.M	34.42	30.02	1.15	0.87
E0CX20_E0CX20_MOUSE	Bud31	Protein BUD31 homolog	R.K#VESLWPIFR@.I	13.34	9.63	1.39	0.72
E0CX20_E0CX20_MOUSE	Bud31	Protein BUD31 homolog	K.VESLWPIFR@.I	9.90	7.83	1.26	0.79
E0CX20_E0CX20_MOUSE	Bud31	Protein BUD31 homolog	R.YIFDLFYK#.R	13.56	8.09	1.68	0.60
O54825_BYST_MOUSE	Bysl	Bystin OS=Mus musculus	K.EALLELLR@.L	19.90	5.42	3.67	0.27
O54825_BYST_MOUSE	Bysl	Bystin OS=Mus musculus	R.FYNLVLLPR@.V	16.49	6.55	2.52	0.40
O54825_BYST_MOUSE	Bysl	Bystin OS=Mus musculus	K.IAEM*EYSGANSIFLR@.L	7.11	3.40	2.09	0.48
O54825_BYST_MOUSE	Bysl	Bystin OS=Mus musculus	R.TLADIIM*EK#.L	7.59	57.75	0.13	7.61
O54825_BYST_MOUSE	Bysl	Bystin OS=Mus musculus	K.EALLELLR@.L	16.74	6.00	2.79	0.36
O54825_BYST_MOUSE	Bysl	Bystin OS=Mus musculus	R.FYNLVLLPR@.V	14.20	6.72	2.11	0.47
Q8R5L1_Q8R5L1_MOUSE	C1qbp	Complement componen	K.AEEQEPELTSTPNFVVEVTK.T	3.24	3.98	0.82	1.23
Q8R5L1_Q8R5L1_MOUSE	C1qbp	Complement componen	K.EVSFQATGDSEWR.D	5.23	6.18	0.85	1.18
Q8VDY9_CAAP1_MOUSE	Caap1	Caspase activity and apo	K.SVNEILGLAESSPK#.E	6.96	3.05	2.28	0.44
Q06138_CAB39_MOUSE	Cab39	Calcium-binding protein	K.DVAQIFNNILR@.R	17.03	7.36	2.31	0.43
Q9DB16_CB39L_MOUSE	Cab39l	Calcium-binding protein	K.KTDKASEEVSK#.S	2.99	2.06	1.45	0.69
Q9CS00_CATIN_MOUSE	Cactin	Cactin OS=Mus musculus	R.AGGPNLDM*GYWESLLQQLR@.A	8.08	3.33	2.43	0.41
Q9CS00_CATIN_MOUSE	Cactin	Cactin OS=Mus musculus	R.EGVNASVSSDVQSVFK#.G	8.28	3.21	2.58	0.39
Q9CS00_CATIN_MOUSE	Cactin	Cactin OS=Mus musculus	K.FNIFYPDLIR@.K	20.09	4.46	4.51	0.22
Q9CS00_CATIN_MOUSE	Cactin	Cactin OS=Mus musculus	K.TYNQLQVIFQGIEGK#.I	5.61	2.52	2.22	0.45
Q8R0X2_CACL1_MOUSE	Cacul1	CDK2-associated and cul	K.FIPNILPPAVESELSEYAAQDQK#.L	7.62	3.43	2.22	0.45
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	R.AAFALGGLGSGFASTK#.E	7.98	3.85	2.07	0.48
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	K.AIVHAVGQELQVTGPFNLQLIAK#.D	4.65	2.59	1.79	0.56
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	R.EAAAGNIGGQTVR@.E	16.78	10.02	1.67	0.60
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	K.LALGIPLPELR@.N	42.44	21.94	1.93	0.52
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	R.LGGAVLSFSEATSSVQK#.G	13.25	6.18	2.14	0.47
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	R.LGYPVLVR@.A	13.29	6.92	1.92	0.52
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	R.LSLDDLLQR@.L	16.40	8.25	1.99	0.50
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	R.M*AEIGEHVAPSEAANSLEQAQAAAER@.L	14.52	6.65	2.19	0.46
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	K.SVGEVM*GIGR@.S	6.80	4.64	1.46	0.68
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	K.TLGVDLVALATR@.I	26.24	14.11	1.86	0.54
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	R.VLGTSPEAIDSAENR@.F	16.54	11.80	1.40	0.71
B2RQC6_PYR1_MOUSE	Cad	CAD protein OS=Mus mu	R.VNEISVEVDSDPR@.A	10.12	4.57	2.21	0.45
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	K.GGSLGENQIK#DEK#.I	4.04	4.25	0.95	1.05
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.LEQYTNAIEGTK#.A	30.07	30.85	0.97	1.03
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.M*QNDSAENETAEGEEK#R@.E	8.25	10.30	0.80	1.25
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.SGR@YEVEETEVVIK#.S	13.75	9.15	1.50	0.67
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.ASGDKEAEGAPQVEAGK.R	26.42	15.74	1.68	0.60
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.GETENEEFEK#.L	4.47	3.55	1.26	0.79

Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	K.GGSLGENQIKDEK.I	16.97	11.49	1.48	0.68
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	K.GSVFSAPSASGTPNK#.E	19.03	14.85	1.28	0.78
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.INEWLTK#.S	17.99	16.17	1.11	0.90
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.LEQYTNAIEGTK#.A	63.12	39.23	1.61	0.62
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	K.LK#QTENAFSPSR@.S	7.34	5.05	1.45	0.69
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.M*QNDSAENETAEGEEK#R@.E	45.61	26.55	1.72	0.58
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.QK#EFDPTITDGSLSGPSR@.R	40.18	15.61	2.57	0.39
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	K.QTENAFSPSR@.S	12.85	7.55	1.70	0.59
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	R.SGR@YEVEETEVVIK#.S	33.03	21.90	1.51	0.66
Q8VCQ8_Q8VCQ8_MOUSE	Cald1	Caldesmon 1 OS=Mus mu	K.VLEEEEQR@.R	32.97	20.07	1.64	0.61
P62204_CALM_MOUSE	Calm1	Calmodulin OS=Mus mus	K.DTDSEEEIR@.E	74.20	44.68	1.66	0.60
P62204_CALM_MOUSE	Calm1	Calmodulin OS=Mus mus	K.DTDSEEEIREAFR.V	20.29	12.85	1.58	0.63
P62204_CALM_MOUSE	Calm1	Calmodulin OS=Mus mus	R.EADIDGDGQVNYEEFVQM*M*TAK#.-	41.17	23.87	1.73	0.58
P62204_CALM_MOUSE	Calm1	Calmodulin OS=Mus mus	K.EAFSLFDK#DGDGTITTK#.E	756.30	405.16	1.87	0.54
P62204_CALM_MOUSE	Calm1	Calmodulin OS=Mus mus	K.ELGTVM*R.S	525.71	380.27	1.38	0.72
P62204_CALM_MOUSE	Calm1	Calmodulin OS=Mus mus	R.KM*KDTDSEEEIR.E	57.10	49.61	1.15	0.87
P62204_CALM_MOUSE	Calm1	Calmodulin OS=Mus mus	K.M*K#DTDSEEEIR@.E	16.66	11.03	1.51	0.66
P62204_CALM_MOUSE	Calm1	Calmodulin OS=Mus mus	R.VFDK#DGNGYISAAELR@.H	245.29	152.34	1.61	0.62
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.EQFLDGDAWTNR.W	15.14	30.47	0.50	2.01
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.FVLSSGK.F	105.75	61.82	1.71	0.58
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	R.FYALSAK.F	35.13	83.16	0.42	2.37
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.GLQTSQDAR@.F	8.62	13.87	0.62	1.61
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.IDNSQVESGSLEDDWDFLPPKK.I	6.17	16.67	0.37	2.70
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.KPEDWDEEM*DGEWEPPVIQNPEYK.G	9.67	22.15	0.44	2.29
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.KPEDWDEEMDGEWEPPVIQNPEYK.G	3.34	4.07	0.82	1.22
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	R.QIDNPDYK.G	16.10	42.93	0.37	2.67
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	R.AKIDDPTDSKPEDWDKPEHIPDPDAK.K	7.23	10.34	0.70	1.43
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.EQFLDGDAWTNR.W	12.32	17.98	0.69	1.46
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.GLQTSQDAR.F	10.37	12.58	0.82	1.21
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.KPEDWDEEM*DGEWEPPVIQNPEYK.G	5.37	8.30	0.65	1.55
P14211_CALR_MOUSE	Calr	Calreticulin OS=Mus mus	K.SGTIFDNFLITNDEAYAEEFGNETWGVTK#.A	17.73	11.14	1.59	0.63
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.DIVVQETM*EDIDK#.N	13.10	9.64	1.36	0.74
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.DIVVQETM*EDIDKNADGFIDLEEYIGDM*YSHDGNADEPEWVK.T	8.81	4.12	2.14	0.47
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.DWILPSDYDHAEAEAR@.H	6.76	3.85	1.76	0.57
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.EEIVDKYDLFVGSQATDFGEALVR.H	228.46	168.80	1.35	0.74
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.EEIVDK#YDLFVGSQATDFGEALVR@HDEF.-	6.44	1.98	3.25	0.31
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	R.EQFVEFR@.D	953.03	576.96	1.65	0.61
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.GHDLNEDGLVSWEEYK#.N	75.26	55.46	1.36	0.74
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.GHDLNEDGLVSWEEYK#.N	11.09	7.15	1.55	0.64
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	R.HLVYESDQNK#DGK#.L	846.27	473.74	1.79	0.56
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	R.HLVYESDQNK#DGK#.L	51.40	29.66	1.73	0.58
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.IDDDK#DGFVTVDELK#.G	823.60	488.61	1.69	0.59
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.LTKEEIVDKYDLFVGSQATDFGEALVR.H	417.99	214.69	1.95	0.51
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.M*ADKDGDLIATK.E	323.75	252.09	1.28	0.78
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.MADK#DGDLIATK#.E	44.34	24.05	1.84	0.54
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.M*DKEETKDWILPSDYDHAEAEAR.H	229.06	147.23	1.56	0.64
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.MDK#EETK#DWILPSDYDHAEAEAR@.H	7.00	4.06	1.72	0.58
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.NADGFIDLEEYIGDM*YSHDGNADEPEWVK#.T	15.00	6.83	2.20	0.46
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.SFDQLTPEESK#.E	143.42	98.31	1.46	0.69
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.SFDQLTPEESKER.L	510.11	344.78	1.48	0.68
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.TER@EQFVEFR@.D	95.11	49.51	1.92	0.52
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	R.VHHEPQLSDK#.V	278.33	187.72	1.48	0.67
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.VHNDAQNFDYDHDAFLGAEEAK.S	50.74	37.57	1.35	0.74
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	R.WIHEDVER.Q	97.94	60.30	1.62	0.62
Q6XLQ8_Q6XLQ8_MOUSE	Calu	Calumenin OS=Mus musc	K.IDADK#DGFVTEGELK#.S	101.01	85.73	1.18	0.85
Q6XLQ8_Q6XLQ8_MOUSE	Calu	Calumenin OS=Mus musc	K.K#YIYDNVENQWQEFDM*NQDGLISWDEYR@.N	5.77	3.44	1.68	0.60
Q6XLQ8_Q6XLQ8_MOUSE	Calu	Calumenin OS=Mus musc	R.LGM*IVDK#.I	57.71	53.14	1.09	0.92
Q6XLQ8_Q6XLQ8_MOUSE	Calu	Calumenin OS=Mus musc	R.LGM*IVDKIDADKDGFVTEGELK.S	249.85	212.37	1.18	0.85
Q6XLQ8_Q6XLQ8_MOUSE	Calu	Calumenin OS=Mus musc	R.LGMIVDK#IDADK#DGFVTEGELK#.S	14.65	9.71	1.51	0.66
Q6XLQ8_Q6XLQ8_MOUSE	Calu	Calumenin OS=Mus musc	K.YIYDNVENQWQEFDM*NQDGLISWDEYR.N	6.39	4.37	1.46	0.68
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.IDDDK#DGFVTVDELK#.G	5.65	5.87	0.96	1.04
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.EEIVDKYDLFVGSQATDFGEALVR.H	6.80	2.61	2.61	0.38
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.IDDDK#DGFVTVDELK#.G	12.20	4.40	2.77	0.36
O35887_CALU_MOUSE	Calu	Calumenin OS=Mus musc	K.LTK#EEIVDK#YDLFVGSQATDFGEALVR@.H	9.29	6.91	1.35	0.74
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.DLK#PENLLLASK#.S	41.68	24.25	1.72	0.58
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	K.ESTESSNTTIEDEDVK#.A	29.15	14.84	1.96	0.51
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.FYFENALSK#.S	41.21	15.98	2.58	0.39
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	K.GAILTTM*LATR@.N	30.71	15.33	2.00	0.50
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	K.IPTGQEYAAK#.I	40.83	20.40	2.00	0.50
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.LTQYM*DGSGM*PK#.T	18.75	8.27	2.27	0.44
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	K.VTEQLIEAINNGDFEAYTK#.I	5.33	3.29	1.62	0.62
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	K.VTEQLIEAINNGDFEAYTK#.I	18.08	7.35	2.46	0.41
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	K.ESTESSNTTIEDEDVK#.A	6.34	2.14	2.97	0.34
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.FYFENALSK#.S	14.11	8.14	1.73	0.58
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.LTQYM*DGSGM*PK#.T	4.71	3.10	1.52	0.66
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.DLK#PENLLLASK#.S	29.96	14.82	2.02	0.49
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	K.ESTESSNTTIEDEDVK#.A	9.28	6.81	1.36	0.73
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.FYFENALSK#.S	14.84	8.23	1.80	0.55
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.LTQYM*DGSGM*PK.T	7.55	4.59	1.64	0.61
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.DLK#PENLLLASK#.S	57.16	26.86	2.13	0.47
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	K.ESTESSNTTIEDEDVK#.A	18.46	8.95	2.06	0.48
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.FTDEYQLFEELGK#.G	33.89	16.35	2.07	0.48
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	R.FYFENALSK#.S	29.01	16.00	1.81	0.55
Q6PHZ2_KCC2D_MOUSE	Camk2d	Calcium/calmodulin-dep	K.VTEQLIEAINNGDFEAYTK#.I	14.37	8.26	1.74	0.57
Q923T9_KCC2G_MOUSE	Camk2g	Calcium/calmodulin-dep	R.FTDDYQLFEELGK#.G	6.99	3.76	1.86	0.54
Q923T9_KCC2G_MOUSE	Camk2g	Calcium/calmodulin-dep	K.FYFENLLSK#.N	9.85	4.86	2.03	0.49
Q923T9_KCC2G_MOUSE	Camk2g	Calcium/calmodulin-dep	K.FYFENLLSK#.N	22.06	7.30	3.02	0.33
Q923T9_KCC2G_MOUSE	Camk2g	Calcium/calmodulin-dep	K.ITEQLIEAINNGDFEAYTK#.I	8.07	2.65	3.04	0.33
Q6ZQ73_CAND2_MOUSE	Cand2	Cullin-associated NEDD8	K.DSIQLDEDSER@.K	8.73	2.42	3.60	0.28
Q6ZQ73_CAND2_MOUSE	Cand2	Cullin-associated NEDD8	K.LVFVNPPYLLPR@.F	4.90	4.00	1.23	0.82
Q6ZQ73_CAND2_MOUSE	Cand2	Cullin-associated NEDD8	R.AVAALLTNPEVR@.K	14.56	5.91	2.47	0.41
Q6ZQ73_CAND2_MOUSE	Cand2	Cullin-associated NEDD8	R.LATLAALDALAQSQGLGLPPPAVR@.T	6.23	2.21	2.81	0.36
Q6ZQ73_CAND2_MOUSE	Cand2	Cullin-associated NEDD8	R.LLDPEPYVGEM*STATLAR@.L	4.48	0.00	#DIV/0!	0.00
Q6ZQ73_CAND2_MOUSE	Cand2	Cullin-associated NEDD8	K.LVFVNPPYLLPR@.F	10.51	4.59	2.29	0.44
Q6ZQ73_CAND2_MOUSE	Cand2	Cullin-associated NEDD8	K.TVLLEALGSPSEDVR@.A	10.07	4.41	2.28	0.44
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	K.APVPTGEVYFADSFDR@.G	63.81	37.70	1.69	0.59
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	R.GSLSGWILSK#.A	32.79	25.77	1.27	0.79
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	K.IPNPDFFEDLEPFK#.M	11.66	7.83	1.49	0.67
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	R.K#IPNPDFFEDLEPFK#.M	38.11	26.46	1.44	0.69
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	K.TAELSLDQFHDK#.T	13.08	9.92	1.32	0.76
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	K.TGVYEEK#.H	18.58	12.59	1.48	0.68
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	K.TYFTDK#K#.T	12.58	7.04	1.79	0.56
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	K.APVPTGEVYFADSFDR@.G	34.96	19.01	1.84	0.54

P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	R.GSLSGWILSK#.A	28.84	17.25	1.67	0.60
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	K.IPNPDFFEDLEPFK#.M	16.74	13.62	1.23	0.81
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	R.K#IPNPDFFEDLEPFK#.M	21.88	14.18	1.54	0.65
P35564_CALX_MOUSE	Canx	Calnexin OS=Mus muscul	K.SDASTPPSPK#.V	20.80	9.82	2.12	0.47
P40124_CAP1_MOUSE	Cap1	Adenylyl cyclase-associat	K.K#EPALLELEGK#.K	14.37	8.93	1.61	0.62
P40124_CAP1_MOUSE	Cap1	Adenylyl cyclase-associat	R.VENQENVSNLVIDDTELK.Q	5.72	6.28	0.91	1.10
P24452_CAPG_MOUSE	Capg	Macrophage-capping prc	K.AQVEIITDGEEPAEM*IQVLGPK#PALK#.E	13.19	4.54	2.91	0.34
P24452_CAPG_MOUSE	Capg	Macrophage-capping prc	K.AQVEIITDGEEPAEMIQVLGPKPALK.E	13.89	5.18	2.68	0.37
P24452_CAPG_MOUSE	Capg	Macrophage-capping prc	R.EVQGNESDLFM*SYFPR@.G	12.63	5.06	2.50	0.40
P24452_CAPG_MOUSE	Capg	Macrophage-capping prc	R.QAALQVADGFISR@.M	63.44	20.87	3.04	0.33
P24452_CAPG_MOUSE	Capg	Macrophage-capping prc	K.VSDATGQMNLTK#.V	11.69	6.37	1.83	0.55
P24452_CAPG_MOUSE	Capg	Macrophage-capping prc	K.VSDATGQM*NLTK#.V	58.44	28.11	2.08	0.48
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	K.APSDLYQIILK#.A	14.38	4.67	3.08	0.32
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	R.DFFLANASR@.A	11.30	5.27	2.14	0.47
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	K.ELQTILNR@.I	13.24	3.08	4.30	0.23
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	K.LVFVHSAQGNEFWSALLEK#.A	8.34	4.43	1.88	0.53
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	K.VLSEEEIDDNFK#.T	12.65	4.54	2.79	0.36
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	K.YLGQDYETLR@.A	9.68	3.07	3.15	0.32
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	K.APSDLYQIILK#.A	17.03	4.73	3.60	0.28
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	R.LPPGEYIVVPSTFEPNK#EGDFLLR@.F	7.81	11.75	0.66	1.50
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	K.LVFVHSAQGNEFWSALLEK#.A	7.54	1.44	5.24	0.19
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	K.R@PTELM*SNPQFIVDGATR@.T	6.96	2.33	2.99	0.33
O35350_CAN1_MOUSE	Capn1	Calpain-1 catalytic subur	K.VLSEEEIDDNFK#.T	16.01	4.36	3.67	0.27
O08529_CAN2_MOUSE	Capn2	Calpain-2 catalytic subur	K.DGELLFVHSAEGSEFWSALLEK#.A	7.40	3.17	2.33	0.43
O08529_CAN2_MOUSE	Capn2	Calpain-2 catalytic subur	K.K#ADYQAVDDEIEANIEEIDANEEDIDDGFR@R@.L	5.52	2.59	2.13	0.47
O88456_CPNS1_MOUSE	Capns1	Calpain small subunit 1 (	R.SHYSNIEANESEEVR@.Q	16.05	4.93	3.25	0.31
O88456_CPNS1_MOUSE	Capns1	Calpain small subunit 1 (	R.SM*VAVM*DSDTTGK#.L	9.42	4.30	2.19	0.46
O88456_CPNS1_MOUSE	Capns1	Calpain small subunit 1 (	R.ILGGVISAISEAAAQYNPEPPPPR.S	16.81	10.00	1.68	0.59
O88456_CPNS1_MOUSE	Capns1	Calpain small subunit 1 (	R.ILGGVISAISEAAAQYNPEPPPPR@.S	7.64	3.41	2.24	0.45
O88456_CPNS1_MOUSE	Capns1	Calpain small subunit 1 (	K.LFVQLAGDDM*EVSATELM*NILNK#.V	5.76	3.68	1.57	0.64
O88456_CPNS1_MOUSE	Capns1	Calpain small subunit 1 (	K.LGFEEFK#.Y	18.40	9.72	1.89	0.53
O88456_CPNS1_MOUSE	Capns1	Calpain small subunit 1 (	R.SHYSNIEANESEEVR@.Q	12.85	6.59	1.95	0.51
O88456_CPNS1_MOUSE	Capns1	Calpain small subunit 1 (	R.SM*VAVM*DSDTTGK#.L	7.41	2.76	2.69	0.37
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	R.LNQDQLDAVSK#.Y	24.11	14.05	1.72	0.58
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	R.DGYQQNFK#.R	21.99	6.96	3.16	0.32
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	K.GK#LDDYQER@.M	26.24	7.37	3.56	0.28
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	R.LNEQYEHASIHLWDLLEGK#.E	94.73	44.31	2.14	0.47
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	R.LNQDQLDAVSK#.Y	199.41	90.16	2.21	0.45
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	K.QILGVIDK#K#.L	26.09	8.60	3.03	0.33
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	R.SFM*ALSQDIQK#.T	87.64	37.14	2.36	0.42
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	R.SFMALSQDIQK#.T	22.37	7.23	3.09	0.32
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	K.TVLELQYVLDK#.L	63.59	25.42	2.50	0.40
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	K.YQEVTNNLEFAK#.E	147.17	67.31	2.19	0.46
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	R.DGYQQNFK#.R	17.10	2.49	6.87	0.15
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	K.GK#LDDYQER@.M	16.23	4.72	3.44	0.29
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	R.LNQDQLDAVSK#.Y	116.92	29.79	3.92	0.25
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	R.SFM*ALSQDIQK#.T	44.40	15.34	2.89	0.35
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	K.TVLELQYVLDK#.L	29.19	7.94	3.68	0.27
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	K.TVLELQYVLDK#LGDDDVR@TDLK#.Q	9.55	2.22	4.30	0.23
Q60865_CAPR1_MOUSE	Caprin1	Caprin-1 OS=Mus muscul	K.YQEVTNNLEFAK#.E	62.40	17.82	3.50	0.29
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.DVQDSVTVSNEIQTTK#.E	19.40	14.34	1.35	0.74
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.EASDPQPEDVDGGLK#.S	57.63	55.11	1.05	0.96
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	R.EGAAHAFAQYNM*DQFTPVK#.I	6.80	8.22	0.83	1.21
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.FITHAPPGEFNEVFNDVR@.L	60.73	39.58	1.53	0.65
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.FTITPPSAQVVGVLK#.I	70.77	61.89	1.14	0.87
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.FTITPPSAQVVGVLK.I	12.89	15.79	0.82	1.22
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.IIESAENEYQTAISENYQTM*SDTTFK#.A	31.44	21.23	1.48	0.68
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.IIESAENEYQTAISENYQTMSDTTFK#.A	6.06	4.00	1.51	0.66
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.FITHAPPGEFNEVFNDVR@.L	11.84	8.89	1.33	0.75
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.FTITPPSAQVVGVLK#.I	10.65	8.16	1.30	0.77
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.FITHAPPGEFNEVFNDVR@.L	7.58	5.43	1.40	0.72
Q5RKN9_Q5RKN9_MOUSE	Capza1	Capping protein (Actin fil	K.FTITPPSAQVVGVLK#.I	10.72	5.66	1.89	0.53
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	K.DIQDSLTVSNEVQTAK#.E	28.97	26.33	1.10	0.91
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	K.EATDPRPYEAENAIESWR.T	56.35	49.02	1.15	0.87
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	K.FIIHAPPGEFNEVFNDVR.L	66.56	48.92	1.36	0.74
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	K.FTVTPSTTQVVGILK#.I	70.86	69.00	1.03	0.97
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	K.IQVHYYEDGNVQLVSHK#.D	18.37	15.68	1.17	0.85
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	K.IVEAAENEYQTAISENYQTM*SDTTFK#.A	21.43	19.78	1.08	0.92
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	R.LLLNNDNLLR@.E	154.90	133.11	1.16	0.86
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	R.TK#IDWNK#.I	32.46	24.10	1.35	0.74
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	R.TSVETALR.A	109.75	80.62	1.36	0.73
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	R.LLLNNDNLLR@.E	22.63	20.85	1.09	0.92
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	K.FTVTPSTTQVVGILK#.I	11.58	4.73	2.45	0.41
P47754_CAZA2_MOUSE	Capza2	F-actin-capping protein s	R.LLLNNDNLLR@.E	27.11	11.63	2.33	0.43
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.K#LEVEANNAFDQYR@.D	129.82	93.75	1.38	0.72
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	K.LEVEANNAFDQYR@.D	22.34	19.72	1.13	0.88
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.LPPQQIEK#.N	32.31	31.13	1.04	0.96
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.LVEDM*ENK#.I	36.49	29.58	1.23	0.81
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	K.NDLVEALKR.K	14.79	12.69	1.17	0.86
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.R@LPPQQIEK#.N	25.44	24.00	1.06	0.94
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	K.SGSGTM*NLGGSLTR@.Q	200.70	159.74	1.26	0.80
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.SPWSNK#YDPPLEDGAM*PSAR@.L	46.89	43.39	1.08	0.93
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.SPWSNKYDPPLEDGAMPSAR.L	13.31	13.75	0.97	1.03
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.STLNEIYFGK#.T	129.33	83.45	1.55	0.65
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.SVQTFADK.S	151.57	123.37	1.23	0.81
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	K.YDPPLEDGAM*PSAR.L	7.79	8.97	0.87	1.15
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.KLEVEANNAFDQYR.D	15.85	13.32	1.19	0.84
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	K.LEVEANNAFDQYR.D	2.25	3.79	0.59	1.68
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	K.SGSGTM*NLGGSLTR@.Q	32.46	27.88	1.16	0.86
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.SPWSNKYDPPLEDGAM*PSAR.L	8.99	7.86	1.14	0.87
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.STLNEIYFGK#.T	52.88	49.27	1.07	0.93
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.K#LEVEANNAFDQYR@.D	13.66	8.94	1.53	0.65
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	K.SGSGTM*NLGGSLTR@.Q	19.66	9.60	2.05	0.49
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	R.STLNEIYFGK#.T	33.71	23.99	1.41	0.71
A2AMW0_A2AMW0_MOUSE	Capzb	Capping protein (Actin fil	K.SGSGTM*NLGGSLTR@.Q	15.03	6.53	2.30	0.43
Q9WVG6_CARM1_MOUSE	Carm1	Histone-arginine methylt	R.GAAVDEYFR@.Q	9.51	3.05	3.12	0.32
O70589_CSKP_MOUSE	Cask	Peripheral plasma memb	R.VGDIIQIISK#.D	9.70	6.83	1.42	0.70
P51125_ICAL_MOUSE	Cast	Calpastatin OS=Mus mus	K.SLSESELIGELSADFDR@.S	14.86	4.64	3.20	0.31
P49817_CAV1_MOUSE	Cav1	Caveolin-1 OS=Mus musc	K.ASFTTFTVTK#.Y	9.47	4.42	2.14	0.47
P49817_CAV1_MOUSE	Cav1	Caveolin-1 OS=Mus musc	K.HLNDDVVK#.I	73.34	28.16	2.60	0.38
P49817_CAV1_MOUSE	Cav1	Caveolin-1 OS=Mus musc	K.HLNDDVVK#IDFEDVIAEPEGTHSFDGIWK#.A	18.05	31.54	0.57	1.75
P49817_CAV1_MOUSE	Cav1	Caveolin-1 OS=Mus musc	K.IDFEDVIAEPEGTHSFDGIWK#.A	22.72	5.67	4.01	0.25
Q08024_PEBB_MOUSE	Cbfb	Core-binding factor subu	R.AQQEDALAQQAFEEAR@.R	12.07	13.17	0.92	1.09

Q08024_PEBB_MOUSE	Cbfb	Core-binding factor subu	R.AQQEDALAQQAFEEAR.R	14.20	15.10	0.94	1.06
Q08024_PEBB_MOUSE	Cbfb	Core-binding factor subu	R.SKFENEEFFR.K	8.94	10.24	0.87	1.15
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	R.IIGATDSSGELM*FLM*K.W	4.68	20.48	0.23	4.38
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	R.IIGATDSSGELM*FLMK.W	3.95	12.77	0.31	3.24
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	K.KKVEEVLEEEEEEYVVEK.V	4.50	13.88	0.32	3.09
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	R.IIGATDSSGELM*FLM*K.W	65.26	257.36	0.25	3.94
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	R.IIGATDSSGELMFLM*K.W	6.07	23.21	0.26	3.82
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	R.IIGATDSSGELM*FLMK.W	36.02	160.54	0.22	4.46
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	R.IIGATDSSGELMFLMK.W	4.44	15.53	0.29	3.50
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	K.KKVEEVLEEEEEEYVVEK.V	18.04	73.27	0.25	4.06
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	K.KVEEVLEEEEEEYVVEK.V	64.69	69.21	0.93	1.07
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	K.VEEVLEEEEEEYVVEK.V	1.95	9.11	0.21	4.68
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	K.VEYLLK.W	8.39	40.90	0.21	4.88
P83917_CBX1_MOUSE	Cbx1	Chromobox protein hom	K.WKNSDEADLVPAK.E	4.97	31.05	0.16	6.25
P30658_CBX2_MOUSE	Cbx2	Chromobox protein hom	K.LPPPLSAPVAGLAALK.A	4.77	5.52	0.86	1.16
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.KVEEAEPEEFVVEK.V	2.95	26.45	0.11	8.97
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.SLSDSESDDSK.S	1.63	6.42	0.25	3.95
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.WKDSDEADLVLAK.E	7.10	36.99	0.19	5.21
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.DSDEADLVLAK.E	8.78	41.75	0.21	4.76
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.KVEEAEPEEFVVEK.V	47.35	282.94	0.17	5.98
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.K#VEEAEPEEFVVEK#.V	12.89	96.65	0.13	7.50
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.SKKVEEAEPEEFVVEK.V	6.28	27.94	0.22	4.45
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.SLSDSESDDSK.S	3.35	22.68	0.15	6.77
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.VEEAEPEEFVVEK.V	18.69	103.64	0.18	5.55
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.WKDSDEADLVLAK.E	10.79	48.82	0.22	4.52
P23198_CBX3_MOUSE	Cbx3	Chromobox protein hom	K.WK#DSDEADLVLAK#.E	37.54	262.60	0.14	7.00
O55187_CBX4_MOUSE	Cbx4	E3 SUMO-protein ligase C	K.GYLGAVK#PLGGGAGAPGK#.G	10.55	3.10	3.40	0.29
Q61686_CBX5_MOUSE	Cbx5	Chromobox protein hom	K.GQVEYLLK.W	11.65	43.67	0.27	3.75
Q61686_CBX5_MOUSE	Cbx5	Chromobox protein hom	R.KSSFSNSADDIK.S	2.64	10.24	0.26	3.88
Q61686_CBX5_MOUSE	Cbx5	Chromobox protein hom	K.SSFSNSADDIK.S	16.04	60.92	0.26	3.80
Q61686_CBX5_MOUSE	Cbx5	Chromobox protein hom	K.WKDTDEADLVLAK.E	16.56	63.72	0.26	3.85
Q9DBY5_CBX6_MOUSE	Cbx6	Chromobox protein hom	K.VAAGVAGATGGGGGTGPSK#.-	40.55	12.04	3.37	0.30
Q9DBY5_CBX6_MOUSE	Cbx6	Chromobox protein hom	R.VFAAESIIK#.R	16.63	5.63	2.95	0.34
Q9DBY5_CBX6_MOUSE	Cbx6	Chromobox protein hom	K.VAAGVAGATGGGGGTGPSK#.-	5.19	1.97	2.64	0.38
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	K.FPAGHSVIQLAR@.R	9.43	7.73	1.22	0.82
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	K.GQGALDPGGAR@.V	33.17	19.59	1.69	0.59
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	R.ILGDPEEESWSPSLTNLEK#.V	12.71	7.07	1.80	0.56
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	R.K#EPLDPSQR@PLGEPSAGLGEYLK#.G	27.64	15.09	1.83	0.55
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	K.LAVDTFPAR@.V	44.70	15.36	2.91	0.34
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	R.LLAAFEER@.E	70.96	26.15	2.71	0.37
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	R.R@QDSDLVQYGVTSPSSAEASSK#.L	50.54	16.73	3.02	0.33
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	R.SPQDLASTSR@.A	95.82	39.31	2.44	0.41
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	R.VDDK#PSSPGDSSK#.K	4.37	1.74	2.52	0.40
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	R.VFAAEALLK#.R	25.06	10.61	2.36	0.42
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	K.VVVTDVTSNFLTVTIK#.E	11.90	6.42	1.85	0.54
Q9QXV1_CBX8_MOUSE	Cbx8	Chromobox protein hom	K.YSTWEPEENILDAR@.L	14.72	7.47	1.97	0.51
Q9D1C2_CBY1_MOUSE	Cby1	Protein chibby homolog	R.NQQLEEENNLLR@.L	15.26	5.65	2.70	0.37
Q8K1A6_C2D1A_MOUSE	Cc2d1a	Coiled-coil and C2 domai	K.SFDPVLEALSR@.G	5.62	3.42	1.64	0.61
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.AGLLQPPVR@.I	16.42	7.68	2.14	0.47
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.DLGQLQENLEVSENM*NLQFENQLNK#.T	5.63	4.29	1.31	0.76
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	R.IQTLPNQNQSQTQPLLK#.T	6.49	3.38	1.92	0.52
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	R.IVSQPQPAR@.R	40.97	14.41	2.84	0.35
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.LHDTFGFVDEDVFFQLGAVK#.G	29.19	7.20	4.05	0.25
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.LQLLEEK#TDEDGK#TILNLENSNK#.S	38.71	10.87	3.56	0.28
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	R.VLVEATYNPNM*PFK#.W	16.04	5.60	2.87	0.35
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	R.YTVQFSK#.F	27.04	13.00	2.08	0.48
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.AGLLQPPVR@.I	16.50	4.93	3.34	0.30
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.DLGQLQENLEVSENM*NLQFENQLNK#.T	6.03	2.91	2.07	0.48
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.IEEQK#EEQK#ELEK#.S	20.67	6.23	3.32	0.30
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	R.IQTLPNQNQSQTQPLLK#.T	9.77	2.47	3.97	0.25
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.K#ADGEQDEEEK#DDGEVK#.E	6.77	2.63	2.57	0.39
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.K#DLGQLQENLEVSENM*NLQFENQLNK#.T	2.52	2.72	0.93	1.08
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.NM*AVLDPPDADHLYSAK#.V	21.63	4.38	4.94	0.20
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	R.SEWETLSR@.G	18.35	5.62	3.26	0.31
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	K.TDEDGK#TILNLENSNK#.S	11.94	2.92	4.08	0.24
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	R.VFTGVVTK#.L	30.09	7.00	4.30	0.23
Q8CH18_CCAR1_MOUSE	Ccar1	Cell division cycle and ap	R.VLVEATYNPNM*PFK#.W	16.36	13.40	1.22	0.82
Q8VDP4_CCAR2_MOUSE	Ccar2	Cell cycle and apoptosis r	R.FAEFQYLQPGPPR@.Q	8.00	4.30	1.86	0.54
Q8VDP4_CCAR2_MOUSE	Ccar2	Cell cycle and apoptosis r	R.K#EEEAVLVGGEWSPSLDGLDPQADPQVLVR@.T	3.71	2.02	1.84	0.54
Q8VDP4_CCAR2_MOUSE	Ccar2	Cell cycle and apoptosis r	K.QGILGAQPQLIFQPHR@.I	8.49	4.01	2.12	0.47
Q8VDP4_CCAR2_MOUSE	Ccar2	Cell cycle and apoptosis r	K.VLLLSSPGLEEFYR@.C	15.84	5.66	2.80	0.36
Q8VDP4_CCAR2_MOUSE	Ccar2	Cell cycle and apoptosis r	K.VQTLSNQPLLK#.S	13.05	5.30	2.46	0.41
Q8VDP4_CCAR2_MOUSE	Ccar2	Cell cycle and apoptosis r	R.K#EEEAVLVGGEWSPSLDGLDPQADPQVLVR@.T	3.74	4.23	0.89	1.13
Q3TMW1_C102A_MOUSE	Ccdc102a	Coiled-coil domain-cont	R.AQVGDLEEALAR@.R	9.44	6.26	1.51	0.66
Q3TMW1_C102A_MOUSE	Ccdc102a	Coiled-coil domain-cont	R.SLDEQTEQSENLQVQLEHLQSR@.L	5.98	4.58	1.31	0.77
Q8R344_CCD12_MOUSE	Ccdc12	Coiled-coil domain-cont	R.AIAELIR.E	44.58	28.39	1.57	0.64
Q8R344_CCD12_MOUSE	Ccdc12	Coiled-coil domain-cont	K.EQLEAAK#PEPVIEEVDLANLAPR@.K	9.98	3.66	2.73	0.37
Q8R344_CCD12_MOUSE	Ccdc12	Coiled-coil domain-cont	R.R@VPQAK#PVAVEEK#.V	82.70	49.09	1.68	0.59
Q8R344_CCD12_MOUSE	Ccdc12	Coiled-coil domain-cont	K.VK#EQLEAAK#PEPVIEEVDLANLAPR@.K	13.43	9.82	1.37	0.73
A2AEV7_A2AEV7_MOUSE	Ccdc120	Coiled-coil domain conta	R.TTGPPDPPR@.A	50.52	1.88	26.87	0.04
Q8CI71_CC132_MOUSE	Ccdc132	Coiled-coil domain-cont	R.DYVDEQTGDVPVK#.S	7.06	4.32	1.64	0.61
Q8CI71_CC132_MOUSE	Ccdc132	Coiled-coil domain-cont	K.LQDTLEQIEEQLDVALSK#.I	3.94	6.38	0.62	1.62
Q8CI71_CC132_MOUSE	Ccdc132	Coiled-coil domain-cont	K.SPPESLNDLGAFESLR@.V	4.99	2.24	2.23	0.45
Q8CI71_CC132_MOUSE	Ccdc132	Coiled-coil domain-cont	K.VNAPILTNTTLNVIR@.L	4.34	0.93	4.66	0.21
Q8C7V8_CC134_MOUSE	Ccdc134	Coiled-coil domain-cont	K.ILDVM*LK#.G	102.54	50.92	2.01	0.50
Q8C7V8_CC134_MOUSE	Ccdc134	Coiled-coil domain-cont	K.NLAQLNDIHQQYK#.I	10.41	2.73	3.81	0.26
Q8C7V8_CC134_MOUSE	Ccdc134	Coiled-coil domain-cont	K.TDQTEFIPSTDPFQK#.A	48.50	20.74	2.34	0.43
Q8C7V8_CC134_MOUSE	Ccdc134	Coiled-coil domain-cont	R.TVLIAADVLPDGPVPQDEK#.L	25.88	13.60	1.90	0.53
Q8C7V8_CC134_MOUSE	Ccdc134	Coiled-coil domain-cont	K.TDQTEFIPSTDPFQK#.A	9.21	3.78	2.44	0.41
Q8C7V8_CC134_MOUSE	Ccdc134	Coiled-coil domain-cont	R.TVLIAADVLPDGPVPQDEK#.L	9.74	5.12	1.90	0.53
Q8R0K4_CC137_MOUSE	Ccdc137	Coiled-coil domain-cont	R.K#GESDVAYVQR@.M	7.36	3.37	2.18	0.46
Q8R0K4_CC137_MOUSE	Ccdc137	Coiled-coil domain-cont	K.M*LLGPGGGSPAPATSLAR@.Q	10.74	4.08	2.63	0.38
Q8R0K4_CC137_MOUSE	Ccdc137	Coiled-coil domain-cont	K.NQDEQEIPFR@.L	15.51	7.93	1.95	0.51
Q8R0K4_CC137_MOUSE	Ccdc137	Coiled-coil domain-cont	R.QEM*TPAQPPGSSFQR@.Q	6.01	2.27	2.64	0.38
Q8C9S4_CC186_MOUSE	Ccdc186	Coiled-coil domain-cont	R.ESELLLFTEK#.L	9.33	3.64	2.56	0.39
Q9JIG7_CCD22_MOUSE	Ccdc22	Coiled-coil domain-cont	R.DLLLFLAER@.L	14.32	7.33	1.95	0.51
Q9JIG7_CCD22_MOUSE	Ccdc22	Coiled-coil domain-cont	K.FTFHLEPQVQAAQVADVPATSQR@.L	11.32	5.48	2.07	0.48
Q9JIG7_CCD22_MOUSE	Ccdc22	Coiled-coil domain-cont	R.ILEIVGNIR@.K	12.55	6.08	2.07	0.48
Q9JIG7_CCD22_MOUSE	Ccdc22	Coiled-coil domain-cont	R.LPSDASEDADQPAGDSAIFLR@.A	4.84	1.65	2.94	0.34
Q9JIG7_CCD22_MOUSE	Ccdc22	Coiled-coil domain-cont	K.LQLVVESSAQR@.L	13.47	3.08	4.37	0.23
Q9JIG7_CCD22_MOUSE	Ccdc22	Coiled-coil domain-cont	K.QLVSELETLPK#.D	10.30	4.99	2.06	0.48
Q9JIG7_CCD22_MOUSE	Ccdc22	Coiled-coil domain-cont	R.QSELSVAEQEQALR@.L	6.74	4.95	1.36	0.73
Q9CR29_CCD43_MOUSE	Ccdc43	Coiled-coil domain-cont	R.LEALGVDR@.A	19.78	6.58	3.01	0.33

Q9CR29_CCD43_MOUSE	Ccdc43	Coiled-coil domain-cont	R.NTNVEDVLNAR@.K	13.63	3.46	3.94	0.25
Q9CR27_CCD53_MOUSE	Ccdc53	WASH complex subunit (	R.IQQIETTLNILDAK#.L	3.37	4.23	0.80	1.26
Q5SNZ0_GRDN_MOUSE	Ccdc88a	Girdin OS=Mus musculus	R.LEESTNYNQQLR@.H	9.41	14.34	0.66	1.52
Q5SNZ0_GRDN_MOUSE	Ccdc88a	Girdin OS=Mus musculus	K.LEM*ENQSLTK#.T	4.20	14.24	0.29	3.40
Q5SNZ0_GRDN_MOUSE	Ccdc88a	Girdin OS=Mus musculus	R.LEVSYQGLDTENQR@.L	9.40	5.63	1.67	0.60
Q5SNZ0_GRDN_MOUSE	Ccdc88a	Girdin OS=Mus musculus	R.LQQENM*NLLSDAR@.S	9.40	3.36	2.80	0.36
Q5SNZ0_GRDN_MOUSE	Ccdc88a	Girdin OS=Mus musculus	R.QASEYESLISK#.H	8.41	3.65	2.31	0.43
Q5SNZ0_GRDN_MOUSE	Ccdc88a	Girdin OS=Mus musculus	R.QQAEIK#DTTLEENNVK#.I	7.82	3.06	2.55	0.39
Q5SNZ0_GRDN_MOUSE	Ccdc88a	Girdin OS=Mus musculus	K.SLEQETSQLEK#.D	9.44	3.25	2.91	0.34
Q5SNZ0_GRDN_MOUSE	Ccdc88a	Girdin OS=Mus musculus	R.TSELAEAPQK#.S	20.87	5.63	3.70	0.27
Q7TQK5_CCD93_MOUSE	Ccdc93	Coiled-coil domain-cont	K.EISLLNSIHENFSQAM*ASPAAR@.D	6.65	2.40	2.76	0.36
Q9DBT3_CCD97_MOUSE	Ccdc97	Coiled-coil domain-cont	R.APLLYEQYIGQYLTQEELNAR@.T	8.26	3.64	2.27	0.44
Q9DBT3_CCD97_MOUSE	Ccdc97	Coiled-coil domain-cont	R.ELIQGGEYFSDEQM*R@.F	6.05	5.02	1.21	0.83
Q9DBT3_CCD97_MOUSE	Ccdc97	Coiled-coil domain-cont	R.VVHWGELSQTPIPSGPQEK#.E	7.36	3.87	1.90	0.53
Q8K2Y9_CCM2_MOUSE	Ccm2	Malcavernin OS=Mus mu	K.YLGQLTSIPGYLNPSSR@.T	4.27	2.25	1.90	0.53
Q62447_CCNC_MOUSE	Ccnc	Cyclin-C OS=Mus muscul	K.VEEFGVVSNTR@.L	10.35	31.80	0.33	3.07
O88874_CCNK_MOUSE	Ccnk	Cyclin-K OS=Mus muscul	K.FDLQVEHPYQFLLK#.Y	6.37	4.05	1.57	0.64
O88874_CCNK_MOUSE	Ccnk	Cyclin-K OS=Mus muscul	R.K#PPLAPALGEAEATGPVETSDLPK#.V	9.84	3.46	2.84	0.35
O88874_CCNK_MOUSE	Ccnk	Cyclin-K OS=Mus muscul	R.SLLNDVQFGQFGDDPK#EEVM*VLER@.I	3.56	2.34	1.52	0.66
Q9QWV9_CCNT1_MOUSE	Ccnt1	Cyclin-T1 OS=Mus muscu	R.TSESLALIGVDHSLQQDGSSAFGSQK#.Q	7.01	4.94	1.42	0.71
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.DAALM*VTNDGATILK#.N	185.54	69.61	2.67	0.38
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.DAALMVTNDGATILK#.N	38.26	17.59	2.17	0.46
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.EAESLIAK#.K	204.84	87.09	2.35	0.43
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.EALLSSAVDHGSDEAR.F	33.40	14.67	2.28	0.44
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.EAVAM*ESFAK#.A	151.27	60.18	2.51	0.40
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.EGTIGDM*AVLGITESFQVK#.R	19.07	6.68	2.85	0.35
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.EGTIGDMAVLGITESFQVK#.R	17.46	4.84	3.61	0.28
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.FWQDLM*NIAGTTLSSK#.L	23.53	10.73	2.19	0.46
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.FWQDLMNIAGTTLSSK#.L	12.40	5.31	2.34	0.43
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.GATQQILDEAER@.S	309.17	110.50	2.80	0.36
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.IHPQTIISGWR@.E	58.51	16.62	3.52	0.28
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.ILIANTGM*DTDK#.I	34.22	8.29	4.13	0.24
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.ILIANTGM*DTDKIK.I	29.04	13.21	2.20	0.45
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.ILLSSGR.D	254.24	107.55	2.36	0.42
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.K#IHPQTIISGWR@.E	51.72	20.14	2.57	0.39
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.K#LGGSLADSYLDEGFLLDK#K#.I	42.76	18.63	2.30	0.44
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.LALVTGGEIASTFDHPELVK#.L	344.80	159.03	2.17	0.46
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.LALVTGGEIASTFDHPELVK#.L	9.92	3.05	3.26	0.31
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.LGGSLADSYLDEGFLLDK#K#.I	5.70	2.25	2.54	0.39
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.LK#GSGNLEAIHVIK#.K	77.17	35.96	2.15	0.47
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.LSSFIGAIAIGDLVK#.S	356.09	133.78	2.66	0.38
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.M*LPTIIADNAGYDSADLVAQLR@.A	148.59	51.30	2.90	0.35
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.M*LPTIIADNAGYDSADLVAQLR.A	18.87	8.98	2.10	0.48
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.MLPTIIADNAGYDSADLVAQLR@.A	18.71	7.83	2.39	0.42
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.NIGVDNPAAK#.V	200.66	87.24	2.30	0.43
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.QLIYNYPEQLFGAAGVMAIEHADFAGVER@.L	11.52	5.33	2.16	0.46
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.QVLLSAAEAAEVILR@.V	110.41	43.95	2.51	0.40
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.R@QVLLSAAEAAEVILR@.V	18.03	8.62	2.09	0.48
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.TPGK#EAVAM*ESFAK#.A	43.52	24.68	1.76	0.57
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.VAEIEHAEK#EK#.M	22.42	12.33	1.82	0.55
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.VLVDM*SR@.V	112.31	47.55	2.36	0.42
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.VQDDEVGDGTTSVTVLAAELLR@.E	176.56	66.56	2.65	0.38
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.VQDDEVGDGTTSVTVLAAELLR.E	95.81	38.73	2.47	0.40
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	K.EAVAM*ESFAK#.A	14.00	6.12	2.29	0.44
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.FWQDLM*NIAGTTLSSK#.L	4.40	2.71	1.62	0.62
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.GATQQILDEAER@.S	35.12	9.90	3.55	0.28
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.LSSFIGAIAIGDLVK#.S	31.69	12.57	2.52	0.40
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.M*LPTIIADNAGYDSADLVAQLR@.A	16.44	6.38	2.58	0.39
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.QVLLSAAEAAEVILR@.V	8.99	3.51	2.56	0.39
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.LSSFIGAIAIGDLVK#.S	18.37	6.57	2.79	0.36
P80314_TCPB_MOUSE	Cct2	T-complex protein 1 subu	R.VQDDEVGDGTTSVTVLAAELLR@.E	11.23	3.22	3.49	0.29
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.AM*TGVEQWPYR@.A	35.44	16.07	2.21	0.45
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.AVAQALEVIPR@.T	82.85	52.54	1.58	0.63
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.EILSEVER@.N	101.59	48.33	2.10	0.48
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.EIQVQHPAAK#.S	23.48	14.38	1.63	0.61
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.ELGIWEPLAVK#.L	56.82	29.16	1.95	0.51
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.EM*M*LSIINSSITTK#.V	24.90	14.75	1.69	0.59
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.IVLLDSSLEYK#.K	85.32	100.97	0.85	1.18
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.IVSRPEELREDDVGTGAGLLEIKK.I	24.53	11.05	2.22	0.45
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.K#VQSGNINAAK#.T	16.84	9.36	1.80	0.56
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.M*ALDDM*ISTLK#.K	20.45	7.76	2.64	0.38
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.TAVETAVLLLR@.I	106.12	49.26	2.15	0.46
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.AM*TGVEQWPYR@.A	33.83	16.28	2.08	0.48
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.ANVTAIR@.R	159.15	67.43	2.36	0.42
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.AVAQALEVIPR@.T	130.21	56.61	2.30	0.43
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.EILSEVER@.N	97.01	37.97	2.55	0.39
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.ELGIWEPLAVK#.L	82.26	39.33	2.09	0.48
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.EM*M*LSIINSSITTK#.V	35.65	13.47	2.65	0.38
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.EMMLSIINSSITTK#.V	4.12	20.11	0.20	4.89
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.IDDIVSGHK#.K	20.10	21.31	0.94	1.06
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.ISTPVDVNNR.E	61.85	27.91	2.22	0.45
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.IVLLDSSLEYK#.K	199.11	43.54	4.57	0.22
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.IVSR@PEELR@EDDVGTGAGLLEIK#.K	16.48	8.24	2.00	0.50
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.IVSRPEELREDDVGTGAGLLEIKK.I	17.30	9.69	1.79	0.56
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.K#GESQTDIEITR@.E	7.88	10.83	0.73	1.37
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.K#VQSGNINAAK#.T	22.89	8.96	2.56	0.39
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.M*ALDDM*ISTLK#.K	14.67	8.14	1.80	0.56
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.NVLLDPQLVPGGGASEMAVAHALTEK#.S	21.29	10.41	2.05	0.49
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.TAVETAVLLLR.I	208.75	85.17	2.45	0.41
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.AM*TGVEQWPYR@.A	17.64	5.75	3.07	0.33
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.AVAQALEVIPR@.T	69.90	13.95	5.01	0.20
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.ELGIWEPLAVK#.L	41.94	7.71	5.44	0.18
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.EM*M*LSIINSSITTK#.V	18.74	4.50	4.16	0.24
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.ISTPVDVNNR@.E	37.19	6.36	5.85	0.17
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.IVLLDSSLEYK#.K	110.80	12.61	8.79	0.11
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	R.K#VQSGNINAAK#.T	10.70	4.60	2.32	0.43
P80318_TCPG_MOUSE	Cct3	T-complex protein 1 subu	K.TAVETAVLLLR@.I	101.62	18.30	5.55	0.18
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.AFADAM*EVIPSTLAENAGLNPISTVTELR@.N	8.66	4.82	1.80	0.56
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.ALIAGGGAPEIELALR@.L	183.21	89.40	2.05	0.49
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.AYILNLVK#.Q	139.66	48.98	2.85	0.35
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.DALSDLALHFLNK#.M	70.76	26.58	2.66	0.38
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.ETLLNSATTSLNSK#.V	42.89	18.78	2.28	0.44
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.FSNISAAK#.A	47.69	21.30	2.24	0.45

P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.GDVTITNDGATILK#.Q	21.18	9.91	2.14	0.47
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.GIHPTIISESFQK#.A	156.47	62.90	2.49	0.40
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.IDDVVNTR@.-	152.38	54.99	2.77	0.36
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.LVIEEAER.S	332.27	43.52	7.63	0.13
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.M*IQDGK#GDVTITNDGATILK#.Q	119.15	44.71	2.67	0.38
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.MIQDGK#GDVTITNDGATILK#.Q	10.29	3.13	3.29	0.30
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.M*LVELSK#.A	64.81	30.49	2.13	0.47
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.MLVELSK#.A	18.46	8.36	2.21	0.45
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.SGAPTAGPGSR@.G	49.76	24.72	2.01	0.50
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.TDM*DNQIVVSDYAQM*DR@.V	32.77	14.22	2.30	0.43
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.TDM*DNQIVVSDYAQMDR@.V	7.18	3.32	2.16	0.46
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.TVTIVVR@.G	69.03	26.55	2.60	0.38
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.VANSGITR@.V	75.75	20.90	3.63	0.28
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.VIDPATATSVDLR.D	182.56	76.74	2.38	0.42
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.VVSQYSSLLSPM*SVNAVM*K#.V	21.18	6.86	3.09	0.32
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.ALIAGGGAPEIELALR@.L	79.80	33.21	2.40	0.42
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.AYILNLVK#.Q	54.95	14.46	3.80	0.26
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.ETLLNSATTSLNSK#.V	12.65	3.38	3.75	0.27
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.GDVTITNDGATILK#.Q	7.68	3.53	2.17	0.46
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.GIHPTIISESFQK#.A	7.73	88.02	0.09	11.38
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.IDDVVNTR@.-	44.35	9.19	4.83	0.21
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.LVIEEAER@.S	82.06	24.74	3.32	0.30
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.M*IQDGKGDVTITNDGATILK.Q	28.80	8.69	3.31	0.30
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.TDM*DNQIVVSDYAQM*DR@.V	9.39	5.29	1.77	0.56
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.VIDPATATSVDLR@.D	63.41	23.25	2.73	0.37
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.ALIAGGGAPEIELALR@.L	51.77	10.17	5.09	0.20
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.AYILNLVK#.Q	18.59	4.79	3.88	0.26
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	R.ETLLNSATTSLNSK#.V	9.11	2.00	4.56	0.22
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.GDVTITNDGATILK#.Q	8.41	2.01	4.18	0.24
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.GIHPTIISESFQK#.A	10.20	127.52	0.08	12.50
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.IDDVVNTR@.-	29.71	9.11	3.26	0.31
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.LVIEEAER@.S	30.02	8.99	3.34	0.30
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.M*IQDGK#GDVTITNDGATILK#.Q	12.64	2.92	4.33	0.23
P80315_TCPD_MOUSE	Cct4	T-complex protein 1 subu	K.VIDPATATSVDLR@.D	35.61	11.31	3.15	0.32
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.AFADALEVIPMALSENSGM*NPIQTM*TEVR@.A	14.19	5.27	2.69	0.37
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.AVTIFIR.G	120.48	43.29	2.78	0.36
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.DK#M*LVIEK#.C	16.03	6.37	2.52	0.40
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.DVDFELIK#.V	49.58	14.50	3.42	0.29
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.DVDFELIK#VEGK#.V	20.72	10.09	2.05	0.49
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.FSELTSEK#.L	180.94	78.65	2.30	0.43
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.GSNDM*QYQHVIETLIGK#.K	43.96	13.27	3.31	0.30
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.IADGYEQAAR.I	216.62	75.87	2.85	0.35
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.IAIQHLDK#.I	29.89	11.81	2.53	0.40
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.IDDIR@K#PGESEE.-	28.23	10.73	2.63	0.38
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.ISDK#VLVDINNPEPLIQTAK#.T	18.81	8.81	2.13	0.47
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.LDVM*SVEDYK#.A	13.97	7.72	1.81	0.55
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.LGFAGVVQEISFGTTK#.D	191.66	77.01	2.49	0.40
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.LM*GLEALK#.S	77.53	37.52	2.07	0.48
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.LMGLEALK#.S	15.92	5.86	2.72	0.37
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.LM*VELSK#.S	58.62	21.67	2.71	0.37
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.LMVELSK#.S	33.62	13.50	2.49	0.40
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.M*LVIEK#.C	39.95	26.03	1.53	0.65
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.QM*AEIAVNAVLTVADM*ER@.R	5.70	3.21	1.77	0.56
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.QQISLATQM*VR@.M	86.13	33.26	2.59	0.39
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.R@DVDFELIK#VEGK#.V	12.83	8.20	1.56	0.64
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.VLVDINNPEPLIQTAK#.T	156.60	69.50	2.25	0.44
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.WVGGPEIELIAIATGGR@.I	109.65	40.62	2.70	0.37
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.AVTIFIR@.G	61.30	21.28	2.88	0.35
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.DVDFELIK#.V	15.34	6.82	2.25	0.44
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.DVDFELIK#VEGK#.V	18.97	4.38	4.33	0.23
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.GSNDM*QYQHVIETLIGK#.K	18.92	8.23	2.30	0.44
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.IADGYEQAAR@.I	86.50	26.98	3.21	0.31
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.IAIQHLDK#.I	25.76	10.08	2.56	0.39
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.IDDIR@K#PGESEE.-	13.33	4.38	3.04	0.33
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.LDVM*SVEDYK#.A	7.77	3.03	2.56	0.39
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.LGFAGVVQEISFGTTK#.D	109.17	40.71	2.68	0.37
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.LM*GLEALK#.S	31.60	14.16	2.23	0.45
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.LMVELSK#.S	10.29	53.96	0.19	5.24
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.QQISLATQM*VR@.M	25.46	8.86	2.87	0.35
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.VLVDINNPEPLIQTAK#.T	98.73	35.56	2.78	0.36
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.WVGGPEIELIAIATGGR@.I	50.28	19.62	2.56	0.39
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.IADGYEQAAR@.I	21.50	5.98	3.60	0.28
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.LGFAGVVQEISFGTTK#.D	27.14	11.34	2.39	0.42
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	K.VLVDINNPEPLIQTAK#.T	20.34	7.64	2.66	0.38
P80316_TCPE_MOUSE	Cct5	T-complex protein 1 subu	R.WVGGPEIELIAIATGGR@.I	7.05	1.89	3.73	0.27
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	R.AGM*SSLK#G.-	31.64	15.99	1.98	0.51
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.ALQFLEQVK#.V	314.86	123.54	2.55	0.39
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	R.AQAALAVNISAAR@.G	49.88	15.17	3.29	0.30
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.EGIVALR@.R	145.17	50.05	2.90	0.34
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.EM*DR@ETLIDVAR@.T	156.69	59.37	2.64	0.38
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.GIDPFSLDALAK#.E	357.73	133.44	2.68	0.37
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	R.GLVLDHGAR.H	79.89	25.86	3.09	0.32
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	R.IITEGFEAAK#.E	204.27	79.35	2.57	0.39
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.M*LVSGAGDIK#.L	283.22	105.77	2.68	0.37
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.MLVSGAGDIK#.L	26.40	13.01	2.03	0.49
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.QADLYISEGLHPR@.I	143.12	64.54	2.22	0.45
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.QADLYISEGLHPR.I	17.67	5.76	3.07	0.33
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.SETDTSLIR@.G	79.75	29.61	2.69	0.37
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	R.SVTLLVK#.G	108.30	42.93	2.52	0.40
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.TEVNSGFFYK#.S	58.64	25.90	2.26	0.44
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.VATAQDDITGDGTTSNVLIIGELLK#.Q	185.46	76.76	2.42	0.41
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.VLAQNSGFDLQETLVK#.V	217.69	78.08	2.79	0.36
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.ALQFLEQVK#.V	83.22	34.84	2.39	0.42
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	R.AQAALAVNISAAR@.G	21.41	7.41	2.89	0.35
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.GIDPFSLDALAK#.E	132.10	53.65	2.46	0.41
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	R.GLQDVLR@.T	65.67	23.59	2.78	0.36
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	R.GLVLDHGAR@.H	38.19	14.54	2.63	0.38
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	R.IITEGFEAAK#.E	100.95	39.08	2.58	0.39
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.M*LVSGAGDIK#.L	73.22	32.52	2.25	0.44
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.QADLYISEGLHPR@.I	56.65	30.47	1.86	0.54
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.SETDTSLIR@.G	35.78	14.23	2.51	0.40
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.VATAQDDITGDGTTSNVLIIGELLK#.Q	105.30	37.01	2.85	0.35
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 subu	K.VLAQNSGFDLQETLVK#.V	80.99	33.76	2.40	0.42

P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 sub	K.ALQFLEQVK#.V	24.44	5.14	4.76	0.21
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 sub	K.GIDPFSLDALAK#.E	20.96	4.84	4.33	0.23
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 sub	K.VATAQDDITGDGTTSNVLIIGELLK#.Q	6.12	1.82	3.36	0.30
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 sub	K.VATAQDDITGDGTTSNVLIIGELLK#.Q	19.86	4.70	4.22	0.24
P80317_TCPZ_MOUSE	Cct6a	T-complex protein 1 sub	K.VLAQNSGFDLQETLVK#.V	18.60	8.45	2.20	0.45
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.AIK#NDSVVAGGGAIEM*ELSK#.Y	26.45	10.91	2.43	0.41
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.AIK#NDSVVAGGGAIEMELSK#.Y	4.79	3.05	1.57	0.64
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.ALEIIPR@.Q	108.61	44.53	2.44	0.41
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.ATISNDGATILK#.L	158.49	71.04	2.23	0.45
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.GGAEQFM*EETER@.S	107.63	47.07	2.29	0.44
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.GGAEQFMEETER@.S	17.69	7.84	2.26	0.44
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.IALLNVELELK#.A	33.51	16.79	2.00	0.50
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.IK#EIAVTVK#.K	35.34	18.70	1.89	0.53
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.K#VQGGALEESQLVAGVAFK#.K	22.95	12.32	1.86	0.54
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.LLDVVHPAAK#.T	36.49	16.11	2.27	0.44
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.LPIGDVATQYFADR@.D	33.78	19.77	1.71	0.59
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.NDSVVAGGGAIEM*ELSK#.Y	30.86	16.32	1.89	0.53
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.NDSVVAGGGAIEMELSK#.Y	7.47	2.79	2.68	0.37
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.SQDAEVGDGTTSVTLLAAEFLK#.Q	95.27	40.96	2.33	0.43
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.TATQLAVNK#.I	145.60	73.45	1.98	0.50
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.TFSYAGFEM*QPK#.K	56.43	24.36	2.32	0.43
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.TFSYAGFEMQPK#.K	13.60	8.54	1.59	0.63
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.VHTVEDYQAIVDAEWNILYDK#.L	8.01	4.06	1.98	0.51
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.VHTVEDYQAIVDAEWNILYDK#LEK#.I	20.84	8.75	2.38	0.42
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.VQGGALEESQLVAGVAFK#.K	42.88	16.24	2.64	0.38
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.AIK#NDSVVAGGGAIEM*ELSK#.Y	8.33	2.54	3.28	0.30
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.ALEIIPR@.Q	48.61	19.47	2.50	0.40
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.ATISNDGATILK#.L	43.94	15.26	2.88	0.35
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.GGAEQFM*EETER@.S	23.77	8.19	2.90	0.34
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.IALLNVELELK#.A	15.97	8.10	1.97	0.51
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.LPIGDVATQYFADR@.D	17.93	8.14	2.20	0.45
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.NDSVVAGGGAIEM*ELSK#.Y	8.47	4.58	1.85	0.54
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.QVK#PYVEEGLHPQIIIR@.A	55.90	19.01	2.94	0.34
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.SQDAEVGDGTTSVTLLAAEFLK#.Q	33.78	10.06	3.36	0.30
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.SQDAEVGDGTTSVTLLAAEFLK#.Q	24.30	9.45	2.57	0.39
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.TATQLAVNK#.I	37.09	14.62	2.54	0.39
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.TFSYAGFEM*QPK#.K	20.32	9.46	2.15	0.47
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.VHTVEDYQAIVDAEWNILYDK#LEK#.I	32.85	14.19	2.31	0.43
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.VQGGALEESQLVAGVAFK.K	13.14	4.24	3.10	0.32
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.AIK#NDSVVAGGGAIEM*ELSK#.Y	5.83	2.76	2.11	0.47
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.ALEIIPR@.Q	49.32	11.38	4.33	0.23
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.ATISNDGATILK#.L	26.91	5.88	4.57	0.22
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.GGAEQFM*EETER@.S	17.04	4.84	3.52	0.28
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.LPIGDVATQYFADR@.D	11.86	4.97	2.39	0.42
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.NDSVVAGGGAIEM*ELSK#.Y	12.41	3.60	3.45	0.29
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.QQLLIGAYAK#.A	30.46	5.92	5.15	0.19
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	R.SLHDAIM*IVR@.R	35.50	7.03	5.05	0.20
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.TFSYAGFEM*QPK#.K	15.26	4.94	3.09	0.32
P80313_TCPH_MOUSE	Cct7	T-complex protein 1 sub	K.VQGGALEESQLVAGVAFK#.K	15.62	5.66	2.76	0.36
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.AIAGTGANVIVTGGK#.V	104.10	51.47	2.02	0.49
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.ALAENSGVK#.A	47.07	70.69	0.67	1.50
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.APGFAQM*LK#.D	77.61	45.80	1.69	0.59
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.AVDDGVNTFK#.V	73.02	37.13	1.97	0.51
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.DVDEVSSLLR@.T	89.84	45.27	1.98	0.50
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.EDGAISTIVLR.G	19.00	8.00	2.37	0.42
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.ETEGDVTSVK#.D	50.51	21.47	2.35	0.43
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.FAEAFEAIPR@.A	127.48	69.09	1.85	0.54
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.GEENLM*DAQVK#.A	14.07	7.38	1.91	0.52
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.GSTDNLM*DDIER@.A	29.94	10.86	2.76	0.36
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.HEK#EDGAISTIVLR@.G	39.95	14.57	2.74	0.36
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.LATNAAVTVLR@.V	50.55	26.34	1.92	0.52
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.LFVTNDAATILR@.E	141.49	61.81	2.29	0.44
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.NVGLDIEAEVPAVK#DM*LEASILDTYLGK#.Y	9.73	4.78	2.03	0.49
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.QYGSETFLAK#.L	47.42	24.21	1.96	0.51
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.TAEELM*NFSK#.G	12.54	4.31	2.91	0.34
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.TAEELM*NFSKGEENLM*DAQVK.A	18.97	9.42	2.01	0.50
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.TAEELMNFSK#GEENLM*DAQVK#.A	5.53	3.46	1.60	0.63
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.TVGATALPK#.L	82.30	36.77	2.24	0.45
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.YNIM*LVR.L	34.08	17.35	1.96	0.51
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.YNIMLVR@.L	11.15	7.55	1.48	0.68
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.AIAGTGANVIVTGGK#.V	110.96	34.10	3.25	0.31
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.APGFAQM*LK#.D	69.06	24.35	2.84	0.35
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.AVDDGVNTFK#.V	79.30	37.64	2.11	0.47
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.DVDEVSSLLR@.T	71.45	24.03	2.97	0.34
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.EDGAISTIVLR@.G	17.32	5.15	3.36	0.30
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.FAEAFEAIPR@.A	93.56	29.66	3.15	0.32
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.GEENLM*DAQVK#.A	17.22	6.94	2.48	0.40
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.GSTDNLM*DDIER@.A	41.16	16.05	2.56	0.39
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.HEK#EDGAISTIVLR@.G	44.59	18.42	2.42	0.41
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.HFSGLEEAVYR.N	28.40	11.44	2.48	0.40
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.LATNAAVTVLR@.V	73.25	24.57	2.98	0.34
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.LFVTNDAATILR@.E	118.68	47.99	2.47	0.40
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.NVGLDIEAEVPAVK#.D	13.48	4.57	2.95	0.34
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.NVGLDIEAEVPAVK#DM*LEASILDTYLGK#.Y	11.02	5.50	2.00	0.50
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.TAEELM*NFSK#.G	10.44	5.12	2.04	0.49
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.TAEELM*NFSKGEENLM*DAQVK.A	15.07	5.88	2.56	0.39
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.AIAGTGANVIVTGGK#.V	56.27	17.00	3.31	0.30
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.AVDDGVNTFK#.V	32.81	9.16	3.58	0.28
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.DVDEVSSLLR@.T	56.63	14.05	4.03	0.25
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.EDGAISTIVLR@.G	22.31	5.42	4.12	0.24
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.FAEAFEAIPR@.A	74.20	24.26	3.06	0.33
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	R.GSTDNLM*DDIER@.A	30.13	8.13	3.70	0.27
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.HEK#EDGAISTIVLR@.G	27.00	5.66	4.77	0.21
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.HFSGLEEAVYR.N	23.42	8.29	2.82	0.35
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.LATNAAVTVLR@.V	56.98	15.79	3.61	0.28
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.LFVTNDAATILR@.E	66.16	18.67	3.54	0.28
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.NVGLDIEAEVPAVK#.D	21.48	4.31	4.99	0.20
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.QYGSETFLAK#.L	14.72	6.98	2.11	0.47
P42932_TCPQ_MOUSE	Cct8	T-complex protein 1 sub	K.TAEELM*NFSK#.G	13.44	3.52	3.82	0.26
Q8R422_CD109_MOUSE	Cd109	CD109 antigen OS=Mus	R.FAEENEANLVDFEDASSVNNVHVR@.K	9.72	4.81	2.02	0.50
Q8R422_CD109_MOUSE	Cd109	CD109 antigen OS=Mus	K.IPVQLVFENK#.V	9.36	5.86	1.60	0.63
Q6XJV6_MO2R2_MOUSE	Cd200r1l	Cell surface glycoprotein	K.ETNETCLGR@.N	31.71	1.92	16.50	0.06
Q9CWK3_CD2B2_MOUSE	Cd2bp2	CD2 antigen cytoplasmic	R.LSGLADQM*VAR@.G	8.67	1.64	5.29	0.19

Q9CWK3_CD2B2_MOUSE	Cd2bp2	CD2 antigen cytoplasmic	K.VTFQGVGDEDGEDEISVPK#.K	11.69	3.89	3.01	0.33
Q76KJ5_RPA34_MOUSE	Cd3eap	DNA-directed RNA polym	R.EATLLASSSEAGGR@.L	15.20	5.03	3.02	0.33
Q76KJ5_RPA34_MOUSE	Cd3eap	DNA-directed RNA polym	K.GTETSQVEHTEPVAQTEPPEGTFLFPTK#.K	5.48	3.25	1.69	0.59
Q76KJ5_RPA34_MOUSE	Cd3eap	DNA-directed RNA polym	R.IM*EGPQEYLLSR@.V	3.36	2.95	1.14	0.88
Q76KJ5_RPA34_MOUSE	Cd3eap	DNA-directed RNA polym	R.VFTSSPQAR@.E	18.65	7.10	2.63	0.38
P15379_CD44_MOUSE	Cd44	CD44 antigen OS=Mus m	R.NLQSVDM*K#.I	7.55	5.05	1.50	0.67
P15379_CD44_MOUSE	Cd44	CD44 antigen OS=Mus m	R.YGFIEGNVVIPR@.I	31.58	13.10	2.41	0.41
P15379_CD44_MOUSE	Cd44	CD44 antigen OS=Mus m	R.YGFIEGNVVIPR@.I	9.49	5.34	1.78	0.56
Q61735_CD47_MOUSE	Cd47	Leukocyte surface antige	K.ISVSDLINGIASLK#.M	34.87	17.54	1.99	0.50
Q61735_CD47_MOUSE	Cd47	Leukocyte surface antige	R.NVEAQSTEEMFVK#.W	9.15	3.37	2.71	0.37
P35762_CD81_MOUSE	Cd81	CD81 antigen OS=Mus m	K.QFYDQALQQAVM*DDDANNAK#.A	15.89	5.25	3.03	0.33
P40240_CD9_MOUSE	Cd9	CD9 antigen OS=Mus mu	R.SK#DEPQR@ETLK#.A	6.33	1.37	4.61	0.22
Q8R349_CDC16_MOUSE	Cdc16	Cell division cycle protei	K.K#YNK#PSETVIPESVDGLQENLDVVVSLAER@.H	4.43	1.87	2.36	0.42
Q8R349_CDC16_MOUSE	Cdc16	Cell division cycle protei	K.YNK#PSETVIPESVDGLQENLDVVVSLAER@.H	6.32	3.28	1.93	0.52
Q8BGZ4_CDC23_MOUSE	Cdc23	Cell division cycle protei	K.ALSIFNELR@.K	11.34	3.06	3.70	0.27
Q8BGZ4_CDC23_MOUSE	Cdc23	Cell division cycle protei	R.IENM*DTFSNLLYVR@.S	6.13	1.80	3.40	0.29
Q8BGZ4_CDC23_MOUSE	Cdc23	Cell division cycle protei	K.LNQLVEAK#.K	8.19	3.44	2.38	0.42
Q8BGZ4_CDC23_MOUSE	Cdc23	Cell division cycle protei	K.NTSAAIQAYR@.H	6.39	2.31	2.77	0.36
Q61081_CDC37_MOUSE	Cdc37	Hsp90 co-chaperone Cdc	K.ELEVAESDGQVELER@.L	7.04	3.10	2.27	0.44
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	K.EVQYNPTYETM*FAPEFGPENPFR.T	5.93	8.05	0.74	1.36
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	R.HLGAVNTIVFVDENRR.F	37.41	24.34	1.54	0.65
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	K.LNIWDWK.T	7.76	8.92	0.87	1.15
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	R.SGEIVQEYDR.H	27.56	23.81	1.16	0.86
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	R.SYLHIPQDVGVNLR@.S	20.59	15.86	1.30	0.77
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	R.TFATYGYALDPSLDNHQVSAK#.Y	16.70	13.60	1.23	0.81
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	R.VWEWDIPVDFK#.Y	21.77	19.10	1.14	0.88
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	K.YIGSVEEAEK#NQGLTVFETGQK#.K	17.78	19.50	0.91	1.10
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	K.EVQYNPTYETM*FAPEFGPENPFR@.T	7.40	2.12	3.49	0.29
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	K.FK#ENDASNIDGFLGPWAK#.Y	9.72	3.62	2.68	0.37
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	R.SYLHIPQDVGVNLR@.S	28.43	5.97	4.76	0.21
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	R.VWEWDIPVDFK#.Y	15.70	7.48	2.10	0.48
Q9DC48_PRP17_MOUSE	Cdc40	Pre-mRNA-processing fac	K.YIGSVEEAEK#NQGLTVFETGQK#.K	20.21	7.93	2.55	0.39
P60766_CDC42_MOUSE	Cdc42	Cell division control prot	K.NVFDEAILAALEPPEPK#.K	7.36	4.28	1.72	0.58
P60766_CDC42_MOUSE	Cdc42	Cell division control prot	K.NVFDEAILAALEPPEPK#.K	12.73	5.58	2.28	0.44
P60766_CDC42_MOUSE	Cdc42	Cell division control prot	K.TPFLLVGTQIDLR@DDPSTIEK#.L	20.76	6.12	3.39	0.29
P60766_CDC42_MOUSE	Cdc42	Cell division control prot	K.TPFLLVGTQIDLR@DDPSTIEK#.L	4.97	3.27	1.52	0.66
P60766_CDC42_MOUSE	Cdc42	Cell division control prot	K.NVFDEAILAALEPPEPK#.K	13.48	7.37	1.83	0.55
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	R.GAFGEVAVVK#.L	11.68	6.13	1.91	0.52
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	K.SM*TQSNTLTK#DEDVQR@.D	7.30	2.55	2.86	0.35
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	K.AVLAAAIVDGDR@.I	37.66	8.52	4.42	0.23
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	R.GAFGEVAVVK#.L	23.76	6.33	3.75	0.27
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	R.GYLQALASK#.M	10.62	5.04	2.11	0.47
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	R.HSEM*EEAIGTVK#.D	4.88	1.47	3.32	0.30
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	R.K#LQESTQTVQSLHGSTR@.A	16.92	4.56	3.71	0.27
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	R.LEDAAAEASK#.E	16.31	6.67	2.44	0.41
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	R.LELQSALEAEIR@.A	11.01	6.74	1.63	0.61
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	K.LFLYDLPEGK#.S	7.68	5.40	1.42	0.70
Q7TT50_MRCKB_MOUSE	Cdc42bpb	Serine/threonine-protei	K.R@LNEELER@.M	9.90	5.60	1.77	0.57
Q91W92_BORG5_MOUSE	Cdc42ep1	Cdc42 effector protein 1	R.EQSSFPSEPTPNPELR@.R	4.58	3.18	1.44	0.69
Q91W92_BORG5_MOUSE	Cdc42ep1	Cdc42 effector protein 1	R.M*ASPAAPSPAPPPISPIIK#.N	14.54	8.06	1.80	0.55
Q91W92_BORG5_MOUSE	Cdc42ep1	Cdc42 effector protein 1	R.M*ASPAAPSPAPPPISPIIK.N	2.45	6.08	0.40	2.48
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.AQDALVQEM*EVVK#.Q	6.37	3.47	1.84	0.54
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.EIDDTYIEDAADVDAR@.K	6.93	7.66	0.90	1.11
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.ESDLPSAILQTSGVSEFTK#.K	5.72	4.56	1.25	0.80
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.GVDYNAEIPFEK#.K	10.82	9.34	1.16	0.86
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.LGLLGLPAPK.N	12.42	10.06	1.23	0.81
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.LVLPAPQISDAELQEVVK.V	11.27	9.66	1.17	0.86
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.AQDALVQEM*EVVK#.Q	5.60	4.80	1.17	0.86
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.AAGIEIQK#.K	21.03	14.13	1.49	0.67
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.AQDALVQEM*EVVK#.Q	17.59	12.33	1.43	0.70
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.AQDALVQEMEVVK#.Q	7.41	3.83	1.94	0.52
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.DK#LNINPEDGM*ADYSDPSYVK#.Q	15.17	4.94	3.07	0.33
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.DLPR@PSEVNETILR@PLNVEPPLTDLQK#.S	67.47	35.41	1.91	0.52
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.EIDDTYIEDAADVDAR@.K	15.37	10.35	1.49	0.67
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.ESDLPSAILQTSGVSEFTK#.K	22.49	12.29	1.83	0.55
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.GVDYNAEIPFEK#.K	40.97	25.62	1.60	0.63
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.ILLGGYQSR@.A	54.72	22.76	2.40	0.42
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.ILQEAQNLM*ALTNVDTPLK#.G	19.74	15.41	1.28	0.78
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.ILQEAQNLM*ALTNVDTPLK#.G	5.88	4.96	1.19	0.84
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.K#PALGFYDTSEENYQALDADFR@.K	9.45	6.52	1.45	0.69
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.K#PALGFYDTSEENYQALDADFR@K#.L	4.79	3.10	1.54	0.65
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.LGLLGLPAPK#.N	56.52	28.66	1.97	0.51
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.LNINPEDGM*ADYSDPSYVK#.Q	10.37	8.57	1.21	0.83
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.LVLPAPQISDAELQEVVK#.V	40.99	24.33	1.68	0.59
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.NDFEIVLPENAEK#ELEER@.E	29.41	15.38	1.91	0.52
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.NVGFATNNSEHITYLEHSPYEK#.F	12.61	9.74	1.29	0.77
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.QQDLDGELR@.S	25.77	12.87	2.00	0.50
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.QTAEESGITNSASSTLLSEYNVTNNSIALR@.T	11.89	4.86	2.45	0.41
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.SGTTPK#PVTNATPGR@.T	29.81	20.05	1.49	0.67
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	R.SK#LVLPAPQISDAELQEVVK#.V	14.11	7.57	1.87	0.54
Q6A068_CDC5L_MOUSE	Cdc5l	Cell division cycle 5-like	K.VGQASEVAR@.Q	31.96	17.39	1.84	0.54
Q8JZM7_CDC73_MOUSE	Cdc73	Parafibromin OS=Mus mu	K.NIFAILQSVK#.A	9.88	8.14	1.21	0.82
Q8JZM7_CDC73_MOUSE	Cdc73	Parafibromin OS=Mus mu	R.SAPLEIGLQR@.S	4.89	4.10	1.20	0.84
Q8JZM7_CDC73_MOUSE	Cdc73	Parafibromin OS=Mus mu	K.NIFAILQSVK#.A	9.18	6.87	1.34	0.75
Q14B71_CDCA2_MOUSE	Cdca2	Cell division cycle-associ	R.DLENTGLVWLSPSPSTLQK#PR@.R	2.33	1.32	1.77	0.57
Q8BHX3_BOREA_MOUSE	Cdca8	Borealin OS=Mus muscul	K.ADR@DITEINNLTAEAIQTPLK#.S	6.40	13.03	0.49	2.04
Q8BHX3_BOREA_MOUSE	Cdca8	Borealin OS=Mus muscul	K.EVENLYNIEILR.L	6.28	11.28	0.56	1.80
Q8BHX3_BOREA_MOUSE	Cdca8	Borealin OS=Mus muscul	R.IDIAQLNPEALGNIR.K	7.38	16.21	0.46	2.19
Q8BHX3_BOREA_MOUSE	Cdca8	Borealin OS=Mus muscul	K.VIEVEESIKEEEEEEEEGGGGGGR.T	4.66	7.69	0.61	1.65
Q8VDP6_CDIPT_MOUSE	Cdipt	CDP-diacylglycerol--inosi	R.M*GLWVTAPIALLK#.S	10.07	4.81	2.09	0.48
Q8VDP6_CDIPT_MOUSE	Cdipt	CDP-diacylglycerol--inosi	K.M*IDLSGNPVLR@.I	6.11	2.68	2.28	0.44
Q8VDP6_CDIPT_MOUSE	Cdipt	CDP-diacylglycerol--inosi	R.NM*AALDAADR@.A	8.74	5.21	1.68	0.60
Q8VDP6_CDIPT_MOUSE	Cdipt	CDP-diacylglycerol--inosi	K.SVISVIHLITAAR@.N	11.10	6.38	1.74	0.57
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.AFGIPIR.V	183.66	64.29	2.86	0.35
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.ALGTPNNEVWPEVESLQDYK#.N	28.55	9.35	3.05	0.33
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.ALGTPNNEVWPEVESLQDYK#.N	16.80	7.73	2.17	0.46
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.DLK#PQNLLIDDK#.G	31.67	17.04	1.86	0.54
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.DLK#PQNLLIDDK#GTIK#.L	70.68	37.22	1.90	0.53
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.DLKPQNLLIDDKGTIK.L	45.07	25.85	1.74	0.57
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.HPNIVSLQDVLM*QDSR@.L	52.24	21.27	2.46	0.41
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.HPNIVSLQDVLMQDSR@.L	6.70	2.88	2.32	0.43
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.HPYFDDLDNQIK#.K	29.12	11.75	2.48	0.40
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.IGEGTYGVVYK#.G	131.82	59.25	2.22	0.45

P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.IR@LESEEEGVPSTAIR@.E	154.41	48.96	3.15	0.32
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.K#PLFHGDSEIDQLFR@.I	52.57	17.72	2.97	0.34
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.LESEEEGVPSTAIR@.E	89.46	31.44	2.85	0.35
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.NLDENGLDLLSK#.M	71.00	32.19	2.21	0.45
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.SPEVLLGSAR.Y	202.34	75.53	2.68	0.37
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.VTGQIVAM*K#K#.I	9.05	2.97	3.05	0.33
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.VYTHEVVTLWYR@.S	46.44	13.97	3.32	0.30
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.YLDSIPPGQFM*DSSLVK#.S	11.84	6.01	1.97	0.51
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.DLK#PQNLLIDDK#GTIK#.L	14.31	6.17	2.32	0.43
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.HPNIVSLQDVLM*QDSR@.L	12.90	8.24	1.57	0.64
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.IGEGTYGVVYK#.G	33.87	15.24	2.22	0.45
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.KPLFHGDSEIDQLFR.I	17.59	10.90	1.61	0.62
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.LESEEEGVPSTAIR@.E	9.75	5.83	1.67	0.60
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.SPEVLLGSAR@.Y	37.21	18.62	2.00	0.50
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.VYTHEVVTLWYR@.S	10.63	3.79	2.81	0.36
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.AFGIPIR@.V	30.43	14.43	2.11	0.47
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.HPNIVSLQDVLM*QDSR@.L	10.75	3.03	3.54	0.28
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.HPYFDDLDNQIK#.K	3.83	2.72	1.41	0.71
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.IGEGTYGVVYK#.G	36.98	19.53	1.89	0.53
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	K.K#PLFHGDSEIDQLFR@.I	8.01	6.55	1.22	0.82
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.LESEEEGVPSTAIR@.E	15.43	6.89	2.24	0.45
P11440_CDK1_MOUSE	Cdk1	Cyclin-dependent kinase	R.SPEVLLGSAR@.Y	38.18	19.26	1.98	0.50
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	R.APELLLGAK#.E	51.91	30.65	1.69	0.59
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	R.ETPLPIDPSM*FPTWPAK#.S	9.41	4.74	1.99	0.50
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	R.FGALLSDQGFDLM*NK#.F	21.85	4.95	4.41	0.23
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	R.IEEGTYGVVYR@.A	34.15	12.48	2.74	0.37
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	K.M*TFSEYPYNNLR@.K	13.98	4.89	2.86	0.35
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	K.SDIDQINK#.I	36.55	11.55	3.17	0.32
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	K.TLM*IQLLSGVK#.H	10.46	2.95	3.55	0.28
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	K.TSNLLLSHAGILK#.V	49.44	16.53	2.99	0.33
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	R.APELLLGAK#.E	15.15	19.84	0.76	1.31
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	R.IEEGTYGVVYR@.A	10.15	3.32	3.05	0.33
P24788_CD11B_MOUSE	Cdk11b	Cyclin-dependent kinase	K.TSNLLLSHAGILK#.V	26.18	7.93	3.30	0.30
Q69ZA1_CDK13_MOUSE	Cdk13	Cyclin-dependent kinase	R.GGDVSPSPYSSSSWR@.R	3.05	1.77	1.73	0.58
Q69ZA1_CDK13_MOUSE	Cdk13	Cyclin-dependent kinase	K.K#PIFQANQELAQLELISR@.I	6.13	5.09	1.21	0.83
Q69ZA1_CDK13_MOUSE	Cdk13	Cyclin-dependent kinase	K.SLGGVQPSQTIQPK#.V	4.66	2.01	2.32	0.43
Q69ZA1_CDK13_MOUSE	Cdk13	Cyclin-dependent kinase	K.VDNNLTVEK#.A	7.70	3.70	2.08	0.48
P97377_CDK2_MOUSE	Cdk2	Cyclin-dependent kinase	R.ALFPGDSEIDQLFR@.I	39.31	15.44	2.55	0.39
P97377_CDK2_MOUSE	Cdk2	Cyclin-dependent kinase	R.DLK#PQNLLINAEGSIK#.L	14.53	5.40	2.69	0.37
P97377_CDK2_MOUSE	Cdk2	Cyclin-dependent kinase	R.ALFPGDSEIDQLFR@.I	17.71	3.01	5.88	0.17
P97377_CDK2_MOUSE	Cdk2	Cyclin-dependent kinase	R.ALFPGDSEIDQLFR@.I	20.00	5.53	3.62	0.28
Q8K389_CK5P2_MOUSE	Cdk5rap2	CDK5 regulatory subunit	K.SQM*ASPDENVSSGELR@.G	4.90	1.41	3.48	0.29
Q03147_CDK7_MOUSE	Cdk7	Cyclin-dependent kinase	R.APELLFGAR@.M	13.69	6.42	2.13	0.47
Q03147_CDK7_MOUSE	Cdk7	Cyclin-dependent kinase	R.VPFLPGDSDLDQLTR@.I	15.53	6.57	2.36	0.42
Q03147_CDK7_MOUSE	Cdk7	Cyclin-dependent kinase	R.VPFLPGDSDLDQLTR@.I	9.34	4.39	2.13	0.47
Q03147_CDK7_MOUSE	Cdk7	Cyclin-dependent kinase	R.APELLFGAR@.M	11.40	5.01	2.28	0.44
Q03147_CDK7_MOUSE	Cdk7	Cyclin-dependent kinase	K.LDFLGEGQFATVYK#.A	6.17	9.80	0.63	1.59
Q03147_CDK7_MOUSE	Cdk7	Cyclin-dependent kinase	R.VPFLPGDSDLDQLTR@.I	8.84	3.58	2.47	0.41
Q99J95_CDK9_MOUSE	Cdk9	Cyclin-dependent kinase	K.AYVR@DPYALDLIDK#.L	13.15	6.35	2.07	0.48
Q99J95_CDK9_MOUSE	Cdk9	Cyclin-dependent kinase	K.IGQGTFGEVFK#.A	12.79	5.10	2.51	0.40
Q99J95_CDK9_MOUSE	Cdk9	Cyclin-dependent kinase	R.NPATTNQTEFER@.V	16.32	4.82	3.38	0.30
Q99J95_CDK9_MOUSE	Cdk9	Cyclin-dependent kinase	K.AANVLITR@.D	10.86	2.75	3.95	0.25
Q99J95_CDK9_MOUSE	Cdk9	Cyclin-dependent kinase	R.NPATTNQTEFER@.V	8.74	3.47	2.52	0.40
P46414_CDN1B_MOUSE	Cdkn1b	Cyclin-dependent kinase	K.VLAQESQDVSGSR@.Q	2.70	1.25	2.17	0.46
P51480_CD2A1_MOUSE	Cdkn2a	Cyclin-dependent kinase	R.ALLEAGVSPNAPNSFGR@.T	7.98	6.27	1.27	0.79
P51480_CD2A1_MOUSE	Cdkn2a	Cyclin-dependent kinase	R.LPLDLAQER@.G	12.01	10.19	1.18	0.85
Q64364_CD2A2_MOUSE	Cdkn2a	Cyclin-dependent kinase	R.NPGPGDDDGQR@.S	26.88	10.21	2.63	0.38
Q8BI72_CARF_MOUSE	Cdkn2aip	CDKN2A-interacting prot	K.SGASLGSVSQLAAK#.S	9.43	5.81	1.62	0.62
Q8BI72_CARF_MOUSE	Cdkn2aip	CDKN2A-interacting prot	K.SSSEANISSSVSK#.N	16.65	4.93	3.38	0.30
Q8BI72_CARF_MOUSE	Cdkn2aip	CDKN2A-interacting prot	K.STAQVAASLLATK#.S	8.26	4.71	1.75	0.57
Q8BI72_CARF_MOUSE	Cdkn2aip	CDKN2A-interacting prot	K.SSSEANISSSVSK#.N	10.58	3.56	2.97	0.34
Q8BI72_CARF_MOUSE	Cdkn2aip	CDKN2A-interacting prot	R.GSEIEDLVLLDEEAR@PVNLPPALK#.H	3.81	2.36	1.61	0.62
Q8BI72_CARF_MOUSE	Cdkn2aip	CDKN2A-interacting prot	K.SGASLGSVSQLAAK#.S	12.67	6.42	1.98	0.51
Q8BI72_CARF_MOUSE	Cdkn2aip	CDKN2A-interacting prot	K.SSSEANISSSVSK#.N	14.38	3.77	3.82	0.26
Q8BI72_CARF_MOUSE	Cdkn2aip	CDKN2A-interacting prot	K.SSSETASSGLTSK#.S	6.98	2.36	2.96	0.34
Q8R4E9_CDT1_MOUSE	Cdt1	DNA replication factor C	R.AR@PPAEPGSDQPAPLAR@.R	14.16	7.13	1.98	0.50
Q8R4E9_CDT1_MOUSE	Cdt1	DNA replication factor C	K.AVDLAGLTAR@.L	248.99	103.88	2.40	0.42
Q8R4E9_CDT1_MOUSE	Cdt1	DNA replication factor C	R.FHALAQPGLPGLVLPYK#.Y	13.50	2.98	4.53	0.22
Q8R4E9_CDT1_MOUSE	Cdt1	DNA replication factor C	K.STTVYVGQQPGK#.I	8.07	3.72	2.17	0.46
Q8R4E9_CDT1_MOUSE	Cdt1	DNA replication factor C	R.VQENAVEPSTPDAK#.V	13.69	3.43	3.99	0.25
P28033_CEBPB_MOUSE	Cebpb	CCAAT/enhancer-binding	K.VLELTAENER@.L	11.20	11.35	0.99	1.01
P28033_CEBPB_MOUSE	Cebpb	CCAAT/enhancer-binding	K.VLELTAENER.L	3.32	7.11	0.47	2.14
P53569_CEBPZ_MOUSE	Cebpz	CCAAT/enhancer-binding	K.EESQIPVDEVFFYR@.Y	9.55	7.27	1.31	0.76
P53569_CEBPZ_MOUSE	Cebpz	CCAAT/enhancer-binding	K.ELLITDLLPDSR@.K	13.23	20.08	0.66	1.52
P53569_CEBPZ_MOUSE	Cebpz	CCAAT/enhancer-binding	K.K#GTIDDLQQGELESFIQNLNLAK#.Y	11.88	7.12	1.67	0.60
P53569_CEBPZ_MOUSE	Cebpz	CCAAT/enhancer-binding	K.QAM*FLNLIYK#.S	5.34	3.32	1.61	0.62
P53569_CEBPZ_MOUSE	Cebpz	CCAAT/enhancer-binding	K.EESQIPVDEVFFYR@.Y	9.86	3.84	2.57	0.39
P53569_CEBPZ_MOUSE	Cebpz	CCAAT/enhancer-binding	K.K#GTIDDLQQGELESFIQNLNLAK#.Y	16.35	6.79	2.41	0.42
P53569_CEBPZ_MOUSE	Cebpz	CCAAT/enhancer-binding	K.QAM*FLNLIYK#.S	8.54	2.74	3.11	0.32
P28659_CELF1_MOUSE	Celf1	CUGBP Elav-like family m	K.AALEAQNALHNM*K#.V	8.11	4.31	1.88	0.53
P28659_CELF1_MOUSE	Celf1	CUGBP Elav-like family m	R.ELFEQYGAVYEINILR@.D	15.25	8.75	1.74	0.57
P28659_CELF1_MOUSE	Celf1	CUGBP Elav-like family m	R.ELFEQYGAVYEINILR@.D	12.24	6.26	1.96	0.51
P28659_CELF1_MOUSE	Celf1	CUGBP Elav-like family m	K.M*FVGQVPR@.T	14.30	7.84	1.83	0.55
P28659_CELF1_MOUSE	Celf1	CUGBP Elav-like family m	K.M*FVGQVPR@.T	4.76	1.80	2.64	0.38
Q6RT24_CENPE_MOUSE	Cenpe	Centromere-associated p	K.SLK#ETTEQLSEVYQTLTASQSVVHLHPTVQPSTR@.D	2.50	2.50	1.00	1.00
Q9CPQ5_CENPQ_MOUSE	Cenpq	Centromere protein Q OS	K.IQILTSEVEEEEQEVK#.Q	5.14	1.65	3.12	0.32
Q3TJM4_CENPT_MOUSE	Cenpt	Centromere protein T OS	R.NILLTAPESSTVM*PDPVVKPAQVPEVAR.S	2.05	2.75	0.74	1.34
Q8C4M7_CENPU_MOUSE	Cenpu	Centromere protein U OS	R.LHSAQLSPVDETPATQSQLK#.T	8.15	4.95	1.65	0.61
Q8C4M7_CENPU_MOUSE	Cenpu	Centromere protein U OS	R.NLDPSEDEASGNESIK#.V	4.85	2.63	1.85	0.54
Q8C4M7_CENPU_MOUSE	Cenpu	Centromere protein U OS	K.YDSSSLPALLFK#.A	10.35	5.70	1.81	0.55
Q62036_CP131_MOUSE	Cep131	Centrosomal protein of 1	R.ATLDDLLDTLK#.L	13.14	7.02	1.87	0.53
Q62036_CP131_MOUSE	Cep131	Centrosomal protein of 1	K.LSAAPGPPDDGTLLSEAK#.L	6.97	3.17	2.20	0.45
Q62036_CP131_MOUSE	Cep131	Centrosomal protein of 1	R.ATLDDLLDTLK#.L	16.32	5.51	2.96	0.34
Q62036_CP131_MOUSE	Cep131	Centrosomal protein of 1	K.LSAAPGPPDDGTLLSEAK#.L	7.65	2.80	2.74	0.37
Q62036_CP131_MOUSE	Cep131	Centrosomal protein of 1	R.VK#VELAELQAR@.Q	12.65	5.35	2.36	0.42
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.DEVM*GDNLLLSSVFQFSR@.K	4.68	1.33	3.52	0.28
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.FNPDGEEEDVTVHE.-	19.37	19.37	1.00	1.00
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.M*QSTGSAM*PASSSFK#.H	7.36	3.21	2.29	0.44
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.VFDESLNFR@.K	10.75	5.79	1.86	0.54
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	K.DTEAVMAFLEAK#.L	6.02	3.33	1.81	0.55
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.FNPDGEEEDVTVHE.-	12.82	12.82	1.00	1.00
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.IDLLAQPR@.R	25.16	9.06	2.78	0.36
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.ISQDLALIAR@.E	27.15	10.09	2.69	0.37

Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.LGEASDSELADADK#.A	8.87	3.34	2.65	0.38
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.LGEASDSELADADK#ASVASEVSTTSSTSK#PPTGR@.R	21.86	6.54	3.34	0.30
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.M*QSTGSAM*PASSSFK#.H	7.90	2.58	3.06	0.33
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.SDSLDTDSSM*DTTLILK#.D	7.52	2.72	2.76	0.36
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	K.TSSM*EISSILQELK#.R	15.30	2.45	6.25	0.16
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.VFDESLNFR@.K	16.99	6.66	2.55	0.39
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	K.ASPGTQDLPGIQTGM*M*APENK#.V	6.16	2.21	2.79	0.36
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.EINDVAGEIDSVTSSGTAPSTTVSTAATTPGSAIDTR@.E	6.61	1.94	3.41	0.29
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.FNPDGEEEDVTVHE.-	11.02	11.02	1.00	1.00
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	K.GTDSK#VEAAAEVQPR@.A	9.31	4.61	2.02	0.50
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.IDLLAQPR@.R	26.34	6.79	3.88	0.26
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.ISQDLALIAR@.E	30.37	10.25	2.96	0.34
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.LGEASDSELADADK#.A	7.80	2.26	3.45	0.29
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.M*QSTGSAM*PASSSFK#.H	10.00	2.72	3.68	0.27
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.SDSEATISR@.S	8.68	4.23	2.05	0.49
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	R.SDSLDTDSSM*DTTLILK#.D	8.41	4.42	1.90	0.53
Q6A065_CE170_MOUSE	Cep170	Centrosomal protein of 1	K.TSSM*EISSILQELK#.R	13.33	3.01	4.44	0.23
Q80U49_C170B_MOUSE	Cep170b	Centrosomal protein of 1	K.TASVSGASAEASGEQVR@.L	9.74	3.91	2.49	0.40
Q80U49_C170B_MOUSE	Cep170b	Centrosomal protein of 1	K.ETTPVETVSAETK#.V	6.91	2.31	2.99	0.33
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	K.EVEDLNQLLSSQR@.K	6.08	2.25	2.70	0.37
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	R.ILYDSLLK#.H	52.48	16.59	3.16	0.32
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	K.K#IESEGYLQVEK#.Q	25.12	9.87	2.55	0.39
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	K.LR@EESSIFK#.G	10.76	4.62	2.33	0.43
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	K.NQQWLVYDQQR@.E	9.71	3.09	3.14	0.32
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	K.NVYYLLEK#.D	16.05	5.74	2.79	0.36
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	K.QLHGFTITEQPFPLQR@.E	12.94	5.33	2.43	0.41
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	R.SEELLSQVR@.I	21.97	8.93	2.46	0.41
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	K.TSLDEITSGK#.G	22.95	7.84	2.93	0.34
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	R.YSSSSLFEQLEEK#.T	17.18	6.80	2.53	0.40
Q8BT07_CEP55_MOUSE	Cep55	Centrosomal protein of 5	K.SQITQLESLK#.Q	10.53	2.54	4.14	0.24
Q8BMK0_CEP85_MOUSE	Cep85	Centrosomal protein of 8	K.ELSVQNQDLIEK#.N	5.91	2.57	2.30	0.44
Q924Z4_CERS2_MOUSE	Cers2	Ceramide synthase 2 OS=	R.AGTLIM*ALHDASDYLLESAK#.M	12.02	6.38	1.88	0.53
Q924Z4_CERS2_MOUSE	Cers2	Ceramide synthase 2 OS=	K.QVEVDLLSR@.Q	13.04	1.62	8.07	0.12
Q9R1K9_CETN2_MOUSE	Cetn2	Centrin-2 OS=Mus muscu	R.EAFDLFDADGTGTIDIK#.E	7.55	3.67	2.06	0.49
Q9R1K9_CETN2_MOUSE	Cetn2	Centrin-2 OS=Mus muscu	K.ELGENLTDEELQEM*IDEADR@DGDGEVNEQEFLR@.I	2.86	1.81	1.58	0.63
Q9R1K9_CETN2_MOUSE	Cetn2	Centrin-2 OS=Mus muscu	K.M*NFSDFLTVM*TQK#.M	4.91	3.55	1.38	0.72
O35648_CETN3_MOUSE	Cetn3	Centrin-3 OS=Mus muscu	K.DAFELFDTDK#DQAIDYHELK#.V	8.72	3.34	2.61	0.38
Q8BTU1_CFA20_MOUSE	Cfap20	Cilia- and flagella-associa	K.LPFLVM*IIK#.N	5.68	2.60	2.18	0.46
Q8BTU1_CFA20_MOUSE	Cfap20	Cilia- and flagella-associa	R.LYSEDELPAEFK#.L	22.64	14.49	1.56	0.64
Q8BTU1_CFA20_MOUSE	Cfap20	Cilia- and flagella-associa	R.LYSEDELPAEFK#.L	5.42	6.04	0.90	1.11
Q8BTU1_CFA20_MOUSE	Cfap20	Cilia- and flagella-associa	R.LYSEDELPAEFK#.L	9.10	10.69	0.85	1.17
Q9D439_CFA53_MOUSE	Cfap53	Cilia- and flagella-associa	K.IESMQR@EYR@.E	8.68	1.98	4.38	0.23
P18760_COF1_MOUSE	Cfl1	Cofilin-1 OS=Mus muscul	K.EILVGDVGQTVDDPYTTFVK#.M	3.66	1.73	2.11	0.47
P18760_COF1_MOUSE	Cfl1	Cofilin-1 OS=Mus muscul	K.LGGSAVISLEGK#PL.-	29.86	19.86	1.50	0.67
P18760_COF1_MOUSE	Cfl1	Cofilin-1 OS=Mus muscul	K.NIILEEGKEILVGDVGQTVDDPYTTFVK.M	12.35	10.50	1.18	0.85
P18760_COF1_MOUSE	Cfl1	Cofilin-1 OS=Mus muscul	R.YALYDATYETK#.E	16.11	11.22	1.44	0.70
Q8BHG9_CGBP1_MOUSE	Cggbp1	CGG triplet repeat-bindi	K.ASVIQDFVK#.M	17.84	12.47	1.43	0.70
Q8BHG9_CGBP1_MOUSE	Cggbp1	CGG triplet repeat-bindi	K.TALYVTPLDR@.V	19.80	17.00	1.16	0.86
P59242_CING_MOUSE	Cgn	Cingulin OS=Mus muscul	R.DQVDQLR@.T	31.53	12.54	2.52	0.40
P59242_CING_MOUSE	Cgn	Cingulin OS=Mus muscul	R.ELEQQNLQLQK#.T	5.51	1.93	2.85	0.35
P59242_CING_MOUSE	Cgn	Cingulin OS=Mus muscul	R.ELLEELLEGK#.Q	9.73	6.87	1.42	0.71
P59242_CING_MOUSE	Cgn	Cingulin OS=Mus muscul	R.GLAEGGEAVEAR@.L	9.71	2.92	3.33	0.30
P59242_CING_MOUSE	Cgn	Cingulin OS=Mus muscul	R.LASSEGFQK#PSASLSQLESQNQLLQER@.L	3.46	1.49	2.32	0.43
Q6AW69_CGNL1_MOUSE	Cgnl1	Cingulin-like protein 1 O	R.ELSQVSQEQK#.E	6.74	3.76	1.79	0.56
Q6AW69_CGNL1_MOUSE	Cgnl1	Cingulin-like protein 1 O	K.GALIEELLQAK#.Q	16.27	8.37	1.94	0.51
Q6AW69_CGNL1_MOUSE	Cgnl1	Cingulin-like protein 1 O	K.GQQELTQQTNEETAK#.Q	12.01	6.28	1.91	0.52
Q6AW69_CGNL1_MOUSE	Cgnl1	Cingulin-like protein 1 O	K.SLEELFQVK#.M	9.29	5.56	1.67	0.60
Q6AW69_CGNL1_MOUSE	Cgnl1	Cingulin-like protein 1 O	R.YIPFLPGTGR@.D	8.10	5.29	1.53	0.65
Q6AW69_CGNL1_MOUSE	Cgnl1	Cingulin-like protein 1 O	K.GALIEELLQAK#.Q	8.24	3.74	2.20	0.45
Q9QWF0_CAF1A_MOUSE	Chaf1a	Chromatin assembly fact	K.LVGGQGPIDSFLR@.A	9.90	9.85	1.00	1.00
Q9QWF0_CAF1A_MOUSE	Chaf1a	Chromatin assembly fact	K.VPVVVLEDILATKPSIASLPM*M*SLDR.S	6.74	10.09	0.67	1.50
Q9D0N7_CAF1B_MOUSE	Chaf1b	Chromatin assembly fact	K.AIVEFLSNLAR.H	10.18	8.90	1.14	0.87
Q9D0N7_CAF1B_MOUSE	Chaf1b	Chromatin assembly fact	R.LASAGVDTAVR@.I	6.36	6.90	0.92	1.09
Q9D0N7_CAF1B_MOUSE	Chaf1b	Chromatin assembly fact	K.AIVEFLSNLAR@.H	12.91	4.91	2.63	0.38
Q9D0N7_CAF1B_MOUSE	Chaf1b	Chromatin assembly fact	R.LASAGVDTAVR@.I	5.36	4.86	1.10	0.91
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.APELSEEIQLEAVDNAK#.C	4.33	4.32	1.00	1.00
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.EAFISEEEIAK#.Y	7.52	4.17	1.80	0.55
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	R.K#HVFLPELPK#.S	12.96	5.12	2.53	0.40
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.LM*EALESPLEEQQI.-	7.18	7.18	1.00	1.00
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.AFLLESLLK#.N	38.85	20.46	1.90	0.53
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.APELSEEIQLEAVDNAK#.C	8.69	6.24	1.39	0.72
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.DSQENSDAELSSSEYIR@.A	7.20	4.26	1.69	0.59
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	R.K#HVFLPELPK#.S	15.37	17.89	0.86	1.16
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.LM*EALESPLEEQQI.-	16.73	16.73	1.00	1.00
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.NVLQFTEEK#EAFISEEEIAK#.Y	4.97	2.81	1.77	0.57
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.SALVSSK#PPK#.H	10.84	6.26	1.73	0.58
Q8K327_CHAP1_MOUSE	Champ1	Chromosome alignment-	K.TSPASLDFPEPQK#.S	11.49	6.91	1.66	0.60
P40201_CHD1_MOUSE	Chd1	Chromodomain-helicase	K.ELEPFLLR@.R	11.50	10.45	1.10	0.91
P40201_CHD1_MOUSE	Chd1	Chromodomain-helicase	K.FGAEELFKEPEGEEQEPQEM*DIDEILK.R	8.65	3.38	2.56	0.39
P40201_CHD1_MOUSE	Chd1	Chromodomain-helicase	K.GSVEEDILER@.A	10.68	6.17	1.73	0.58
P40201_CHD1_MOUSE	Chd1	Chromodomain-helicase	R.LLITGTPLQNSLK#.E	12.72	6.66	1.91	0.52
P40201_CHD1_MOUSE	Chd1	Chromodomain-helicase	R.M*LDILAEYLK#.Y	13.26	8.62	1.54	0.65
P40201_CHD1_MOUSE	Chd1	Chromodomain-helicase	K.SVVSDAPVHITASGEPVPIAEESEELDQK#.T	10.79	5.71	1.89	0.53
Q9CXF7_CHD1L_MOUSE	Chd1l	Chromodomain-helicase	K.ILSPEELEDR@.R	7.25	2.81	2.58	0.39
E9PZM4_CHD2_MOUSE	Chd2	Chromodomain-helicase	R.SFHTDK#LGEYKQPMPSLHTALSDPR@.S	2.01	2.40	0.84	1.20
E9PZM4_CHD2_MOUSE	Chd2	Chromodomain-helicase	R.ENEVSTSATDELLSQFK#.V	5.32	5.55	0.96	1.04
E9PZM4_CHD2_MOUSE	Chd2	Chromodomain-helicase	K.GTVEEEIIER@.A	20.23	6.15	3.29	0.30
E9PZM4_CHD2_MOUSE	Chd2	Chromodomain-helicase	K.SNSVILADEM*GLGK#.T	5.69	4.33	1.31	0.76
E9PZM4_CHD2_MOUSE	Chd2	Chromodomain-helicase	K.VLEPFLLR@.R	10.01	4.49	2.23	0.45
E9Q614_E9Q614_MOUSE	Chd3	Protein Chd3 OS=Mus mu	K.ELQGDGPPSSPTNDPTVK#.Y	8.30	2.15	3.87	0.26
E9Q614_E9Q614_MOUSE	Chd3	Protein Chd3 OS=Mus mu	R.ENEFSFEDNAIK#.G	17.78	4.80	3.70	0.27
E9Q614_E9Q614_MOUSE	Chd3	Protein Chd3 OS=Mus mu	K.FGTEELFK#DENEGENK#EEDSSVIHYDNEAIAR@.L	9.86	2.96	3.33	0.30
E9Q614_E9Q614_MOUSE	Chd3	Protein Chd3 OS=Mus mu	R.IDGGITGALR@.Q	24.33	7.19	3.39	0.30
E9Q614_E9Q614_MOUSE	Chd3	Protein Chd3 OS=Mus mu	K.ILLEDEAPGVPGETEPEPGYR@GDR@.E	5.50	1.77	3.11	0.32
E9Q614_E9Q614_MOUSE	Chd3	Protein Chd3 OS=Mus mu	K.LPSGAYEGGALIK#.S	26.90	13.62	1.97	0.51
E9Q614_E9Q614_MOUSE	Chd3	Protein Chd3 OS=Mus mu	K.SESGGSEYGTGPGR@.K	6.80	2.60	2.61	0.38
E9Q614_E9Q614_MOUSE	Chd3	Protein Chd3 OS=Mus mu	R.TPLDK#DDTENQEEK#PEK#.N	11.80	2.72	4.34	0.23
E9Q614_E9Q614_MOUSE	Chd3	Protein Chd3 OS=Mus mu	R.VGGNIEVLGFNTR@.Q	17.52	5.24	3.35	0.30
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.APEPPPQQVAQQQ.-	7.20	7.20	1.00	1.00
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.AGGLGINLATADTVIIYDSDWNPHNDIQAFSR@.A	4.20	1.54	2.72	0.37
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.APEPPPQQVAQQQ.-	32.99	32.99	1.00	1.00
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.AYVSLFM*R@.H	46.51	16.23	2.87	0.35
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.ENEFSFEDNAIR@.G	37.73	12.59	3.00	0.33

Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.ER@TEEPM*ETEAK#.G	7.18	4.33	1.66	0.60
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.FGTEELFK#DEATDGGGDNK#EGEDSSVIHYDDK#.A	8.83	5.04	1.75	0.57
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.FHNLEGFLEEFADIAK#.E	7.91	3.81	2.07	0.48
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.FHNLEGFLEEFADIAK#EDQIK#.K	6.62	1.53	4.32	0.23
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.FM*FNIADGGFTELHSLWQNEER@.A	27.65	9.79	2.83	0.35
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.FSWAQGTDTILADEM*GLGK#.T	16.20	3.80	4.27	0.23
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.FSWAQGTDTILADEM*GLGK#.T	11.64	4.23	2.75	0.36
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.GGGNQVSLLNVVM*DLK#K#.C	15.88	6.27	2.53	0.39
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.GNFLEIK#.N	38.50	19.82	1.94	0.51
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.HHYEQQQEDLAR@.N	42.16	17.58	2.40	0.42
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.IDGGITGNM*R@.Q	30.15	11.12	2.71	0.37
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.IGVM*SLIR@.K	35.87	12.52	2.87	0.35
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.KEEEEEEDEDDDSKEPK.S	3.39	2.64	1.29	0.78
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.LLDR@NQDETEDTELQGM*NEYLSSFK#.V	3.39	1.48	2.30	0.44
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.LLEQALVIEEQLR@.R	36.15	11.24	3.22	0.31
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.LPATIAR@.I	82.35	110.89	0.74	1.35
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.M*LDLLEDFLEHEGYK#.Y	15.68	6.29	2.49	0.40
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.M*LDLLEDFLEHEGYKYER.I	35.89	12.25	2.93	0.34
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.NDK#DK#PLPPLLAR@.V	35.41	20.83	1.70	0.59
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.NFEALNAR@.G	36.09	12.48	2.89	0.35
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.QVNYNDGSQEDR@.D	7.23	2.12	3.41	0.29
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.TEEPM*ETEAK#.G	12.09	5.18	2.34	0.43
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.TVQTAVFLYSLYK#.E	31.69	10.89	2.91	0.34
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.VGGNIEVLGFNAR@.Q	61.19	21.08	2.90	0.34
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.VLIFSQM*TK#.M	31.24	9.81	3.19	0.31
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.YGM*PPQDAFTTQWLVR@.D	16.09	7.36	2.19	0.46
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.AAYLNM*SEDPSHPSM*ALNTR@.F	21.30	9.87	2.16	0.46
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.AGGLGINLATADTVIIYDSDWNPHNDIQAFSR@.A	8.89	4.13	2.15	0.46
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.APEPPPQQVAQQQ.-	34.26	34.26	1.00	1.00
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.AYVSLFM*R@.H	50.54	14.77	3.42	0.29
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.EEEM*GEEEEVER@.E	15.53	6.42	2.42	0.41
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.ENEFSFEDNAIR@.G	156.57	46.17	3.39	0.29
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.ER@TEEPM*ETEAK#.G	9.62	2.84	3.39	0.29
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.FAEM*EER@.F	85.68	28.02	3.06	0.33
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.FGTEELFK#DEATDGGGDNK#.E	8.35	15.99	0.52	1.91
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.FGTEELFKDEATDGGGDNKEGEDSSVIHYDDK.A	37.72	9.85	3.83	0.26
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.FHNLEGFLEEFADIAK#.E	14.64	5.57	2.63	0.38
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.FHNLEGFLEEFADIAK#EDQIK#K#.L	11.54	4.46	2.59	0.39
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.FM*FNIADGGFTELHSLWQNEER@.A	18.39	4.67	3.93	0.25
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.FSWAQGTDTILADEM*GLGK#.T	63.67	21.59	2.95	0.34
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.GGGNQVSLLNVVM*DLK#.K	46.53	16.63	2.80	0.36
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.GGGNQVSLLNVVMDLK#.K	22.30	6.61	3.37	0.30
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.GGGNQVSLLNVVM*DLK#K#.C	53.19	14.51	3.67	0.27
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.GGGNQVSLLNVVMDLK#K#.C	12.47	1.68	7.44	0.13
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.GHVHYLIK#.W	14.50	5.02	2.89	0.35
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.GNFLEIK#.N	34.85	16.96	2.05	0.49
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.GPFLVSAPLSTIINWER@.E	55.87	20.32	2.75	0.36
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.HHYEQQQEDLAR@.N	95.25	38.00	2.51	0.40
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.IDGGITGNM*R@.Q	170.40	56.91	2.99	0.33
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.IEENSLK#EEESTEGEK#.E	12.51	5.44	2.30	0.43
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.IEENSLKEEESTEGEKEVK.S	8.44	4.19	2.01	0.50
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.IGVM*SLIR@.K	52.95	23.35	2.27	0.44
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.IGVMSLIR@.K	17.51	6.63	2.64	0.38
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.K#EEEEEEDEDDDSK#EPK#.S	24.75	10.21	2.42	0.41
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.K#NDM*DEPPSGDFGGDEEK#.S	30.47	13.70	2.22	0.45
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.LK#ADVFK#.N	44.70	13.11	3.41	0.29
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.LLDR@NQDETEDTELQGM*NEYLSSFK#.V	28.89	7.99	3.61	0.28
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.LLEQALVIEEQLR@.R	52.05	18.11	2.87	0.35
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.M*LDLLEDFLEHEGYK#.Y	105.66	35.30	2.99	0.33
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.M*LDLLEDFLEHEGYK#YER@.I	74.36	23.75	3.13	0.32
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.M*PNGM*YDGSALIR@.A	10.54	5.00	2.11	0.47
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.M*SQPGSPSPK#.T	17.15	6.77	2.53	0.39
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.NDKDKPLPPLLAR.V	46.88	24.09	1.95	0.51
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.NFEALNAR@.G	170.22	51.23	3.32	0.30
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.NQDETEDTELQGM*NEYLSSFK#.V	13.61	6.99	1.95	0.51
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.QPEYLDATGGTLHPYQMEGLNWLR@.F	5.83	2.85	2.04	0.49
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.QVNYNDGSQEDR@.D	4.99	1.79	2.79	0.36
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.SDSEGSDYTPGK#.K	8.57	3.05	2.81	0.36
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.SSAQLLEDWGM*EDIDHVFSEEDYR@.T	95.50	22.35	4.27	0.23
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.SSAQLLEDWGMEDIDHVFSEEDYR@.T	18.51	4.13	4.49	0.22
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.TGSM*SK#QELDDILK#.F	19.86	5.92	3.36	0.30
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.TPTPSTPGDTQPNTPAPVPPAEDGIK#.I	8.06	4.13	1.95	0.51
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.TVQTAVFLYSLYK#.E	111.75	28.32	3.95	0.25
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	K.VAQYVVR@EEEM*GEEEEVER@.E	19.43	5.02	3.87	0.26
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.VGGNIEVLGFNAR@.Q	67.02	20.37	3.29	0.30
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.VLIFSQM*TK#.M	105.47	39.00	2.70	0.37
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.WQDIQNDPR@.Y	18.22	8.51	2.14	0.47
Q6PDQ2_CHD4_MOUSE	Chd4	Chromodomain-helicase	R.YGM*PPQDAFTTQWLVR@.D	16.12	5.08	3.17	0.32
Q09XV5_CHD8_MOUSE	Chd8	Chromodomain-helicase	K.ASFVASENR@.T	6.60	2.27	2.90	0.34
Q09XV5_CHD8_MOUSE	Chd8	Chromodomain-helicase	R.DGNITGIQQFSK#.K	7.69	2.09	3.69	0.27
Q09XV5_CHD8_MOUSE	Chd8	Chromodomain-helicase	R.SGSAASM*AEEEASAVTTAAAQFTK#.L	4.89	1.96	2.49	0.40
Q09XV5_CHD8_MOUSE	Chd8	Chromodomain-helicase	R.TDISLDDPNFWQK#.W	11.38	2.84	4.01	0.25
F6W5S9_F6W5S9_MOUSE	Chd8	Chromodomain-helicase	R.VSPFPGLSIPVPR@.G	10.93	4.68	2.34	0.43
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.DEFSTFGTR@.K	30.05	9.49	3.17	0.32
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.ELLAALQK#.V	132.27	41.03	3.22	0.31
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.GDPGWNGQR@.D	27.91	6.01	4.64	0.22
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	K.GVGVALDDPYENYR@.R	20.04	4.87	4.11	0.24
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.ITADGAHFELR@.L	19.24	13.48	1.43	0.70
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	K.LAQFVAR@.N	113.21	36.35	3.11	0.32
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.LLAAVEAFYSPPSHDR@PR@.N	56.82	12.59	4.51	0.22
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.LLQLWEK#.N	99.29	31.92	3.11	0.32
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	K.M*GWSGSGGLGAK#.E	16.18	3.52	4.60	0.22
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.NSEGWEQNGLYEFFR@.A	14.23	4.34	3.28	0.30
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.QEQVTTAVAHAVEQQM*QK#.L	50.74	19.06	2.66	0.38
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	K.SYSFIAR@.M	53.16	13.74	3.87	0.26
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	K.LAQFVAR@.N	82.88	21.39	3.88	0.26
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.LLAAVEAFYSPPSHDR@PR@.N	20.28	1.61	12.56	0.08
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	K.M*GWSGSGGLGAK#.E	6.43	2.84	2.27	0.44
Q8CGZ0_CHERP_MOUSE	Cherp	Calcium homeostasis enc	R.NGPEFEK#.M	26.81	8.95	2.99	0.33
Q8BJF9_CHM2B_MOUSE	Chmp2b	Charged multivesicular b	K.MAGAMSTTAK#TM*QAVNK#.K	3.59	1.90	1.88	0.53
Q9D8B3_CHM4B_MOUSE	Chmp4b	Charged multivesicular b	R.EALENANTNTEVLK.N	7.23	7.73	0.93	1.07
Q9D7S9_CHMP5_MOUSE	Chmp5	Charged multivesicular b	K.NKDGVLVDEFGLPQIPAS.-	3.40	3.26	1.04	0.96
P0C0A3_CHMP6_MOUSE	Chmp6	Charged multivesicular b	R.ILDETQEAVEYQR@.Q	9.92	5.91	1.68	0.60

P61022_CHP1_MOUSE	Chp1	Calcineurin B homologou	R.EDFQRIPELAINPLGDR.I	18.77	11.09	1.69	0.59
P61022_CHP1_MOUSE	Chp1	Calcineurin B homologou	R.IINAFFSEGEDQVNFR@.G	20.08	13.74	1.46	0.68
P61022_CHP1_MOUSE	Chp1	Calcineurin B homologou	R.IPELAINPLGDR@.I	21.72	19.24	1.13	0.89
P61022_CHP1_MOUSE	Chp1	Calcineurin B homologou	R.M*M*VGVNISDEQLGSIADR@.T	5.12	3.33	1.54	0.65
P61022_CHP1_MOUSE	Chp1	Calcineurin B homologou	R.TIQEADQDGDSAISFTEFVK#.V	10.19	5.35	1.91	0.52
Q9JKP8_CHRC1_MOUSE	Chrac1	Chromatin accessibility c	K.SSPEVSSINQEALVLTAK#.A	13.02	5.58	2.33	0.43
Q8BIW9_CTF18_MOUSE	Chtf18	Chromosome transmissio	R.K#GPQEADQGGTAVAAGGR@.R	8.46	3.08	2.74	0.36
Q8BIW9_CTF18_MOUSE	Chtf18	Chromosome transmissio	K.VVQGLFDNFLR@.L	20.04	2.43	8.24	0.12
P0CG15_CTF8_MOUSE	Chtf8	Chromosome transmissio	R.GTGTQYLVTALIK#.N	18.34	6.56	2.80	0.36
P0CG15_CTF8_MOUSE	Chtf8	Chromosome transmissio	K.TR@PK#PIITNVPK#.K	19.23	7.74	2.49	0.40
Q9CY57_CHTOP_MOUSE	Chtop	Chromatin target of PRM	R.ASM*QQQQQLASAR@.N	48.86	31.46	1.55	0.64
Q9CY57_CHTOP_MOUSE	Chtop	Chromatin target of PRM	R.ASMQQQQQLASAR@.N	11.86	7.49	1.58	0.63
Q9CY57_CHTOP_MOUSE	Chtop	Chromatin target of PRM	K.EQLDNQLDAYM*SK#.T	52.09	28.16	1.85	0.54
Q9CY57_CHTOP_MOUSE	Chtop	Chromatin target of PRM	K.GHLDAELDAYM*AQTDPETND.-	7.85	7.85	1.00	1.00
Q9CY57_CHTOP_MOUSE	Chtop	Chromatin target of PRM	K.TK#GHLDAELDAYM*AQTDPETND.-	9.23	6.21	1.49	0.67
Q9CY57_CHTOP_MOUSE	Chtop	Chromatin target of PRM	R.ASMQQQQQLASAR@.N	2.18	1.49	1.46	0.68
Q9CY57_CHTOP_MOUSE	Chtop	Chromatin target of PRM	K.EQLDNQLDAYM*SK#.T	19.63	9.70	2.02	0.49
Q9CY57_CHTOP_MOUSE	Chtop	Chromatin target of PRM	K.TK#GHLDAELDAYM*AQTDPETND.-	5.70	3.16	1.80	0.56
P60824_CIRBP_MOUSE	Cirbp	Cold-inducible RNA-bind	K.YGQISEVVVVK#.D	8.53	9.49	0.90	1.11
Q8R2N2_CIR1A_MOUSE	Cirh1a	Cirhin OS=Mus musculus	K.IYK#PLLFM*DLLDER@.T	12.14	5.79	2.10	0.48
Q8R2N2_CIR1A_MOUSE	Cirh1a	Cirhin OS=Mus musculus	R.TDGTVEIYNLSANYFQEK#.F	5.12	2.54	2.01	0.50
Q8R2N2_CIR1A_MOUSE	Cirh1a	Cirhin OS=Mus musculus	R.K#MVLDR@.Q	24.35	3.19	7.63	0.13
Q3V1H1_CKAP2_MOUSE	Ckap2	Cytoskeleton-associated	R.HIIIDILTTK#.S	9.31	8.62	1.08	0.93
Q3V1H1_CKAP2_MOUSE	Ckap2	Cytoskeleton-associated	R.IEPITSPIENIISIYEK#.A	10.08	7.18	1.41	0.71
Q3V1H1_CKAP2_MOUSE	Ckap2	Cytoskeleton-associated	K.AILAGAQPIEEM*R@.H	8.35	2.35	3.55	0.28
Q3V1H1_CKAP2_MOUSE	Ckap2	Cytoskeleton-associated	K.AQSEPANTVSVK#.A	8.40	2.16	3.90	0.26
Q3V1H1_CKAP2_MOUSE	Ckap2	Cytoskeleton-associated	R.IEPITSPIENIISIYEK#.A	5.80	3.80	1.53	0.66
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	R.LAM*LQEHVGNLGSSSDLASTVR@.S	5.52	3.42	1.61	0.62
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	R.DFTSLENTVEER@.L	6.65	7.46	0.89	1.12
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	K.GGHGAASPSDK#GAHPSGGADDVAK#.K	4.72	3.76	1.26	0.80
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	R.HTESLESLLSK#.S	23.98	18.40	1.30	0.77
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	K.IETNENNLESAK#.G	33.44	22.30	1.50	0.67
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	R.LALQALTEK#.L	62.84	45.36	1.39	0.72
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	R.LAM*LQEHVGNLGSSSDLASTVR@.S	20.70	15.05	1.38	0.73
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	R.LQYVEDGVYSM*QVASAR@.H	9.29	8.07	1.15	0.87
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	R.QRDELGQGLQGVEQK.V	22.71	11.79	1.93	0.52
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	K.SSLQTM*ESDVYTEVR@.E	19.19	11.99	1.60	0.62
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	K.SSLQTMESDVYTEVR@.E	5.62	6.00	0.94	1.07
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	K.SSVSQVESDLK#.M	41.09	21.26	1.93	0.52
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	K.VGAHGSEEGAVFK#.D	36.60	32.07	1.14	0.88
Q8BMK4_CKAP4_MOUSE	Ckap4	Cytoskeleton-associated	K.VQSLQATFGTFESLLR@.N	24.53	20.53	1.19	0.84
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.IEDLEEGQQVIR@.S	12.47	4.81	2.59	0.39
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.LDDIFEPVLIPEPK#.I	5.78	3.61	1.60	0.62
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.EGLAELYEYK#.K	12.76	4.87	2.62	0.38
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.IEDLEEGQQVIR@.S	26.41	7.65	3.45	0.29
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.LDDIFEPVLIPEPK#.I	12.13	5.67	2.14	0.47
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.LLPDTINSINLDR@.I	28.70	11.02	2.60	0.38
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.NSSQFFQSYVER@.G	15.68	5.36	2.92	0.34
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.SVNLLVVK#.V	30.87	8.92	3.46	0.29
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.DQVLAM*LEK#.A	11.38	3.34	3.41	0.29
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.EALEAVEVLVK#.N	22.22	6.71	3.31	0.30
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.EFQLDLDEIENDNGTVR@.C	4.02	1.99	2.02	0.50
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.EGLAELYEYK#.K	15.82	5.00	3.16	0.32
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.EGLDEVAGIINEAK#.F	25.78	16.43	1.57	0.64
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.FGQYAGHVVPTILEK#.F	29.94	11.53	2.60	0.39
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.FIQPNIGELPTALK#.G	35.29	14.81	2.38	0.42
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.GLEAALVYVENAHVAGK#.T	25.78	7.81	3.30	0.30
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.HINDSAPEVR.D	12.23	4.69	2.61	0.38
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.HSTSATDEGEDGEEPGEGGNDVVDLLPR@.I	7.63	2.19	3.48	0.29
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.IEDLEEGQQVIR@.S	33.44	11.70	2.86	0.35
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.LDDIFEPVLIPEPK#.I	33.14	16.34	2.03	0.49
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.LEAGDYADLVK#.A	21.83	8.08	2.70	0.37
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.LFAIEIYR@.W	12.63	3.27	3.86	0.26
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.LLPDTINSINLDR@.I	38.04	15.74	2.42	0.41
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.M*IFEDEK#PALLSQIDAEFQK#.M	15.69	5.95	2.64	0.38
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.M*QGQSPPAPTR@.G	31.24	10.29	3.04	0.33
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.NLGIPVITVLGDSK#.N	45.04	14.55	3.10	0.32
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.NQSETLNWLSNAIK#.E	11.83	5.41	2.19	0.46
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.NSSQFFQSYVER@.G	18.52	6.54	2.83	0.35
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.SVNLLVVK#.V	29.75	11.61	2.56	0.39
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.TALAATNPAVR@.T	19.87	6.90	2.88	0.35
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	R.TQNINSNANM*LR@.K	15.78	3.63	4.35	0.23
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.TSAQIVLDGLVDK#.I	20.12	4.43	4.54	0.22
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.VNDFLAEIFK#.K	7.61	1.58	4.81	0.21
A2AGT5_CKAP5_MOUSE	Ckap5	Cytoskeleton-associated	K.YSDTDIEPFLK#.N	19.24	9.58	2.01	0.50
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.AQTTNSNSSSSSDVSTHS.-	1.96	1.96	1.00	1.00
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.EYNPYPYSDTINTYDK#.T	7.58	3.51	2.16	0.46
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.FIVDQTQTPNLK#.V	14.83	12.10	1.23	0.82
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.NSSNTGVGSPSNTIGR@.T	61.72	4.96	12.44	0.08
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.AQIGTVLPSLIDR@.L	7.43	2.23	3.33	0.30
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.AQTTNSNSSSSSDVSTHS.-	1.66	1.66	1.00	1.00
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.DSFPFDQQFNILM*R@.F	11.73	4.83	2.43	0.41
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.DSFPFDQQFNILMR@.F	4.88	2.95	1.65	0.61
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.EYNPYPYSDTINTYDK#.T	5.11	2.56	1.99	0.50
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.FIVDQTQTPNLK#.V	18.84	11.05	1.71	0.59
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.IITWTTEPK#.S	13.32	5.94	2.24	0.45
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.NSSNTGVGSPSNTIGR@.T	44.89	5.26	8.54	0.12
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.QM*DPTDFVNSSETR@.L	4.64	3.05	1.52	0.66
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.AFDDVPVVQIYSSR@.D	4.94	2.73	1.81	0.55
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.AQIGTVLPSLIDR@.L	17.23	4.92	3.50	0.29
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.DAAINSLVEIYR@.H	7.98	3.09	2.59	0.39
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.DSFPFDQQFNILM*R@.F	9.10	4.75	1.92	0.52
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.EGAGAVDEEDFIK#.A	7.70	3.44	2.24	0.45
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.FIVDQTQTPNLK#.V	18.75	7.26	2.58	0.39
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.IM*ATSGVVAVR@.L	6.65	5.85	1.14	0.88
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.LLGSGLAGGSSR@.G	14.16	4.08	3.47	0.29
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.NSDSIVSLPQSDR@.S	5.77	8.61	0.67	1.49
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	R.QSSGSTTNVASTPSDSR@.G	5.49	3.70	1.49	0.67
E9Q6L0_E9Q6L0_MOUSE	Clasp1	CLIP-associating protein	K.VVSQSQPGSR@.S	7.09	3.22	2.20	0.45
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	R.AGGDAADGSQPALDNK#.A	18.30	4.05	4.52	0.22
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	R.DYNPYNYSDSISPFNK#.S	4.09	2.06	1.98	0.50
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	K.EAM*FDDDADQFPDDLSLDHSDLVAELLK#.E	48.05	2.06	23.31	0.04
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	R.FTVDQTQTPSLK#.V	21.00	3.92	5.36	0.19

Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	K.NYAELTVM*K#.T	9.44	2.91	3.24	0.31
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	R.SFQPLGPGYGISQSSR@.L	6.83	2.94	2.32	0.43
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	K.AFTDVPSVQIYSSR@.E	5.88	3.06	1.92	0.52
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	K.EGGAGAVDEDDFIK#.A	11.60	2.59	4.49	0.22
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	K.EGLLGLQNLLK#.S	23.27	12.19	1.91	0.52
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	R.FTVDQTQTPSLK#.V	6.71	1.80	3.73	0.27
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	R.SFQPLGPGYGISQSSR@.L	7.24	2.12	3.42	0.29
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	K.AFTDVPSVQIYSSR@.E	6.49	2.12	3.07	0.33
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	K.EGGAGAVDEDDFIK#.A	11.99	4.05	2.96	0.34
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	K.EGLLGLQNLLK#.S	27.33	10.85	2.52	0.40
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	R.FTVDQTQTPSLK#.V	11.95	2.00	5.97	0.17
Q8BRT1_CLAP2_MOUSE	Clasp2	CLIP-associating protein	K.SSGSVASLPQSDR@.S	8.71	3.93	2.22	0.45
Q8CFC7_CLASR_MOUSE	Clasrp	CLK4-associating serine/	K.ASIGYTYEDSTVAEVEK#.V	4.94	3.70	1.33	0.75
Q8CFC7_CLASR_MOUSE	Clasrp	CLK4-associating serine/	K.QATTYGM*ADGDFVR@.M	6.09	3.54	1.72	0.58
Q9Z1Q5_CLIC1_MOUSE	Clic1	Chloride intracellular ch	K.LAALNPESNTSGLDIFAK#.F	3.61	3.76	0.96	1.04
Q5SUH6_Q5SUH6_MOUSE	Clint1	Clathrin interactor 1 OS=	K.ATNVVM*NYSEIESK#.V	8.87	7.87	1.13	0.89
Q5SUH6_Q5SUH6_MOUSE	Clint1	Clathrin interactor 1 OS=	K.IGSTIDDTISK#.F	23.67	17.16	1.38	0.72
Q5SUH6_Q5SUH6_MOUSE	Clint1	Clathrin interactor 1 OS=	K.ATNVVM*NYSEIESK#.V	15.74	6.53	2.41	0.41
Q5SUH6_Q5SUH6_MOUSE	Clint1	Clathrin interactor 1 OS=	K.GEFK#DEEETVTTK#.H	10.76	6.30	1.71	0.59
Q5SUH6_Q5SUH6_MOUSE	Clint1	Clathrin interactor 1 OS=	K.HIHITQATETTTTR@.H	6.15	4.46	1.38	0.73
Q5SUH6_Q5SUH6_MOUSE	Clint1	Clathrin interactor 1 OS=	K.IGSTIDDTISK#.F	27.85	13.32	2.09	0.48
Q5SUH6_Q5SUH6_MOUSE	Clint1	Clathrin interactor 1 OS=	K.LGELSDK#IGSTIDDTISK#.F	13.24	7.03	1.88	0.53
Q5SUH6_Q5SUH6_MOUSE	Clint1	Clathrin interactor 1 OS=	K.QDAFANFANFSK#.-	12.34	7.31	1.69	0.59
Q5SUH6_Q5SUH6_MOUSE	Clint1	Clathrin interactor 1 OS=	K.YVGVSSDSVGGFR@.Y	22.93	9.95	2.30	0.43
Q922J3_CLIP1_MOUSE	Clip1	CAP-Gly domain-contain	K.ASGPPSSETQEEFVDDFR@.V	4.12	2.17	1.90	0.53
Q922J3_CLIP1_MOUSE	Clip1	CAP-Gly domain-contain	K.ATSHVGEIEQELALAR@.D	16.80	4.28	3.93	0.25
Q922J3_CLIP1_MOUSE	Clip1	CAP-Gly domain-contain	R.DGHDQHVLELEAK#.M	9.46	3.97	2.38	0.42
Q922J3_CLIP1_MOUSE	Clip1	CAP-Gly domain-contain	K.ELVLTGLQDSLNQVNQVK#.E	4.50	2.62	1.72	0.58
Q922J3_CLIP1_MOUSE	Clip1	CAP-Gly domain-contain	K.GIGTDSAEFAELK#.T	11.65	10.10	1.15	0.87
Q922J3_CLIP1_MOUSE	Clip1	CAP-Gly domain-contain	K.SQQLSALQEENVK#.L	9.84	2.26	4.34	0.23
Q922J3_CLIP1_MOUSE	Clip1	CAP-Gly domain-contain	K.TASESISNLSEAGSVK#.K	11.49	3.68	3.12	0.32
Q922J3_CLIP1_MOUSE	Clip1	CAP-Gly domain-contain	K.SQQLSALQEENVK#.L	9.16	3.08	2.97	0.34
Q922J3_CLIP1_MOUSE	Clip1	CAP-Gly domain-contain	K.TASESISNLSEAGSVK#.K	7.27	3.25	2.23	0.45
O35492_CLK3_MOUSE	Clk3	Dual specificity protein k	R.YEIVGNLGEGTFGK#.V	8.08	3.51	2.30	0.44
Q8C5W0_CLMN_MOUSE	Clmn	Calmin OS=Mus musculu	R.FPELEPEDFVNPDK#EAPIESTFVR@.I	4.35	1.51	2.88	0.35
Q8C5W0_CLMN_MOUSE	Clmn	Calmin OS=Mus musculu	R.FPELEPEDFVNPDK#EAPIESTFVR@.I	14.50	5.00	2.90	0.34
Q8C5W0_CLMN_MOUSE	Clmn	Calmin OS=Mus musculu	R.FPELEPEDFVNPDK#EAPIESTFVR@.I	4.95	2.15	2.30	0.43
Q60649_CLPB_MOUSE	Clpb	Caseinolytic peptidase B	R.IAENLGDVQM*SDK#.I	4.42	1.90	2.33	0.43
Q8VBZ3_CLPT1_MOUSE	Clptm1	Cleft lip and palate trans	R.AQASTAAGALTPAPSTAVSGEDASTVPK#.A	5.99	4.86	1.23	0.81
Q8VBZ3_CLPT1_MOUSE	Clptm1	Cleft lip and palate trans	R.AQASTAAGALTPAPSTAVSGEDASTVPK#.A	5.49	1.88	2.92	0.34
Q9JHS4_CLPX_MOUSE	Clpx	ATP-dependent Clp prote	R.DLIEFGM*IPEFVGR@.L	5.91	1.63	3.62	0.28
Q9JHS4_CLPX_MOUSE	Clpx	ATP-dependent Clp prote	K.LLEGTIVNVPEK#.N	11.98	9.75	1.23	0.81
Q9JHS4_CLPX_MOUSE	Clpx	ATP-dependent Clp prote	R.LPVVVPLHSLDEK#.T	10.91	4.87	2.24	0.45
Q9JHS4_CLPX_MOUSE	Clpx	ATP-dependent Clp prote	K.SNILLLGPTGSGK#.T	11.22	4.53	2.47	0.40
Q9JHS4_CLPX_MOUSE	Clpx	ATP-dependent Clp prote	K.TLVQILTEPR@.N	16.71	3.33	5.03	0.20
Q9JHS4_CLPX_MOUSE	Clpx	ATP-dependent Clp prote	K.LLQDANYNVEK#.A	5.45	1.16	4.71	0.21
Q6PFA2_Q6PFA2_MOUSE	Clta	Clathrin light chain A OS	R.LEALDANSR@.K	51.22	24.51	2.09	0.48
Q6PFA2_Q6PFA2_MOUSE	Clta	Clathrin light chain A OS	R.AAEEAFVNDIDESSPGTEWER.V	3.54	3.23	1.10	0.91
Q6PFA2_Q6PFA2_MOUSE	Clta	Clathrin light chain A OS	R.LEALDANSR@.K	7.69	8.87	0.87	1.15
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.ALEHFTDLYDIK#.R	13.57	5.16	2.63	0.38
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.ESYVETELIFALAK#.T	16.13	4.07	3.96	0.25
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.HDVVFLITK#.Y	15.29	7.15	2.14	0.47
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.HELIEFR@.R	15.74	3.74	4.21	0.24
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.ISGETIFVTAPHEATAGIIGVNR@.K	34.65	9.91	3.50	0.29
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.IYIDSNNNPER@.F	16.32	5.12	3.19	0.31
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.K#FDVNTSAVQVLIEHIGNLDR@.A	20.92	6.61	3.16	0.32
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.K#VGYTPDWIFLLR@.N	19.02	4.24	4.49	0.22
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.LAELEEFINGPNNAHIQQVGDR@.C	7.26	2.32	3.13	0.32
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.LLLPWLEAR.I	55.78	12.27	4.55	0.22
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.LLYNNVSNFGR@.L	22.35	39.12	0.57	1.75
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.NLQNLLILTAIK#.A	32.41	6.46	5.02	0.20
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.NNLAGAEELFAR@.K	27.47	6.11	4.49	0.22
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.R@PLIDQVVQTALSETQDPEEVSVTVK#.A	14.96	3.72	4.02	0.25
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.SVNESLNNLFITEEDYQALR@.T	14.47	4.78	3.02	0.33
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.TLQIFNIEM*K#.S	12.35	5.11	2.42	0.41
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.TSIDAYDNFDNISLAQR@.L	15.29	4.43	3.45	0.29
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.VANVELYYK#.A	16.84	4.68	3.60	0.28
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.VGYTPDWIFLLR@.N	13.74	4.94	2.78	0.36
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.WLLLTGISAQQNR@.V	8.27	2.01	4.12	0.24
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.AHM*GM*FTELAILYSK#.F	47.19	30.52	1.55	0.65
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.ALEHFTDLYDIK#.R	33.56	14.07	2.39	0.42
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.ALEHFTDLYDIKR.A	32.97	11.86	2.78	0.36
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.AVNYFSK#.V	33.85	17.64	1.92	0.52
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.AYEFAER@.C	45.26	17.47	2.59	0.39
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.DAM*QYASESK#.D	13.91	5.34	2.60	0.38
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.ESYVETELIFALAK#.T	33.72	14.05	2.40	0.42
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.FDVNTSAVQVLIEHIGNLDR@.A	18.07	7.83	2.31	0.43
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.FNALFAQGNYSEAAK#.V	15.61	8.07	1.93	0.52
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.GQFSTDELVAEVEK#.R	16.18	9.58	1.69	0.59
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.HDVVFLITK#.Y	57.40	26.79	2.14	0.47
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.HNIM*DFAM*PYFIQVMK#.E	6.36	2.77	2.30	0.43
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.ISGETIFVTAPHEATAGIIGVNR@.K	121.97	62.08	1.96	0.51
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.IYIDSNNNPER@.F	81.80	33.91	2.41	0.41
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.KAVDVFFPPEAQNDFPVAM*QISEK.H	7.52	4.55	1.65	0.60
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.K#DPELWGSVLLESNPYR@.R	11.96	9.47	1.26	0.79
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.K#FDVNTSAVQVLIEHIGNLDR@.A	24.16	9.50	2.54	0.39
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.KFDVNTSAVQVLIEHIGNLDR.A	22.39	12.78	1.75	0.57
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.K#FNALFAQGNYSEAAK#.V	47.22	16.45	2.87	0.35
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.K#VGYTPDWIFLLR@.N	25.83	14.65	1.76	0.57
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.K#VSQPIEGHAASFAQFK#.M	13.48	11.77	1.15	0.87
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.LASTLVHLGEYQAAVDGAR@.K	150.04	53.37	2.81	0.36
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.LEK#HELIEFR@.R	22.42	6.91	3.25	0.31
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.LLLPWLEAR@.I	153.93	70.29	2.19	0.46
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.LLYNNVSNFGR@.L	94.50	32.64	2.90	0.35
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.NLILVVR@.G	46.50	17.97	2.59	0.39
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.NLQNLLILTAIK#.A	123.79	51.25	2.42	0.41
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.NNLAGAEELFAR@.K	76.73	33.70	2.28	0.44
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.NNRPSEGPLQTR.L	43.23	20.67	2.09	0.48
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.NNR@PSEGPLQTR@.L	3.77	3.59	1.05	0.95
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.R@PISADSAIM*NPASK#.V	42.60	19.07	2.23	0.45
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.R@PLIDQVVQTALSETQDPEEVSVTVK#.A	58.82	28.08	2.09	0.48
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	R.R@PLIDQVVQTALSETQDPEEVSVTVK#.A	9.03	5.16	1.75	0.57
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O	K.SVDPTLALSVYLR.A	33.22	15.21	2.18	0.46

Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O K.SVNESLNNLFITEEDYQALR@.T	82.36	28.92	2.85	0.35
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O K.SVNESLNNLFITEEDYQALR.T	20.82	9.67	2.15	0.46
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O K.TLQIFNIEM*K#.S	56.48	20.08	2.81	0.36
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O R.TSIDAYDNFDNISLAQR@.L	50.15	19.40	2.59	0.39
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O K.VANVELYYK#.A	72.41	31.66	2.29	0.44
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O K.VDKLDASESLR.K	32.10	12.37	2.60	0.39
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O K.VGEQAQVVIIDM*NDPSNPIR.R	7.30	5.72	1.28	0.78
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O K.VGYTPDWIFLLR@.N	40.90	20.86	1.96	0.51
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O R.VM*EYINR@.L	36.15	16.63	2.17	0.46
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O K.VSQPIEGHAASFAQFK#.M	71.20	27.83	2.56	0.39
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O R.VVGAM*QLYSVDR@.K	20.67	19.09	1.08	0.92
Q68FD5_CLH1_MOUSE	Cltc	Clathrin heavy chain 1 O K.WLLLTGISAQQNR@.V	32.27	15.69	2.06	0.49
Q9D1A2_CNDP2_MOUSE	Cndp2	Cytosolic non-specific di K.AVFQYIDENQDR@.Y	4.64	1.65	2.81	0.36
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus K.GLQSGVDIGVK#.Y	232.83	54.95	4.24	0.24
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus K.GPSYGLSAEVK#.N	237.12	76.37	3.10	0.32
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus R.NFDDATM*K#.A	49.86	17.48	2.85	0.35
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus R.SM*QNWHQLENLSNFIK#.A	66.89	18.06	3.70	0.27
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus R.SM*QNWHQLENLSNFIK#.A	6.24	1.81	3.44	0.29
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus R.SWIEGLTGLSIGPDFQK#.G	159.67	37.26	4.29	0.23
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus K.GLQSGVDIGVK#.Y	50.19	22.92	2.19	0.46
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus K.GPSYGLSAEVK#.N	41.64	17.50	2.38	0.42
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus R.SM*QNWHQLENLSNFIK#.A	48.65	22.28	2.18	0.46
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus R.SWIEGLTGLSIGPDFQK#.G	55.01	26.41	2.08	0.48
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus K.YDPQK#EAELR@.S	14.84	5.51	2.69	0.37
Q08093_CNN2_MOUSE	Cnn2	Calponin-2 OS=Mus mus R.SWIEGLTGLSIGPDFQK#.G	10.16	3.89	2.61	0.38
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.AGQSVIGLQM*GTNK#.C	38.18	13.43	2.84	0.35
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.GASQAGMLAPGTR@.R	11.09	2.97	3.73	0.27
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.GASQAGM*LAPGTR@.R	129.35	36.76	3.52	0.28
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.GM*SVYGLGR@.Q	87.34	24.52	3.56	0.28
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.K#VNESSLNWPQLENIGNFIK#.A	18.33	6.37	2.88	0.35
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.LTLQPVDNSTISLQM*GTNK#.V	15.03	3.42	4.39	0.23
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.M*QTDKPFDQTTISLQM*GTNK.G	36.87	12.22	3.02	0.33
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.MQTDK#PFDQTTISLQM*GTNK#.G	3.71	2.02	1.84	0.54
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.VNESSLNWPQLENIGNFIK#.A	15.14	4.82	3.14	0.32
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.VNESSLNWPQLENIGNFIK#.A	27.96	9.02	3.10	0.32
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.YDQQAEEDLR@.N	28.43	6.95	4.09	0.24
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.AGQSVIGLQM*GTNK#.C	9.29	4.35	2.13	0.47
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.GM*SVYGLGR@.Q	5.77	4.59	1.26	0.79
Q9DAW9_CNN3_MOUSE	Cnn3	Calponin-3 OS=Mus mus K.LTLQPVDNSTISLQM*GTNK#.V	3.72	3.41	1.09	0.92
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.LAEVGQYEQVK#.Q	13.42	2.67	5.03	0.20
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.SLDLIESLLR@.L	12.03	4.72	2.55	0.39
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.GAFGVGQEQIDAFLK#.T	10.48	3.31	3.17	0.32
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.IVEPPENIQEK#.I	6.95	1.30	5.36	0.19
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.LAEVGQYEQVK#.Q	18.37	7.55	2.43	0.41
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.SLDLIESLLR@.L	23.94	9.59	2.50	0.40
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.SLLEVVVLSR@.N	8.27	1.34	6.17	0.16
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.AQAEQQHNPAANPTM*IR@.A	29.47	9.28	3.18	0.31
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.AVEGLLDATSGADADLLLR@.Y	42.59	10.43	4.08	0.24
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.DAIAALGLLQK#.A	43.22	9.69	4.46	0.22
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.DVPPSINTTNIDTLLVATDQTER@.I	23.04	4.93	4.68	0.21
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.EIDDEANSYFQR@.I	34.52	7.31	4.72	0.21
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.ELNPSLNFK#.E	22.99	5.60	4.11	0.24
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.GLHNVVYGIQR@.G	20.04	4.96	4.04	0.25
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.GQQELLYVVPFVAK#.V	56.55	10.90	5.19	0.19
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.GSTPSM*STITHSAHM*DIFQNLAVDLDTEGR@.Y	14.66	4.23	3.46	0.29
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.IAFIFNNLSQSNM*TQK#.V	20.62	4.65	4.43	0.23
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.IVEPPENIQEK#.I	55.20	14.07	3.92	0.25
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.K#DFALDSEESR@.M	19.29	4.49	4.29	0.23
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.K#DVPPSINTTNIDTLLVATDQTER@.I	4.79	2.13	2.25	0.44
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.LAEVGQYEQVK#.Q	43.04	12.53	3.43	0.29
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.LATEFELR@.K	15.49	4.99	3.11	0.32
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.LGTSGLNQPTFQQSK#.M	15.13	2.77	5.46	0.18
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.LIALLVK#.H	24.14	5.98	4.04	0.25
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.LK#NLDEQLSAPK#.K	11.31	1.56	7.24	0.14
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.LPDPFTPNLK#.V	33.04	10.05	3.29	0.30
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.M*QGSITTPGSIALAQAQAQAQVPAK#.A	35.22	8.14	4.33	0.23
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.M*VLNETYR@.N	35.85	9.80	3.66	0.27
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.M*YYFGIAALDR@.F	18.99	5.72	3.32	0.30
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.NIIM*QFGVR@.E	16.57	5.80	2.86	0.35
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.NLDEQLSAPK#.K	42.30	20.57	2.06	0.49
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.NLFEEYR@.F	29.63	6.01	4.93	0.20
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.NLILSAFPR@.N	67.02	21.34	3.14	0.32
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.NSFASALR@.T	28.61	8.20	3.49	0.29
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.NVPGFLPTNDLSQPTGFLAQPM*K#.Q	40.79	13.20	3.09	0.32
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.SLDLIESLLR@.L	129.63	37.15	3.49	0.29
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.SLLEVVVLSR@.N	53.48	12.61	4.24	0.24
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.SLLLEAYVK#.G	32.57	7.62	4.27	0.23
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.SNLQVSNEPGNR@.Y	18.32	6.71	2.73	0.37
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.SNYEAM*IDR@.A	26.41	7.03	3.76	0.27
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.SPVTFLSDLR@.S	84.18	20.32	4.14	0.24
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.SVAHITEADLFHTIETLM*R@.I	34.99	4.86	7.20	0.14
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.SVAHITEADLFHTIETLM*R@.I	15.51	7.03	2.21	0.45
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.VQEVIFGLALLNSSSPDLR@.G	5.11	1.37	3.71	0.27
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.VSIEPNFHSLYSNFLDTLK#.N	13.46	3.91	3.44	0.29
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.YLAPFLR@.N	15.38	7.31	2.10	0.48
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription R.YLFLNAIANQLR@.Y	50.40	11.73	4.30	0.23
Q6ZQ08_CNOT1_MOUSE	Cnot1	CCR4-NOT transcription K.YNVEAVELLIR.N	26.80	6.25	4.29	0.23
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.IILNTAVAEFFK#.N	41.14	16.16	2.55	0.39
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.LYQFIEPFEEK#.F	7.98	2.30	3.46	0.29
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription R.QYTEAISVGEK#.L	5.80	4.80	1.21	0.83
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.FLGHLYAAEALISLDR@.I	7.64	2.37	3.22	0.31
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.IILNTAVAEFFK#.N	50.53	9.25	5.46	0.18
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription R.ISDAITHLNPENVTDVSLGISSNEQDQGSDK#GENEAM*ESSGK#.R	4.74	2.23	2.13	0.47
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.TVFQPVHPIQPIQM*PAFTTVQR@.K	4.13	2.04	2.03	0.49
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.AESAALIEAAK#.S	18.07	3.58	5.05	0.20
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.HNLGIFYFK#.K	6.85	3.45	1.99	0.50
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.IILNTAVAEFFK#.N	52.01	10.36	5.02	0.20
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.NNQTTTDNLR@.Q	12.01	3.49	3.44	0.29
Q8BH15_CNO10_MOUSE	Cnot10	CCR4-NOT transcription K.SNFEYLR@.G	15.09	3.24	4.65	0.22
Q9CWN7_CNO11_MOUSE	Cnot11	CCR4-NOT transcription K.FFLSQLM*LAPPR@.E	16.84	7.93	2.12	0.47
Q9CWN7_CNO11_MOUSE	Cnot11	CCR4-NOT transcription R.GGAGGPGPGIGGPAGR@.M	6.33	3.21	1.97	0.51
Q9CWN7_CNO11_MOUSE	Cnot11	CCR4-NOT transcription R.GGQEPDR@PPLSGFLPPITPPEK#.F	21.45	8.29	2.59	0.39
Q9CWN7_CNO11_MOUSE	Cnot11	CCR4-NOT transcription R.LGSVLVM*LLQQPDLLPSAAQR@.L	23.57	7.00	3.37	0.30

Q9CWN7_CNO11_MOUSE	Cnot11	CCR4-NOT transcription	K.LVYHIGLTPAK#.L	34.63	7.59	4.56	0.22
Q9CWN7_CNO11_MOUSE	Cnot11	CCR4-NOT transcription	K.TLDTGETPSETK#.I	50.81	18.10	2.81	0.36
Q9CWN7_CNO11_MOUSE	Cnot11	CCR4-NOT transcription	R.LGSVLVM*LLQQPDLLPSAAQR@.L	8.41	1.09	7.69	0.13
Q9CWN7_CNO11_MOUSE	Cnot11	CCR4-NOT transcription	K.TLDTGETPSETK#.I	15.72	3.72	4.22	0.24
Q9CWN7_CNO11_MOUSE	Cnot11	CCR4-NOT transcription	K.TLDTGETPSETK#.I	19.45	3.47	5.60	0.18
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.APYVGMVTK#PANEQSQDFSIHNEDFPALPGSSYK#DPTSSNDDSK#.S	4.81	1.66	2.90	0.35
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.EGSGNPTPLINPLAGR@.A	32.93	15.07	2.19	0.46
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	K.GIQVLPDGR@.V	34.98	21.29	1.64	0.61
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.GM*SNNTPQLNR@.S	18.53	5.99	3.09	0.32
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.NM*M*NHSQVGQGIGIPSR@.T	15.22	3.68	4.14	0.24
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.AAETDPGM*VHLALGSDLTTLGLNLNSPENLYPK#.F	13.43	3.99	3.37	0.30
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.EGSGNPTPLINPLAGR@.A	56.50	10.67	5.30	0.19
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	K.GIQVLPDGR@.V	23.63	18.54	1.27	0.78
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.NM*M*NHSQVGQGIGIPSR@.T	21.58	5.06	4.26	0.23
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.AAETDPGM*VHLALGSDLTTLGLNLNSPENLYPK#.F	4.19	1.73	2.42	0.41
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.EGSGNPTPLINPLAGR@.A	12.67	3.14	4.03	0.25
Q8C5L3_CNOT2_MOUSE	Cnot2	CCR4-NOT transcription	R.TNSM*SSSGLGSPNR@.S	8.73	1.26	6.95	0.14
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	K.AAGTLLNGPPQFSTTPEIK#.A	9.40	3.50	2.68	0.37
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	K.EGFTFEYR@.Y	11.64	4.29	2.71	0.37
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	K.TITDEFEQGTYIYFDYEK#.W	7.54	1.83	4.11	0.24
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	R.YLEDR@DLQ.-	153.16	92.25	1.66	0.60
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	K.AAGTLLNGPPQFSTTPEIK#.A	12.78	2.65	4.83	0.21
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	R.AAISSGIEDPVPTLHLTDR@.D	11.74	2.77	4.24	0.24
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	K.APEPLSSLK#.S	38.78	6.46	6.00	0.17
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	K.EGFTFEYR@.Y	16.08	4.30	3.74	0.27
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	R.STDSEVSQSPAK#.N	10.00	3.28	3.05	0.33
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	K.TITDEFEQGTYIYFDYEK#.W	6.47	2.28	2.84	0.35
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	K.YM*M*WFQR@.H	11.21	3.41	3.29	0.30
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	R.M*LDNDSILVDAIR@.K	7.82	14.93	0.52	1.91
Q8K0V4_CNOT3_MOUSE	Cnot3	CCR4-NOT transcription	R.STDSEVSQSPAK#.N	8.00	2.34	3.42	0.29
Q8K3P5_CNOT6_MOUSE	Cnot6	CCR4-NOT transcription	K.LFQLQTLSLK#.G	11.47	3.21	3.57	0.28
Q8VEG6_CNO6L_MOUSE	Cnot6l	CCR4-NOT transcription	K.HTVEFNQVAM*ANSDGSEAM*LNR@.V	3.39	1.96	1.74	0.58
Q8VEG6_CNO6L_MOUSE	Cnot6l	CCR4-NOT transcription	R.ELLLNDNYLR@.V	7.08	3.08	2.30	0.43
Q8VEG6_CNO6L_MOUSE	Cnot6l	CCR4-NOT transcription	K.GVIDYIFYSK#.T	4.93	1.40	3.53	0.28
Q8VEG6_CNO6L_MOUSE	Cnot6l	CCR4-NOT transcription	K.HTVEFNQVAM*ANSDGSEAM*LNR@.V	5.73	2.43	2.36	0.42
Q60809_CNOT7_MOUSE	Cnot7	CCR4-NOT transcription	K.GGLQEVAEQLELER@.I	51.63	14.50	3.56	0.28
Q60809_CNOT7_MOUSE	Cnot7	CCR4-NOT transcription	R.IGPQHQAGSDSLLTGM*AFFK#.M	14.36	5.85	2.45	0.41
Q60809_CNOT7_MOUSE	Cnot7	CCR4-NOT transcription	R.LFFPVIYDVK#.Y	79.96	20.60	3.88	0.26
Q60809_CNOT7_MOUSE	Cnot7	CCR4-NOT transcription	K.GGLQEVAEQLELER@.I	20.00	5.55	3.61	0.28
Q60809_CNOT7_MOUSE	Cnot7	CCR4-NOT transcription	R.IGPQHQAGSDSLLTGM*AFFK#.M	7.69	2.52	3.05	0.33
Q60809_CNOT7_MOUSE	Cnot7	CCR4-NOT transcription	R.LFFPVIYDVK#.Y	25.14	7.96	3.16	0.32
Q60809_CNOT7_MOUSE	Cnot7	CCR4-NOT transcription	K.GGLQEVAEQLELER@.I	18.24	7.31	2.50	0.40
Q60809_CNOT7_MOUSE	Cnot7	CCR4-NOT transcription	R.IGPQHQAGSDSLLTGM*AFFK#.M	11.44	1.99	5.75	0.17
Q60809_CNOT7_MOUSE	Cnot7	CCR4-NOT transcription	R.LFFPVIYDVK#.Y	42.31	10.70	3.96	0.25
Q9D8X5_CNOT8_MOUSE	Cnot8	CCR4-NOT transcription	K.GGLQEVADQLDLQR@.I	12.81	3.80	3.37	0.30
Q9D8X5_CNOT8_MOUSE	Cnot8	CCR4-NOT transcription	R.LYGLGTGVAQK#.Q	17.31	5.93	2.92	0.34
Q9D8X5_CNOT8_MOUSE	Cnot8	CCR4-NOT transcription	R.LYGLGTGVAQK#.Q	8.25	2.75	3.00	0.33
Q9D8X5_CNOT8_MOUSE	Cnot8	CCR4-NOT transcription	K.FNLTEDM*YSQDSIDLLANSGLQFQK#.H	5.65	1.54	3.66	0.27
Q9D8X5_CNOT8_MOUSE	Cnot8	CCR4-NOT transcription	R.LYGLGTGVAQK#.Q	15.97	4.00	3.99	0.25
P16330_CN37_MOUSE	Cnp	2',3'-cyclic-nucleotide 3'	K.GGSQGEAVGELPR@.G	8.01	3.06	2.62	0.38
Q9QXT0_CNPY2_MOUSE	Cnpy2	Protein canopy homolog	R.ALVDELEWEIAR@.V	16.89	21.01	0.80	1.24
Q9QXT0_CNPY2_MOUSE	Cnpy2	Protein canopy homolog	R.INPDGSQSVVEVPYAR@.S	9.41	6.84	1.38	0.73
Q8BQ47_CNPY4_MOUSE	Cnpy4	Protein canopy homolog	K.LLSM*ELQEALSR@.T	7.43	5.14	1.44	0.69
Q9Z160_COG1_MOUSE	Cog1	Conserved oligomeric Gc	R.ALQLLYDLR@.Y	11.26	3.26	3.46	0.29
Q9Z160_COG1_MOUSE	Cog1	Conserved oligomeric Gc	R.HLPTSIIEFQPTLR@.T	9.22	4.20	2.20	0.46
Q9Z160_COG1_MOUSE	Cog1	Conserved oligomeric Gc	R.SVETQAQVGPPALSR@.V	5.76	2.29	2.52	0.40
Q9Z160_COG1_MOUSE	Cog1	Conserved oligomeric Gc	R.TSVLFGLVTGTENQFASR@.S	6.59	1.51	4.38	0.23
Q9Z160_COG1_MOUSE	Cog1	Conserved oligomeric Gc	K.VK#LDDLLAYLPSSDTPLLK#.D	17.08	6.08	2.81	0.36
Q921L5_COG2_MOUSE	Cog2	Conserved oligomeric Gc	K.DVSSQEASSPLLTGQVLER@.I	5.99	2.39	2.51	0.40
Q921L5_COG2_MOUSE	Cog2	Conserved oligomeric Gc	K.LPSLFNPGDPDAFHQK#.Y	13.79	8.60	1.60	0.62
Q921L5_COG2_MOUSE	Cog2	Conserved oligomeric Gc	R.LQEWLPDLLETVK#.Q	12.06	2.59	4.65	0.22
Q921L5_COG2_MOUSE	Cog2	Conserved oligomeric Gc	R.SSVSEGILAVDER@.M	12.27	3.87	3.17	0.32
E9QL65_E9QL65_MOUSE	Cog3	Conserved oligomeric Gc	R.LFVEQLEEFM*TK#.V	7.48	9.31	0.80	1.25
Q8R1U1_COG4_MOUSE	Cog4	Conserved oligomeric Gc	K.LFSQGIGGEQAQAK#.F	6.72	5.88	1.14	0.88
Q8R1U1_COG4_MOUSE	Cog4	Conserved oligomeric Gc	R.LSQM*ATILNLER@.V	14.56	3.42	4.26	0.23
Q8C0L8_COG5_MOUSE	Cog5	Conserved oligomeric Gc	R.LLEQGVETQNPTQVGTALQVFHNLGTLK#.E	3.17	1.58	2.01	0.50
Q8R3I3_COG6_MOUSE	Cog6	Conserved oligomeric Gc	K.ALSAFFVENSLR@.T	10.53	18.06	0.58	1.71
Q8R3I3_COG6_MOUSE	Cog6	Conserved oligomeric Gc	K.ALSAFFVENSLR@.T	10.21	3.40	3.00	0.33
Q8R3I3_COG6_MOUSE	Cog6	Conserved oligomeric Gc	R.IEQVILAEPGAVLLYK#.I	5.99	2.79	2.15	0.47
Q8R3I3_COG6_MOUSE	Cog6	Conserved oligomeric Gc	R.SLAINEEFVNIFK#.D	10.24	3.21	3.19	0.31
Q8R3I3_COG6_MOUSE	Cog6	Conserved oligomeric Gc	K.TTLALFEFTDR@.R	6.17	2.23	2.77	0.36
Q5SU73_COIL_MOUSE	Coil	Coilin OS=Mus musculus	K.LM*EDEETDQGYK#.S	4.74	1.52	3.12	0.32
Q5SU73_COIL_MOUSE	Coil	Coilin OS=Mus musculus	R.VVTDLISLIR@.Q	14.77	6.23	2.37	0.42
Q5SU73_COIL_MOUSE	Coil	Coilin OS=Mus musculus	R.VVTDLISLIR@.Q	16.51	5.25	3.15	0.32
Q5SU73_COIL_MOUSE	Coil	Coilin OS=Mus musculus	K.LM*EDEETDQGYK#.S	9.26	2.43	3.82	0.26
Q61245_COBA1_MOUSE	Col11a1	Collagen alpha-1(XI) chai	R.ILETDVFQGDIQQFLITGDPK#.A	9.42	8.60	1.10	0.91
Q61245_COBA1_MOUSE	Col11a1	Collagen alpha-1(XI) chai	R.VTEEAQISAPTK#.Q	11.63	8.54	1.36	0.73
P11087_CO1A1_MOUSE	Col1a1	Collagen alpha-1(I) chain	R.DRDLEVDTTLK.S	3.10	10.08	0.31	3.26
P11087_CO1A1_MOUSE	Col1a1	Collagen alpha-1(I) chain	K.SLSQQIENIR.S	138.62	10.63	13.04	0.08
Q30D77_COOA1_MOUSE	Col24a1	Collagen alpha-1(XXIV) c	K.GFR@GETGPQGPR@.G	5.46	2.04	2.68	0.37
Q3U962_CO5A2_MOUSE	Col5a2	Collagen alpha-2(V) chai	R.NTVGYM*DDQAK.N	4.96	8.26	0.60	1.66
Q04857_CO6A1_MOUSE	Col6a1	Collagen alpha-1(VI) chai	K.TAEYDVAFGER.H	1.97	8.22	0.24	4.17
Q8K297_GT251_MOUSE	Colgalt1	Procollagen galactosyltra	K.NSDVLQSPLDSTARDEL.-	3.20	4.34	0.74	1.36
Q8K4M5_COMD1_MOUSE	Commd1	COMM domain-containi	K.SIASADM*DFNQLEAFLTAQTK#.K	9.09	2.61	3.48	0.29
Q8JZY2_COMDA_MOUSE	Commd10	COMM domain-containi	K.AVPLINAIDTGR@.F	12.17	4.77	2.55	0.39
Q8JZY2_COMDA_MOUSE	Commd10	COMM domain-containi	K.DK#AEAFASAWSAM*GQETVEK#.F	5.24	2.87	1.83	0.55
Q8BXC6_COMD2_MOUSE	Commd2	COMM domain-containi	R.IAVEFLR.R	36.59	19.13	1.91	0.52
Q8BXC6_COMD2_MOUSE	Commd2	COMM domain-containi	R.LDVQLASR@.S	12.81	30.70	0.42	2.40
Q8BXC6_COMD2_MOUSE	Commd2	COMM domain-containi	R.TILNELAPR@.L	29.00	13.96	2.08	0.48
Q63829_COMD3_MOUSE	Commd3	COMM domain-containi	K.NSLETLLGSIGR.S	28.71	8.98	3.20	0.31
Q9CQ02_COMD4_MOUSE	Commd4	COMM domain-containi	K.ELLGQGIDYEK#.I	8.12	4.73	1.72	0.58
Q8R395_COMD5_MOUSE	Commd5	COMM domain-containi	R.LAVLLAGTHTLLQQALR@.L	2.88	2.51	1.15	0.87
Q8R395_COMD5_MOUSE	Commd5	COMM domain-containi	R.YSVALVLK#.E	7.69	3.17	2.43	0.41
Q3V4B5_COMD6_MOUSE	Commd6	COMM domain-containi	K.SEVTGQLIDFQWK#.L	13.25	8.30	1.60	0.63
Q3V4B5_COMD6_MOUSE	Commd6	COMM domain-containi	K.SIEM*TIPQFQNFYK#.Q	10.17	6.14	1.66	0.60
Q8BG94_COMD7_MOUSE	Commd7	COMM domain-containi	R.FGVTSGSSELEK#.V	8.23	4.20	1.96	0.51
Q8BG94_COMD7_MOUSE	Commd7	COMM domain-containi	R.TDLQTLGLSEEK#.A	7.90	4.18	1.89	0.53
Q9CZG3_COMD8_MOUSE	Commd8	COMM domain-containi	K.HVLEDVTTFFK#.A	12.88	3.72	3.46	0.29
Q8K2Q0_COMD9_MOUSE	Commd9	COMM domain-containi	R.AEAQANQISLPR@.L	8.66	2.92	2.97	0.34
Q8K2Q0_COMD9_MOUSE	Commd9	COMM domain-containi	K.ETLDTM*LDGLGR@.I	7.50	4.38	1.72	0.58
Q8K2Q0_COMD9_MOUSE	Commd9	COMM domain-containi	R.IR@DQLSAVANK#.-	7.01	1.48	4.75	0.21
Q8K2Q0_COMD9_MOUSE	Commd9	COMM domain-containi	R.LVDLDWR@.V	7.64	3.38	2.26	0.44
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.ASNLENSTYDLYTIPK#.D	21.42	12.73	1.68	0.59

Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.DADSITLFDVQQK#.R	29.21	16.62	1.76	0.57
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.DADSQNPDAPEGK#.R	8.18	4.47	1.83	0.55
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.FAVLDR@.M	17.98	11.22	1.60	0.62
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.GFFEGSIASK#.G	27.84	13.55	2.05	0.49
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.GITGVDLFGTTDAVVK#.H	38.48	18.36	2.10	0.48
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.GVNWAAFHPTM*PLIVSGADDR@.Q	23.39	8.98	2.61	0.38
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.LLELGPK#PEVAQQTR@.K	25.45	16.29	1.56	0.64
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.LLHDQVGVIQFGPYK#.Q	31.76	15.58	2.04	0.49
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.LVGQSIIAYLQK#.K	45.09	17.93	2.51	0.40
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.NLSPGAVESDVR@.G	31.21	13.51	2.31	0.43
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.QQPLFVSGGDDYK.I	8.05	6.37	1.26	0.79
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.SGAWDESGVFIYTTSNHIK#.Y	10.15	5.34	1.90	0.53
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.SILLSVPLLVVDNK#.Q	22.70	10.99	2.07	0.48
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.SLAYLSAATHGLDEEAESLKETFDPEKETIPDIDPNAK.L	6.62	2.82	2.35	0.43
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.SSGLTAVWVAR@.N	9.12	4.46	2.05	0.49
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.TALNLFFK#.L	33.67	18.60	1.81	0.55
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.TLDLPIYVTR@.V	42.04	22.06	1.91	0.52
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.VLTIDPTEFK#.F	33.99	19.96	1.70	0.59
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.VTTVTEIGK#DVIGLR@.I	78.72	35.48	2.22	0.45
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.VWDISGLR@.K	23.71	11.04	2.15	0.47
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.ASNLENSTYDLYTIPK#.D	75.35	19.78	3.81	0.26
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.DADSITLFDVQQK#.R	74.66	23.58	3.17	0.32
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.DADSQNPDAPEGK#.R	34.50	13.43	2.57	0.39
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.DVAVM*QLR@.S	116.01	39.54	2.93	0.34
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.FAVLDR@.M	59.39	19.35	3.07	0.33
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.GFFEGSIASK#.G	86.09	27.49	3.13	0.32
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.GITGVDLFGTTDAVVK#.H	147.31	49.15	3.00	0.33
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.GVNWAAFHPTM*PLIVSGADDR@.Q	55.58	17.31	3.21	0.31
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.GVNWAAFHPTMPLIVSGADDR@.Q	9.13	2.53	3.61	0.28
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.K#DM*SGHYQNALYLGDVSER@.V	21.12	8.90	2.37	0.42
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.K#YDEVLHM*VR@.N	37.82	8.60	4.40	0.23
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.LLELGPK#PEVAQQTR@.K	98.95	32.28	3.07	0.33
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.LLHDQVGVIQFGPYK#.Q	85.76	30.85	2.78	0.36
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.LLQPPAPIM*PLDTNWPLLTVSK#.G	48.67	16.86	2.89	0.35
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.LVGQSIIAYLQK#.K	152.95	53.14	2.88	0.35
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.NLSPGAVESDVR@.G	98.85	31.96	3.09	0.32
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.QELILSNSEDK#.S	64.17	20.38	3.15	0.32
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.QLFLQTYAR@.G	39.31	12.77	3.08	0.32
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.QQPLFVSGGDDYK#.I	38.92	14.62	2.66	0.38
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	K.SGAWDESGVFIYTTSNHIK#.Y	38.31	13.18	2.91	0.34
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.SILLSVPLLVVDNK#.Q	88.00	31.97	2.75	0.36
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.SSGLTAVWVAR@.N	21.47	6.35	3.38	0.30
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.TALNLFFK#.L	83.61	29.24	2.86	0.35
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.TGVQTFR@.R	75.33	26.26	2.87	0.35
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.TLDLPIYVTR@.V	176.53	55.60	3.18	0.31
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.VLTIDPTEFK#.F	158.64	51.29	3.09	0.32
Q8CIE6_COPA_MOUSE	Copa	Coatomer subunit alpha	R.VWDISGLR@.K	78.71	22.94	3.43	0.29
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.LVEK#PSPLTLAPHDFANIK#.A	6.73	4.13	1.63	0.61
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.EAELLEPLM*PAIR@.A	9.21	11.20	0.82	1.22
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.EAGELK#PEEEITVGPVQK#.L	61.00	35.28	1.73	0.58
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.LK#EAELLEPLM*PAIR@.A	29.71	16.93	1.75	0.57
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.LK#EAELLEPLMPAIR@.A	10.02	4.25	2.36	0.42
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.LVEK#PSPLTLAPHDFANIK#.A	53.88	31.06	1.74	0.58
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.LVEKPSPLTLAPHDFANIK.A	10.92	6.77	1.61	0.62
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.NAVLAIYTIYR@.N	25.89	10.45	2.48	0.40
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.NVEELVIVLK#.K	24.19	9.20	2.63	0.38
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.NVTVQPDDPISFM*QLTAK#.N	12.01	2.75	4.36	0.23
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.QSLSQM*LSAK#.L	23.87	6.91	3.46	0.29
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.TLQLALDLVSSR@.N	26.25	14.20	1.85	0.54
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.TNNVSEHEDTDK#YR@.Q	1.71	2.15	0.79	1.26
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.VLQDLVM*DILR@.V	53.86	23.63	2.28	0.44
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.VLQDLVMDILR@.V	14.86	5.91	2.51	0.40
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.VLSTPDLEVR@.K	81.77	35.38	2.31	0.43
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.YVALVQEK#.K	52.67	21.57	2.44	0.41
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.EAELLEPLM*PAIR@.A	18.80	24.77	0.76	1.32
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.EAGELK#PEEEITVGPVQK#.L	116.13	37.51	3.10	0.32
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.EDIQSVM*TEVR@.R	15.76	2.80	5.62	0.18
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.LEEEK#LSQK#.K	8.34	5.43	1.54	0.65
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.LK#EAELLEPLM*PAIR@.A	47.61	14.06	3.39	0.30
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.LVEK#PSPLTLAPHDFANIK#.A	94.60	30.00	3.15	0.32
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.LVEKPSPLTLAPHDFANIK.A	17.88	9.83	1.82	0.55
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.NFEHLIPDAPELIHDFLVNEK#.D	10.08	4.50	2.24	0.45
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.NVEELVIVLK#.K	31.28	15.90	1.97	0.51
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.NVTVQPDDPISFM*QLTAK#.N	17.34	7.32	2.37	0.42
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.NVTVQPDDPISFM*QLTAK#.N	7.51	5.01	1.50	0.67
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.QSLSQM*LSAK#.L	38.52	15.87	2.43	0.41
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.R@SLGEIPIVESEIK#K#.E	10.06	1.57	6.40	0.16
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.SLGEIPIVESEIK#.K	17.82	5.37	3.32	0.30
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.TLQLALDLVSSR@.N	42.83	15.36	2.79	0.36
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.TNNVSEHEDTDK#YR@.Q	48.25	11.72	4.12	0.24
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.VASTENGIIFGNIVYDVSGAASDR@.N	12.61	3.91	3.22	0.31
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.VLQDLVM*DILR@.V	114.73	37.76	3.04	0.33
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.VLQDLVMDILR@.V	19.19	4.09	4.69	0.21
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.VLSTPDLEVR.K	88.04	36.00	2.45	0.41
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	K.YEAAGTLVTLSSAPTAIK#.A	52.50	15.13	3.47	0.29
Q9JIF7_COPB_MOUSE	Copb1	Coatomer subunit beta C	R.YVALVQEK#.K	51.47	14.64	3.52	0.28
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.AM*GDTEIK#DGER@.L	5.81	1.72	3.37	0.30
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.DNNQFASASLDR@.T	63.09	19.33	3.26	0.31
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.FELALQLGELK#.I	10.56	5.10	2.07	0.48
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.HSEVQQANLK#.A	37.91	10.67	3.55	0.28
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.IAYQLAVEAESEQK#.W	18.23	6.32	2.88	0.35
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.IWDYQNK#.T	22.24	10.88	2.04	0.49
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.K#NWVVTGADDM*QIR@.V	11.53	3.93	2.94	0.34
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.LESTLNYGM*ER.V	42.82	12.51	3.42	0.29
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.LPEAAFLAR.T	99.09	31.64	3.13	0.32
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.QLAELAISK#.C	33.85	13.16	2.57	0.39
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.QQALTVSTDPEHR@.F	3.90	1.97	1.98	0.50
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.QYPLVTPNEER@.N	22.42	11.82	1.90	0.53
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.SFK#PDFGAESIYGGFLLGVR@.S	31.23	12.51	2.50	0.40
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.SVNGLAFYDWENTELIR@.R	11.54	4.61	2.50	0.40
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.TM*YLLGYIPK#.D	19.85	7.92	2.51	0.40
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.TMYLLGYIPK#.D	13.53	5.22	2.59	0.39
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.TYLPSQVSR.V	77.31	27.42	2.82	0.35

O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.VFNYNTLER@.V	58.17	18.64	3.12	0.32
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.AM*GDTEIK#DGER@.L	7.86	2.38	3.30	0.30
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.DNNQFASASLDR@.T	119.75	39.40	3.04	0.33
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.EAFVVEEWVK#.E	64.82	17.57	3.69	0.27
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.FELALQLGELK#.I	29.20	10.71	2.73	0.37
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.GSNNVALGYDEGSIIVK#.L	144.73	63.42	2.28	0.44
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.HSEVQQANLK#.A	165.96	51.96	3.19	0.31
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.IAYQLAVEAESEQK#.W	18.42	118.34	0.16	6.43
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.IWDYQNK#.T	35.38	13.16	2.69	0.37
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.K#NWVVTGADDM*QIR@.V	24.82	8.23	3.02	0.33
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.LESTLNYGM*ER@.V	61.31	21.71	2.82	0.35
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.LPEAAFLAR@.T	201.11	66.22	3.04	0.33
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.NWVVTGADDM*QIR@.V	10.27	3.26	3.15	0.32
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.QLAELAISK#.C	62.00	15.71	3.95	0.25
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.QQALTVSTDPEHR@.F	53.17	17.74	3.00	0.33
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.QYPLVTPNEER@.N	43.99	16.60	2.65	0.38
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	K.SFK#PDFGAESIYGGFLLGVR@.S	31.08	10.21	3.04	0.33
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.SVNGLAFYDWENTELIR@.R	23.57	8.44	2.79	0.36
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.TM*YLLGYIPK#.D	36.21	11.78	3.07	0.33
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.TMYLLGYIPK#.D	27.62	10.29	2.69	0.37
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.TYLPSQVSR.V	100.51	34.54	2.91	0.34
O55029_COPB2_MOUSE	Copb2	Coatomer subunit beta' (	R.VFNYNTLER@.V	154.23	44.88	3.44	0.29
O89079_COPE_MOUSE	Cope	Coatomer subunit epsilo	R.DSIVLELDR.E	25.37	12.36	2.05	0.49
O89079_COPE_MOUSE	Cope	Coatomer subunit epsilo	R.DSIVLELDR@EM*SR@.S	56.62	17.00	3.33	0.30
O89079_COPE_MOUSE	Cope	Coatomer subunit epsilo	R.K#YGVVLDEIK#PSSAPELQAVR@.M	202.14	73.50	2.75	0.36
O89079_COPE_MOUSE	Cope	Coatomer subunit epsilo	R.LAM*QYAPSA.-	86.95	86.95	1.00	1.00
O89079_COPE_MOUSE	Cope	Coatomer subunit epsilo	K.LQEAYYIFQELADK#.C	17.97	4.87	3.69	0.27
O89079_COPE_MOUSE	Cope	Coatomer subunit epsilo	R.M*FAEYLASENQR@.D	79.44	30.01	2.65	0.38
O89079_COPE_MOUSE	Cope	Coatomer subunit epsilo	R.MFAEYLASENQR@.D	29.71	10.90	2.73	0.37
O89079_COPE_MOUSE	Cope	Coatomer subunit epsilo	R.SVDVTNTTFLLM*AASIYFHDQNPDAALR@.T	35.10	12.89	2.72	0.37
O89079_COPE_MOUSE	Cope	Coatomer subunit epsilo	K.YGVVLDEIK#PSSAPELQAVR@.M	114.24	55.33	2.06	0.48
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.SIATLAITTLLK#.T	20.40	3.59	5.68	0.18
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.VFNETPINPR@.K	7.33	1.99	3.69	0.27
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.ALQQYTLEPSEK#PFDLK#.S	65.96	34.16	1.93	0.52
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.ATFYLNVLEQK#.Q	44.77	16.30	2.75	0.36
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.FGAQNEEM*LPSILVLLK#.R	14.16	9.03	1.57	0.64
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.ILHLLGQEGPK#.T	64.69	53.24	1.22	0.82
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.ILYLINQGEHLGTTEATEAFFAM*TK#.L	32.35	11.65	2.78	0.36
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.ILYLINQGEHLGTTEATEAFFAMTK#.L	9.13	5.48	1.67	0.60
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.K#DEESGGGSNPLQHLEK#.S	8.24	3.32	2.48	0.40
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.LFQSNDPTLR@.R	37.73	8.47	4.46	0.22
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.LLLLDTVTM*QVTAR@.S	29.59	8.04	3.68	0.27
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.NTHTLLLAGVFR@.G	31.43	11.41	2.76	0.36
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.QISSFM*SEISDEFK#.V	6.88	2.85	2.42	0.41
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.SIATLAITTLLK#.T	90.86	31.76	2.86	0.35
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.SSPEPVALTESETEYVIR@.C	34.11	16.08	2.12	0.47
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.TLEEAVGNIVK#.F	66.25	23.43	2.83	0.35
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.VFNETPINPR@.K	41.19	16.90	2.44	0.41
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.VPSVSSSALVSSLHLLK#.C	12.70	4.32	2.94	0.34
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.AGAVSALAK#.F	104.13	26.89	3.87	0.26
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.ALNAGYILNGLTVSIPGLEK#.A	18.27	2.49	7.34	0.14
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.ALQQYTLEPSEK#PFDLK#.S	114.64	39.70	2.89	0.35
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.ATFYLNVLEQK#.Q	75.08	18.66	4.02	0.25
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.FGAQNEEM*LPSILVLLK.R	26.70	6.94	3.85	0.26
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.FGAQNEEM*LPSILVLLK#R@.C	9.23	3.26	2.83	0.35
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.GGHDILVR@.S	21.19	4.59	4.62	0.22
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.ILHLLGQEGPK#.T	125.32	36.08	3.47	0.29
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.ILYLINQGEHLGTTEATEAFFAM*TK#.L	52.32	13.47	3.89	0.26
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.ILYLINQGEHLGTTEATEAFFAMTK#.L	10.11	5.54	1.82	0.55
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.LFQSNDPTLR@.R	52.55	14.91	3.52	0.28
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.LLLLDTVTM*QVTAR@.S	52.22	16.22	3.22	0.31
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.NTHTLLLAGVFR@.G	37.15	7.58	4.90	0.20
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.QAIVDK#VPSVSSSALVSSLHLLK#.C	41.88	9.90	4.23	0.24
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.QISSFM*SEISDEFK#.V	127.38	65.58	1.94	0.51
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.SAVLQEAR@.V	130.31	37.21	3.50	0.29
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.SIATLAITTLLK#.T	249.89	63.77	3.92	0.26
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.SSEELPVDIILASVG.-	19.03	19.03	1.00	1.00
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.SSPEPVALTESETEYVIR@.C	59.39	18.87	3.15	0.32
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.TLEEAVGNIVK#.F	131.08	49.15	2.67	0.37
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	R.VFNETPINPR@.K	79.44	22.02	3.61	0.28
Q9QZE5_COPG1_MOUSE	Copg1	Coatomer subunit gamm	K.VPSVSSSALVSSLHLLK#.C	21.40	7.62	2.81	0.36
Q9QXK3_COPG2_MOUSE	Copg2	Coatomer subunit gamm	K.ILK#PNFAAAWEEVGDAFEK#EETFALSSTK#.T	8.07	4.05	1.99	0.50
Q9QXK3_COPG2_MOUSE	Copg2	Coatomer subunit gamm	R.IFNETPINPR@.R	14.62	6.32	2.31	0.43
Q9QXK3_COPG2_MOUSE	Copg2	Coatomer subunit gamm	R.ITDGTM*LQAVER@.Y	9.25	3.39	2.73	0.37
Q9QXK3_COPG2_MOUSE	Copg2	Coatomer subunit gamm	K.SIPLAM*APVFEQK#.S	16.22	4.96	3.27	0.31
Q9QXK3_COPG2_MOUSE	Copg2	Coatomer subunit gamm	K.SSEPVQLTEAETEYFVR@.C	8.20	3.34	2.45	0.41
P61202_CSN2_MOUSE	Cops2	COP9 signalosome comp	K.AALSSFQK#.V	25.46	14.22	1.79	0.56
P61202_CSN2_MOUSE	Cops2	COP9 signalosome comp	K.LTNFPEM*M*NR@.Y	8.64	3.10	2.79	0.36
P61202_CSN2_MOUSE	Cops2	COP9 signalosome comp	K.SINSILDYISTSK#.Q	20.96	6.67	3.14	0.32
P61202_CSN2_MOUSE	Cops2	COP9 signalosome comp	K.SINSILDYISTSK#.Q	9.64	3.88	2.49	0.40
O88543_CSN3_MOUSE	Cops3	COP9 signalosome comp	K.AM*DQEITVNPQFVQK#.S	7.06	3.62	1.95	0.51
O88543_CSN3_MOUSE	Cops3	COP9 signalosome comp	K.SM*GSQEDDSGNK#PSSYS.-	3.26	1.48	2.21	0.45
O88544_CSN4_MOUSE	Cops4	COP9 signalosome comp	K.AIQLSGTEQLEALK#.A	31.76	14.86	2.14	0.47
O88544_CSN4_MOUSE	Cops4	COP9 signalosome comp	K.ATTADGSSILDR@.A	28.79	11.80	2.44	0.41
O88544_CSN4_MOUSE	Cops4	COP9 signalosome comp	K.IASQM*ITEGR@.M	55.44	20.97	2.64	0.38
O88544_CSN4_MOUSE	Cops4	COP9 signalosome comp	R.K#FIEAAQR@.Y	15.50	13.90	1.12	0.90
O88544_CSN4_MOUSE	Cops4	COP9 signalosome comp	R.LYLEDDDPVQAEAYINR@.A	15.68	3.45	4.55	0.22
O88544_CSN4_MOUSE	Cops4	COP9 signalosome comp	R.NAAQVLVGIPLETGQK#.Q	29.73	10.39	2.86	0.35
O88544_CSN4_MOUSE	Cops4	COP9 signalosome comp	R.VISFEEQVASIR@.Q	56.00	18.40	3.04	0.33
O35864_CSN5_MOUSE	Cops5	COP9 signalosome comp	K.GYKPPDEGPSEYQTIPLNK.I	12.88	7.06	1.82	0.55
O35864_CSN5_MOUSE	Cops5	COP9 signalosome comp	K.ISALALLK#.M	19.43	6.60	2.94	0.34
O35864_CSN5_MOUSE	Cops5	COP9 signalosome comp	K.LEQSEAQLGR@.G	22.70	8.28	2.74	0.36
O35864_CSN5_MOUSE	Cops5	COP9 signalosome comp	K.LFNQINVA.-	15.48	15.48	1.00	1.00
O35864_CSN5_MOUSE	Cops5	COP9 signalosome comp	K.LLELLWNK#.Y	9.56	4.71	2.03	0.49
O35864_CSN5_MOUSE	Cops5	COP9 signalosome comp	K.QQQEILAAK#PWTK#.D	13.52	23.02	0.59	1.70
O35864_CSN5_MOUSE	Cops5	COP9 signalosome comp	K.VNLGAFR@.T	25.58	5.86	4.36	0.23
O88545_CSN6_MOUSE	Cops6	COP9 signalosome comp	K.FNVLYDR@.Q	22.08	6.66	3.32	0.30
Q9CZ04_CSN7A_MOUSE	Cops7a	COP9 signalosome comp	R.ELAESDFASTFR@.L	33.39	8.16	4.09	0.24
Q9CZ04_CSN7A_MOUSE	Cops7a	COP9 signalosome comp	R.LLTVFAYGTYADYLAEAR@.N	14.55	4.31	3.37	0.30
Q9CZ04_CSN7A_MOUSE	Cops7a	COP9 signalosome comp	K.VTGQNQEQFLLLAK#.S	18.48	5.69	3.25	0.31
Q8BV13_CSN7B_MOUSE	Cops7b	COP9 signalosome comp	K.ESLPELSVAQQNK#.L	8.95	6.57	1.36	0.73
Q8BV13_CSN7B_MOUSE	Cops7b	COP9 signalosome comp	R.TQQQVEAEVSNIK#K#.T	15.64	6.72	2.33	0.43
Q8VBV7_CSN8_MOUSE	Cops8	COP9 signalosome comp	R.FIPLSEPAPVPPIPNEQQLAR@.L	10.23	4.81	2.12	0.47

Q8VBV7_CSN8_MOUSE	Cops8	COP9 signalosome comp	R.FIPLSEPAPVPPIPNEQQLAR@.L	36.60	11.30	3.24	0.31
Q8VBV7_CSN8_MOUSE	Cops8	COP9 signalosome comp	K.GVLEQGWQADSTTR@.M	17.33	6.71	2.58	0.39
Q8VBV7_CSN8_MOUSE	Cops8	COP9 signalosome comp	K.SANSELGGIWSVGQR@.I	23.45	8.11	2.89	0.35
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	R.VALR@GEDVPLTEQTVSQVLQSAK#.E	9.36	2.94	3.18	0.31
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	K.YYDDTYPSVK#.E	9.53	2.49	3.83	0.26
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	K.AILILDNDGDR.L	142.40	46.22	3.08	0.32
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	R.GEDVPLTEQTVSQVLQSAK#.E	57.80	19.98	2.89	0.35
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	R.TDSEIALLEGLTVVYK#.S	31.61	12.38	2.55	0.39
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	R.VALR@GEDVPLTEQTVSQVLQSAK#.E	394.12	108.27	3.64	0.27
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	K.YYDDTYPSVK#.E	136.58	45.62	2.99	0.33
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	R.VALR@GEDVPLTEQTVSQVLQSAK#.E	20.95	4.37	4.79	0.21
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	K.AILILDNDGDR@.L	8.92	4.29	2.08	0.48
P61924_COPZ1_MOUSE	Copz1	Coatomer subunit zeta-1	R.VALR@GEDVPLTEQTVSQVLQSAK#.E	12.73	7.03	1.81	0.55
Q9JHH9_COPZ2_MOUSE	Copz2	Coatomer subunit zeta-2	R.TDDSGLTEQSVAQVLQSAK#.E	36.84	13.18	2.80	0.36
Q9JHH9_COPZ2_MOUSE	Copz2	Coatomer subunit zeta-2	K.YYDDTFPSVK#.E	37.67	8.49	4.44	0.23
P19783_COX41_MOUSE	Cox4i1	Cytochrome c oxidase su	K.ADWSSLSR.D	6.96	5.75	1.21	0.83
P19783_COX41_MOUSE	Cox4i1	Cytochrome c oxidase su	R.IQFNESFAEM*NR.G	10.36	8.97	1.16	0.87
P19783_COX41_MOUSE	Cox4i1	Cytochrome c oxidase su	K.SEDYAFPTYADR@.R	3.59	2.24	1.60	0.62
P12787_COX5A_MOUSE	Cox5a	Cytochrome c oxidase su	K.GM*NTLVGYDLVPEPK#.I	8.02	10.54	0.76	1.31
P36552_HEM6_MOUSE	Cpox	Oxygen-dependent copro	K.K#HCDDSYTPRDK#.L	1.24	4.23	0.29	3.40
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.DALLLSFK#.D	18.80	5.73	3.28	0.30
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.DVSGM*FTTESR@.L	5.34	2.89	1.85	0.54
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.EVLLVALGSR@.Q	35.25	16.64	2.12	0.47
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.GGEIYVLTLITDGM*R@.S	9.55	3.39	2.82	0.36
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.HGFLILSR@.E	38.64	14.00	2.76	0.36
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.IGTTPDIILDDLLETDR@.V	10.30	4.82	2.14	0.47
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.ISVLPAYLSYDAPWPVR@.K	12.17	5.83	2.09	0.48
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.LGNSLLLK#.Y	32.76	11.26	2.91	0.34
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.LQEPPASSVR@.E	16.94	7.35	2.30	0.43
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.LVFLVK#.N	23.28	8.72	2.67	0.37
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.LVVLPFR@.R	22.08	8.85	2.49	0.40
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.NVLDGELLNR@.Y	30.40	13.46	2.26	0.44
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.SSFLPSYIIDVR@.A	39.29	17.15	2.29	0.44
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.TLSLHYFEEPELR@.D	55.38	21.23	2.61	0.38
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.VLVDSSFGQPTTQGEVR@.K	38.31	12.38	3.10	0.32
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.YIVQVSPLGIR@.L	42.85	15.02	2.85	0.35
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.YLYLSTM*ER@.S	14.68	9.16	1.60	0.62
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.AAASVLTTSM*VTM*EPGYLFLGSR@.L	44.74	10.62	4.21	0.24
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.AESTEQEPSAPK#.A	15.22	6.50	2.34	0.43
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.DALLLSFK#.D	47.93	9.18	5.22	0.19
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.DVSGM*FTTESR@.L	24.80	7.38	3.36	0.30
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.EAADK#EEPPSK#.K	6.93	1.37	5.05	0.20
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.ESLAEEHEGLM*GEGQR@.S	50.32	12.11	4.16	0.24
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.EVLLVALGSR@.Q	116.12	28.04	4.14	0.24
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.GFLYFNR@.Q	36.46	6.64	5.49	0.18
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.GGEIYVLTLITDGM*R@.S	25.02	3.32	7.54	0.13
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.HGFLILSR@.E	102.64	28.08	3.66	0.27
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.IGTTPDIILDDLLETDR@.V	67.63	24.54	2.76	0.36
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.ILIM*DVIEVVPEPGQPLTK#.N	13.30	4.81	2.76	0.36
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.ILIMDVIEVVPEPGQPLTK#.N	14.29	2.49	5.74	0.17
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.ISVLPAYLSYDAPWPVR@.K	38.30	12.25	3.12	0.32
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.K#IGTTPDIILDDLLETDR@VTAHF.-	35.61	15.68	2.27	0.44
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.LGNSLLLK#.Y	87.63	20.06	4.37	0.23
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.LQEPPASSVR@.E	53.73	16.86	3.19	0.31
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.LSVVEYDPGTHDLK#.T	92.78	32.32	2.87	0.35
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.LVFLVK#.N	69.62	16.17	4.31	0.23
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.LVVLPFR@.R	91.12	27.71	3.29	0.30
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.NFILAADVM*K#.S	41.32	16.91	2.44	0.41
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.NLM*VYM*YLPEAK#.E	7.20	4.40	1.63	0.61
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.NLM*VYMYLPEAK#.E	6.66	4.98	1.34	0.75
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.NVLDGELLNR@.Y	135.98	43.88	3.10	0.32
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.R@DALLLSFK#.D	13.74	1.67	8.20	0.12
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.SEETVSGLK#.G	54.57	17.72	3.08	0.32
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.SSFLPSYIIDVR@.A	142.91	44.39	3.22	0.31
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	K.TLSLHYFEEPELR@.D	95.63	29.20	3.27	0.31
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.VLVDSSFGQPTTQGEVR@.K	103.56	28.56	3.63	0.28
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.YIVQVSPLGIR@.L	101.01	28.28	3.57	0.28
Q9EPU4_CPSF1_MOUSE	Cpsf1	Cleavage and polyadenyl	R.YLYLSTM*ER@.S	47.30	11.40	4.15	0.24
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.DEQLLTNVLETLR@.G	28.72	10.55	2.72	0.37
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.FLIDNPTEK#.V	37.05	21.42	1.73	0.58
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.FSQIVNLK#.G	39.84	15.89	2.51	0.40
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.HNTEDFTLFTLDDVDAAFDK#.I	18.09	9.57	1.89	0.53
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.HNTEDFTLFTLDDVDAAFDK#IQQLK#.F	10.91	4.20	2.60	0.38
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.HVHQIDAVLLSHPDPLHLGALPFAVGK#.L	13.26	8.39	1.58	0.63
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.IR@DLLYEQYAIV.-	42.38	13.04	3.25	0.31
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.IVK#DGEEEIVYAVDFNHK#.R	9.26	4.18	2.22	0.45
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.NSIILTYR@.T	22.54	12.88	1.75	0.57
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.QR@DEQLLTNVLETLR@.G	12.74	4.72	2.70	0.37
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.VTEIELR@.K	42.39	14.95	2.84	0.35
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.VTYIDYEGR@.S	41.68	16.34	2.55	0.39
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.DEQLLTNVLETLR@.G	28.42	6.69	4.25	0.24
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.FLIDNPTEK#.V	29.96	10.90	2.75	0.36
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.FSQIVNLK#.G	24.58	6.08	4.05	0.25
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.GDGNVLIAVDTAGR@.V	20.83	5.53	3.77	0.27
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.NSIILTYR@.T	20.47	130.75	0.16	6.39
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.QR@DEQLLTNVLETLR@.G	14.18	2.36	6.02	0.17
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.SLFGEDEK#ELGEETEIIPTLEPLPPHEVPGHQSVFM*NEPR@.L	2.23	2.74	0.81	1.23
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	K.VTEIELR@.K	32.84	6.55	5.01	0.20
O35218_CPSF2_MOUSE	Cpsf2	Cleavage and polyadenyl	R.VTYIDYEGR@.S	15.37	3.92	3.92	0.25
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	R.GLIPVFALGR@.A	193.84	64.55	3.00	0.33
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	R.K#QININNPFVFK#.H	17.25	4.28	4.03	0.25
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	K.LLYTGDFSR@.Q	70.83	21.85	3.24	0.31
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	R.LYEALTPVH.-	89.45	89.45	1.00	1.00
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	K.M*SVDYISFSAHTDYQQTSEFIR@.A	9.14	4.72	1.93	0.52
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	R.NTEAVTLNFR@.G	36.07	13.79	2.62	0.38
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	K.QININNPFVFK#.H	11.91	5.03	2.37	0.42
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	K.TANINLETR@.A	63.27	22.20	2.85	0.35
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	R.VSGILVK#.R	40.28	16.68	2.41	0.41
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	R.WLLSDYVK#.V	37.13	13.87	2.68	0.37
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	R.GLIPVFALGR@.A	17.56	8.42	2.09	0.48
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	K.LLYTGDFSR@.Q	11.53	5.38	2.15	0.47
Q9QXK7_CPSF3_MOUSE	Cpsf3	Cleavage and polyadenyl	R.LYEALTPVH.-	19.85	19.85	1.00	1.00
Q9CWS4_INT11_MOUSE	Cpsf3l	Integrator complex subu	K.VLIPVFALGR@.A	13.98	7.10	1.97	0.51

Q9CWS4_INT11_MOUSE	Cpsf3l	Integrator complex subu	R.VTPLGAGQDVGR@.S	21.69	15.74	1.38	0.73
Q9CWS4_INT11_MOUSE	Cpsf3l	Integrator complex subu	K.VLIPVFALGR@.A	16.28	5.62	2.90	0.35
Q9CWS4_INT11_MOUSE	Cpsf3l	Integrator complex subu	K.VGSESVVYTGDYNM*TPDR@.H	5.17	2.52	2.05	0.49
Q9CWS4_INT11_MOUSE	Cpsf3l	Integrator complex subu	K.VLIPVFALGR@.A	24.32	7.99	3.04	0.33
Q9CWS4_INT11_MOUSE	Cpsf3l	Integrator complex subu	R.VTPLGAGQDVGR@.S	15.14	5.40	2.81	0.36
Q8BQZ5_CPSF4_MOUSE	Cpsf4	Cleavage and polyadenyl	R.APQVIGVM*QSQNSSAGNR@.G	17.18	5.62	3.05	0.33
Q8BQZ5_CPSF4_MOUSE	Cpsf4	Cleavage and polyadenyl	K.GHLAFLSGQ.-	39.92	39.92	1.00	1.00
Q8BQZ5_CPSF4_MOUSE	Cpsf4	Cleavage and polyadenyl	K.R@APQVIGVM*QSQNSSAGNR@.G	7.69	2.60	2.96	0.34
Q8BQZ5_CPSF4_MOUSE	Cpsf4	Cleavage and polyadenyl	R.APQVIGVM*QSQNSSAGNR@.G	6.43	2.50	2.57	0.39
Q8BQZ5_CPSF4_MOUSE	Cpsf4	Cleavage and polyadenyl	R.FELPM*GTTEQPPLPQQTQPPTK#.R	36.75	17.54	2.10	0.48
Q8BQZ5_CPSF4_MOUSE	Cpsf4	Cleavage and polyadenyl	K.R@APQVIGVM*QSQNSSAGNR@.G	6.97	2.14	3.26	0.31
Q6NVF9_CPSF6_MOUSE	Cpsf6	Cleavage and polyadenyl	K.GAAPNVVYTYTGK#.R	10.93	5.04	2.17	0.46
Q6NVF9_CPSF6_MOUSE	Cpsf6	Cleavage and polyadenyl	R.AVSDASAGDYGSAIETLVTAISLIK#.Q	46.78	17.66	2.65	0.38
Q6NVF9_CPSF6_MOUSE	Cpsf6	Cleavage and polyadenyl	K.GAAPNVVYTYTGK#.R	37.11	10.19	3.64	0.27
Q6NVF9_CPSF6_MOUSE	Cpsf6	Cleavage and polyadenyl	K.GFALVGVGSEASSK#.K	42.01	13.01	3.23	0.31
Q6NVF9_CPSF6_MOUSE	Cpsf6	Cleavage and polyadenyl	K.K#LM*DLLPK#.R	12.26	4.89	2.51	0.40
Q6NVF9_CPSF6_MOUSE	Cpsf6	Cleavage and polyadenyl	K.QFLSQFEM*QSR@.K	7.79	1.69	4.60	0.22
Q6NVF9_CPSF6_MOUSE	Cpsf6	Cleavage and polyadenyl	R.TPLSEAEFEEIM*NR@.N	21.40	7.02	3.05	0.33
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	R.AISSSAISK#.A	60.87	18.60	3.27	0.31
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	K.LLELLPGK#.V	22.91	6.73	3.40	0.29
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	R.QNLSQFEAQAR@.K	51.50	15.03	3.43	0.29
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	R.SIGVYDVVELK#.F	33.75	12.41	2.72	0.37
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	R.SSSTEPPPPVR@.Q	22.79	6.76	3.37	0.30
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	K.TPAILYTYSGLR@.S	37.02	7.56	4.90	0.20
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	R.ATPSENLVPSSAR@.V	23.77	5.26	4.52	0.22
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	K.LLELLPGK#.V	22.68	7.37	3.08	0.32
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	R.QNLSQFEAQAR@.K	17.12	2.83	6.06	0.17
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	R.SIGVYDVVELK#.F	21.74	6.31	3.45	0.29
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	K.SYSVGASGSSSR@.K	14.49	6.30	2.30	0.43
Q8BTV2_CPSF7_MOUSE	Cpsf7	Cleavage and polyadenyl	K.TPAILYTYSGLR@.S	22.93	7.83	2.93	0.34
Q9DCT8_CRIP2_MOUSE	Crip2	Cysteine-rich protein 2 O	K.GVNIGGAGSYIYEK#PQTEAPQVTGPIEVPVVR@.T	8.72	5.05	1.73	0.58
Q9DCT8_CRIP2_MOUSE	Crip2	Cysteine-rich protein 2 O	K.GVNIGGAGSYIYEK#PQTEAPQVTGPIEVPVVR@.T	9.66	5.17	1.87	0.54
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	R.AIYELAISQPR@.L	39.28	24.54	1.60	0.62
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	R.ALDVDYR@.N	31.52	21.84	1.44	0.69
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.ANPHNYDAWFDYLR@.L	11.87	6.55	1.81	0.55
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.FAELETILGDIER@.A	39.90	20.30	1.97	0.51
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	R.LDM*PEVLWK#.S	8.10	4.57	1.77	0.56
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	R.LM*LLESWR@.S	17.17	10.58	1.62	0.62
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	R.LVESDAEADTVR@.E	26.02	16.48	1.58	0.63
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.SYIDFEIEQEETER@.T	9.42	6.22	1.51	0.66
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.VWISFAQFELSSGK#.E	5.96	2.87	2.08	0.48
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.YTYM*EEM*LGNVAGAR@.Q	9.57	3.15	3.04	0.33
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.APAEVQITAEQLLR@.E	13.09	8.80	1.49	0.67
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.FAELETILGDIER.A	44.46	26.58	1.67	0.60
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	R.LDM*PEVLWK#.S	11.06	5.62	1.97	0.51
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	R.LM*LLESWR@.S	16.26	9.10	1.79	0.56
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	R.LVESDAEADTVR@.E	26.21	14.59	1.80	0.56
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.NK#APAEVQITAEQLLR@.E	13.25	10.90	1.22	0.82
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.SYIDFEIEQEETER@.T	13.92	6.30	2.21	0.45
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	R.TVISNWIK#.Y	17.87	11.08	1.61	0.62
P63154_CRNL1_MOUSE	Crnkl1	Crooked neck-like protei	K.YTYM*EEM*LGNVAGAR@.Q	6.81	1.78	3.82	0.26
Q9CYD3_CRTAP_MOUSE	Crtap	Cartilage-associated prot	K.SYESLFVR@.A	19.15	12.35	1.55	0.64
Q91W50_CSDE1_MOUSE	Csde1	Cold shock domain-cont	K.EAFGFIER@.G	11.96	5.99	2.00	0.50
Q91W50_CSDE1_MOUSE	Csde1	Cold shock domain-cont	R.GPDNSM*GFGAER@.K	7.37	4.68	1.57	0.63
Q9ERK4_XPO2_MOUSE	Cse1l	Exportin-2 OS=Mus musc	R.GSSTIATAAADK#IPGLLGVFQK#.L	12.45	6.24	2.00	0.50
Q9ERK4_XPO2_MOUSE	Cse1l	Exportin-2 OS=Mus musc	K.ALTLPGSSENEYIM*K#.A	8.33	3.37	2.47	0.40
Q9ERK4_XPO2_MOUSE	Cse1l	Exportin-2 OS=Mus musc	R.GSSTIATAAADK#IPGLLGVFQK#.L	14.28	6.96	2.05	0.49
Q9ERK4_XPO2_MOUSE	Cse1l	Exportin-2 OS=Mus musc	K.LLQTDDEEEAGLLELLK#.S	8.40	6.18	1.36	0.74
P41241_CSK_MOUSE	Csk	Tyrosine-protein kinase C	R.LLYPPETGLFLVR@.E	3.86	3.45	1.12	0.89
Q60737_CSK21_MOUSE	Csnk2a1	Casein kinase II subunit a	R.EYWDYESHVVEWGNQDDYQLVR@.K	14.57	3.95	3.69	0.27
Q60737_CSK21_MOUSE	Csnk2a1	Casein kinase II subunit a	R.FNDILGR@.H	68.58	23.22	2.95	0.34
Q60737_CSK21_MOUSE	Csnk2a1	Casein kinase II subunit a	R.GGPNIITLADIVK#.D	19.31	11.86	1.63	0.61
Q60737_CSK21_MOUSE	Csnk2a1	Casein kinase II subunit a	R.GKYSEVFEAINITNNEK.V	46.07	15.58	2.96	0.34
Q60737_CSK21_MOUSE	Csnk2a1	Casein kinase II subunit a	R.LIDWGLAEFYHPGQEYNVR@.V	66.30	20.06	3.30	0.30
Q60737_CSK21_MOUSE	Csnk2a1	Casein kinase II subunit a	K.QLYQTLTDYDIR.F	34.66	16.55	2.09	0.48
Q60737_CSK21_MOUSE	Csnk2a1	Casein kinase II subunit a	R.TPALVFEHVNNTDFK#.Q	104.65	32.98	3.17	0.32
Q60737_CSK21_MOUSE	Csnk2a1	Casein kinase II subunit a	K.VLGTEDLYDYIDK#.Y	6.95	3.44	2.02	0.50
Q60737_CSK21_MOUSE	Csnk2a1	Casein kinase II subunit a	K.VLGTEDLYDYIDKYNIELDPR.F	78.73	25.34	3.11	0.32
O54833_CSK22_MOUSE	Csnk2a2	Casein kinase II subunit a	K.EAM*EHPYFYPVVK#.E	11.79	3.66	3.22	0.31
O54833_CSK22_MOUSE	Csnk2a2	Casein kinase II subunit a	R.LIDWGLAEFYHPAQEYNVR@.V	19.48	10.04	1.94	0.52
O54833_CSK22_MOUSE	Csnk2a2	Casein kinase II subunit a	K.TPALVFEYINNTDFK#.Q	14.34	9.97	1.44	0.70
O54833_CSK22_MOUSE	Csnk2a2	Casein kinase II subunit a	K.VLGTDELYGYLK#.K	26.00	6.48	4.01	0.25
O54833_CSK22_MOUSE	Csnk2a2	Casein kinase II subunit a	R.VYAEVNSLR@.S	46.53	11.71	3.97	0.25
O54833_CSK22_MOUSE	Csnk2a2	Casein kinase II subunit a	K.YSEVFEAINITNNER@.V	7.39	2.96	2.50	0.40
P67871_CSK2B_MOUSE	Csnk2b	Casein kinase II subunit b	R.GIAQM*LEK#.Y	38.78	15.49	2.50	0.40
P67871_CSK2B_MOUSE	Csnk2b	Casein kinase II subunit b	K.R@PANQFVPR@.L	35.56	13.52	2.63	0.38
P67871_CSK2B_MOUSE	Csnk2b	Casein kinase II subunit b	K.FNLTGLNEQVPHYR@.Q	26.16	10.62	2.46	0.41
P67871_CSK2B_MOUSE	Csnk2b	Casein kinase II subunit b	R.GIAQM*LEK#.Y	53.05	21.70	2.44	0.41
P67871_CSK2B_MOUSE	Csnk2b	Casein kinase II subunit b	K.IHPM*AYQLQLQAASNFK#.S	16.47	9.94	1.66	0.60
P67871_CSK2B_MOUSE	Csnk2b	Casein kinase II subunit b	K.R@PANQFVPR@.L	64.33	23.56	2.73	0.37
Q99388_CSPRS_MOUSE	Csprs	Component of Sp100-rs (	R.SLVPVDK#.V	66.20	34.65	1.91	0.52
Q99388_CSPRS_MOUSE	Csprs	Component of Sp100-rs (	K.VAISNAIR.S	27.79	22.57	1.23	0.81
P97315_CSRP1_MOUSE	Csrp1	Cysteine and glycine-rich	K.GFGFGQGAGALVHSE.-	13.38	13.38	1.00	1.00
P97315_CSRP1_MOUSE	Csrp1	Cysteine and glycine-rich	K.GYGYGQGAGTLSTDKGESLGIK.H	30.45	12.48	2.44	0.41
P97314_CSRP2_MOUSE	Csrp2	Cysteine and glycine-rich	K.GFGYGQGAGALVHAQ.-	12.03	12.03	1.00	1.00
P97314_CSRP2_MOUSE	Csrp2	Cysteine and glycine-rich	K.GYGYGQGAGTLNM*DR@.G	40.58	27.95	1.45	0.69
P97314_CSRP2_MOUSE	Csrp2	Cysteine and glycine-rich	K.SLESTTLTEK#.E	132.39	98.11	1.35	0.74
Q8CID0_CSR2B_MOUSE	Csrp2bp	Cysteine-rich protein 2-b	R.LVGSEDLAVDQSIISPYTSR@.I	3.25	2.04	1.59	0.63
Q8CID0_CSR2B_MOUSE	Csrp2bp	Cysteine-rich protein 2-b	R.NPVESAM*ELK#.E	7.96	2.45	3.25	0.31
Q99LC2_CSTF1_MOUSE	Cstf1	Cleavage stimulation fact	R.DGQLIATGSADASIK#.I	64.41	80.05	0.80	1.24
Q99LC2_CSTF1_MOUSE	Cstf1	Cleavage stimulation fact	K.LGM*ENDDTAVQYAIGR@.S	19.65	8.16	2.41	0.42
Q99LC2_CSTF1_MOUSE	Cstf1	Cleavage stimulation fact	R.SISFHPSGDFILVGTQHPTLR@.L	3.11	2.19	1.42	0.70
Q99LC2_CSTF1_MOUSE	Cstf1	Cleavage stimulation fact	R.TQAVFNHTEDYILLPDER@.T	23.64	12.33	1.92	0.52
Q99LC2_CSTF1_MOUSE	Cstf1	Cleavage stimulation fact	K.YIQEAEM*LR@.S	20.31	6.93	2.93	0.34
Q99LC2_CSTF1_MOUSE	Cstf1	Cleavage stimulation fact	K.LGM*ENDDTAVQYAIGR@.S	10.74	2.68	4.01	0.25
Q99LC2_CSTF1_MOUSE	Cstf1	Cleavage stimulation fact	R.TQAVFNHTEDYILLPDER@.T	15.61	5.43	2.88	0.35
Q99LC2_CSTF1_MOUSE	Cstf1	Cleavage stimulation fact	K.LGM*ENDDTAVQYAIGR@.S	6.82	1.54	4.43	0.23
Q99LC2_CSTF1_MOUSE	Cstf1	Cleavage stimulation fact	R.TQAVFNHTEDYILLPDER@.T	11.36	2.51	4.53	0.22
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	R.DYNK#YEEGINIHLAK#.K	17.67	6.83	2.59	0.39
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	K.GVEAVGSYAENQR@.I	29.95	7.81	3.84	0.26
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	R.IITGGAPELAVEGNGPVESSAVLTK#.A	22.82	6.15	3.71	0.27
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	K.IPNTVEEAVR@.I	15.72	5.00	3.14	0.32
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	K.K#LEENPYDLDAWSILIR@.E	65.32	22.42	2.91	0.34

Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	K.LFSDEAANIYER@.A	49.08	15.52	3.16	0.32
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	R.LLAIEDIDPTLVYIQYM*K#.F	15.84	3.64	4.36	0.23
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	R.LVAQFPSSGR@.F	44.03	13.25	3.32	0.30
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	K.M*AQAYDFALDK#.I	17.49	6.93	2.52	0.40
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	K.NM*LLYFAYADYEESR@.M	6.03	3.10	1.94	0.51
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	R.TEDQTLITK#.R	31.15	7.87	3.96	0.25
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	R.VLTSGSLPPEK#.S	10.10	4.00	2.52	0.40
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	K.GVEAVGSYAENQR@.I	5.60	2.80	2.00	0.50
Q99LI7_CSTF3_MOUSE	Cstf3	Cleavage stimulation fact	K.K#LEENPYDLDAWSILIR@.E	5.63	4.39	1.28	0.78
O88712_CTBP1_MOUSE	Ctbp1	C-terminal-binding prote	K.ALAQALK#.E	38.54	20.58	1.87	0.53
O88712_CTBP1_MOUSE	Ctbp1	C-terminal-binding prote	R.GAALDVHESEPFSFSQGPLK#.D	32.34	19.97	1.62	0.62
O88712_CTBP1_MOUSE	Ctbp1	C-terminal-binding prote	R.IGSGFDNIDIK#.S	50.00	29.05	1.72	0.58
O88712_CTBP1_MOUSE	Ctbp1	C-terminal-binding prote	R.IRGETLGIIGLGR.V	55.82	26.54	2.10	0.48
O88712_CTBP1_MOUSE	Ctbp1	C-terminal-binding prote	R.QGAFLVNTAR@.G	43.27	18.35	2.36	0.42
O88712_CTBP1_MOUSE	Ctbp1	C-terminal-binding prote	R.VGQAVALR@.A	36.36	17.43	2.09	0.48
O88712_CTBP1_MOUSE	Ctbp1	C-terminal-binding prote	K.VLNEAVGALMYHTITLTR@.E	11.38	8.42	1.35	0.74
P56546_CTBP2_MOUSE	Ctbp2	C-terminal-binding prote	R.GAALDVHESEPFSFAQGPLK#.D	18.15	9.13	1.99	0.50
P56546_CTBP2_MOUSE	Ctbp2	C-terminal-binding prote	R.IGSGYDNVDIK#.A	15.11	7.98	1.89	0.53
P56546_CTBP2_MOUSE	Ctbp2	C-terminal-binding prote	R.IRGETLGLIGFGR.T	29.01	8.84	3.28	0.30
P56546_CTBP2_MOUSE	Ctbp2	C-terminal-binding prote	R.QGAFLVNAAR@.G	18.51	10.84	1.71	0.59
Q5SUQ9_CTC1_MOUSE	Ctc1	CST complex subunit CTC	R.VALQFTGLGGQTESASK#.T	4.58	3.66	1.25	0.80
Q5SUQ9_CTC1_MOUSE	Ctc1	CST complex subunit CTC	R.VALQFTGLGGQTESASK#.T	7.59	2.56	2.96	0.34
Q61164_CTCF_MOUSE	Ctcf	Transcriptional repressor	R.YTEEGK#DVDVSVYDFEEEQQEGLLSEVNAEK#.V	4.81	1.79	2.68	0.37
Q61164_CTCF_MOUSE	Ctcf	Transcriptional repressor	R.K#SDLGVHLR@.K	20.51	6.27	3.27	0.31
Q61164_CTCF_MOUSE	Ctcf	Transcriptional repressor	K.QNQPTAIIQVEDQNTGAIENIIVEVK#.K	22.58	6.57	3.44	0.29
Q61164_CTCF_MOUSE	Ctcf	Transcriptional repressor	R.YALIQHQK#.S	35.45	12.26	2.89	0.35
Q61164_CTCF_MOUSE	Ctcf	Transcriptional repressor	R.YTEEGK#DVDVSVYDFEEEQQEGLLSEVNAEK#.V	28.42	10.90	2.61	0.38
Q61164_CTCF_MOUSE	Ctcf	Transcriptional repressor	R.YTEEGK#DVDVSVYDFEEEQQEGLLSEVNAEK#.V	10.30	4.13	2.50	0.40
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	R.AIM*AQLPQEQK#.A	18.60	7.91	2.35	0.43
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	R.ALLSAVTR@.L	23.06	9.62	2.40	0.42
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	K.ESQFLK#EELVVAVEDVR@.K	15.98	5.78	2.76	0.36
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	K.ESQFLK#EELVVAVEDVR@K#.Q	5.15	3.22	1.60	0.63
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	R.FTEQVEAAVEALSSDPAQPM*DENEFIDASR@.L	5.18	2.27	2.28	0.44
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	K.IAEQVASFQEEK#.S	30.08	15.93	1.89	0.53
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	R.LLILADM*ADVYK#.L	11.37	4.37	2.60	0.38
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	K.LLSNTVM*PR@.F	12.96	7.23	1.79	0.56
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	R.NAGNEQDLGIQYK#.A	24.14	9.93	2.43	0.41
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	K.QIIVDPLSFSEER@.F	17.78	8.52	2.09	0.48
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	R.SDALNSAIDK#.M	16.60	8.93	1.86	0.54
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	R.TSVQTEDDQLIAGQSAR@.A	15.65	7.02	2.23	0.45
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	R.VIHVVTSEM*DNYEPGVYTEK#.V	25.28	11.21	2.26	0.44
P26231_CTNA1_MOUSE	Ctnna1	Catenin alpha-1 OS=Mus	K.VK#AEVQNLGGELVVSGVDSAM*SLIQAAK#.N	9.86	7.12	1.38	0.72
Q02248_CTNB1_MOUSE	Ctnnb1	Catenin beta-1 OS=Mus n	K.HAVVNLINYQDDAELATR@.A	9.72	9.16	1.06	0.94
Q02248_CTNB1_MOUSE	Ctnnb1	Catenin beta-1 OS=Mus n	K.LLNDEDQVVVNK#.A	14.37	6.77	2.12	0.47
Q02248_CTNB1_MOUSE	Ctnnb1	Catenin beta-1 OS=Mus n	R.LVQLLVR@.A	17.31	8.18	2.12	0.47
Q02248_CTNB1_MOUSE	Ctnnb1	Catenin beta-1 OS=Mus n	K.SGGIPALVK#.M	11.73	2.27	5.18	0.19
Q02248_CTNB1_MOUSE	Ctnnb1	Catenin beta-1 OS=Mus n	R.TM*QNTNDVETAR@.C	10.38	3.56	2.91	0.34
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.QDVYGPQPQVR@.V	6.95	6.86	1.01	0.99
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.AAALVLQTIWGYK#.E	11.04	4.74	2.33	0.43
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.GK#K#PTEDPANDTVDFPK#.R	4.28	3.80	1.12	0.89
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.GYELLFQPEVVR@.I	25.63	11.20	2.29	0.44
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.HYEDGYPGGSDNYGSLSR@.V	11.17	7.11	1.57	0.64
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.QDVYGPQPQVR@.V	20.67	9.83	2.10	0.48
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	K.SDFQVNLNNASR@.S	14.90	5.53	2.69	0.37
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	K.SLDNNYSTLNER@.G	7.34	2.03	3.62	0.28
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.GYELLFQPEVVR@.I	15.47	8.62	1.79	0.56
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	K.HAIPNLVK#.N	14.59	3.91	3.73	0.27
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.HYEDGYPGGSDNYGSLSR@.V	8.25	2.90	2.85	0.35
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.IYISLLK#.E	25.42	5.26	4.83	0.21
P30999_CTND1_MOUSE	Ctnnd1	Catenin delta-1 OS=Mus	R.QDVYGPQPQVR@.V	10.05	4.98	2.02	0.50
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.FSDSYASVIK#.A	23.81	13.83	1.72	0.58
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.FVGQDVEGER@.M	20.77	9.15	2.27	0.44
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	R.NVLGWQDANSTEFDPK#.T	8.39	3.31	2.54	0.39
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	R.RLDLPIER.Q	21.23	8.73	2.43	0.41
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.TVQVVPHITDAIQEWVM*R@.Q	81.40	5.42	15.02	0.07
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.YIDSTDLEPSTLQEEPVR@.Y	11.18	7.95	1.41	0.71
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.GVIASSVGTILK.S	2.99	3.68	0.81	1.23
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.FSDSYASVIK#.A	58.16	31.71	1.83	0.55
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.FVGQDVEGER@.M	50.83	28.18	1.80	0.55
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.GVIASSVGTILK#.S	9.83	10.38	0.95	1.06
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.IYQYVINK#.E	48.45	26.83	1.81	0.55
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	R.K#LYGDTDYLEER@.H	23.32	19.99	1.17	0.86
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.LYGDTDYLEER@.H	28.63	18.17	1.58	0.63
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	R.NVLGWQDANSTEFDPK#.T	21.10	9.59	2.20	0.45
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	R.R@LDLPIER@.Q	49.81	27.40	1.82	0.55
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.YIDSTDLEPSTLQEEPVR@.Y	26.41	13.18	2.00	0.50
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.FVGQDVEGER@.M	22.82	6.94	3.29	0.30
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.IYQYVINK#.E	15.99	5.13	3.12	0.32
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.LYGDTDYLEER@.H	15.46	4.40	3.51	0.28
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	R.NVLGWQDANSTEFDPK#.T	11.40	3.23	3.53	0.28
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	R.R@LDLPIER@.Q	27.38	6.48	4.23	0.24
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.TVQVVPHITDAIQEWVM*R@.Q	26.30	18.10	1.45	0.69
P70698_PYRG1_MOUSE	Ctps1	CTP synthase 1 OS=Mus n	K.YIDSTDLEPSTLQEEPVR@.Y	17.57	5.93	2.96	0.34
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.ASAGHAVSITQDDGGADDWETDPDFVNDVSEK#.E	2.51	1.70	1.47	0.68
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.SAVGFEYQGK#.T	15.43	15.06	1.02	0.98
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	R.ANFENLAK#.E	83.50	44.82	1.86	0.54
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.ASAGHAVSITQDDGGADDWETDPDFVNDVSEK#EQR@.W	14.34	7.98	1.80	0.56
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.EK#ELETGPK#.A	14.05	18.28	0.77	1.30
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.FGVQM*DR@.V	43.18	17.87	2.42	0.41
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.FGVQTDR.Q	80.50	42.60	1.89	0.53
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.HESQQDYAK#.G	9.29	4.53	2.05	0.49
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.LR@ENVFQEHQTLK#.E	46.16	18.67	2.47	0.40
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.NASTFEEVVQVPSAYQK#.T	33.87	15.64	2.17	0.46
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	R.QDSSAVGFDYK#.E	38.81	15.85	2.45	0.41
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.SAVGFDYQGK#.T	74.82	33.58	2.23	0.45
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.SAVGFEYQGK#.T	90.59	52.94	1.71	0.58
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	R.SAVGHEYQSK#.L	12.95	7.00	1.85	0.54
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	R.YGLFPANYVELR@.Q	60.19	25.20	2.39	0.42
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	R.YGLFPANYVELR@Q.-	41.62	15.66	2.66	0.38
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.YGVQADR@VDK#.S	25.50	19.87	1.28	0.78
Q60598_SRC8_MOUSE	Cttn	Src substrate cortactin O	K.NASTFEEVVQVPSAYQK#.T	4.80	1.93	2.48	0.40
Q99LJ0_CT2NL_MOUSE	Cttnbp2nl	CTTNBP2 N-terminal-like	R.ELTSDSSTENQGPPR@.E	6.99	2.49	2.80	0.36
Q99LJ0_CT2NL_MOUSE	Cttnbp2nl	CTTNBP2 N-terminal-like	K.LTDTGLPGPTTAAYSYAK#.A	6.39	4.25	1.50	0.67

Q99LJ0_CT2NL_MOUSE	Cttnbp2nl	CTTNBP2 N-terminal-like	R.DLVIEALK#.A	15.14	3.58	4.23	0.24
Q99LJ0_CT2NL_MOUSE	Cttnbp2nl	CTTNBP2 N-terminal-like	R.ELTSDSSTENQGPPR@.E	13.36	3.63	3.68	0.27
Q99LJ0_CT2NL_MOUSE	Cttnbp2nl	CTTNBP2 N-terminal-like	R.GLQTEAQVEK#.Q	8.78	2.46	3.56	0.28
Q99LJ0_CT2NL_MOUSE	Cttnbp2nl	CTTNBP2 N-terminal-like	K.LTDTGLPGPTTAAYSYAK#.A	10.22	3.77	2.71	0.37
Q99LJ0_CT2NL_MOUSE	Cttnbp2nl	CTTNBP2 N-terminal-like	K.VSSPLSPLSPGIK#.S	5.41	1.96	2.76	0.36
A2A432_CUL4B_MOUSE	Cul4b	Cullin-4B OS=Mus muscu	K.ETVEEQASTTER@.V	13.62	3.29	4.14	0.24
A2A432_CUL4B_MOUSE	Cul4b	Cullin-4B OS=Mus muscu	K.TIDGILLLIER@.E	13.57	8.44	1.61	0.62
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	R.EAAPPVVAIPR@.S	20.87	8.83	2.36	0.42
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	K.ELNTVNVM*PSASR@.V	9.33	5.80	1.61	0.62
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	R.FLPDM*EAAQALSK#.T	12.16	5.15	2.36	0.42
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	R.GLEVLGPK#PTFWPVFR@.E	8.29	3.04	2.73	0.37
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	R.GPLDLQEQK#.N	12.53	4.86	2.58	0.39
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	R.HEQNFAER@.F	4.35	52.65	0.08	12.09
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	R.LHIVDLLQDHLEEER@.V	18.31	4.02	4.56	0.22
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	K.SSSELFGPR@.A	17.98	3.60	5.00	0.20
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	R.TQILLSLSQQEAIEK#.H	14.74	4.05	3.63	0.28
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	K.VEVSSNPQR@.A	19.63	3.48	5.63	0.18
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	R.VPLGPGLHAYPDELIR@.Q	35.15	9.69	3.63	0.28
Q8VE73_CUL7_MOUSE	Cul7	Cullin-7 OS=Mus muscul	R.VTLLENLTR@.F	21.95	5.58	3.93	0.25
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	R.LIDVPDPVPALDVGQQLEIK#.V	3.11	1.84	1.69	0.59
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	K.APDVAIEVLTR@.S	10.12	6.56	1.54	0.65
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	R.ASETGSDEAIK#.S	11.17	30.25	0.37	2.71
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	R.ELDATATVLANR@.Q	17.91	4.06	4.41	0.23
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	R.ISNSDLSGSAR@.R	11.87	6.08	1.95	0.51
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	R.LIDVPDPVPALDVGQQLEIK#.V	7.70	3.77	2.04	0.49
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	K.LQTLQTALEK#.T	17.05	5.83	2.92	0.34
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	K.LR@ENSASQISQLEQQLNAK#.N	10.68	6.57	1.63	0.62
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	R.SLQSENATLR.I	13.30	4.48	2.97	0.34
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	K.SM*EFAPSEGAGTQDSTK#PLEVLLLEK#.N	16.10	7.05	2.28	0.44
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	K.SQGGLAEVAAAPADR@EEATQPAEK#.A	23.89	5.47	4.37	0.23
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	R.SQLQGPSASAEYWK#.E	5.77	2.97	1.94	0.51
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	R.SSALPSTSAPANAPAR@.R	11.89	3.59	3.31	0.30
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	K.TAEPVQTSSTSSSGNSDDAIR@.S	8.65	2.07	4.19	0.24
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	K.TPAAPETSTAALPSAPALK#.K	2.17	2.20	0.99	1.01
P53564_CUX1_MOUSE	Cux1	Homeobox protein cut-li	K.TPAAPETSTAALPSAPALK#K#.E	10.85	5.54	1.96	0.51
Q9JHS9_CWC15_MOUSE	Cwc15	Spliceosome-associated	R.FVNDTLR@.S	52.11	25.12	2.07	0.48
Q9JHS9_CWC15_MOUSE	Cwc15	Spliceosome-associated	R.GKGEGDLSQLSK.Q	10.07	6.81	1.48	0.68
Q9JHS9_CWC15_MOUSE	Cwc15	Spliceosome-associated	R.IR@M*ENILSGNPLLNLTGPSQPQANFK#.V	17.55	11.94	1.47	0.68
Q9JHS9_CWC15_MOUSE	Cwc15	Spliceosome-associated	R.M*ENILSGNPLLNLTGPSQPQANFK#.V	9.77	7.65	1.28	0.78
Q9JHS9_CWC15_MOUSE	Cwc15	Spliceosome-associated	R.MENILSGNPLLNLTGPSQPQANFK#.V	9.85	2.99	3.29	0.30
Q9JHS9_CWC15_MOUSE	Cwc15	Spliceosome-associated	R.QTTQDAPEEVR@.N	29.39	22.65	1.30	0.77
Q9JHS9_CWC15_MOUSE	Cwc15	Spliceosome-associated	R.IRM*ENILSGNPLLNLTGPSQPQANFK.V	1.49	4.20	0.35	2.83
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	K.EYM*ESFESIFK#.E	11.48	2.77	4.15	0.24
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	K.FFGLLAGR@.F	30.44	8.88	3.43	0.29
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	R.GINAIFER@.L	45.58	15.32	2.98	0.34
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	R.GYSYDDSM*ESR@.S	10.25	2.98	3.44	0.29
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	R.LK#DETLQPFFEGLLPR@.D	83.59	25.97	3.22	0.31
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	K.LTQVSPR@.G	28.92	9.75	2.96	0.34
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	K.M*EFAESQTK#.E	20.19	5.72	3.53	0.28
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	R.NILHESEIDK#R@.V	32.31	15.49	2.09	0.48
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	K.TEINLVSFR@.R	18.36	6.40	2.87	0.35
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	K.VIVAQK#PEAEQK#.K	14.82	3.67	4.04	0.25
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	R.GINAIFER@.L	27.17	8.38	3.24	0.31
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	R.HQEGRTER@.A	9.47	1.09	8.71	0.11
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	R.LILNFR@.K	33.06	10.08	3.28	0.30
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	R.LK#DETLQPFFEGLLPR@.D	67.70	28.08	2.41	0.41
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	R.M*M*QEQITDK#.S	19.20	9.64	1.99	0.50
Q8C5N3_CWC22_MOUSE	Cwc22	Pre-mRNA-splicing factor	K.TEINLVSFR@.R	18.40	5.52	3.33	0.30
Q9DBF7_CWC25_MOUSE	Cwc25	Pre-mRNA-splicing factor	R.EVLNNPVK#.M	37.37	25.41	1.47	0.68
Q9DBF7_CWC25_MOUSE	Cwc25	Pre-mRNA-splicing factor	R.GLQGSLGEQR@.A	51.16	34.04	1.50	0.67
Q9DBF7_CWC25_MOUSE	Cwc25	Pre-mRNA-splicing factor	K.IR@EDPLFIIR@.K	30.12	24.32	1.24	0.81
Q9DBF7_CWC25_MOUSE	Cwc25	Pre-mRNA-splicing factor	R.KLSAEELER.K	23.27	22.02	1.06	0.95
Q9DBF7_CWC25_MOUSE	Cwc25	Pre-mRNA-splicing factor	K.VPGYGLQVR@.D	38.02	29.00	1.31	0.76
Q9DBF7_CWC25_MOUSE	Cwc25	Pre-mRNA-splicing factor	R.YAEDVGAVK#.K	20.03	15.93	1.26	0.80
Q9DBF7_CWC25_MOUSE	Cwc25	Pre-mRNA-splicing factor	R.KLSAEELER.K	2.58	9.77	0.26	3.79
Q3TKY6_CWC27_MOUSE	Cwc27	Peptidyl-prolyl cis-trans	R.EDQTLALLSQFK#.S	19.54	9.34	2.09	0.48
Q3TKY6_CWC27_MOUSE	Cwc27	Peptidyl-prolyl cis-trans	K.ETAIK#VEEGR@EEEEAAPDGAVAEYR@.R	5.89	2.57	2.29	0.44
Q3TKY6_CWC27_MOUSE	Cwc27	Peptidyl-prolyl cis-trans	K.NFSLLSFGEEAEEEEEEVNR@.V	7.76	3.12	2.49	0.40
Q3TKY6_CWC27_MOUSE	Cwc27	Peptidyl-prolyl cis-trans	K.VEEGR@EEEEAAPDGAVAEYR@.R	10.24	7.62	1.34	0.74
Q3TKY6_CWC27_MOUSE	Cwc27	Peptidyl-prolyl cis-trans	K.VTGDTVYNM*LR@.L	9.11	4.89	1.86	0.54
Q9CQX2_CYB5B_MOUSE	Cyb5b	Cytochrome b5 type B O	R.FLSEHPGGEEVLLEQAGADATESFEDVGHSPDAR@.E	24.45	8.28	2.95	0.34
Q9CQX2_CYB5B_MOUSE	Cyb5b	Cytochrome b5 type B O	K.VEGSEPSVTYYR@.L	6.21	4.29	1.45	0.69
Q9CQX2_CYB5B_MOUSE	Cyb5b	Cytochrome b5 type B O	K.VEGSEPSVTYYR@.L	7.37	3.05	2.42	0.41
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.GPNGLLVYQGK#.G	22.67	9.72	2.33	0.43
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.IDGNLVIRPYTPVSSDDDKGFVDLVVK.V	9.28	1.99	4.67	0.21
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	K.IGDTIEFR.G	124.52	31.95	3.90	0.26
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.LIDK#EVISPDTR@.R	80.98	24.26	3.34	0.30
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.LIDK#EVISPDTR@R@.F	26.12	9.58	2.73	0.37
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	K.LWYTVDK#APDAWDYSQGFVNEEM*IR@.D	4.31	2.83	1.52	0.66
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.STPAITLENPDIK#.Y	31.53	11.37	2.77	0.36
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.STPAITLENPDIK#YPLR@.L	33.06	10.57	3.13	0.32
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	K.SVGM*IAGGTGITPM*LQVIR@.A	24.04	5.92	4.06	0.25
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	K.SVGMIAGGTGITPM*LQVIR@.A	6.99	1.94	3.59	0.28
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.IDGNLVIR@PYTPVSSDDDK#GFVDLVVK#.V	22.47	8.86	2.54	0.39
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.LIDKEVISPDTR.R	25.32	11.61	2.18	0.46
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.STPAITLENPDIK#.Y	8.67	4.88	1.78	0.56
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.LIDK#EVISPDTR@.R	35.07	14.93	2.35	0.43
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	K.M*SQYLENM*K#.I	11.25	6.17	1.82	0.55
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	R.STPAITLENPDIK#.Y	12.65	6.83	1.85	0.54
Q9DCN2_NB5R3_MOUSE	Cyb5r3	NADH-cytochrome b5 re	K.SVGM*IAGGTGITPM*LQVIR@.A	7.86	3.63	2.16	0.46
Q8BKE6_CP20A_MOUSE	Cyp20a1	Cytochrome P450 20A1	R.M*VLGSTFEDEQEVIR@.F	6.42	2.91	2.21	0.45
Q8BKE6_CP20A_MOUSE	Cyp20a1	Cytochrome P450 20A1	R.LVVSLGTTDVLK#.Q	5.78	3.16	1.83	0.55
Q8BKE6_CP20A_MOUSE	Cyp20a1	Cytochrome P450 20A1	R.M*VLGSTFEDEQEVIR@.F	4.98	3.39	1.47	0.68
Q8K0C4_CP51A_MOUSE	Cyp51a1	Lanosterol 14-alpha dem	K.SPIEFLENAYEK#.Y	6.35	4.50	1.41	0.71
Q9D172_ES1_MOUSE	D10Jhu81e	ES1 protein homolog, mi	K.ITSLAQLNAANHDAAIFPGGFGAAK#.N	5.63	3.18	1.77	0.56
P61804_DAD1_MOUSE	Dad1	Dolichyl-diphosphoolig	K.ADFQGISPER.A	23.85	19.86	1.20	0.83
P61804_DAD1_MOUSE	Dad1	Dolichyl-diphosphoolig	R.FLEEYLSSTPQR@.L	25.46	14.60	1.74	0.57
Q62165_DAG1_MOUSE	Dag1	Dystroglycan OS=Mus mu	K.LTLEDQATFIK#.K	6.35	4.55	1.39	0.72
Q62165_DAG1_MOUSE	Dag1	Dystroglycan OS=Mus mu	K.LTLEDQATFIK#K#.G	21.61	4.77	4.53	0.22
Q62165_DAG1_MOUSE	Dag1	Dystroglycan OS=Mus mu	K.LTLEDQATFIK#.K	5.98	3.23	1.85	0.54
Q80YE7_DAPK1_MOUSE	Dapk1	Death-associated protei	R.LLDPPDPMGK#.D	13.15	3.66	3.59	0.28
O54784_DAPK3_MOUSE	Dapk3	Death-associated protei	R.VLEDVAAAEQGLR@.E	11.73	9.64	1.22	0.82
Q922B2_SYDC_MOUSE	Dars	Aspartate--tRNA ligase, c	R.EIVDAAEDYAK#.E	7.68	6.28	1.22	0.82

Q922B2_SYDC_MOUSE	Dars	Aspartate--tRNA ligase, c	K.ESIIDVEGVVR@.K	4.54	3.76	1.21	0.83
Q922B2_SYDC_MOUSE	Dars	Aspartate--tRNA ligase, c	K.IISAASEGGANVFTVSYFK#.N	5.30	1.69	3.13	0.32
Q3UKR0_Q3UKR0_MOUSE	Daxx	Death domain-associate	K.ELDLSELDDPDSSYLQEAR@.L	7.61	2.79	2.72	0.37
Q3UKR0_Q3UKR0_MOUSE	Daxx	Death domain-associate	R.LEQLLALYVAEIR@.R	12.02	3.68	3.27	0.31
Q3UKR0_Q3UKR0_MOUSE	Daxx	Death domain-associate	R.LINK#PGLDTFPDYGDVLR@.A	23.02	14.63	1.57	0.64
Q3UKR0_Q3UKR0_MOUSE	Daxx	Death domain-associate	R.LLGTAPQPSDPPK#.A	8.55	3.82	2.24	0.45
Q9JII5_DAZP1_MOUSE	Dazap1	DAZ-associated protein 1	K.FGVVTEVVM*IYDAEK.Q	3.66	5.04	0.73	1.38
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.SESEVEEAAAIIAQRPDNPR.E	16.46	17.21	0.96	1.05
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.SPSDSSTASTPIAEQIER@.A	7.30	6.60	1.11	0.90
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.VAEFFQGVDVIVNASSVEDIDAGAIGQR.L	6.91	10.68	0.65	1.55
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.YVLINWVGEDVPDAR@.K	10.75	10.19	1.05	0.95
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.DSQAALPK#.Y	81.30	73.20	1.11	0.90
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.EESAADWALYTYEDGSDDLK.L	6.21	5.95	1.04	0.96
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.EQFWEQAK#.K	32.31	31.32	1.03	0.97
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.K#QQSLEAEEAK#.R	15.47	12.38	1.25	0.80
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.K#SESEVEEAAAIIAQR@PDNPR@.E	28.01	24.42	1.15	0.87
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.LAASGEGGLQELSGHFENQK#.V	140.07	104.96	1.33	0.75
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.LAASGEGGLQELSGHFENQK#.V	5.50	3.06	1.80	0.56
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.LELLAAYEEVIR@.E	45.53	34.07	1.34	0.75
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.LR@EDENAEPVGTTYQK#.T	29.38	22.57	1.30	0.77
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.M*APTPIPTR@.S	107.19	89.34	1.20	0.83
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.QQSLEAEEAK#.R	60.37	42.02	1.44	0.70
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.SESEVEEAAAIIAQR@PDNPR@.E	133.21	105.15	1.27	0.79
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.SPSDSSTASTPIAEQIER@.A	102.00	87.24	1.17	0.86
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.TDAAVEM*K#R@.I	16.93	12.39	1.37	0.73
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.VAEFFQGVDVIVNASSVEDIDAGAIGQR@.L	35.73	23.16	1.54	0.65
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.YVLINWVGEDVPDAR.K	57.08	44.39	1.29	0.78
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.DSQAALPK#.Y	16.21	10.38	1.56	0.64
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.LREDENAEPVGTTYQK.T	25.66	20.83	1.23	0.81
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.M*APTPIPTR.S	10.56	9.41	1.12	0.89
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.SESEVEEAAAIIAQR@PDNPR@.E	22.63	20.51	1.10	0.91
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	R.SPSDSSTASTPIAEQIER@.A	13.97	12.80	1.09	0.92
Q9QXS6_DREB_MOUSE	Dbn1	Drebrin OS=Mus muscul	K.YVLINWVGEDVPDAR@.K	11.39	7.84	1.45	0.69
P53395_ODB2_MOUSE	Dbt	Lipoamide acyltransferas	R.ILK#EDILSFLEK#.Q	28.80	11.55	2.49	0.40
P53395_ODB2_MOUSE	Dbt	Lipoamide acyltransferas	K.LSDIGEGIR@.E	15.77	27.05	0.58	1.72
P53395_ODB2_MOUSE	Dbt	Lipoamide acyltransferas	R.SVFEIAM*ELNR@.L	13.37	3.23	4.15	0.24
P61963_DCAF7_MOUSE	Dcaf7	DDB1- and CUL4-associat	R.DM*FASVGADGSVR@.M	9.11	5.56	1.64	0.61
P61963_DCAF7_MOUSE	Dcaf7	DDB1- and CUL4-associat	K.GVYPDLLATSGDYLR@.V	17.73	9.44	1.88	0.53
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	R.AVSSLATAK#.G	59.20	13.63	4.34	0.23
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	R.DLYR@PLSSDDLDSVGDSV.-	22.65	5.27	4.30	0.23
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	K.GIVYAISPDR@.F	50.99	12.24	4.17	0.24
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	R.LYTLDGK#.Q	32.85	7.45	4.41	0.23
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	K.NVNPNWSVNVK#.T	29.04	6.92	4.20	0.24
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	R.SFEALLADLTR@.T	141.72	30.75	4.61	0.22
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	K.TAHSFEQVLTDITDAIK#.L	39.08	7.91	4.94	0.20
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	R.TLSDNVNLPQGVR@.T	72.43	18.84	3.84	0.26
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	R.SFEALLADLTR@.T	7.17	3.20	2.24	0.45
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	R.SFEALLADLTR@.T	13.83	4.83	2.87	0.35
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	K.TAHSFEQVLTDITDAIK#.L	8.05	5.89	1.37	0.73
Q80VB6_Q80VB6_MOUSE	Dclk1	Dclk1 protein OS=Mus m	R.TLSDNVNLPQGVR@.T	6.53	2.19	2.98	0.34
Q91YD3_DCP1A_MOUSE	Dcp1a	mRNA-decapping enzym	R.APVSLANPAGTALPSVDLLQK#.L	7.87	2.23	3.53	0.28
Q91YD3_DCP1A_MOUSE	Dcp1a	mRNA-decapping enzym	K.SQLQDTLIHLIK#.N	7.97	1.40	5.69	0.18
Q91YD3_DCP1A_MOUSE	Dcp1a	mRNA-decapping enzym	K.TDIEGTLFVYR@.R	12.53	7.71	1.62	0.62
Q9CYC6_DCP2_MOUSE	Dcp2	m7GpppN-mRNA hydrol	K.SHSNHGEVSDLLK#.A	25.25	8.31	3.04	0.33
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.AEITDAEGLGLK#.L	38.31	21.90	1.75	0.57
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.AFLQGGQEATDIALLLR@.D	30.16	12.33	2.45	0.41
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.ASLAALPPLHVAK#.L	27.48	15.31	1.79	0.56
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.DFEETM*DALQADIDQLEAEK#AELK#.Q	11.92	4.81	2.48	0.40
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.DLEEK#LETLR@.L	11.22	3.87	2.90	0.34
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.ELTNQQEASVER@.Q	49.60	18.43	2.69	0.37
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.ETVGDLEAM*NEM*NDELQENAR@.E	6.10	2.70	2.26	0.44
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.ETVTQRPGATVPTDFATFPSSAFLR.A	48.20	13.96	3.45	0.29
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.GPPPSGIATLVSGIAGGGAPGQAPGALPGPGLVK#.D	24.46	13.09	1.87	0.54
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.GSDGAASSYQLK#.Q	21.58	9.62	2.24	0.45
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.IK#GEELSEANVR@.L	56.08	19.81	2.83	0.35
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.IQLEQVQEWK#.S	18.61	5.90	3.15	0.32
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.K#NQELEVVR@.Q	8.63	4.80	1.80	0.56
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.LDETQTLLR@.K	45.65	19.12	2.39	0.42
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.LNQLSTHTHVVDITR@.S	10.56	6.88	1.54	0.65
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.M*QEQQADLQR@.R	11.52	7.24	1.59	0.63
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.NQELEVVR@.Q	21.80	10.34	2.11	0.47
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.QQQPPPETFDFK#.I	9.73	5.58	1.74	0.57
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.QSQIQVFEDGADTTSPETPDSSASK#.V	9.68	5.11	1.89	0.53
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.R@VEAAQETVADYQQTIK#K#.Y	16.90	4.40	3.84	0.26
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.SPSAQLM*EQVAQLK#.S	15.80	10.72	1.48	0.68
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.VDELTTDLEILK#.A	6.87	4.21	1.63	0.61
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.VDELTTDLEILK#AEIEEK#.G	53.48	21.58	2.48	0.40
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.VEAAQETVADYQQTIK#.K	6.90	2.83	2.44	0.41
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.WVGVILDEAK#.G	19.67	9.13	2.16	0.46
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.AEITDAEGLGLK#.L	31.07	39.24	0.79	1.26
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.AFLQGGQEATDIALLLR@.D	38.39	14.45	2.66	0.38
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.ASLAALPPLHVAK#.L	52.27	16.03	3.26	0.31
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.DFEETM*DALQADIDQLEAEK#AELK#.Q	6.18	2.98	2.08	0.48
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.ELTNQQEASVER@.Q	55.29	17.41	3.18	0.31
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.ETVGDLEAM*NEM*NDELQENAR@.E	7.25	3.98	1.82	0.55
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.ETVTQR@PGATVPTDFATFPSSAFLR@.A	26.76	10.19	2.63	0.38
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.GSDGAASSYQLK#.Q	21.31	8.39	2.54	0.39
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.IKGEELSEANVR.L	60.77	21.10	2.88	0.35
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.IK#GEELSEANVR@.L	12.46	2.76	4.51	0.22
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.K#NQELEVVR@.Q	8.59	2.32	3.71	0.27
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.LDETQTLLR@.K	53.57	14.02	3.82	0.26
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.M*QEQQADLQR@.R	25.85	7.57	3.41	0.29
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.NQELEVVR@.Q	20.04	3.65	5.49	0.18
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.QQQPPPETFDFK#.I	13.40	3.34	4.01	0.25
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.QSQIQVFEDGADTTSPETPDSSASK#.V	10.05	4.10	2.45	0.41
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.R@VEAAQETVADYQQTIK#.K	12.40	4.81	2.58	0.39
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.R@VEAAQETVADYQQTIK#K#.Y	12.50	3.31	3.78	0.26
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.SPSAQLM*EQVAQLK#.S	17.65	6.44	2.74	0.37
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.VDELTTDLEILK#.A	8.85	2.65	3.33	0.30
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	R.VDELTTDLEILK#AEIEEK#.G	82.59	21.53	3.84	0.26
E9Q586_E9Q586_MOUSE	Dctn1	Dynactin subunit 1 OS=	K.WVGVILDEAK#.G	18.10	5.76	3.14	0.32
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.ASVEDADTQNK#.V	38.17	13.29	2.87	0.35
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.ASVEDADTQNK#VHQLYETIQR@.W	13.25	3.94	3.36	0.30

Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.DNTALLTQVQTTM*R@.E	46.43	18.66	2.49	0.40
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.DNTALLTQVQTTMR@.E	10.12	4.68	2.16	0.46
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	R.ENLATVEGNFASIDAR@.M	96.43	33.78	2.85	0.35
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.GLDFSDR@.I	97.24	30.68	3.17	0.32
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.LLGPDAAINLADPDGALAK#.R	90.50	41.67	2.17	0.46
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.LLGPDAAINLADPDGALAK#.R	17.01	8.59	1.98	0.51
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.LLGPDAAINLADPDGALAKR.L	33.60	15.26	2.20	0.45
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	R.LLHEVQELTTEVEK#.I	68.83	24.78	2.78	0.36
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	R.LLLQLEATK#.S	129.67	41.16	3.15	0.32
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	R.LQSVLGK#.V	132.42	49.90	2.65	0.38
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	R.LTELEATVR@.C	141.27	49.01	2.88	0.35
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.R@LLLQLEATK#.S	16.90	5.63	3.00	0.33
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.R@LTELEATVR@.C	13.16	4.24	3.11	0.32
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.R@TGYESGDYEM*LGEGLGVK#.E	14.73	4.74	3.11	0.32
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	R.TGYESGDYEM*LGEGLGVK#.E	54.84	18.52	2.96	0.34
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	R.TGYESGDYEMLGEGLGVK#.E	10.49	4.58	2.29	0.44
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.VHQLYETIQR@.W	71.49	25.77	2.77	0.36
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.VHQLYETIQR.W	23.89	8.32	2.87	0.35
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.VSALDLAVLDQVEAR@.L	115.01	44.08	2.61	0.38
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	R.WSPVASTLPELVQR@.L	83.93	26.10	3.22	0.31
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.YADLPGIAR@.N	152.56	61.91	2.46	0.41
Q99KJ8_DCTN2_MOUSE	Dctn2	Dynactin subunit 2 OS=	K.LLGPDAAINLADPDGALAK#.R	4.29	1.88	2.29	0.44
Q9Z0Y1_DCTN3_MOUSE	Dctn3	Dynactin subunit 3 OS=	K.VQVALGNIASK#.R	34.14	11.44	2.98	0.34
Q9Z0Y1_DCTN3_MOUSE	Dctn3	Dynactin subunit 3 OS=	K.YLDPEYIDR@.I	29.94	10.93	2.74	0.36
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	R.AGASISTLAGLSLR@.E	8.67	3.67	2.36	0.42
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	R.ATSISTQLPDDPAK#.T	13.56	8.93	1.52	0.66
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	K.IEPAQAVAEVEPLPEDYYTR@PVNLTEVTTLQQR@.L	7.31	4.64	1.58	0.63
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	K.IQLVAVNYIPEVR@.I	16.10	7.48	2.15	0.46
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	K.LIEYYQQLAQK#.E	20.77	11.22	1.85	0.54
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	R.LLQPDLQPVSASQLYPR@.H	10.14	9.20	1.10	0.91
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	R.LLQPDLQPVSASQLYPR.H	11.16	4.99	2.24	0.45
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	K.IQLVAVNYIPEVR@.I	9.06	4.20	2.16	0.46
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	K.LIEYYQQLAQK#.E	12.29	3.86	3.18	0.31
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	R.LLQPDLQPVSASQLYPR@.H	9.36	4.52	2.07	0.48
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	R.VLYLVQGEK#.K	10.46	4.31	2.43	0.41
Q8CBY8_DCTN4_MOUSE	Dctn4	Dynactin subunit 4 OS=	R.ATSISTQLPDDPAK#.T	7.26	7.11	1.02	0.98
Q9CXV9_DCNL5_MOUSE	Dcun1d5	DCN1-like protein 5 OS=	K.SM*LALLLGR@.T	12.16	13.08	0.93	1.08
Q9CXV9_DCNL5_MOUSE	Dcun1d5	DCN1-like protein 5 OS=	R.SQLNDISSFK#.N	10.13	18.39	0.55	1.82
Q9D9Z5_DDA1_MOUSE	Dda1	DET1- and DDB1-associat	R.EYPSEQIIVTEK#.T	5.80	2.96	1.96	0.51
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.DLLFILTAK#.Y	24.64	14.11	1.75	0.57
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.EATADDLIK#.V	16.75	9.70	1.73	0.58
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.EM*LGGEIIPR@.S	18.06	6.29	2.87	0.35
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.GAVYSM*VEFNGK#.L	5.54	2.48	2.24	0.45
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.IEVQDSSGGTTALR@PSASTQALSSSVSSSK#.L	39.78	16.98	2.34	0.43
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.IVVFQYSDGK#.L	33.33	20.66	1.61	0.62
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.K#TEPATGFIDGDLIESFLDISR@PK#.M	26.00	15.64	1.66	0.60
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.LGDSQLVK#.L	54.74	21.30	2.57	0.39
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.LGK#DPNTYFIVGTAM*VYPEEAEPK#.Q	14.31	6.72	2.13	0.47
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.LLASINSTVR@.L	34.72	17.97	1.93	0.52
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.LPSFELLHK#.E	24.60	9.82	2.51	0.40
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.LVFSNVNLK#.E	43.52	19.62	2.22	0.45
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.SDPGR@ETDDTLVLSFVGQTR@.V	30.34	17.11	1.77	0.56
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.SVLLLAYK#PM*EGNFEEIAR@.D	28.85	12.15	2.37	0.42
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.VTLGTQPTVLR.T	32.06	13.35	2.40	0.42
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.VVEELTR@.I	28.22	17.01	1.66	0.60
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.YLAIAPPIIK#.Q	22.81	12.71	1.79	0.56
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.YLLGDM*EGR@.L	10.53	3.77	2.79	0.36
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.IEVQDSSGGTTALR@PSASTQALSSSVSSSK#.L	15.89	7.20	2.21	0.45
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.IVVFQYSDGK#.L	15.22	8.76	1.74	0.58
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.LGKDPNTYFIVGTAM*VYPEEAEPK.Q	3.80	3.13	1.21	0.82
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.LLASINSTVR@.L	13.84	4.93	2.81	0.36
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.SDPGR@ETDDTLVLSFVGQTR@.V	15.98	10.49	1.52	0.66
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	R.SVLLLAYK#PM*EGNFEEIAR@.D	12.19	4.90	2.49	0.40
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.VTLGTQPTVLR@.T	10.72	5.41	1.98	0.51
Q3U1J4_DDB1_MOUSE	Ddb1	DNA damage-binding prc	K.YLAIAPPIIK#.Q	9.03	6.02	1.50	0.67
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	R.GFELTFK#.T	22.85	17.56	1.30	0.77
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	R.GVGM*VADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGR.N	6.87	4.18	1.64	0.61
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	K.LPDVYGVFQFK#.V	18.48	10.00	1.85	0.54
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	R.NTLLIAGLQAR@.N	25.38	11.59	2.19	0.46
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	K.SSLNPILFR@.G	29.71	23.66	1.26	0.80
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	K.TADDPSLSLIK#.Y	17.18	12.58	1.37	0.73
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	K.TAVIDHHNYDVSDLGQHTLIVADTENLLK#.A	12.40	5.71	2.17	0.46
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	R.TLVLLDNLNVR@.D	34.67	26.21	1.32	0.76
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	K.WVPFDGDDIQLEFVR@.I	7.76	6.06	1.28	0.78
O54734_OST48_MOUSE	Ddost	Dolichyl-diphosphooligc	R.YSQTGNYELAVALSR@.W	8.82	13.47	0.65	1.53
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.ALIVEPSR@ELAEQTLNNVK#.Q	25.49	12.24	2.08	0.48
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.APDNYIVK#.S	53.59	20.95	2.56	0.39
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.DGFVALSK#.A	26.60	11.78	2.26	0.44
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.DLGLAFEIPAHIK#.N	33.48	13.86	2.41	0.41
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.EAQTSFLHLGYLPNQLFR@.T	37.90	13.89	2.73	0.37
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	R.ELAEQTLNNVK#.Q	50.68	16.91	3.00	0.33
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	R.ELLIIGGVAAR@.D	68.70	31.80	2.16	0.46
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	R.FLVLDEADGLLSQGYSDFINR@.M	48.91	19.22	2.54	0.39
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.GHVDVLAPTVQELAALEK#.E	68.47	32.70	2.09	0.48
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	R.GIDIHGVPYVINVTLPDEK#.Q	59.07	29.30	2.02	0.50
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	R.M*GLAISLVATEK#.E	14.58	1.57	9.27	0.11
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.SQHTGNAQVSQTK#.F	3.43	1.49	2.31	0.43
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	R.VGWSTM*QASLDLGTDK#.F	9.13	5.86	1.56	0.64
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.VPVDEFDGK#.V	24.34	12.21	1.99	0.50
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.EAQTSFLHLGYLPNQLFR@.T	7.84	3.76	2.08	0.48
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	R.ELAEQTLNNVK#.Q	8.68	2.68	3.23	0.31
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	R.ELLIIGGVAAR@.D	10.96	4.24	2.59	0.39
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	R.FLVLDEADGLLSQGYSDFINR@.M	21.90	8.20	2.67	0.37
Q91VR5_DDX1_MOUSE	Ddx1	ATP-dependent RNA heli	K.GHVDVLAPTVQELAALEK#.E	12.25	2.75	4.46	0.22
Q80Y44_DDX10_MOUSE	Ddx10	Probable ATP-dependent	R.ELAYQTFEVLR@.K	12.91	4.28	3.02	0.33
Q80Y44_DDX10_MOUSE	Ddx10	Probable ATP-dependent	R.YK#EDGEALLILLPSEEQGM*VQQLLQK#.K	4.64	1.77	2.62	0.38
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.APILIATDVASR@.G	928.96	512.73	1.81	0.55
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.ELAQQVQQVADDYGK#.C	12.11	7.70	1.57	0.64
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.GLDVEDVK#.F	408.43	219.00	1.86	0.54
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.M*LDM*GFEPQIR@.K	115.42	60.29	1.91	0.52
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.MLDM*GFEPQIR@.K	9.40	5.32	1.77	0.57
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.QTLM*WSATWPK#.E	68.71	32.42	2.12	0.47
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.QTLMWSATWPK#.E	10.39	19.48	0.53	1.88

Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.VLEEANQAINPK#.L	7.49	9.48	0.79	1.27
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.SSQSSSQQFSGIGR@.S	9.96	4.78	2.09	0.48
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.APILIATDVASR@.G	1108.81	431.75	2.57	0.39
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.DM*VGIAQTGSGK#.T	53.13	27.08	1.96	0.51
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.DWVLNEFR@.S	31.53	16.67	1.89	0.53
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.ELAQQVQQVADDYGK#.C	95.50	56.93	1.68	0.60
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.FVINYDYPNSSEDYVHR@.I	92.28	48.49	1.90	0.53
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.GLDVEDVK#.F	474.22	220.28	2.15	0.46
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.GTAYTFFTPGNLK#.Q	103.37	63.41	1.63	0.61
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.IVDQIRPDR.Q	98.65	37.23	2.65	0.38
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.K#K#WDLSELPK#.F	19.64	6.69	2.94	0.34
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.KWDLSELPK.F	10.36	17.18	0.60	1.66
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.LIDFLESGK#.T	143.28	74.99	1.91	0.52
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.LIQLM*EEIM*AEK#.E	10.48	5.73	1.83	0.55
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.LM*QLVDHR@.G	21.76	10.04	2.17	0.46
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.M*LDM*GFEPQIR@.K	151.87	64.64	2.35	0.43
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.MLDM*GFEPQIR@.K	29.81	11.29	2.64	0.38
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.M*LDMGFEPQIR@.K	12.60	5.24	2.41	0.42
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.MLDMGFEPQIR@.K	9.90	4.98	1.99	0.50
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.QLAEDFLR@.D	88.09	38.92	2.26	0.44
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.QTLM*WSATWPK#.E	87.40	36.16	2.42	0.41
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.SGK#APILIATDVASR@.G	14.09	6.99	2.02	0.50
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.SQPER@DWVLNEFR@.S	26.51	12.73	2.08	0.48
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.SSQSSSQQFSGIGR@.S	89.30	45.82	1.95	0.51
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.TIIFVETK#.R	129.36	69.04	1.87	0.53
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.VLEEANQAINPK#.L	140.18	77.17	1.82	0.55
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.WDLSELPK#.F	27.91	19.19	1.45	0.69
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.APILIATDVASR@.G	188.70	53.64	3.52	0.28
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.GLDVEDVK#.F	72.56	19.50	3.72	0.27
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.GTAYTFFTPGNLK#.Q	11.41	3.64	3.14	0.32
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.LIDFLESGK#.T	10.54	4.50	2.34	0.43
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.M*LDM*GFEPQIR@.K	23.83	9.48	2.51	0.40
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.QTLM*WSATWPK#.E	9.63	3.70	2.60	0.38
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	R.SSQSSSQQFSGIGR@.S	7.42	6.55	1.13	0.88
Q501J6_DDX17_MOUSE	Ddx17	Probable ATP-dependent	K.VLEEANQAINPK#.L	14.92	8.04	1.85	0.54
Q8K363_DDX18_MOUSE	Ddx18	ATP-dependent RNA heli	K.VSDIQSQLEK#.L	22.87	13.26	1.73	0.58
Q8K363_DDX18_MOUSE	Ddx18	ATP-dependent RNA heli	K.VSDIQSQLEK#.L	17.32	8.25	2.10	0.48
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.DPSSPLYSVK#.S	61.09	25.47	2.40	0.42
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.EEETLDTIK#.Q	66.84	20.13	3.32	0.30
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.EGHQVALLSGEM*M*VEQR@.A	60.11	20.78	2.89	0.35
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.GLAVNM*VDSK#.H	17.30	6.23	2.77	0.36
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.GLAVNMVDSK#.H	5.59	2.70	2.07	0.48
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.HSM*NILNR@.I	82.96	30.86	2.69	0.37
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.IER@LDTDDLDEIEK#.I	14.72	4.74	3.11	0.32
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.K#TASWLAAELSK#.E	14.08	4.67	3.02	0.33
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.LDTDDLDEIEK#.I	93.13	39.87	2.34	0.43
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.LDTDDLDEIEK#IAN.-	13.79	7.43	1.85	0.54
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.LK#R@EEETLDTIK#.Q	23.10	10.23	2.26	0.44
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.SNLVDNTNQVEVLQR@.D	65.56	22.31	2.94	0.34
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.SNLVDNTNQVEVLQR@DPSSPLYSVK#.S	7.65	1.85	4.15	0.24
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.TAAFVLAM*LSR@.V	45.25	17.13	2.64	0.38
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.TAAFVLAMLSR@.V	14.85	4.57	3.25	0.31
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.TASWLAAELSK#.E	34.34	22.34	1.54	0.65
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.TSTTAEK#TEEEEK#EDR@.A	54.12	19.12	2.83	0.35
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.TSTTAEK#TEEEEK#EDR@.A	3.26	2.56	1.27	0.79
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.VFVLDEADVM*IATQGHQDQSIR@.I	44.81	16.97	2.64	0.38
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.DPSSPLYSVK#.S	17.55	7.15	2.45	0.41
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.EGHQVALLSGEM*M*VEQR@.A	12.96	6.14	2.11	0.47
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.GLAVNM*VDSK#.H	9.60	6.98	1.38	0.73
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.HSM*NILNR@.I	16.64	6.57	2.53	0.40
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.LDTDDLDEIEK#.I	24.48	11.88	2.06	0.49
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.SNLVDNTNQVEVLQR@.D	23.41	7.70	3.04	0.33
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.SNLVDNTNQVEVLQR@.D	8.08	1.52	5.32	0.19
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.TAAFVLAM*LSR@.V	20.82	5.99	3.48	0.29
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.TSTTAEK#TEEEEK#EDR@.A	24.11	7.53	3.20	0.31
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.VFVLDEADVM*IATQGHQDQSIR@.I	14.98	6.32	2.37	0.42
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.DPSSPLYSVK#.S	13.18	10.53	1.25	0.80
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.EGHQVALLSGEM*M*VEQR@.A	14.22	3.34	4.26	0.23
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.LDTDDLDEIEK#.I	21.09	6.39	3.30	0.30
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	R.SNLVDNTNQVEVLQR@.D	18.60	3.75	4.96	0.20
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.TAAFVLAM*LSR@.V	15.51	15.72	0.99	1.01
Q61655_DD19A_MOUSE	Ddx19a	ATP-dependent RNA heli	K.VFVLDEADVM*IATQGHQDQSIR@.I	18.17	6.03	3.01	0.33
Q9JJY4_DDX20_MOUSE	Ddx20	Probable ATP-dependent	K.TQHLQELFSK#.V	6.64	6.25	1.06	0.94
Q9JJY4_DDX20_MOUSE	Ddx20	Probable ATP-dependent	R.VLISTDLTSR@.G	9.77	3.41	2.86	0.35
Q9JJY4_DDX20_MOUSE	Ddx20	Probable ATP-dependent	K.VPFNQALVFSNLHSR@.A	7.83	3.92	2.00	0.50
Q9JJY4_DDX20_MOUSE	Ddx20	Probable ATP-dependent	R.VLISTDLTSR@.G	10.91	2.93	3.72	0.27
Q9JJY4_DDX20_MOUSE	Ddx20	Probable ATP-dependent	K.VPFNQALVFSNLHSR@.A	12.77	3.15	4.06	0.25
Q9JJY4_DDX20_MOUSE	Ddx20	Probable ATP-dependent	K.QLIELDYLNPGSIR@.L	8.03	1.00	8.07	0.12
Q9JJY4_DDX20_MOUSE	Ddx20	Probable ATP-dependent	K.VPFNQALVFSNLHSR@.A	12.51	2.50	5.01	0.20
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.EGAFSNFPISEETVK.L	3.96	3.67	1.08	0.93
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.GAVEALAAALAHISGATSVDQR@.S	17.14	12.85	1.33	0.75
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.TFSFAIPLIEK#.L	11.76	13.82	0.85	1.18
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.AAVIGDVIR@.V	250.35	106.78	2.34	0.43
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.APQVLVLAPTR@.E	114.40	52.98	2.16	0.46
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.DFSDITK#K#.L	36.52	21.08	1.73	0.58
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.EGAFSNFPISEETVK#.L	146.61	71.90	2.04	0.49
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.ELANQVSK#.D	142.59	65.28	2.18	0.46
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.ELK#EQLGESIDAK#.V	83.45	48.66	1.72	0.58
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.EQLGESIDAK#.V	55.20	19.24	2.87	0.35
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.GAVEALAAALAHISGATSVDQR@.S	66.11	31.58	2.09	0.48
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.GAVEALAAALAHISGATSVDQR.S	13.98	6.15	2.27	0.44
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.GM*VFLK#.G	38.77	13.11	2.96	0.34
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.GPSEDDVDPPK#.S	10.10	5.02	2.01	0.50
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.GR@APQVLVLAPTR@.E	76.83	28.06	2.74	0.37
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.GVNFLFPIQAK#.T	262.56	128.91	2.04	0.49
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.IGVPSATEIIK#.A	136.32	70.28	1.94	0.52
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.KGPSEDDVDPPK.S	49.64	27.43	1.81	0.55
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.KQEEEPQDDTASTSK.T	11.86	9.00	1.32	0.76
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.LGSDGAEESM*ETLPK#PSEK#.K	68.17	27.66	2.46	0.41
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.LK#DGLSQPSEPK#.S	150.77	78.16	1.93	0.52
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.LLDSVPPTAISHFK#.Q	72.65	40.07	1.81	0.55
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.R@WQLTVATEQPELEGPPDGYR@.G	6.95	3.56	1.95	0.51
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.SGIDILVGTPGR@.I	140.74	66.14	2.13	0.47

Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.SK#TEEATEGMEEAVSSK#.A	14.96	7.59	1.97	0.51
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.SLINSQAGFVTM*ILR@.C	31.12	16.15	1.93	0.52
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.SLINSQAGFVTMILR@.C	27.79	11.39	2.44	0.41
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.SNSSDAPGEESSSETEK#EIPVEQK#.E	71.27	29.40	2.42	0.41
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.STYEQVDLIGK#.K	71.16	27.95	2.55	0.39
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.TEAVTEIQEK#.W	180.05	81.27	2.22	0.45
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.TEEATEGMEEAVSSK#.A	3.88	1.79	2.17	0.46
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.TEEATEGM*EEAVSSK#.A	18.13	7.95	2.28	0.44
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.TFHHVYSGK#.D	110.37	56.31	1.96	0.51
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.TFSFAIPLIEK#.L	371.48	200.97	1.85	0.54
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.WQLTVATEQPELEGPPDGYR@.G	14.46	9.33	1.55	0.65
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.AAITVEHLAIK#.C	8.52	2.36	3.61	0.28
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.AAVIGDVIR@.V	87.39	28.31	3.09	0.32
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.EEYQLAQVEQK#.A	8.36	8.51	0.98	1.02
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.EGAFSNFPISEETVK#.L	49.06	15.79	3.11	0.32
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.EQLGESIDAK#.V	15.17	9.89	1.53	0.65
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.GAVEALAAALAHISGATSVDQR@.S	115.11	29.55	3.90	0.26
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.GR@APQVLVLAPTR@.E	23.17	7.38	3.14	0.32
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.GVNFLFPIQAK#.T	91.41	31.24	2.93	0.34
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.IGVPSATEIIK#.A	33.28	9.30	3.58	0.28
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.K#QEEEPQDDTASTSK#.T	4.12	1.45	2.84	0.35
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.K#QEEEPQDDTASTSK#.T	17.45	5.05	3.46	0.29
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.LGSDGAEESM*ETLPK#PSEK#.K	24.48	8.55	2.86	0.35
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.LQGGLQER.K	61.84	18.79	3.29	0.30
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.SGIDILVGTPGR@.I	57.11	22.41	2.55	0.39
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.SK#TEEATEGM*EEAVSSK#.A	9.75	2.79	3.50	0.29
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.SKTEEATEGM*EEAVSSK.A	64.13	20.33	3.16	0.32
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.SLINSQAGFVTM*ILR@.C	6.46	4.51	1.43	0.70
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.SLINSQAGFVTMILR@.C	8.94	2.19	4.09	0.24
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.STYEQVDLIGK#.K	23.64	9.83	2.40	0.42
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	R.TEAVTEIQEK#.W	45.68	17.94	2.55	0.39
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.TEEATEGM*EEAVSSK#.A	10.82	2.85	3.79	0.26
Q9JIK5_DDX21_MOUSE	Ddx21	Nucleolar RNA helicase 2	K.TFSFAIPLIEK#.L	124.06	45.41	2.73	0.37
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.DIIGVAETGSGK#.T	39.16	12.37	3.16	0.32
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	K.DILVATDVAGR@.G	22.48	9.08	2.47	0.40
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.ELAQQIEEETIK#.F	51.29	13.68	3.75	0.27
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.GFIAGIDLK#.Q	36.91	15.80	2.34	0.43
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.GIDIQDVSM*VVNYDM*AK#.N	5.93	3.18	1.86	0.54
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	K.IDR@IEESDQGPYAIILAPTR@.E	26.99	7.86	3.43	0.29
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.IEESDQGPYAIILAPTR@.E	11.32	3.32	3.41	0.29
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.IFR@EDYSITTK#.G	38.32	12.33	3.11	0.32
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.LIDVLENR@.Y	53.99	19.67	2.74	0.36
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	K.M*LEDPQER@.E	9.77	3.91	2.50	0.40
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.QTVM*FTATM*PPAVER@.L	6.73	2.85	2.36	0.42
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	K.SGVAITFLTK#.E	61.66	27.94	2.21	0.45
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.TLEEKEQEEAR.L	9.21	5.94	1.55	0.65
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.TVAVIGGISR@.E	47.25	17.48	2.70	0.37
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	K.VFLM*SESEK#.R	9.45	3.80	2.48	0.40
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.DIIGVAETGSGK#.T	15.50	4.07	3.81	0.26
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	K.EDSAVFYELK#.Q	8.69	3.66	2.37	0.42
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.GFIAGIDLK#.Q	15.29	5.05	3.03	0.33
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.HQVQLLGR@.G	17.32	3.45	5.03	0.20
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	K.IDR@IEESDQGPYAIILAPTR@.E	8.94	3.11	2.87	0.35
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.IEESDQGPYAIILAPTR@.E	5.66	2.06	2.74	0.36
D3Z0M9_D3Z0M9_MOUSE	Ddx23	MCG18410, isoform CRA	R.TLEEK#EQEEAR@.L	4.68	2.44	1.92	0.52
Q9ESV0_DDX24_MOUSE	Ddx24	ATP-dependent RNA helic	R.AAEGAAAQNEYEVK#.A	7.60	2.19	3.48	0.29
Q9ESV0_DDX24_MOUSE	Ddx24	ATP-dependent RNA helic	R.NEGTVETLTETK.I	10.13	9.04	1.12	0.89
Q9ESV0_DDX24_MOUSE	Ddx24	ATP-dependent RNA helic	K.SESLAQAAPR.K	6.54	10.54	0.62	1.61
Q9ESV0_DDX24_MOUSE	Ddx24	ATP-dependent RNA helic	K.TLQK#DEDIPLFPVQSK#.Y	7.80	7.53	1.04	0.97
Q9ESV0_DDX24_MOUSE	Ddx24	ATP-dependent RNA helic	R.AAEGAAAQNEYEVK#.A	10.80	2.99	3.61	0.28
Q9ESV0_DDX24_MOUSE	Ddx24	ATP-dependent RNA helic	R.AASEGLSLM*LIGPEDVINFKK.I	4.73	4.67	1.01	0.99
Q921N6_DDX27_MOUSE	Ddx27	Probable ATP-dependent	R.IFVNSNTDVAPFLR.Q	7.06	5.77	1.22	0.82
Q6NZQ2_Q6NZQ2_MOUSE	Ddx31	DEAD/H (Asp-Glu-Ala-Asp	R.SDGPYALVLVPTR@.E	9.13	2.14	4.27	0.23
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.DVQEIFR@.L	372.12	143.67	2.59	0.39
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.FEVNVAELPEEIDISTYIEQSR@.-	16.41	6.58	2.49	0.40
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.FM*QDPM*EVFVDDETK#.L	7.68	3.39	2.26	0.44
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.GLAVTFVSDENDAK#.I	155.49	56.06	2.77	0.36
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.GSYVSIHSSGFR.D	92.65	42.17	2.20	0.46
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.ILNDVQDR@.F	101.09	36.67	2.76	0.36
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.ILNDVQDR@FEVNVAELPEEIDISTYIEQSR@.-	20.04	3.31	6.06	0.16
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.ILVATNLFGR@.G	779.04	325.29	2.39	0.42
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.LTLHGLQQYYVK#.L	255.13	103.02	2.48	0.40
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.R@ILVATNLFGR@.G	57.69	24.52	2.35	0.43
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.VNIVFNYDM*PEDSDTYLHR@.V	49.98	22.64	2.21	0.45
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.VSVFFGGLSIK#.K	65.84	24.48	2.69	0.37
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.GLAVTFVSDENDAK#.I	11.20	2.11	5.30	0.19
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.ILVATNLFGR@.G	58.95	15.38	3.83	0.26
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.DVQEIFR@.L	195.98	68.12	2.88	0.35
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.GLAVTFVSDENDAK#.I	93.49	29.37	3.18	0.31
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.ILVATNLFGR@.G	326.53	106.49	3.07	0.33
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.LTLHGLQQYYVK#.L	151.56	49.85	3.04	0.33
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.VNIVFNYDM*PEDSDTYLHR@.V	30.46	13.22	2.30	0.43
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.VSVFFGGLSIK#.K	58.57	18.74	3.13	0.32
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.DVQEIFR@.L	234.50	65.25	3.59	0.28
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.ELAFQISK#.E	197.27	57.29	3.44	0.29
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.FM*QDPM*EVFVDDETK#.L	8.02	2.37	3.38	0.30
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.GLAVTFVSDENDAK#.I	105.86	27.72	3.82	0.26
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.ILNDVQDR@.F	64.47	15.94	4.04	0.25
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.ILVATNLFGR@.G	381.06	106.79	3.57	0.28
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.LTLHGLQQYYVK#.L	141.27	43.73	3.23	0.31
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.R@ILVATNLFGR@.G	18.77	6.02	3.12	0.32
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	R.VNIVFNYDM*PEDSDTYLHR@.V	55.46	16.49	3.36	0.30
Q8VDW0_DX39A_MOUSE	Ddx39a	ATP-dependent RNA helic	K.VSVFFGGLSIK#.K	67.91	13.52	5.02	0.20
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.FEVNISELPDEIDISSYIEQTR@.-	6.35	5.08	1.25	0.80
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.FM*QDPM*EIFVDDETK#.L	24.52	9.96	2.46	0.41
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.GLAITFVSDENDAK#.I	426.55	178.86	2.38	0.42
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.ILNDVQDR@FEVNISELPDEIDISSYIEQTR@.-	56.87	18.90	3.01	0.33
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.K#DEEVLK#K#.N	10.45	5.50	1.90	0.53
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.KFM*QDPM*EIFVDDETK.L	23.35	10.46	2.23	0.45
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.QVM*M*FSATLSK#.E	102.73	50.59	2.03	0.49
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.VAVFFGGLSIK#.K	222.70	73.32	3.04	0.33
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.VNIAFNYDM*PEDSDTYLHR@.V	217.14	92.00	2.36	0.42
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.VNIAFNYDMPEDSDTYLHR@.V	24.69	12.13	2.04	0.49

Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.GLAITFVSDENDAK#.I	20.64	3.64	5.68	0.18
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.VAVFFGGLSIK#.K	4.53	1.76	2.57	0.39
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.VNIAFNYDM*PEDSDTYLHR@.V	5.57	2.27	2.46	0.41
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.FEVNISELPDEIDISSYIEQTR@.-	24.08	3.20	7.53	0.13
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.FM*QDPM*EIFVDDETK#.L	6.90	3.29	2.10	0.48
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.GLAITFVSDENDAK#.I	180.76	67.11	2.69	0.37
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.ILNDVQDR@FEVNISELPDEIDISSYIEQTR@.-	17.41	19.73	0.88	1.13
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.QVM*M*FSATLSK#.E	20.58	8.93	2.30	0.43
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.VAVFFGGLSIK#.K	104.84	32.46	3.23	0.31
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.VNIAFNYDM*PEDSDTYLHR@.V	73.48	22.89	3.21	0.31
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.FEVNISELPDEIDISSYIEQTR@.-	36.59	12.64	2.90	0.35
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.FM*QDPM*EIFVDDETK#.L	23.90	8.97	2.67	0.38
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.GLAITFVSDENDAK#.I	247.39	71.27	3.47	0.29
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.QVM*M*FSATLSK#.E	31.03	9.77	3.17	0.32
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.VAVFFGGLSIK#.K	80.57	23.50	3.43	0.29
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.VNIAFNYDM*PEDSDTYLHR@.V	89.40	24.61	3.63	0.28
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	R.VNIAFNYDMPEDSDTYLHR@.V	11.52	2.81	4.10	0.24
Q9Z1N5_DX39B_MOUSE	Ddx39b	Spliceosome RNA helicas	K.YM*PNVK#.V	67.85	30.23	2.24	0.45
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.DLLDLLVEAK#.Q	167.49	105.61	1.59	0.63
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.DR@EEALHQFR@.S	86.31	55.75	1.55	0.65
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.ELAVQIYEEAR@.K	33.56	64.16	0.52	1.91
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.FSGGFGAR@.D	94.05	65.08	1.45	0.69
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.GLDISNVK#.H	52.49	35.24	1.49	0.67
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.HAIPIIK#.E	51.99	38.12	1.36	0.73
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.HTM*M*FSATFPK#.E	21.30	18.11	1.18	0.85
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.HVINFDLPSDIEEYVHR@.I	78.04	42.67	1.83	0.55
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.IVEQDTM*PPK#.G	57.91	38.66	1.50	0.67
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.LEQELFSGGNTGINFEK#.Y	11.81	10.50	1.12	0.89
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.LVDM*M*ER@.G	38.02	19.96	1.91	0.52
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.QSSGASSSSFSSSR@.A	23.16	15.59	1.49	0.67
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.QYPISLVLAPTR@.E	50.08	46.94	1.07	0.94
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.RIVEQDTM*PPK.G	5.27	2.19	2.41	0.42
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.SFLLDLLNATGK#.D	163.49	126.85	1.29	0.78
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.SPILVATAVAAR@.G	137.84	80.50	1.71	0.58
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.VGNLGLATSFFNER@.N	107.84	76.09	1.42	0.71
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.VGSTSENITQK#.V	103.32	78.86	1.31	0.76
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.YLVLDEADR@.M	59.78	38.64	1.55	0.65
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.YLVLDEADRM*LDM*GFEPQIR.R	24.04	14.97	1.61	0.62
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.LEQELFSGGNTGINFEK.Y	4.00	6.09	0.66	1.52
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.DKDAYSSFGSR.S	49.75	14.51	3.43	0.29
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.DLLDLLVEAK#.Q	489.66	175.46	2.79	0.36
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.DR@EEALHQFR@.S	333.97	104.96	3.18	0.31
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.DSLTLVFVETK#.K	54.17	25.89	2.09	0.48
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.DSLTLVFVETK#K#.G	17.62	4.26	4.13	0.24
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.EIQM*LAR@.D	97.52	33.74	2.89	0.35
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.ELAVQIYEEAR@.K	169.24	53.30	3.18	0.31
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.FSGGFGAR@.D	205.05	75.07	2.73	0.37
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.GLDISNVK#.H	161.29	48.47	3.33	0.30
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.GR@GDYDGIGGR@.G	17.77	6.34	2.80	0.36
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.HAIPIIK#.E	201.44	88.86	2.27	0.44
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.HTM*M*FSATFPK#.E	38.35	17.78	2.16	0.46
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.HVINFDLPSDIEEYVHR@.I	189.97	73.42	2.59	0.39
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.IVEQDTM*PPK#.G	90.37	43.63	2.07	0.48
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.K#QYPISLVLAPTR@.E	8.19	4.52	1.81	0.55
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.KQYPISLVLAPTR.E	30.82	12.99	2.37	0.42
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.LEQELFSGGNTGINFEK#.Y	51.62	21.77	2.37	0.42
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.LVDM*M*ER.G	61.92	22.84	2.71	0.37
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.QSSGASSSSFSSSR@.A	38.17	9.65	3.96	0.25
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.QYPISLVLAPTR@.E	142.66	58.81	2.43	0.41
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.RIVEQDTM*PPK.G	11.56	5.84	1.98	0.51
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.SFLLDLLNATGK#.D	438.17	128.40	3.41	0.29
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.SGFGK#FER@.G	16.32	5.17	3.15	0.32
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.SPILVATAVAAR@.G	400.59	165.74	2.42	0.41
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.VGNLGLATSFFNER@.N	352.96	119.71	2.95	0.34
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.VGSTSENITQK#.V	338.33	124.17	2.72	0.37
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.YLVLDEADR@.M	97.17	38.52	2.52	0.40
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.YLVLDEADRM*LDM*GFEPQIR.R	70.56	24.98	2.83	0.35
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.DLLDLLVEAK#.Q	145.36	42.21	3.44	0.29
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.DR@EEALHQFR@.S	68.77	17.32	3.97	0.25
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.DSLTLVFVETK#.K	11.60	4.57	2.54	0.39
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.ELAVQIYEEAR@.K	37.41	9.70	3.85	0.26
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.GLDISNVK#.H	28.97	9.37	3.09	0.32
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.HTM*M*FSATFPK#.E	10.22	3.86	2.65	0.38
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.HVINFDLPSDIEEYVHR@.I	43.42	11.29	3.85	0.26
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.IVEQDTM*PPK#.G	5.69	4.13	1.38	0.73
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.LEQELFSGGNTGINFEK#.Y	12.09	5.35	2.26	0.44
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.QSSGASSSSFSSSR@.A	15.13	6.07	2.49	0.40
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.QYPISLVLAPTR@.E	31.99	11.72	2.73	0.37
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.SFLLDLLNATGK#.D	101.63	36.19	2.81	0.36
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	K.SPILVATAVAAR@.G	69.95	17.70	3.95	0.25
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.VGNLGLATSFFNER@.N	82.44	21.34	3.86	0.26
Q62167_DDX3X_MOUSE	Ddx3x	ATP-dependent RNA heli	R.VGSTSENITQK#.V	51.50	12.98	3.97	0.25
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	R.LLQEDSSPLLR@.C	5.16	3.45	1.50	0.67
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	K.DVLVATDVASK#.G	20.70	11.71	1.77	0.57
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	K.DYLAHSSM*DF.-	12.62	12.62	1.00	1.00
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	K.FPAAILR@.G	13.10	8.35	1.57	0.64
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	K.ILESVAEGR@.A	32.05	19.34	1.66	0.60
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	K.K#ADVDAIHEYLLLK#.G	40.55	19.97	2.03	0.49
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	R.LLQEDSSPLLR.C	23.54	14.23	1.65	0.60
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	R.QTLLFSATM*PK#.K	7.83	6.94	1.13	0.89
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	K.SALVK#PVTINVGR@.A	41.92	16.96	2.47	0.40
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	R.SEDEDEDDEDYVPYVPLR@.Q	7.14	4.99	1.43	0.70
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	R.SGNTGIATTFINK#.A	16.14	9.07	1.78	0.56
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	K.TPPPVLIFAEK#.K	24.30	13.56	1.79	0.56
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	R.YLALDEADR@.M	11.63	6.15	1.89	0.53
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	K.K#ADVDAIHEYLLLK#.G	13.61	6.75	2.02	0.50
Q91VN6_DDX41_MOUSE	Ddx41	Probable ATP-dependent	K.SALVK#PVTINVGR@.A	18.45	4.31	4.28	0.23
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	R.DILIDPIR@.V	42.02	17.55	2.39	0.42
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	K.DIPVLVATDVAAR@.G	62.88	25.68	2.45	0.41
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	R.DM*IGIAK#.T	28.55	9.90	2.88	0.35
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	K.DSNFAGDLVR@.N	33.88	16.76	2.02	0.49
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	R.GFGFGGFAISAGK#.K	14.25	5.72	2.49	0.40
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	K.GIRDDIEEEDDQEAYFR.Y	34.84	11.99	2.91	0.34

Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	R.GLDIPSIK#.T	32.18	15.20	2.12	0.47
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	K.GVAYTLLTPK#.D	38.68	18.32	2.11	0.47
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	K.NFYNEHEEITNLTPQQLIDLR@.H	40.99	16.41	2.50	0.40
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	R.QTLLFSATFR@.K	12.32	5.89	2.09	0.48
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	K.SHFVAASLSNQK#.A	7.33	4.23	1.73	0.58
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	R.SVAVYGGGSM*WEQAK#.A	6.59	2.33	2.83	0.35
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	K.TVINYDVAR@.D	45.73	18.67	2.45	0.41
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	R.VVQGDIGEANEDVTQIVEILHSGPSK#.W	48.01	18.01	2.67	0.38
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	K.DIPVLVATDVAAR@.G	11.80	6.28	1.88	0.53
Q810A7_DDX42_MOUSE	Ddx42	ATP-dependent RNA heli	R.VVQGDIGEANEDVTQIVEILHSGPSK#.W	14.89	4.42	3.37	0.30
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.AALGLQDSDDEDAAVDIDEQIESM*FNSK#.K	4.04	1.58	2.56	0.39
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.ALELSGTAVPPDLEK#.L	20.29	7.46	2.72	0.37
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.DLIGIAK#.T	83.76	23.98	3.49	0.29
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.ELALQITK#.E	250.35	27.41	9.13	0.11
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.FDETEQALANER@.K	32.60	10.64	3.06	0.33
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.GFK#FDETEQALANER@.K	81.01	21.22	3.82	0.26
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.GGTILAPTVSAK#.T	95.92	29.04	3.30	0.30
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.GYAYTFITEDQAR@.Y	126.92	30.69	4.14	0.24
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.HGYEK#PTPIQTQAIPAIM*SGR@.D	8.50	2.80	3.03	0.33
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.ILSK#PIEVQVGGR@.S	99.15	33.42	2.97	0.34
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.ISEYSEAAITIR@.G	34.43	9.57	3.60	0.28
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.IYLAIESANELAVQK#.A	14.25	12.05	1.18	0.85
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.K#IYLAIESANELAVQK#.A	16.05	5.62	2.85	0.35
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.K#LLEPVDHGK#.I	51.62	27.92	1.85	0.54
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.LEM*EGITVK#.G	46.29	12.98	3.56	0.28
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.LIK#EELIR@.L	13.47	4.13	3.26	0.31
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.LLVATSVAAR@.G	115.52	32.13	3.60	0.28
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.LNYVPLEK#.Q	64.42	18.92	3.40	0.29
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.LQNSYQPTNK#.G	59.79	19.54	3.06	0.33
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.M*IDM*LAANSGR@.V	23.86	8.24	2.90	0.35
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.M*SQEEVNVFR@.L	61.49	21.69	2.83	0.35
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.NFYVEVPELAK#.M	88.44	30.11	2.94	0.34
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.NLGIESQVDVM*QQATNAILR@.G	20.66	5.52	3.74	0.27
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.QTVM*FSATFPR@.A	38.05	11.67	3.26	0.31
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.RILSKPIEVQVGGR.S	34.63	11.64	2.98	0.34
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.R@YEEELEINDFPQTAR@.W	42.27	10.55	4.01	0.25
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.SLEEGEGPIAVIM*TPTR@.E	44.39	22.92	1.94	0.52
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.SLEEGEGPIAVIMTPTR@.E	13.75	6.68	2.06	0.49
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.TIAEQLAEK#.I	91.38	27.02	3.38	0.30
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.TIAFLLPM*FR@.H	96.68	28.50	3.39	0.29
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.VK#DM*AAPGTSSVPAPTAGNAEK#.L	36.17	13.92	2.60	0.38
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.VTYVVLDEADR@.M	30.63	14.30	2.14	0.47
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.VVTVVTTK#.K	80.31	19.69	4.08	0.25
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.YEEELEINDFPQTAR@.W	13.19	4.93	2.67	0.37
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.GGTILAPTVSAK#.T	32.55	8.94	3.64	0.27
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.GYAYTFITEDQAR@.Y	22.55	6.95	3.24	0.31
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.ISEYSEAAITIR@.G	8.98	3.02	2.97	0.34
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.M*IDM*LAANSGR@.V	8.38	3.52	2.38	0.42
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.M*SQEEVNVFR@.L	19.09	5.92	3.23	0.31
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.NFYVEVPELAK#.M	35.09	7.57	4.64	0.22
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.NLGIESQVDVM*QQATNAILR@.G	4.72	11.43	0.41	2.42
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.QTVM*FSATFPR@.A	17.36	5.73	3.03	0.33
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	R.SLEEGEGPIAVIM*TPTR@.E	12.70	5.93	2.14	0.47
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.TIAEQLAEK#.I	26.85	4.90	5.48	0.18
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.TIAFLLPM*FR@.H	35.62	11.35	3.14	0.32
Q569Z5_DDX46_MOUSE	Ddx46	Probable ATP-dependent	K.VVTVVTTK#.K	27.51	5.79	4.75	0.21
Q9CWX9_DDX47_MOUSE	Ddx47	Probable ATP-dependent	R.DIIGLAETGSGK#.T	13.61	9.25	1.47	0.68
Q9CWX9_DDX47_MOUSE	Ddx47	Probable ATP-dependent	K.IQIEAIPLALQGR@.D	22.57	15.59	1.45	0.69
Q9CWX9_DDX47_MOUSE	Ddx47	Probable ATP-dependent	R.LFALVLTPTR.E	14.94	11.87	1.26	0.79
Q4FZF3_DDX49_MOUSE	Ddx49	Probable ATP-dependent	R.ELAYQIAEQFR@.V	4.81	2.84	1.69	0.59
Q4FZF3_DDX49_MOUSE	Ddx49	Probable ATP-dependent	K.TAAFVLPILQK.L	7.04	7.81	0.90	1.11
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.DWVLNEFK#.H	140.05	72.99	1.92	0.52
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.EANQAINPK#.L	81.13	39.83	2.04	0.49
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.FGNPGEK#.L	95.89	49.63	1.93	0.52
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.FVINYDYPNSSEDYIHR@.I	309.00	167.08	1.85	0.54
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.GYSNLLK#.R	142.31	75.92	1.87	0.53
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.K#K#WNLDELPK#.F	16.30	13.05	1.25	0.80
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.LLQLVEDR@.G	299.10	153.13	1.95	0.51
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.LMEEIMSEK#.E	6.85	3.06	2.24	0.45
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.LM*EEIM*SEK#.E	80.37	44.61	1.80	0.56
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.LM*EEIM*SEKENK.T	17.53	9.49	1.85	0.54
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.QNFTEPTAIQAQGWPVALSGLDM*VGVAQTGSGK#.T	28.11	9.72	2.89	0.35
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.QVSDLISVLR@.E	377.00	172.55	2.18	0.46
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.R@GGFNTFR@.D	41.19	21.14	1.95	0.51
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.SQQER@DWVLNEFK#.H	27.40	17.69	1.55	0.65
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.TAQEVDTYR@.R	56.82	31.24	1.82	0.55
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.TGTAYTFFTPNNIK#.Q	104.11	54.39	1.91	0.52
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.TIVFVETK#.R	200.94	102.58	1.96	0.51
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.TIVFVETK#R@.R	7.63	3.63	2.10	0.48
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.TTYLVLDEADR@.M	168.65	79.20	2.13	0.47
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.TTYLVLDEADRM*LDM*GFEPQIR.K	78.77	42.43	1.86	0.54
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.WNLDELPK#.F	41.52	28.72	1.45	0.69
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.WNLDELPK#FEK#.N	39.23	25.09	1.56	0.64
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.DWVLNEFK#.H	239.86	102.24	2.35	0.43
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.EANQAINPK#.L	127.07	45.77	2.78	0.36
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.FGNPGEK#.L	159.13	66.81	2.38	0.42
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.FVINYDYPNSSEDYIHR@.I	437.68	165.05	2.65	0.38
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.FVINYDYPNSSEDYIHR.I	11.41	4.15	2.75	0.36
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.GGFNTFR@.D	98.30	45.76	2.15	0.47
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.GYSNLLK#.R	282.25	112.44	2.51	0.40
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.K#K#WNLDELPK#.F	25.63	9.65	2.66	0.38
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.K#WNLDELPK#.F	9.87	5.35	1.84	0.54
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.K#WNLDELPK#FEK#.N	15.55	5.37	2.89	0.35
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.LLQLVEDR@.G	579.28	199.69	2.90	0.34
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.LM*EEIM*SEK#.E	67.36	27.79	2.42	0.41
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.QLAEDFLK#.D	62.87	20.30	3.10	0.32
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.QNFTEPTAIQAQGWPVALSGLDM*VGVAQTGSGK#.T	49.02	12.53	3.91	0.26
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.QVSDLISVLR@.E	405.70	144.37	2.81	0.36
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.SQQER@DWVLNEFK#.H	40.93	10.52	3.89	0.26
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.TAQEVDTYR@.R	79.71	29.62	2.69	0.37
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.TGTAYTFFTPNNIK#.Q	306.81	112.29	2.73	0.37
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.TIVFVETK#.R	369.96	143.01	2.59	0.39
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.TTYLVLDEADR@.M	187.83	73.15	2.57	0.39

Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.TTYLVLDEADRM*LDM*GFEPQIR.K	142.07	45.42	3.13	0.32
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.TTYLVLDEADR@M*LDMGFEPQIR@.K	3.77	1.86	2.03	0.49
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.WNLDELPK#.F	107.98	39.46	2.74	0.37
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.WNLDELPKFEK.N	121.34	46.94	2.58	0.39
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.DWVLNEFK#.H	28.90	9.50	3.04	0.33
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.EANQAINPK#.L	35.82	9.66	3.71	0.27
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	R.LM*EEIM*SEK#.E	10.06	3.67	2.74	0.37
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.QVSDLISVLR@.E	50.45	13.84	3.65	0.27
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.TGTAYTFFTPNNIK#.Q	29.85	7.63	3.91	0.26
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.TIVFVETK#.R	54.68	21.85	2.50	0.40
Q61656_DDX5_MOUSE	Ddx5	Probable ATP-dependent	K.WNLDELPK#.F	10.13	1.13	8.97	0.11
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	K.EGAFSNFSISEETIK#.L	30.63	13.40	2.29	0.44
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	R.ELANQVAK#.D	27.01	17.13	1.58	0.63
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	K.GAVDALAAALAHISGASSFEPR@.S	54.63	37.39	1.46	0.68
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	R.GVTYLFPIQVK#.T	33.93	23.00	1.47	0.68
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	R.LQAEWHDSDWILSVPAK#.L	6.89	4.42	1.56	0.64
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	R.NGIDILVGTPGR@.I	6.86	7.38	0.93	1.08
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	R.SLASVSYAAVDFFR@PSAQR@.L	35.37	19.39	1.82	0.55
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	K.TFSFAIPLIER@.L	82.94	44.69	1.86	0.54
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	R.VGVPSTM*DLVK#.S	526.61	303.82	1.73	0.58
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	K.VLVATNVAAR@.G	35.30	23.79	1.48	0.67
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	K.VLVLAPTR@.E	43.00	30.43	1.41	0.71
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	K.GAVDALAAALAHISGASSFEPR@.S	11.35	5.52	2.06	0.49
Q99MJ9_DDX50_MOUSE	Ddx50	ATP-dependent RNA heli	K.TFSFAIPLIER@.L	23.19	9.45	2.45	0.41
Q6P9R1_DDX51_MOUSE	Ddx51	ATP-dependent RNA heli	K.SVTEDLTPIEDIPEVHPDLQK#.Q	11.62	7.45	1.56	0.64
Q6P9R1_DDX51_MOUSE	Ddx51	ATP-dependent RNA heli	K.TGQAFTLLLK#.V	9.57	2.98	3.21	0.31
Q6P9R1_DDX51_MOUSE	Ddx51	ATP-dependent RNA heli	R.YAGPEAAGQGDTDAEAGSR@.A	5.08	2.33	2.18	0.46
Q6P9R1_DDX51_MOUSE	Ddx51	ATP-dependent RNA heli	K.EQESLVQK#.T	8.51	4.53	1.88	0.53
Q6P9R1_DDX51_MOUSE	Ddx51	ATP-dependent RNA heli	K.LLFSATLTQDPEK#.L	10.45	4.00	2.61	0.38
Q6P9R1_DDX51_MOUSE	Ddx51	ATP-dependent RNA heli	K.SVTEDLTPIEDIPEVHPDLQK#.Q	11.40	7.86	1.45	0.69
Q6P9R1_DDX51_MOUSE	Ddx51	ATP-dependent RNA heli	K.TGQAFTLLLK#.V	17.13	6.95	2.46	0.41
Q6P9R1_DDX51_MOUSE	Ddx51	ATP-dependent RNA heli	R.YAGPEAAGQGDTDAEAGSR@.A	7.02	2.13	3.30	0.30
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.IHVQGTDLPDPIATFQQLDQEYK#.I	4.37	1.80	2.43	0.41
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.NSAVETVEQELLFVGSETGK#.L	8.35	4.00	2.09	0.48
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.TLAFSIPILM*QLK#.Q	6.52	1.05	6.18	0.16
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.ALVISPTR@.E	34.10	15.78	2.16	0.46
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.DNTVHSFR@.A	15.38	4.15	3.70	0.27
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.ELFHELIYEGINVDVIHAER@.T	3.13	1.92	1.63	0.61
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.ELLASAPTGSGK#.T	41.70	13.77	3.03	0.33
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.GFK#PPVLVFVQSIER@.A	21.11	10.47	2.02	0.50
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.IHVQGTDLPDPIATFQQLDQEYK#.I	33.39	14.78	2.26	0.44
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.ISEGTGFR@.I	38.91	13.46	2.89	0.35
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.K#FDSESLEVLK#.G	15.81	4.50	3.51	0.28
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.K#GFK#PPVLVFVQSIER@.A	9.14	3.39	2.70	0.37
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.LIYLLK#.Q	33.77	7.76	4.35	0.23
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.NSAVETVEQELLFVGSETGK#.L	57.38	18.60	3.08	0.32
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.NSAVETVEQELLFVGSETGK#.L	21.29	8.75	2.43	0.41
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.TLAFSIPILM*QLK#.Q	56.46	18.98	2.98	0.34
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.YFLEQAK#.Q	28.81	16.73	1.72	0.58
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.ELLASAPTGSGK#.T	18.77	4.62	4.06	0.25
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.LLQNILDAGFQVPTPIQM*QAIPVM*LHGR@.E	5.19	2.12	2.45	0.41
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.NSAVETVEQELLFVGSETGK#.L	12.24	5.26	2.33	0.43
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	R.NSAVETVEQELLFVGSETGK#.L	38.02	11.81	3.22	0.31
Q8K301_DDX52_MOUSE	Ddx52	Probable ATP-dependent	K.TLAFSIPILM*QLK#.Q	14.14	5.44	2.60	0.38
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	R.AGLTEPVLIR@.L	19.22	7.07	2.72	0.37
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	R.ELPQEEEEEM*VETVEGVFTEVVGQK#.R	5.79	3.00	1.93	0.52
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	K.LLVEFAR.A	39.62	14.29	2.77	0.36
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	K.SGGFQSM*GLSYPVFK#.G	10.48	2.62	3.99	0.25
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	R.VANNAQQQYVR@.S	16.00	6.36	2.52	0.40
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	R.VPQSVVDDEDSSLQTAM*GASLDLQGLHR@.V	6.21	2.68	2.32	0.43
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	R.AGLTEPVLIR@.L	14.80	5.07	2.92	0.34
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	R.ELPQEEEEEM*VETVEGVFTEVVGQK#.R	7.80	3.05	2.56	0.39
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	R.QEGPADPAPQR@.E	9.00	4.51	2.00	0.50
Q8K4L0_DDX54_MOUSE	Ddx54	ATP-dependent RNA heli	R.VPQSVVDDEDSSLQTAM*GASLDLQGLHR@.V	8.63	2.21	3.90	0.26
Q6ZPL9_DDX55_MOUSE	Ddx55	ATP-dependent RNA heli	R.TVQLTDLGVSDLEEDS.-	3.18	3.18	1.00	1.00
Q9D0R4_DDX56_MOUSE	Ddx56	Probable ATP-dependent	K.ALLFVNTLER@.G	10.63	4.74	2.24	0.45
Q9D0R4_DDX56_MOUSE	Ddx56	Probable ATP-dependent	R.VANVSAAEDSASQR@.A	14.55	6.00	2.43	0.41
Q9D0R4_DDX56_MOUSE	Ddx56	Probable ATP-dependent	K.ALLFVNTLER@.G	11.41	4.30	2.65	0.38
Q6Q899_DDX58_MOUSE	Ddx58	Probable ATP-dependent	K.FSELWIVDK#.G	9.99	7.94	1.26	0.79
Q6Q899_DDX58_MOUSE	Ddx58	Probable ATP-dependent	K.VVFFANQIPVYEQQATVFSR@.Y	11.14	6.17	1.80	0.55
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.DNIQAM*VIVPTR@.E	73.56	23.13	3.18	0.31
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.DNIQAMVIVPTR@.E	16.00	3.85	4.15	0.24
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	R.ELLM*GIFEM*GWEKPSPIQEESIPIALSGR.D	15.17	4.21	3.60	0.28
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	R.ELLM*GIFEMGWEK#PSPIQEESIPIALSGR@.D	9.23	4.13	2.24	0.45
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.GVTQYYAYVTER@.Q	81.99	24.56	3.34	0.30
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.K#DNIQAM*VIVPTR@.E	21.18	8.71	2.43	0.41
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.LAETYLHR@.I	55.02	36.36	1.51	0.66
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	R.QILLYSATFPLSVQK#.F	80.82	32.08	2.52	0.40
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.SGAYLIPLLER@.L	375.66	120.29	3.12	0.32
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.SIEEQLGTEIK#PIPSNIDK#.S	116.91	30.09	3.89	0.26
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.SLYVAEYHSEPAEDEK#P.-	162.50	66.81	2.43	0.41
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.VM*ATTGGTNLR.D	69.80	25.39	2.75	0.36
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.DNIQAM*VIVPTR@.E	8.95	4.76	1.88	0.53
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	R.LDDTVHVVIATPGR@.I	26.48	12.56	2.11	0.47
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.SGAYLIPLLER@.L	39.16	14.48	2.71	0.37
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.DNIQAM*VIVPTR@.E	11.04	4.68	2.36	0.42
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	R.QILLYSATFPLSVQK#.F	16.89	6.57	2.57	0.39
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.SGAYLIPLLER.L	34.55	21.22	1.63	0.61
P54823_DDX6_MOUSE	Ddx6	Probable ATP-dependent	K.SLYVAEYHSEPAEDEK#P.-	15.90	6.40	2.49	0.40
Q3U1T9_DEN1B_MOUSE	Dennd1b	DENN domain-containin	K.ELEEDLNETLK#.S	73.28	5.64	12.99	0.08
Q8C4S8_DEN2A_MOUSE	Dennd2a	DENN domain-containin	R.K#LQVALEHILEQR@.N	10.43	6.76	1.54	0.65
Q8C4S8_DEN2A_MOUSE	Dennd2a	DENN domain-containin	R.LEHVDFESLFSSLSVR@.H	11.26	6.85	1.64	0.61
Q99J56_DERL1_MOUSE	Derl1	Derlin-1 OS=Mus muscul	R.GGVSGFGVPPASM*R@.R	6.07	3.82	1.59	0.63
Q99J56_DERL1_MOUSE	Derl1	Derlin-1 OS=Mus muscul	R.HNWGQGFR@.L	7.39	3.98	1.85	0.54
Q99J56_DERL1_MOUSE	Derl1	Derlin-1 OS=Mus muscul	R.NFLSTPQFLYR@.W	85.56	44.77	1.91	0.52
Q9EQM6_DGCR8_MOUSE	Dgcr8	Microprocessor complex	R.ATLEILIPDFVK#.Q	12.83	5.15	2.49	0.40
Q9EQM6_DGCR8_MOUSE	Dgcr8	Microprocessor complex	R.ATLEILIPDFVK#.Q	18.22	5.63	3.24	0.31
Q99L04_DHRS1_MOUSE	Dhrs1	Dehydrogenase/reductas	R.ATAQEAQSLGGR@.C	7.28	4.57	1.59	0.63
Q99LB2_DHRS4_MOUSE	Dhrs4	Dehydrogenase/reductas	K.VALVTASTDGIGFAIAR.R	3.68	4.43	0.83	1.21
Q99LB2_DHRS4_MOUSE	Dhrs4	Dehydrogenase/reductas	K.TALLGLTK.N	7.18	10.48	0.68	1.46
Q99LB2_DHRS4_MOUSE	Dhrs4	Dehydrogenase/reductas	K.VALVTASTDGIGFAIAR.R	4.18	8.24	0.51	1.97
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	K.ALVTGYFMQVAHLER@.T	8.93	7.79	1.15	0.87
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.EAM*NDPLLER@.Y	28.89	18.29	1.58	0.63

O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.EVDDLGPEVGDIK#.I	64.06	48.55	1.32	0.76
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.FAHIDGDHLTLLNVYHAFK#.Q	30.59	22.59	1.35	0.74
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.FTDILVR.H	78.28	47.13	1.66	0.60
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.HQSFVLVGETGSGK#.T	37.95	31.63	1.20	0.83
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.HR@LDLGEDYPSGK#.K	56.60	32.93	1.72	0.58
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.IFEPPPPK#.K	41.50	31.72	1.31	0.76
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	K.IIPLYSTLPPQQQQR@.I	13.00	8.30	1.57	0.64
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.IR@VESLLVTAISK#.A	40.76	24.00	1.70	0.59
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	K.LGIDDLVHFDFM*DPPAPETLM*R@.A	17.60	15.40	1.14	0.88
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.LQLPVWEYK#.D	31.53	22.41	1.41	0.71
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.SLM*SADNVR@.Q	38.03	26.81	1.42	0.70
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.SNLGSVVLQLK#.K	69.27	55.56	1.25	0.80
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	K.TEM*QDNTYPEILR@.S	19.31	13.86	1.39	0.72
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.TLATDILM*GVLK#.E	187.82	136.30	1.38	0.73
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.TLATDILMGVLK#.E	16.30	14.08	1.16	0.86
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.VADEM*DVM*LGQEVGYSIR@.F	9.83	6.41	1.53	0.65
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.VESLLVTAISK#.A	8.42	4.43	1.90	0.53
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	K.VIVM*SATLDAGK#.F	12.96	8.85	1.46	0.68
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.YGVIILDEAHER@.T	72.92	64.93	1.12	0.89
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	K.YM*TDGM*LLR@.E	12.39	9.92	1.25	0.80
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.ASTNAM*LISAGLPPLK#.A	13.90	6.87	2.02	0.49
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.EVDDLGPEVGDIK#.I	42.41	23.08	1.84	0.54
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.FTDILVR@.H	49.98	24.69	2.02	0.49
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.IFEPPPPK#.K	12.86	8.09	1.59	0.63
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	K.IIPLYSTLPPQQQQR@.I	6.73	4.32	1.56	0.64
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.IR@VESLLVTAISK#.A	12.40	8.16	1.52	0.66
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	K.LGIDDLVHFDFM*DPPAPETLM*R@.A	16.59	8.71	1.91	0.52
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.SNLGSVVLQLK#.K	51.26	28.47	1.80	0.56
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	K.TEM*QDNTYPEILR@.S	10.76	4.28	2.52	0.40
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.TLATDILM*GVLK#.E	99.60	64.77	1.54	0.65
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.TLATDILMGVLK#.E	11.91	6.18	1.93	0.52
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.VADEM*DVM*LGQEVGYSIR@.F	6.15	5.42	1.13	0.88
O35286_DHX15_MOUSE	Dhx15	Putative pre-mRNA-splici	R.YGVIILDEAHER@.T	54.82	24.46	2.24	0.45
G3X8X0_G3X8X0_MOUSE	Dhx16	DEAH (Asp-Glu-Ala-His) b	R.TSLGNVVLLLK#.S	11.00	5.95	1.85	0.54
G3X8X0_G3X8X0_MOUSE	Dhx16	DEAH (Asp-Glu-Ala-His) b	R.AAQLQGDEEPSGPPLSAQAQQK#.E	4.09	3.65	1.12	0.89
G3X8X0_G3X8X0_MOUSE	Dhx16	DEAH (Asp-Glu-Ala-His) b	R.FSAFFDDAPVFR@.I	14.82	5.88	2.52	0.40
G3X8X0_G3X8X0_MOUSE	Dhx16	DEAH (Asp-Glu-Ala-His) b	K.VLVASATLDTAR@.F	7.05	5.96	1.18	0.85
Q6PGC1_DHX29_MOUSE	Dhx29	ATP-dependent RNA heli	R.K#LQEDGLLADVSHVIVDEVHER@.S	14.22	4.99	2.85	0.35
Q6PGC1_DHX29_MOUSE	Dhx29	ATP-dependent RNA heli	R.DLQTYGWLLYQEK#.V	5.53	2.81	1.97	0.51
Q6PGC1_DHX29_MOUSE	Dhx29	ATP-dependent RNA heli	K.LQEDGLLADVSHVIVDEVHER@.S	11.13	2.27	4.91	0.20
Q6PGC1_DHX29_MOUSE	Dhx29	ATP-dependent RNA heli	K.SPFITPIGR@.K	18.13	7.76	2.34	0.43
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.ATISLSDSDLLR@.L	13.11	16.44	0.80	1.25
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.ENYLEENLLYAPSLR@.F	9.03	5.03	1.79	0.56
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.GGSFEM*TDDDSAIR@.A	6.96	2.78	2.50	0.40
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	K.GVLM*AGLYPNLIQVR@.Q	35.92	2.36	15.23	0.07
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.IPQLLLER@.Y	19.98	7.05	2.83	0.35
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.LQSDDILPLGK#.D	16.36	8.53	1.92	0.52
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.LSQSLLELWR@.R	13.32	6.97	1.91	0.52
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	K.TAVEFLSK#.A	20.48	5.13	3.99	0.25
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.TPLENLVLQAK#.I	12.93	5.77	2.24	0.45
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.DSSQVHPLAVLLLTDGDVHIR@.D	7.65	3.78	2.02	0.49
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.LSQSLLELWR@.R	11.60	3.43	3.39	0.30
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	K.M*VPFQVPEILR@.T	6.66	5.60	1.19	0.84
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	K.NLLNSVIGR@.A	11.15	4.91	2.27	0.44
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	R.TPLENLVLQAK#.I	13.44	4.78	2.81	0.36
Q99PU8_DHX30_MOUSE	Dhx30	Putative ATP-dependent	K.VIQIATSSSTAK#.N	10.14	3.75	2.71	0.37
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	R.ASLLDDYQLPEILR@.T	21.36	12.62	1.69	0.59
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	R.DSEYLLQENEPNLSLDQHLLEDLQR@.K	3.42	3.05	1.12	0.89
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	K.HLM*ELSALDK#QEELTPLGVHLAR@.L	6.72	6.04	1.11	0.90
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	R.ISAISVAER@.V	12.74	7.72	1.65	0.61
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	R.LGGIAYFLSR@.L	19.97	9.99	2.00	0.50
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	R.LM*DPPSNEAVVLSIK#.H	6.42	4.44	1.44	0.69
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	R.NLQSDVLM*TVIK#.D	6.62	5.21	1.27	0.79
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	K.TTQVTQFILDNYIER@.G	6.93	10.03	0.69	1.45
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	R.ASLLDDYQLPEILR@.T	14.66	5.65	2.59	0.39
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	R.LGGIAYFLSR@.L	10.35	4.20	2.47	0.41
Q8VHK9_DHX36_MOUSE	Dhx36	ATP-dependent RNA heli	R.LM*DPPSNEAVVLSIK#.H	4.31	1.83	2.36	0.42
Q6NZL1_Q6NZL1_MOUSE	Dhx37	DEAH (Asp-Glu-Ala-His) b	K.TPLLDDPVFIHPSSVLFK#.E	16.22	6.44	2.52	0.40
Q80X98_Q80X98_MOUSE	Dhx38	DEAH (Asp-Glu-Ala-His) b	R.SLNTDVLFGLLR@.E	10.93	2.48	4.40	0.23
Q6P5D3_DHX57_MOUSE	Dhx57	Putative ATP-dependent	R.LSELEEDADEDEGPASIIVENESYVNLK#.K	2.93	3.35	0.88	1.14
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.DAAEAGLQEQR.V	13.07	8.74	1.50	0.67
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.NIIIWLPTGAGK#.T	15.63	6.44	2.43	0.41
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.VVVLVNR@.V	16.77	5.34	3.14	0.32
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.YGLLTNEISM*VQAR@.G	4.23	2.59	1.63	0.61
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.AEPLPQVLGLTASPGTGGATK#.L	3.07	0.00	#DIV/0!	0.00
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.ELTNEALEVLM*EK#.A	9.57	4.08	2.34	0.43
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.VVVLVNR@.V	8.21	1.59	5.16	0.19
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.AEPLPQVLGLTASPGTGGATK#.L	6.22	5.17	1.20	0.83
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.AESWLLK#.L	27.06	3.36	8.05	0.12
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.AGFGLM*AR@.S	26.05	8.60	3.03	0.33
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.AGQSVYSFLATEGSR@.E	28.28	8.37	3.38	0.30
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.AQDPFGDLIK#.K	17.97	14.84	1.21	0.83
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.DLQQASLVK#.R	8.89	3.13	2.84	0.35
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.DQQEVIQEFR@.D	35.04	10.85	3.23	0.31
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.ELTNEALEVLM*EK#.A	27.48	8.55	3.21	0.31
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.ELTNEALEVLMEK#.A	12.19	4.98	2.45	0.41
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.IGSILLETPR@.G	73.64	19.61	3.75	0.27
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.IR@DLQQASLVK#.R	41.46	13.04	3.18	0.31
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.K#AEPLPQVLGLTASPGTGGATK#.L	16.54	5.94	2.78	0.36
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.NIIIWLPTGAGK#.T	34.83	11.44	3.05	0.33
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.VVVLVNR@.V	53.54	13.69	3.91	0.26
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.YNDALFIHDTVR@.A	28.30	9.52	2.97	0.34
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.AEPLPQVLGLTASPGTGGATK#.L	7.79	3.07	2.54	0.39
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.AGQSVYSFLATEGSR@.E	26.54	7.99	3.32	0.30
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.DAAEAGLQEQR@.V	20.84	7.23	2.88	0.35
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.DQQEVIQEFR@.D	31.63	7.53	4.20	0.24
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.DTVYNTILSR@.Y	14.80	4.27	3.47	0.29
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.ELTNEALEVLM*EK#.A	25.50	5.29	4.82	0.21
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.IGSILLETPR@.G	54.67	9.47	5.77	0.17
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.IR@DLQQASLVK#.R	22.85	4.22	5.42	0.18
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.K#AEPLPQVLGLTASPGTGGATK#.L	12.44	2.68	4.65	0.22
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.NIIIWLPTGAGK#.T	49.69	9.42	5.28	0.19
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.NVLGQLAAR@.G	17.06	2.14	7.99	0.13

Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	K.VVVLVNR@.V	44.25	6.56	6.74	0.15
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.YGLLTNEISM*VQAR@.G	47.00	15.43	3.05	0.33
Q99J87_DHX58_MOUSE	Dhx58	Probable ATP-dependent	R.YNDALFIHDTVR@.A	20.83	6.86	3.04	0.33
A2A4P0_DHX8_MOUSE	Dhx8	ATP-dependent RNA helic	K.LIVTSATLDAVK#.F	17.69	6.27	2.82	0.35
A2A4P0_DHX8_MOUSE	Dhx8	ATP-dependent RNA helic	K.TGIDQLVVTPISQAQAK#.Q	8.18	7.63	1.07	0.93
A2A4P0_DHX8_MOUSE	Dhx8	ATP-dependent RNA helic	R.VANVADVVSK#.G	15.75	6.87	2.29	0.44
A2A4P0_DHX8_MOUSE	Dhx8	ATP-dependent RNA helic	R.WLVEFAPAFFK#.V	9.55	6.19	1.54	0.65
A2A4P0_DHX8_MOUSE	Dhx8	ATP-dependent RNA helic	K.FSQYFYEAPIFTIPGR@.T	5.78	3.42	1.69	0.59
A2A4P0_DHX8_MOUSE	Dhx8	ATP-dependent RNA helic	K.LIVTSATLDAVK#.F	11.84	4.56	2.60	0.38
A2A4P0_DHX8_MOUSE	Dhx8	ATP-dependent RNA helic	K.TGIDQLVVTPISQAQAK#.Q	7.05	5.45	1.29	0.77
A2A4P0_DHX8_MOUSE	Dhx8	ATP-dependent RNA helic	R.TLIDQQVVYIHPSSALFNR@.Q	5.96	5.88	1.01	0.99
A2A4P0_DHX8_MOUSE	Dhx8	ATP-dependent RNA helic	R.TNLASTVLSLK#.A	11.93	7.47	1.60	0.63
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.K#FEAEILEAISSNSVVIIR@.G	14.43	10.91	1.32	0.76
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.DFVNYLVR@.I	10.74	11.34	0.95	1.06
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.AAM*EALVVEVSK#.Q	123.66	77.04	1.61	0.62
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.AAMEALVVEVSK#.Q	71.64	39.31	1.82	0.55
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.AEAENNSGVESSGYGSPGPTWDR@.G	24.92	15.19	1.64	0.61
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.AEAENNSGVESSGYGSPGPTWDR.G	14.90	8.36	1.78	0.56
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.AIEPPPLDAVIEAEHTLR.E	9.35	6.41	1.46	0.69
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.DFVNYLVR@.I	347.95	185.99	1.87	0.53
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.DVVLAYPEVR@.I	258.89	147.19	1.76	0.57
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.ELDALDANDELTPLGR@.I	257.03	171.53	1.50	0.67
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.FEAEILEAISSNSVVIIR@.G	19.29	6.61	2.92	0.34
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.FSDHVALLSVFQAWDDAR@.M	152.00	93.43	1.63	0.61
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.GANLK#DYYSR@.K	68.48	33.44	2.05	0.49
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.GANLKDYYSR.K	23.42	14.80	1.58	0.63
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.GISHVIVDEIHER@.D	426.12	230.60	1.85	0.54
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.HLENNSHFGSHR.Y	4.77	3.57	1.34	0.75
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.HLENNSHFGSHR@.Y	83.34	49.75	1.68	0.60
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.ISAVAVAER@.V	317.18	195.95	1.62	0.62
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.K#EEQEVQATLESEEVDLNAGLHGNWTLENAK#.A	15.78	10.71	1.47	0.68
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.K#FEAEILEAISSNSVVIIR@.G	110.62	66.94	1.65	0.61
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.K#M*TPAYEIR@.A	27.15	15.05	1.80	0.55
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.KVFDPVPDGVTK.V	47.67	32.88	1.45	0.69
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.KVQSDGQIVFIDDWIR.L	129.68	62.03	2.09	0.48
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.LAHFEPSQR.Q	56.56	32.06	1.76	0.57
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.LFTAHNNM*TNYATVWASK#.T	109.03	53.47	2.04	0.49
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.LFTAHNNMTNYATVWASK#.T	10.64	9.89	1.08	0.93
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LGGIGQFLAK#.A	365.88	235.81	1.55	0.64
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LGYIHR@.N	117.19	70.87	1.65	0.60
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LNM*ATLR@.M	123.58	72.80	1.70	0.59
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LNMATLR@.M	30.19	15.67	1.93	0.52
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LNQYFQK#.E	218.24	140.02	1.56	0.64
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.LPIEPR@.F	333.48	241.06	1.38	0.72
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.LSM*SQLNEK#.E	67.11	39.85	1.68	0.59
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.M*SGEEAEIR@.F	141.05	88.64	1.59	0.63
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.NELTYQM*EQDHNLQSVLQER@.E	132.45	81.22	1.63	0.61
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.NELTYQMEQDHNLQSVLQER@.E	20.59	10.48	1.96	0.51
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.NNFGGDYR@.G	23.96	18.88	1.27	0.79
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.QISRPSAAGINLM*IGSVR.Y	60.67	30.71	1.98	0.51
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.QLYHLGVIEAYSGLTK#.K	254.09	136.83	1.86	0.54
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.RISAVAVAER.V	155.95	92.79	1.68	0.60
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.SFIAEM*TIYIK#.Q	63.87	31.56	2.02	0.49
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.TPLHEIALSIK#.L	299.93	237.14	1.26	0.79
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.TTQVPQYILDDFIQNDR@.A	90.05	63.59	1.42	0.71
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.TTQVPQYILDDFIQNDR@.A	150.59	92.51	1.63	0.61
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.VEGFNYAGM*GNSTNK#.K	22.30	9.93	2.24	0.45
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.VFDPVPDGVTK#.V	155.09	107.43	1.44	0.69
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.VQSDGQIVFIDDWIR@.L	45.85	27.75	1.65	0.61
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.YGDGPRPPK.M	24.15	18.41	1.31	0.76
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.YPSPFFVFGEK#.I	108.98	79.02	1.38	0.73
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.YQILPLHSQIPR@.E	280.43	194.18	1.44	0.69
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.YQILPLHSQIPR.E	20.26	11.06	1.83	0.55
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.YTQVGPDHNR.S	40.69	26.29	1.55	0.65
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.AAM*EALVVEVSK#.Q	168.79	90.85	1.86	0.54
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.AAMEALVVEVSK#.Q	91.67	50.08	1.83	0.55
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.AEAENNSGVESSGYGSPGPTWDR@.G	57.32	24.21	2.37	0.42
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.AIEPPPLDAVIEAEHTLR.E	11.60	6.37	1.82	0.55
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.DAQSNAAR@.D	12.05	6.42	1.88	0.53
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.DFVNYLVR@.I	418.58	183.60	2.28	0.44
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.DVVLAYPEVR@.I	321.02	152.19	2.11	0.47
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.ELDALDANDELTPLGR@.I	458.51	230.17	1.99	0.50
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.ETPFELIEALLK#.Y	213.76	118.77	1.80	0.56
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.FEAEILEAISSNSVVIIR@.G	21.01	11.72	1.79	0.56
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.FSDHVALLSVFQAWDDAR@.M	156.41	69.14	2.26	0.44
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.GANLK#DYYSR@.K	121.18	65.34	1.85	0.54
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.GISHVIVDEIHER@.D	557.10	256.81	2.17	0.46
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.GM*TLVTPLQLLLFASK#.K	157.35	72.83	2.16	0.46
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.HLENNSHFGSHR@.Y	128.83	57.83	2.23	0.45
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.ILTTEGR@.N	404.00	211.65	1.91	0.52
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.ISAVAVAER@.V	296.87	135.16	2.20	0.46
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.KEEQEVQATLESEEVDLNAGLHGNWTLENAK.A	11.61	6.44	1.80	0.55
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.K#FEAEILEAISSNSVVIIR@.G	50.04	22.27	2.25	0.44
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.K#LEAGIR@.G	204.76	122.90	1.67	0.60
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.K#M*TPAYEIR@.A	31.44	10.54	2.98	0.34
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.KVFDPVPDGVTK.V	63.84	34.86	1.83	0.55
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.K#VQSDGQIVFIDDWIR@.L	111.70	129.26	0.86	1.16
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.K#VQSDGQIVFIDDWIR@.L	13.05	302.91	0.04	23.21
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.LAHFEPSQR.Q	136.21	65.37	2.08	0.48
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LETHM*TPEM*FR.T	8.17	3.89	2.10	0.48
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.LFTAHNNM*TNYATVWASK#.T	145.95	64.63	2.26	0.44
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LGGIGQFLAK#.A	476.31	241.86	1.97	0.51
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LGYIHR@.N	90.66	28.16	3.22	0.31
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LNM*ATLR@.M	233.39	113.90	2.05	0.49
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.LNQYFQK#.E	286.17	166.73	1.72	0.58
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.LPIEPR@.F	700.52	333.10	2.10	0.48
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.LSM*SQLNEK#.E	88.63	45.51	1.95	0.51
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.M*SGEEAEIR@.F	178.89	92.13	1.94	0.51
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.MSGEEAEIR@.F	17.53	10.14	1.73	0.58
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	K.NELTYQM*EQDHNLQSVLQER@.E	210.65	90.84	2.32	0.43
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.NNFGGDYR@.G	45.68	24.88	1.84	0.54
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.QISR@PSAAGINLM*IGSVR@.Y	58.73	24.44	2.40	0.42
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA helic	R.QLYHLGVIEAYSGLTK#.K	297.09	142.97	2.08	0.48

E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	R.R@ISAVAVAER@.V	200.83	91.97	2.18	0.46
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	R.SFIAEM*TIYIK#.Q	87.45	48.83	1.79	0.56
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	R.TPLHEIALSIK#.L	350.07	187.65	1.87	0.54
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	K.TTQVPQYILDDFIQNDR@.A	289.58	135.82	2.13	0.47
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	R.VEGFNYAGM*GNSTNK#.K	44.06	20.03	2.20	0.45
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	K.VFDPVPDGVTK#.V	225.48	126.31	1.79	0.56
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	K.VQSDGQIVFIDDWIR@.L	98.42	46.40	2.12	0.47
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	R.YGDGPRPPK.M	48.33	27.82	1.74	0.58
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	K.YPSPFFVFGEK#.I	165.82	88.29	1.88	0.53
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	R.YQILPLHSQIPR@.E	525.08	274.08	1.92	0.52
E9QNN1_E9QNN1_MOUSE	Dhx9	ATP-dependent RNA heli	K.YTQVGPDHNR.S	69.37	36.51	1.90	0.53
Q9Z207_DIAP3_MOUSE	Diaph3	Protein diaphanous hom	K.INELQAELQAFK#.S	10.71	9.54	1.12	0.89
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	K.AK#GEDTM*SAAPLLDPIVQQFGQFSK#.D	6.45	2.05	3.14	0.32
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.K#PM*SANVPAASPAPGR@.L	10.88	1.19	9.12	0.11
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.LGPVSPAPSQPNSQIR@.Q	15.31	1.91	8.03	0.12
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.LQQEELETSVYPK#.V	7.50	2.05	3.67	0.27
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	K.SAAPLLDVFSSM*LK#.D	10.10	3.27	3.09	0.32
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.SPPEGDTTLFLSR@.L	6.07	2.93	2.07	0.48
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.VEEFLTTVR@.R	6.41	22.93	0.28	3.58
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.VNDSDDLIM*TENEVGK#.I	4.06	1.98	2.05	0.49
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	K.AK#GEDTM*SAAPLLDPIVQQFGQFSK#.D	9.25	2.51	3.69	0.27
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.APTGSTPGPQGTLPAR@.E	5.70	2.33	2.45	0.41
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.EGAGDTEVDPSEQQPQQHNLSLR@.R	13.03	1.33	9.78	0.10
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	K.GFINM*QSVAK#.F	12.15	1.30	9.32	0.11
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.LGPVSPAPSQPNSQIR@.Q	22.03	3.34	6.59	0.15
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	K.SAAPLLDVFSSM*LK#.D	17.37	4.14	4.20	0.24
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.SPPEGDTTLFLSR@.L	13.75	2.73	5.04	0.20
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	R.VEEFLTTVR@.R	12.62	21.15	0.60	1.68
Q8C9B9_DIDO1_MOUSE	Dido1	Death-inducer obliterat	K.VSATER@PADFTTDASSASLVEQQK#.M	8.74	2.01	4.34	0.23
Q9D0D4_DIM1_MOUSE	Dimt1	Probable dimethyladeno	K.AALR@PTDVVLEVGPGTGNM*TVK#.L	11.35	4.90	2.32	0.43
Q9D0D4_DIM1_MOUSE	Dimt1	Probable dimethyladeno	K.SSAVQQLLEK#.N	10.75	3.38	3.19	0.31
Q9D0D4_DIM1_MOUSE	Dimt1	Probable dimethyladeno	K.AALR@PTDVVLEVGPGTGNM*TVK#.L	5.58	2.96	1.88	0.53
Q9D0D4_DIM1_MOUSE	Dimt1	Probable dimethyladeno	K.AALR@PTDVVLEVGPGTGNM*TVK#.L	8.08	3.66	2.21	0.45
Q9D0D4_DIM1_MOUSE	Dimt1	Probable dimethyladeno	R.LLHGFNAEGIHFS.-	15.27	15.27	1.00	1.00
Q9D0D4_DIM1_MOUSE	Dimt1	Probable dimethyladeno	K.LQVLVGDVLK#.S	18.34	8.58	2.14	0.47
Q9D0D4_DIM1_MOUSE	Dimt1	Probable dimethyladeno	R.LSINTQLLAR@.V	11.95	3.66	3.26	0.31
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.AESPDFPYLNTLLR@.I	11.65	4.97	2.35	0.43
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.ASLTYAEAQM*R@.I	12.29	6.16	2.00	0.50
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.AVHEDIVAVELLPR@.S	20.67	12.57	1.64	0.61
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.GALTLSSPEIR@.F	24.23	10.91	2.22	0.45
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.GIVSEEAYILFVR@.K	16.53	13.71	1.21	0.83
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.IDSAAM*NDDITTSLR@.G	18.46	11.24	1.64	0.61
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.IEGTVFHVFDK#.V	12.56	5.10	2.46	0.41
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.LAYDDEIPSLR@.I	30.34	18.98	1.60	0.63
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.NAIVVLIPK#.Y	15.20	11.86	1.28	0.78
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.NVIVLQTVM*QEVR@.N	12.56	4.37	2.88	0.35
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.NVIVLQTVMQEVR@.N	5.62	3.57	1.57	0.64
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.SLADSLDR@AESPDFPYLNTLLR@.I	14.45	9.10	1.59	0.63
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.SLTANPELIDR@.L	25.87	12.59	2.06	0.49
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.SQWVAPSSVVLDDEGQNEDDVEKDEER.E	8.22	5.01	1.64	0.61
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.YGLEGTVFFEEK#.D	6.99	2.59	2.70	0.37
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.AESPDFPYLNTLLR@.I	19.07	7.27	2.62	0.38
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.ASLTYAEAQM*R@.I	21.10	8.21	2.57	0.39
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.FHM*DSETHDPIDLQTK#.E	10.13	2.92	3.47	0.29
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.GALTLSSPEIR@.F	24.34	8.36	2.91	0.34
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.GIVSEEAYILFVR@.K	14.54	16.58	0.88	1.14
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.IDSAAM*NDDITTSLR@.G	29.79	10.47	2.85	0.35
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.IIVAIDGWPR@.N	25.36	8.47	2.99	0.33
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.LAYLSDEM*NEIESGK#.I	16.66	5.53	3.01	0.33
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.NAIVVLIPK#.Y	29.92	8.98	3.33	0.30
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.NLGDVGEK#ETETEVLLLEHDVPHQPFSQAVLSFLPR@.M	4.17	1.78	2.35	0.43
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.NVIVLQTVM*QEVR@.N	20.71	7.46	2.78	0.36
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	R.NVIVLQTVMQEVR@.N	8.10	4.50	1.80	0.56
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.SGSYLQGTFR@.A	25.94	7.37	3.52	0.28
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.SLADSLDR@AESPDFPYLNTLLR@.I	26.56	9.58	2.77	0.36
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.SLTANPELIDR.L	50.31	15.03	3.35	0.30
Q9CSH3_RRP44_MOUSE	Dis3	Exosome complex exonu	K.YGLEGTVFFEEK#.D	14.77	4.44	3.33	0.30
Q9ESX5_DKC1_MOUSE	Dkc1	H/ACA ribonucleoprotei	R.ALETLTGALFQRPPLIAAVK.R	8.31	10.79	0.77	1.30
Q9ESX5_DKC1_MOUSE	Dkc1	H/ACA ribonucleoprotei	K.NTLVTEAVQAPQLAAEAVNVIK#.R	6.87	7.51	0.92	1.09
Q8BMF4_ODP2_MOUSE	Dlat	Dihydrolipoyllysine-resi	K.GIDLTQVK#.G	17.05	8.47	2.01	0.50
Q8BMF4_ODP2_MOUSE	Dlat	Dihydrolipoyllysine-resi	K.GLETIASDVVSLASK#.A	34.71	13.05	2.66	0.38
Q8BMF4_ODP2_MOUSE	Dlat	Dihydrolipoyllysine-resi	K.ISVNDFIIK#.A	20.34	4.05	5.02	0.20
Q8BMF4_ODP2_MOUSE	Dlat	Dihydrolipoyllysine-resi	R.VAPAPAGVFTDIPISNIR@.R	20.82	9.29	2.24	0.45
Q8BMF4_ODP2_MOUSE	Dlat	Dihydrolipoyllysine-resi	K.VPEANSSWM*DTVIR@.Q	5.13	9.07	0.57	1.77
Q8BMF4_ODP2_MOUSE	Dlat	Dihydrolipoyllysine-resi	K.YLEK#PITM*LL.-	12.46	7.05	1.77	0.57
Q8BMF4_ODP2_MOUSE	Dlat	Dihydrolipoyllysine-resi	K.GLETIASDVVSLASK#.A	10.45	3.04	3.44	0.29
Q8BMF4_ODP2_MOUSE	Dlat	Dihydrolipoyllysine-resi	R.VAPAPAGVFTDIPISNIR@.R	8.17	1.98	4.12	0.24
Q811D0_DLG1_MOUSE	Dlg1	Disks large homolog 1 OS	R.EQM*M*NSSVSSGSGSLR@.T	5.65	2.43	2.33	0.43
Q811D0_DLG1_MOUSE	Dlg1	Disks large homolog 1 OS	R.FGDILHVINASDDEWWQAR@.Q	11.72	5.02	2.33	0.43
Q811D0_DLG1_MOUSE	Dlg1	Disks large homolog 1 OS	R.GNSGLGFSIAGGTDNPHIGDDSSIFITK#.I	7.60	3.80	2.00	0.50
Q811D0_DLG1_MOUSE	Dlg1	Disks large homolog 1 OS	K.NAGQAVTIVAQYR@PEEYSR@.F	20.28	8.97	2.26	0.44
Q811D0_DLG1_MOUSE	Dlg1	Disks large homolog 1 OS	R.YQDEEVLPPEHISPQVTNEVLGPELVHVSEK#.N	4.98	3.25	1.53	0.65
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	K.DAPPLLPSDTGQGYR@.T	28.62	11.53	2.48	0.40
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	R.DILELGGPEGDAASGTISK#.K	13.06	5.91	2.21	0.45
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	K.LITAADTTAEQR@.R	37.83	14.63	2.59	0.39
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	R.SDLVLLYELK#.Q	47.80	18.14	2.64	0.38
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	R.TPEQVAEEEYLLQELR@.K	30.73	9.93	3.10	0.32
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	R.TPEQVAEEEYLLQELR@K#.I	10.47	7.99	1.31	0.76
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	K.WM*PFTNPAR@.K	8.88	5.03	1.77	0.57
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	K.DAPPLLPSDTGQGYR@.T	18.43	9.60	1.92	0.52
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	R.DILELGGPEGDAASGTISK#.K	14.36	6.54	2.19	0.46
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	K.LITAADTTAEQR@.R	43.26	18.98	2.28	0.44
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	R.SDLVLLYELK#.Q	34.34	9.56	3.59	0.28
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	R.TPEQVAEEEYLLQELR@.K	25.19	12.11	2.08	0.48
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	R.TPEQVAEEEYLLQELR.K	10.14	3.32	3.06	0.33
Q9JI44_DMAP1_MOUSE	Dmap1	DNA methyltransferase 1	R.TPEQVAEEEYLLQELR@K#.I	8.46	6.30	1.34	0.74
P63037_DNJA1_MOUSE	Dnaja1	DnaJ homolog subfamily	K.EGGAGGGFGSPM*DIFDM*FFGGGGR@.M	45.89	8.27	5.55	0.18
P63037_DNJA1_MOUSE	Dnaja1	DnaJ homolog subfamily	K.EGGAGGGFGSPM*DIFDM*FFGGGGR.M	4.11	5.20	0.79	1.27
P63037_DNJA1_MOUSE	Dnaja1	DnaJ homolog subfamily	R.ELYDKGGEQAIK.E	30.74	15.74	1.95	0.51
P63037_DNJA1_MOUSE	Dnaja1	DnaJ homolog subfamily	K.EVEETDEM*DQVELVDFDPNQER@.R	44.98	26.93	1.67	0.60
P63037_DNJA1_MOUSE	Dnaja1	DnaJ homolog subfamily	K.ILEVHIDK#.G	26.09	11.94	2.19	0.46
P63037_DNJA1_MOUSE	Dnaja1	DnaJ homolog subfamily	K.ITFHGEGDQEPGLEPGDIIIVLDQK#.D	118.52	65.98	1.80	0.56
P63037_DNJA1_MOUSE	Dnaja1	DnaJ homolog subfamily	R.K#EVEETDEM*DQVELVDFDPNQER@.R	10.59	7.59	1.40	0.72

P63037_DNJA1_MOUSE	Dnaja1	DnaJ homolog subfamily	K.QISQAYEVLADSK#.K	130.36	59.22	2.20	0.45
P63037_DNJA1_MOUSE	Dnaja1	DnaJ homolog subfamily	K.QISQAYEVLADSK#.K	10.55	6.15	1.72	0.58
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	R.EGSGGGGGM*DDIFSHIFGGGLFGFM*GNQSR@.S	77.95	32.27	2.42	0.41
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	K.EISFAYEVLSNPEK#.R	11.37	7.86	1.45	0.69
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	K.FDVQFPENNWINPDK#.L	8.55	2.73	3.13	0.32
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	K.GDLYIK#.F	49.67	32.93	1.51	0.66
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	R.GEGM*PQYR@.N	26.98	11.20	2.41	0.41
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	R.ITFTGEADQAPGVEPGDIVLLLQEK#.E	138.80	68.30	2.03	0.49
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	K.LSELEDLLPSRPEVPNVIGETEEVELQEFDSTR.G	11.24	2.68	4.19	0.24
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	K.LYDILGVPPGASENELK#K#.A	40.37	15.03	2.69	0.37
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	K.VSLEDLYNGK#.T	58.98	23.93	2.46	0.41
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	R.YGEQGLR@.E	91.82	43.49	2.11	0.47
Q9QYJ0_DNJA2_MOUSE	Dnaja2	DnaJ homolog subfamily	R.ITFTGEADQAPGVEPGDIVLLLQEK#.E	7.32	2.34	3.12	0.32
Q99M87_DNJA3_MOUSE	Dnaja3	DnaJ homolog subfamily	R.EIFVTFR@.V	11.52	5.86	1.97	0.51
Q99M87_DNJA3_MOUSE	Dnaja3	DnaJ homolog subfamily	K.FSQLAEAYEVLSDEVK#R@.K	6.21	4.14	1.50	0.67
Q9QYJ3_DNJB1_MOUSE	Dnajb1	DnaJ homolog subfamily	R.DGSDVIYPAR@.I	14.57	12.67	1.15	0.87
Q9QYJ3_DNJB1_MOUSE	Dnajb1	DnaJ homolog subfamily	K.ILTIEVK#.R	8.99	10.31	0.87	1.15
Q9QYJ3_DNJB1_MOUSE	Dnajb1	DnaJ homolog subfamily	R.TILEQVLPI.-	45.07	45.07	1.00	1.00
Q99KV1_DJB11_MOUSE	Dnajb11	DnaJ homolog subfamily	R.DGM*EYPFIGEGEPHVDGEPGDLR@.F	14.53	14.71	0.99	1.01
Q99KV1_DJB11_MOUSE	Dnajb11	DnaJ homolog subfamily	K.FQDLGAAYEVLSDSEK#.R	19.45	17.93	1.08	0.92
Q99KV1_DJB11_MOUSE	Dnajb11	DnaJ homolog subfamily	R.TLEVEIEPGVR@.D	27.59	19.06	1.45	0.69
Q99KV1_DJB11_MOUSE	Dnajb11	DnaJ homolog subfamily	R.TTQLGPGR@.F	45.55	28.82	1.58	0.63
O54946_DNJB6_MOUSE	Dnajb6	DnaJ homolog subfamily	R.GQPTPALAPGPAPAPVR@.V	4.54	4.99	0.91	1.10
O54946_DNJB6_MOUSE	Dnajb6	DnaJ homolog subfamily	K.QVAEAYEVLSDAK#.K	8.85	3.90	2.27	0.44
Q9DC23_DJC10_MOUSE	Dnajc10	DnaJ homolog subfamily	K.ILYDILAFAK#.E	11.91	5.40	2.21	0.45
Q9DC23_DJC10_MOUSE	Dnajc10	DnaJ homolog subfamily	R.YDFGIYDDDPEIITLER@.R	6.05	2.81	2.15	0.47
Q9DC23_DJC10_MOUSE	Dnajc10	DnaJ homolog subfamily	R.YDFGIYDDDPEIITLER@.R	4.67	2.45	1.91	0.52
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	R.AELLEFLESQQENM*IK#.K	9.21	4.61	2.00	0.50
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	R.DSLLASLLDGVR@.A	25.05	9.63	2.60	0.38
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	K.ELIVGEIFVR@.V	11.62	5.55	2.10	0.48
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	R.FLAAPPNGNFADAVFR@.F	3.25	2.65	1.23	0.82
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	R.IFIAQPAWVLR@.K	9.28	4.86	1.91	0.52
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	K.IVDGPDPENIILILK#.T	21.87	12.29	1.78	0.56
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	K.KPVVLEVTPGGFDQINPVTNR.V	14.47	6.26	2.31	0.43
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	R.LGGYLSEDQATPENPTVR@.K	6.96	4.93	1.41	0.71
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	K.LLEGVGLENLDSPAATK#.A	14.42	5.88	2.45	0.41
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	R.LLLEEDENEESGSIK#.R	6.29	1.81	3.48	0.29
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	K.NEETNQQEVANSLAK#.L	5.08	5.01	1.01	0.99
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	R.TELLTEALR@.F	12.63	3.84	3.29	0.30
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	R.TITM*ETSDDLLFSK#.E	8.76	4.36	2.01	0.50
G3X922_G3X922_MOUSE	Dnajc13	MCG115602 OS=Mus mu	K.YSTDESITSLAEFVVQK#.I	7.20	3.48	2.07	0.48
Q91YW3_DNJC3_MOUSE	Dnajc3	DnaJ homolog subfamily	K.LIESAEELIR@.D	17.50	14.35	1.22	0.82
Q91YW3_DNJC3_MOUSE	Dnajc3	DnaJ homolog subfamily	R.SQALDAFDGADYTAAITFLDK#.I	5.89	4.11	1.43	0.70
Q91YW3_DNJC3_MOUSE	Dnajc3	DnaJ homolog subfamily	R.SQALDAFDGADYTAAITFLDK#.I	4.55	4.31	1.06	0.95
Q91WN1_DNJC9_MOUSE	Dnajc9	DnaJ homolog subfamily	K.AVYDEQGTVDEDSAGLNQDRDWDAYWR.L	10.59	10.95	0.97	1.03
Q91WN1_DNJC9_MOUSE	Dnajc9	DnaJ homolog subfamily	K.ELGLEEGVDNLK.A	56.15	60.41	0.93	1.08
Q91WN1_DNJC9_MOUSE	Dnajc9	DnaJ homolog subfamily	K.GSEEELNDIK.Q	15.15	28.91	0.52	1.91
Q91WN1_DNJC9_MOUSE	Dnajc9	DnaJ homolog subfamily	K.ISLEDIQAFEK#.T	23.07	45.45	0.51	1.97
Q91WN1_DNJC9_MOUSE	Dnajc9	DnaJ homolog subfamily	R.KELGLEEGVDNLK.A	9.68	14.85	0.65	1.53
Q91WN1_DNJC9_MOUSE	Dnajc9	DnaJ homolog subfamily	K.KISLEDIQAFEK.T	6.19	9.82	0.63	1.59
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.EISYAIK#.N	27.53	64.39	0.43	2.34
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.LQDAFSAIGQNADLDLPQIAVVGGQSAGK#.S	4.40	2.08	2.11	0.47
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.TGLFTPDM*AFETIVK#.K	4.06	3.24	1.25	0.80
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.VYSPHVLNLTLVDLPGM*TK#.V	7.99	2.74	2.91	0.34
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.SSVLENFVGR@.D	6.76	2.41	2.81	0.36
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.AGVYPER@.V	25.25	4.97	5.08	0.20
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.ALLQM*VQQFAVDFEK#.R	18.32	4.56	4.02	0.25
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.ASETEENGSDSFM*HSM*DPQLER@.Q	7.46	3.20	2.33	0.43
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.EISYAIK#.N	57.11	226.94	0.25	3.97
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.GISPVPINLR@.V	115.23	42.55	2.71	0.37
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.GM*EDLIPLVNR@.L	28.64	9.99	2.87	0.35
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.GYIGVVNR@.S	103.67	37.06	2.80	0.36
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.IEGSGDQIDTYELSGGAR@.I	16.81	3.61	4.66	0.21
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.LDLM*DEGTDAR@.D	25.46	8.28	3.07	0.33
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.LDLM*DEGTDARDVLENK.L	41.48	11.32	3.67	0.27
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.M*GTPYLQK#.V	18.13	4.91	3.69	0.27
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.NLVDSYM*AIVNK#.T	19.62	5.22	3.76	0.27
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.R@IEGSGDQIDTYELSGGAR@.I	21.44	7.02	3.05	0.33
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.SSVLENFVGR@.D	123.31	42.37	2.91	0.34
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.TGLFTPDM*AFETIVK#.K	38.03	11.11	3.42	0.29
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.VPVGDQPPDIEFQIR@.D	31.99	8.01	3.99	0.25
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.VYSPHVLNLTLVDLPGM*TK#.V	43.96	12.59	3.49	0.29
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.YM*LSVDNLK#.L	17.67	6.10	2.90	0.35
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.GISPVPINLR@.V	64.30	14.00	4.59	0.22
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.GM*EDLIPLVNR@.L	15.30	1.90	8.04	0.12
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.GYIGVVNR@.S	44.87	10.81	4.15	0.24
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.IEGSGDQIDTYELSGGAR@.I	12.33	1.82	6.77	0.15
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.LDLM*DEGTDAR@.D	16.41	2.51	6.53	0.15
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.LDLM*DEGTDAR@DVLENK#.L	24.59	5.88	4.18	0.24
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.SSVLENFVGR@.D	73.58	15.05	4.89	0.20
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	R.TGLFTPDM*AFETIVK#.K	12.25	3.22	3.81	0.26
P39053_DYN1_MOUSE	Dnm1	Dynamin-1 OS=Mus musc	K.VPVGDQPPDIEFQIR@.D	13.42	4.77	2.81	0.36
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	R.FISNPNSIILAVTAANTDM*ATSEALK#.I	8.62	4.23	2.04	0.49
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.SSVLESLVGR@.D	13.04	6.13	2.13	0.47
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.VFSPNVVNLTLVDLPGM*TK#.V	6.63	2.61	2.54	0.39
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.ALQGASQIIAEIR@.E	31.49	14.88	2.12	0.47
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.DTLQSELVGQLYK#.S	13.85	6.92	2.00	0.50
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.SSLLDDLLTESEDM*AQR@.R	3.18	1.33	2.40	0.42
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.SYFLIVR@.K	17.24	7.67	2.25	0.44
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.AEELLAEEK#.S	17.25	5.45	3.17	0.32
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.ALQGASQIIAEIR.E	29.19	10.59	2.76	0.36
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	R.DK#VPSAGGGIGDGGQEPTTGNWR@.G	7.09	4.90	1.45	0.69
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.DTLQSELVGQLYK#.S	31.69	21.84	1.45	0.69
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	R.FISNPNSIILAVTAANTDMATSEALK#.I	6.12	1.39	4.42	0.23
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.LYTDFDEIR@QEIENETER@.I	21.32	4.05	5.26	0.19
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	R.R@PLILQLVHVSPEDK#.R	21.13	11.55	1.83	0.55
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.SATLLQLITK#.F	10.08	3.73	2.70	0.37
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.SSLLDDLLTESEDM*AQR@.R	10.20	2.56	3.98	0.25
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.SSVLESLVGR@.D	32.75	6.79	4.83	0.21
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.SYFLIVR@.K	22.26	5.53	4.03	0.25
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.TSK#AEELLAEEK#.S	16.80	7.00	2.40	0.42
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	K.VFSPNVVNLTLVDLPGM*TK#.V	16.70	8.03	2.08	0.48
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein O	R.DK#VPSAGGGIGDGGQEPTTGNWR@.G	5.31	2.22	2.39	0.42

E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein	K.DTLQSELVGQLYK#.S	16.87	23.00	0.73	1.36
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein	R.FISNPNSIILAVTAANTDM*ATSEALK#.I	17.61	5.14	3.42	0.29
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein	K.LGIIGVVNR@.S	30.73	9.35	3.29	0.30
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein	R.R@PLILQLVHVSPEDK#.R	17.88	3.09	5.78	0.17
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein	K.SSVLESLVGR@.D	22.40	3.51	6.39	0.16
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein	R.TLAVITK#.L	17.25	4.74	3.64	0.27
E9PUD2_E9PUD2_MOUSE	Dnm1l	Dynamin-1-like protein	K.VFSPNVVNLTLVDLPGM*TK#.V	15.37	3.86	3.98	0.25
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.AGVYPEK#DQAENEDGAQENTFSM*DPQLER@.Q	8.34	2.39	3.49	0.29
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.GM*EELIPLVNK#.L	20.59	10.04	2.05	0.49
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.IEGSGDQVDTLELSGGAR@.I	15.57	2.98	5.23	0.19
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.IVTTYIR@.E	14.48	5.20	2.79	0.36
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.K#FFLSHPAYR@.H	14.44	6.07	2.38	0.42
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.NLVDSYVAIINK#.S	37.84	8.12	4.66	0.21
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.R@IEGSGDQVDTLELSGGAR@.I	16.76	2.25	7.44	0.13
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.TGLFTPDLAFEAIVK#.K	23.35	4.49	5.19	0.19
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.VPVGDQPPDIEYQIK#.D	12.15	3.09	3.94	0.25
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.VYSPHVLNLTLIDLPGITK#.V	29.19	7.13	4.09	0.24
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.AFIHHELLAYLYSSADQSSLM*EESAEQAQR@.R	6.18	2.33	2.65	0.38
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.AGVYPEKDQAENEDGAQENTFSM*DPQLER.Q	28.26	9.87	2.86	0.35
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.ALLQM*VQQFGVDFEK#.R	19.26	7.27	2.65	0.38
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.DM*ILQFISR@.E	23.65	11.00	2.15	0.47
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.DMILQFISR@.E	10.85	3.71	2.92	0.34
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.ESSLILAVTPANMDLANSDALK#.L	5.50	1.78	3.10	0.32
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.EVDPQGLR@.T	75.44	26.14	2.89	0.35
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.FTDFDEVR@.Q	14.74	5.89	2.50	0.40
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.FTDFDEVRQEIEAETDR.V	25.88	9.53	2.72	0.37
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.GM*EELIPLVNK#.L	60.99	16.61	3.67	0.27
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.GWLTINNISLM*K#.G	6.12	3.54	1.72	0.58
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.IEGSGDQVDTLELSGGAR@.I	38.94	14.16	2.75	0.36
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.IVTTYIR@.E	80.51	26.75	3.01	0.33
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.K#FFLSHPAYR@.H	33.02	7.36	4.49	0.22
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.NLVDSYVAIINK#.S	79.23	32.97	2.40	0.42
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.R@GWLTINNISLM*K#.G	12.75	4.19	3.04	0.33
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.R@IEGSGDQVDTLELSGGAR@.I	36.59	8.46	4.33	0.23
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.R@PLILQLIFSK#.T	23.42	5.75	4.07	0.25
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.SK#LQSQLLSLEK#.E	15.45	7.26	2.13	0.47
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.TGLFTPDLAFEAIVK#.K	61.06	19.55	3.12	0.32
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.VPVGDQPPDIEYQIK#.D	33.61	14.84	2.26	0.44
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.VPVGDQPPDIEYQIK#DM*ILQFISR@.E	21.14	10.91	1.94	0.52
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.VYSPHVLNLTLIDLPGITK#.V	111.22	42.59	2.61	0.38
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.YM*LPLDNLK#.I	24.04	9.85	2.44	0.41
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.ALLQM*VQQFGVDFEK#.R	12.85	3.00	4.28	0.23
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.DM*ILQFISR@.E	11.30	3.21	3.53	0.28
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.FTDFDEVR@QEIEAETDR@.V	13.42	3.92	3.42	0.29
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.GM*EELIPLVNK#.L	35.38	10.01	3.53	0.28
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.IEGSGDQVDTLELSGGAR@.I	24.75	4.41	5.61	0.18
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.NLVDSYVAIINK#.S	62.43	15.58	4.01	0.25
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.R@IEGSGDQVDTLELSGGAR@.I	17.08	3.06	5.59	0.18
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.SK#LQSQLLSLEK#.E	14.29	1.57	9.08	0.11
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.TGLFTPDLAFEAIVK#.K	42.19	9.84	4.29	0.23
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.VPVGDQPPDIEYQIK#.D	19.61	4.64	4.23	0.24
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.VPVGDQPPDIEYQIK#DM*ILQFISR@.E	9.67	3.13	3.09	0.32
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	R.VYSPHVLNLTLIDLPGITK#.V	48.16	13.64	3.53	0.28
P39054_DYN2_MOUSE	Dnm2	Dynamin-2 OS=Mus musc	K.YM*LPLDNLK#.I	13.22	5.54	2.39	0.42
Q8BZ98_DYN3_MOUSE	Dnm3	Dynamin-3 OS=Mus musc	R.TGLFTPDM*AFEAIVK#.K	10.16	5.31	1.91	0.52
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.NLGPINQWWLSGFDGGEK.V	3.08	6.42	0.48	2.09
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.AIILAAAPGEK#.L	33.66	29.26	1.15	0.87
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.ALIHLAGVSLGQR@.R	54.04	39.11	1.38	0.72
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.DLPNIQVR@.L	57.77	51.68	1.12	0.89
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.EADDDEEADDDVSEM*PSPK#.K	8.30	6.67	1.24	0.80
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.EAEPEQVAPETPEDR@.D	6.82	6.43	1.06	0.94
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.EAEPEQVAPETPEDR@DEDER@EEK#.R	7.01	7.45	0.94	1.06
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.EAR@PETHLDEDEDGK#K#.D	6.24	10.64	0.59	1.71
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.EESEEGNSAESAAEER@.D	12.88	6.92	1.86	0.54
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.FFGNILDR@.H	58.52	32.38	1.81	0.55
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.FFLLENVR@.N	91.29	73.15	1.25	0.80
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.FTEDSLLR@.H	75.06	53.74	1.40	0.72
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.FYFLEAYNSK#.T	44.90	33.40	1.34	0.74
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.GSNLDAPEPYR.I	50.42	47.35	1.06	0.94
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.IVVEFLQNNPDAVYEDLINK#.I	26.71	23.18	1.15	0.87
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.IVVEFLQNNPDAVYEDLINK.I	8.80	5.30	1.66	0.60
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.KDPVNETLYPEHYR.K	25.96	27.37	0.95	1.05
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.LEWDGFFSTTVTNPEPM*GK#.Q	9.12	7.44	1.23	0.82
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.LGDGVIAHK#.L	18.64	15.16	1.23	0.81
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.LGDSVYLPPEAFTFNIK.V	48.43	36.61	1.32	0.76
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.LNLLHEFLQTEIK#.S	27.34	8.61	3.18	0.31
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.LPLFPEPLHVFAPR.A	144.77	147.20	0.98	1.02
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.LVM*AGEVTNSLGQR@.L	32.10	21.32	1.51	0.66
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.LVMAGEVTNSLGQR@.L	7.31	5.02	1.45	0.69
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.NGYSSTGALR@.G	5.09	6.15	0.83	1.21
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.NLGPINQWWLSGFDGGEK#.V	26.53	17.30	1.53	0.65
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.SDSDTLSVETSPSSVATR@.R	15.49	8.33	1.86	0.54
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.SKSDSDTLSVETSPSSVATR.R	15.36	11.17	1.37	0.73
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.SQGFPDSYR@.F	20.57	13.15	1.56	0.64
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.VLEQIEEVDGR.V	87.51	87.86	1.00	1.00
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.VVDTESGAAAAVEK#.L	34.88	22.14	1.58	0.63
P13864_DNMT1_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.YQQHPEDAVDEPQM*LTSEK#.L	55.34	41.14	1.35	0.74
J3QNW0_J3QNW0_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	K.SDSDTLFETSPSSVATR@.R	8.80	7.62	1.15	0.87
J3QNW0_J3QNW0_MOUSE	Dnmt1	DNA (cytosine-5)-methyl	R.SK#SDSDTLFETSPSSVATR@.R	11.60	5.71	2.03	0.49
Q9Z2W0_DNPEP_MOUSE	Dnpep	Aspartyl aminopeptidase	R.EVAGQVGVPLQDLM*VR@.N	11.08	5.39	2.06	0.49
Q9Z2W0_DNPEP_MOUSE	Dnpep	Aspartyl aminopeptidase	K.GFFELFPSVSR@.N	32.06	20.51	1.56	0.64
Q9Z2W0_DNPEP_MOUSE	Dnpep	Aspartyl aminopeptidase	K.GTPEPGPLGATDER@.H	27.54	23.95	1.15	0.87
Q9Z2W0_DNPEP_MOUSE	Dnpep	Aspartyl aminopeptidase	R.LTAFEEAIPK#.S	49.61	30.34	1.64	0.61
Q9Z2W0_DNPEP_MOUSE	Dnpep	Aspartyl aminopeptidase	R.YASNAVSESM*IR@.E	12.79	10.87	1.18	0.85
Q9Z2W0_DNPEP_MOUSE	Dnpep	Aspartyl aminopeptidase	K.GFFELFPSVSR@.N	21.35	5.49	3.89	0.26
Q9Z2W0_DNPEP_MOUSE	Dnpep	Aspartyl aminopeptidase	R.LTAFEEAIPK#.S	29.80	6.38	4.67	0.21
Q99LB0_TDIF1_MOUSE	Dnttip1	Deoxynucleotidyltransfe	R.AVLQPSINEEIQGVFNK#.Y	10.76	10.28	1.05	0.96
Q99LB0_TDIF1_MOUSE	Dnttip1	Deoxynucleotidyltransfe	R.LNESTTFVLGSR@.A	12.14	2.37	5.12	0.20
Q8R2M2_TDIF2_MOUSE	Dnttip2	Deoxynucleotidyltransfe	K.LTSSSIDPGLNIK.Q	5.22	32.27	0.16	6.18
Q8R2M2_TDIF2_MOUSE	Dnttip2	Deoxynucleotidyltransfe	K.FAVVNVER@.W	11.66	4.62	2.53	0.40
Q8VDR9_DOCK6_MOUSE	Dock6	Dedicator of cytokinesis	K.EILEFPAR@.E	33.88	18.66	1.82	0.55
Q8VDR9_DOCK6_MOUSE	Dock6	Dedicator of cytokinesis	R.NLAADSLLPTLLEQAAPEDVDR@R@.N	8.56	3.74	2.29	0.44
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.LGTGFNPNTLDK#.Q	11.09	50.70	0.22	4.57

Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.NSLPDALLPNLLDR@.T	6.26	5.63	1.11	0.90
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.AK#LEEAILGSIGAR@.Q	5.43	2.69	2.02	0.50
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.DLVEFPPDDIEVVYSPR@.D	9.55	4.03	2.37	0.42
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.DSTEVEISTGER@.K	14.26	7.21	1.98	0.51
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.DVYVPNTTYR@.N	23.35	10.43	2.24	0.45
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.EAYTAVVYHNR@.S	8.94	3.95	2.27	0.44
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.ESILGGVLK#.V	25.78	11.75	2.19	0.46
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.FGDLDEQEFVYK#EPAITK#.L	43.97	31.65	1.39	0.72
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.GFVFSLIK#.S	15.28	5.53	2.76	0.36
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.GYQTSPDLR@.L	25.39	9.42	2.69	0.37
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.IANM*FELSLPFR@.Q	22.88	10.65	2.15	0.47
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.ISENFYFDLNSEQM*K#.G	9.07	3.92	2.31	0.43
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.LEGFYGER@.F	17.44	8.94	1.95	0.51
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.LGTGFNPNTLDK#.Q	23.36	11.60	2.01	0.50
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.LPNTYPNSPSPGPGGLGGSVHYATM*AR@.S	3.45	3.48	0.99	1.01
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.M*QVTM*SLSSLVGTSQNFNEEFLR@.R	4.89	2.10	2.33	0.43
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.NLLYIYPQSLNFANR@.Q	20.92	10.12	2.07	0.48
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.QISGQYSGSPQLLK#.N	7.32	14.18	0.52	1.94
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.QNFEIGNNFAR@.V	14.61	5.86	2.49	0.40
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.QVFESDEAPDGSSYQDEQDDLK#R@.R	4.50	2.56	1.76	0.57
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.SLIGPDQK#.E	7.74	14.38	0.54	1.86
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.SPSGSAFGSQENLR@.W	28.77	14.35	2.00	0.50
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.TILTYAEEDLELR@.E	20.61	12.21	1.69	0.59
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.TPNEEIDHQNDDQR@.K	30.53	13.71	2.23	0.45
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	K.WFTDLSVLQLNR@.L	6.42	2.35	2.73	0.37
Q8R1A4_DOCK7_MOUSE	Dock7	Dedicator of cytokinesis	R.YSDPQIK#.A	46.58	22.91	2.03	0.49
P97465_DOK1_MOUSE	Dok1	Docking protein 1 OS=Mu	R.GLYDLPQEPR@.D	5.69	3.83	1.48	0.67
P97465_DOK1_MOUSE	Dok1	Docking protein 1 OS=Mu	K.LTDSK#EDPIYDEPEGLAPAPPR@.G	4.12	2.80	1.47	0.68
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	K.ASIYQNQNSS.-	14.79	14.79	1.00	1.00
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	K.EGLISQDGSSLEALLR.T	60.54	18.86	3.21	0.31
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	K.EGLISQDGSSLEALLR@.T	13.73	3.71	3.70	0.27
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	R.GPGLASGQLYSYPAR@.R	37.93	13.92	2.72	0.37
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	R.IIEPDDFLDDLDDEDYEEDTPK#.R	19.94	8.69	2.29	0.44
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	R.K#K#LDASILEDR@.D	37.14	11.58	3.21	0.31
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	K.LLGEQYYK#.D	53.05	21.45	2.47	0.40
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	R.VDDDSLGEFPVSNSR@.A	39.29	12.60	3.12	0.32
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	K.EGLISQDGSSLEALLR.T	29.14	9.55	3.05	0.33
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	R.GPGLASGQLYSYPAR@.R	5.73	1.89	3.03	0.33
Q61103_REQU_MOUSE	Dpf2	Zinc finger protein ubi-d	K.EGLISQDGSSLEALLR@.T	4.58	1.88	2.43	0.41
O70152_DPM1_MOUSE	Dpm1	Dolichol-phosphate man	K.LGGNEIVSFLK#.G	8.48	3.45	2.46	0.41
Q99LT0_DPY30_MOUSE	Dpy30	Protein dpy-30 homolog	R.IVENEK#INAEK#.S	11.82	5.06	2.33	0.43
Q99LT0_DPY30_MOUSE	Dpy30	Protein dpy-30 homolog	K.VDLQSLPTR@.A	16.79	18.44	0.91	1.10
Q91WV0_NC2B_MOUSE	Dr1	Protein Dr1 OS=Mus mus	R.LENLGIPEEELLR@.Q	47.80	27.12	1.76	0.57
Q9D6N5_NC2A_MOUSE	Drap1	Dr1-associated corepress	K.VAAAVPVIISR@.A	32.64	15.88	2.05	0.49
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.GGGGGGPGEGFDVAK#.T	17.65	7.38	2.39	0.42
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.GQLPDYTSPVVLPYSR@.T	19.30	13.03	1.48	0.68
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.IAEIEAEM*AR@.T	29.50	14.96	1.97	0.51
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.IAEIEAEMAR@.T	15.84	3.27	4.84	0.21
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.IDQISIEELDIIYK#.V	9.28	1.14	8.13	0.12
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	R.IGFVGFPSVGK#.S	44.96	16.90	2.66	0.38
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.IIENELEGFGIR@.L	30.26	11.37	2.66	0.38
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.IQLLDLPGIIEGAK#.D	88.18	44.22	1.99	0.50
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	R.SDATADDLIDVVEGNR@.V	17.75	12.62	1.41	0.71
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.VGK#DHTLEDEDVIQIVK#.K	11.09	4.58	2.42	0.41
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	R.WNFDDLLEK#.I	7.37	6.27	1.18	0.85
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.GGGGGGPGEGFDVAK#.T	14.90	6.24	2.39	0.42
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	R.IGFVGFPSVGK#.S	35.59	16.86	2.11	0.47
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.IIENELEGFGIR@.L	18.65	6.43	2.90	0.34
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.IQLLDLPGIIEGAK#.D	37.16	15.67	2.37	0.42
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	R.SDATADDLIDVVEGNR@.V	16.21	2.50	6.47	0.15
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.DHTLEDEDVIQIVK#.K	7.31	1.64	4.46	0.22
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.GGGGGGPGEGFDVAK#.T	17.55	8.63	2.03	0.49
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	R.IGFVGFPSVGK#.S	42.95	14.85	2.89	0.35
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.IIENELEGFGIR@.L	34.45	9.32	3.70	0.27
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	K.IQLLDLPGIIEGAK#.D	92.69	28.94	3.20	0.31
P32233_DRG1_MOUSE	Drg1	Developmentally-regulat	R.SDATADDLIDVVEGNR.V	20.63	6.75	3.06	0.33
Q9QXB9_DRG2_MOUSE	Drg2	Developmentally-regulat	K.GANIQLLDLPGIIEGAAQGR@.G	14.12	3.36	4.21	0.24
Q9QXB9_DRG2_MOUSE	Drg2	Developmentally-regulat	R.GQR@PDFTDAIILR@.K	12.87	5.00	2.57	0.39
Q9QXB9_DRG2_MOUSE	Drg2	Developmentally-regulat	K.IDQISM*EEVDR@.L	10.53	3.32	3.18	0.31
Q9QXB9_DRG2_MOUSE	Drg2	Developmentally-regulat	R.VALIGFPSVGK#.S	20.91	8.79	2.38	0.42
Q9QXB9_DRG2_MOUSE	Drg2	Developmentally-regulat	K.GANIQLLDLPGIIEGAAQGR@.G	6.41	2.90	2.21	0.45
Q9QXB9_DRG2_MOUSE	Drg2	Developmentally-regulat	R.VALIGFPSVGK#.S	11.70	4.13	2.83	0.35
Q9QXB9_DRG2_MOUSE	Drg2	Developmentally-regulat	K.GANIQLLDLPGIIEGAAQGR@.G	9.65	4.52	2.13	0.47
Q9QXB9_DRG2_MOUSE	Drg2	Developmentally-regulat	K.IDQISM*EEVDR@.L	8.47	2.05	4.13	0.24
Q9QXB9_DRG2_MOUSE	Drg2	Developmentally-regulat	R.VALIGFPSVGK#.S	18.47	9.52	1.94	0.52
Q5HZJ0_RNC_MOUSE	Drosha	Ribonuclease 3 OS=Mus r	R.LLFNDPDLR@.E	8.08	3.17	2.55	0.39
Q5HZJ0_RNC_MOUSE	Drosha	Ribonuclease 3 OS=Mus r	K.LTEFEEAIGVIFTHVR@.L	12.75	3.70	3.45	0.29
Q14AI0_DCC1_MOUSE	DSCC1	Sister chromatid cohesio	R.FNSLFSLR@.E	9.57	4.06	2.36	0.42
Q14AI0_DCC1_MOUSE	DSCC1	Sister chromatid cohesio	R.ILEFDYEIK#.L	19.66	10.02	1.96	0.51
Q14AI0_DCC1_MOUSE	DSCC1	Sister chromatid cohesio	R.LLM*ENTYEGPDSQK#EEDASR@.S	14.94	4.82	3.10	0.32
O35075_DSCR3_MOUSE	Dscr3	Down syndrome critical	R.SIELQLVR@.V	7.49	3.50	2.14	0.47
O35075_DSCR3_MOUSE	Dscr3	Down syndrome critical	K.TEVPFEFPLLVK#.G	13.39	8.24	1.62	0.62
O35075_DSCR3_MOUSE	Dscr3	Down syndrome critical	K.TEVPFEFPLLVK#.G	7.89	4.10	1.92	0.52
O35075_DSCR3_MOUSE	Dscr3	Down syndrome critical	K.TEVPFEFPLLVK#.G	6.65	4.64	1.43	0.70
Q9CYC5_DSN1_MOUSE	Dsn1	Kinetochore-associated	K.AADFSLEASVAEVK#.E	7.62	4.55	1.67	0.60
E9Q557_DESP_MOUSE	Dsp	Desmoplakin OS=Mus mu	K.AEYQEEAKR.R	8.98	15.95	0.56	1.78
Q91ZU6_DYST_MOUSE	Dst	Dystonin OS=Mus muscu	R.FFLGNQFGDSQQLR@.L	8.84	2.23	3.96	0.25
Q91ZU6_DYST_MOUSE	Dst	Dystonin OS=Mus muscu	R.LLDPEDVDVSSPDEK#.S	4.41	1.77	2.49	0.40
Q91ZU6_DYST_MOUSE	Dst	Dystonin OS=Mus muscu	R.LVSDTITQK#VEEIDAAILR@.S	9.16	11.21	0.82	1.22
Q91ZU6_DYST_MOUSE	Dst	Dystonin OS=Mus muscu	R.VGGGWM*ALDEFLVK#.N	10.72	3.74	2.86	0.35
Q91WZ8_DTBP1_MOUSE	Dtnbp1	Dysbindin OS=Mus musc	R.LLSVQQDFTSGLK#.T	18.97	4.67	4.06	0.25
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	R.ATGVSDVITWNDIHHK#.T	29.79	16.86	1.77	0.57
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.DK#DLDLSVQSYTGFTDAFQR@.A	41.83	15.35	2.73	0.37
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.FGGPANFGYPDPDYLK#.R	11.96	8.99	1.33	0.75
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.FGGPANFGYPDPDYLK#R@.V	32.46	14.23	2.28	0.44
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.GNQPEGTM*SYSTQK#.G	13.48	10.59	1.27	0.79
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.HTPPDVEREPPDQSSIQVPVLLLEYFK.H	93.81	54.16	1.73	0.58
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.IHHFLSEQLLER@.E	55.18	22.94	2.41	0.42
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.ITASGYTTGIEVDSTR@.F	68.06	33.96	2.00	0.50
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	R.K#VLDLLHEAFK#.H	13.37	8.67	1.54	0.65
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.LLEPELLQEISEIEQK#.F	110.68	65.76	1.68	0.59
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	R.M*GLAPSSGEK#.L	42.83	19.94	2.15	0.47
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	R.TEVLSLK#.G	50.86	23.82	2.14	0.47

Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	R.TLTLLGSPADISAATEK#.V	63.24	35.60	1.78	0.56
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.DK#DLDLSVQSYTGFTDAFQR@.A	8.32	3.44	2.42	0.41
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.GNQPEGTM*SYSTQK#.G	4.02	3.41	1.18	0.85
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.ITASGYTTGIEVDSTR@.F	11.81	4.86	2.43	0.41
Q3UIR3_DTX3L_MOUSE	Dtx3l	E3 ubiquitin-protein liga	K.LLEPELLQEISEIEQK#.F	32.39	15.57	2.08	0.48
Q9D7X3_DUS3_MOUSE	Dusp3	Dual specificity protein p	R.VYVGNASVAQDITQLQK#.L	7.28	2.92	2.49	0.40
Q60838_DVL2_MOUSE	Dvl2	Segment polarity protei	R.VVSWLVSSDTPQPEVAPPAHESR@.T	5.00	3.02	1.66	0.60
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	K.ASVVTLPVYLNFTR@.A	8.01	2.40	3.34	0.30
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	R.ESPEVLLTLDILK#.H	8.41	6.66	1.26	0.79
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	R.K#LVPLLLEDGGDAPAALEAALEEK#.S	7.59	5.15	1.47	0.68
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	K.QLQNISQAAASGGAK#.E	11.83	3.60	3.29	0.30
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	R.TLINELVK#.G	18.47	6.39	2.89	0.35
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	R.VLLTTQGVDM*ISK#.M	6.32	2.96	2.14	0.47
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	K.VTDFGDK#VEDPTFLNQLQSGVNR@.W	11.47	5.75	1.99	0.50
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	R.ESPEVLLTLDILK#.H	7.15	3.80	1.88	0.53
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	K.VNFLPEIITLSK#.E	8.20	2.60	3.15	0.32
Q9JHU4_DYHC1_MOUSE	Dync1h1	Cytoplasmic dynein 1 he	K.VTDFGDK#VEDPTFLNQLQSGVNR@.W	5.01	3.83	1.31	0.76
O88487_DC1I2_MOUSE	Dync1i2	Cytoplasmic dynein 1 int	R.ADAEEEAATR@.I	11.29	5.19	2.18	0.46
O88487_DC1I2_MOUSE	Dync1i2	Cytoplasmic dynein 1 int	R.ALSEQINIFFDYSGR@.D	9.92	5.60	1.77	0.56
O88487_DC1I2_MOUSE	Dync1i2	Cytoplasmic dynein 1 int	R.DLEDK#EGEIQAGAK#.L	60.18	13.68	4.40	0.23
O88487_DC1I2_MOUSE	Dync1i2	Cytoplasmic dynein 1 int	K.EAAVSVQEESDLEK#.K	124.83	61.36	2.03	0.49
O88487_DC1I2_MOUSE	Dync1i2	Cytoplasmic dynein 1 int	K.ETQTPVTAQPK#.E	6.39	4.23	1.51	0.66
O88487_DC1I2_MOUSE	Dync1i2	Cytoplasmic dynein 1 int	R.LDLWNLNNDTEVPTASISVEGNPALNR@.V	13.33	6.30	2.12	0.47
O88487_DC1I2_MOUSE	Dync1i2	Cytoplasmic dynein 1 int	R.TLAEINANR@ADAEEEAATR@.I	25.91	7.62	3.40	0.29
O88487_DC1I2_MOUSE	Dync1i2	Cytoplasmic dynein 1 int	R.ADAEEEAATR@.I	14.00	3.32	4.22	0.24
O88487_DC1I2_MOUSE	Dync1i2	Cytoplasmic dynein 1 int	K.ETQTPVTAQPK#.E	6.44	2.19	2.94	0.34
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	R.DFQEYVEPGEDFPASPQR@.R	5.85	3.37	1.74	0.58
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	K.EIM*AEDDQVFLM*K#.L	13.02	4.05	3.22	0.31
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	K.FSLDALSLR@.D	56.06	16.14	3.47	0.29
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	R.K#PASVSPTTPTSPTEGEAS.-	22.56	9.95	2.27	0.44
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	K.K#TGSPGGPGVGGSPGGGAAGASPSLPPSAK#.K	4.73	3.05	1.55	0.64
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	K.NVLLLGEDGAGK#.T	39.60	16.36	2.42	0.41
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	R.SVSSNVASVSPIPAGSK#.K	22.58	7.28	3.10	0.32
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	K.VEDNFEDIITK#PPVR@K#.F	19.38	4.56	4.25	0.24
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	K.FSLDALSLR@.D	15.87	5.59	2.84	0.35
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	R.K#PASVSPTTPTSPTEGEAS.-	11.20	3.85	2.91	0.34
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	K.NVLLLGEDGAGK#.T	23.32	7.60	3.07	0.33
Q8R1Q8_DC1L1_MOUSE	Dync1li1	Cytoplasmic dynein 1 lig	R.SVSSNVASVSPIPAGSK#.K	9.52	3.34	2.85	0.35
Q6PDL0_DC1L2_MOUSE	Dync1li2	Cytoplasmic dynein 1 lig	K.FAVSAESLR@.E	29.38	10.14	2.90	0.35
Q6PDL0_DC1L2_MOUSE	Dync1li2	Cytoplasmic dynein 1 lig	R.GGPASVPSASPGTSVK#.K	32.12	11.89	2.70	0.37
Q6PDL0_DC1L2_MOUSE	Dync1li2	Cytoplasmic dynein 1 lig	R.K#PDSM*VTNSSTENEA.-	12.25	1.80	6.83	0.15
Q6PDL0_DC1L2_MOUSE	Dync1li2	Cytoplasmic dynein 1 lig	K.NILVFGEDGSGK#.T	22.15	9.51	2.33	0.43
Q6PDL0_DC1L2_MOUSE	Dync1li2	Cytoplasmic dynein 1 lig	K.TGSPGSPSAGGVQSTAK#.K	4.51	1.67	2.70	0.37
Q6PDL0_DC1L2_MOUSE	Dync1li2	Cytoplasmic dynein 1 lig	K.TVLSNVQEELDR@.M	36.26	10.68	3.40	0.29
Q6PDL0_DC1L2_MOUSE	Dync1li2	Cytoplasmic dynein 1 lig	K.TYGFHFTIPALVVEK#.D	21.32	4.60	4.63	0.22
P63168_DYL1_MOUSE	Dynll1	Dynein light chain 1, cyt	R.NFGSYVTHETK#.H	13.74	5.94	2.31	0.43
P63168_DYL1_MOUSE	Dynll1	Dynein light chain 1, cyt	K.YNIEK#DIAAHIK#.K	90.84	48.12	1.89	0.53
Q9D0M5_DYL2_MOUSE	Dynll2	Dynein light chain 2, cyt	K.YNIEK#DIAAYIK#.K	36.65	13.17	2.78	0.36
Q9D0M5_DYL2_MOUSE	Dynll2	Dynein light chain 2, cyt	K.YNIEK#DIAAYIK#K#.E	16.05	5.39	2.98	0.34
P62627_DLRB1_MOUSE	Dynlrb1	Dynein light chain roadb	R.EIDPQNDLTFLR@.I	18.15	8.55	2.12	0.47
P62627_DLRB1_MOUSE	Dynlrb1	Dynein light chain roadb	K.GVQGIIVVNTEGIPIK#.S	14.78	5.84	2.53	0.40
P51807_DYLT1_MOUSE	Dynlt1	Dynein light chain Tctex-	K.VNQWTTNVLEQTLSQLTK#.L	8.41	2.67	3.14	0.32
A1L341_A1L341_MOUSE	Dyrk1a	Dual-specificity tyrosine-	R.GVSLNLTR@.K	16.88	7.28	2.32	0.43
A1L341_A1L341_MOUSE	Dyrk1a	Dual-specificity tyrosine-	K.HINEVYYAK#.K	13.48	2.53	5.34	0.19
A1L341_A1L341_MOUSE	Dyrk1a	Dual-specificity tyrosine-	K.IVEVLGIPPAHILDQAPK#.A	12.48	4.65	2.68	0.37
A1L341_A1L341_MOUSE	Dyrk1a	Dual-specificity tyrosine-	R.K#VYNDGYDDDNYDYIVK#.N	6.95	1.68	4.13	0.24
A1L341_A1L341_MOUSE	Dyrk1a	Dual-specificity tyrosine-	R.LLELM*NK#.H	15.56	7.36	2.11	0.47
A1L341_A1L341_MOUSE	Dyrk1a	Dual-specificity tyrosine-	R.R@QPSISDQQVSALPYSDQIQQPLTNQR@.R	6.29	2.15	2.93	0.34
Q07802_COE1_MOUSE	Ebf1	Transcription factor COE	R.QGQPVEIER.T	2.17	6.49	0.33	2.99
Q9D903_EBP2_MOUSE	Ebna1bp2	Probable rRNA-processin	K.ESYDDVSSFR@.A	39.13	20.40	1.92	0.52
Q9D903_EBP2_MOUSE	Ebna1bp2	Probable rRNA-processin	K.K#AVNDVSGLK#.Q	16.09	9.22	1.75	0.57
Q9D903_EBP2_MOUSE	Ebna1bp2	Probable rRNA-processin	K.K#VQTEVLQK#.R	31.79	24.44	1.30	0.77
Q9D903_EBP2_MOUSE	Ebna1bp2	Probable rRNA-processin	R.LHQLQVPTK#.R	8.61	6.08	1.42	0.71
Q9D903_EBP2_MOUSE	Ebna1bp2	Probable rRNA-processin	R.QAQAAVLAVLPR@.L	19.60	13.03	1.50	0.66
Q9WUR2_ECI2_MOUSE	Eci2	Enoyl-CoA delta isomera	R.ASQQDFENALNQVK#.L	5.63	1.66	3.39	0.30
Q9WUR2_ECI2_MOUSE	Eci2	Enoyl-CoA delta isomera	K.DILVTSEDGITK#.I	6.12	0.96	6.39	0.16
Q6PDI5_ECM29_MOUSE	Ecm29	Proteasome-associated p	R.FQEFSDIVIPLIK#.K	8.34	4.51	1.85	0.54
Q6PDI5_ECM29_MOUSE	Ecm29	Proteasome-associated p	R.ALM*SSSQATASSSNK#.S	4.67	2.57	1.82	0.55
Q6PDI5_ECM29_MOUSE	Ecm29	Proteasome-associated p	R.FQEFSDIVIPLIK#.K	13.75	2.65	5.20	0.19
Q6PDI5_ECM29_MOUSE	Ecm29	Proteasome-associated p	K.LLLQGLM*DSVEAK#.Q	7.77	4.57	1.70	0.59
Q6PDI5_ECM29_MOUSE	Ecm29	Proteasome-associated p	R.NGPLPIPSEGSGFTK#.L	13.87	6.78	2.05	0.49
Q6PDI5_ECM29_MOUSE	Ecm29	Proteasome-associated p	K.VYLGDIPLK#.T	11.37	6.37	1.79	0.56
Q6PDI5_ECM29_MOUSE	Ecm29	Proteasome-associated p	R.YQFDPNLGIR@.Q	10.96	4.04	2.71	0.37
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.AAVFEEIDTYER@.R	11.41	6.03	1.89	0.53
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	R.APVLSIDPPVHEVEQGIDAK#.W	10.22	6.16	1.66	0.60
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.FVIPLHSA.-	26.53	26.53	1.00	1.00
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.K#PASSSSAPQSIPK#.R	6.06	3.84	1.58	0.63
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.M*LESITNELSLFSK#.T	16.89	7.12	2.37	0.42
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.TQGQQVSSLR@.D	34.27	11.57	2.96	0.34
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.AAVFEEIDTYER@.R	10.11	3.30	3.06	0.33
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	R.APVLSIDPPVHEVEQGIDAK#.W	7.90	6.40	1.24	0.81
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.FVIPLHSA.-	11.73	11.73	1.00	1.00
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.K#PASSSSAPQSIPK#.R	5.89	3.14	1.87	0.53
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.M*LESITNELSLFSK#.T	8.71	6.93	1.26	0.80
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.TQGQQVSSLR@.D	13.32	3.79	3.52	0.28
Q8K2D3_EDC3_MOUSE	Edc3	Enhancer of mRNA-deca	K.TQGQQVSSLR@.D	7.83	3.79	2.06	0.48
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.AAADTLQGPM*QAAYR@.E	9.74	3.19	3.06	0.33
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.EAFQSVVLPAFEK#.S	24.88	21.99	1.13	0.88
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.ELAELWHNQEELLQR@.L	10.69	7.71	1.39	0.72
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.SLEPVAGQLSNSVATK#.L	32.22	13.10	2.46	0.41
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.AAADTLQGPM*QAAYR@.E	34.24	10.45	3.28	0.31
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.AAADTLQGPMQAAYR@.E	7.16	6.93	1.03	0.97
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	K.ALQDVQIR@.F	24.16	8.81	2.74	0.36
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.EAFQSVVLPAFEK#.S	64.16	24.64	2.60	0.38
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.ELAELWHNQEELLQR@.L	55.27	21.84	2.53	0.40
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	K.EQQATVTSSIM*QAM*R@.S	15.87	4.37	3.63	0.28
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	K.EVEIVASSDSSISSK#.A	9.15	9.75	0.94	1.07
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.FLITGADQNR@.E	31.18	13.98	2.23	0.45
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.GGQLQEQLTQQLSQALSSAVAGR@.L	124.82	43.58	2.86	0.35
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.GLVSTLQSATEQM*AATVSSSVR@.A	52.77	13.11	4.02	0.25
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.GLVSTLQSATEQMAATVSSSVR@.A	18.28	8.09	2.26	0.44
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	K.GPGQVSTAASALSLDLQEVEPLGLPQASPSR@.T	17.82	6.52	2.73	0.37
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-deca	R.HSTPSLLEAALTQEVATPDSQVWPTAPDITR@.E	10.17	2.66	3.83	0.26

Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.IQEEILVHIR@.Q	23.84	5.70	4.19	0.24
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.LFQFLQADPHNSLSK#.A	70.31	21.13	3.33	0.30
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.LGTQEYLQQLESHM*K#.S	72.51	21.78	3.33	0.30
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.LQLDGSLTLNSSSSSLQASPR@.S	8.83	3.41	2.59	0.39
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.LSLM*LHGLVTPSLP.-	7.76	7.76	1.00	1.00
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.LTAVEGSM*K#.E	22.04	7.71	2.86	0.35
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.LTEHQVAEPPEDWPALIWQQQR@.E	23.15	9.58	2.42	0.41
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.QGFIVVK#.G	15.62	4.65	3.36	0.30
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.QGPELGSQLGLDGGPGDGDR@.H	9.98	3.86	2.58	0.39
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.SLEPVAGQLSNSVATK#.L	87.10	27.34	3.19	0.31
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.SLEPVAGQLSNSVATK#.L	17.64	3.59	4.91	0.20
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.SLLPGLLPGPADK#.L	49.19	20.58	2.39	0.42
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.AAADTLQGPM*QAAYR@.E	17.71	6.05	2.93	0.34
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.AEVQHQLHVAVGSLQESILAQVQR@.I	17.91	13.04	1.37	0.73
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.AEVWDLDM*LR@.S	19.94	6.76	2.95	0.34
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.ALQDVQIR@.F	41.39	10.68	3.87	0.26
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.DHM*GSVM*AQVR@.Q	13.56	3.62	3.74	0.27
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.EAFQSVVLPAFEK#.S	59.87	15.54	3.85	0.26
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.ELAELWHNQEELLQR@.L	30.43	7.58	4.02	0.25
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.EPVLAQLR.G	38.43	15.72	2.44	0.41
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.EQQATVTSSIM*QAM*R@.S	5.20	2.94	1.77	0.57
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.EVEIVASSDSSISSK#.A	14.40	4.83	2.98	0.34
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.FWQIYIEGQDEPR@.C	10.88	4.78	2.28	0.44
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.GGQLQEQLTQQLSQALSSAVAGR@.L	109.14	24.76	4.41	0.23
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.GGQLQEQLTQQLSQALSSAVAGR@.L	7.08	2.53	2.80	0.36
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.GLVSTLQSATEQM*AATVSSSVR@.A	27.80	9.46	2.94	0.34
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.GPGQVSTAASALSLDLQEVEPLGLPQASPSR@.T	18.77	7.39	2.54	0.39
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.HSTPSLLEAALTQEVATPDSQVWPTAPDITR@.E	10.03	1.69	5.94	0.17
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.IQEEILVHIR@.Q	31.55	33.32	0.95	1.06
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	K.LFQFLQADPHNSLSK#.A	51.39	16.02	3.21	0.31
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.LTEHQVAEPPEDWPALIWQQQR@.E	19.20	6.33	3.03	0.33
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.QGPELGSQLGLDGGPGDGDR@.H	13.78	5.13	2.69	0.37
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.SLEPVAGQLSNSVATK#.L	58.24	19.36	3.01	0.33
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.SLLPGLLPGPADK#.L	91.52	31.89	2.87	0.35
Q3UJB9_EDC4_MOUSE	Edc4	Enhancer of mRNA-decap	R.VISVSTSER@.T	52.44	15.37	3.41	0.29
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.IQAGEGETAVLNQLQEK#.N	5.19	3.27	1.58	0.63
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.LTLAQEDLISNR@.N	8.17	3.61	2.26	0.44
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	R.VLSLETSVSELSSQLNESK#.E	3.99	2.16	1.85	0.54
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.AAQLATEIADIK#.S	27.42	12.15	2.26	0.44
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	R.ADLQNHLDTAQHALQDK#.Q	12.82	4.61	2.78	0.36
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.DALLAELSTTK#.E	25.81	8.54	3.02	0.33
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.EQALQSLQQQR@.Q	15.77	5.25	3.00	0.33
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.HYQAVHDAGNDSGHGGEAGLALTR@.D	18.86	4.19	4.51	0.22
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.IQAGEGETAVLNQLQEK#.N	12.02	20.49	0.59	1.70
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.IQNLEALLQK#.G	22.28	12.09	1.84	0.54
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.K#EEENVVLK#QEFEK#.L	12.19	4.68	2.60	0.38
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.K#LEADALEVK#.A	12.62	7.25	1.74	0.57
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.LQQQSSQAAQELAAEK#.G	23.77	8.58	2.77	0.36
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.LQSEHAHLEATINQLR@.S	5.82	2.67	2.18	0.46
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.LSALQSNYEK#.C	9.44	7.16	1.32	0.76
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	R.LTASESSLQR@.A	25.75	9.91	2.60	0.38
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.LTLAQEDLISNR@.N	29.83	8.04	3.71	0.27
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.LTM*QVTTLNENLGTVK#.K	7.15	6.10	1.17	0.85
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	R.M*QAAVTELTAVK#.A	19.12	9.11	2.10	0.48
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.QQHQEQQALQQSATAK#.L	16.41	7.94	2.07	0.48
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.QTDDLR@GEIAVLEATVQNNQDER@.R	8.33	2.16	3.86	0.26
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.SEILENIK#.Q	114.72	26.18	4.38	0.23
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	R.VLSLETSVSELSSQLNESK#.E	7.00	4.00	1.75	0.57
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.VSVQLDQLTAK#.F	24.02	10.70	2.25	0.45
Q8BL66_EEA1_MOUSE	Eea1	Early endosome antigen	K.VTHLTEDLNK#.Q	23.95	7.12	3.37	0.30
Q921E6_EED_MOUSE	Eed	Polycomb protein EED O	R.DPNLLLSVSK#.D	11.86	9.23	1.28	0.78
Q921E6_EED_MOUSE	Eed	Polycomb protein EED O	K.EGDPLVFATVGSNR.V	6.10	10.04	0.61	1.65
Q921E6_EED_MOUSE	Eed	Polycomb protein EED O	K.TNR@PFISQK#.I	6.93	12.66	0.55	1.83
Q921E6_EED_MOUSE	Eed	Polycomb protein EED O	R.WLGDLILSK.S	8.07	11.48	0.70	1.42
Q921E6_EED_MOUSE	Eed	Polycomb protein EED O	R.EVSTAPAGTDM*PAAK#.K	3.80	1.66	2.28	0.44
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.EHALLAYTLGVK#.Q	230.25	85.84	2.68	0.37
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.EVSTYIK#K#.I	83.85	36.89	2.27	0.44
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.IGGIGTVPVGR@.V	1276.32	551.94	2.31	0.43
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.KIGYNPDTVAFVPISGWNGDNM*LEPSANM*PWFK.G	10.88	4.75	2.29	0.44
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.K#LEDGPK#.F	112.03	65.28	1.72	0.58
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.LPLQDVYK#.I	729.23	319.84	2.28	0.44
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.M*DSTEPPYSQK#.R	245.49	93.50	2.63	0.38
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.QLIVGVNK#.M	607.09	216.09	2.81	0.36
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.QLIVGVNK#M*DSTEPPYSQK#.R	97.85	35.95	2.72	0.37
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.QLIVGVNK#M*DSTEPPYSQK#.R	1.79	1.84	0.97	1.03
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.R@YEEIVK#.E	1215.77	393.98	3.09	0.32
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.STTTGHLIYK#.C	269.13	136.22	1.98	0.51
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.THINIVVIGHVDSGK#.S	151.05	58.22	2.59	0.39
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.TIEK#FEK#.E	155.07	61.43	2.52	0.40
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.VETGVLK#PGM*VVTFAPVNVTTEVK#.S	452.00	178.52	2.53	0.39
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.VETGVLK#PGMVVTFAPVNVTTEVK#.S	310.48	147.64	2.10	0.48
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.YEEIVK#EVSTYIK#.K	45.33	20.39	2.22	0.45
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.YYVTIIDAPGHR@.D	665.91	292.45	2.28	0.44
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.YYVTIIDAPGHR.D	82.29	29.98	2.74	0.36
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.YYVTIIDAPGHRDFIK.N	25.97	8.00	3.24	0.31
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.EHALLAYTLGVK#.Q	9.43	3.20	2.95	0.34
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.LPLQDVYK#.I	12.39	6.36	1.95	0.51
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.M*DSTEPPYSQK#.R	7.68	5.35	1.44	0.70
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.STTTGHLIYK#.C	9.36	9.08	1.03	0.97
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.VETGVLKPGM*VVTFAPVNVTTEVK.S	11.93	7.80	1.53	0.65
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.IGGIGTVPVGR@.V	246.90	89.10	2.77	0.36
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.K#LEDGPK#.F	21.38	10.83	1.97	0.51
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.LPLQDVYK#.I	134.72	55.32	2.44	0.41
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.M*DSTEPPYSQK#.R	41.87	14.86	2.82	0.35
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.QLIVGVNK#M*DSTEPPYSQK#.R	19.37	4.76	4.07	0.25
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.R@YEEIVK#.E	109.76	52.70	2.08	0.48
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.STTTGHLIYK#.C	60.95	21.85	2.79	0.36
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.THINIVVIGHVDSGK#.S	33.02	11.73	2.81	0.36
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.VETGVLK#PGM*VVTFAPVNVTTEVK#.S	84.74	32.41	2.61	0.38
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.VETGVLK#PGMVVTFAPVNVTTEVK#.S	45.67	18.61	2.45	0.41
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	R.EHALLAYTLGVK#.Q	74.91	22.38	3.35	0.30
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.IGGIGTVPVGR@.V	243.17	77.02	3.16	0.32
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alph	K.K#LEDGPK#.F	26.76	15.18	1.76	0.57

P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alpha	R.LPLQDVYK#.I	109.85	38.56	2.85	0.35
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alpha	K.M*DSTEPPYSQK#.R	12.97	4.05	3.21	0.31
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alpha	K.QLIVGVNK#.M	60.92	17.20	3.54	0.28
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alpha	K.STTTGHLIYK#.C	54.03	19.77	2.73	0.37
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alpha	K.THINIVVIGHVDSGK#.S	20.61	4.04	5.10	0.20
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alpha	R.VETGVLK#PGM*VVTFAPVNVTTEVK#.S	90.32	30.69	2.94	0.34
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alpha	R.VETGVLK#PGMVVTFAPVNVTTEVK#.S	28.34	8.67	3.27	0.31
P10126_EF1A1_MOUSE	Eef1a1	Elongation factor 1-alpha	K.YYVTIIDAPGHR@.D	12.31	3.72	3.31	0.30
O70251_EF1B_MOUSE	Eef1b	Elongation factor 1-beta	K.LVPVGYGIK#.K	26.87	20.00	1.34	0.74
P57776_EF1D_MOUSE	Eef1d	Elongation factor 1-delta	R.FYEQM*NGPVTSGSR@.Q	17.35	6.63	2.62	0.38
P57776_EF1D_MOUSE	Eef1d	Elongation factor 1-delta	R.GVVQDLQQAISK#.L	85.61	42.76	2.00	0.50
P57776_EF1D_MOUSE	Eef1d	Elongation factor 1-delta	R.ITSLEVENQNLR@.G	81.05	37.30	2.17	0.46
P57776_EF1D_MOUSE	Eef1d	Elongation factor 1-delta	R.SIQLDGLVWGASK#.L	32.71	12.30	2.66	0.38
P57776_EF1D_MOUSE	Eef1d	Elongation factor 1-delta	K.SLAGSSGPGASSGPGGDHSELIVR@.I	63.55	29.46	2.16	0.46
Q9D8N0_EF1G_MOUSE	Eef1g	Elongation factor 1-gamm	K.ALIAAQYSGAQVR@.V	40.79	24.47	1.67	0.60
Q9D8N0_EF1G_MOUSE	Eef1g	Elongation factor 1-gamm	R.FPEELTQTFM*SCNLITGMFQR@LDK#LR.K	2.50	4.90	0.51	1.96
Q9D8N0_EF1G_MOUSE	Eef1g	Elongation factor 1-gamm	R.ILGLLDTHLK#.T	14.79	5.67	2.61	0.38
Q9D8N0_EF1G_MOUSE	Eef1g	Elongation factor 1-gamm	R.K#LDPGSEETQTLVR@.E	25.32	10.95	2.31	0.43
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	R.ALLELQLEPEELYQTFQR@.I	45.64	28.72	1.59	0.63
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.AYLPVNESFGFTADLR.S	26.35	15.66	1.68	0.59
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.FSVSPVVR@.V	50.89	28.63	1.78	0.56
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.GEGQLSAAER.A	50.09	31.02	1.61	0.62
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	R.GGGQIIPTAR@.R	120.74	74.73	1.62	0.62
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	R.GHVFEESQVAGTPM*FVVK#.A	21.35	10.16	2.10	0.48
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.GVQYLNEIK#DSVVAGFQWATK#.E	11.78	8.15	1.45	0.69
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	R.IM*GPNYTPGK#.K	12.80	7.47	1.71	0.58
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.NPADLPK#.L	34.86	26.25	1.33	0.75
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.SDPVVSYR@.E	34.04	18.34	1.86	0.54
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.VFDAIM*NFR@.K	31.02	16.73	1.85	0.54
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	R.VFSGVVSTGLK#.V	39.50	32.17	1.23	0.81
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.YEWDVAEAR@.K	15.28	7.77	1.97	0.51
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	R.YLAEK#YEWDVAEAR@.K	13.52	4.34	3.12	0.32
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.AGIIASAR@.A	30.12	13.03	2.31	0.43
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	R.ALLELQLEPEELYQTFQR@.I	31.98	13.84	2.31	0.43
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.GEGQLSAAER@.A	20.33	7.42	2.74	0.36
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	R.GGGQIIPTAR@.R	53.60	27.54	1.95	0.51
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.GVQYLNEIK#DSVVAGFQWATK#.E	6.82	5.75	1.19	0.84
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.K#EDLYLK#PIQR@.T	14.92	3.63	4.11	0.24
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.NPADLPK#.L	31.15	16.60	1.88	0.53
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.VFDAIM*NFR@.K	14.60	6.23	2.34	0.43
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	R.VFSGVVSTGLK#.V	40.13	13.13	3.06	0.33
P58252_EF2_MOUSE	Eef2	Elongation factor 2 OS=M	K.YEWDVAEAR@.K	12.08	3.55	3.41	0.29
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	R.ADLNQGIGEPQSPSR.R	18.08	24.17	0.75	1.34
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	R.DGFIDLM*ELK#.L	32.47	40.75	0.80	1.26
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	R.DGFIDLMELK.L	19.77	20.73	0.95	1.05
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	R.EFLLIFR@.K	67.15	84.86	0.79	1.26
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	K.LGAPQTHLGLK#.S	78.80	90.53	0.87	1.15
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	R.LSEIDVSTEGVK#.G	78.88	115.58	0.68	1.47
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	R.RADLNQGIGEPQSPSR.R	21.66	29.61	0.73	1.37
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	R.R@ADLNQGIGEPQSPSR@.R	4.33	3.89	1.11	0.90
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	R.RVFNPYTEFK.E	10.72	10.05	1.07	0.94
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	K.SM*IQEVDEDFDSK.L	33.88	42.04	0.81	1.24
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	K.SMIQEVDEDFDSK.L	5.36	9.30	0.58	1.73
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	R.VFNPYTEFK.E	56.82	74.72	0.76	1.32
Q9D8Y0_EFHD2_MOUSE	Efhd2	EF-hand domain-contain	K.VQAINVSSR@.F	83.99	98.03	0.86	1.17
Q8C0D5_ETUD1_MOUSE	Eftud1	Elongation factor Tu GTP	K.IVTSLGLK#.I	44.30	20.67	2.14	0.47
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.AFIPAIDSFGFETDLR@.T	32.56	19.36	1.68	0.59
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.AFIPAIDSFGFETDLR.T	115.42	59.36	1.94	0.51
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.DSIVQGFQWGTR@.E	43.44	20.16	2.15	0.46
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.FFDDPM*LLELAK#.Q	79.38	42.09	1.89	0.53
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.FNTTSVIK#.I	56.63	30.15	1.88	0.53
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.GHVTQDAPIPGSPLYTIK#.A	71.14	44.92	1.58	0.63
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.GLAEDIENEVVQITWNR@.K	90.19	49.45	1.82	0.55
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.GLSEDVSISK#.F	73.61	44.18	1.67	0.60
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.IAVEPVNPSELPK#.M	180.22	111.24	1.62	0.62
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.ILAQVVGDVDTSLPR@.T	93.75	49.82	1.88	0.53
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.ILDAVVAQEPLHR@.G	231.50	124.01	1.87	0.54
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.ILDAVVAQEPLHR.G	22.99	13.85	1.66	0.60
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.ISDGVVLFIDAAEGVM*LNTER@.L	23.06	16.28	1.42	0.71
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.ITM*IAEPLEK#.G	62.80	36.30	1.73	0.58
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.ITMIAEPLEK#.G	17.02	11.44	1.49	0.67
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.IYADTFGDINYQEFAK#.R	95.57	54.14	1.77	0.57
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.K#GLSEDVSISK#.F	17.82	14.23	1.25	0.80
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.LGEFFQTK#.Y	95.60	58.77	1.63	0.61
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.LWGDIYFNPK#.T	33.88	21.01	1.61	0.62
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.LWISVAR.Y	103.90	61.80	1.68	0.59
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.M*YSEIDIK#.V	32.94	20.50	1.61	0.62
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.QDVVLNYPM*.-	16.48	16.48	1.00	1.00
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.R@LWGDIYFNPK#.T	12.89	4.89	2.64	0.38
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.SIVIR@PLEPQPAPHLAR@.E	29.47	19.43	1.52	0.66
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.SIWAFGPDATGPNILVDDTLPSEVDK#.A	4.41	2.59	1.70	0.59
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.STPVTVVLPDTK#.G	118.18	90.15	1.31	0.76
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.SYLFNIM*DTPGHVNFSDEVTAGLR@.I	83.93	41.05	2.04	0.49
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.TATITEPR@.G	114.11	71.42	1.60	0.63
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.THTQGQAFSLSVFHHWQIVPGDPLDK#.S	6.82	4.03	1.69	0.59
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.TLDELGIHLTKEELK.L	70.45	29.63	2.38	0.42
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.VPAGNWVLIEGVDQPIVK#.T	58.63	38.17	1.54	0.65
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.VVYSAFLM*ATPR@.L	26.96	26.48	1.02	0.98
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.YDWDLLAAR@.S	100.25	50.35	1.99	0.50
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.YHIEVNR@.V	41.75	22.50	1.86	0.54
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.YYPTAEEVYGPEVETIVQEEDTQPLTEPIIK#PVK#.T	27.70	12.27	2.26	0.44
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.AFIPAIDSFGFETDLR.T	80.22	36.54	2.20	0.46
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.DLDEDEDEDEDDVGEHEDDHPGM*EVVLHEDK#K#.Y	4.71	1.44	3.26	0.31
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.DSIVQGFQWGTR@.E	27.61	13.05	2.12	0.47
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.FFDDPM*LLELAK#.Q	39.30	14.41	2.73	0.37
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.GLAEDIENEVVQITWNR@.K	9.20	2.53	3.64	0.27
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.IAVEPVNPSELPK#.M	115.46	52.05	2.22	0.45
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.ILAQVVGDVDTSLPR.T	73.52	18.82	3.91	0.26
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.ILDAVVAQEPLHR@.G	119.99	54.52	2.20	0.45
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.ISDGVVLFIDAAEGVM*LNTER@.L	4.04	3.79	1.07	0.94
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.ITM*IAEPLEK#.G	32.58	13.08	2.49	0.40
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.ITMIAEPLEK#.G	11.43	5.46	2.09	0.48
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.IYADTFGDINYQEFAK#.R	56.80	20.59	2.76	0.36

O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.K#GLSEDVSISK#.F	7.98	63.73	0.13	7.99
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.LGEFFQTK#.Y	51.76	19.92	2.60	0.38
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.LWGDIYFNPK#.T	14.83	7.55	1.96	0.51
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.M*YSEIDIK#.V	16.59	9.65	1.72	0.58
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.STPVTVVLPDTK#.G	80.35	47.30	1.70	0.59
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.SYLFNIM*DTPGHVNFSDEVTAGLR@.I	50.74	21.72	2.34	0.43
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.VPAGNWVLIEGVDQPIVK#.T	38.41	18.52	2.07	0.48
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	R.VVYSAFLM*ATPR@.L	14.35	8.71	1.65	0.61
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.YDWDLLAAR@.S	46.76	20.08	2.33	0.43
O08810_U5S1_MOUSE	Eftud2	116 kDa U5 small nuclea	K.YYPTAEEVYGPEVETIVQEEDTQPLTEPIIKPVK.T	20.29	10.62	1.91	0.52
P08046_EGR1_MOUSE	Egr1	Early growth response pr	K.AFATQSGSQDLK#.A	21.08	7.55	2.79	0.36
P08046_EGR1_MOUSE	Egr1	Early growth response pr	K.AFATQSGSQDLK#.A	16.36	8.86	1.85	0.54
P08046_EGR1_MOUSE	Egr1	Early growth response pr	R.TQQPSLTPLSTIK#.A	11.58	8.61	1.34	0.74
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.ELVNNLGEIYQK#.I	23.18	6.19	3.75	0.27
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	R.IGPEPTTDSFIAVM*HGPTEGVVPGNALVVDPR@.R	4.38	1.82	2.41	0.42
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	R.IILLFDAHK#LDISDEFSEVIK#.A	14.91	6.86	2.17	0.46
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.IINTPEVVR@.V	23.58	9.74	2.42	0.41
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.LDISDEFSEVIK#.A	9.06	9.45	0.96	1.04
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.LFEAEEQDLFK#DIQSLPR@.N	12.97	2.93	4.43	0.23
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.LLDTVDDM*LANDIAR@.L	6.59	2.91	2.27	0.44
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.M*QELLQTQDFSK#.F	7.30	2.62	2.78	0.36
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	R.QEESLM*PSQAVK#.G	8.80	4.12	2.14	0.47
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.ADQIETQQLM*R@.V	18.64	5.92	3.15	0.32
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.ELVNNLGEIYQK#.I	31.12	10.32	3.02	0.33
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	R.FHEFHSPALEDADFDNK#PM*VLLVGQYSTGK#.T	7.22	2.55	2.83	0.35
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.FQALK#PK#.L	17.51	6.35	2.76	0.36
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	R.IGPEPTTDSFIAVM*HGPTEGVVPGNALVVDPR@.R	6.44	2.27	2.84	0.35
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	R.IILLFDAHK#.L	13.63	4.01	3.40	0.29
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	R.IILLFDAHK#LDISDEFSEVIK#.A	11.77	2.85	4.13	0.24
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.IINTPEVVR@.V	30.95	11.58	2.67	0.37
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	R.K#LNDLIK#.R	16.93	7.27	2.33	0.43
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.LFEAEEQDLFK#DIQSLPR@.N	17.96	6.44	2.79	0.36
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.LLDTVDDM*LANDIAR@.L	10.68	2.80	3.81	0.26
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.M*QELLQTQDFSK#.F	9.88	4.08	2.42	0.41
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	R.QEESLM*PSQAVK#.G	14.25	4.07	3.50	0.29
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.ELVNNLGEIYQK#.I	11.89	3.29	3.61	0.28
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.IINTPEVVR@.V	8.68	3.35	2.59	0.39
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.LFEAEEQDLFK#DIQSLPR@.N	7.18	2.36	3.04	0.33
Q9WVK4_EHD1_MOUSE	Ehd1	EH domain-containing pr	K.M*QELLQTQDFSK#.F	4.00	2.41	1.66	0.60
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.ADM*VETQQLM*R@.V	8.82	3.57	2.47	0.40
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	R.FGSFHSPALEDADFDGK#PM*VLVAGQYSTGK#.T	11.12	6.02	1.85	0.54
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.LEGHGLPTNLPR@.R	32.45	18.89	1.72	0.58
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	R.LFELEEQDLFR@.D	43.65	22.84	1.91	0.52
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.LLEALDDM*LAQDIAK#.L	13.30	7.62	1.75	0.57
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.LNPFGNTFLNR@.F	16.26	9.44	1.72	0.58
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.LPNSVLGR@.I	26.63	14.62	1.82	0.55
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.LPVIFAK#.I	24.35	14.02	1.74	0.58
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	R.QEELESVEAGVQGGAFEGTR@.M	2.95	1.99	1.48	0.67
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.SK#YDEIFYNLAPADGK#.L	13.65	7.56	1.81	0.55
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.TSFIQYLLEQEVPGSR@.V	27.70	13.71	2.02	0.50
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.LLEALDDM*LAQDIAK#.L	6.62	3.68	1.80	0.56
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.LPNSVLGR@.I	13.63	6.80	2.01	0.50
Q8BH64_EHD2_MOUSE	Ehd2	EH domain-containing pr	K.TSFIQYLLEQEVPGSR@.V	16.68	11.03	1.51	0.66
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.LFEAEAQDLFR@.D	5.82	4.53	1.28	0.78
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	K.AM*QEQLENYDFTK#.F	14.65	7.71	1.90	0.53
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.DIQSLPQK#.A	23.86	10.77	2.22	0.45
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.EYQISAGDFPEVK#.A	25.47	9.83	2.59	0.39
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.FGNAFLNR@.F	23.50	7.39	3.18	0.31
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.FHEFHSPALEDADFENK#PM*ILLVGQYSTGK#.T	8.62	2.28	3.77	0.26
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.LFEAEAQDLFR@.D	36.90	12.78	2.89	0.35
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	K.LIEAVDNM*LTNK#.I	15.40	8.04	1.92	0.52
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.LPEIYVQLQR@.E	10.95	3.72	2.94	0.34
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.SGGM*DAVQTVTGGLR@.S	13.84	8.80	1.57	0.64
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	K.SISIIDSPGILSGEK#.Q	32.15	13.45	2.39	0.42
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	K.AM*QEQLENYDFTK#.F	5.59	3.11	1.80	0.56
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.LFEAEAQDLFR@.D	13.34	4.28	3.12	0.32
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	R.SGGM*DAVQTVTGGLR@.S	8.82	2.78	3.17	0.32
Q9EQP2_EHD4_MOUSE	Ehd4	EH domain-containing pr	K.SISIIDSPGILSGEK#.Q	12.07	4.77	2.53	0.40
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	K.ADTTSTVTLAPGQEK#.S	22.35	6.53	3.42	0.29
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	R.ADTTTGSIAGAPEDER@.S	14.33	9.73	1.47	0.68
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	R.DSAPDK#PVAVEK#.T	13.99	6.61	2.12	0.47
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	R.IAFFSTR@.L	18.43	8.28	2.22	0.45
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	R.LIQAGEQLGFDYGER@.F	15.10	4.62	3.27	0.31
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	K.VLLM*LVDGIDPNFK#.M	6.87	4.72	1.46	0.69
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	K.ADTTSTVTLAPGQEK#.S	14.67	4.37	3.36	0.30
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	R.ADTTTGSIAGAPEDER@.S	9.11	5.23	1.74	0.57
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	R.DSAPDK#PVAVEK#.T	12.04	3.57	3.37	0.30
Q5DW34_EHMT1_MOUSE	Ehmt1	Histone-lysine N-methylt	R.LIQAGEQLGFDYGER@.F	12.84	4.67	2.75	0.36
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	R.GVSNDTSSLETER@.G	8.49	2.91	2.92	0.34
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	R.LDPHPELLPDLSSLPPINT.-	13.46	13.46	1.00	1.00
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	R.TGEELGFDYGDRFWDIK.S	11.53	4.01	2.87	0.35
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	R.TPLM*EAVVNNHLEVAR@.Y	11.77	5.51	2.14	0.47
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	K.VILM*LLDNLDPNFQSDQQSK#.R	2.35	3.66	0.64	1.56
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	K.VILM*LLDNLDPNFQSDQQSK#.R	11.05	4.68	2.36	0.42
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	R.GVSNDTSSLETER@.G	6.78	1.40	4.84	0.21
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	R.LDPHPELLPDLSSLPPINT.-	16.47	16.47	1.00	1.00
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	R.NK#EGDTAWDLTPER@.S	8.18	3.07	2.66	0.38
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	R.TPLM*EAVVNNHLEVAR@.Y	13.41	5.15	2.61	0.38
A2CG76_A2CG76_MOUSE	Ehmt2	Histone-lysine N-methylt	K.VILM*LLDNLDPNFQSDQQSK#.R	10.93	3.47	3.15	0.32
Q9CXU9_EIF1B_MOUSE	Eif1b	Eukaryotic translation in	K.TLTTVQGIADDYDK#.K	4.97	2.53	1.96	0.51
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	R.DLK#PGNIFLVDER@.H	32.93	22.57	1.46	0.69
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	K.GDFSNDIFDNK#.E	4.12	2.12	1.95	0.51
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	K.IGDFGLATALENDGK#.S	40.94	25.97	1.58	0.63
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	K.IGQTM*YGTGSGVTK#.Q	37.66	48.25	0.78	1.28
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	R.TGTLQYM*SPEQLFLK#.H	12.01	6.68	1.80	0.56
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	R.DLK#PGNIFLVDER@.H	38.62	14.02	2.75	0.36
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	K.DR@PETSEILK#.T	18.52	11.96	1.55	0.65
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	R.FTFQVLIDEK#EFPEAK#.G	9.05	4.98	1.82	0.55
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	K.IGDFGLATALENDGK#.S	30.21	14.17	2.13	0.47
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	K.IGQTM*YGTGSGVTK#.Q	13.40	23.25	0.58	1.73
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	R.TGTLQYM*SPEQLFLK#.H	11.32	4.49	2.52	0.40
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	R.DLK#PGNIFLVDER@.H	19.07	8.54	2.23	0.45
Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, dou	K.IGDFGLATALENDGK#.S	21.48	4.91	4.37	0.23

Q03963_E2AK2_MOUSE	Eif2ak2	Interferon-induced, doul	R.TGTLQYM*SPEQLFLK#.H	5.66	2.31	2.45	0.41
Q99LC8_EI2BA_MOUSE	Eif2b1	Translation initiation fac	K.ADLVIVGAEGVVENGGIINK#.I	4.97	1.57	3.17	0.32
Q99LC8_EI2BA_MOUSE	Eif2b1	Translation initiation fac	R.ANLTYAIK#.T	16.79	5.84	2.87	0.35
Q99LC8_EI2BA_MOUSE	Eif2b1	Translation initiation fac	K.AQNK#PFYVVAESFK#.F	16.67	9.58	1.74	0.57
Q99LC8_EI2BA_MOUSE	Eif2b1	Translation initiation fac	R.VLEEAVAAK#.K	39.37	17.54	2.25	0.45
Q99LC8_EI2BA_MOUSE	Eif2b1	Translation initiation fac	K.AQNK#PFYVVAESFK#.F	6.40	2.72	2.36	0.42
Q99LC8_EI2BA_MOUSE	Eif2b1	Translation initiation fac	R.FISLTSLEYSDYSK#.C	6.03	3.68	1.64	0.61
Q99LC8_EI2BA_MOUSE	Eif2b1	Translation initiation fac	K.AQNK#PFYVVAESFK#.F	15.03	3.78	3.97	0.25
Q99LC8_EI2BA_MOUSE	Eif2b1	Translation initiation fac	R.VLEEAVAAK#.K	21.25	9.32	2.28	0.44
Q99LD9_EI2BB_MOUSE	Eif2b2	Translation initiation fac	K.FVAPEEVLPFTEGDILEK#.V	30.34	15.48	1.96	0.51
Q99LD9_EI2BB_MOUSE	Eif2b2	Translation initiation fac	K.FVAPEEVLPFTEGDILEK#.V	24.91	14.53	1.71	0.58
Q99LD9_EI2BB_MOUSE	Eif2b2	Translation initiation fac	R.M*TAAQPSETTVGNM*VR@.R	19.69	11.72	1.68	0.60
Q99LD9_EI2BB_MOUSE	Eif2b2	Translation initiation fac	R.SDESDQQESLHK#.L	5.33	3.06	1.74	0.57
Q99LD9_EI2BB_MOUSE	Eif2b2	Translation initiation fac	K.FVAPEEVLPFTEGDILEK#.V	10.84	3.70	2.93	0.34
Q3UKV0_Q3UKV0_MOUSE	Eif2b3	Protein Eif2b3 OS=Mus m	R.SELIPYLVR@.K	15.03	10.09	1.49	0.67
Q3UKV0_Q3UKV0_MOUSE	Eif2b3	Protein Eif2b3 OS=Mus m	K.SLDIYSFIK#.K	11.26	6.33	1.78	0.56
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.AGVPTSYLLIPAASYVLPEVSK#.V	25.41	22.75	1.12	0.90
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.AGVPTSYLLIPAASYVLPEVSK.V	5.85	7.88	0.74	1.35
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	K.GADQEIGSAVSAAQR.Q	17.19	13.10	1.31	0.76
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	K.IVLAAQAISR@.F	23.96	21.12	1.13	0.88
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.LGLQYSQGLISGSNAR.C	20.32	8.41	2.42	0.41
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.VGTAQLALVAR@.A	15.12	7.80	1.94	0.52
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	K.VSLFSHLPQYSR@.Q	18.71	10.33	1.81	0.55
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.AGVPTSYLLIPAASYVLPEVSK#.V	23.97	9.86	2.43	0.41
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.AGVPTSYLLIPAASYVLPEVSK#.V	7.07	4.97	1.42	0.70
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	K.GADQEIGSAVSAAQR@.Q	10.87	6.57	1.65	0.60
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	K.IVLAAQAISR@.F	28.26	12.13	2.33	0.43
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.LGLQYSQGLISGSNAR@.C	10.04	6.52	1.54	0.65
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.VGTAQLALVAR@.A	13.39	8.20	1.63	0.61
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.AGVPTSYLLIPAASYVLPEVSK#.V	14.95	4.29	3.49	0.29
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.ELPGPGSQLGGTAGEK#.L	6.56	3.21	2.04	0.49
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	K.GADQEIGSAVSAAQR@.Q	10.66	5.90	1.81	0.55
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.LGLQYSQGLISGSNAR@.C	9.13	4.17	2.19	0.46
Q61749_EI2BD_MOUSE	Eif2b4	Translation initiation fac	R.VGTAQLALVAR@.A	16.84	6.07	2.78	0.36
Q8CHW4_EI2BE_MOUSE	Eif2b5	Translation initiation fac	R.VFQNEVLGTLQR@.G	20.14	11.06	1.82	0.55
Q8CHW4_EI2BE_MOUSE	Eif2b5	Translation initiation fac	R.VFQNEVLGTLQR@.G	10.54	3.72	2.84	0.35
Q6ZWX6_IF2A_MOUSE	Eif2s1	Eukaryotic translation in	R.ENAEVDGDDDAEEM*EAK#.A	6.94	2.48	2.80	0.36
Q6ZWX6_IF2A_MOUSE	Eif2s1	Eukaryotic translation in	R.EVLINNINR@.R	7.74	36.10	0.21	4.66
Q6ZWX6_IF2A_MOUSE	Eif2s1	Eukaryotic translation in	R.GVFNVQM*EPK#.V	11.59	7.92	1.46	0.68
Q6ZWX6_IF2A_MOUSE	Eif2s1	Eukaryotic translation in	R.LER@ENAEVDGDDDAEEM*EAK#.A	9.42	4.74	1.99	0.50
Q6ZWX6_IF2A_MOUSE	Eif2s1	Eukaryotic translation in	K.R@PGYGAYDAFK#.H	10.74	9.07	1.18	0.84
Q6ZWX6_IF2A_MOUSE	Eif2s1	Eukaryotic translation in	R.TEGLSVLNQAM*AVIK#.E	23.82	9.23	2.58	0.39
Q6ZWX6_IF2A_MOUSE	Eif2s1	Eukaryotic translation in	R.TEGLSVLNQAMAVIK#.E	8.94	5.37	1.66	0.60
Q6ZWX6_IF2A_MOUSE	Eif2s1	Eukaryotic translation in	K.VVTDTDETELAR.Q	99.74	52.57	1.90	0.53
Q6ZWX6_IF2A_MOUSE	Eif2s1	Eukaryotic translation in	R.YVM*TTTTLER@.T	17.92	11.18	1.60	0.62
Q99L45_IF2B_MOUSE	Eif2s2	Eukaryotic translation in	K.DASDDLDDLNFFNQK#.K	14.13	6.04	2.34	0.43
Q99L45_IF2B_MOUSE	Eif2s2	Eukaryotic translation in	R.DYTYEELLNR.V	38.26	23.61	1.62	0.62
Q99L45_IF2B_MOUSE	Eif2s2	Eukaryotic translation in	K.IESDAQEPAEPEDDLDIM*LGNK#K#.K	11.43	6.64	1.72	0.58
Q99L45_IF2B_MOUSE	Eif2s2	Eukaryotic translation in	R.K#K#DASDDLDDLNFFNQK#.K	13.02	1.24	10.49	0.10
Q99L45_IF2B_MOUSE	Eif2s2	Eukaryotic translation in	K.QIENVLR@.R	38.66	19.54	1.98	0.51
Q99L45_IF2B_MOUSE	Eif2s2	Eukaryotic translation in	R.SPDTILQK#.D	57.22	29.13	1.96	0.51
Q99L45_IF2B_MOUSE	Eif2s2	Eukaryotic translation in	K.TGFQAVTGK#.R	67.25	38.44	1.75	0.57
Q99L45_IF2B_MOUSE	Eif2s2	Eukaryotic translation in	R.VFNIM*R@.E	62.32	24.21	2.57	0.39
Q9Z0N1_IF2G_MOUSE	Eif2s3x	Eukaryotic translation in	K.HILILQNK#.I	22.66	9.99	2.27	0.44
Q9Z0N1_IF2G_MOUSE	Eif2s3x	Eukaryotic translation in	K.IVSLFAEHNDLQYAAPGGLIGVGTK#.I	27.13	12.97	2.09	0.48
Q9Z0N1_IF2G_MOUSE	Eif2s3x	Eukaryotic translation in	K.VGQEIEVR@PGIVSK#.D	70.39	39.31	1.79	0.56
Q9Z0N1_IF2G_MOUSE	Eif2s3x	Eukaryotic translation in	R.QDLATLDVTK#.L	11.64	4.28	2.72	0.37
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.AFK#DIDIEDLEELDPDFIM*AK#.Q	20.27	7.80	2.60	0.38
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.DIDIEDLEELDPDFIM*AK#.Q	16.72	6.72	2.49	0.40
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.EDAPVGPHLQSM*PSEQIR@.N	28.61	12.97	2.21	0.45
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.EQPEK#EPELQQYVPQLQNNTILR@.L	22.31	9.24	2.41	0.41
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.FSVLQYVVPEVK#.D	49.86	24.55	2.03	0.49
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.IGLINDM*VR@.F	30.57	10.93	2.80	0.36
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.ILQEHEQIK#.K	13.05	8.06	1.62	0.62
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.ITTM*QLER@.E	36.23	17.67	2.05	0.49
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.K#IDYFER@.A	37.17	12.84	2.89	0.35
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LEEIPLIK#.S	26.54	13.02	2.04	0.49
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LLDM*DGIIVEK#.Q	50.25	10.77	4.67	0.21
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LLLTPWVK#.F	44.73	14.70	3.04	0.33
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LLQQVAQIYQSIEFSR@.L	58.40	48.62	1.20	0.83
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LTSLVPFVDAFQLER@.A	99.18	34.71	2.86	0.35
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LVQLDSAISM*ELWQEAFK#.A	12.27	4.22	2.91	0.34
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.NQLTAM*SSVLAK#.A	26.14	10.42	2.51	0.40
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.TLSFGSDLNYATR@.E	47.94	17.27	2.78	0.36
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.VLLATLSIPITPER@.T	59.40	26.23	2.26	0.44
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.AFK#DIDIEDLEELDPDFIM*AK#.Q	52.16	11.94	4.37	0.23
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.ANEFLEVGK#.K	47.47	10.43	4.55	0.22
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.DIDIEDLEELDPDFIM*AK#.Q	29.60	8.44	3.51	0.29
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.DNQDR@EENDK#DLER@.D	6.47	1.44	4.49	0.22
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.EQPEK#EPELQQYVPQLQNNTILR@.L	56.99	18.91	3.01	0.33
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.FSVLQYVVPEVK#.D	95.40	27.19	3.51	0.29
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.GPAEESSSWR@.D	8.64	2.26	3.83	0.26
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.IGLINDM*VR@.F	64.78	13.51	4.80	0.21
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.ILQEHEQIK#.K	33.71	7.56	4.46	0.22
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.ITTM*QLER@.E	46.22	14.63	3.16	0.32
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.K#GPEADSEWR@.R	11.11	3.18	3.49	0.29
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.K#IDYFER@.A	34.41	15.50	2.22	0.45
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.K#QPALDVLYDVM*K#.S	13.52	5.15	2.63	0.38
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LATLLGLQAPPTR@.I	41.18	12.49	3.30	0.30
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LEEIPLIK#.S	50.00	13.57	3.69	0.27
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LESLNIQR@.E	96.34	20.59	4.68	0.21
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LLDM*DGIIVEK#.Q	52.90	15.46	3.42	0.29
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LLLTPWVK#.F	72.77	22.69	3.21	0.31
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LLQQVAQIYQSIEFSR@.L	94.31	25.29	3.73	0.27
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LTSLVPFVDAFQLER@.A	165.50	46.18	3.58	0.28
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.LVQLDSAISM*ELWQEAFK#.A	49.61	11.87	4.18	0.24
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.M*HLSQIQR@.H	26.97	6.13	4.40	0.23
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.NLTQEEM*QR@.M	44.23	13.22	3.35	0.30
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.NQLTAM*SSVLAK#.A	55.10	13.55	4.07	0.25
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.RLEEIPLIK.S	48.07	14.75	3.26	0.31
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.SGNALFHASTLHR@.L	28.95	6.17	4.70	0.21
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.TEAAK#EESQQM*VLDIEDLDNIQTPESVLLSAVSGEDTQDR@.T	11.32	2.11	5.36	0.19
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.TLSFGSDLNYATR@.E	108.08	31.74	3.41	0.29

P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.VK#DM*DLWEQQEEER@.I	20.72	3.85	5.38	0.19
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	R.VLLATLSIPITPER@.T	120.66	33.04	3.65	0.27
P23116_EIF3A_MOUSE	Eif3a	Eukaryotic translation in	K.VSTVFWK#.S	46.82	12.36	3.79	0.26
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.AEAVGEQAR@.G	37.11	11.82	3.14	0.32
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.AK#PAAQSEEETATSPAASPTPQSAER@.S	55.80	23.18	2.41	0.42
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.DQYSVIFESGDR@.T	36.74	10.67	3.44	0.29
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.DR@PQEADGIDSVIVVDNVPQVGPDR@.L	71.66	17.46	4.10	0.24
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.DR@PQEADGIDSVIVVDNVPQVGPDR@LEK#.L	12.20	3.24	3.76	0.27
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.ETIIAFAWEPNGSK#.F	11.06	4.86	2.28	0.44
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.GHPSAGAEEEGGSDGSAAEAEPR@.A	53.71	16.33	3.29	0.30
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.GIALWGGDK#.F	30.26	12.39	2.44	0.41
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.GTQGVVTNFEIFR@.M	194.56	50.70	3.84	0.26
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.GYIFLEYASPAHAVDAVK#.N	179.34	42.84	4.19	0.24
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.IINDYYPEEDGK#.T	21.54	6.19	3.48	0.29
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.M*AQELYM*K#.Q	32.53	11.49	2.83	0.35
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.M*TLDTLSIYETPSMGLLDK#K#.S	6.36	2.12	3.00	0.33
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.NADGYK#LDK#.Q	37.96	38.81	0.98	1.02
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.QQANTIFWSPQGQFVVLAGLR@.S	20.35	3.80	5.35	0.19
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.SPSQEPSAPGK#.A	52.42	18.62	2.81	0.36
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.SPSQEPSAPGK#AEAVGEQAR@.G	57.55	15.73	3.66	0.27
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.TM*M*EDFR@.Q	96.37	29.50	3.27	0.31
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.TSIFWNDVK#DPVSIEER@.A	142.40	38.76	3.67	0.27
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.VDNAYWLWTFQGR.L	43.14	11.17	3.86	0.26
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.VNLFTDFDK#.Y	19.95	5.87	3.40	0.29
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.VNLFTDFDK#YM*TISDEWDIPEK#.Q	13.91	3.64	3.82	0.26
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.VTLM*QLPTR@.Q	91.96	30.37	3.03	0.33
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.VTLMQLPTR@.Q	33.04	11.61	2.84	0.35
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.WTETYVR@.W	91.11	24.43	3.73	0.27
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.AK#PAAQSEEETATSPAASPTPQSAER@.S	11.64	2.43	4.80	0.21
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.DR@PQEADGIDSVIVVDNVPQVGPDR@.L	13.65	5.68	2.40	0.42
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.GHPSAGAEEEGGSDGSAAEAEPR@.A	19.23	12.23	1.57	0.64
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.GTQGVVTNFEIFR@.M	28.23	5.66	4.99	0.20
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	K.GYIFLEYASPAHAVDAVK#.N	46.72	10.24	4.56	0.22
Q8JZQ9_EIF3B_MOUSE	Eif3b	Eukaryotic translation in	R.TSIFWNDVK#DPVSIEER@.A	16.81	7.11	2.37	0.42
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	R.AK#ELLGQGLLLR@.S	44.62	12.43	3.59	0.28
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	R.DLM*LM*SHLQDNIQHADPPVQILYNR@.T	8.07	4.09	1.97	0.51
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.ELLGQGLLLR@.S	29.16	9.61	3.03	0.33
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	R.FEELTNLIR@.T	57.47	17.06	3.37	0.30
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.LGSLVENNER@.V	40.89	5.22	7.84	0.13
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.LNEILQVR@.G	30.42	10.62	2.86	0.35
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.QGTYGGYFR@.D	20.73	6.71	3.09	0.32
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	R.QPLLGPPESM*R@.E	7.67	3.48	2.20	0.45
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.SEQDQAENEGEDSAVLM*ER@.L	19.22	5.77	3.33	0.30
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	R.TEPTAQQNLALQLAEK#.L	32.74	10.77	3.04	0.33
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.VWDLFPEADK#VR@.T	22.14	6.42	3.45	0.29
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	R.AK#ELLGQGLLLR@.S	65.21	19.81	3.29	0.30
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.DAHNALLDIQSSGR@.A	59.46	15.65	3.80	0.26
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.ELLGQGLLLR@.S	56.15	11.14	5.04	0.20
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	R.FEELTNLIR@.T	84.30	21.46	3.93	0.25
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	R.FFTTGSDSESESSLSGEELVTK#PVSGNYGK#.Q	11.87	1.65	7.17	0.14
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.LGSLVENNER@.V	46.99	16.48	2.85	0.35
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.R@LDEEEEDNEGGEWER@.V	20.26	5.41	3.75	0.27
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.SEQDQAENEGEDSAVLM*ER@.L	33.95	11.85	2.86	0.35
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	K.SIVDK#EGVPR@.F	16.34	5.21	3.14	0.32
Q8R1B4_EIF3C_MOUSE	Eif3c	Eukaryotic translation in	R.TEPTAQQNLALQLAEK#.L	48.59	14.87	3.27	0.31
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.DNSDFDLLTVSETANEPPQDEGNSFNSPR@.N	7.38	1.55	4.76	0.21
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.IFHTVTTTDDPVIR@.K	20.78	11.31	1.84	0.54
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.NM*VQFNLQTLPK#.S	14.40	7.89	1.82	0.55
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.YNFPNPNPFVEDDM*DK#NEIASVAYR@.Y	9.15	3.56	2.57	0.39
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	K.YSSQFGGGSQYAYFHEEDETSFQLVDTAR@.T	5.35	1.83	2.93	0.34
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.IFHTVTTTDDPVIR@.K	53.12	20.25	2.62	0.38
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	K.LGDDIDLIVR@.C	39.04	14.36	2.72	0.37
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.NM*VQFNLQTLPK#.S	48.62	21.48	2.26	0.44
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.SVYSWDIVVQR@.V	33.93	12.57	2.70	0.37
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	K.TLNEWDSR@.H	19.72	9.91	1.99	0.50
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	K.VADWTGATYQDK#.R	8.61	8.29	1.04	0.96
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	K.YSSQFGGGSQYAYFHEEDETSFQLVDTAR@.T	10.79	5.30	2.04	0.49
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.DNSDFDLLTVSETANEPPQDEGNSFNSPR@.N	15.68	2.80	5.61	0.18
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.IFHTVTTTDDPVIR@.K	36.46	8.08	4.51	0.22
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	K.LGDDIDLIVR@.C	28.34	11.05	2.56	0.39
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.NM*VQFNLQTLPK#.S	29.08	8.83	3.29	0.30
O70194_EIF3D_MOUSE	Eif3d	Eukaryotic translation in	R.SVYSWDIVVQR@.V	21.15	5.98	3.54	0.28
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LASEILM*QNWDAAM*EDLTR@.L	8.20	7.90	1.04	0.96
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LASEILM*QNWDAAM*EDLTR@.L	2.95	1.98	1.49	0.67
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LASEILM*QNWDAAMEDLTR@.L	5.68	2.74	2.07	0.48
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LDLLSDTNM*VDFAM*DVYK#.N	18.31	8.85	2.07	0.48
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LGHVVM*GNNAVSPYQQVIEK#.T	37.53	18.75	2.00	0.50
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.LK#ETIDNNSVSSPLQSLQQR@.T	58.91	18.82	3.13	0.32
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LNM*TPEEAER@.W	13.06	238.91	0.05	18.30
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.M*FEDPETTR@.Q	25.55	9.83	2.60	0.38
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.M*LFDYLADK#.H	49.42	14.45	3.42	0.29
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.NALSSLWGK#.L	30.92	11.13	2.78	0.36
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.QEYLDTLYR@.Y	34.80	13.39	2.60	0.38
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.QLQAETEPIVK#.M	59.05	24.12	2.45	0.41
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.SEAPNWATQDSGFY.-	7.56	7.56	1.00	1.00
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.TTVVAQLK#.Q	45.57	13.29	3.43	0.29
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.WIVNLIR@.N	22.83	5.43	4.21	0.24
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.YLTTAVITNK#.D	72.10	22.57	3.20	0.31
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LDLLSDTNM*VDFAM*DVYK#.N	11.98	2.92	4.11	0.24
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LGHVVM*GNNAVSPYQQVIEK#.T	26.79	7.42	3.61	0.28
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.LKETIDNNSVSSPLQSLQQR.T	29.83	5.99	4.98	0.20
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.M*FEDPETTR@.Q	14.45	2.90	4.98	0.20
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.NALSSLWGK#.L	19.73	9.17	2.15	0.46
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.QLQAETEPIVK#.M	34.22	9.12	3.75	0.27
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.SEAPNWATQDSGFY.-	6.50	6.50	1.00	1.00
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.SQM*LAM*NIEK#.K	13.78	4.96	2.78	0.36
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.WIVNLIR@.N	17.85	5.18	3.45	0.29
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.YLTTAVITNK#.D	39.04	7.08	5.52	0.18
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LASEILM*QNWDAAM*EDLTR@.L	5.18	1.25	4.13	0.24
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LDLLSDTNM*VDFAM*DVYK#.N	9.80	5.59	1.75	0.57
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.LDLLSDTNM*VDFAM*DVYK#.N	5.76	1.92	3.01	0.33
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.LK#ETIDNNSVSSPLQSLQQR@.T	28.70	8.02	3.58	0.28
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.M*FEDPETTR@.Q	13.53	6.14	2.20	0.45

P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.M*LFDYLADK#.H	18.79	6.40	2.93	0.34
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.NALSSLWGK#.L	24.99	5.65	4.42	0.23
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	K.QLQAETEPIVK#.M	32.31	9.92	3.26	0.31
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.SEAPNWATQDSGFY.-	5.51	5.51	1.00	1.00
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.TTVVAQLK#.Q	56.81	15.92	3.57	0.28
P60229_EIF3E_MOUSE	Eif3e	Eukaryotic translation in	R.YLTTAVITNK#.D	42.70	14.21	3.00	0.33
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	K.AYVSTLM*GVPGR@.T	87.93	34.01	2.59	0.39
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	K.AYVSTLMGVPGR@.T	8.21	2.42	3.39	0.30
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.FLM*SLVNQVPK#.I	45.92	20.89	2.20	0.45
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.IGVDLIM*K#.T	62.50	26.98	2.32	0.43
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.LHPVILASIVDSYER@.R	111.08	41.17	2.70	0.37
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.TM*GVM*FTPLTVK#.Y	51.11	20.52	2.49	0.40
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.TMGVM*FTPLTVK#.Y	7.63	2.30	3.31	0.30
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.TM*GVMFTPLTVK#.Y	10.80	3.93	2.74	0.36
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.VIGLSSDLQQVGGASAR@.I	131.17	48.43	2.71	0.37
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.VIGTLLGTVDK#.H	115.79	37.63	3.08	0.32
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	K.VSADNTVGR@.F	56.84	18.78	3.03	0.33
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	K.YAYYDTER@.I	44.75	14.24	3.14	0.32
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	K.AYVSTLM*GVPGR@.T	20.70	6.01	3.44	0.29
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.FLM*SLVNQVPK#.I	10.68	3.81	2.81	0.36
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.LHPVILASIVDSYER@.R	27.64	11.05	2.50	0.40
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.TM*GVM*FTPLTVK#.Y	15.08	3.47	4.35	0.23
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.VIGLSSDLQQVGGASAR@.I	26.15	7.60	3.44	0.29
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.VIGTLLGTVDK#.H	36.89	8.94	4.13	0.24
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	K.AYVSTLM*GVPGR@.T	21.60	3.86	5.60	0.18
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.IGVDLIM*K#.T	12.32	1.72	7.14	0.14
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.LHPVILASIVDSYER@.R	32.16	7.67	4.19	0.24
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.TM*GVM*FTPLTVK#.Y	11.36	2.78	4.08	0.25
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.VIGLSSDLQQVGGASAR@.I	30.93	4.96	6.23	0.16
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	R.VIGTLLGTVDK#.H	17.48	3.18	5.50	0.18
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	K.VSADNTVGR@.F	15.14	10.02	1.51	0.66
Q9DCH4_EIF3F_MOUSE	Eif3f	Eukaryotic translation in	K.YAYYDTER@.I	9.37	2.56	3.67	0.27
Q9Z1D1_EIF3G_MOUSE	Eif3g	Eukaryotic translation in	K.EK#LPGELEPVQAAQSK#.T	48.81	13.55	3.60	0.28
Q9Z1D1_EIF3G_MOUSE	Eif3g	Eukaryotic translation in	K.ELAEQLGLSTGEK#.E	73.56	17.99	4.09	0.24
Q9Z1D1_EIF3G_MOUSE	Eif3g	Eukaryotic translation in	K.ELAEQLGLSTGEK#EK#LPGELEPVQAAQSK#.T	6.12	1.99	3.07	0.33
Q9Z1D1_EIF3G_MOUSE	Eif3g	Eukaryotic translation in	R.ETDLQELFR@PFGSISR@.I	170.20	46.95	3.63	0.28
Q9Z1D1_EIF3G_MOUSE	Eif3g	Eukaryotic translation in	K.FGNSEFDPPGPNVATTTVSDDVSM*TFITSK#.E	5.34	2.75	1.94	0.52
Q9Z1D1_EIF3G_MOUSE	Eif3g	Eukaryotic translation in	K.K#FGNSEFDPPGPNVATTTVSDDVSM*TFITSK#.E	3.57	2.48	1.44	0.70
Q9Z1D1_EIF3G_MOUSE	Eif3g	Eukaryotic translation in	R.R@ADDNATIR@.V	15.08	4.01	3.76	0.27
Q9Z1D1_EIF3G_MOUSE	Eif3g	Eukaryotic translation in	R.VTNLSEDTR@.E	112.06	30.74	3.65	0.27
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	R.ALLDSQFSYQHAIEESVVLIYDPIK#.T	45.80	14.65	3.13	0.32
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.ASITFEHM*FEEVPIVIK#.N	80.01	25.53	3.13	0.32
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.ASITFEHMFEEVPIVIK#.N	48.07	17.73	2.71	0.37
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.EGTGSTATSSGSAGGAVGK#.G	148.42	48.66	3.05	0.33
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.HYQEEGQGTEVVQGVLLGLVVEDR@.L	37.40	10.85	3.45	0.29
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	R.K#EGTGSTATSSGSAGGAVGK#.G	4.45	2.75	1.61	0.62
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.LFM*AQALQEYNN.-	57.20	57.20	1.00	1.00
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.NSHLINVLM*WELEK#.K	5.50	8.40	0.65	1.53
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.NSHLINVLM*WELEK#K#.S	7.83	3.74	2.09	0.48
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.QVQIDGLVVLK#.I	54.14	16.94	3.20	0.31
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.SLQLLM*DR@.V	19.22	9.60	2.00	0.50
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.SLQLLM*DR@VDEMSQDIIK#.Y	6.05	2.88	2.10	0.48
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.SLQLLMDR@VDEMSQDIIK#.Y	11.15	2.74	4.07	0.25
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.TAQGSLSLK#.A	114.80	36.75	3.12	0.32
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	R.VDEM*SQDIIK#.Y	40.83	13.97	2.92	0.34
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.HYQEEGQGTEVVQGVLLGLVVEDR@.L	3.68	3.15	1.17	0.85
Q91WK2_EIF3H_MOUSE	Eif3h	Eukaryotic translation in	K.EGTGSTATSSGSAGGAVGK#.G	12.00	2.89	4.15	0.24
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	R.DM*TM*FVTASK#.D	39.68	14.17	2.80	0.36
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	R.DPSQIDSNEPYM*K#.I	7.85	1.37	5.71	0.18
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	R.EGDLLFTVAK#.D	25.61	13.03	1.97	0.51
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	R.EGDLLFTVAK#DPIVNVWYSVNGER@.L	16.21	4.76	3.41	0.29
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	R.FFHLAFEEEFGR@.V	37.38	12.09	3.09	0.32
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	K.GHFGPINSVAFHPDGK#.S	51.14	18.75	2.73	0.37
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	R.IHYFDPQYFEFEFEA.-	7.38	7.38	1.00	1.00
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	K.LFDSTTLEHQK#.T	118.07	40.39	2.92	0.34
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	-.M*K#PILLQGHER@.S	58.48	22.03	2.65	0.38
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	R.QINDIQLSR@.D	43.17	16.61	2.60	0.38
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	K.SYSSGGEDGYVR@.I	132.27	40.32	3.28	0.30
Q9QZD9_EIF3I_MOUSE	Eif3i	Eukaryotic translation in	R.TERPVNSAALSPNYDHVVLGGGQEAM*DVTTTSTR.I	32.50	11.66	2.79	0.36
Q3UGC7_EI3JA_MOUSE	Eif3j1	Eukaryotic translation in	K.ATM*K#DDLADYGGYEGGYVQDYEDFM*.-	8.40	4.75	1.77	0.57
Q3UGC7_EI3JA_MOUSE	Eif3j1	Eukaryotic translation in	K.ETFGVNNTVYGIDAM*NPSSR@.D	7.56	4.59	1.65	0.61
Q3UGC7_EI3JA_MOUSE	Eif3j1	Eukaryotic translation in	K.ETFGVNNTVYGIDAM*NPSSR@DDFTEFGK#.L	8.23	4.64	1.78	0.56
Q3UGC7_EI3JA_MOUSE	Eif3j1	Eukaryotic translation in	K.K#LQEESDLELAK#.E	12.93	5.62	2.30	0.43
Q3UGC7_EI3JA_MOUSE	Eif3j1	Eukaryotic translation in	K.LQEESDLELAK#.E	68.50	38.99	1.76	0.57
Q3UGC7_EI3JA_MOUSE	Eif3j1	Eukaryotic translation in	K.LQEESDLELAK#ETFGVNNTVYGIDAM*NPSSR@.D	8.65	6.20	1.40	0.72
Q9DBZ5_EIF3K_MOUSE	Eif3k	Eukaryotic translation in	K.ENAYDLEANLAVLK#.L	71.77	20.47	3.51	0.29
Q9DBZ5_EIF3K_MOUSE	Eif3k	Eukaryotic translation in	K.GIDRYNPENLATLER.Y	36.84	9.13	4.03	0.25
Q9DBZ5_EIF3K_MOUSE	Eif3k	Eukaryotic translation in	R.YNPENLATLER.Y	66.60	21.19	3.14	0.32
Q9DBZ5_EIF3K_MOUSE	Eif3k	Eukaryotic translation in	K.ENAYDLEANLAVLK#.L	14.82	7.14	2.07	0.48
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.LAGFLDLTEQEFR@.I	9.31	2.88	3.24	0.31
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.VFSDEVQQQAQLSTIR@.S	4.50	2.02	2.23	0.45
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.IQLLVFK#.H	84.95	29.27	2.90	0.34
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.K#SEGEM*DFLR@.S	31.29	12.24	2.56	0.39
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.LAGFLDLTEQEFR@.I	104.61	30.34	3.45	0.29
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.LHSLLGDYYQAIK#.V	35.46	10.06	3.52	0.28
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.LYTTM*PVAK#.L	51.06	19.84	2.57	0.39
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.M*LGYFSLVGLLR@.L	46.96	11.89	3.95	0.25
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.QDLAYER@.Q	43.51	15.25	2.85	0.35
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.QLEVYTSGGDPESVAGEYGR@.H	25.71	8.07	3.19	0.31
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.QYEQQTYQVIPEVIK#.N	12.17	4.35	2.80	0.36
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.R@YGDFFIR@.Q	26.54	9.59	2.77	0.36
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.SEGEM*DFLR@.S	10.88	3.63	2.99	0.33
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.TVSDLIDQK#.V	44.72	13.78	3.25	0.31
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.VFSDEVQQQAQLSTIR@.S	55.42	18.25	3.04	0.33
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.VSGGPSLEQR@.F	95.74	29.44	3.25	0.31
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.VSSDVIDQK#.V	72.72	23.18	3.14	0.32
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.VYEIQDIYENSWTK#.L	37.42	11.74	3.19	0.31
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.VYELQASR@.V	51.29	16.81	3.05	0.33
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.YGDFFIR@.Q	30.41	10.94	2.78	0.36
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.EPFLQQLK#.V	12.01	3.91	3.07	0.33
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.IQLLVFK#.H	59.31	22.23	2.67	0.37
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.LAGFLDLTEQEFR@.I	77.48	23.27	3.33	0.30
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.LHSLLGDYYQAIK#.V	39.42	10.86	3.63	0.28

Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.M*LGYFSLVGLLR@.L	24.46	3.83	6.38	0.16
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.QDLAYER@.Q	37.55	9.22	4.07	0.25
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.QLEVYTSGGDPESVAGEYGR@.H	16.42	5.55	2.96	0.34
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.QYEQQTYQVIPEVIK#.N	11.41	3.47	3.29	0.30
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.SEGEM*DFLR@.S	9.21	3.87	2.38	0.42
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.TVSDLIDQK#.V	26.92	3.04	8.86	0.11
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.VFSDEVQQQAQLSTIR@.S	45.71	12.48	3.66	0.27
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.VSGGPSLEQR@.F	93.40	26.76	3.49	0.29
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.VSSDVIDQK#.V	49.40	21.67	2.28	0.44
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.VYEIQDIYENSWTK#.L	24.53	7.06	3.47	0.29
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	K.VYELQASR@.V	46.98	15.61	3.01	0.33
Q8QZY1_EIF3L_MOUSE	Eif3l	Eukaryotic translation in	R.YGDFFIR@.Q	27.51	7.02	3.92	0.26
Q99JX4_EIF3M_MOUSE	Eif3m	Eukaryotic translation in	R.ALK#DPNAFLFDHLLTLK#PVK#.F	69.46	13.90	5.00	0.20
Q99JX4_EIF3M_MOUSE	Eif3m	Eukaryotic translation in	R.LLTFM*GM*AVENK#.E	60.34	14.74	4.09	0.24
Q99JX4_EIF3M_MOUSE	Eif3m	Eukaryotic translation in	K.QQWQQLYDTLNAWK#.Q	14.77	4.26	3.46	0.29
Q99JX4_EIF3M_MOUSE	Eif3m	Eukaryotic translation in	K.VM*VELLGSYTEDNASQAR@.V	17.21	6.95	2.48	0.40
Q99JX4_EIF3M_MOUSE	Eif3m	Eukaryotic translation in	K.VM*VELLGSYTEDNASQAR.V	25.18	9.04	2.79	0.36
Q99JX4_EIF3M_MOUSE	Eif3m	Eukaryotic translation in	K.VMVELLGSYTEDNASQAR@.V	8.86	2.56	3.46	0.29
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.ATQALVLAPTR@.E	243.66	103.15	2.36	0.42
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.DFTVSAM*HGDM*DQK#.E	30.90	14.23	2.17	0.46
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.DIETFYNTSIEEM*PLNVADLI.-	80.82	80.82	1.00	1.00
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.DQIYDIFQK#.L	49.80	26.56	1.88	0.53
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.EELTLEGIR@.Q	138.23	56.56	2.44	0.41
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.ELAQQIQK#.V	645.24	236.14	2.73	0.37
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GFKDQIYDIFQK.L	398.42	176.03	2.26	0.44
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GIDVQQVSLVINYDLPTNR@.E	97.52	38.58	2.53	0.40
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GIYAYGFEK#PSAIQQR@.A	1018.68	397.71	2.56	0.39
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.GYDVIAQAQSGTGK#.T	435.58	199.81	2.18	0.46
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.K#GVAINMVTEEDK#R@.T	76.94	29.17	2.64	0.38
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.K#VDWLTEK#.M	368.68	180.05	2.05	0.49
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATM*PSDVLEVTK#.K	88.28	33.03	2.67	0.37
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATMPSDVLEVTK#.K	9.73	3.73	2.61	0.38
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATMPSDVLEVTK#.K	30.55	18.58	1.64	0.61
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATM*PSDVLEVTK#K#.F	61.77	24.24	2.55	0.39
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATMPSDVLEVTK#K#.F	32.73	14.36	2.28	0.44
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LQM*EAPHIIVGTPGR@.V	438.90	201.92	2.17	0.46
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.M*FVLDEADEM*LSR@.G	327.81	130.45	2.51	0.40
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.MFVLDEADEM*LSR@.G	50.56	24.64	2.05	0.49
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.M*FVLDEADEMLSR@.G	39.01	20.67	1.89	0.53
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.MFVLDEADEMLSR@.G	22.65	7.83	2.89	0.35
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.QFYINVER.E	244.15	100.48	2.43	0.41
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.R@K#VDWLTEK#.M	259.83	120.24	2.16	0.46
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.VFDM*LNR@.R	99.79	42.67	2.34	0.43
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.VFDMLNR.R	30.75	16.81	1.83	0.55
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.VLITTDLLAR.G	1416.08	585.24	2.42	0.41
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.ATQALVLAPTR@.E	7.08	5.46	1.30	0.77
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GIYAYGFEK#PSAIQQR@.A	33.39	13.77	2.42	0.41
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.GYDVIAQAQSGTGK#.T	13.40	6.41	2.09	0.48
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.VLITTDLLAR@.G	41.50	10.95	3.79	0.26
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.ATQALVLAPTR@.E	90.41	33.05	2.74	0.37
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.DQIYDIFQK#.L	21.82	10.37	2.10	0.48
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.EELTLEGIR@.Q	34.78	12.19	2.85	0.35
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.ELAQQIQK#.V	181.78	51.28	3.54	0.28
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GFK#DQIYDIFQK#.L	52.83	10.41	5.07	0.20
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GFKDQIYDIFQK.L	100.37	27.46	3.66	0.27
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GIDVQQVSLVINYDLPTNR@.E	48.74	35.94	1.36	0.74
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GIYAYGFEK#PSAIQQR@.A	220.48	59.19	3.73	0.27
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.GYDVIAQAQSGTGK#.T	125.75	37.50	3.35	0.30
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.K#EELTLEGIR@.Q	120.99	29.54	4.10	0.24
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.K#VDWLTEK#.M	65.08	21.76	2.99	0.33
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATM*PSDVLEVTK#.K	24.58	8.95	2.75	0.36
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATM*PSDVLEVTK#.K	5.81	2.27	2.56	0.39
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATM*PSDVLEVTK#K#.F	20.21	4.49	4.50	0.22
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LQM*EAPHIIVGTPGR@.V	154.83	49.94	3.10	0.32
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.M*FVLDEADEM*LSR@.G	107.62	35.81	3.01	0.33
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.MFVLDEADEM*LSR@.G	9.27	3.62	2.56	0.39
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.QFYINVER.E	65.99	21.01	3.14	0.32
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.VDWLTEK#.M	20.51	8.33	2.46	0.41
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.VFDM*LNR@.R	32.77	8.68	3.78	0.26
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.VLITTDLLAR@.G	402.18	127.81	3.15	0.32
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.ATQALVLAPTR@.E	63.28	14.17	4.46	0.22
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.DFTVSAM*HGDM*DQK#.E	11.67	3.74	3.12	0.32
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.DQIYDIFQK#.L	34.74	11.55	3.01	0.33
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.EELTLEGIR@.Q	50.47	12.95	3.90	0.26
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.ELAQQIQK#.V	294.42	54.29	5.42	0.18
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GFK#DQIYDIFQK#.L	115.52	22.75	5.08	0.20
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GIDVQQVSLVINYDLPTNR@.E	91.98	26.30	3.50	0.29
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.GIYAYGFEK#PSAIQQR@.A	253.18	63.31	4.00	0.25
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.GYDVIAQAQSGTGK#.T	164.14	46.19	3.55	0.28
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.K#GVAINMVTEEDK#R@.T	18.49	7.29	2.54	0.39
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.K#VDWLTEK#.M	66.72	15.68	4.26	0.24
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATM*PSDVLEVTK#.K	41.21	9.45	4.36	0.23
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATM*PSDVLEVTK#K#.F	29.43	6.78	4.34	0.23
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LNSNTQVVLLSATMPSDVLEVTK#K#.F	9.56	3.47	2.75	0.36
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.LQM*EAPHIIVGTPGR@.V	190.85	46.73	4.08	0.24
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.M*FVLDEADEM*LSR@.G	128.92	31.63	4.08	0.25
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	K.MFVLDEADEM*LSR@.G	13.22	4.50	2.94	0.34
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.QFYINVER@.E	75.33	17.69	4.26	0.23
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.VFDM*LNR@.R	37.50	10.58	3.55	0.28
P60843_IF4A1_MOUSE	Eif4a1	Eukaryotic initiation fact	R.VLITTDLLAR@.G	421.33	106.33	3.96	0.25
P10630_IF4A2_MOUSE	Eif4a2	Eukaryotic initiation fact	R.DFTVSALHGDM*DQK#.E	5.61	2.23	2.52	0.40
P10630_IF4A2_MOUSE	Eif4a2	Eukaryotic initiation fact	K.EELTLEGIK#.Q	8.07	3.68	2.19	0.46
P10630_IF4A2_MOUSE	Eif4a2	Eukaryotic initiation fact	K.ETQALVLAPTR@.E	22.53	8.43	2.67	0.37
P10630_IF4A2_MOUSE	Eif4a2	Eukaryotic initiation fact	R.GFK#DQIYEIFQK#.L	39.08	14.70	2.66	0.38
P10630_IF4A2_MOUSE	Eif4a2	Eukaryotic initiation fact	K.K#EELTLEGIK#.Q	19.59	8.47	2.31	0.43
P10630_IF4A2_MOUSE	Eif4a2	Eukaryotic initiation fact	R.K#GVAINFVTEEDK#R@.I	82.98	34.06	2.44	0.41
P10630_IF4A2_MOUSE	Eif4a2	Eukaryotic initiation fact	K.LNTSIQVVLLSATM*PTDVLEVTK#.K	5.79	2.00	2.90	0.34
P10630_IF4A2_MOUSE	Eif4a2	Eukaryotic initiation fact	R.GFK#DQIYEIFQK#.L	11.31	1.79	6.33	0.16
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.DELTLEGIK#.Q	106.99	43.46	2.46	0.41
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.DIEQYYSTQIDEM*PM*NVADLI.-	80.36	80.36	1.00	1.00
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.DVIAQSQSGTGK#.T	212.20	91.78	2.31	0.43
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.ELAVQIQK#.G	643.43	294.07	2.19	0.46
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.EQIYDVYR@.Y	288.77	110.87	2.60	0.38

Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.ETQALILAPTR@.E	485.90	1049.26	0.46	2.16
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.FM*TDPIR@.I	425.90	193.01	2.21	0.45
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.GFK#EQIYDVYR@.Y	137.95	56.60	2.44	0.41
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.GFKEQIYDVYR.Y	46.23	19.87	2.33	0.43
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.GR@DVIAQSQSGTGK#.T	37.34	19.92	1.88	0.53
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.GVAINFVK#.N	102.54	50.92	2.01	0.50
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.KGVAINFVK.N	348.14	171.83	2.03	0.49
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.K#LDYGQHVVAGTPGR@.V	349.12	146.87	2.38	0.42
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.LDYGQHVVAGTPGR@.V	386.70	167.59	2.31	0.43
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.LDYGQHVVAGTPGR.V	19.55	9.41	2.08	0.48
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.M*LVLDEADEM*LNK#.G	191.39	90.09	2.12	0.47
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.MLVLDEADEM*LNK#.G	18.02	5.65	3.19	0.31
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.M*LVLDEADEMLNK#.G	28.62	10.13	2.83	0.35
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.MLVLDEADEMLNK#.G	16.53	11.02	1.50	0.67
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.QFFVAVER.E	223.88	91.39	2.45	0.41
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.R@DELTLEGIK#.Q	197.94	81.83	2.42	0.41
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.VEFETSEEVDVTPTFDTM*GLR.E	8.10	4.99	1.62	0.62
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.VEFETSEEVDVTPTFDTM*GLR@EDLLR@.G	14.37	5.91	2.43	0.41
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.VLISTDVWAR@.G	396.35	155.99	2.54	0.39
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.DELTLEGIK#.Q	8.56	17.26	0.50	2.02
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.DIEQYYSTQIDEM*PM*NVADLI.-	9.91	9.91	1.00	1.00
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.DIEQYYSTQIDEM*PM*NVADLI.-	3.38	3.38	1.00	1.00
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.ELAVQIQK#.G	46.63	16.67	2.80	0.36
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.EQIYDVYR@.Y	27.83	10.84	2.57	0.39
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.ETQALILAPTR@.E	50.42	21.07	2.39	0.42
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.FM*TDPIR.I	52.97	16.10	3.29	0.30
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.GFK#EQIYDVYR@.Y	14.90	6.04	2.47	0.41
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.K#GVAINFVK#.N	34.66	12.67	2.74	0.37
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.K#LDYGQHVVAGTPGR@.V	38.22	13.82	2.77	0.36
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.M*LVLDEADEM*LNK#.G	21.95	8.64	2.54	0.39
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.QFFVAVER@.E	22.44	8.16	2.75	0.36
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.VLISTDVWAR@.G	42.16	12.79	3.30	0.30
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.DIEQYYSTQIDEM*PM*NVADLI.-	3.49	3.49	1.00	1.00
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.DVIAQSQSGTGK#.T	13.49	1.41	9.58	0.10
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.ELAVQIQK#.G	51.91	9.36	5.55	0.18
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.ETQALILAPTR@.E	54.95	16.40	3.35	0.30
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.FM*TDPIR@.I	46.32	11.22	4.13	0.24
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.GR@DVIAQSQSGTGK#.T	11.80	2.54	4.65	0.21
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.GVAINFVK#.N	15.25	5.32	2.87	0.35
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.K#GVAINFVK#.N	39.00	9.20	4.24	0.24
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.M*LVLDEADEM*LNK#.G	28.78	8.08	3.56	0.28
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.QFFVAVER@.E	23.17	7.87	2.94	0.34
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	K.R@DELTLEGIK#.Q	39.31	4.32	9.10	0.11
Q91VC3_IF4A3_MOUSE	Eif4a3	Eukaryotic initiation fact	R.VLISTDVWAR@.G	32.06	7.17	4.47	0.22
Q8BGD9_IF4B_MOUSE	Eif4b	Eukaryotic translation in	R.SQSSDTEQPSPTSGGGK#.V	4.08	3.29	1.24	0.80
Q8BMB3_IF4E2_MOUSE	Eif4e2	Eukaryotic translation in	R.FQEDIISIWNK#.T	40.13	12.26	3.27	0.31
Q8BMB3_IF4E2_MOUSE	Eif4e2	Eukaryotic translation in	K.QIGTFASVEQFWK#.F	21.59	2.33	9.25	0.11
Q8BMB3_IF4E2_MOUSE	Eif4e2	Eukaryotic translation in	K.TASDQATTAR@.I	7.43	4.64	1.60	0.62
Q8BMB3_IF4E2_MOUSE	Eif4e2	Eukaryotic translation in	R.TPGR@PTSSQSYEQNIK#.Q	35.84	11.31	3.17	0.32
Q8BMB3_IF4E2_MOUSE	Eif4e2	Eukaryotic translation in	R.VLNLPPNTIM*EYK#.T	12.85	5.30	2.42	0.41
Q9EST3_4ET_MOUSE	Eif4enif1	Eukaryotic translation in	K.VDLK#PLLSSLSANK#.E	7.81	1.97	3.96	0.25
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.EFLAEGQDVGSFVAEK#.K	14.50	7.61	1.90	0.53
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.GGPGGELPR@.G	15.48	10.80	1.43	0.70
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.GLPLVDDGGWNTVPISK#.G	9.34	6.82	1.37	0.73
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.GVIDLIFEK#.A	13.21	8.35	1.58	0.63
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.IISSVIM*TEDIK#.L	11.06	3.82	2.90	0.35
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.K#VEYTLGEESEAPGQR@.T	9.02	7.76	1.16	0.86
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.M*DQYFNQM*EK#.I	8.36	6.20	1.35	0.74
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.VFDWIDANLNEQQIASNTLVR@.A	5.91	4.23	1.40	0.72
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.DITEEIM*SGAR@.T	8.69	4.23	2.06	0.49
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.EAVGDLLDAFK#.E	43.22	10.58	4.08	0.24
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.EFLAEGQDVGSFVAEK#.K	33.98	9.73	3.49	0.29
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.FIGELFK#.L	35.62	12.17	2.93	0.34
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.GGPGGELPR@.G	35.00	11.09	3.16	0.32
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.GLPLVDDGGWNTVPISK#.G	16.80	4.78	3.52	0.28
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.GPAGLGPR@.R	17.37	6.75	2.57	0.39
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.GSSGGSGAKPSDTASEATRPATLNR.F	23.55	9.16	2.57	0.39
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.GVIDLIFEK#.A	49.02	15.22	3.22	0.31
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.IHNAENIQPGEQK#.Y	4.25	2.50	1.70	0.59
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.IISSVIM*TEDIK#.L	10.74	3.46	3.10	0.32
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.K#IISSVIM*TEDIK#.L	17.72	8.06	2.20	0.45
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.LGIESTLER@.S	57.45	91.59	0.63	1.59
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.LK#GVIDLIFEK#.A	16.36	3.97	4.12	0.24
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.LLTTIGK#.D	53.88	9.54	5.65	0.18
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.M*DQYFNQM*EK#.I	16.69	2.95	5.66	0.18
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.QVTQLAIDTEER.L	38.98	11.67	3.34	0.30
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.SDQWK#PLNLEEK#.K	28.72	9.40	3.05	0.33
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.SVTAFFNWLR@.E	24.83	5.67	4.38	0.23
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.TASTPTPPQTGGSLEPQPNGESPQVAVIIR@PDDR@.S	1.70	1.99	0.85	1.17
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.VDVQVLK#.V	15.30	3.67	4.17	0.24
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.VFDWIDANLNEQQIASNTLVR@.A	22.79	9.06	2.52	0.40
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.VPTTEK#PTVTVNFR@.K	45.54	11.95	3.81	0.26
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.AALSVDEVEK#K#.S	5.38	2.79	1.93	0.52
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.EAVGDLLDAFK#.E	27.34	9.56	2.86	0.35
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.EFLAEGQDVGSFVAEK#.K	40.02	15.33	2.61	0.38
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.FSALQQTLPAENTDNR@.R	3.62	2.51	1.44	0.69
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.GGPGGELPR@.G	45.29	11.01	4.11	0.24
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.GGPPGPPINR@.G	24.53	9.24	2.65	0.38
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.GLPLVDDGGWNTVPISK#.G	23.51	6.03	3.90	0.26
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.GSSGGSGAK#PSDTASEATR@PATLNR@.F	26.90	4.89	5.50	0.18
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.IISSVIM*TEDIK#.L	14.27	4.75	3.00	0.33
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.ITKPGSIDSNNQLFAPGGR.L	57.10	13.80	4.14	0.24
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.K#IISSVIM*TEDIK#.L	16.13	4.60	3.50	0.29
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.K#VEYTLGEESEAPGQR@.T	32.05	5.94	5.40	0.19
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.LGIESTLER@.S	41.01	10.91	3.76	0.27
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.LK#EELEEAR@.D	16.87	5.73	2.95	0.34
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.M*DQYFNQM*EK#.I	16.75	4.07	4.12	0.24
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	K.SVTAFFNWLR@.E	16.15	3.88	4.16	0.24
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.VDVQVLK#.V	16.42	6.85	2.40	0.42
Q6NZJ6_IF4G1_MOUSE	Eif4g1	Eukaryotic translation in	R.VFDWIDANLNEQQIASNTLVR@.A	25.09	7.66	3.28	0.31
Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	K.ASSLISLLK#.Q	7.46	2.87	2.60	0.39
Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	K.ASSLISLLK#.Q	16.73	7.66	2.18	0.46
Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	R.ENPLLPEEEEQR@.A	10.72	24.35	0.44	2.27

Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	K.LEVDIPLVK#.S	15.50	6.23	2.49	0.40
Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	K.LQDEFENR@.T	133.40	86.84	1.54	0.65
Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	K.LTEAVVTDYLNSGNANDAVSGVR@.E	12.15	4.08	2.98	0.34
Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	K.SQGLSQLYHNQSQGLLSQLQGQSK#.D	16.11	4.57	3.53	0.28
Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	K.LEVDIPLVK#.S	10.83	3.61	3.00	0.33
Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	K.LQDEFENR@.T	8.96	1.26	7.11	0.14
Q62448_IF4G2_MOUSE	Eif4g2	Eukaryotic translation in	K.LTEAVVTDYLNSGNANDAVSGVR@.E	7.80	3.20	2.44	0.41
Q80XI3_IF4G3_MOUSE	Eif4g3	Eukaryotic translation in	R.SPAPVQTATTAPK#.S	8.28	4.93	1.68	0.60
Q80XI3_IF4G3_MOUSE	Eif4g3	Eukaryotic translation in	K.YLDSDTEK#ELQALYALQASIVK#.L	28.21	7.28	3.88	0.26
Q05D44_IF2P_MOUSE	Eif5b	Eukaryotic translation in	R.LK#EGDTIIVPGVEGPIVTQIR@.G	11.15	4.36	2.56	0.39
O55135_IF6_MOUSE	Eif6	Eukaryotic translation in	R.NSLPDSVQIR.R	17.84	10.30	1.73	0.58
O55135_IF6_MOUSE	Eif6	Eukaryotic translation in	K.TSIEDQDELSSLLQVPLVAGTVNR@.G	24.20	10.17	2.38	0.42
O55135_IF6_MOUSE	Eif6	Eukaryotic translation in	R.HGLLVPNNTTDQELQHIR@.N	9.58	8.26	1.16	0.86
O55135_IF6_MOUSE	Eif6	Eukaryotic translation in	K.LNEAK#PSTIATSM*R@.D	16.04	11.41	1.41	0.71
O55135_IF6_MOUSE	Eif6	Eukaryotic translation in	R.NSLPDSVQIR@.R	35.68	21.48	1.66	0.60
O55135_IF6_MOUSE	Eif6	Eukaryotic translation in	K.TSIEDQDELSSLLQVPLVAGTVNR@.G	21.15	14.97	1.41	0.71
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.AISTLNGLR@.L	85.17	51.00	1.67	0.60
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.DANLYISGLPR@.T	175.24	121.15	1.45	0.69
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.DK#VAGHSLGYGFVNYVTAK#.D	46.17	30.34	1.52	0.66
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.DVEDM*FSR.F	113.83	74.12	1.54	0.65
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.FAANPNQNK#.N	56.10	45.66	1.23	0.81
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.FGGPVHHQAQR@.F	8.04	3.28	2.45	0.41
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.GFGFVTM*TNYEEAAM*AIASLNGYR@.L	6.62	5.40	1.23	0.82
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.ILQVSFK#.T	358.47	213.54	1.68	0.60
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.NM*ALLSQLYHSPAR.R	14.66	10.60	1.38	0.72
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.NMALLSQLYHSPAR@.R	5.90	4.97	1.19	0.84
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.SEAEEAITSFNGHKPPGSSEPITVK.F	13.74	12.08	1.14	0.88
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.SLFSSIGEVESAK#.L	312.30	203.62	1.53	0.65
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.TM*TQKDVEDM*FSR.F	27.41	15.11	1.81	0.55
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.TNLIVNYLPQNM*TQEELR@.S	150.86	87.78	1.72	0.58
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.TNLIVNYLPQNM*TQEELR.S	53.25	33.64	1.58	0.63
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.TNLIVNYLPQNMTQEELR@.S	32.59	25.81	1.26	0.79
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.VAGHSLGYGFVNYVTAK#.D	68.09	44.04	1.55	0.65
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.VAGHSLGYGFVNYVTAK#.D	5.44	5.03	1.08	0.92
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.VLVDQTTGLSR@.G	728.09	475.60	1.53	0.65
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.VSYAR@PSSEVIK#.D	21.11	10.02	2.11	0.47
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.ILQVSFK#.T	17.69	11.45	1.55	0.65
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.TNLIVNYLPQNM*TQEELR@.S	7.22	3.92	1.84	0.54
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	R.VLVDQTTGLSR@.G	27.75	17.09	1.62	0.62
P70372_ELAV1_MOUSE	Elavl1	ELAV-like protein 1 OS=M	K.ILQVSFK#.T	16.60	6.91	2.40	0.42
Q60775_ELF1_MOUSE	Elf1	ETS-related transcription	R.TVQPSQAPYPTQLFR@.T	7.14	1.48	4.81	0.21
Q9JHC9_ELF2_MOUSE	Elf2	ETS-related transcription	R.SPTTTAPVSAAAAPR@.T	9.33	2.65	3.52	0.28
Q9JHC9_ELF2_MOUSE	Elf2	ETS-related transcription	R.VSLSAESLLK#.A	12.90	8.18	1.58	0.63
Q9JHC9_ELF2_MOUSE	Elf2	ETS-related transcription	R.SPTTTAPVSAAAAPR@.T	8.42	2.81	3.00	0.33
E9Q2I4_E9Q2I4_MOUSE	Elmsan1	Protein Elmsan1 OS=Mus	R.VSQEANLLTLAQK#.A	7.82	4.62	1.69	0.59
Q91WG4_ELP2_MOUSE	Elp2	Elongator complex prote	R.FQFVSGADEK#.V	14.35	4.80	2.99	0.33
Q91WG4_ELP2_MOUSE	Elp2	Elongator complex prote	R.NFVENFSVISR@.Q	20.12	6.19	3.25	0.31
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	R.GTGLYELWK#.S	7.77	6.82	1.14	0.88
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	R.ILALVPPWTR.V	13.83	9.03	1.53	0.65
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	R.SYSPSDLIELVAR.I	12.44	4.96	2.51	0.40
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	R.ILALVPPWTR@.V	20.28	8.00	2.54	0.39
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	R.LEIGVQSVYEDVAR.D	10.77	6.42	1.68	0.60
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	R.SYSPSDLIELVAR@.I	28.00	9.36	2.99	0.33
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	K.FQHQGFGM*LLM*EEAER@.I	6.25	2.80	2.23	0.45
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	R.ILALVPPWTR@.V	25.04	8.85	2.83	0.35
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	R.LEIGVQSVYEDVAR@.D	15.78	4.75	3.32	0.30
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	K.LYPTLVIR@.G	20.15	6.13	3.29	0.30
Q9CZX0_ELP3_MOUSE	Elp3	Elongator complex prote	R.SYSPSDLIELVAR.I	25.33	7.35	3.45	0.29
Q99L85_ELP5_MOUSE	Elp5	Elongator complex prote	R.DSLTLPFQFSSEK#.Q	4.41	5.00	0.88	1.13
P21995_EMB_MOUSE	Emb	Embigin OS=Mus muscul	K.SLIAYVGDSTVLK#.C	5.03	1.86	2.70	0.37
Q3TAS6_EMC10_MOUSE	Emc10	ER membrane protein co	R.GLLLWNQQDGTLSATQR@.Q	2.92	2.20	1.33	0.75
Q9CRD2_EMC2_MOUSE	Emc2	ER membrane protein co	R.ILQEDPTNTAAR@.K	20.09	16.13	1.25	0.80
Q99KI3_EMC3_MOUSE	Emc3	ER membrane protein co	K.LTQEQVSDSQVLIR@.S	7.17	4.68	1.53	0.65
Q99KI3_EMC3_MOUSE	Emc3	ER membrane protein co	R.SIYSLILGQDNAADQSR@.M	7.62	5.80	1.31	0.76
Q99KI3_EMC3_MOUSE	Emc3	ER membrane protein co	K.VPFPLTLR.F	9.24	7.09	1.30	0.77
O70378_EMC8_MOUSE	Emc8	ER membrane protein co	R.SYETLVDFDNHLDDIR@.S	1.68	2.40	0.70	1.43
O70378_EMC8_MOUSE	Emc8	ER membrane protein co	R.VK#DASPNQVAEK#.V	4.10	5.42	0.76	1.32
O08579_EMD_MOUSE	Emd	Emerin OS=Mus musculu	K.DYNDDYYEESYLTTK#.T	6.85	5.93	1.15	0.87
O08579_EMD_MOUSE	Emd	Emerin OS=Mus musculu	K.QAPAAALGQDR@.Q	13.41	10.22	1.31	0.76
O08579_EMD_MOUSE	Emd	Emerin OS=Mus musculu	K.TYGEPESVGM*SK#.S	20.70	13.64	1.52	0.66
O35130_NEP1_MOUSE	Emg1	Ribosomal RNA small sub	K.IGTSFSVEDISDIR@.E	6.08	5.06	1.20	0.83
O35130_NEP1_MOUSE	Emg1	Ribosomal RNA small sub	K.VTTAFEEVWGVI.-	9.02	9.02	1.00	1.00
O35130_NEP1_MOUSE	Emg1	Ribosomal RNA small sub	K.IGTSFSVEDISDIR@.E	8.24	7.14	1.15	0.87
O35130_NEP1_MOUSE	Emg1	Ribosomal RNA small sub	K.NVLIEVNPQTR@.I	5.00	6.32	0.79	1.26
O35130_NEP1_MOUSE	Emg1	Ribosomal RNA small sub	R.LIVVLEGASLETVK#.V	5.84	2.56	2.28	0.44
Q8BMB0_EMSY_MOUSE	Emsy	Protein EMSY OS=Mus mu	K.LSQPQLEQTQLQVK#.T	12.49	6.35	1.97	0.51
Q8BMB0_EMSY_MOUSE	Emsy	Protein EMSY OS=Mus mu	K.NVVTTLLNAGGEK#.T	10.18	4.91	2.07	0.48
Q8BMB0_EMSY_MOUSE	Emsy	Protein EMSY OS=Mus mu	R.QLVTETLQQASR@.V	14.02	3.74	3.75	0.27
Q8BMB0_EMSY_MOUSE	Emsy	Protein EMSY OS=Mus mu	R.SQPQQPSQPQR@.T	5.01	6.77	0.74	1.35
Q8BMB0_EMSY_MOUSE	Emsy	Protein EMSY OS=Mus mu	R.VATTPGAATYVK#.T	9.03	5.51	1.64	0.61
Q8BMB0_EMSY_MOUSE	Emsy	Protein EMSY OS=Mus mu	K.LSQPQLEQTQLQVK#.T	4.20	1.74	2.41	0.42
Q8BMB0_EMSY_MOUSE	Emsy	Protein EMSY OS=Mus mu	K.SLVSGPTQILAQFPK#.Q	5.28	1.44	3.67	0.27
Q8C522_ENDD1_MOUSE	Endod1	Endonuclease domain-c	K.ILEVVNQVQDEER@.S	5.30	3.10	1.71	0.58
P17182_ENOA_MOUSE	Eno1	Alpha-enolase OS=Mus m	K.DATNVGDEGGFAPNILENK.E	1.93	5.02	0.39	2.60
P17182_ENOA_MOUSE	Eno1	Alpha-enolase OS=Mus m	R.AAVPSGASTGIYEALELR.D	2.25	2.24	1.00	1.00
Q9JIX0_ENY2_MOUSE	Eny2	Transcription and mRNA	K.GLEHVTVDDLVAEITPK#.G	14.78	10.93	1.35	0.74
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	K.AIQPQVAQGQAAVQQK#.L	4.85	2.03	2.39	0.42
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	K.EAELPLIDLM*K#.L	8.00	4.60	1.74	0.58
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	R.IDENANSEQR@.Q	4.67	1.46	3.20	0.31
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	K.LAGTQQVQTQIQVAK#.L	5.85	1.74	3.36	0.30
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	R.LVQFDSGK#LEALAILLQK#.L	16.24	4.07	3.99	0.25
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	R.LVSGNSIEEK#.L	11.17	7.98	1.40	0.71
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	R.SLQFPELR@.L	11.90	4.11	2.89	0.35
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	R.SLVTQVSQATGVQLPGK#.T	7.39	2.13	3.47	0.29
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	K.TAGQTVVAQPVNVQQLLK#.Y	5.31	1.87	2.85	0.35
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	R.VAVSAM*AVGEPGLASK#PASPAAGPTQEEK#.S	3.60	1.91	1.89	0.53
Q8CHI8_EP400_MOUSE	Ep400	E1A-binding protein p40	R.VPGSSFAAGSLQYK#.S	7.99	3.69	2.16	0.46
P48193_41_MOUSE	Epb41	Protein 4.1 OS=Mus mus	K.APIAAPEPELK#.T	8.18	4.80	1.71	0.59
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.AKEVENEQTPVSEPEEEKGSQPGPPVER.Q	13.00	7.68	1.69	0.59
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.DK#EETIQDTQEEK#LEGGAAK#.R	8.92	8.49	1.05	0.95
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.EVPIVQTETK#.T	28.10	18.33	1.53	0.65
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.FYPPDPSQLTEDITR@.Y	8.22	4.15	1.98	0.50
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.GLSPAQADSQFLENAK#.R	20.75	12.58	1.65	0.61

O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.HLEVQVEVR@.E	12.41	5.85	2.12	0.47
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.HSNLM*LEDLDKAQEAILK.H	8.19	6.05	1.35	0.74
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.NLPWLFTFNVK#.F	13.59	8.44	1.61	0.62
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.QAGASVLPVETEAQEHVVAQK#.L	49.24	23.28	2.12	0.47
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.SSVETQPAEEVR@.K	10.06	8.08	1.25	0.80
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.SYNLVVAK#.D	25.58	12.79	2.00	0.50
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.TEM*VTISDASQR@.T	14.10	9.13	1.54	0.65
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.TITYESPQIDGGAGGDSGVLLTAQTITSESASTTTTTHITK#.T	5.55	4.37	1.27	0.79
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.VDGDNIYVR@.H	26.61	14.04	1.90	0.53
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.VR@PAELEQFESTIGFK#.L	42.42	32.93	1.29	0.78
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.VR@PAELEQFESTIGFK#.L	4.81	3.78	1.27	0.79
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.DK#EETIQDTQEEK#.L	4.04	1.43	2.83	0.35
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.DK#EETIQDTQEEK#LEGGAAK#.R	11.62	3.00	3.87	0.26
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.DSEGVDIK#.L	18.54	8.11	2.29	0.44
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.EVPIVQTETK#.T	40.49	18.59	2.18	0.46
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.GLSPAQADSQFLENAK#.R	24.42	11.98	2.04	0.49
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.HLEVQVEVR@.E	11.20	5.22	2.15	0.47
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.HSNLM*LEDLDK#AQEAILK#.H	15.52	4.41	3.52	0.28
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.IVITGDAALDHDQALAQAIR@.E	47.31	18.04	2.62	0.38
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.LVSPEQPPK#.T	27.21	12.19	2.23	0.45
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.QAGASVLPVETEAQEHVVAQK#.L	55.30	22.17	2.49	0.40
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.SLDGAPIGVVDQSPPGEGSVPGPGVISYTTIQDGR@.R	12.44	3.96	3.14	0.32
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.SLDGAPIGVVDQSPPGEGSVPGPGVISYTTIQDGR@R@.D	5.28	2.42	2.18	0.46
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.SSVETQPAEEVR@.K	21.76	7.55	2.88	0.35
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.SYNLVVAK#.D	28.22	9.58	2.95	0.34
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.TEM*VTISDASQR@.T	16.80	8.10	2.08	0.48
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	R.VDGDNIYVR@.H	30.70	15.00	2.05	0.49
O70318_E41L2_MOUSE	Epb41l2	Band 4.1-like protein 2 O	K.VR@PAELEQFESTIGFK#.L	62.70	28.20	2.22	0.45
Q9WV92_E41L3_MOUSE	Epb41l3	Band 4.1-like protein 3 O	R.GEEVDQSAPEQEQPATVSHEEEQASTIR@.T	9.26	3.35	2.76	0.36
Q9WV92_E41L3_MOUSE	Epb41l3	Band 4.1-like protein 3 O	K.GISQTNLITTVTPEK#.K	8.75	3.68	2.38	0.42
Q9WV92_E41L3_MOUSE	Epb41l3	Band 4.1-like protein 3 O	K.IR@PGEFEQFESTIGFK#.L	26.57	2.43	10.93	0.09
Q9WV92_E41L3_MOUSE	Epb41l3	Band 4.1-like protein 3 O	K.TEPVEAEVESTPHPQPLSTEK#.V	18.06	6.31	2.86	0.35
Q9WV92_E41L3_MOUSE	Epb41l3	Band 4.1-like protein 3 O	K.VLQETILVEER@.H	24.89	6.88	3.62	0.28
Q8C9X6_EPC1_MOUSE	Epc1	Enhancer of polycomb ho	R.AISAQQVYGEK#.R	7.18	1.42	5.05	0.20
Q8C9X6_EPC1_MOUSE	Epc1	Enhancer of polycomb ho	R.DGSSTNDPYVAFR@.R	6.39	1.82	3.51	0.29
Q8C9X6_EPC1_MOUSE	Epc1	Enhancer of polycomb ho	K.DLSQILVDIK#.S	9.07	2.67	3.40	0.29
Q8C0I4_EPC2_MOUSE	Epc2	Enhancer of polycomb ho	K.ASSNQLVTLQEAK#.L	7.49	3.24	2.31	0.43
Q9D379_HYEP_MOUSE	Ephx1	Epoxide hydrolase 1 OS=I	R.FLGYTEK#DLELLYPFK#.E	10.62	3.57	2.98	0.34
Q9D379_HYEP_MOUSE	Ephx1	Epoxide hydrolase 1 OS=I	K.VFYNIM*R@.E	6.26	4.72	1.33	0.75
Q8VEH5_EPMIP_MOUSE	Epm2aip1	EPM2A-interacting prote	K.DLELFSNPFSFK#PEYAPISVR@.V	6.12	2.47	2.48	0.40
Q91W69_EPN3_MOUSE	Epn3	Epsin-3 OS=Mus musculu	R.GSPSSYTSASSSPR@.Y	5.00	3.31	1.51	0.66
Q91W69_EPN3_MOUSE	Epn3	Epsin-3 OS=Mus musculu	R.M*ALEGM*GIGSGQLGYSR@.R	4.26	1.56	2.73	0.37
Q91W69_EPN3_MOUSE	Epn3	Epsin-3 OS=Mus musculu	R.TPESFLGPSASSLVNLDSLVK#.A	2.45	1.70	1.44	0.69
Q8CGC7_SYEP_MOUSE	Eprs	Bifunctional glutamate/p	K.ASK#DQVDSAVQELLQLK#.A	14.95	7.91	1.89	0.53
Q8CGC7_SYEP_MOUSE	Eprs	Bifunctional glutamate/p	R.LNLNNTVLSK#.R	7.36	2.91	2.53	0.40
Q8CGC7_SYEP_MOUSE	Eprs	Bifunctional glutamate/p	K.SQGSGLSSGGAGEGQGPK#.K	8.50	3.76	2.26	0.44
Q8CGC7_SYEP_MOUSE	Eprs	Bifunctional glutamate/p	R.VSETVAFTDVNSILR@.Y	8.50	2.94	2.89	0.35
P42567_EPS15_MOUSE	Eps15	Epidermal growth factor	R.LQQETAQLEESVESGK#.A	6.06	3.08	1.97	0.51
P42567_EPS15_MOUSE	Eps15	Epidermal growth factor	R.TSEVQDLQDEVQR@.E	6.33	1.66	3.82	0.26
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	R.AQLETILR@.S	26.43	10.28	2.57	0.39
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	K.ELDDISQEIAQLQR@.E	9.58	3.79	2.52	0.40
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	K.LDPFESSDPFSSSSISSK#.G	6.23	2.11	2.95	0.34
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	R.LQQEETQLEQSIQAGR@.A	17.43	2.69	6.48	0.15
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	K.NDPFTSDPFTK#.N	8.00	2.66	3.00	0.33
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	K.QGFYVALR@.L	11.63	4.91	2.37	0.42
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	K.SGLSDIILGK#.I	16.60	4.65	3.57	0.28
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	K.TQIQSQESDLK#.S	16.01	2.87	5.58	0.18
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	K.TQIQSQESDLK#SQEDDLNR@.A	29.41	5.83	5.04	0.20
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	R.VGASEAALFLK#.K	23.29	4.55	5.12	0.20
Q60902_EP15R_MOUSE	Eps15l1	Epidermal growth factor	K.YSLEQDIR@.E	13.42	2.76	4.87	0.21
D3Z5I5_D3Z5I5_MOUSE	Eps8	Epidermal growth factor	K.ALYGTDGAYFFR@SSSK.Q	1.95	2.01	0.97	1.03
D3Z5I5_D3Z5I5_MOUSE	Eps8	Epidermal growth factor	K.ANLISEDIESAISDSK#.G	7.22	4.13	1.75	0.57
D3Z5I5_D3Z5I5_MOUSE	Eps8	Epidermal growth factor	R.DSVSSVSDVSQYR@.V	6.67	4.13	1.61	0.62
Q99K30_ES8L2_MOUSE	Eps8l2	Epidermal growth factor	R.SQPVHLPLTFESGPDEVR@.A	11.31	5.81	1.95	0.51
Q99K30_ES8L2_MOUSE	Eps8l2	Epidermal growth factor	R.SVSSPLLSTDAVSFLR@.G	9.96	2.86	3.48	0.29
Q99K30_ES8L2_MOUSE	Eps8l2	Epidermal growth factor	R.VGLPLPVPFSEPGYR@.R	16.39	3.78	4.34	0.23
Q99K30_ES8L2_MOUSE	Eps8l2	Epidermal growth factor	R.VGLPLPVPFSEPGYR@.R	5.88	2.24	2.62	0.38
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.AAGLQSEIGQVK#.Q	9.33	4.04	2.31	0.43
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.DNTIM*DLQTQLK#.E	9.09	4.04	2.25	0.44
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.EM*VLAQEESAR@.T	8.58	3.48	2.46	0.41
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.R@FENAPDSAK#.T	9.65	3.08	3.13	0.32
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.R@R@EDSLSDSSQQLQDSLR@.K	7.43	5.24	1.42	0.70
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	K.SAQM*LEEAR@.R	6.17	3.14	1.96	0.51
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	K.SLQADTTNTDTALTTLEEALADK#ER@.T	32.52	12.94	2.51	0.40
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.SNQTNHK#PSPDQIIQPLLELDQNR@.S	9.25	2.58	3.58	0.28
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.VVQEENQHM*QM*TIQALQDELR@.I	8.00	3.79	2.11	0.47
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.AAGLQSEIGQVK#.Q	6.43	2.86	2.25	0.45
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.DLNQLFQQDSSSR@.T	8.68	4.50	1.93	0.52
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	K.LETLTNQFSDSK#.Q	10.45	3.73	2.80	0.36
Q99MI1_RB6I2_MOUSE	Erc1	ELKS/Rab6-interacting/C	R.SNQTNHK#PSPDQIIQPLLELDQNR@.S	7.16	2.44	2.93	0.34
O08811_ERCC2_MOUSE	Ercc2	TFIIH basal transcription	R.EDQLGLSLLSLEQLQSEETLQR@.I	5.34	1.74	3.06	0.33
Q8BHK9_ERC6L_MOUSE	Ercc6l	DNA excision repair prot	K.AQFLVESESQNTVQR@.Q	5.90	2.18	2.71	0.37
Q8BHK9_ERC6L_MOUSE	Ercc6l	DNA excision repair prot	R.SLINVVLDDVEDM*EER@.L	7.24	3.12	2.32	0.43
Q9DC16_ERGI1_MOUSE	Ergic1	Endoplasmic reticulum-(	R.IIPAIWFR.Y	46.16	15.88	2.91	0.34
Q9DC16_ERGI1_MOUSE	Ergic1	Endoplasmic reticulum-(	R.YSYQYTVANK#.E	28.83	8.30	3.47	0.29
Q9CR89_ERGI2_MOUSE	Ergic2	Endoplasmic reticulum-(	R.IDHLSFGELVPGIINPLDGTEK#.I	9.89	3.49	2.83	0.35
P84089_ERH_MOUSE	Erh	Enhancer of rudimentary	R.ADTQTYQPYNK#.D	36.06	21.50	1.68	0.60
P84089_ERH_MOUSE	Erh	Enhancer of rudimentary	R.ADTQTYQPYNKDWIK.E	8.50	3.50	2.43	0.41
P84089_ERH_MOUSE	Erh	Enhancer of rudimentary	K.IYVLLR@.R	333.17	177.84	1.87	0.53
P57759_ERP29_MOUSE	Erp29	Endoplasmic reticulum r	K.ILDQGEDFPASEM*AR.I	5.58	7.16	0.78	1.28
P57759_ERP29_MOUSE	Erp29	Endoplasmic reticulum r	K.SLNILTAFR@.K	7.43	10.58	0.70	1.42
P57759_ERP29_MOUSE	Erp29	Endoplasmic reticulum r	K.WASQYLK#.I	40.71	13.58	3.00	0.33
P57759_ERP29_MOUSE	Erp29	Endoplasmic reticulum r	K.WASQYLK#.I	21.11	3.00	7.03	0.14
O08580_ERR1_MOUSE	Esrra	Steroid hormone recepto	R.LLLTLPLLR@.Q	8.69	1.47	5.90	0.17
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.ALTLGALTLPLAR@.L	90.55	37.89	2.39	0.42
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.ATYSTNSPVWEEAFR@.F	16.69	9.87	1.69	0.59
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.DLPDPYVSVLLLPDK#.N	9.06	4.09	2.21	0.45
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.FEWDLPLDGTLR@.R	15.94	6.14	2.60	0.39
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.GITSRPEPPSAAILVVYLDR.A	28.72	15.64	1.84	0.54
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.IHVLEAQDLIAK#.D	26.15	10.16	2.57	0.39
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.IVAQVWPFLGQYM*EK#.L	6.73	6.61	1.02	0.98
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.K#PHAESLELQVR@.G	22.72	10.30	2.20	0.45
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.LLAETVAPAVR@.G	37.36	15.80	2.36	0.42

Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.LLTASELTLDQWFQLSSSGPNSR@.L	8.50	4.68	1.82	0.55
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.LTHGDSPSEAPVGPLGQVK#.L	22.84	10.74	2.13	0.47
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.LTPR@PTAAELEEVLQVNSLIQTQK#.S	26.57	7.52	3.53	0.28
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.SQELDVQVK#.D	22.35	7.35	3.04	0.33
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.TVSQSSAPVWEESASFLIR@.K	6.98	5.17	1.35	0.74
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.VLQAGVLDNWYPLQGGQGQVHLR@.L	15.05	7.74	1.94	0.51
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.VQLDLAEIDLSQGAAQWYDLM*DDR@DK#GGS.-	3.93	1.46	2.69	0.37
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.ALTLGALTLPLAR@.L	52.11	22.61	2.30	0.43
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.ATYSTNSPVWEEAFR@.F	15.28	7.36	2.08	0.48
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.DLPDPYVSVLLLPDK#.N	14.22	7.47	1.90	0.53
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.FFLQDPR@.S	19.40	5.15	3.77	0.27
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.GITSR@PEPPSAAILVVYLDR@.A	12.32	5.01	2.46	0.41
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.ILYLDYSEIR@.F	16.18	5.95	2.72	0.37
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.K#PHAESLELQVR@.G	13.75	5.51	2.50	0.40
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.LLAETVAPAVR@.G	33.16	14.04	2.36	0.42
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.LTPR@PTAAELEEVLQVNSLIQTQK#.S	24.63	9.83	2.50	0.40
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	R.SQELDVQVK#.D	18.26	5.53	3.30	0.30
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.TVSQSSAPVWEESASFLIR@.K	8.65	4.10	2.11	0.47
Q3U7R1_ESYT1_MOUSE	Esyt1	Extended synaptotagmin	K.VLQAGVLDNWYPLQGGQGQVHLR@.L	10.19	4.59	2.22	0.45
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.ADK#DQASDGLSSALLILYLDSAR@.N	12.32	4.99	2.47	0.40
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.ALALLEDEEQAVR@.L	12.07	3.29	3.67	0.27
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.FQLSNSGPNSTLK#.M	9.61	5.25	1.83	0.55
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.ITVPLVSEVQIAQLR@.F	15.48	3.86	4.02	0.25
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.LLDEWFTLDEVPK#.G	9.67	4.44	2.18	0.46
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	K.VDVGQQPLR@.V	10.24	3.96	2.59	0.39
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.VGNQIFQSK#.V	16.78	7.94	2.11	0.47
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.ALALLEDEEQAVR@.L	9.98	4.79	2.08	0.48
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.FQLSNSGPNSTLK#.M	7.47	2.75	2.72	0.37
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.IPLSQLLTSDNM*TINQR@.F	11.09	6.76	1.64	0.61
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.ITVPLVSEVQIAQLR@.F	12.61	5.24	2.41	0.42
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	R.VGNQIFQSK#.V	12.57	5.24	2.40	0.42
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	K.VLVVLASEELAK#.G	13.10	3.16	4.15	0.24
Q3TZZ7_ESYT2_MOUSE	Esyt2	Extended synaptotagmin	K.VYTENVDK#R@.Q	5.16	1.73	2.99	0.33
Q8BWY3_ERF1_MOUSE	Etf1	Eukaryotic peptide chain	K.GFGGIGGILR@.Y	17.94	13.06	1.37	0.73
Q8BWY3_ERF1_MOUSE	Etf1	Eukaryotic peptide chain	R.LSVLGAITSVQQR@.L	27.48	15.24	1.80	0.55
Q8BWY3_ERF1_MOUSE	Etf1	Eukaryotic peptide chain	K.TELSQSDM*FDQR@.L	7.15	5.31	1.35	0.74
P97360_ETV6_MOUSE	Etv6	Transcription factor ETV	K.ALLLLTK#.E	39.18	7.15	5.48	0.18
P97360_ETV6_MOUSE	Etv6	Transcription factor ETV	K.TPDEIM*SGR@.T	27.18	12.03	2.26	0.44
P97360_ETV6_MOUSE	Etv6	Transcription factor ETV	K.ALLLLTK#.E	21.53	8.28	2.60	0.38
P97360_ETV6_MOUSE	Etv6	Transcription factor ETV	R.DDVAQWLK#.W	9.17	3.98	2.31	0.43
P97360_ETV6_MOUSE	Etv6	Transcription factor ETV	K.TPDEIM*SGR@.T	14.03	5.91	2.37	0.42
Q61545_EWS_MOUSE	Ewsr1	RNA-binding protein EW	R.QDHPSSM*GVYGQESGGFSGPGENR@.S	6.15	1.25	4.91	0.20
Q61545_EWS_MOUSE	Ewsr1	RNA-binding protein EW	K.GDATVSYEDPPTAK#.A	46.77	16.69	2.80	0.36
Q61545_EWS_MOUSE	Ewsr1	RNA-binding protein EW	R.QDHPSSM*GVYGQESGGFSGPGENR@.S	25.09	9.44	2.66	0.38
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	R.YAKLMEWLK#STDYGK#.Y	3.87	31.00	0.12	8.02
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	K.ALQEGDLVSSR@.G	13.97	5.95	2.35	0.43
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	K.DAIK#ENPEFDLHFEK#.V	11.86	7.74	1.53	0.65
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	R.GVFINVEK#.V	13.25	9.36	1.42	0.71
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	K.LQQHQNM*SASM*TEAEDLDGGSLLR@.Q	7.88	4.85	1.63	0.62
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	K.ALQEGDLVSSR@.G	11.87	3.58	3.31	0.30
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	R.ELQVLDGANIQSIM*ASEK#.Q	4.02	2.38	1.69	0.59
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	K.LNHFFEGVEAR@.V	23.96	8.08	2.96	0.34
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	K.LQQHQNM*SASM*TEAEDLDGGSLLR@.Q	52.81	15.51	3.41	0.29
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	K.LSSYEEM*LQSVK#.E	11.00	6.04	1.82	0.55
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	K.LTGSTSSLNK#.L	10.22	2.55	4.02	0.25
Q8R3S6_EXOC1_MOUSE	Exoc1	Exocyst complex compo	R.VAQGIR@EEEVSYQLAFNK#.Q	9.20	4.46	2.06	0.49
Q9D4H1_EXOC2_MOUSE	Exoc2	Exocyst complex compo	K.ITQVSM*ASLK#.E	8.98	4.27	2.10	0.48
Q9D4H1_EXOC2_MOUSE	Exoc2	Exocyst complex compo	R.LFENYIELK#.A	11.36	6.82	1.67	0.60
Q9D4H1_EXOC2_MOUSE	Exoc2	Exocyst complex compo	R.NALNVLQR@.F	21.55	1.98	10.90	0.09
Q9D4H1_EXOC2_MOUSE	Exoc2	Exocyst complex compo	R.VVEAVSEELSR@.L	13.85	6.11	2.27	0.44
Q9D4H1_EXOC2_MOUSE	Exoc2	Exocyst complex compo	R.ASNTADTLFQEVLGR@.K	17.65	6.23	2.83	0.35
Q9D4H1_EXOC2_MOUSE	Exoc2	Exocyst complex compo	K.ITQVSM*ASLK#.E	12.64	5.48	2.31	0.43
Q9D4H1_EXOC2_MOUSE	Exoc2	Exocyst complex compo	R.LFENYIELK#.A	17.44	5.73	3.05	0.33
Q9D4H1_EXOC2_MOUSE	Exoc2	Exocyst complex compo	R.VVEAVSEELSR@.L	19.36	7.84	2.47	0.40
Q6KAR6_EXOC3_MOUSE	Exoc3	Exocyst complex compo	K.NIFSVPEIVR@.E	14.33	8.42	1.70	0.59
Q6KAR6_EXOC3_MOUSE	Exoc3	Exocyst complex compo	R.R@DPTLLVSVVR@.I	8.44	3.34	2.53	0.40
Q6KAR6_EXOC3_MOUSE	Exoc3	Exocyst complex compo	K.YPDIR@DDHIGALLALR@.G	15.55	5.43	2.86	0.35
Q6KAR6_EXOC3_MOUSE	Exoc3	Exocyst complex compo	R.DM*TLIHGYFGSTQGLSDELAK#.Q	9.66	2.20	4.38	0.23
Q6KAR6_EXOC3_MOUSE	Exoc3	Exocyst complex compo	K.NIFSVPEIVR@.E	15.99	2.77	5.78	0.17
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	R.GESLTVDNQPR@.L	14.29	4.97	2.88	0.35
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	R.K#FLDASQYSAAGGSSVR@.E	8.24	3.43	2.40	0.42
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	K.SK#DPSGLLISVIR@.T	15.78	6.93	2.28	0.44
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	R.STTQVADSAYQR.G	26.72	6.55	4.08	0.25
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	R.TYQSITER@.I	18.46	6.90	2.68	0.37
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	K.ESEVLIGNLGDK#.L	17.86	3.30	5.41	0.18
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	R.SGELQGGPDDNLIEGGGTK#.F	5.86	2.06	2.85	0.35
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	R.SQTGVGDQTTQNTR@.L	5.46	1.57	3.48	0.29
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	K.ALANM*HESLEWLAGR@.T	7.22	2.54	2.84	0.35
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	K.ESEVLIGNLGDK#.L	14.19	4.85	2.93	0.34
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	R.SGELQGGPDDNLIEGGGTK#.F	12.01	3.52	3.41	0.29
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	R.STTQVADSAYQR.G	10.10	3.83	2.64	0.38
O35382_EXOC4_MOUSE	Exoc4	Exocyst complex compo	R.TASEPSAQLSYASTGR@.E	8.13	2.58	3.14	0.32
Q3TPX4_EXOC5_MOUSE	Exoc5	Exocyst complex compo	K.QVGDIFSNPEAVLAK#.L	3.25	2.91	1.12	0.89
Q3TPX4_EXOC5_MOUSE	Exoc5	Exocyst complex compo	K.QVGDIFSNPEAVLAK#.L	5.89	1.70	3.46	0.29
A6H5Z3_EXC6B_MOUSE	Exoc6b	Exocyst complex compo	R.VNPVTALTLLEK#.M	11.26	2.89	3.89	0.26
O35250_EXOC7_MOUSE	Exoc7	Exocyst complex compo	K.AVEYFQDNSPDSPELNK#.V	4.22	2.65	1.59	0.63
O35250_EXOC7_MOUSE	Exoc7	Exocyst complex compo	R.HDFSTVLTVFPILR@.H	10.69	2.65	4.03	0.25
O35250_EXOC7_MOUSE	Exoc7	Exocyst complex compo	R.LEEYLGSM*AK#.I	10.11	67.68	0.15	6.69
O35250_EXOC7_MOUSE	Exoc7	Exocyst complex compo	K.SELIQLVAVTQK#.T	9.60	5.77	1.66	0.60
O35250_EXOC7_MOUSE	Exoc7	Exocyst complex compo	K.VLGNLQLNLLSK#.S	7.22	3.44	2.10	0.48
O35250_EXOC7_MOUSE	Exoc7	Exocyst complex compo	K.SELIQLVAVTQK#.T	8.00	1.35	5.92	0.17
Q6PGF7_EXOC8_MOUSE	Exoc8	Exocyst complex compo	R.GAVQAGFLPGPAGVPR@.E	12.32	2.99	4.12	0.24
Q6PGF7_EXOC8_MOUSE	Exoc8	Exocyst complex compo	R.GAVQAGFLPGPAGVPR@.E	12.07	4.04	2.99	0.33
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	K.FALGSVVAVTK#.A	7.27	6.02	1.21	0.83
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	K.ASGGLPQFGDEYDFYR@.S	9.23	4.61	2.00	0.50
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	R.ER@PQDR@PEDLDVPPALADFIHQQR@.T	7.72	3.12	2.47	0.40
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	K.FALGSVVAVTK#.A	11.68	4.97	2.35	0.43
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	R.SDM*YILNESLTDPAIVK#.V	4.45	3.37	1.32	0.76
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	R.TEDFIVDTLELR.S	16.85	7.97	2.11	0.47
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	K.VTELEDK#FDLLVDTNDVILER@.V	4.66	4.95	0.94	1.06
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	K.ASGGLPQFGDEYDFYR@.S	12.73	3.27	3.89	0.26
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	R.ER@PQDR@PEDLDVPPALADFIHQQR@.T	11.78	3.72	3.16	0.32
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	K.FVK#PIFTDESYLELYR@.K	16.37	3.52	4.65	0.22

P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	K.HQQPVLPAGLQVPK#.T	24.23	6.64	3.65	0.27
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	R.SDM*YILNESLTDPAIVK#.V	9.44	2.19	4.30	0.23
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	R.TEDFIVDTLELR@.S	35.56	9.86	3.61	0.28
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	R.VGM*LLDEASGVNK#.H	8.27	21.96	0.38	2.66
P56960_EXOSX_MOUSE	Exosc10	Exosome component 10	K.VTELEDK#FDLLVDTNDVILER@.V	8.61	3.63	2.37	0.42
Q8VBV3_EXOS2_MOUSE	Exosc2	Exosome complex comp	R.LDSVLLLSSM*NLPGGELR@.R	6.57	2.49	2.63	0.38
Q8VBV3_EXOS2_MOUSE	Exosc2	Exosome complex comp	K.LGQGVLVQVSPSLVK.R	2.94	3.81	0.77	1.30
Q8VBV3_EXOS2_MOUSE	Exosc2	Exosome complex comp	K.LIASVAGSVER@.V	7.69	2.71	2.84	0.35
Q921I9_EXOS4_MOUSE	Exosc4	Exosome complex comp	R.LHEDHLEQVLEAAAQAAR@.G	11.78	4.71	2.50	0.40
Q921I9_EXOS4_MOUSE	Exosc4	Exosome complex comp	R.QHVQEASVSLGD.-	11.66	11.66	1.00	1.00
Q921I9_EXOS4_MOUSE	Exosc4	Exosome complex comp	R.QTFEAAILTQLHPR@.S	18.89	6.92	2.73	0.37
Q8BTW3_EXOS6_MOUSE	Exosc6	Exosome complex comp	R.GSGPAGAGGEAPAALR@.G	23.73	12.20	1.95	0.51
Q8BTW3_EXOS6_MOUSE	Exosc6	Exosome complex comp	R.IR@GPEESQPPQLYAAEDDETPAAR@.D	9.69	4.29	2.26	0.44
Q9D753_EXOS8_MOUSE	Exosc8	Exosome complex comp	R.ATTVNIGSISTADGSALVK#.L	5.87	2.33	2.52	0.40
Q9D753_EXOS8_MOUSE	Exosc8	Exosome complex comp	K.LLDEVIQSM*R@.H	7.33	3.38	2.17	0.46
Q9D753_EXOS8_MOUSE	Exosc8	Exosome complex comp	K.NVQLPEVTINEETALAEVNLK#.K	4.44	3.82	1.16	0.86
Q9JHI7_EXOS9_MOUSE	Exosc9	Exosome complex comp	K.M*ETAPIDTSNIEER@.A	8.03	3.74	2.15	0.47
Q9JHI7_EXOS9_MOUSE	Exosc9	Exosome complex comp	K.VAEITELIQK#.A	10.38	4.02	2.59	0.39
P26040_EZRI_MOUSE	Ezr	Ezrin OS=Mus musculus	K.IGFPWSEIR@.N	9.61	5.51	1.74	0.57
O88792_JAM1_MOUSE	F11r	Junctional adhesion mol	K.VIYSQPSTR@.S	25.11	3.60	6.97	0.14
O88792_JAM1_MOUSE	F11r	Junctional adhesion mol	R.VTFSSSGITFSSVTR@.K	7.20	2.84	2.53	0.39
Q00558_F8I2_MOUSE	F8a1	Factor VIII intron 22 prot	R.DYTGALALFTR@.M	6.23	3.14	1.98	0.50
P54731_FAF1_MOUSE	Faf1	FAS-associated factor 1	R.EYNLNFSGSSTVQEVK#.R	7.94	7.16	1.11	0.90
P54731_FAF1_MOUSE	Faf1	FAS-associated factor 1	R.NVYDLTSIPVR@.H	11.58	17.74	0.65	1.53
Q3TDN2_FAF2_MOUSE	Faf2	FAS-associated factor 2	R.QQQDEAYLASLR@.A	7.88	4.81	1.64	0.61
Q9D281_NXP20_MOUSE	Fam114a1	Protein Noxp20 OS=Mus	R.LAQQLTVER@.T	9.96	4.09	2.43	0.41
Q9D281_NXP20_MOUSE	Fam114a1	Protein Noxp20 OS=Mus	K.SVLTGGLDALEFIGK#.K	9.02	1.61	5.59	0.18
Q8VE88_F1142_MOUSE	Fam114a2	Protein FAM114A2 OS=	K.SILSSLSGEELQTTR@.L	7.78	1.89	4.12	0.24
Q8VE88_F1142_MOUSE	Fam114a2	Protein FAM114A2 OS=	K.SLLSSASATVATVGQGISNVIEK#.A	10.53	4.11	2.56	0.39
Q3U3E2_F117B_MOUSE	Fam117b	Protein FAM117B OS=M	R.TSPTVATQTGASVTSTR@.G	6.56	1.37	4.78	0.21
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.EAALEAAVLNK#EE.-	11.19	5.69	1.97	0.51
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.GVISTPVIR.T	29.85	16.09	1.86	0.54
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.LYEPDQLQELK#.I	25.82	16.76	1.54	0.65
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.NIHDTSDLDAIAK#.D	22.15	19.52	1.13	0.88
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.QNHPLPFPPPPALPFYPASVYPR@.H	14.84	11.33	1.31	0.76
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.QSILEGLSFSR@.Q	13.50	7.56	1.79	0.56
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.SPQTPELVEALAFR@.E	22.96	13.61	1.69	0.59
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.SQGAIQGRPPYAASAEEVAK.E	30.29	14.44	2.10	0.48
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.SQGGVQPIPSQGGK#.L	16.93	8.46	2.00	0.50
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.VEGSSTASSGSQLAEGK#.G	31.97	13.28	2.41	0.42
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.AVADYVR@.N	33.42	15.27	2.19	0.46
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.EAALEAAVLNK#EE.-	22.29	9.39	2.37	0.42
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.IDNLDPR@.G	15.92	8.67	1.84	0.54
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.LPPEFSPLIIK#.E	16.95	6.84	2.48	0.40
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.LYEPDQLQELK#.I	45.52	16.11	2.83	0.35
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.NIHDTSDLDAIAK#.D	28.10	15.27	1.84	0.54
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.NLTEQNSYSNIPHEGK#.H	30.57	11.86	2.58	0.39
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.NR@LPPEFSPLIIK#.E	10.83	4.54	2.39	0.42
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.QNHPLPFPPPPALPFYPASVYPR@.H	27.84	15.88	1.75	0.57
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	R.QSILEGLSFSR@.Q	28.13	11.08	2.54	0.39
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.SPQTPELVEALAFR@.E	34.27	14.34	2.39	0.42
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.SQGAIQGR@PPYAASAEEVAK#.E	31.59	7.49	4.22	0.24
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.SQGGVQPIPSQGGK#.L	33.70	14.60	2.31	0.43
Q6A0A9_F120A_MOUSE	FAM120A	Constitutive coactivator	K.VEGSSTASSGSQLAEGK#.G	30.04	10.86	2.77	0.36
Q8C3F2_F120C_MOUSE	Fam120c	Constitutive coactivator	K.LSSLPVGPSFLGFR@.N	16.22	5.61	2.89	0.35
Q8R1F1_NIBL1_MOUSE	Fam129b	Niban-like protein 1 OS=	R.FQELIFEDFAR@.F	18.61	13.08	1.42	0.70
Q8R1F1_NIBL1_MOUSE	Fam129b	Niban-like protein 1 OS=	R.FSLVPHNYGLVLYENK#.V	20.78	4.01	5.18	0.19
Q8R1F1_NIBL1_MOUSE	Fam129b	Niban-like protein 1 OS=	R.FDVSSTSVFK#.Q	15.44	8.12	1.90	0.53
Q8R1F1_NIBL1_MOUSE	Fam129b	Niban-like protein 1 OS=	R.FQELIFEDFAR@.F	19.04	5.01	3.80	0.26
Q8R1F1_NIBL1_MOUSE	Fam129b	Niban-like protein 1 OS=	R.FYEDQYGVSLFNSM*R@.H	4.38	2.64	1.66	0.60
Q8R1F1_NIBL1_MOUSE	Fam129b	Niban-like protein 1 OS=	R.HEIEGTGPPQAQLLWR@.K	6.49	4.28	1.52	0.66
Q8R1F1_NIBL1_MOUSE	Fam129b	Niban-like protein 1 OS=	R.NHVQPYIPSILEALM*VPTSQGFTEVR@.D	6.86	1.44	4.77	0.21
Q8R1F1_NIBL1_MOUSE	Fam129b	Niban-like protein 1 OS=	K.VLTSVDQYLELVGNSLPGTTSK#.S	12.73	6.04	2.11	0.47
Q9CQV4_F134C_MOUSE	Fam134c	Protein FAM134C OS=M	R.TLVEVLGPYEPLLSR@.V	14.23	2.64	5.39	0.19
Q8BPZ8_F175A_MOUSE	Fam175a	BRCA1-A complex subun	K.LLM*DVNQLK#.E	9.51	3.69	2.58	0.39
Q8BPZ8_F175A_MOUSE	Fam175a	BRCA1-A complex subun	R.VPLVVTNLGM*SDQLGYK#.T	11.73	3.92	3.00	0.33
Q8BPZ8_F175A_MOUSE	Fam175a	BRCA1-A complex subun	K.VVYTIDIQK#.Y	14.00	3.29	4.25	0.24
Q8BR63_F177A_MOUSE	Fam177a1	Protein FAM177A1 OS=	K.IASVLGISTPK#.Y	6.97	5.25	1.33	0.75
Q8CGI1_F193A_MOUSE	Fam193a	Protein FAM193A OS=M	R.TSSSLDDVFLPK#.D	7.45	6.05	1.23	0.81
P58468_F207A_MOUSE	Fam207a	Protein FAM207A OS=M	K.LLASPTYR@.A	16.80	7.70	2.18	0.46
P58468_F207A_MOUSE	Fam207a	Protein FAM207A OS=M	R.TQIDPSALVQR@.L	12.17	6.90	1.76	0.57
P58468_F207A_MOUSE	Fam207a	Protein FAM207A OS=M	R.TQIDPSALVQR.L	5.93	4.54	1.31	0.77
Q69ZR9_F208A_MOUSE	Fam208a	Protein FAM208A OS=M	R.VSEITENTVLGEFHLFSR@.K	11.70	7.30	1.60	0.62
Q69ZR9_F208A_MOUSE	Fam208a	Protein FAM208A OS=M	R.VVSISSSDFSAK#.E	9.68	6.68	1.45	0.69
Q5DTT3_F208B_MOUSE	Fam208b	Protein FAM208B OS=M	K.ILQTFSLVFPK.Q	5.64	6.02	0.94	1.07
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	R.LHNVFNDFLM*LSNTQFIENR@.V	12.09	3.47	3.49	0.29
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.NQDPLDSTQGSK#.E	4.86	2.29	2.12	0.47
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	R.VSPEVGSADVASIAQK#.E	10.66	1.62	6.58	0.15
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	R.VYDEEVEEQVLK#.A	8.32	3.28	2.53	0.39
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.DLYIDR@PLPYLIGSK#.L	18.80	4.30	4.38	0.23
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.DNDPDVDLFAGTK#.K	7.53	2.04	3.69	0.27
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.EGLLPASDQEAGGPSDIFSSSSPLDK#.G	9.28	2.90	3.21	0.31
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.EIDLIPK#.V	13.28	4.83	2.75	0.36
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	R.GGLFSNGQGLFDDEDESDLFK#EAPR@.A	6.19	1.55	4.00	0.25
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.IPAGAVSVLLGHPDVSGSTSAPSLK#.E	17.34	2.91	5.95	0.17
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.K#TNLFEDDDDDEVDLFAIAK#.D	6.83	2.71	2.52	0.40
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	R.LHNVFNDFLM*LSNTQFIENR@.V	9.48	4.24	2.23	0.45
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.NQDPLDSTQGSK#.E	13.84	4.08	3.39	0.29
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.QVDGLIQETK#.A	9.48	2.30	4.12	0.24
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.SM*FDDDTDDIFSSGLQAK#.A	6.37	2.10	3.04	0.33
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.SR@PQTGNEADLFDSGDIFPK#.S	13.88	3.78	3.67	0.27
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	R.SSVPSGGSLFGDDEDDDLFSSAK#.T	12.65	1.92	6.59	0.15
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.TEPAQDSSGLTPFK#.S	12.61	4.17	3.02	0.33
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.TNLFEDDDDDEVDLFAIAK#.D	12.24	2.09	5.86	0.17
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	K.VPLLFSDEEDSEVPSGVK#PEDLK#.V	45.49	14.11	3.22	0.31
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	R.VSPEVGSADVASIAQK#.E	21.99	3.20	6.87	0.15
Q6PGL7_FAM21_MOUSE	Fam21	WASH complex subunit	R.VYDEEVEEQVLK#.A	10.69	2.94	3.63	0.28
Q9CYH2_F213A_MOUSE	Fam213a	Redox-regulatory protei	K.LDELGVPLYAVVK#.E	5.03	1.79	2.81	0.36
Q91VU0_FAM3C_MOUSE	Fam3c	Protein FAM3C OS=Mus	R.LIAELGSTSITSLGFR@.D	16.80	5.16	3.25	0.31
Q91VU0_FAM3C_MOUSE	Fam3c	Protein FAM3C OS=Mus	K.M*ASGAANVVGPK#.I	23.13	7.98	2.90	0.35
Q91VU0_FAM3C_MOUSE	Fam3c	Protein FAM3C OS=Mus	K.M*DASLGNLFAR@.S	7.72	4.49	1.72	0.58
Q9D8N2_FA45A_MOUSE	Fam45a	Protein FAM45A OS=Mus	K.EIGQLIVQSAEDPEKSDSQVIQDIALK.T	3.05	2.32	1.32	0.76
Q9D8N2_FA45A_MOUSE	Fam45a	Protein FAM45A OS=Mus	K.EIGQLIVQSAEDPEK#SDSQVIQDIALK#.T	3.58	2.85	1.26	0.80

Q68FE6_FA65A_MOUSE	Fam65a	Protein FAM65A OS=Mus	R.LGFLYDLDK#.Q	8.20	1.59	5.16	0.19
Q922G2_FA76A_MOUSE	Fam76a	Protein FAM76A OS=Mus	K.TLSTSSIQNEIPK#.K	7.83	7.51	1.04	0.96
Q80XP8_FA76B_MOUSE	Fam76b	Protein FAM76B OS=Mus	K.ADFQYQESNLR@.T	21.88	10.62	2.06	0.49
Q80XP8_FA76B_MOUSE	Fam76b	Protein FAM76B OS=Mus	K.SSAAIQNETPK#.K	35.72	19.18	1.86	0.54
Q80XP8_FA76B_MOUSE	Fam76b	Protein FAM76B OS=Mus	K.ADFQYQESNLR@.T	6.97	1.26	5.53	0.18
Q80XP8_FA76B_MOUSE	Fam76b	Protein FAM76B OS=Mus	K.SSAAIQNETPK#.K	8.39	2.79	3.01	0.33
Q148V8_FA83H_MOUSE	Fam83h	Protein FAM83H OS=Mus	R.ILFAQSEPLVPSAGALAR@.M	9.09	4.76	1.91	0.52
Q148V8_FA83H_MOUSE	Fam83h	Protein FAM83H OS=Mus	R.LAVDALTEGGPEAYNR@.F	10.74	3.60	2.98	0.34
Q148V8_FA83H_MOUSE	Fam83h	Protein FAM83H OS=Mus	K.EQTVSETLGPSGEAVR@.S	5.40	3.65	1.48	0.67
Q148V8_FA83H_MOUSE	Fam83h	Protein FAM83H OS=Mus	R.ILFAQSEPLVPSAGALAR@.M	7.34	3.51	2.09	0.48
Q148V8_FA83H_MOUSE	Fam83h	Protein FAM83H OS=Mus	R.LAVDALTEGGPEAYNR@.F	6.16	3.94	1.56	0.64
Q3UVG3_F91A1_MOUSE	Fam91a1	Protein FAM91A1 OS=Mu	K.LSDESLDSFLIELEK#.V	11.43	10.77	1.06	0.94
Q3UVG3_F91A1_MOUSE	Fam91a1	Protein FAM91A1 OS=Mu	R.SPSSLLIASLHL.-	21.74	21.74	1.00	1.00
Q3UVG3_F91A1_MOUSE	Fam91a1	Protein FAM91A1 OS=Mu	R.VQGDYFETLLYK#.I	13.82	6.42	2.15	0.46
Q3UVG3_F91A1_MOUSE	Fam91a1	Protein FAM91A1 OS=Mu	K.IIDSGPQLSGSLDYNVVHSLYNK#.G	15.90	6.23	2.55	0.39
Q3UVG3_F91A1_MOUSE	Fam91a1	Protein FAM91A1 OS=Mu	K.LSDESLDSFLIELEK#.V	16.47	6.90	2.39	0.42
Q3UVG3_F91A1_MOUSE	Fam91a1	Protein FAM91A1 OS=Mu	R.SPSSLLIASLHL.-	26.24	26.24	1.00	1.00
Q3UVG3_F91A1_MOUSE	Fam91a1	Protein FAM91A1 OS=Mu	R.VQGDYFETLLYK#.I	11.13	7.78	1.43	0.70
Q3TJZ6_FA98A_MOUSE	Fam98a	Protein FAM98A OS=Mus	K.AQEGGGSEVFQELK#.G	13.54	8.60	1.57	0.64
Q3TJZ6_FA98A_MOUSE	Fam98a	Protein FAM98A OS=Mus	R.GGRPNEIEPPPPEM*PPWQK.R	20.41	9.54	2.14	0.47
Q3TJZ6_FA98A_MOUSE	Fam98a	Protein FAM98A OS=Mus	K.K#AQEGGGSEVFQELK#.G	9.91	8.77	1.13	0.89
Q3TJZ6_FA98A_MOUSE	Fam98a	Protein FAM98A OS=Mus	R.LDVTVQSFGWSDR@.A	10.68	6.07	1.76	0.57
Q3TJZ6_FA98A_MOUSE	Fam98a	Protein FAM98A OS=Mus	K.R@LDVTVQSFGWSDR@.A	19.74	6.83	2.89	0.35
Q3TJZ6_FA98A_MOUSE	Fam98a	Protein FAM98A OS=Mus	K.AQEGGGSEVFQELK#.G	4.91	3.96	1.24	0.81
Q3TJZ6_FA98A_MOUSE	Fam98a	Protein FAM98A OS=Mus	K.IEAINQAIANEYEVR@.R	10.50	7.93	1.32	0.76
Q80VD1_FA98B_MOUSE	Fam98b	Protein FAM98B OS=Mus	R.DDLESFQLEISGFLK#.E	5.63	2.49	2.26	0.44
Q80VD1_FA98B_MOUSE	Fam98b	Protein FAM98B OS=Mus	R.GPELGPETSM*EGDVLDTLEALGYK#.G	4.33	3.68	1.18	0.85
Q80VD1_FA98B_MOUSE	Fam98b	Protein FAM98B OS=Mus	K.GPLLEEQALSK#.A	93.85	40.98	2.29	0.44
Q80VD1_FA98B_MOUSE	Fam98b	Protein FAM98B OS=Mus	-.M*RGPELGPETSM*EGDVLDTLEALGYK.G	6.74	2.64	2.55	0.39
Q80VD1_FA98B_MOUSE	Fam98b	Protein FAM98B OS=Mus	-.M*R@GPELGPETSMEGDVLDTLEALGYK#.G	4.52	1.05	4.29	0.23
Q80VD1_FA98B_MOUSE	Fam98b	Protein FAM98B OS=Mus	K.SDTSDIPLLLSQVESK#.V	57.57	24.30	2.37	0.42
Q80VD1_FA98B_MOUSE	Fam98b	Protein FAM98B OS=Mus	K.TTVTLAHLLAAR@.E	15.97	4.94	3.23	0.31
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	K.DLIGIDNLVTPGR@.E	25.39	10.55	2.41	0.42
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	K.HSEALEALETSIK#.G	11.43	5.09	2.24	0.45
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.IM*EFHHSHVGQTPAESDFQLLEVAR@.R	5.70	3.32	1.71	0.58
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.LGAPENSGISTLER@.G	26.20	11.46	2.29	0.44
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	K.LR@PDVNSSYQDTLEFLM*AGR@.D	12.56	4.72	2.66	0.38
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.SLVSQPTAPNSEVPK#.Q	16.75	7.57	2.21	0.45
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.AALAEITEM*VAQLHGTM*IK#.M	15.00	6.71	2.23	0.45
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.AESEYTFER@.W	17.27	6.07	2.85	0.35
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	K.DLIGIDNLVTPGR@.E	62.82	22.00	2.86	0.35
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.GLTASNQFK#.V	29.35	8.28	3.55	0.28
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	K.HSEALEALETSIK#.G	26.75	10.48	2.55	0.39
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	K.INAFNWAK#.V	17.71	5.17	3.42	0.29
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	K.IQM*LDDTQEAFEVPQR@.A	7.60	2.57	2.95	0.34
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.LALWEGR@.S	19.92	8.21	2.43	0.41
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.LGAPENSGISTLER@.G	59.30	19.91	2.98	0.34
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	K.LR@PDVNSSYQDTLEFLM*AGR@.D	27.58	4.51	6.12	0.16
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.SLVSQPTAPNSEVPK#.Q	42.07	15.95	2.64	0.38
F8VPU2_FARP1_MOUSE	Farp1	FERM, RhoGEF and pleck	R.YLFALQVK#.Q	20.62	7.06	2.92	0.34
Q91VS8_FARP2_MOUSE	Farp2	FERM, RhoGEF and pleck	K.LLDSTVELFDIEPK#.C	6.99	2.58	2.71	0.37
Q99M01_SYFM_MOUSE	Fars2	Phenylalanine--tRNA liga	R.TVGGDLVEKVDLIDK#.F	5.32	48.51	0.11	9.12
Q8C0C7_SYFA_MOUSE	Farsa	Phenylalanine--tRNA liga	K.LGITQLR@.F	14.87	6.73	2.21	0.45
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.AGLYGLPK#.R	22.93	16.16	1.42	0.70
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.DHK#DNLEFFLTNLGK#.V	20.45	10.66	1.92	0.52
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.EEEPEAVLPGAQPTLISAISK.T	2.49	4.40	0.56	1.77
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.FDASFFGVHPK#.Q	40.81	23.80	1.71	0.58
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.FPQLDDTSFANSR@.D	22.34	15.22	1.47	0.68
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.GNAGQTNYGFANSTM*ER@.I	9.68	3.47	2.79	0.36
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.GVDLVLNSLAEEK#.L	41.88	18.95	2.21	0.45
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.GYTVLGVEGR@.V	42.56	12.78	3.33	0.30
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.HDLVM*NVYR@.D	11.61	5.65	2.06	0.49
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.IPALLNTQPM*LQLEYTATDR@.H	9.79	6.46	1.51	0.66
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.LDPGSPELQQVLK#.H	28.62	15.70	1.82	0.55
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.LGPVGGVFNLAM*VLR@.D	70.32	42.08	1.67	0.60
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.LK#EDTQVADVTTSR@.C	19.49	13.01	1.50	0.67
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.LLEASHAFEVSDTGNLIVSGK#.V	33.92	17.22	1.97	0.51
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.QGIQVLVSTSNVSSLEGAR@.A	7.19	3.20	2.24	0.45
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.RQQEQLVPTLEK.F	15.39	11.91	1.29	0.77
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.SEAVVAVLLTK#.K	23.04	12.96	1.78	0.56
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.SNM*GHPEPASGLAALTK#.V	22.02	16.23	1.36	0.74
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.SYIITGGLGGFGLELAR@.W	17.75	11.08	1.60	0.62
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.TGTVALEVR@.L	33.67	20.48	1.64	0.61
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.TLEAVQDLLEQGR@.Q	41.11	39.25	1.05	0.95
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.VAASVDLITK#.S	26.02	13.72	1.90	0.53
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.VHLTGINVNPNALFPPVEFPAPR@.G	44.72	27.84	1.61	0.62
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.VLEALLPLK#.S	22.87	13.22	1.73	0.58
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	K.VLVQVREEEPEAVLPGAQPTLISAISK.T	5.58	4.74	1.18	0.85
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.VTAIYIDPATHR@.Q	55.02	26.67	2.06	0.48
P19096_FAS_MOUSE	Fasn	Fatty acid synthase OS=M	R.VYATILNAGTNTDGSK#.E	4.79	3.81	1.26	0.79
P62862_RS30_MOUSE	Fau	40S ribosomal protein S3	R.FVNVVPTFGK#.K	299.65	98.20	3.05	0.33
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.DHAVVVGVYR@PPPK#.S	219.32	139.76	1.57	0.64
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.GK#EDALVTK#.N	149.10	88.77	1.68	0.60
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.LAAAILGGVDQIHIKPGAK.V	167.45	69.94	2.39	0.42
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.M*LIAM*VDVIFADVAQPDQTR@.I	42.34	23.13	1.83	0.55
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.M*LIAM*VDVIFADVAQPDQTR.I	6.03	2.20	2.74	0.37
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.M*QQENM*KPQEQLTLEPYER.D	135.14	59.19	2.28	0.44
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.MQQENM*K#PQEQLTLEPYER@.D	9.17	4.26	2.15	0.47
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.M*QQENMK#PQEQLTLEPYER@.D	15.51	6.10	2.54	0.39
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.MQQENMK#PQEQLTLEPYER@.D	9.03	5.76	1.57	0.64
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.RVSISEGDDKIEYR.A	105.98	47.72	2.22	0.45
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.GK#EDALVTK#.N	37.57	31.92	1.18	0.85
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.LAAAILGGVDQIHIK#PGAK#.V	16.25	16.31	1.00	1.00
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.M*LIAM*VDVIFADVAQPDQTR@.I	9.46	7.45	1.27	0.79
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.M*QQENM*KPQEQLTLEPYER.D	24.74	14.59	1.70	0.59
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.VLYLGAASGTTVSHVSDIVGPDGLVYAVEFSHR@.S	3.62	1.65	2.19	0.46
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.VSISEGDDK#IEYR@.A	103.03	59.78	1.72	0.58
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.GK#EDALVTK#.N	29.92	11.83	2.53	0.40
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.M*LIAM*VDVIFADVAQPDQTR@.I	9.18	3.29	2.79	0.36
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.M*QQENM*KPQEQLTLEPYER.D	21.58	6.60	3.27	0.31
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.DHAVVVGVYR@PPPK#.S	27.87	7.48	3.73	0.27
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	K.LAAAILGGVDQIHIK#PGAK#.V	27.15	7.11	3.82	0.26
P35550_FBRL_MOUSE	Fbl	rRNA 2'-O-methyltransfer	R.M*LIAM*VDVIFADVAQPDQTR@.I	7.88	2.88	2.73	0.37

Q71FD7_FBLI1_MOUSE	Fblim1	Filamin-binding LIM prot	K.SLISDLEQLHLPPPPPPPPPQAPSK#.G	4.57	4.32	1.06	0.94
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.IGPAPAFAGDTISLTITK#.G	17.28	26.52	0.65	1.53
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.LNAYTGVVSLQR@.S	9.07	9.87	0.92	1.09
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.IGPAPAFAGDTISLTITK#.G	30.71	27.72	1.11	0.90
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.LNAYTGVVSLQR@.S	12.14	6.34	1.92	0.52
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.SVM*QEGAAPLPR@.S	10.91	21.71	0.50	1.99
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.DFALDVEM*K#.L	32.26	29.14	1.11	0.90
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.FRAEEDIDPNSVHSVPR.G	105.78	99.62	1.06	0.94
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.GAPQLDTAR@.E	81.45	63.44	1.28	0.78
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	K.GNEEGYFVTR.R	95.25	87.51	1.09	0.92
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.IGPAPAFAGDTISLTITK#.G	150.21	157.99	0.95	1.05
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.LNAYTGVVSLQR@.S	40.32	25.85	1.56	0.64
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	K.M*YIFFTTFAP.-	33.22	33.22	1.00	1.00
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.QGSVTTFLAK#.M	55.91	53.50	1.05	0.96
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.R@LNAYTGVVSLQR@.S	34.82	30.37	1.15	0.87
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.RPPEPEAAPR.R	55.28	62.58	0.88	1.13
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.R@PPEPEAAPR@.R	122.20	113.59	1.08	0.93
P37889_FBLN2_MOUSE	Fbln2	Fibulin-2 OS=Mus muscu	R.SVM*QEGAAPLPR@.S	63.80	55.15	1.16	0.86
Q8BIA4_FBXW8_MOUSE	Fbxw8	F-box/WD repeat-contai	R.DLNELDDVPFFDVR@.L	17.27	10.20	1.69	0.59
Q8BIA4_FBXW8_MOUSE	Fbxw8	F-box/WD repeat-contai	R.YPVAIATAGDLVYLLK#.A	6.92	3.02	2.29	0.44
Q3UQN2_FCHO2_MOUSE	Fcho2	F-BAR domain only prote	K.TK#EEVAGTLEAVQAIQNITQALQK#.S	4.03	1.59	2.54	0.39
Q91Z50_Q91Z50_MOUSE	Fen1	Flap endonuclease 1 OS=	K.EAQQLFLEPEVLDPESVELK#.W	24.51	8.08	3.03	0.33
Q91Z50_Q91Z50_MOUSE	Fen1	Flap endonuclease 1 OS=	R.LDDFFK#.V	26.12	10.98	2.38	0.42
Q91Z50_Q91Z50_MOUSE	Fen1	Flap endonuclease 1 OS=	K.LIADVAPSAIR@.E	87.76	33.63	2.61	0.38
Q91Z50_Q91Z50_MOUSE	Fen1	Flap endonuclease 1 OS=	K.QLQQAQEAGM*EEEVEK#.F	25.29	10.12	2.50	0.40
Q91Z50_Q91Z50_MOUSE	Fen1	Flap endonuclease 1 OS=	K.VAIDASM*SIYQFLIAVR@.Q	5.43	2.41	2.25	0.44
Q91Z50_Q91Z50_MOUSE	Fen1	Flap endonuclease 1 OS=	K.WSEPNEEELVK#.F	23.53	7.36	3.20	0.31
Q8CIB5_FERM2_MOUSE	Fermt2	Fermitin family homolog	R.EELIGIAYNR@.L	10.37	3.78	2.74	0.36
Q8CIB5_FERM2_MOUSE	Fermt2	Fermitin family homolog	R.FIQAWQSLPEFGITHFIAR@.F	24.42	11.34	2.15	0.46
Q8CIB5_FERM2_MOUSE	Fermt2	Fermitin family homolog	R.ILEAHQNVAQM*SLIEAK#.M	23.81	8.01	2.97	0.34
Q8CIB5_FERM2_MOUSE	Fermt2	Fermitin family homolog	R.INQLYEQAK#.W	20.25	7.72	2.62	0.38
Q8CIB5_FERM2_MOUSE	Fermt2	Fermitin family homolog	R.SLM*EQDVK#ENEALLLR@.F	33.78	8.47	3.99	0.25
Q8CIB5_FERM2_MOUSE	Fermt2	Fermitin family homolog	K.TNQGWLDSSR@.S	7.86	2.45	3.21	0.31
Q8CIB5_FERM2_MOUSE	Fermt2	Fermitin family homolog	R.ILEAHQNVAQM*SLIEAK#.M	24.74	10.09	2.45	0.41
Q8CIB5_FERM2_MOUSE	Fermt2	Fermitin family homolog	K.K#LDDQSEDEALELEGPLIM*PGSGSIYSSPGLYSK#.T	5.75	1.70	3.39	0.30
Q8CIB5_FERM2_MOUSE	Fermt2	Fermitin family homolog	R.M*DASTGDAIK#.T	13.41	4.60	2.92	0.34
Q6TYB5_FEZ2_MOUSE	Fez2	Fasciculation and elonga	K.SGPPSVEDLQILTK#.I	9.45	4.68	2.02	0.50
Q6TYB5_FEZ2_MOUSE	Fez2	Fasciculation and elonga	R.TLHLLTLNLSEK#.G	10.48	5.58	1.88	0.53
Q66JX5_FR1OP_MOUSE	Fgfr1op	FGFR1 oncogene partner	R.IASFLSSSAVDAR@.D	6.73	5.42	1.24	0.80
Q3ULZ2_FHDC1_MOUSE	Fhdc1	FH2 domain-containing	K.GGSEDSASK.D	2.01	7.71	0.26	3.83
P97447_FHL1_MOUSE	Fhl1	Four and a half LIM dom	K.AIVAGDQNVEYK#.G	24.34	6.63	3.67	0.27
P97447_FHL1_MOUSE	Fhl1	Four and a half LIM dom	K.AIVAGDQNVEYK#.G	3.38	2.39	1.41	0.71
Q9R059_FHL3_MOUSE	Fhl3	Four and a half LIM dom	R.ELFYEDR@.H	22.86	12.92	1.77	0.57
Q9R059_FHL3_MOUSE	Fhl3	Four and a half LIM dom	K.R@PITGGSGGGEGAGLGGGK#.Y	10.63	8.25	1.29	0.78
Q9R059_FHL3_MOUSE	Fhl3	Four and a half LIM dom	K.TLTQGGVTYR.D	49.61	29.91	1.66	0.60
Q9R059_FHL3_MOUSE	Fhl3	Four and a half LIM dom	K.TPLAGQQFTSR@.D	31.75	21.56	1.47	0.68
Q9R059_FHL3_MOUSE	Fhl3	Four and a half LIM dom	K.TLTQGGVTYR@.D	15.16	10.96	1.38	0.72
Q9R059_FHL3_MOUSE	Fhl3	Four and a half LIM dom	K.TPLAGQQFTSR@.D	11.91	8.60	1.39	0.72
Q6P9Q4_FHOD1_MOUSE	Fhod1	FH1/FH2 domain-contai	K.AALLNFDEFAVSK#.D	8.33	2.39	3.48	0.29
Q6P9Q4_FHOD1_MOUSE	Fhod1	FH1/FH2 domain-contai	R.EIAEPLFDLK#.V	5.88	3.49	1.69	0.59
Q91WF7_FIG4_MOUSE	Fig4	Polyphosphoinositide p	R.FGSPIIILNLVK#.E	7.71	3.84	2.01	0.50
Q6P6L0_FIL1L_MOUSE	Filip1l	Filamin A-interacting pr	K.AIEDDLM*K#TEDEYETLER@.R	5.56	4.65	1.20	0.84
Q6P6L0_FIL1L_MOUSE	Filip1l	Filamin A-interacting pr	R.ITILQNASITPIK#.S	10.57	6.59	1.60	0.62
Q6P6L0_FIL1L_MOUSE	Filip1l	Filamin A-interacting pr	R.KAEEELQDIKDK.I	20.48	15.00	1.37	0.73
Q6P6L0_FIL1L_MOUSE	Filip1l	Filamin A-interacting pr	K.LQSTTSQLQAEQNK#.V	7.68	6.47	1.19	0.84
Q6P6L0_FIL1L_MOUSE	Filip1l	Filamin A-interacting pr	K.QLSEELESLNAR@.I	15.89	10.49	1.51	0.66
Q6P6L0_FIL1L_MOUSE	Filip1l	Filamin A-interacting pr	K.VTSSITITPTATPLPR.Q	4.67	4.78	0.98	1.02
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.ANENSNIQVLSDR@.S	22.98	13.58	1.69	0.59
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	K.GVDLDAPGSINGVPLLEVDLDSFEDK#PWR@.K	6.76	4.77	1.42	0.71
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.K#PGADLSDYFNYGFNEDTWK#.A	12.43	5.79	2.14	0.47
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.LPGAIDVIGQTITISR@.V	17.14	10.86	1.58	0.63
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.M*GLEVIPVTSTTNK#.I	29.04	17.88	1.62	0.62
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.MGLEVIPVTSTTNK#.I	12.30	4.59	2.68	0.37
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.R@LPGAIDVIGQTITISR@.V	73.26	32.69	2.24	0.45
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	K.TGAPQYGSYGTAPVNLNIK#.A	29.61	14.30	2.07	0.48
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.TGNSEK#EAALPSTK#.A	12.92	34.29	0.38	2.65
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	K.VTETEDDSDSDSDDDEDDVHVTIGDIK#.T	5.60	1.48	3.79	0.26
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	K.AEFTSPPSLFK#.T	123.59	50.18	2.46	0.41
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.AFPYGNVAFPHLTSSAPSWPSLVDTTK#.Q	49.93	18.44	2.71	0.37
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.ANENSNIQVLSDR@.S	92.38	33.50	2.76	0.36
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	K.GVDLDAPGSINGVPLLEVDLDSFEDK#PWR@.K	22.10	6.77	3.26	0.31
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.K#PGADLSDYFNYGFNEDTWK#.A	36.14	12.38	2.92	0.34
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.LPGAIDVIGQTITISR@.V	37.50	11.45	3.28	0.31
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.M*GLEVIPVTSTTNK#.I	61.50	27.47	2.24	0.45
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	R.R@LPGAIDVIGQTITISR@.V	140.23	57.33	2.45	0.41
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	K.TGAPQYGSYGTAPVNLNIK#.A	75.41	28.29	2.67	0.38
Q9D824_FIP1_MOUSE	Fip1l1	Pre-mRNA 3'-end-proces	K.VTETEDDSDSDSDDDEDDVHVTIGDIK#.T	19.67	3.73	5.28	0.19
Q9CQ92_FIS1_MOUSE	Fis1	Mitochondrial fission 1	K.FQSEQAAGSVSK#.S	9.98	3.51	2.85	0.35
Q9CQ92_FIS1_MOUSE	Fis1	Mitochondrial fission 1	R.GLLQTEPQNNQAK#.E	27.80	10.54	2.64	0.38
Q61576_FKB10_MOUSE	Fkbp10	Peptidyl-prolyl cis-trans	R.EVQM*GDFVR@.Y	11.76	6.44	1.83	0.55
Q61576_FKB10_MOUSE	Fkbp10	Peptidyl-prolyl cis-trans	R.GGTYDTYIGSGWLIK#.G	6.83	11.91	0.57	1.74
Q61576_FKB10_MOUSE	Fkbp10	Peptidyl-prolyl cis-trans	K.IGDFIR@.Y	18.69	8.21	2.28	0.44
Q61576_FKB10_MOUSE	Fkbp10	Peptidyl-prolyl cis-trans	R.M*VQNSDFVR@.Y	10.02	5.65	1.77	0.56
Q61576_FKB10_MOUSE	Fkbp10	Peptidyl-prolyl cis-trans	R.EVQM*GDFVR@.Y	5.86	3.40	1.73	0.58
Q9D1M7_FKB11_MOUSE	Fkbp11	Peptidyl-prolyl cis-trans	R.DPLVIELGQK#.Q	4.99	3.52	1.42	0.71
Q9D1M7_FKB11_MOUSE	Fkbp11	Peptidyl-prolyl cis-trans	R.IIDTSLTR@DPLVIELGQK#.Q	16.18	8.81	1.84	0.54
Q6P9Q6_FKB15_MOUSE	Fkbp15	FK506-binding protein 1	R.GEFELEESYDGGTILR@.T	9.89	3.60	2.75	0.36
Q6P9Q6_FKB15_MOUSE	Fkbp15	FK506-binding protein 1	R.IIQENER@.L	10.70	2.56	4.19	0.24
Q6P9Q6_FKB15_MOUSE	Fkbp15	FK506-binding protein 1	R.DSAAPSPIPASDSLSADPVVTPLPLPLK#PGEPGLR@.S	10.81	3.68	2.93	0.34
Q6P9Q6_FKB15_MOUSE	Fkbp15	FK506-binding protein 1	R.GEFELEESYDGGTILR@.T	7.80	3.87	2.02	0.50
Q6P9Q6_FKB15_MOUSE	Fkbp15	FK506-binding protein 1	R.LQADLSELR@.E	18.20	6.64	2.74	0.37
Q6P9Q6_FKB15_MOUSE	Fkbp15	FK506-binding protein 1	K.VPR@PTAQPEEEDEDEVSM*K#.G	5.56	3.04	1.83	0.55
Q6P9Q6_FKB15_MOUSE	Fkbp15	FK506-binding protein 1	R.YVEQSNLM*M*EK#.R	8.39	4.12	2.04	0.49
O35465_FKBP8_MOUSE	Fkbp8	Peptidyl-prolyl cis-trans	K.TAEDGPDLEM*LSGQER@.V	5.31	5.34	0.99	1.01
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 hom	K.ADLTALFLPR@.Q	22.49	11.99	1.88	0.53
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 hom	R.GAQATLSNTTK#.A	19.31	10.65	1.81	0.55
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 hom	R.LLQSLLDTR@.C	12.41	6.08	2.04	0.49
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 hom	K.LYLNSNK#LDFDGLPSGIGK#.L	6.79	7.02	0.97	1.03
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 hom	R.NAEAVLQGQGLSGK#.V	14.35	8.67	1.66	0.60
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 hom	R.TAEWYNIDFSLQNQLR@.L	5.47	4.43	1.23	0.81
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 hom	K.VGLGLGYLELPQINYK#.L	14.38	9.52	1.51	0.66
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 hom	K.VPFESEDNQGIVYAWVGR@.A	5.60	3.54	1.58	0.63
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 hom	K.VTQGTLQPTLYQIR@.T	7.33	4.64	1.58	0.63

Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 homc	K.ADLTALFLPR@.Q	32.60	16.30	2.00	0.50
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 homc	R.EGEEAAAEAEEK#.Q	10.21	2.55	4.01	0.25
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 homc	R.GAQATLSNTTK#.A	12.35	4.28	2.88	0.35
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 homc	R.GVDLSGNDFK#.G	11.04	2.84	3.88	0.26
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 homc	R.LLQSLLDTR@.C	15.08	6.50	2.32	0.43
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 homc	R.NAEAVLQGQGLSGK#.V	23.01	8.13	2.83	0.35
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 homc	K.VGLGLGYLELPQINYK#.L	22.62	9.41	2.40	0.42
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 homc	K.VPFESEDNQGIVYAWVGR@.A	5.67	2.73	2.07	0.48
Q9JJ28_FLII_MOUSE	Flii	Protein flightless-1 homc	K.VTQGTLQPTLYQIR@.T	6.99	5.42	1.29	0.77
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.DAGEGLLAVQITDPEGKPKK#.T	2.96	1.44	2.05	0.49
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.LIALLEVLSQK#.K	12.40	8.23	1.51	0.66
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.LIALLEVLSQK#.K	11.76	5.91	1.99	0.50
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.VATVPQHATSGPGPADVSK#.V	11.50	7.20	1.60	0.63
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.AEFTVETR.S	32.80	13.42	2.44	0.41
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.AEISFEDR@.K	15.68	5.78	2.71	0.37
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.AEVGVPAEFGIWTR.E	152.83	62.40	2.45	0.41
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.AFGPGLQGGNAGSPAR@.F	130.29	60.13	2.17	0.46
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.AGGPGLER@.A	132.73	54.54	2.43	0.41
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.AGNNM*LLVGVHGPR@.T	61.93	28.67	2.16	0.46
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.AGVAPLQVK#.V	120.70	48.42	2.49	0.40
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.AIVDGNLK#.L	236.32	79.39	2.98	0.34
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.ALTQTGGPHVK#.A	40.15	18.21	2.21	0.45
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.ANLPQSFQVDTSK#.A	163.15	69.14	2.36	0.42
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.ASGPGLNTTGVPASLPVEFTIDAK#.D	103.95	49.35	2.11	0.47
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.AWGPGLEGGIVGK#.S	129.90	56.14	2.31	0.43
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.AYGPGIEPTGNM*VK#.K	63.90	32.44	1.97	0.51
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.AYGPGIEPTGNMVK#.K	15.70	7.29	2.16	0.46
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.DAGEGGLSLAIEGPSK#.A	79.63	32.99	2.41	0.41
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.DAGYGGLSLSIEGPSK#.V	25.46	15.26	1.67	0.60
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.DKGEYTLVVK.W	54.85	23.18	2.37	0.42
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.DVDIIDHHDNTYTVK#.Y	130.57	51.59	2.53	0.40
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.EAGAGGLAIAVEGPSK#.A	78.80	33.10	2.38	0.42
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.EAPQDFHPDR@.V	25.58	11.77	2.17	0.46
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.EATTEFSVDAR@.A	143.36	61.92	2.32	0.43
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTK#PSK#.V	25.55	15.95	1.60	0.62
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.EGSYSISVLYGEEEVPR.S	95.70	40.97	2.34	0.43
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.EGSYSISVLYGEEEVPR@.S	19.97	6.21	3.22	0.31
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.ENGIYLIDVK#.F	22.28	11.31	1.97	0.51
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.ETGEHLVHVK#.K	20.13	10.58	1.90	0.53
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.FADQHVPGSPFSVK#.V	76.37	30.29	2.52	0.40
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.FGGEHVPNSPFQVTALAGDQPTVQTPLR@.S	81.61	39.91	2.04	0.49
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.FNEEHIPDSPFVVPVASPSGDAR@.R	124.54	53.33	2.34	0.43
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.FTVETR@.G	334.58	111.42	3.00	0.33
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.GAGTGGLGLAVEGPSEAK#.M	157.69	67.84	2.32	0.43
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.GK#LDVQFSGLAK#.G	61.10	20.47	2.98	0.34
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.GLVEPVDVVDNADGTQTVNYVPSR@.E	142.36	58.91	2.42	0.41
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.GQHVPGSPFQFTVGPLGEGGAHK#.V	191.89	64.02	3.00	0.33
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.GTVEPQLEAR@.G	162.04	65.71	2.47	0.41
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.HTAM*VSWGGVSIPNSPFR@.V	21.86	10.84	2.02	0.50
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.IANLQTDLSDGLR@.L	180.61	73.32	2.46	0.41
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.IPEISIQDM*TAQVTSPSGK#.T	10.50	4.80	2.19	0.46
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.IQQNTFTR@.W	266.08	83.79	3.18	0.31
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.K#GEITGEVR@.M	62.61	24.15	2.59	0.39
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.LDVQFSGLAK#.G	42.11	22.13	1.90	0.53
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.LIALLEVLSQK#.K	604.74	225.17	2.69	0.37
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.LPQLPITNFSR@.D	108.56	50.98	2.13	0.47
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.LTVSSLQESGLK#.V	63.39	22.65	2.80	0.36
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.LVSIDSK#.A	298.68	102.24	2.92	0.34
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.LVSNHSLHETSSVFVDSLTK#.V	66.30	25.09	2.64	0.38
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.LYSVSYLLK#.D	118.90	41.13	2.89	0.35
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.NDNDTFTVK#.Y	24.45	9.72	2.52	0.40
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.NGQHVASSPIPVVISQSEIGDASR@.V	16.61	7.12	2.33	0.43
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.QM*QLENVSVALEFLDR@.E	10.11	3.66	2.76	0.36
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.QM*QLENVSVALEFLDR@ESIK#.L	61.67	24.39	2.53	0.40
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.QMQLENVSVALEFLDR@ESIK#.L	5.59	2.33	2.40	0.42
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.R@AEFTVETR@.S	29.22	13.72	2.13	0.47
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.SADFVVEAIGDDVGTLGFSVEGPSQAK#.I	66.12	26.70	2.48	0.40
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.SAGQGEVLVYVEDPAGHQEEAK#.V	158.16	71.65	2.21	0.45
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.SPFEVK#.V	66.05	33.81	1.95	0.51
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.SPFEVYVDK#.S	104.56	47.69	2.19	0.46
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.SPFEVYVDKSQGDASK.V	31.46	11.27	2.79	0.36
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.SPFSVGVSPSLDLSK#.I	165.68	70.65	2.35	0.43
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.TFSVWYVPEVTGTHK#.V	90.25	38.11	2.37	0.42
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.TGVAVNK#PAEFTVDAK#.H	162.76	79.85	2.04	0.49
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.VATVPQHATSGPGPADVSK#.V	233.66	113.84	2.05	0.49
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.VEPGLGADNSVVR@.F	58.69	22.42	2.62	0.38
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.VK#ETADFK#.V	30.01	14.55	2.06	0.48
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.VKVEPSHDASK.V	14.76	6.17	2.39	0.42
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.VNQPASFAVSLNGAK#.G	15.27	6.79	2.25	0.44
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.VNVGAGSHPNK#.V	43.80	18.46	2.37	0.42
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.VPVHDVTDASK#.V	109.62	57.70	1.90	0.53
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.VSGQGLHEGHTFEPAEFIIDTR@.D	15.97	5.10	3.13	0.32
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.VTAQGPGLEPSGNIANK#.T	124.09	48.44	2.56	0.39
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.VTYTPM*APGSYLISIK#.Y	60.73	21.26	2.86	0.35
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	R.VTYTPMAPGSYLISIK#.Y	18.86	12.69	1.49	0.67
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.YGGDEIPFSPYR@.V	114.07	52.49	2.17	0.46
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.YGGPYHIGGSPFK#.A	86.50	38.44	2.25	0.44
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.YGGQPVPNFPSK#.L	80.93	37.92	2.13	0.47
Q8BTM8_FLNA_MOUSE	Flna	Filamin-A OS=Mus muscu	K.YNDQHIPGSPFTAR@.V	80.10	33.62	2.38	0.42
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.IGNLQTDLSDGLR.L	10.52	9.94	1.06	0.94
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.AAGSGELGVTVK#.G	41.47	21.65	1.91	0.52
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.ADIEM*PFDPSK#.V	14.84	8.36	1.78	0.56
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.AEVSIQNNK#.D	18.77	9.65	1.95	0.51
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.AFGPGIEGK#.D	42.83	28.16	1.52	0.66
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.AGLAPLEVR@.V	45.92	22.21	2.07	0.48
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.AHGPGLEGGLVGK#PAEFTIDTK#.G	45.68	23.95	1.91	0.52
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.APLNVQFSSPLPGEAVK#DLDIIDNYDYSHTVK#.Y	21.63	5.07	4.26	0.23
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.ATVHDNK#DGTYAVTYIPDK#.T	13.74	11.41	1.20	0.83
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.ATVHDNKDGTYAVTYIPDK.T	11.87	6.31	1.88	0.53
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.DAGEGLLAVQITDQEGKPQR.A	89.46	38.06	2.35	0.43
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.DAGYGGISLAVEGPSK#.V	16.42	10.91	1.50	0.66
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.DNADGTYQVEYTPFEK#.G	9.35	4.52	2.07	0.48
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.EAGAGGLSIAVEGPSK#.A	145.77	55.67	2.62	0.38

Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.EAM*QQADDWLGVPQVITPEEIIHPDVDEHSVM*TYLSQFPK#.A	14.73	4.57	3.22	0.31
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.FADEHVPGSPFTVK#.I	62.85	28.57	2.20	0.45
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.FTVDTISAGQGDVM*VFVEDPEGNK#EEAR@.V	7.42	5.42	1.37	0.73
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.GAGIGGLGITVEGPSESK#.I	45.05	19.75	2.28	0.44
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.GEAGIPAEFSIWTR@.E	43.99	46.19	0.95	1.05
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.GFHVVEVTYDDVPIPNSPFK#.V	36.73	14.78	2.49	0.40
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.GFLDGVYSFEYYPSTPGK#.Y	16.76	8.45	1.98	0.50
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.GLEELVK#.Q	42.93	17.55	2.45	0.41
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.GLVEPVNVVDNGDGTHTVTYTPSQEGPYIVSVK#.Y	12.58	4.39	2.87	0.35
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.GSHIPESPLQFYVNYPNSGSVSAYGPGLVYGVANK#.T	9.32	4.21	2.22	0.45
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.IGNLQTDLSDGLR@.L	55.59	30.21	1.84	0.54
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.ILAQDGEGQPIDIQM*K#.S	13.81	5.56	2.49	0.40
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.ILAQDGEGQPIDIQMK#.S	7.25	5.21	1.39	0.72
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.IPYLPITNFNQNWQDGK#.A	9.52	5.47	1.74	0.57
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.LVSPGSANETSSILVESVTR@.S	44.86	16.26	2.76	0.36
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.NSVELLVEDR@.G	32.89	16.12	2.04	0.49
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.SADFVVESIGSEVGTLGFAIEGPSQAK#.I	31.48	19.87	1.58	0.63
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.SNVFTVVTR.G	42.53	21.65	1.96	0.51
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.SPFEVQVGPEAGM*QK#.V	21.49	9.55	2.25	0.44
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.SPFTVGVAAPLDLSK#.I	63.12	32.29	1.95	0.51
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.TFEM*SDFIVDTR@.D	25.64	12.92	1.98	0.50
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.TGEEVGFVVDAK#.T	31.50	21.08	1.49	0.67
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.TYSVEYLPK#.V	34.34	24.35	1.41	0.71
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.VEVGK#DQEFAIDTNGAGGQGK#.L	8.20	5.64	1.45	0.69
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.VLFASQEIPASPFR@.V	71.79	40.88	1.76	0.57
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.VLSDDEEDVDFDIIHNANDTFTVK#.Y	32.74	17.60	1.86	0.54
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.VNQPASFAIR@.L	33.94	19.89	1.71	0.59
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.VSFAGDAIPK#.S	43.48	18.94	2.30	0.44
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.VSYFPTVPGVYIVSTK#.F	37.14	20.58	1.80	0.55
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.VYGQGLSEGR@.T	28.06	17.09	1.64	0.61
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.YADEEIPR.S	54.33	18.57	2.93	0.34
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.YGGELVPHFPAWVK#.V	32.46	13.57	2.39	0.42
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	R.YM*IGVTYGGDNIPLSPYR@.I	15.14	9.72	1.56	0.64
Q80X90_FLNB_MOUSE	Flnb	Filamin-B OS=Mus muscu	K.YTPTQQGNM*QVLVTYGGDPIPK#.S	19.33	9.65	2.00	0.50
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.ILVGPSEIGDASK#.V	4.39	2.99	1.47	0.68
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.TEAAEIVEGEDSAYSVR@.F	5.62	2.82	2.00	0.50
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.AEIAFEDR@.K	16.08	6.76	2.38	0.42
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.AEIAFEDR@K#.D	24.22	7.53	3.22	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.AEVLIQNNADGTYHITYSPAFPGTYTITIK#.Y	4.57	4.50	1.02	0.98
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.AFGPGLEGGLVNK#.A	312.59	100.77	3.10	0.32
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.AGGTGLER@.G	171.46	71.39	2.40	0.42
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.AKLDVHFAGAAK.G	44.58	14.90	2.99	0.33
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.APLQVAVLGPTGVAEPVEVR@.D	75.60	22.41	3.37	0.30
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.ASGPGLNASGIPASLPVEFTIDAR@.D	104.76	32.65	3.21	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.ASGPGLNASGIPASLPVEFTIDAR.D	19.84	7.84	2.53	0.40
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.ATIQPVFDPSK#.V	127.22	48.81	2.61	0.38
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.AWGPGLETGQVGK#.S	103.92	31.82	3.27	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.DAGEGGLSLAVEGPSK#.A	68.59	23.93	2.87	0.35
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.DNGDGTYTVSYLPDM*SGR@.Y	14.96	3.47	4.32	0.23
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.DTVEVALEDK#.G	13.62	6.15	2.22	0.45
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.DTVEVALEDK#GDNTFR@.C	72.74	19.65	3.70	0.27
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.EK#GDYILIVK#.W	65.13	21.04	3.10	0.32
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.EVGEHVVSVR@.K	84.48	25.96	3.25	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.EVTTEFTVDAR@.S	79.48	21.71	3.66	0.27
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.FDDK#HIPGSPFTAK#.I	87.47	31.97	2.74	0.37
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.FNDEHIPDSPFVVPVASLSDDAR@.R	227.02	83.31	2.73	0.37
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.FNDEHIPDSPFVVPVASLSDDAR@R@.L	21.46	7.92	2.71	0.37
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.FNGAHIPGSPFK#.I	50.10	15.51	3.23	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.GAGGQGQLDVR@.M	278.90	78.33	3.56	0.28
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.GAGTGGLGLAIEGPSEAK#.M	175.47	63.90	2.75	0.36
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.GASYSSIPK#.F	108.71	34.94	3.11	0.32
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.GDYILIVK#.W	28.28	10.31	2.74	0.36
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.GEAVR@DFEIIDNHDYSYTVK#.Y	50.80	8.53	5.96	0.17
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.GGLVGTPAPFSIDTK#.G	213.48	81.34	2.62	0.38
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.GLHQM*GIK#.Y	40.69	11.54	3.53	0.28
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.GLSEGQTFQVAEFIVDTR@.N	134.76	45.20	2.98	0.34
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.GLSEGQTFQVAEFIVDTR.N	77.14	24.89	3.10	0.32
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.GPGLEPVGNVANK#PTYFDIYTAGAGTGDVAVVIVDPQGR@.R	21.59	6.61	3.26	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.GPGLEPVGNVANKPTYFDIYTAGAGTGDVAVVIVDPQGR.R	15.64	5.01	3.12	0.32
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.GPGLSQAFVGQK#.N	231.69	69.61	3.33	0.30
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.GVAGVPAEFSIWTR@.E	176.29	53.50	3.30	0.30
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.HIGISFTPK#.E	247.35	77.47	3.19	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.HVTNSPFK#.I	252.54	78.71	3.21	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.ILVGPSEIGDASK#.V	244.24	64.51	3.79	0.26
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.IPGNWFQM*VSAQER@.L	40.13	15.06	2.66	0.38
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.IPGNWFQMVSAQER@.L	8.92	5.35	1.67	0.60
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.IQIGEETVITVDAK#.A	18.63	6.97	2.67	0.37
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.ITEGDLSQLTASIR@.A	225.60	74.24	3.04	0.33
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.LEPGGGAEAQAVR@.Y	103.41	37.93	2.73	0.37
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.LGSFGSITR@.Q	201.61	117.13	1.72	0.58
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.LLGWIQNK#VPQLPITNFNR@.D	7.27	2.22	3.28	0.30
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.LSGGHSLHETSTVLVETVTK#.S	100.07	25.44	3.93	0.25
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.LTVTSLQETGLK#.V	114.72	35.56	3.23	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.LTVTSLQETGLK#VNQPASFAVQLNGAR@.G	7.01	2.03	3.46	0.29
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.NAGYGGLGLSIEGPSK#.V	45.85	15.37	2.98	0.34
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.QQEGEASSQDM*TAQVTSPSGK#.T	29.88	9.00	3.32	0.30
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.R@DTVEVALEDK#GDNTFR@.C	40.15	12.96	3.10	0.32
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.R@LTVTSLQETGLK#.V	48.39	16.23	2.98	0.34
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.SPFEVNVGM*ALGDANK#.V	28.73	10.44	2.75	0.36
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.SPFVVNVAPPLDLSK#.V	284.92	106.27	2.68	0.37
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.TAR@PNITDNK#.D	68.33	18.32	3.73	0.27
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.TDTYVTDNGDGTYR@.V	31.13	9.96	3.13	0.32
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.TEAAEIVEGEDSAYSVR@.F	226.25	65.41	3.46	0.29
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.TGVEVGK#PTHFTVLTK#.G	206.28	54.74	3.77	0.27
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.TSQLNVGTSTDVSLK#.I	142.46	44.23	3.22	0.31
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.TYAVSYVPK#.V	33.43	12.50	2.67	0.37
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.VAVGQEQAFSVNTR@.G	242.69	71.98	3.37	0.30
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.VEESTQVGGDPFPAVFGDFLGR@.E	114.74	43.30	2.65	0.38
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.VEESTQVGGDPFPAVFGDFLGR.E	38.12	10.81	3.53	0.28
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.VK#EVADFK#.V	49.90	14.83	3.36	0.30
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.VNQPASFAVQLNGAR@.G	22.12	11.33	1.95	0.51
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.VPQLPITNFNR@.D	147.92	43.98	3.36	0.30
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.VTVLFAGQNIER@.S	42.58	10.61	4.01	0.25

Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.VYGPGVEK#.T	16.70	6.38	2.62	0.38
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	R.VYNVTYTVK#.E	111.92	31.19	3.59	0.28
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.WGDESVPGSPFK#.V	70.02	26.36	2.66	0.38
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.YADQEVPR@.S	135.68	46.40	2.92	0.34
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.YDGNHIPGSPLQFYVDAINSR@.H	109.29	37.34	2.93	0.34
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.YGGDEIPYSPFR@.I	65.61	17.09	3.84	0.26
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.YGGPQHIVGSPFK#.A	164.99	64.09	2.57	0.39
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.YTAVQQGNM*AVTVTYGGDPVPK#.S	47.83	11.29	4.24	0.24
Q8VHX6_FLNC_MOUSE	Flnc	Filamin-C OS=Mus muscu	K.YVITIR@.F	188.61	43.18	4.37	0.23
O08917_FLOT1_MOUSE	Flot1	Flotillin-1 OS=Mus muscu	R.AQQVAVQEQEIAR@.R	6.74	2.51	2.69	0.37
Q60634_FLOT2_MOUSE	Flot2	Flotillin-2 OS=Mus muscu	R.DADIGVAEAER@.D	6.83	4.98	1.37	0.73
Q60634_FLOT2_MOUSE	Flot2	Flotillin-2 OS=Mus muscu	K.M*ALVLEALPQIAAK#.I	7.23	3.63	1.99	0.50
Q6ZPF4_FMNL3_MOUSE	Fmnl3	Formin-like protein 3 OS	K.AAAVSLENVLLDVK#.E	8.06	1.89	4.27	0.23
Q6ZPF4_FMNL3_MOUSE	Fmnl3	Formin-like protein 3 OS	K.LQSLDLLLDTK#.S	9.53	1.90	5.01	0.20
Q6ZPF4_FMNL3_MOUSE	Fmnl3	Formin-like protein 3 OS	K.AAAVSLENVLLDVK#.E	21.59	9.03	2.39	0.42
Q6ZPF4_FMNL3_MOUSE	Fmnl3	Formin-like protein 3 OS	K.DGTIEDIITVLK#.S	8.54	4.17	2.05	0.49
Q6ZPF4_FMNL3_MOUSE	Fmnl3	Formin-like protein 3 OS	K.LGLEEFLQK#.S	13.20	4.48	2.95	0.34
Q6ZPF4_FMNL3_MOUSE	Fmnl3	Formin-like protein 3 OS	K.LLDLENENM*M*R@.V	6.09	1.38	4.43	0.23
Q6ZPF4_FMNL3_MOUSE	Fmnl3	Formin-like protein 3 OS	K.LQSLDLLLDTK#.S	13.37	4.00	3.35	0.30
Q6ZPF4_FMNL3_MOUSE	Fmnl3	Formin-like protein 3 OS	K.TAEEAYNAVVR@.Y	12.07	2.38	5.07	0.20
Q6ZPF4_FMNL3_MOUSE	Fmnl3	Formin-like protein 3 OS	K.TTPPSVFFPVFVR@.F	19.84	5.94	3.34	0.30
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	K.DINESDEVEVYSR@.A	15.53	12.62	1.23	0.81
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	R.GM*VPFVFVGTK#.D	10.24	5.24	1.95	0.51
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	R.SFLEFAEDVIQVPR@.N	40.75	22.21	1.83	0.55
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	R.TADGSLQSASSEGSR@.L	12.78	9.76	1.31	0.76
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	K.DINESDEVEVYSR@.A	39.39	11.72	3.36	0.30
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	K.DSIANATVLLDYHLNYLK#.E	44.72	12.99	3.44	0.29
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	K.DVHEDSITVAFENNWQPER@.Q	19.95	5.60	3.56	0.28
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	R.GM*VPFVFVGTK#.D	25.12	8.95	2.81	0.36
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	R.SFLEFAEDVIQVPR@.N	75.52	24.96	3.03	0.33
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	R.SVNPNK#PATK#.D	9.44	10.40	0.91	1.10
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	R.TADGSLQSASSEGSR@.L	61.08	16.47	3.71	0.27
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	K.DINESDEVEVYSR@.A	3.44	1.79	1.92	0.52
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	R.SFLEFAEDVIQVPR@.N	15.65	5.48	2.86	0.35
E9QNF5_E9QNF5_MOUSE	Fmr1	Fragile X mental retardat	R.TADGSLQSASSEGSR@.L	6.25	3.16	1.98	0.50
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.GVTYNIIVEALQNQR.R	1.81	7.73	0.23	4.28
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.APITGYIIR.H	3.85	146.67	0.03	38.07
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.ATGVFTTLQPLR.S	8.54	126.77	0.07	14.85
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.EINLSPDSSSVIVSGLM*VATK.Y	2.43	4.17	0.58	1.72
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.EINLSPDSSSVIVSGLM*VATK.Y	4.11	8.52	0.48	2.07
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.EINLSPDSSSVIVSGLMVATK.Y	1.42	6.03	0.24	4.23
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.ESNPLTAQQTTK.L	2.84	61.24	0.05	21.55
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.EVTSDSGSIVVSGLTPGVEYTYTIQVLR.D	2.48	13.27	0.19	5.36
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.FLTTTPNSLLVSWQAPR.A	1.44	19.84	0.07	13.78
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.FSQVTPTSFTAQWIAPSVQLTGYR.V	2.92	20.75	0.14	7.11
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.FTNIGPDTM*R.V	14.54	55.91	0.26	3.85
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.GLAFTDVDVDSIK.I	11.43	117.53	0.10	10.28
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.GVTYNIIVEALQNQR.R	7.10	54.84	0.13	7.72
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.HALQSASAGSGSFTDVR.T	13.45	103.23	0.13	7.67
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.HYQINQQWER.T	2.60	23.90	0.11	9.19
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.IAWESPQGQVSR.Y	1.72	48.03	0.04	27.96
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.IHLYTLNDNAR.S	5.93	53.62	0.11	9.05
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.KKTDELPQLVTLPHPNLHGPEILDVPSTVQK.T	2.94	38.19	0.08	12.99
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.LGVRPSQGGEAPR.E	5.66	149.79	0.04	26.45
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.LRPRPYLPNVDEEVQIGHVPR.G	2.80	17.80	0.16	6.36
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.NSITLTNLNPGTEYVVSIIAVNGR.E	1.94	9.16	0.21	4.73
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.NTFAEITGLSPGVTYLFK.V	8.86	76.25	0.12	8.60
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.SDNVPPPTDLQFVELTDVK.V	4.14	25.99	0.16	6.28
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.SSPVIIDASTAIDAPSNLR.F	4.22	36.73	0.11	8.70
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.SYTITGLQPGTDYK.I	5.49	62.64	0.09	11.40
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TASPDQTEM*TIEGLQPTVEYVVSVYAQNR.N	5.66	23.01	0.25	4.07
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TDELPQLVTLPHPNLHGPEILDVPSTVQK.T	10.27	18.08	0.57	1.76
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TEIDKPSQM*QVTDVQDNSISVR.W	2.03	47.67	0.04	23.52
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TEIDKPSQMQVTDVQDNSISVR.W	1.61	18.17	0.09	11.32
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.TFYQIGDSWEK.F	5.12	38.48	0.13	7.51
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TGLDSPTGFDSSDITANSFTVHWVAPR.A	4.53	50.84	0.09	11.23
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TPFITNPGYDTENGIQLPGTTHQQPSVGQQM*IFEEHGFR.R	2.71	3.37	0.81	1.24
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.TVLVTWTPPR.A	7.54	54.41	0.14	7.22
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.VFAVHQGR.E	1.73	23.53	0.07	13.57
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.VGDTYERPK.D	1.38	13.14	0.11	9.49
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.VTIM*WTPPDSVVSGYR.V	9.31	15.91	0.59	1.71
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VTWAPPPSIELTNLLVR.Y	4.76	78.59	0.06	16.50
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VTYSSPEDGIR.E	2.34	45.46	0.05	19.41
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VVTPLSPPTNLHLEANPDTGVLTVSWER.S	3.39	29.67	0.11	8.76
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.WSRPQAPITGYR.I	2.98	53.08	0.06	17.82
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.YEVSVYALK.D	3.45	51.93	0.07	15.05
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.YIVNVYQISEEGK.Q	6.93	80.99	0.09	11.69
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.APITGYIIR.H	52.98	1052.88	0.05	19.87
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.ATGVFTTLQPLR.S	43.29	774.62	0.06	17.89
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.DAPIVNR.V	40.51	443.76	0.09	10.95
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.DTLTSRPAQGVITTLENVSPPR.R	5.22	96.42	0.05	18.47
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.EESPPLIGQQATVSDIPR.D	5.08	117.83	0.04	23.18
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.EINLSPDSSSVIVSGLM*VATK.Y	12.91	48.63	0.27	3.77
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.EINLSPDSSSVIVSGLM*VATK.Y	6.79	41.21	0.16	6.07
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.EINLSPDSSSVIVSGLMVATK.Y	8.87	46.21	0.19	5.21
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.EINLSPDSSSVIVSGLMVATK.Y	4.89	33.56	0.15	6.86
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.ESNPLTAQQTTK.L	23.43	376.33	0.06	16.06
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.EVTSDSGSIVVSGLTPGVEYTYTIQVLR.D	8.41	77.97	0.11	9.27
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.EVVPRPRPGVTEATITGLEPGTEYTIYVIALK.N	1.69	10.55	0.16	6.26
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.FLTTTPNSLLVSWQAPR.A	10.72	169.68	0.06	15.83
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.FSQVTPTSFTAQWIAPSVQLTGYR.V	10.94	131.28	0.08	12.00
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.FTNIGPDTM*R.V	27.07	452.34	0.06	16.71
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.GLAFTDVDVDSIK.I	34.76	525.73	0.07	15.12
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.GVTYNIIVEALQNQR.R	19.52	291.92	0.07	14.95
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.GVTYNIIVEALQNQR@.R	16.89	229.14	0.07	13.57
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.HALQSASAGSGSFTDVR.T	21.45	371.39	0.06	17.32
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.HYQINQQWER.T	9.47	118.56	0.08	12.53
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.IAWESPQGQVSR.Y	8.66	266.96	0.03	30.82
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.IGDTWSK.K	7.57	196.56	0.04	25.95
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.ITYGETGGNSPVQEFTVPGSK.S	32.07	160.61	0.20	5.01
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.KTDELPQLVTLPHPNLHGPEILDVPSTVQK.T	2.75	47.67	0.06	17.31
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.KYIVNVYQISEEGK.Q	2.86	34.61	0.08	12.09
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.LGVRPSQGGEAPR.E	70.60	1231.77	0.06	17.45

P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.NLQPGSEYTVTLVAVK.G	51.72	589.71	0.09	11.40
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.NSITLTNLNPGTEYVVSIIAVNGR.E	6.48	69.83	0.09	10.78
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.NTFAEITGLSPGVTYLFK.V	51.38	396.18	0.13	7.71
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.QKTGLDSPTGFDSSDITANSFTVHWVAPR.A	4.98	66.21	0.08	13.31
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.QYNVGPLASK.Y	13.93	280.84	0.05	20.16
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.SDNVPPPTDLQFVELTDVK.V	48.13	321.36	0.15	6.68
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.SSPVIIDASTAIDAPSNLR.F	26.75	435.21	0.06	16.27
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.STATINNIKPGADYTITLYAVTGR.G	5.45	93.20	0.06	17.11
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.SYTITGLQPGTDYK.I	36.78	473.57	0.08	12.88
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TASPDQTEM*TIEGLQPTVEYVVSVYAQNR.N	24.13	153.49	0.16	6.36
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TASPDQTEMTIEGLQPTVEYVVSVYAQNR.N	6.41	50.47	0.13	7.87
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TEIDKPSQM*QVTDVQDNSISVR.W	16.07	258.53	0.06	16.09
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TEIDKPSQMQVTDVQDNSISVR.W	4.45	87.16	0.05	19.60
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TETITGFQVDAIPANGQTPVQR.S	1.73	12.00	0.14	6.92
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.TFYQIGDSWEK.F	14.36	236.46	0.06	16.46
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TGLDSPTGFDSSDITANSFTVHWVAPR.A	38.51	413.29	0.09	10.73
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.TKTETITGFQVDAIPANGQTPVQR.S	4.40	119.24	0.04	27.07
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TPFITNPGYDTENGIQLPGTTHQQPSVGQQM*IFEEHGFR.R	17.31	30.65	0.56	1.77
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.TPFITNPGYDTENGIQLPGTTHQQPSVGQQM*IFEEHGFRR.T	4.01	28.80	0.14	7.18
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.TVLVTWTPPR.A	21.20	329.90	0.06	15.56
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VEVLPVSLPGEHGQR.L	47.57	1005.92	0.05	21.15
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGR.K	6.50	25.45	0.26	3.92
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK.Y	3.59	47.05	0.08	13.12
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.VFAVHQGR.E	8.26	129.26	0.06	15.65
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.VGDTYERPK.D	8.45	135.68	0.06	16.06
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VTDATETTITISWR.T	2.62	39.72	0.07	15.17
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.VTIM*WTPPDSVVSGYR.V	9.14	137.13	0.07	15.01
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.VTIMWTPPDSVVSGYR.V	4.21	41.58	0.10	9.88
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VTWAPPPSIELTNLLVR.Y	28.07	501.46	0.06	17.87
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VTYSSPEDGIR.E	17.05	248.54	0.07	14.57
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.VVTPLSPPTNLHLEANPDTGVLTVSWER.S	26.24	275.86	0.10	10.51
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.WLPSTSPVTGYR.V	15.68	285.55	0.05	18.21
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	R.WSRPQAPITGYR.I	30.31	471.38	0.06	15.55
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.YEVSVYALK.D	9.62	222.39	0.04	23.12
P11276_FINC_MOUSE	Fn1	Fibronectin OS=Mus mus	K.YIVNVYQISEEGK.Q	31.68	350.65	0.09	11.07
B7ZNJ1_B7ZNJ1_MOUSE	Fn1	Fibronectin OS=Mus mus	R.NGESQPLVQTAVTTIPAPTNLK.F	5.86	26.76	0.22	4.57
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	R.ALEEGDGSVSGSSPR@.S	17.21	1.35	12.79	0.08
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	K.EVNEGIQALSNSEEER@.K	12.54	2.97	4.22	0.24
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	K.FEFLGINR@.Q	45.47	7.04	6.46	0.15
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	K.FQIGELANTLTSK#.F	18.89	4.54	4.16	0.24
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	K.GVAAALLAPLLPEGVK#EEEER@.W	10.82	2.54	4.27	0.23
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	R.SDISQPASQDGVR@.R	19.94	4.18	4.77	0.21
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	K.VEEEQDLK#.F	31.15	5.45	5.71	0.18
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	K.VEEEQDLK#FQIGELANTLTSK#.F	10.66	2.60	4.11	0.24
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	R.ALEEGDGSVSGSSPR@.S	6.72	1.79	3.76	0.27
Q6ZQ03_FNBP4_MOUSE	Fnbp4	Formin-binding protein	K.FQIGELANTLTSK#.F	6.36	1.23	5.16	0.19
P47930_FOSL2_MOUSE	Fosl2	Fos-related antigen 2 OS=	R.GSSGSPAHAESYSSGGGGQQK.F	4.30	8.17	0.53	1.90
P47930_FOSL2_MOUSE	Fosl2	Fos-related antigen 2 OS=	R.GTGSAVGPVVVK.Q	6.06	11.12	0.55	1.83
P47930_FOSL2_MOUSE	Fosl2	Fos-related antigen 2 OS=	K.LQAETEELEEEK.S	6.53	13.75	0.48	2.10
Q61572_FOXC1_MOUSE	Foxc1	Forkhead box protein C1	R.AYGPYTPQPQPK.D	6.67	9.97	0.67	1.50
P58462_FOXP1_MOUSE	Foxp1	Forkhead box protein P1	K.AAPQPLNLVSSVTLSK#.S	13.07	9.84	1.33	0.75
P58462_FOXP1_MOUSE	Foxp1	Forkhead box protein P1	K.GAVWTVDEVEFQK#.R	13.31	7.39	1.80	0.55
P58462_FOXP1_MOUSE	Foxp1	Forkhead box protein P1	R.YSDK#YNVPISSADIAQNQEFYK#.N	10.77	7.12	1.51	0.66
P58462_FOXP1_MOUSE	Foxp1	Forkhead box protein P1	K.AAPQPLNLVSSVTLSK#.S	30.77	16.55	1.86	0.54
P58462_FOXP1_MOUSE	Foxp1	Forkhead box protein P1	K.GAVWTVDEVEFQK#.R	20.86	11.24	1.86	0.54
P58462_FOXP1_MOUSE	Foxp1	Forkhead box protein P1	K.NAEVRPPFTYASLIR.Q	29.35	11.37	2.58	0.39
P58462_FOXP1_MOUSE	Foxp1	Forkhead box protein P1	R.YSDK#YNVPISSADIAQNQEFYK#.N	15.22	10.71	1.42	0.70
P97376_FRG1_MOUSE	Frg1	Protein FRG1 OS=Mus mu	K.YLGINSDGLVVGR@.S	14.58	10.46	1.39	0.72
Q3UFK8_FRMD8_MOUSE	Frmd8	FERM domain-containin	K.TGPGEQGLLNAYR@.Q	7.60	3.84	1.98	0.50
F8VQ05_F8VQ05_MOUSE	Fryl	Protein Fryl OS=Mus mus	K.EAEAASENEEIDISK#.A	4.05	2.16	1.88	0.53
P29391_FRIL1_MOUSE	Ftl1	Ferritin light chain 1 OS=	R.LLEFQNDR@.G	7.77	5.14	1.51	0.66
P29391_FRIL1_MOUSE	Ftl1	Ferritin light chain 1 OS=	K.TQEAM*EAALAM*EK#.N	2.85	2.23	1.28	0.78
P29391_FRIL1_MOUSE	Ftl1	Ferritin light chain 1 OS=	K.NLNQALLDLHALGSAR@.T	12.70	5.30	2.39	0.42
Q9DBE9_SPB1_MOUSE	Ftsj3	pre-rRNA processing prot	K.DGFSGIEDDADEALEISQAQLLYK#.S	7.94	2.40	3.31	0.30
Q9DBE9_SPB1_MOUSE	Ftsj3	pre-rRNA processing prot	R.FTQVDDNK#EEEGENPLLVPLEEK#.A	11.21	6.95	1.61	0.62
Q91WJ8_FUBP1_MOUSE	Fubp1	Far upstream element-bi	K.IQIAPDSGGLPER@.S	8.54	4.58	1.86	0.54
Q91WJ8_FUBP1_MOUSE	Fubp1	Far upstream element-bi	K.IQNDAGVR@.I	30.27	14.04	2.16	0.46
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.EILGGLTVTR@.G	42.41	17.24	2.46	0.41
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	K.IDSIPHLNNSTPLVDPSVYGYGVQK#.R	16.16	5.76	2.81	0.36
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.IINELILTAQER@.E	34.95	16.70	2.09	0.48
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.IQFKPDDGISPER.A	51.59	20.95	2.46	0.41
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	K.M*VGFIIGR@.G	13.57	5.60	2.42	0.41
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.NGPGFHNDM*DGNSTIQELLIPASK#.V	11.56	4.27	2.71	0.37
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.NPPPNTDPNLR@.I	9.94	8.51	1.17	0.86
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.SDWSVGTPGGVQEITYTVPADK#.C	4.66	2.79	1.67	0.60
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.AAQVM*GPPDR@.C	23.16	10.35	2.24	0.45
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.AGGGSIEVSVPR@.F	46.58	21.30	2.19	0.46
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.EILGGLTVTR@.G	70.02	26.34	2.66	0.38
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.FVVGIVIGR@.N	11.47	4.72	2.43	0.41
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	K.IDSIPHLNNSTPLVDPSVYGYGVQK#.R	28.44	15.72	1.81	0.55
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.IINELILTAQER@.E	48.21	18.52	2.60	0.38
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.IQFK#PDDGISPER@.A	71.65	29.60	2.42	0.41
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.LLGQIVDR@.C	58.30	20.37	2.86	0.35
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	K.M*VGFIIGR@.G	38.86	15.22	2.55	0.39
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.NGPGFHNDM*DGNSTIQELLIPASK#.V	13.45	4.29	3.14	0.32
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.QQAAFYGQTLGQAQAHSQEQ.-	12.75	12.75	1.00	1.00
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	K.QSHPTSAAPQASSPPDYTM*AWAEYYR@.Q	4.96	4.19	1.18	0.84
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	R.SDWSVGTPGGVQEITYTVPADK#.C	6.72	3.55	1.90	0.53
A2AJ72_A2AJ72_MOUSE	Fubp3	MCG130458 OS=Mus mu	K.VGGASLGAPAAFGQSPFSQPPAAPHQNTFPPR@.G	3.32	3.20	1.04	0.96
Q9D6K8_FUND2_MOUSE	Fundc2	FUN14 domain-containi	K.SK#AEEVVSFVK#.K	8.83	3.49	2.53	0.40
P56959_FUS_MOUSE	Fus	RNA-binding protein FUS	R.HDSEQDNSDNNTIFVQGLGENVTIESVADYFK#.Q	4.53	1.99	2.27	0.44
P56959_FUS_MOUSE	Fus	RNA-binding protein FUS	K.LKGEATVSFDDPPSAK.A	13.24	11.34	1.17	0.86
P56959_FUS_MOUSE	Fus	RNA-binding protein FUS	K.AAIDWFDGK#.E	11.19	6.11	1.83	0.55
P56959_FUS_MOUSE	Fus	RNA-binding protein FUS	K.GEATVSFDDPPSAK#.A	50.11	16.27	3.08	0.32
P56959_FUS_MOUSE	Fus	RNA-binding protein FUS	K.LK#GEATVSFDDPPSAK#.A	20.60	12.30	1.68	0.60
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.EDGM*VPFVFVGTK#.E	11.49	7.70	1.49	0.67
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	K.EISEGDEVEVYSR@.A	11.99	8.25	1.45	0.69
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.KVPGVTAIELDEDTGTFR.I	30.26	24.63	1.23	0.81
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.LQIDEQLR.Q	83.00	54.28	1.53	0.65
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	K.VIQEIVDK#.S	26.12	14.65	1.78	0.56
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.LQIDEQLR.Q	11.51	12.03	0.96	1.05
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	K.DVHEDSLTVVFENNWQPER@.Q	11.03	5.06	2.18	0.46
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.EDGM*VPFVFVGTK#.E	41.46	16.58	2.50	0.40

Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.EDGMVPFVFVGTK#.E	10.46	4.04	2.59	0.39
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.EDLM*GLAIGTHGSNIQQAR@.K	28.37	9.05	3.13	0.32
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	K.EISEGDEVEVYSR@.A	79.78	27.64	2.89	0.35
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	K.GYATDESTVSSVQGSR@.S	12.13	4.53	2.68	0.37
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.IFYHPETTQLM*ILSASEATVK#.R	30.24	11.40	2.65	0.38
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.IYGESAEAVK#.K	35.10	12.20	2.88	0.35
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.K#VPGVTAIELDEDTGTFR@.I	144.00	58.65	2.46	0.41
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.LQIDEQLR.Q	251.24	94.69	2.65	0.38
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	K.SSISSVLK#DPDSNPYSLLDNTESDQTADTDASESHHSTNR@.R	8.28	2.14	3.87	0.26
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	K.SSISSVLK#DPDSNPYSLLDNTESDQTADTDASESHHSTNR@R@.R	8.91	2.17	4.12	0.24
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	K.VIQEIVDK#.S	140.18	53.86	2.60	0.38
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	K.VPGVTAIELDEDTGTFR@.I	17.68	1.54	11.50	0.09
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.EDGM*VPFVFVGTK#.E	9.77	6.75	1.45	0.69
Q61584_FXR1_MOUSE	Fxr1	Fragile X mental retardat	R.K#VPGVTAIELDEDTGTFR@.I	21.74	7.35	2.96	0.34
Q9WVR4_FXR2_MOUSE	Fxr2	Fragile X mental retardat	K.DVHEDSVTIFFENNWQSER@.Q	16.07	7.70	2.09	0.48
Q9WVR4_FXR2_MOUSE	Fxr2	Fragile X mental retardat	R.EDLM*GLAIGTHGANIQQAR@.K	40.72	15.90	2.56	0.39
Q9WVR4_FXR2_MOUSE	Fxr2	Fragile X mental retardat	R.EDLMGLAIGTHGANIQQAR@.K	13.45	4.95	2.71	0.37
Q9WVR4_FXR2_MOUSE	Fxr2	Fragile X mental retardat	K.QLAAAFQEEFTVR@.E	6.57	4.17	1.57	0.63
Q9WVR4_FXR2_MOUSE	Fxr2	Fragile X mental retardat	R.SYLEFSEDSVQVPR@.D	32.04	16.35	1.96	0.51
Q9WVR4_FXR2_MOUSE	Fxr2	Fragile X mental retardat	R.TDGSISGDR@QPVTVADYISR@.A	13.00	3.62	3.59	0.28
Q9WVR4_FXR2_MOUSE	Fxr2	Fragile X mental retardat	R.TGGPAYGPSSDPSTASETESEK#R@.E	6.88	4.55	1.51	0.66
Q9WVR4_FXR2_MOUSE	Fxr2	Fragile X mental retardat	R.SYLEFSEDSVQVPR@.D	9.34	3.63	2.57	0.39
Q8VDC1_FYCO1_MOUSE	Fyco1	FYVE and coiled-coil dom	R.LQAEAQAQELR@.A	7.76	2.60	2.98	0.34
Q91Z49_UIF_MOUSE	Fyttd1	UAP56-interacting factor	R.ANLTFSK#.G	42.07	10.48	4.01	0.25
Q91Z49_UIF_MOUSE	Fyttd1	UAP56-interacting factor	K.GVPLQFDINSVGK#.Q	51.85	17.42	2.98	0.34
Q91Z49_UIF_MOUSE	Fyttd1	UAP56-interacting factor	R.K#NNIPANFTR@.N	11.62	10.88	1.07	0.94
Q91Z49_UIF_MOUSE	Fyttd1	UAP56-interacting factor	R.LVGATATPPPPPK#.A	31.08	15.54	2.00	0.50
Q91Z49_UIF_MOUSE	Fyttd1	UAP56-interacting factor	R.TAVPSFLTK#.R	30.49	17.07	1.79	0.56
Q91Z49_UIF_MOUSE	Fyttd1	UAP56-interacting factor	K.VQTQLNTEQLIDDVVAK#.R	26.62	9.21	2.89	0.35
Q91Z49_UIF_MOUSE	Fyttd1	UAP56-interacting factor	R.WGIQQNSGFGK#.T	18.56	19.88	0.93	1.07
Q91Z49_UIF_MOUSE	Fyttd1	UAP56-interacting factor	R.LVGATATPPPPPK#.A	5.70	4.01	1.42	0.70
Q91Z49_UIF_MOUSE	Fyttd1	UAP56-interacting factor	K.VQTQLNTEQLIDDVVAK#.R	2.62	1.77	1.47	0.68
P97855_G3BP1_MOUSE	G3bp1	Ras GTPase-activating pro	R.EAGEPGDVEPR@.R	11.63	4.81	2.42	0.41
P97855_G3BP1_MOUSE	G3bp1	Ras GTPase-activating pro	K.LPNFGFVVFDDSEPVQK#.V	12.69	6.51	1.95	0.51
P97855_G3BP1_MOUSE	G3bp1	Ras GTPase-activating pro	K.LPNFGFVVFDDSEPVQK#.V	7.78	4.43	1.76	0.57
P97379_G3BP2_MOUSE	G3bp2	Ras GTPase-activating pro	K.FM*QTFVLAPEGSVPNK.F	3.94	2.50	1.58	0.63
P97379_G3BP2_MOUSE	G3bp2	Ras GTPase-activating pro	K.LPNFGFVVFDDSEPVQR@.I	14.04	7.83	1.79	0.56
P97379_G3BP2_MOUSE	G3bp2	Ras GTPase-activating pro	R.VDAK#PEVQSQPPR@.V	27.51	10.92	2.52	0.40
E0CXU4_E0CXU4_MOUSE	G930045G22Rik	Protein G930045G22Rik	R.ESRMEQPR@.G	8.15	2.57	3.17	0.32
Q00422_GABPA_MOUSE	Gabpa	GA-binding protein alpha	K.HITTISDETSEQVTR@.W	32.35	10.19	3.17	0.32
Q00422_GABPA_MOUSE	Gabpa	GA-binding protein alpha	K.LNILEIVK#.T	47.90	10.38	4.62	0.22
Q00422_GABPA_MOUSE	Gabpa	GA-binding protein alpha	K.LNQPELVAQK#.W	22.64	7.20	3.14	0.32
Q00422_GABPA_MOUSE	Gabpa	GA-binding protein alpha	K.TLIGYSAAELNR@.L	24.03	7.00	3.43	0.29
Q00422_GABPA_MOUSE	Gabpa	GA-binding protein alpha	K.LNILEIVK#.T	40.35	10.44	3.87	0.26
P81069_GABP2_MOUSE	Gabpb2	GA-binding protein subu	K.ATSAHLEEM*EEGNSLDSSTQQVVGSGGQR@.V	9.09	3.42	2.65	0.38
P81069_GABP2_MOUSE	Gabpb2	GA-binding protein subu	R.TTEPHTNVSIETISS.-	10.22	10.22	1.00	1.00
P81069_GABP2_MOUSE	Gabpb2	GA-binding protein subu	K.YGADVYAFSK#.F	5.23	2.01	2.60	0.38
Q99KY4_GAK_MOUSE	Gak	Cyclin-G-associated kinas	R.DQSDFVGQTVELGELR@.L	4.38	3.26	1.34	0.74
Q99KY4_GAK_MOUSE	Gak	Cyclin-G-associated kinas	R.DQSDFVGQTVELGELR@.L	9.81	4.71	2.08	0.48
Q99KY4_GAK_MOUSE	Gak	Cyclin-G-associated kinas	R.IAVM*SFPAEGVESAIK.N	6.30	8.42	0.75	1.34
Q99KY4_GAK_MOUSE	Gak	Cyclin-G-associated kinas	K.VSENDFEDLLPNQGFSK#.S	3.73	2.67	1.40	0.71
Q99KY4_GAK_MOUSE	Gak	Cyclin-G-associated kinas	R.DQSDFVGQTVELGELR@.L	16.32	7.01	2.33	0.43
Q99KY4_GAK_MOUSE	Gak	Cyclin-G-associated kinas	K.GDLDISYITSR@.I	14.91	9.50	1.57	0.64
Q99KY4_GAK_MOUSE	Gak	Cyclin-G-associated kinas	K.SVVM*TPVPLFSK#.Q	50.53	18.03	2.80	0.36
Q99KY4_GAK_MOUSE	Gak	Cyclin-G-associated kinas	K.VIQSVANYAK#.G	12.92	4.75	2.72	0.37
Q99KY4_GAK_MOUSE	Gak	Cyclin-G-associated kinas	K.VSENDFEDLLPNQGFSK#.S	5.13	3.49	1.47	0.68
P16858_G3P_MOUSE	Gapdh	Glyceraldehyde-3-phospl	R.GAAQNIIPASTGAAK#.A	69.49	38.94	1.78	0.56
P16858_G3P_MOUSE	Gapdh	Glyceraldehyde-3-phospl	K.LISWYDNEYGYSNR@.V	32.09	13.76	2.33	0.43
P16858_G3P_MOUSE	Gapdh	Glyceraldehyde-3-phospl	K.VIHDNFGIVEGLM*TTVHAITATQK#.T	19.41	13.92	1.39	0.72
P16858_G3P_MOUSE	Gapdh	Glyceraldehyde-3-phospl	R.VVDLM*AYM*ASK#E.-	15.34	7.17	2.14	0.47
P16858_G3P_MOUSE	Gapdh	Glyceraldehyde-3-phospl	K.WGEAGAEYVVESTGVFTTM*EK#.A	12.00	8.76	1.37	0.73
P16858_G3P_MOUSE	Gapdh	Glyceraldehyde-3-phospl	R.GAAQNIIPASTGAAK.A	6.64	6.77	0.98	1.02
P16858_G3P_MOUSE	Gapdh	Glyceraldehyde-3-phospl	K.LISWYDNEYGYSNR.V	3.74	3.99	0.94	1.07
P16858_G3P_MOUSE	Gapdh	Glyceraldehyde-3-phospl	R.GAAQNIIPASTGAAK#.A	5.95	4.08	1.46	0.69
P16858_G3P_MOUSE	Gapdh	Glyceraldehyde-3-phospl	R.GAAQNIIPASTGAAK#.A	5.64	3.67	1.54	0.65
Q9CY66_GAR1_MOUSE	Gar1	H/ACA ribonucleoprotei	K.FQDQGPPER.V	5.36	6.35	0.84	1.19
Q9CY66_GAR1_MOUSE	Gar1	H/ACA ribonucleoprotei	K.FQDQGPPER.V	16.02	31.47	0.51	1.96
Q9CY66_GAR1_MOUSE	Gar1	H/ACA ribonucleoprotei	K.VDEIFGQLR.D	6.15	14.15	0.43	2.30
Q61169_GATA6_MOUSE	Gata6	Transcription factor GAT.	R.GPSTDLLEDLSESR@.E	8.37	7.37	1.14	0.88
Q920S3_GATD1_MOUSE	Gatad1	GATA zinc finger domain-	R.DQFDPASYIIGPEEDLPR@.K	11.28	11.30	1.00	1.00
Q920S3_GATD1_MOUSE	Gatad1	GATA zinc finger domain-	K.GVYYQIGDVVSVIDEQDGK#PYYAQIR@.G	5.48	4.28	1.28	0.78
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.ALQQEQEM*EQR@.L	17.51	6.52	2.69	0.37
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.EATAQK#PTASSGSTVTTPPPLVR@.G	8.19	4.31	1.90	0.53
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	R.IPGSIIPPPLVR@.G	6.62	2.98	2.22	0.45
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	R.LLQQGVGTASIK#.A	58.65	19.20	3.05	0.33
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.LQNAASATALVSR@.T	22.78	6.22	3.66	0.27
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	R.LLQQGVGTASIK#.A	3.97	2.50	1.59	0.63
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.ALQQEQEM*EQR@.L	14.39	6.24	2.31	0.43
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.EATAQK#PTASSGSTVTTPPPLVR@.G	18.70	6.87	2.72	0.37
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.GSSELTVDGDSR@.V	12.62	4.15	3.04	0.33
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	R.IIQQGLIR@.V	18.77	9.64	1.95	0.51
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	R.IPGSIIPPPLVR@.G	13.39	6.06	2.21	0.45
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.LGPQASSQVVM*PPLVR@.G	4.79	4.09	1.17	0.85
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	R.LLQQGVGTASIK#.A	35.02	13.92	2.52	0.40
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.LQNAASATALVSR@.T	19.10	6.42	2.98	0.34
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.TPLSTGGTLAFVSPSLAVHK#.T	18.83	9.20	2.05	0.49
Q8CHY6_P66A_MOUSE	Gatad2a	Transcriptional repressor	K.TSLQTSSTR@.I	10.01	2.43	4.11	0.24
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	K.AANLEM*FK#.G	8.37	4.14	2.02	0.49
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	K.ALQQEQEIEQR@.L	99.10	31.85	3.11	0.32
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	K.LPSR@PGAQGIEPQNM*R@.T	24.66	14.23	1.73	0.58
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.LQQQAALSPTTAPAVSSVSK#.Q	22.83	8.89	2.57	0.39
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.QAPQPQSSLQR@.G	49.84	17.81	2.80	0.36
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.SISQSISGQK#.-	34.04	9.53	3.57	0.28
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	K.TPVVQNAASIVQPSPAHVGQQGLSK#.L	32.82	10.82	3.03	0.33
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.TTSSAIYM*NLASHIQPGTVNR@.V	8.02	7.35	1.09	0.92
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.VIAPNPAQLQGQR@.G	34.98	14.94	2.34	0.43
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.VSSPLPSPSAM*SDAANSQAAAK#.L	21.23	7.75	2.74	0.36
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	K.ALQQEQEIEQR@.L	12.45	4.28	2.91	0.34
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	K.ALQQEQEIEQR@.L	28.46	9.36	3.04	0.33
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	K.LPSR@PGAQGIEPQNM*R@.T	21.53	5.52	3.90	0.26
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.LQQQAALSPTTAPAVSSVSK#.Q	9.66	3.06	3.16	0.32
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.QAPQPQSSLQR@.G	19.84	7.27	2.73	0.37
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.TTSSAIYM*NLASHIQPGTVNR@.V	10.34	5.49	1.88	0.53

Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.VIAPNPAQLQGQR.G	34.64	12.01	2.88	0.35
Q8VHR5_P66B_MOUSE	Gatad2b	Transcriptional repressor	R.VSSPLPSPSAM*SDAANSQAAAK#.L	10.87	3.71	2.93	0.34
P17439_GLCM_MOUSE	Gba	Glucosylceramidase OS=	R.NFVDSPIIVDIPK.D	5.50	4.12	1.34	0.75
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	K.LLENISPADVGGM*EETR@.M	5.37	3.89	1.38	0.72
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	R.FVGTDPASDEVVLM*K#.I	6.93	2.58	2.69	0.37
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	R.SEDTTGPITGLALTSVNK#.F	7.33	49.80	0.15	6.80
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	R.ADAPDAGAQSDSELPSYHQNDVSLDR@.G	6.43	2.33	2.76	0.36
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	R.APSSSSPGSPM*ASSPSK#.L	11.22	3.25	3.45	0.29
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	R.DLEEAGDSGADK#K#.F	2.63	2.02	1.30	0.77
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	K.FLSYALIDPTHEGTAEGM*ENM*ADAVTHAR@.F	8.91	3.17	2.81	0.36
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	K.FTALSSESIENLPSVFGSNPK#.A	4.88	1.53	3.19	0.31
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	R.FVGTDPASDEVVLM*K#.I	10.85	4.40	2.46	0.41
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	R.GASPEGVFLR@.V	15.02	3.98	3.78	0.26
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	K.LLENISPADVGGM*EETR@.M	9.62	3.24	2.97	0.34
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	R.SEDTTGPITGLALTSVNK#.F	14.12	81.28	0.17	5.75
Q6A099_Q6A099_MOUSE	Gbf1	MKIAA0248 protein (Frag	K.SLEETIIQK#.A	15.79	15.51	1.02	0.98
Q61107_GBP4_MOUSE	Gbp4	Guanylate-binding prote	R.LLLQIENVPENQLER@.N	5.34	3.25	1.64	0.61
Q91Z40_Q91Z40_MOUSE	Gbp7	Gbp6 protein OS=Mus m	R.VITADEYLENALK#.L	6.52	2.34	2.79	0.36
E9PWY6_E9PWY6_MOUSE	Gcat	2-amino-3-ketobutyrate	K.WLTSRTFR@.W	1.01	4.11	0.25	4.07
Q9D4H2_GCC1_MOUSE	Gcc1	GRIP and coiled-coil dom	R.ALAVLAEK#DLELEQLR@.S	6.83	4.22	1.62	0.62
Q9D4H2_GCC1_MOUSE	Gcc1	GRIP and coiled-coil dom	R.AYAADQVEGFELQTK#.Q	5.42	2.72	1.99	0.50
Q9D4H2_GCC1_MOUSE	Gcc1	GRIP and coiled-coil dom	R.VAALESQISEVSELLGTYEK#.A	9.63	2.22	4.33	0.23
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.LIQAVGESLVK#.V	9.16	3.09	2.96	0.34
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.TM*TEDQEALSSK#.I	6.68	2.09	3.20	0.31
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.AEQAAVTSEFESYK#.V	34.21	9.23	3.70	0.27
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.ASILEENEEEDVVK#.L	40.73	14.16	2.88	0.35
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.ATHK#EEVTELM*SQIETSAK#.E	4.37	4.53	0.97	1.04
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.DINTFQAEILQLR@.A	45.96	11.30	4.07	0.25
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.DTM*LQELEAK#.I	10.47	4.47	2.34	0.43
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.EALQLDLLEM*K#.N	21.07	7.39	2.85	0.35
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.EAQTLR@EELESVR@.S	35.96	7.85	4.58	0.22
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.EFLQGAESYK#.S	19.25	11.24	1.71	0.58
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.EM*M*EILQTELGESAGK#.I	16.03	4.03	3.98	0.25
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.ETEATNAILM*EQIK#.L	15.97	4.76	3.36	0.30
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.EVSELSETFISGSEK#.E	21.81	5.18	4.21	0.24
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.GELEASQQQVEVYK#.I	16.57	13.87	1.19	0.84
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.IETLQANAK#.L	45.64	11.99	3.81	0.26
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.INELLLAK#.E	26.41	8.02	3.29	0.30
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.INELLLAK#EEQGYVVEK#.L	13.49	2.98	4.52	0.22
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.IQLAEM*TSEK#.H	22.01	15.82	1.39	0.72
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.ISQEFETM*K#.Q	14.21	4.50	3.16	0.32
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.LATVAQGEEESASR@.S	45.55	10.47	4.35	0.23
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.LEAQLFQLK#.S	47.38	10.67	4.44	0.23
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.LIQAVGESLVK#.V	54.53	15.81	3.45	0.29
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.LLEAQILEVQK#.A	65.66	20.43	3.21	0.31
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.LLENEQVQK#.S	22.51	9.19	2.45	0.41
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.LLPVIDTM*LQLSPEEK#.G	19.37	6.44	3.01	0.33
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.LLSQQELVPELESTIK#.N	36.13	9.13	3.96	0.25
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.LQDSQNSLQISVSEYQTLQAEHDTLLER@.H	8.11	3.21	2.53	0.40
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.LSVELR@.E	26.81	9.04	2.96	0.34
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.LTSDNEDLLAR@.I	38.63	11.58	3.34	0.30
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.M*LQETVTK#.E	20.65	7.31	2.82	0.35
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.NDQLSLVK#.E	27.03	7.76	3.49	0.29
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.NLQADNSM*YLASLGQK#.D	21.10	5.66	3.73	0.27
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.NSTIEDLEQEM*K#.I	9.51	4.02	2.36	0.42
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.QEVVLNYESLR@.E	23.83	7.52	3.17	0.32
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.SAFNEK#DALLETVNR@.L	20.41	5.67	3.60	0.28
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.SQNDQSITVQM*K#.T	14.55	3.86	3.77	0.27
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.SVSQVETEGAK#.Q	17.48	4.37	4.00	0.25
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.TLSAYQQR@.V	23.40	10.19	2.30	0.44
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.TM*TEDQEALSSK#.I	21.51	2.97	7.23	0.14
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	K.TQLYEYLK#.Q	23.90	4.05	5.90	0.17
B2RSU7_B2RSU7_MOUSE	Gcc2	GRIP and coiled-coil dom	R.VVALQEESR@.A	36.16	14.45	2.50	0.40
Q8BKT3_GCFC2_MOUSE	Gcfc2	GC-rich sequence DNA-bi	R.VAFEQFASENEVSK#.N	6.87	3.10	2.22	0.45
Q8BKT3_GCFC2_MOUSE	Gcfc2	GC-rich sequence DNA-bi	K.SIEDDIFIPLYPK#.S	6.86	2.88	2.38	0.42
O09172_GSH0_MOUSE	Gclm	Glutamate--cysteine ligas	K.LFIVGSNSSSSTR@.S	5.51	3.22	1.71	0.58
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.AASQGTQVPTVTEGVAAALLLSK#.L	11.99	5.38	2.23	0.45
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.ALQAAIQQLAEAQPEATAK#.N	10.26	2.21	4.65	0.22
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.IIIEDLLEATR@.S	13.53	1.53	8.85	0.11
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.VLPLEALVTDAGEVTEM*GK#.T	14.57	3.75	3.89	0.26
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.AASQGTQVPTVTEGVAAALLLSK#.L	20.39	9.42	2.16	0.46
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.ALADENEFVR@.D	19.21	5.07	3.79	0.26
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.ALQAAIQQLAEAQPEATAK#.N	25.16	8.31	3.03	0.33
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.ASLLDPVPEVR@.T	18.17	6.32	2.87	0.35
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.DAPNDASYDAVR@.Q	4.02	2.17	1.85	0.54
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.DAVLFFSESLVPTAR@.K	19.57	7.16	2.73	0.37
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.EEFSIM*QTPAGELFDK#.S	3.94	2.03	1.94	0.51
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.GLGILSLK#.Q	15.13	5.14	2.94	0.34
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.GVTSILPVLR@.E	10.38	4.54	2.29	0.44
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.IIIEDLLEATR@.S	46.62	12.73	3.66	0.27
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.K#LDAGNQLALIEELHK#.E	20.06	10.82	1.85	0.54
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.LANGLLDELK#.T	9.03	1.64	5.52	0.18
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.LDAGNQLALIEELHK#.E	14.24	5.13	2.78	0.36
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.LM*DEAVLALR@.N	21.08	0.00	#DIV/0!	0.00
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.LSGFWQLVVDEK#.R	11.22	3.63	3.09	0.32
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.LTIIAQK#.M	13.82	5.74	2.41	0.42
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.LYR@PPPVLDALGR@.V	15.07	4.48	3.36	0.30
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.R@ALQAAIQQLAEAQPEATAK#.N	10.21	4.36	2.34	0.43
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.SLVSGLIR@.L	18.38	7.26	2.53	0.39
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.STLLEFYVK#.N	12.74	7.35	1.73	0.58
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.VGK#GEPDAAPLSAPAFSLVFPM*LK#.M	14.36	4.00	3.59	0.28
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.VISESPPDQWEAR@.C	3.54	1.78	1.98	0.50
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	R.VLAFLSSVAGDALTR@.H	25.56	7.42	3.45	0.29
E9PVA8_E9PVA8_MOUSE	Gcn1l1	Protein Gcn1l1 OS=Mus	K.VLPLEALVTDAGEVTEM*GK#.T	48.85	18.16	2.69	0.37
Q9CQQ4_GEMI2_MOUSE	Gemin2	Gem-associated protein	K.SQQLDSNVAM*PK#.S	17.42	5.33	3.26	0.31
Q6P6L6_Q6P6L6_MOUSE	Gemin4	Gem (Nuclear organelle)	K.AVASVAHLVILNPEVVVK#.K	6.68	1.35	4.94	0.20
Q6P6L6_Q6P6L6_MOUSE	Gemin4	Gem (Nuclear organelle)	K.VLQPSPVSPSDTDTR@.W	6.10	1.85	3.29	0.30
Q6P6L6_Q6P6L6_MOUSE	Gemin4	Gem (Nuclear organelle)	K.GLEDITASIAM*AIIEQK#.M	3.91	1.66	2.36	0.42
Q6P6L6_Q6P6L6_MOUSE	Gemin4	Gem (Nuclear organelle)	K.SDWEHVGQPIVEALK#.E	9.43	3.70	2.55	0.39
A2AFQ9_A2AFQ9_MOUSE	Gemin5	Gem-associated protein	K.ELNEDVSADLEER@.F	5.15	2.36	2.19	0.46
A2AFQ9_A2AFQ9_MOUSE	Gemin5	Gem-associated protein	K.VLALGNEDGSIEIFQVPNLR@.L	24.48	6.32	3.88	0.26
A2AFQ9_A2AFQ9_MOUSE	Gemin5	Gem-associated protein	K.VLALGNEDGSIEIFQVPNLR.L	8.71	2.63	3.32	0.30
A2AFQ9_A2AFQ9_MOUSE	Gemin5	Gem-associated protein	K.VYEAVELLK#.S	8.65	3.05	2.84	0.35

A2AFQ9_A2AFQ9_MOUSE	Gemin5	Gem-associated protein	K.YPSATSNTPFR@.Q	12.38	22.37	0.55	1.81
Q9D1H7_GET4_MOUSE	Get4	Golgi to ER traffic protei	K.AEVDVADELLENLAK#.V	21.96	7.39	2.97	0.34
Q9D1H7_GET4_MOUSE	Get4	Golgi to ER traffic protei	K.VFSLM*DPNSPER@.V	10.67	4.90	2.18	0.46
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.AVEYYFASDASAVIEHTNR@.V	37.84	10.46	3.62	0.28
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.AVQTLQM*ELQQIM*K#.G	7.06	2.50	2.82	0.35
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.AVQTLQM*ELQQIMK#.G	2.16	1.88	1.15	0.87
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.EIFEQPESVVNTM*R.G	27.30	13.05	2.09	0.48
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.EVLSM*DDEIQK#.L	29.95	8.67	3.46	0.29
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.GSPLLIGVR@.S	29.94	7.56	3.96	0.25
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.GYDFESETDTETIAK#.L	40.17	12.04	3.34	0.30
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.GYDVDFPR@.N	39.97	13.92	2.87	0.35
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.HGPLALVDK#.L	21.72	6.71	3.24	0.31
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.R@GSPLLIGVR@.S	19.20	16.06	1.20	0.84
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.VIFLEDDDVAAVVDGR@.L	42.65	14.19	3.00	0.33
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.VIQQLEGAFALVFK#.S	31.43	8.71	3.61	0.28
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.VNFDDYTVNLGGLK#.D	7.80	3.33	2.34	0.43
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.AVEYYFASDASAVIEHTNR@.V	43.17	13.01	3.32	0.30
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.AVQTLQM*ELQQIM*K#.G	8.08	2.39	3.38	0.30
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.EVLSM*DDEIQK#.L	27.79	8.68	3.20	0.31
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.GNFSSFM*QK#.E	8.72	4.93	1.77	0.57
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.GSPLLIGVR@.S	40.60	10.87	3.74	0.27
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.GYDFESETDTETIAK#.L	38.58	13.32	2.90	0.35
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.GYDVDFPR@.N	30.45	8.07	3.77	0.27
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.HGPLALVDK#.L	17.62	6.79	2.59	0.39
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.SDK#NNEFIVIHNGIITNYK#.D	5.42	23.11	0.23	4.26
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	K.SVHFPGQAVGTR@.R	39.70	8.98	4.42	0.23
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.VIFLEDDDVAAVVDGR@.L	90.35	25.44	3.55	0.28
P47856_GFPT1_MOUSE	Gfpt1	Glutamine--fructose-6-p	R.VIQQLEGAFALVFK#.S	19.79	3.35	5.92	0.17
Q9Z2Z9_GFPT2_MOUSE	Gfpt2	Glutamine--fructose-6-p	K.GYEFESETDTETIAK#.L	5.51	2.44	2.26	0.44
Q9Z2Z9_GFPT2_MOUSE	Gfpt2	Glutamine--fructose-6-p	R.ETEDITFSTLVER@.V	12.38	1.86	6.68	0.15
Q8R0H9_GGA1_MOUSE	Gga1	ADP-ribosylation factor-	R.VNAIEEVNNNVK#.L	5.86	2.04	2.87	0.35
Q9D7M1_GID8_MOUSE	Gid8	Glucose-induced degrad	R.LIMNYLVTEGFK#.E	11.02	4.51	2.45	0.41
Q9D7M1_GID8_MOUSE	Gid8	Glucose-induced degrad	K.LLLWAQNELDQK#.K	16.44	6.95	2.37	0.42
Q9D7M1_GID8_MOUSE	Gid8	Glucose-induced degrad	R.M*ESGIEPSVDLETLDER@.I	10.15	4.47	2.27	0.44
Q9D7M1_GID8_MOUSE	Gid8	Glucose-induced degrad	R.QK#VWSEVNQAVLDYENR@.E	3.40	2.83	1.20	0.83
Q9D7M1_GID8_MOUSE	Gid8	Glucose-induced degrad	R.QR@ETEAALEFAQTQLAEQGEESR@.E	5.27	3.39	1.56	0.64
Q9D7M1_GID8_MOUSE	Gid8	Glucose-induced degrad	R.TLALLAFDSPEESPFGDLLHM*M*QR@.Q	20.45	13.83	1.48	0.68
Q9D7M1_GID8_MOUSE	Gid8	Glucose-induced degrad	K.VWSEVNQAVLDYENR@.E	9.74	4.04	2.41	0.41
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.ALSSGGSITSPPLSPALPK#.Y	4.43	2.54	1.74	0.57
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.DVGR@PNFEESGPTSVGR@.K	8.36	3.89	2.15	0.47
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.NFSM*SVNSAAVLR@.L	5.15	2.85	1.81	0.55
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.AALSSQQQQQLALLLQQFQALK#.M	69.63	30.64	2.27	0.44
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.AEEENR@SENSLSAK#.V	1.99	1.51	1.32	0.76
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.AEQVEK#AEEENR@SENSLSAK#.V	8.15	4.28	1.90	0.53
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.ALQQQQQQQQQQK#.L	6.21	4.06	1.53	0.65
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.ALSSGGSITSPPLSPALPK#.Y	12.30	8.40	1.46	0.68
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.DVGRPNFEESGPTSVGR.K	22.73	11.78	1.93	0.52
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.IPFDLLEK#.E	19.84	10.18	1.95	0.51
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.LFQGVNK#.A	21.31	10.50	2.03	0.49
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.LQQQQQQQQLAQM*K#.L	4.70	2.60	1.81	0.55
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.M*SDQNIIPSVTR@.S	28.44	9.84	2.89	0.35
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.M*VAYLQDSALDDER@.L	5.95	3.41	1.74	0.57
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.M*VAYLQDSALDDERLTSK.L	28.45	12.04	2.36	0.42
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.SLLEIQQEEAR.Q	38.52	14.48	2.66	0.38
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.VPFSPGPAPPPHM*GELDQER@.L	28.10	14.41	1.95	0.51
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.AALSSQQQQQLALLLQQFQALK#.M	105.35	37.38	2.82	0.35
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.ADPSLLGFSVNASSER@.L	16.96	9.10	1.86	0.54
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.ALQQQQQQQQQQK#.L	11.34	2.98	3.80	0.26
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.ALSSGGSITSPPLSPALPK#.Y	32.99	14.25	2.32	0.43
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.AYLGDTSEAK#.E	38.44	12.16	3.16	0.32
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.DVGRPNFEESGPTSVGR.K	53.37	17.75	3.01	0.33
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.FEFDFR@.D	15.24	4.04	3.77	0.27
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.IFR@EEQNGEDEDGGWR@.L	3.66	2.34	1.56	0.64
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.IPFDLLEK#.E	42.10	16.03	2.63	0.38
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.LNM*GEIETLDDY.-	11.19	11.19	1.00	1.00
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.M*SDQNIIPSVTR@.S	31.80	10.00	3.18	0.31
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.M*VAYLQDSALDDER@.L	9.11	2.69	3.39	0.29
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.NFSM*SVNSAAVLR@.L	11.99	5.00	2.40	0.42
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.NSNM*GFWDDAVK#.E	9.67	3.00	3.22	0.31
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.QQQEEALR@.R	16.23	5.49	2.96	0.34
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	K.SLLEIQQEEAR@.Q	56.37	18.01	3.13	0.32
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.VPFSPGPAPPPHM*GELDQER@.L	46.53	19.54	2.38	0.42
Q6Y7W8_PERQ2_MOUSE	Gigyf2	PERQ amino acid-rich wi	R.YGR@EEM*LALFLK#.D	7.09	1.92	3.70	0.27
Q68FF6_GIT1_MOUSE	Git1	ARF GTPase-activating pr	K.LQAENLQLR@.Q	9.23	4.31	2.14	0.47
Q68FF6_GIT1_MOUSE	Git1	ARF GTPase-activating pr	R.SAVPFLPVNPEYSATR@.N	17.03	6.09	2.79	0.36
Q68FF6_GIT1_MOUSE	Git1	ARF GTPase-activating pr	K.SLSSPTDNLELSAR@.S	12.57	9.23	1.36	0.73
Q68FF6_GIT1_MOUSE	Git1	ARF GTPase-activating pr	K.SLSSPTDNLELSAR@.S	11.41	3.91	2.92	0.34
Q80XR8_Q80XR8_MOUSE	Git2	ARF GTPase-activating pr	R.ADSSLDLSELAK#.A	8.64	4.35	1.99	0.50
Q80XR8_Q80XR8_MOUSE	Git2	ARF GTPase-activating pr	K.AGQILQAELLAVYGADPGTQDSSGK#.T	7.41	4.64	1.60	0.63
Q80XR8_Q80XR8_MOUSE	Git2	ARF GTPase-activating pr	R.SM*LWQGDGLLPDTAEPHSVPSPTLPSTEDVIR@.K	6.21	3.01	2.07	0.48
Q9JMB0_GKAP1_MOUSE	Gkap1	G kinase-anchoring prot	K.EQQQSEANELR@.N	3.74	2.65	1.41	0.71
Q61543_GSLG1_MOUSE	Glg1	Golgi apparatus protein	R.IIIQESALDYR@.L	15.04	4.94	3.04	0.33
Q61543_GSLG1_MOUSE	Glg1	Golgi apparatus protein	K.LDPVLYR@.K	27.02	6.88	3.93	0.25
Q61543_GSLG1_MOUSE	Glg1	Golgi apparatus protein	R.LLELQYFISR@.D	26.54	5.76	4.61	0.22
Q61543_GSLG1_MOUSE	Glg1	Golgi apparatus protein	K.MTAIIFSDYR@.L	12.03	4.32	2.78	0.36
Q61543_GSLG1_MOUSE	Glg1	Golgi apparatus protein	R.QITQNTDYR@.L	19.20	4.94	3.88	0.26
Q9CYL5_GAPR1_MOUSE	Glipr2	Golgi-associated plant p	K.ASASDGSSFVVAR@.Y	45.67	25.84	1.77	0.57
Q9CYL5_GAPR1_MOUSE	Glipr2	Golgi-associated plant p	R.EAQQYSEALASTR@.I	45.02	34.22	1.32	0.76
Q9CYL5_GAPR1_MOUSE	Glipr2	Golgi-associated plant p	K.QFNNEVLK#.A	22.53	18.33	1.23	0.81
Q9CQM9_GLRX3_MOUSE	Glrx3	Glutaredoxin-3 OS=Mus	R.GDLVGGLDIVK#.E	6.27	5.16	1.22	0.82
Q80Y14_GLRX5_MOUSE	Glrx5	Glutaredoxin-related pro	R.DYAAYNVLDDPELR@.Q	5.77	5.60	1.03	0.97
F8VPZ9_F8VPZ9_MOUSE	Gltscr1	Protein Gltscr1 OS=Mus	K.AFASNLPTLSVAK#.A	6.10	1.73	3.52	0.28
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.ALDQSDNDM*SAVYR@.A	138.94	40.65	3.42	0.29
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.ALDQSDNDMSAVYR@.A	8.99	3.01	2.99	0.33
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.FLEAPVSGNQQLSNDGM*LVILAAGDR@.G	48.90	18.57	2.63	0.38
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.FLEAPVSGNQQLSNDGMLVILAAGDR@.G	26.14	10.89	2.40	0.42
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.FQQAVDAVEEFLR@.R	71.31	23.99	2.97	0.34
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.K#LSLSEGK#.V	15.47	305.61	0.05	19.76
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.LAIALGDAVNHPTPM*AAAANEVYK#.R	14.58	6.88	2.12	0.47
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.LGDLVWGK#.L	50.49	17.94	2.81	0.36
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.M*GHTVTVWNR@.T	47.95	14.41	3.33	0.30
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.TSFFLGEVGNAAK#.M	95.09	32.03	2.97	0.34
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.ALDQSDNDM*SAVYR@.A	46.40	11.80	3.93	0.25

Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.ALDQSDNDMSAVYR@.A	3.63	1.90	1.90	0.52
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.FLEAPVSGNQQLSNDGM*LVILAAGDR@.G	49.60	17.82	2.78	0.36
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.FLEAPVSGNQQLSNDGMLVILAAGDR@.G	14.55	4.23	3.44	0.29
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.FQQAVDAVEEFLR@.R	51.96	12.44	4.18	0.24
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.K#LSLSEGK#.V	16.73	21.66	0.77	1.29
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.LAIALGDAVNHPTPM*AAAANEVYK#.R	18.96	6.17	3.07	0.33
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.M*GHTVTVWNR@.T	7.38	2.27	3.24	0.31
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.TSFFLGEVGNAAK#.M	65.19	15.45	4.22	0.24
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.ALDQSDNDM*SAVYR@.A	20.38	4.85	4.20	0.24
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	R.FQQAVDAVEEFLR@.R	25.16	6.02	4.18	0.24
Q922P9_GLYR1_MOUSE	Glyr1	Putative oxidoreductase	K.TSFFLGEVGNAAK#.M	13.79	2.48	5.57	0.18
A0A087WPH4_A0A087WPH4_MOUSE	Gm6358	Protein Gm6358 OS=Mu	-.M*VTPR@LK#.K	16.32	6.07	2.69	0.37
E9Q070_E9Q070_MOUSE	Gm8730	Uncharacterized protein	R.VLALSVETEYTFPLAEK#.V	444.80	136.23	3.27	0.31
E9Q070_E9Q070_MOUSE	Gm8730	Uncharacterized protein	R.VLALSVETEYTFPLAEK#.V	184.80	63.35	2.92	0.34
E9Q070_E9Q070_MOUSE	Gm8730	Uncharacterized protein	R.VLALSVETEYTFPLAEK#.V	13.27	6.46	2.06	0.49
E9Q070_E9Q070_MOUSE	Gm8730	Uncharacterized protein	R.VLALSVETEYTFPLAEK#.V	98.68	22.68	4.35	0.23
E9Q070_E9Q070_MOUSE	Gm8730	Uncharacterized protein	R.VLALSVETEYTFPLAEK#.V	112.36	21.75	5.17	0.19
Q3THK7_GUAA_MOUSE	Gmps	GMP synthase [glutamin	K.TLNM*TTSPEEK#.R	5.04	3.12	1.61	0.62
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	R.IAQSDYIPTQQDVLR@.T	9.80	4.92	1.99	0.50
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	K.AM*GNLQIDFADPQR@.A	6.39	3.08	2.08	0.48
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	R.IAQSDYIPTQQDVLR@.T	26.80	8.57	3.13	0.32
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	K.AM*GNLQIDFADPQR@.A	13.72	4.48	3.06	0.33
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	R.AVVYSNTIQSIM*AIVK#.A	14.47	4.36	3.32	0.30
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	R.EYQLNDSAAYYLNDLER@.I	5.81	2.11	2.75	0.36
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	R.IAQSDYIPTQQDVLR@.T	39.07	15.14	2.58	0.39
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	K.M*FDVGGQR@.S	22.30	6.02	3.70	0.27
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	R.SR@EYQLNDSAAYYLNDLER@.I	6.11	2.33	2.62	0.38
P08752_GNAI2_MOUSE	Gnai2	Guanine nucleotide-binc	K.YDEAASYIQSK#.F	16.70	5.53	3.02	0.33
Q9DC51_GNAI3_MOUSE	Gnai3	Guanine nucleotide-binc	R.ISQTNYIPTQQDVLR@.T	11.99	7.89	1.52	0.66
P21279_GNAQ_MOUSE	Gnaq	Guanine nucleotide-binc	K.LLLLGTGESGK#.S	11.82	4.10	2.88	0.35
P21279_GNAQ_MOUSE	Gnaq	Guanine nucleotide-binc	K.VSAFENPYVDAIK#.S	9.65	2.61	3.70	0.27
P21279_GNAQ_MOUSE	Gnaq	Guanine nucleotide-binc	K.LLLLGTGESGK#.S	10.27	1.42	7.21	0.14
P21279_GNAQ_MOUSE	Gnaq	Guanine nucleotide-binc	K.LLLLGTGESGK#.S	12.38	4.59	2.70	0.37
Q6R0H7_GNAS1_MOUSE	Gnas	Guanine nucleotide-binc	R.LQEALNLFK#.S	9.36	2.58	3.63	0.28
Q6R0H7_GNAS1_MOUSE	Gnas	Guanine nucleotide-binc	R.YTTPEDATPEPGEDPR@.V	7.68	2.86	2.68	0.37
P62874_GBB1_MOUSE	Gnb1	Guanine nucleotide-binc	K.LIIWDSYTTNK#.V	65.69	42.50	1.55	0.65
P62874_GBB1_MOUSE	Gnb1	Guanine nucleotide-binc	R.LLVSASQDGK#.L	166.20	105.55	1.57	0.64
P62874_GBB1_MOUSE	Gnb1	Guanine nucleotide-binc	K.LIIWDSYTTNK#.V	30.37	9.63	3.15	0.32
P62874_GBB1_MOUSE	Gnb1	Guanine nucleotide-binc	K.LIIWDSYTTNK#.V	42.97	16.46	2.61	0.38
P62874_GBB1_MOUSE	Gnb1	Guanine nucleotide-binc	R.LLVSASQDGK#.L	61.61	21.01	2.93	0.34
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	R.DETNYGIPQR.A	57.93	44.76	1.29	0.77
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.DGQAM*LWDLNEGK#.H	7.49	4.69	1.60	0.63
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.DVLSVAFSSDNR@.Q	47.64	42.10	1.13	0.88
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.IIVDELK#QEVISTSSK#.A	81.63	57.81	1.41	0.71
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.LTRDETNYGIPQR.A	26.69	20.09	1.33	0.75
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	R.LWDLTTGTTTR@.R	46.56	29.96	1.55	0.64
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	R.VWQVTIGTR@.-	21.26	18.94	1.12	0.89
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.IIVDELK#QEVISTSSK#.A	4.42	3.57	1.24	0.81
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	R.LWDLTTGTTTR@.R	4.50	4.40	1.02	0.98
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.DVLSVAFSSDNR@.Q	9.69	4.40	2.20	0.45
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.IIVDELKQEVISTSSK.A	6.28	5.24	1.20	0.83
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.IIVDELK#QEVISTSSK#.A	16.52	9.46	1.75	0.57
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.DVLSVAFSSDNR@.Q	17.71	5.96	2.97	0.34
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	K.IIVDELK#QEVISTSSK#.A	21.17	18.93	1.12	0.89
P68040_GBLP_MOUSE	Gnb2l1	Guanine nucleotide-binc	R.VWQVTIGTR@.-	9.77	2.10	4.66	0.21
Q9DAS9_GBG12_MOUSE	Gng12	Guanine nucleotide-binc	R.SDPLLM*GIPTSENPFK#.D	7.83	2.27	3.45	0.29
Q9DAS9_GBG12_MOUSE	Gng12	Guanine nucleotide-binc	K.TASTNSIAQAR@.R	18.71	8.03	2.33	0.43
Q8CI11_GNL3_MOUSE	Gnl3	Guanine nucleotide-binc	K.ENLENWLNYLNK#.E	8.91	4.51	1.97	0.51
Q8CI11_GNL3_MOUSE	Gnl3	Guanine nucleotide-binc	K.K#VIEASDIVLEVLDAR@.D	5.99	1.65	3.62	0.28
Q8CI11_GNL3_MOUSE	Gnl3	Guanine nucleotide-binc	R.NAEISDVAPVEETR@.E	13.47	4.96	2.71	0.37
Q8CI11_GNL3_MOUSE	Gnl3	Guanine nucleotide-binc	R.SPASIEELR@PLEAASAILSQADNEQVVLK#.Y	32.69	8.40	3.89	0.26
Q8CI11_GNL3_MOUSE	Gnl3	Guanine nucleotide-binc	K.VIEASDIVLEVLDAR@.D	18.11	0.00	#DIV/0!	0.00
Q8CI11_GNL3_MOUSE	Gnl3	Guanine nucleotide-binc	K.YTVPEYK#.D	23.15	5.73	4.04	0.25
Q9CW79_GOGA1_MOUSE	Golga1	Golgin subfamily A meml	R.SLQAAEEQLSQSR@.N	9.22	21.38	0.43	2.32
Q9CW79_GOGA1_MOUSE	Golga1	Golgin subfamily A meml	R.LSDYAEQVR@.N	11.47	5.63	2.04	0.49
Q9CW79_GOGA1_MOUSE	Golga1	Golgin subfamily A meml	K.M*AEGLALALAR@.K	9.12	5.08	1.80	0.56
Q9CW79_GOGA1_MOUSE	Golga1	Golgin subfamily A meml	K.TVAEQNLEDTR@.Q	9.02	2.51	3.60	0.28
Q921M4_GOGA2_MOUSE	Golga2	Golgin subfamily A meml	K.LLELQELVLR@.L	34.43	31.35	1.10	0.91
Q921M4_GOGA2_MOUSE	Golga2	Golgin subfamily A meml	R.LTNENM*EITSALQSEQHVK#.K	25.46	6.70	3.80	0.26
Q921M4_GOGA2_MOUSE	Golga2	Golgin subfamily A meml	R.TLSTVSTQQK#.Q	14.38	12.19	1.18	0.85
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.AELQAQLAALSTR@.L	11.20	3.41	3.28	0.30
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.EATDAELNQLR@.A	11.02	4.88	2.26	0.44
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.EHLVQTLQAEVDELQIQDGK#.H	10.66	3.31	3.22	0.31
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.LTGLGQSNAALR@.E	11.72	2.54	4.61	0.22
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.NASLASSNNDLQVAEEQYQR@.L	10.42	3.11	3.35	0.30
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.QLTSTQEALQAK#.G	7.70	2.90	2.66	0.38
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.R@LEEDTEETSGLLEQLR@.Q	6.33	4.13	1.53	0.65
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.R@LEEFEGER@EQLQK#.V	15.20	5.55	2.74	0.36
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.R@LEGQVEALSLEASQALQEK#.A	10.33	4.07	2.54	0.39
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.SLADYR@TEDPSDSGGLGSTADAVGSSLK#.Q	2.70	1.50	1.80	0.56
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.SNQVEHLQQETATLR@.K	11.35	6.20	1.83	0.55
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.TEDPSDSGGLGSTADAVGSSLK#.Q	4.71	3.21	1.47	0.68
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.TLLQQNQQLK#.L	12.51	7.37	1.70	0.59
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.VADAAASLEQQLEQVK#.L	5.68	18.09	0.31	3.19
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.VLELEDELQESR@.G	22.66	8.98	2.52	0.40
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.AELQAQLAALSTR@.L	9.26	3.87	2.39	0.42
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.ALEVELQNVGQSK#.I	21.74	6.92	3.14	0.32
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.AM*TDLQSM*LEAK#.N	12.78	4.16	3.07	0.33
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.DVLQAAAAQHQDQNQEANGEVR@.S	8.54	2.01	4.24	0.24
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.EHLVQTLQAEVDELQIQDGK#.H	28.36	8.83	3.21	0.31
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.HSQEIAQFQTELAEAR@.T	15.72	5.23	3.00	0.33
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.IAVQLQSIEADM*LDQEAAFVQIR@.E	8.42	2.43	3.46	0.29
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.IVLEVALQSAK#.S	14.04	5.42	2.59	0.39
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.LFSTLDPELM*LNPENLPR@.A	6.96	2.76	2.52	0.40
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.LFSTLDPELM*LNPENLPR@.A	8.20	1.84	4.45	0.22
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.LGSDLTSAQK#.E	22.74	9.22	2.47	0.41
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.NASLASSNNDLQVAEEQYQR@.L	10.98	3.93	2.79	0.36
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.QDSLSSEVDTLK#.Q	14.26	37.06	0.38	2.60
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	K.QLTSTQEALQAK#.G	13.89	4.60	3.02	0.33
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.QQM*TALQSQLQQVQLER@.T	7.32	2.96	2.47	0.40
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.R@LEEDTEETSGLLEQLR@.Q	12.79	4.94	2.59	0.39
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.R@LEGQVEALSLEASQALQEK#.A	20.12	4.05	4.97	0.20
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A meml	R.SLADYR@TEDPSDSGGLGSTADAVGSSLK#.Q	7.03	1.82	3.85	0.26

P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A mem	K.SNQVEHLQQETATLR@.K	19.68	4.07	4.84	0.21
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A mem	R.TEDPSDSGGLGSTADAVGSSLK#.Q	6.71	4.52	1.49	0.67
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A mem	R.TQLQLLQK#.K	23.79	18.34	1.30	0.77
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A mem	K.VGSLGLLAHSK#.E	10.95	3.05	3.60	0.28
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A mem	K.VLELEDELQESR@.G	33.40	11.24	2.97	0.34
P55937_GOGA3_MOUSE	Golga3	Golgin subfamily A mem	R.YDELQAR@.L	37.55	9.22	4.07	0.25
Q91VW5_GOGA4_MOUSE	Golga4	Golgin subfamily A mem	K.AILTESENK#LQELGQEAEAYR@.T	12.35	4.40	2.81	0.36
Q91VW5_GOGA4_MOUSE	Golga4	Golgin subfamily A mem	K.ELENTVLELSQK#.E	13.36	1.79	7.48	0.13
Q91VW5_GOGA4_MOUSE	Golga4	Golgin subfamily A mem	R.EVGSISEQQELTVR@.R	17.80	2.07	8.62	0.12
Q91VW5_GOGA4_MOUSE	Golga4	Golgin subfamily A mem	R.LEQEESTK#DSVTILELQTQLAQK#.T	4.51	2.00	2.25	0.44
Q91VW5_GOGA4_MOUSE	Golga4	Golgin subfamily A mem	R.LK#EAVSGQDVALAGLQGQLEQK#.S	8.20	2.37	3.45	0.29
Q91VW5_GOGA4_MOUSE	Golga4	Golgin subfamily A mem	K.NSEEQVAALQK#.L	8.57	3.57	2.40	0.42
Q91VW5_GOGA4_MOUSE	Golga4	Golgin subfamily A mem	K.SAGELQQALAK#.L	11.28	2.79	4.04	0.25
Q91VW5_GOGA4_MOUSE	Golga4	Golgin subfamily A mem	R.VSELTGQVQAAEK#.E	10.53	6.16	1.71	0.58
Q91W53_GOGA7_MOUSE	Golga7	Golgin subfamily A mem	K.IYAPQGLLLTDPIER@.G	5.10	3.44	1.48	0.68
Q91W53_GOGA7_MOUSE	Golga7	Golgin subfamily A mem	R.VIEITIYEDR@.G	9.71	2.10	4.62	0.22
D3YVW2_D3YVW2_MOUSE	Golim4	Golgi integral membrane	K.DAGFQALEEQNQVEPR@.E	5.42	2.92	1.86	0.54
D3YVW2_D3YVW2_MOUSE	Golim4	Golgi integral membrane	K.LEAQETLNK#.G	17.39	7.21	2.41	0.41
D3YVW2_D3YVW2_MOUSE	Golim4	Golgi integral membrane	K.LTGELQEVQPNHEAGPR@.R	16.66	7.42	2.24	0.45
D3YVW2_D3YVW2_MOUSE	Golim4	Golgi integral membrane	K.SALAAAQTQVAEYK#.Q	16.84	5.63	2.99	0.33
Q9CRA5_GOLP3_MOUSE	Golph3	Golgi phosphoprotein 3	R.LTLM*EEVLLLGLK#.D	9.95	5.54	1.80	0.56
Q9CRA5_GOLP3_MOUSE	Golph3	Golgi phosphoprotein 3	K.SDAPTGDVLLDEALK#.H	10.91	5.46	2.00	0.50
Q9CR60_GOT1B_MOUSE	Golt1b	Vesicle transport protein	R.SFVDK#VGESNNM*V.-	11.38	4.44	2.56	0.39
Q9CR60_GOT1B_MOUSE	Golt1b	Vesicle transport protein	R.VPVLGSLLNLPGIR@.S	10.23	5.23	1.96	0.51
Q9CR60_GOT1B_MOUSE	Golt1b	Vesicle transport protein	R.R@VPVLGSLLNLPGIR@.S	44.23	19.02	2.33	0.43
Q9CR60_GOT1B_MOUSE	Golt1b	Vesicle transport protein	R.SFVDK#VGESNNM*V.-	31.92	13.95	2.29	0.44
Q9CR60_GOT1B_MOUSE	Golt1b	Vesicle transport protein	R.VPVLGSLLNLPGIR@.S	18.55	8.19	2.26	0.44
Q8BH60_GOPC_MOUSE	Gopc	Golgi-associated PDZ an	K.LEAQLVDLR.S	15.40	8.39	1.84	0.54
Q8BH60_GOPC_MOUSE	Gopc	Golgi-associated PDZ an	R.VQQIQLLGR@.D	16.13	7.10	2.27	0.44
Q99JX3_GORS2_MOUSE	Gorasp2	Golgi reassembly-stackin	K.ADASSLTVDVTSPASK#.V	8.98	5.58	1.61	0.62
Q99JX3_GORS2_MOUSE	Gorasp2	Golgi reassembly-stackin	K.ISLPGQM*TGTPITPLK#.D	5.98	3.10	1.93	0.52
O88630_GOSR1_MOUSE	Gosr1	Golgi SNAP receptor com	R.LIEETISIAM*ATK#.E	12.37	4.22	2.93	0.34
P05202_AATM_MOUSE	Got2	Aspartate aminotransfera	K.ASAELALGENNEVLK.S	3.57	5.10	0.70	1.43
Q3TFK5_GPTC4_MOUSE	Gpatch4	G patch domain-containi	K.ALGTSQPLTDSEPSQK.K	9.02	6.53	1.38	0.72
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	R.M*EM*ELDYAEDATER@.R	4.63	2.31	2.00	0.50
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	R.EPNK#SQEEEQDVVLSSEGR@.V	5.15	2.27	2.27	0.44
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	K.GAGLPSQNSNTGTGR@.G	12.83	6.93	1.85	0.54
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	K.VGDTDGTGNLDGK#K#EDEDPQDGGSLASTLSK#.L	5.49	2.16	2.55	0.39
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	K.DISQATPATK.A	21.97	15.83	1.39	0.72
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	K.EAAVAGPSEPGGK#.T	23.76	11.97	1.99	0.50
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	R.EPNK#SQEEEQDVVLSSEGR@.V	16.35	8.00	2.04	0.49
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	K.GAGLPSQNSNTGTGR.G	21.29	8.49	2.51	0.40
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	K.LQQAAQQHIQQQLLAK#.Q	47.82	20.07	2.38	0.42
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	K.SQEEEQDVVLSSEGR@.V	7.00	5.13	1.36	0.73
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	R.SSDAPFGHQFSEEAAGPLSDPPPEEPK#.S	6.78	3.97	1.71	0.59
A2A6A1_GPTC8_MOUSE	Gpatch8	G patch domain-containi	R.TVSEASELQK#.E	44.54	18.19	2.45	0.41
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	K.DLFVELK#R@.Y	12.79	9.29	1.38	0.73
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	K.FDEFFK#ELLENAEK#.S	27.72	22.22	1.25	0.80
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	K.ISDAIM*NM*QDNSVQVSQK#.V	15.04	11.48	1.31	0.76
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	R.LEGPFNIESVM*DPIDVK#.I	28.22	22.40	1.26	0.79
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	R.LEGPFNIESVMDPIDVK#.I	4.68	3.50	1.34	0.75
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	R.TFAQGLAVAR@.D	57.60	34.58	1.67	0.60
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	K.TYGHLYM*QNSELFK#.D	19.20	11.98	1.60	0.62
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	K.YTEQLK#PFGDVPR@.K	29.91	18.88	1.58	0.63
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	K.FDEFFK#ELLENAEK#.S	8.89	3.47	2.56	0.39
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	R.TFAQGLAVAR@.D	12.17	9.71	1.25	0.80
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	R.YLFAVTGNGLANQGNNPEVQVDTSK#PDILILR@.Q	4.32	2.93	1.47	0.68
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	K.FDEFFK#ELLENAEK#.S	7.54	7.76	0.97	1.03
P51655_GPC4_MOUSE	Gpc4	Glypican-4 OS=Mus musc	R.LEGPFNIESVM*DPIDVK#.I	13.74	7.09	1.94	0.52
Q3UN16_GP162_MOUSE	Gpr162	Probable G-protein coup	R.QFLESGVLGSGGGPPR.G	3.24	25.16	0.13	7.77
Q5U4C1_GASP1_MOUSE	Gprasp1	G-protein coupled recep	K.SSM*ESGPK#.A	112.12	70.61	1.59	0.63
Q99LD4_CSN1_MOUSE	Gps1	COP9 signalosome comp	K.AESTPEIAEQR@.G	18.37	4.59	4.00	0.25
Q99LD4_CSN1_MOUSE	Gps1	COP9 signalosome comp	R.EGSQGELTPANSQSR@.M	16.96	5.41	3.13	0.32
Q99LD4_CSN1_MOUSE	Gps1	COP9 signalosome comp	K.AESTPEIAEQR@.G	11.74	2.80	4.18	0.24
Q99LD4_CSN1_MOUSE	Gps1	COP9 signalosome comp	K.LFLELEPQVR@.D	10.95	1.09	10.02	0.10
Q99LD4_CSN1_MOUSE	Gps1	COP9 signalosome comp	K.AESTPEIAEQR@.G	11.46	3.08	3.72	0.27
Q99LD4_CSN1_MOUSE	Gps1	COP9 signalosome comp	R.EGSQGELTPANSQSR@.M	5.62	1.44	3.90	0.26
P11352_GPX1_MOUSE	Gpx1	Glutathione peroxidase 1	R.NALPTPSDDPTALM*TDPK#.Y	4.15	3.08	1.35	0.74
Q60631_GRB2_MOUSE	Grb2	Growth factor receptor-	R.ESESAPGDFSLSVK#.F	5.04	8.89	0.57	1.76
Q8C5Q4_GRSF1_MOUSE	Grsf1	G-rich sequence factor 1	K.LGDEVDDVYLIR@.A	6.74	4.00	1.69	0.59
Q8C5Q4_GRSF1_MOUSE	Grsf1	G-rich sequence factor 1	K.SLQVK#PSPVLSDGVVR@.L	13.55	5.00	2.71	0.37
Q9D8T2_GSDMD_MOUSE	Gsdmdc1	Gasdermin-D OS=Mus mu	R.SR@GDDLFVVTEVLQTK#.E	8.74	2.79	3.13	0.32
Q9WV60_GSK3B_MOUSE	Gsk3b	Glycogen synthase kinas	R.DIK#PQNLLLDPDTAVLK#.L	7.96	2.34	3.40	0.29
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.EVQGFESSTFSGYFK.S	5.39	7.30	0.74	1.35
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.AGK#EPGLQIWR@.V	221.10	153.03	1.44	0.69
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.AQVHVSEEGGEPEAM*LQVLGPK#PALPEGTEDTAK#.E	11.53	6.70	1.72	0.58
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.AVEVMPK#.S	35.06	32.13	1.09	0.92
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.DGGQTAPASIR.L	200.75	145.63	1.38	0.73
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.DSQEEEK#TEALTSAK#.R	221.63	184.39	1.20	0.83
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.EPGLQIWR.V	36.80	37.35	0.99	1.02
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.EVQGFESSTFSGYFK#.S	183.42	124.16	1.48	0.68
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.HVVPNEVVVQR@.L	153.01	99.41	1.54	0.65
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.IEGSNK#VPVDPATYGQFYGGDSYIILYNYR@.H	50.16	28.34	1.77	0.56
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.NWR@DPDQTDGPGLGYLSSHIANVER@.V	17.15	10.44	1.64	0.61
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.QTQVSVLPEGGETPLFK#.Q	158.29	109.62	1.44	0.69
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.R@TPITVVR@.Q	128.38	73.09	1.76	0.57
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.SGALNSNDAFVLK#.T	269.17	177.94	1.51	0.66
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.SQHVQVEEGSEPDAFWEALGGK#.T	144.16	100.55	1.43	0.70
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.TASDFISK.M	242.82	143.88	1.69	0.59
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.TGAQELLK#.V	423.74	280.18	1.51	0.66
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.TPITVVR@.Q	149.76	88.69	1.69	0.59
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.TPSAAYLWVGAGASEAEK#.T	127.56	87.99	1.45	0.69
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK#.Q	33.80	22.76	1.48	0.67
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.VPVDPATYGQFYGGDSYIILYNYR@.H	44.73	33.37	1.34	0.75
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.YIETDPANR@.D	68.14	46.70	1.46	0.69
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.DGGQTAPASIR@.L	28.76	12.07	2.38	0.42
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.DSQEEEKTEALTSAK.R	15.33	5.98	2.56	0.39
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.EVQGFESSTFSGYFK#.S	15.63	9.32	1.68	0.60
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.NWR@DPDQTDGPGLGYLSSHIANVER@.V	9.84	5.03	1.95	0.51
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	K.SGALNSNDAFVLK#.T	24.26	10.39	2.34	0.43
P13020_GELS_MOUSE	Gsn	Gelsolin OS=Mus muscul	R.SQHVQVEEGSEPDAFWEALGGK#.T	15.85	6.55	2.42	0.41
P19157_GSTP1_MOUSE	Gstp1	Glutathione S-transfera	K.ALPGHLKPFETLLSQNQGGK.A	1.51	5.01	0.30	3.33
P19157_GSTP1_MOUSE	Gstp1	Glutathione S-transfera	K.FEDGDLTLYQSNAILR.H	3.15	4.95	0.64	1.57

Q99L20_Q99L20_MOUSE	Gstt3	Glutathione S-transferase	K.GQQYTDSFAQVNPLR@.K	2.94	2.11	1.40	0.71
P62915_TF2B_MOUSE	Gtf2b	Transcription initiation f	K.ALETSVDLITTGDFM*SR@.F	7.28	3.14	2.32	0.43
P62915_TF2B_MOUSE	Gtf2b	Transcription initiation f	K.AVELDLVPGR@.S	7.64	4.92	1.55	0.64
P62915_TF2B_MOUSE	Gtf2b	Transcription initiation f	K.EIGDIAGVADVTIR@.Q	29.81	6.63	4.49	0.22
P62915_TF2B_MOUSE	Gtf2b	Transcription initiation f	R.SPISVAAAAIYM*ASQASAEK#.R	7.10	2.93	2.42	0.41
P62915_TF2B_MOUSE	Gtf2b	Transcription initiation f	R.VGDSQNPLLSDGDLSTM*IGK#.G	11.91	3.90	3.05	0.33
P62915_TF2B_MOUSE	Gtf2b	Transcription initiation f	R.VIDVGSEWR.T	21.85	9.11	2.40	0.42
Q9D0D5_T2EA_MOUSE	Gtf2e1	General transcription fac	R.FNEQIEPIYALLR@.E	15.16	9.18	1.65	0.61
Q9D0D5_T2EA_MOUSE	Gtf2e1	General transcription fac	R.FNEQIEPIYALLR@.E	12.81	5.77	2.22	0.45
Q9D902_T2EB_MOUSE	Gtf2e2	General transcription fac	R.GLGGILLEDIEEGLPNSQK#.A	7.13	2.28	3.13	0.32
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.AGISFIIK#.R	31.23	8.05	3.88	0.26
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.APSYLEISSM*R@.R	25.18	8.06	3.12	0.32
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.APSYLEISSMR@.R	6.08	2.68	2.27	0.44
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.DQSAVVVQGLPEGVAFK#.H	34.70	7.98	4.35	0.23
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.EQVNDLFSR@.K	43.69	12.36	3.54	0.28
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.FAEALGSTEAK#.A	11.35	22.36	0.51	1.97
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.FAQALGLTEAVK#.V	21.66	9.87	2.19	0.46
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.FGEAIGM*GFPVK#.V	6.30	56.12	0.11	8.91
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.ILDSAEFIK#.F	58.14	17.59	3.30	0.30
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.K#PEM*FETAIK#.E	10.71	6.32	1.69	0.59
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.M*SVDAVEIETLR@.K	13.27	4.65	2.86	0.35
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.R@PELLTHSTTEVTQPR@.T	13.51	5.89	2.29	0.44
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.SPPIFLSGK#.I	18.31	8.71	2.10	0.48
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.SPTWFGIPR@.L	13.50	6.43	2.10	0.48
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.STVVPVPYEK#.M	43.63	13.63	3.20	0.31
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.VLAAEAER@.S	89.15	22.95	3.88	0.26
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.AGISFIIK#.R	69.84	8.42	8.30	0.12
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.APSYLEISSM*R@.R	31.00	4.30	7.21	0.14
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.APSYLEISSMR@.R	13.94	4.62	3.02	0.33
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.DQSAVVVQGLPEGVAFK#.H	80.25	12.76	6.29	0.16
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.EQVNDLFSR@.K	66.33	8.79	7.54	0.13
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.FAEALGSTEAK#.A	109.90	18.01	6.10	0.16
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.FAQALGLTEAVK#.V	130.11	24.95	5.21	0.19
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.FEAHPNDLYVEGLPENIPFR@.S	101.08	15.05	6.72	0.15
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.GR@EFSFEAWNAK#.I	22.88	5.12	4.47	0.22
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.ILDSAEFIK#.F	86.05	12.93	6.65	0.15
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.INSSPNVNTTASGVEDLNIIQVTIPDDDNER@.L	12.29	3.02	4.07	0.25
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.K#FAEALGSTEAK#.A	10.30	4.79	2.15	0.47
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.K#FGEAIGM*GFPVK#.V	11.90	3.79	3.14	0.32
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.K#PEM*FETAIK#.E	20.97	4.86	4.32	0.23
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.M*SVDAVEIETLR@.K	18.06	3.96	4.56	0.22
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.M*SVDAVEIETLR@K#.T	52.27	11.02	4.74	0.21
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.R@ILDSAEFIK#.F	17.42	4.88	3.57	0.28
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.RPELLTHSTTEVTQPR.T	73.49	11.21	6.55	0.15
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.R@PSTFGIPR@.L	28.94	4.84	5.98	0.17
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.R@PSTYGIPR@.L	47.35	10.59	4.47	0.22
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.SPPIFLSGK#.I	35.45	7.17	4.94	0.20
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.SPSWYGIPR@.L	55.01	13.26	4.15	0.24
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.SPTWFGIPR@.L	94.41	21.64	4.36	0.23
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.STVVPVPYEK#.M	84.42	16.30	5.18	0.19
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.VLAAEAER@.S	114.07	20.74	5.50	0.18
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.AGISFIIK#.R	26.50	3.69	7.18	0.14
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.APSYLEISSM*R@.R	18.96	4.30	4.41	0.23
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.DQSAVVVQGLPEGVAFK#.H	38.87	4.34	8.96	0.11
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.EQVNDLFSR@.K	30.50	5.81	5.25	0.19
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.FAEALGSTEAK#.A	28.68	4.86	5.90	0.17
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.FAQALGLTEAVK#.V	58.43	13.11	4.46	0.22
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.ILDSAEFIK#.F	31.57	11.98	2.63	0.38
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.K#PEM*FETAIK#.E	10.37	3.92	2.65	0.38
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.K#QVEEIFNLK#.F	6.23	2.69	2.31	0.43
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.M*SVDAVEIETLR@.K	11.28	1.86	6.05	0.17
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.R@PELLTHSTTEVTQPR@.T	32.29	3.58	9.02	0.11
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.SPTWFGIPR@.L	29.27	6.29	4.65	0.21
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.STEPPPPPPVPEPANAGK#.R	4.94	2.16	2.28	0.44
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	K.STVVPVPYEK#.M	36.64	5.95	6.16	0.16
Q3UHU8_Q3UHU8_MOUSE	Gtf2i	General transcription fac	R.VLAAEAER@.S	65.53	12.23	5.36	0.19
Q9JI57_GT2D1_MOUSE	Gtf2ird1	General transcription fac	K.FLM*HPEELFVLGLPEGISLR@.R	9.55	3.37	2.83	0.35
Q9JI57_GT2D1_MOUSE	Gtf2ird1	General transcription fac	K.YGEALGLNR@PVLVPYK#.L	10.36	6.06	1.71	0.58
Q8K284_TF3C1_MOUSE	Gtf3c1	General transcription fac	R.NLIIEAVTNLR@.L	12.11	4.79	2.53	0.40
Q8K284_TF3C1_MOUSE	Gtf3c1	General transcription fac	R.YQDEADQNALR@.M	7.00	3.76	1.86	0.54
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	K.ADLIPYQDSPEDQDYSSTSSETPNPPK#.A	7.62	5.35	1.42	0.70
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	K.AYFTAPR@.K	36.14	10.75	3.36	0.30
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	R.EGIPEDGTIYR@.I	19.35	7.00	2.76	0.36
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	R.FSPNLDSYGWLVSGGQSGLVR@.I	8.06	3.43	2.35	0.43
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	R.KPPSTPLVPGLLDQSNPLSTPM*PK.K	12.05	7.17	1.68	0.59
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	R.LEQQDLSSEM*SK#.V	13.95	4.39	3.18	0.31
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	K.SPLFSVQR@.E	24.28	11.15	2.18	0.46
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	K.WQLLSELEAAPYLPQEEK#.S	5.10	2.69	1.90	0.53
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	R.EGIPEDGTIYR@.I	7.41	1.33	5.59	0.18
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	R.LEQQDLSSEM*SK#.V	6.40	2.59	2.47	0.41
Q8BL74_TF3C2_MOUSE	Gtf3c2	General transcription fac	K.SPLFSVQR@.E	9.86	3.51	2.81	0.36
Q3TMP1_Q3TMP1_MOUSE	Gtf3c3	General transcription fac	K.AIYTLSDLAR@.F	10.28	2.32	4.44	0.23
Q3TMP1_Q3TMP1_MOUSE	Gtf3c3	General transcription fac	K.ALEALEPM*YDPDTLAQDANAAQQELK#.L	11.66	2.24	5.19	0.19
Q3TMP1_Q3TMP1_MOUSE	Gtf3c3	General transcription fac	K.ALEVITDFSGIILEK#.E	7.46	2.02	3.69	0.27
Q3TMP1_Q3TMP1_MOUSE	Gtf3c3	General transcription fac	R.DK#ISDNNEQETSNYDAK#.A	8.71	2.51	3.47	0.29
Q3TMP1_Q3TMP1_MOUSE	Gtf3c3	General transcription fac	K.ETLEEGTSEENK#.A	7.67	2.61	2.94	0.34
Q3TMP1_Q3TMP1_MOUSE	Gtf3c3	General transcription fac	R.ILNLLSPSDGER@.F	14.25	15.00	0.95	1.05
Q3TMP1_Q3TMP1_MOUSE	Gtf3c3	General transcription fac	K.ISFEEFER@.R	8.56	2.77	3.09	0.32
Q3TMP1_Q3TMP1_MOUSE	Gtf3c3	General transcription fac	R.LAEM*SLEQDNIK#.Q	7.93	4.30	1.84	0.54
Q3TMP1_Q3TMP1_MOUSE	Gtf3c3	General transcription fac	K.VVDLAPLHLDAR@.I	20.25	5.80	3.49	0.29
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	K.EAAADAAPGPSASFR@.L	6.38	2.34	2.73	0.37
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	R.LQWVQLVDLTEIYGDR@.L	4.95	2.05	2.41	0.41
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	K.LSDVFGSVR@.T	14.48	7.41	1.95	0.51
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	K.NYQVQFVTLK#.T	13.74	4.38	3.14	0.32
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	K.QVDLIDLVR@.W	17.91	9.26	1.93	0.52
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	K.SKEGDTEETPEDSLTAGGDTGGREPVEEK.L	32.33	6.69	4.83	0.21
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	K.LSDVFGSVR@.T	4.21	17.17	0.25	4.07
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	K.NEAPEGNLGDFAEFQR@.R	3.53	1.76	2.01	0.50
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	K.NYQVQFVTLK#.T	9.95	1.81	5.50	0.18
Q8BMQ2_TF3C4_MOUSE	Gtf3c4	General transcription fac	K.QVDLIDLVR@.W	12.73	3.46	3.68	0.27
Q8R2T8_TF3C5_MOUSE	Gtf3c5	General transcription fac	R.STYNYSLPITVK#.K	7.31	2.66	2.75	0.36
Q8R2T8_TF3C5_MOUSE	Gtf3c5	General transcription fac	R.EGYHNPTISGENLIGLSR@.A	19.24	4.10	4.69	0.21
Q8R2T8_TF3C5_MOUSE	Gtf3c5	General transcription fac	R.FSTSSLLLR@.I	17.52	4.91	3.57	0.28

Q8R2T8_TF3C5_MOUSE	Gtf3c5	General transcription fac	K.IYQVLDFR@.I	20.81	5.54	3.76	0.27
Q8R2T8_TF3C5_MOUSE	Gtf3c5	General transcription fac	K.QGLGPSGTDGPR@.K	14.67	3.11	4.71	0.21
Q8R2T8_TF3C5_MOUSE	Gtf3c5	General transcription fac	R.STYNYSLPITVK#.K	14.52	4.02	3.61	0.28
O08582_GTPB1_MOUSE	Gtpbp1	GTP-binding protein 1 O	K.LVLVSPTSEQYDSLLR@.Q	25.73	6.76	3.81	0.26
O08582_GTPB1_MOUSE	Gtpbp1	GTP-binding protein 1 O	R.VAVVGNVDAGK#.S	24.97	6.27	3.99	0.25
O08582_GTPB1_MOUSE	Gtpbp1	GTP-binding protein 1 O	K.LVLVSPTSEQYDSLLR@.Q	13.28	4.11	3.23	0.31
O08582_GTPB1_MOUSE	Gtpbp1	GTP-binding protein 1 O	R.TSYR@EEEPAEFQIDDTYSVPGVGTVVSGTTLR@.G	5.12	2.00	2.56	0.39
Q99ME9_NOG1_MOUSE	Gtpbp4	Nucleolar GTP-binding p	R.ADVDVQPYAFTTK#.S	8.21	2.89	2.84	0.35
Q99ME9_NOG1_MOUSE	Gtpbp4	Nucleolar GTP-binding p	K.DFIDLTLSK#.T	13.42	4.98	2.69	0.37
Q99ME9_NOG1_MOUSE	Gtpbp4	Nucleolar GTP-binding p	R.IAELSEEDQK#.I	13.66	3.92	3.48	0.29
Q99ME9_NOG1_MOUSE	Gtpbp4	Nucleolar GTP-binding p	K.LALGQINIAK#.N	9.68	4.56	2.13	0.47
Q99ME9_NOG1_MOUSE	Gtpbp4	Nucleolar GTP-binding p	R.LPTIDPNTR@.T	13.76	5.62	2.45	0.41
Q99ME9_NOG1_MOUSE	Gtpbp4	Nucleolar GTP-binding p	R.LSQILSDFPK#.L	10.12	5.19	1.95	0.51
Q99ME9_NOG1_MOUSE	Gtpbp4	Nucleolar GTP-binding p	K.VNEVLNR@.L	51.51	31.96	1.61	0.62
Q99ME9_NOG1_MOUSE	Gtpbp4	Nucleolar GTP-binding p	K.YGDSLYR@.C	7.78	3.55	2.19	0.46
Q8K2A1_GULP1_MOUSE	Gulp1	PTB domain-containing	K.FLGSTEVEQPK#.G	42.43	30.19	1.41	0.71
Q8K2A1_GULP1_MOUSE	Gulp1	PTB domain-containing	R.IQDLETENM*ELK#.N	18.23	11.11	1.64	0.61
Q8K2A1_GULP1_MOUSE	Gulp1	PTB domain-containing	R.IQDLETENMELK#.N	5.13	3.36	1.53	0.65
Q8K2A1_GULP1_MOUSE	Gulp1	PTB domain-containing	K.LDEM*QEGFK#.M	12.44	8.06	1.54	0.65
Q8K2A1_GULP1_MOUSE	Gulp1	PTB domain-containing	R.TTQVSTSPAHGVTVM*SPSTDIFDM*IPFSPISHQSPTSAR@.N	5.49	3.12	1.76	0.57
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	K.LLDFSQPNSVAELQETPR.E	2.41	5.21	0.46	2.16
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	K.LQEDLGVTSAQALQYLDRNDLQK.L	4.48	6.81	0.66	1.52
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	R.EVGQIYEALEETSSSR.D	4.95	9.54	0.52	1.93
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	K.FTETLTNIWK#.Q	8.82	7.37	1.20	0.83
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	K.ILTLTSNLLEEPLSR.K	15.20	19.55	0.78	1.29
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	R.LGLDNYYPK.R	8.73	8.91	0.98	1.02
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	K.LLDFSQPNSVAELQETPR@.E	5.69	3.87	1.47	0.68
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	K.NEAPETVEEAER.T	6.68	9.57	0.70	1.43
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	R.NEILSTAQQESR.G	7.04	7.15	0.98	1.02
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	K.NSQEILDNQK.S	9.58	16.51	0.58	1.72
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	K.SQYENQLLER.S	8.88	9.07	0.98	1.02
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	R.TATYEVTTALSSFLK.Y	9.64	15.18	0.63	1.58
Q80SU7_GVIN1_MOUSE	Gvin1	Interferon-induced very l	K.VTNFPEAHSIIQWINQSEYGEEQVK#.I	3.93	6.29	0.62	1.60
Q4VBD9_GZF1_MOUSE	Gzf1	GDNF-inducible zinc fing	R.CGQCGKGLSSK.T	3.11	26.84	0.12	8.62
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	K.GVGASGSFR@.L	2255.47	876.46	2.57	0.39
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	R.LAK#GDEPK#.R	46.34	18.27	2.54	0.39
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	R.LAK#GDEPK#R@.S	13.02	4.92	2.65	0.38
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	-.M*TENSTSAPAAKPK.R	6.98	3.03	2.30	0.43
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	K.R@LVTTGVLK#.Q	1197.01	430.59	2.78	0.36
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	K.VGENADSQIK#.L	3069.33	1260.54	2.43	0.41
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	K.YSDM*IVAAIQAEK#.N	998.19	437.30	2.28	0.44
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	K.YSDMIVAAIQAEK#.N	535.13	223.13	2.40	0.42
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	K.VGENADSQIK#.L	53.34	23.73	2.25	0.44
P10922_H10_MOUSE	H1f0	Histone H1.0 OS=Mus mu	K.YSDM*IVAAIQAEK#.N	12.85	7.53	1.71	0.59
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	K.AGGSAAPTQPK#.R	41.78	17.01	2.46	0.41
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	R.ALVQNDTLLQVK#.G	132.72	46.80	2.84	0.35
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	R.GASAASSPAPK#.A	18.83	8.61	2.19	0.46
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	R.K#VAWFDQQNGR@.T	16.69	2.44	6.84	0.15
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	K.YSQLVVETIR@.K	107.47	39.24	2.74	0.37
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	K.AGGSAAPTQPK#.R	115.49	41.82	2.76	0.36
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	R.ALVQNDTLLQVK#.G	505.74	163.45	3.09	0.32
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	R.K#VAWFDQQNGR@.T	32.94	8.06	4.09	0.24
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	R.R@GASAASSPAPK#.A	31.30	13.53	2.31	0.43
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	K.VAWFDQQNGR@.T	10.74	6.73	1.60	0.63
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	K.YSQLVVETIR@.K	351.36	120.86	2.91	0.34
Q80ZM5_Q80ZM5_MOUSE	H1fx	H1 histone family, memb	K.YSQLVVETIR@K#.L	116.43	42.36	2.75	0.36
Q3THW5_H2AV_MOUSE	H2afv	Histone H2A.V OS=Mus m	R.GDEELDSLIK.A	3.78	26.91	0.14	7.12
Q3THW5_H2AV_MOUSE	H2afv	Histone H2A.V OS=Mus m	K.ATIAGGGVIPHIHK.S	3.81	24.10	0.16	6.32
Q3THW5_H2AV_MOUSE	H2afv	Histone H2A.V OS=Mus m	R.GDEELDSLIK.A	209.38	1399.86	0.15	6.69
Q3THW5_H2AV_MOUSE	H2afv	Histone H2A.V OS=Mus m	R.HLQLAIRGDEELDSLIK.A	84.67	592.95	0.14	7.00
P27661_H2AX_MOUSE	H2afx	Histone H2AX OS=Mus m	K.KASQASQEY.-	9.02	29.57	0.31	3.28
P27661_H2AX_MOUSE	H2afx	Histone H2AX OS=Mus m	K.KSSATVGPK.A	34.69	228.83	0.15	6.60
P27661_H2AX_MOUSE	H2afx	Histone H2AX OS=Mus m	K.LLGGVTIAQGGVLPNIQAVLLPKKSSATVGPK.A	2.77	6.94	0.40	2.51
P27661_H2AX_MOUSE	H2afx	Histone H2AX OS=Mus m	K.SSATVGPK.A	29.53	173.59	0.17	5.88
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.AASADSTTEGTPTDGFTVLSTK.S	23.21	67.40	0.34	2.90
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.AISSYFVSTM*SSSIK.T	16.88	72.08	0.23	4.27
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.EFVEAVLELR.K	8.01	75.50	0.11	9.43
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.GGKEFVEAVLELR.K	4.06	10.95	0.37	2.69
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.GKLEAIITPPPAK.K	8.60	47.04	0.18	5.47
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.GVTIASGGVLPNIHPELLAK.K	55.08	200.27	0.28	3.64
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.KGGKEFVEAVLELR.K	1.33	8.16	0.16	6.11
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.LEAIITPPPAK.K	1.42	7.23	0.20	5.11
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.QTAAQLILK.A	40.19	192.06	0.21	4.78
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.SIAFPSIGSGR.N	25.31	106.34	0.24	4.20
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.SLFLGQK.L	37.55	137.16	0.27	3.65
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.AASADSTTEGTPTDGFTVLSTK.S	6.51	22.91	0.28	3.52
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.EFVEAVLELR.K	8.94	19.93	0.45	2.23
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.GVTIASGGVLPNIHPELLAK.K	15.59	52.42	0.30	3.36
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.QTAAQLILK.A	11.65	34.50	0.34	2.96
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.SIAFPSIGSGR.N	8.02	28.54	0.28	3.56
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.AASADSTTEGTPTDGFTVLSTK.S	7.52	17.78	0.42	2.36
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.AISSYFVSTM*SSSIK.T	7.95	19.11	0.42	2.40
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.EFVEAVLELR.K	8.60	24.33	0.35	2.83
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.GVTIASGGVLPNIHPELLAK.K	32.11	87.72	0.37	2.73
Q9QZQ8_H2AY_MOUSE	H2afy	Core histone macro-H2A	K.SIAFPSIGSGR.N	10.83	46.74	0.23	4.31
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	K.AGGKEFLETVK.E	3.97	14.80	0.27	3.73
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	R.AGVIFPVGR.L	53.66	255.74	0.21	4.77
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	K.DSDKEGTSNSTSEDGPGDGFTILSSK.S	4.26	15.10	0.28	3.55
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	K.GVTIASGGVLPR.I	26.32	71.85	0.37	2.73
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	R.HILLAVANDEELNQLLK.G	41.69	139.36	0.30	3.34
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	R.KSQGPLEVAEAAVSQSSGLAAK.F	5.18	14.18	0.37	2.74
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	K.QTAAQVTLK.A	16.30	40.96	0.40	2.51
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	K.SQGPLEVAEAAVSQSSGLAAK.F	13.31	16.99	0.78	1.28
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	K.SVAFPPFPSGR.N	3.07	10.01	0.31	3.26
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	R.VEGIVHPTTAEIDLKEEIGK.A	21.10	58.50	0.36	2.77
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	R.HILLAVANDEELNQLLK.G	5.97	13.93	0.43	2.33
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	R.AGVIFPVGR.L	20.83	71.41	0.29	3.43
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	K.GVTIASGGVLPR.I	2.89	8.80	0.33	3.04
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	R.HILLAVANDEELNQLLK.G	8.71	27.28	0.32	3.13
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	R.AGVIFPVGR.L	30.65	95.89	0.32	3.13
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	R.HILLAVANDEELNQLLK.G	13.64	44.75	0.30	3.28
Q8CCK0_H2AW_MOUSE	H2afy2	Core histone macro-H2A	K.SQGPLEVAEAAVSQSSGLAAK.F	2.95	4.48	0.66	1.52
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.APWM*EQEGPEYWER@.E	10.90	4.92	2.22	0.45

P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.APWMEQEGPEYWER@.E	5.59	2.78	2.01	0.50
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.DYIALNEDLK#.T	63.46	32.98	1.92	0.52
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.FDSDAENPR.Y	32.06	15.24	2.10	0.48
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.GGDYALAPGSQSSEM*SLR@.D	18.96	11.95	1.59	0.63
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.GYLQFAYEGR.D	78.16	29.46	2.65	0.38
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.TWTAADM*AAQITR@.R	31.84	12.20	2.61	0.38
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.TWTAADMAAQITR@.R	15.48	5.92	2.61	0.38
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.VYHEGLPEPLTLR@.W	63.54	30.04	2.12	0.47
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.WASVVVPLGK#.E	40.82	17.44	2.34	0.43
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.YFETAVSRPGLEEPR.Y	179.61	63.98	2.81	0.36
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.GYLQFAYEGR@.D	11.60	6.90	1.68	0.59
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.APWM*EQEGPEYWER@.E	3.03	3.75	0.81	1.24
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.DYIALNEDLK#.T	24.49	16.94	1.45	0.69
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.FDSDAENPR@.Y	19.39	16.50	1.18	0.85
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.GGDYALAPGSQSSEM*SLR.D	13.64	8.97	1.52	0.66
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.TWTAADM*AAQITR@.R	11.95	8.07	1.48	0.68
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.WASVVVPLGK#.E	23.41	17.86	1.31	0.76
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.APWM*EQEGPEYWER@.E	2.68	2.81	0.95	1.05
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.FDSDAENPR@.Y	45.77	38.51	1.19	0.84
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.GGDYALAPGSQSSEM*SLR@.D	12.80	9.88	1.30	0.77
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.GQEQWFR.V	11.45	9.04	1.27	0.79
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.GYLQFAYEGR@.D	18.74	8.76	2.14	0.47
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.TWTAADM*AAQITR.R	14.99	10.02	1.50	0.67
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.VYHEGLPEPLTLR@.W	37.23	30.79	1.21	0.83
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	K.WASVVVPLGK#.E	39.96	28.25	1.41	0.71
P01899_HA11_MOUSE	H2-D1	H-2 class I histocompatib	R.YFETAVSR@PGLEEPR@.Y	58.71	38.50	1.53	0.66
P01902_HA1D_MOUSE	H2-K1	H-2 class I histocompatib	R.GYQQFAYDGR@.D	10.44	3.97	2.63	0.38
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	K.TWTAADM*AALITK#.H	15.00	6.56	2.29	0.44
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	R.WM*EQEGPEYWER@.E	9.21	7.77	1.19	0.84
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	R.YFVTAVSR@PGLGEPR@.Y	61.22	525.16	0.12	8.58
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	R.YM*EVGYVDDTEFVR.F	22.96	9.22	2.49	0.40
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	R.WM*EQEGPEYWER.E	1.80	2.57	0.70	1.42
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	R.YFVTAVSRPGLGEPR.Y	29.90	86.91	0.34	2.91
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	R.YM*EVGYVDDTEFVR@.F	10.06	6.64	1.51	0.66
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	K.TWTAADM*AALITK#.H	6.46	4.73	1.36	0.73
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	R.YFVTAVSRPGLGEPR.Y	31.57	18.71	1.69	0.59
P01901_HA1B_MOUSE	H2-K1	H-2 class I histocompatib	R.YM*EVGYVDDTEFVR@.F	13.07	8.90	1.47	0.68
Q85ZW6_Q85ZW6_MOUSE	H2-M10.3	Histocompatibility 2, M	K.NRWENM*SEAER@.W	3.37	7.80	0.43	2.31
Q61425_HCDH_MOUSE	Hadh	Hydroxyacyl-coenzyme A	R.LLVPYLIEAVR.L	4.67	7.46	0.63	1.60
Q8BMS1_ECHA_MOUSE	Hadha	Trifunctional enzyme sub	K.AGLEQGSDAGYLAESQK#.F	11.46	5.18	2.21	0.45
Q8BMS1_ECHA_MOUSE	Hadha	Trifunctional enzyme sub	K.DTTASAVAVGLR@.Q	14.95	36.30	0.41	2.43
Q8BMS1_ECHA_MOUSE	Hadha	Trifunctional enzyme sub	R.FGGGSVELLK#.Q	20.71	9.14	2.27	0.44
Q8BMS1_ECHA_MOUSE	Hadha	Trifunctional enzyme sub	K.GFYIYQEGSK#.N	8.72	5.39	1.62	0.62
Q8BMS1_ECHA_MOUSE	Hadha	Trifunctional enzyme sub	R.LPAK#PEVSSDEDVQYR@.V	28.03	7.54	3.72	0.27
Q8BMS1_ECHA_MOUSE	Hadha	Trifunctional enzyme sub	K.M*QLLEIITTDK#.T	8.64	5.19	1.66	0.60
Q8BMS1_ECHA_MOUSE	Hadha	Trifunctional enzyme sub	R.TIEYLEEVAVNFAK#.G	12.73	4.20	3.03	0.33
Q99JY0_ECHB_MOUSE	Hadhb	Trifunctional enzyme sub	K.DQLLLGPTYATPK#.V	8.53	5.86	1.45	0.69
Q99JY0_ECHB_MOUSE	Hadhb	Trifunctional enzyme sub	R.EAALGAGFSDK#.T	21.76	12.15	1.79	0.56
Q99JY0_ECHB_MOUSE	Hadhb	Trifunctional enzyme sub	R.LAAAFAVSR.M	54.39	26.01	2.09	0.48
Q99JY0_ECHB_MOUSE	Hadhb	Trifunctional enzyme sub	R.M*EQDEYALR@.S	24.10	11.85	2.03	0.49
Q99JY0_ECHB_MOUSE	Hadhb	Trifunctional enzyme sub	K.NIVVVEGVR@.I	28.42	15.02	1.89	0.53
Q99JY0_ECHB_MOUSE	Hadhb	Trifunctional enzyme sub	R.IPFLLSGTSYK#.D	5.55	14.71	0.38	2.65
Q8BY71_HAT1_MOUSE	Hat1	Histone acetyltransferase	R.LLVTDM*SDAEQYR@.S	17.74	8.50	2.09	0.48
Q8BY71_HAT1_MOUSE	Hat1	Histone acetyltransferase	R.LLVTDM*SDAEQYR@.S	4.09	3.48	1.18	0.85
Q8BHX1_HAUS1_MOUSE	Haus1	HAUS augmin-like compl	K.AAEEQLSAR@.G	20.36	8.80	2.31	0.43
Q8BHX1_HAUS1_MOUSE	Haus1	HAUS augmin-like compl	K.ALQVAEWLK#.K	7.10	3.03	2.35	0.43
Q8BHX1_HAUS1_MOUSE	Haus1	HAUS augmin-like compl	R.DISLVIEDLK#.Q	12.38	5.28	2.34	0.43
Q8BHX1_HAUS1_MOUSE	Haus1	HAUS augmin-like compl	R.DR@DISLVIEDLK#.Q	11.72	5.09	2.30	0.43
Q8BHX1_HAUS1_MOUSE	Haus1	HAUS augmin-like compl	K.K#LESYLDLM*PSPSLAQLK#.I	15.97	6.80	2.35	0.43
Q8BHX1_HAUS1_MOUSE	Haus1	HAUS augmin-like compl	K.NLTATLVLEK#.C	12.33	8.75	1.41	0.71
Q8BHX1_HAUS1_MOUSE	Haus1	HAUS augmin-like compl	K.R@LEDFLM*ESVNFSPANLSK#.S	17.22	9.72	1.77	0.56
Q9CQS9_HAUS2_MOUSE	Haus2	HAUS augmin-like compl	R.ELQTEISLYIPK#.M	16.08	5.29	3.04	0.33
Q9CQS9_HAUS2_MOUSE	Haus2	HAUS augmin-like compl	K.M*DILVNK#TEELAENILK#.W	18.82	6.95	2.71	0.37
Q8QZX2_HAUS3_MOUSE	Haus3	HAUS augmin-like compl	K.LDDK#EIQILEDEVQTLQK#.L	14.85	7.36	2.02	0.50
Q8QZX2_HAUS3_MOUSE	Haus3	HAUS augmin-like compl	R.LYELLEGDNK#.K	4.91	3.75	1.31	0.76
Q8QZX2_HAUS3_MOUSE	Haus3	HAUS augmin-like compl	R.QELVLNELIK#.Q	11.51	4.75	2.42	0.41
Q8QZX2_HAUS3_MOUSE	Haus3	HAUS augmin-like compl	R.SGKPILEGTALDEVLR.T	15.87	9.48	1.67	0.60
Q8BFT2_HAUS4_MOUSE	Haus4	HAUS augmin-like compl	R.VIQELLVDYYVK#.A	9.86	3.29	3.00	0.33
Q8BFT2_HAUS4_MOUSE	Haus4	HAUS augmin-like compl	K.VWTLTEVLVR@.E	12.70	7.75	1.64	0.61
Q9D786_HAUS5_MOUSE	Haus5	HAUS augmin-like compl	K.ASELLLPR@.A	7.15	2.98	2.40	0.42
Q9D786_HAUS5_MOUSE	Haus5	HAUS augmin-like compl	R.ASSLILLSHTLGLPVGK#.A	10.75	6.56	1.64	0.61
Q9D786_HAUS5_MOUSE	Haus5	HAUS augmin-like compl	K.LVPTSEAVAPQSQELLR@.C	8.92	4.49	1.99	0.50
Q9D786_HAUS5_MOUSE	Haus5	HAUS augmin-like compl	K.VDVTFGPVVSAAPALEPEVLGDVR@.A	6.67	6.37	1.05	0.95
Q6NV99_Q6NV99_MOUSE	Haus6	Protein Haus6 OS=Mus m	R.FLQILQR@.E	9.30	4.01	2.32	0.43
Q6NV99_Q6NV99_MOUSE	Haus6	Protein Haus6 OS=Mus m	K.TIADSEEEDSPLSDTAK#.N	5.77	3.06	1.88	0.53
Q8BKT8_HAUS7_MOUSE	Haus7	HAUS augmin-like compl	R.AVM*EIADTSAEAM*K#.A	7.17	3.40	2.11	0.47
Q99L00_HAUS8_MOUSE	Haus8	HAUS augmin-like compl	R.LVSQVVELSSQASK#.E	24.86	15.32	1.62	0.62
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	R.ANTNSLEVSWGAVATADSYLLQLQK#.Y	6.92	2.09	3.31	0.30
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.ENQWFDVGVIK#.G	12.86	2.50	5.13	0.19
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	R.GPFSEISAFK#.T	12.13	4.14	2.93	0.34
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.GPLPAGTILK#.L	29.47	6.85	4.30	0.23
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.IATGHGQQGVTQVVLK#.G	45.98	6.31	7.29	0.14
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	R.LGHSFSLVGNK#.C	14.91	3.60	4.14	0.24
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	R.LYIWSGR@.D	17.38	4.70	3.70	0.27
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.M*YVFGGWVPLVM*DDVK#.V	8.56	4.58	1.87	0.53
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.SPISVPGGSALISNLGK#.V	37.72	8.80	4.28	0.23
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.SSTPAQLAFM*R@.V	7.48	2.77	2.70	0.37
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.VASSPVM*VSNPATR@.M	31.26	6.62	4.72	0.21
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.YSNDLYELQASR@.W	22.66	6.36	3.56	0.28
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.GPLPAGTILK#.L	15.99	4.68	3.42	0.29
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.IATGHGQQGVTQVVLK#.G	17.06	4.63	3.68	0.27
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	R.ITVAPGALER@.V	6.58	3.65	1.80	0.55
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.SPISVPGGSALISNLGK#.V	21.81	6.65	3.28	0.30
Q61191_HCFC1_MOUSE	Hcfc1	Host cell factor 1 OS=Mus	K.VASSPVM*VSNPATR@.M	8.96	3.07	2.92	0.34
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	R.DGIDDESYEAIFK#PVM*SK#.V	12.64	5.61	2.25	0.44
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.LHISPSNM*TNQNTNEYLEK#.I	43.64	19.10	2.29	0.44
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.LHISPSNMTNQNTNEYLEK#.I	4.69	3.77	1.25	0.80
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	R.M*THNLLLNYGLYR@.K	21.63	10.38	2.08	0.48
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.SFNLPM*LM*LGGGGYTIR@.N	7.22	2.52	2.87	0.35
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	R.VM*TVSFHK#.Y	9.24	15.94	0.58	1.73
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.YGEYFPGTGDLR@.D	61.35	26.62	2.31	0.43
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	R.LFENLR@.M	169.09	58.12	2.91	0.34
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.LHISPSNM*TNQNTNEYLEK#.I	73.47	24.98	2.94	0.34

O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	R.M*THNLLLNYGLYR@.K	6.22	1.09	5.69	0.18
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.SFNLPM*LM*LGGGGYTIR@.N	16.26	6.46	2.52	0.40
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	R.VM*TVSFHK#.Y	15.93	3.45	4.61	0.22
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.YGEYFPGTGDLR@.D	147.47	46.25	3.19	0.31
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.YHSDDYIK#.F	41.91	15.26	2.75	0.36
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.YYAVNYPLR@.D	40.54	14.21	2.85	0.35
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	R.DGIDDESYEAIFK#PVM*SK#.V	24.53	7.29	3.36	0.30
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.LHISPSNM*TNQNTNEYLEK#.I	49.64	19.09	2.60	0.38
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.LHISPSNMTNQNTNEYLEK#.I	4.81	2.11	2.28	0.44
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	R.M*THNLLLNYGLYR@.K	33.39	13.26	2.52	0.40
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.SFNLPM*LM*LGGGGYTIR@.N	14.34	4.91	2.92	0.34
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	R.VM*TVSFHK#.Y	12.40	5.13	2.42	0.41
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.YGEYFPGTGDLR@.D	86.75	30.74	2.82	0.35
O09106_HDAC1_MOUSE	Hdac1	Histone deacetylase 1 OS	K.YYAVNYPLR@.D	21.73	8.66	2.51	0.40
Q6P3E7_HDA10_MOUSE	Hdac10	Histone deacetylase 10 O	K.ILCLLDGIM*DGQIR@.N	9.84	5.51	1.79	0.56
P70288_HDAC2_MOUSE	Hdac2	Histone deacetylase 2 OS	K.LHISPSNM*TNQNTPEYM*EK#.I	12.74	5.00	2.55	0.39
P70288_HDAC2_MOUSE	Hdac2	Histone deacetylase 2 OS	K.TFNLPLLM*LGGGGYTIR@.N	15.01	5.94	2.53	0.40
P70288_HDAC2_MOUSE	Hdac2	Histone deacetylase 2 OS	R.DGIDDESYGQIFK#PIISK#.V	22.24	7.17	3.10	0.32
P70288_HDAC2_MOUSE	Hdac2	Histone deacetylase 2 OS	K.LHISPSNM*TNQNTPEYM*EK#.I	18.34	8.00	2.29	0.44
P70288_HDAC2_MOUSE	Hdac2	Histone deacetylase 2 OS	K.TFNLPLLM*LGGGGYTIR@.N	9.74	2.50	3.90	0.26
P70288_HDAC2_MOUSE	Hdac2	Histone deacetylase 2 OS	R.DGIDDESYGQIFK#PIISK#.V	25.80	7.64	3.38	0.30
P70288_HDAC2_MOUSE	Hdac2	Histone deacetylase 2 OS	K.LHISPSNM*TNQNTPEYM*EK#.I	17.77	6.74	2.64	0.38
Q9Z2V5_HDAC6_MOUSE	Hdac6	Histone deacetylase 6 OS	K.AVLAQGQSSEQAAK#.G	5.12	2.68	1.91	0.52
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.AFHPFIAGPYNR@.L	81.99	26.78	3.06	0.33
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.AFHPFIAGPYNR@.L	9.02	3.89	2.32	0.43
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.AR@HEVLLISAEQDK#R@.A	28.14	6.98	4.03	0.25
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.ASVITQVFHVPLEER@.K	149.99	52.55	2.85	0.35
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.DAFPPLPEK#.A	17.26	1.49	11.56	0.09
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.DAPWTSNSSEK#APDM*SSSEEFPSFGAQVAPK#.T	8.47	3.09	2.74	0.37
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.DK#FPEVIINFPDPAQK#.S	74.54	30.38	2.45	0.41
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.DLANIAEVEVSIPAK#.L	64.63	23.35	2.77	0.36
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.DM*NQFGEGEQAK#.I	12.91	3.27	3.94	0.25
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.DYNVQIK#.F	85.76	33.60	2.55	0.39
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.EALEALVPVTIEVEVPFDLHR@.Y	22.94	6.90	3.33	0.30
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.EIAEEYGGVM*VSFPR@.S	72.08	22.64	3.18	0.31
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.ELLELASR.M	106.52	38.09	2.80	0.36
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.ELQAEQEDR@.A	47.66	5.57	8.56	0.12
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.FPDR@EENPVHSVEPSIQENGDEAGEGR@.E	15.60	83.76	0.19	5.37
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.GAVITQIR@.L	49.63	12.27	4.04	0.25
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.GEPEK#LGQALTEVYAK#.A	5.40	1.57	3.44	0.29
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.GNSLQEILER@.T	115.33	35.59	3.24	0.31
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.GPSSDVEK#.A	22.67	9.85	2.30	0.43
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.HEVLLISAEQDK#R@.A	84.16	27.64	3.05	0.33
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.IDLPAENSNSETIIITGK#.R	62.69	15.64	4.01	0.25
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.IEGDPQGVQQAK#.R	194.81	67.25	2.90	0.35
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.IIFPAAEDK#DQDLITIIGK#EDAVR@.E	22.33	4.41	5.07	0.20
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.INIPPPSVNR@.T	43.19	18.25	2.37	0.42
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.IQIPR@PDDPSNQIK#.I	85.91	29.94	2.87	0.35
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.KGAVITQIR.L	32.49	12.50	2.60	0.38
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.K#QLLHLAEEK#.Q	22.78	8.76	2.60	0.38
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.LEHEVNIQFPDK#DDGNQPQDQITITGYEK#.N	42.84	14.02	3.06	0.33
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.LGQALTEVYAK#.A	145.37	46.79	3.11	0.32
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.LHNSLIGTK#.G	42.80	12.24	3.50	0.29
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.LQTQASATVPIPK#.E	103.17	33.06	3.12	0.32
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.LSVTVDPK#.Y	63.16	29.44	2.15	0.47
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.LVGEIM*QETGTR@.I	95.17	27.98	3.40	0.29
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.LVGEIMQETGTR@.I	20.59	5.21	3.95	0.25
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.M*DYVEINIDHK#.F	45.92	13.29	3.46	0.29
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.M*VADLVENSYSISVPIFK#.Q	115.81	37.92	3.05	0.33
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.MVADLVENSYSISVPIFK#.Q	9.92	3.28	3.02	0.33
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.SDIVQLR@.G	139.87	42.19	3.31	0.30
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.SGLVPQQIK#.V	87.82	24.79	3.54	0.28
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.TEIVFTGEK#.E	19.49	8.18	2.38	0.42
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.TEIVFTGEK#EQLAQAVAR@.I	153.51	46.48	3.30	0.30
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.TGAHLELSLAK#.D	83.00	30.44	2.73	0.37
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.TGVSVEIPPSDSISETVILR@.G	13.48	5.48	2.46	0.41
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.TK#DLIIEQR@.F	38.40	8.70	4.41	0.23
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.TTTIAVEVK#.K	64.94	24.14	2.69	0.37
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.VATLNSEEENDPPTYK#.D	36.64	12.13	3.02	0.33
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.VATLNSEEENDPPTYK#DAFPPLPEK#.A	7.43	28.63	0.26	3.86
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.VHIEFTEGEDK#ITLEGPTEDVNVAQEQIEGM*VK#.D	28.26	11.32	2.50	0.40
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.VK#ELQAEQEDR@.A	60.72	21.46	2.83	0.35
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.YIIGQK#.G	68.78	23.73	2.90	0.35
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.AFHPFIAGPYNR@.L	45.85	12.03	3.81	0.26
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.APDM*SSSEEFPSFGAQVAPK#.T	11.44	3.23	3.54	0.28
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.APDM*SSSEEFPSFGAQVAPK#.T	7.57	2.72	2.78	0.36
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.DAPWTSNSSEK#APDM*SSSEEFPSFGAQVAPK#.T	4.09	3.26	1.26	0.80
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.DK#FPEVIINFPDPAQK#.S	39.50	11.80	3.35	0.30
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.DLANIAEVEVSIPAK#.L	48.05	11.71	4.10	0.24
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.EIAEEYGGVM*VSFPR@.S	43.51	13.64	3.19	0.31
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.EIAEEYGGVMVSFPR@.S	5.82	6.23	0.93	1.07
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.ELLELASR.M	53.68	17.02	3.15	0.32
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.FPDR@EENPVHSVEPSIQENGDEAGEGR@.E	6.25	5.09	1.23	0.81
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.GAVITQIR@.L	13.73	4.42	3.11	0.32
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.GNSLQEILER@.T	85.13	20.41	4.17	0.24
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.HEVLLISAEQDK#R@.A	23.00	3.72	6.19	0.16
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.IDLPAENSNSETIIITGK#.R	43.92	15.69	2.80	0.36
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.IEGDPQGVQQAK#.R	55.58	13.76	4.04	0.25
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.IIFPAAEDK#DQDLITIIGK#.E	5.17	1.60	3.23	0.31
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.IIFPAAEDKDQDLITIIGK.E	94.42	32.46	2.91	0.34
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.ITLEGPTEDVNVAQEQIEGM*VK#.D	6.91	3.00	2.31	0.43
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.LEHEVNIQFPDK#DDGNQPQDQITITGYEK#.N	23.62	8.05	2.93	0.34
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.LGQALTEVYAK#.A	52.53	14.02	3.75	0.27
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.LQDLELK#.T	55.54	9.28	5.98	0.17
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.LQTQASATVPIPK#.E	49.12	18.27	2.69	0.37
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.LSVTVDPK#.Y	31.86	11.38	2.80	0.36
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.LVGEIM*QETGTR@.I	41.60	13.72	3.03	0.33
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.LVGEIMQETGTR@.I	11.07	2.42	4.58	0.22
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.M*VADLVENSYSISVPIFK#.Q	53.90	16.53	3.26	0.31
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.MVADLVENSYSISVPIFK#.Q	7.04	0.93	7.56	0.13
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.SDIVQLR.G	61.01	17.97	3.39	0.29
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.SGLVPQQIK#.V	50.40	13.29	3.79	0.26
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.TEIVFTGEK#EQLAQAVAR@.I	80.25	16.43	4.89	0.20

Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.TGVSVEIPPSDSISETVILR@.G	10.74	2.99	3.59	0.28
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.VATLNSEEENDPPTYK#.D	20.94	8.47	2.47	0.40
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	K.VATLNSEEENDPPTYK#DAFPPLPEK#.A	3.38	1.78	1.89	0.53
Q8VDJ3_VIGLN_MOUSE	Hdlbp	Vigilin OS=Mus musculus	R.VK#ELQAEQEDR@.A	14.31	4.03	3.55	0.28
G3X9B1_G3X9B1_MOUSE	Heatr1	HEAT repeat containing 1	R.EAEDEQAINR.Q	4.79	5.43	0.88	1.13
G3X9B1_G3X9B1_MOUSE	Heatr1	HEAT repeat containing 1	K.M*VIPALIQSDTGDSVEVTR@.N	2.66	2.60	1.02	0.98
Q8BQM4_HEAT3_MOUSE	Heatr3	HEAT repeat-containing p	K.DIM*TPLVALLR@.E	4.67	2.48	1.89	0.53
Q8BQM4_HEAT3_MOUSE	Heatr3	HEAT repeat-containing p	R.LGPLLLDSSLAVR@.E	12.93	2.98	4.34	0.23
Q5QNV8_HEAT9_MOUSE	Heatr9	Protein HEATR9 OS=Mus	K.LM*EAQLMSPDVSDR@.Q	6.79	3.34	2.03	0.49
Q69ZR2_HECD1_MOUSE	Hectd1	E3 ubiquitin-protein liga	R.GQVK#PSTSSQPILSAPGPTK#.L	7.23	4.30	1.68	0.60
Q69ZR2_HECD1_MOUSE	Hectd1	E3 ubiquitin-protein liga	K.IFLDESAPDNVLEVTAR@.A	7.27	2.58	2.82	0.36
Q69ZR2_HECD1_MOUSE	Hectd1	E3 ubiquitin-protein liga	R.LEDILSR@.D	13.57	10.49	1.29	0.77
Q69ZR2_HECD1_MOUSE	Hectd1	E3 ubiquitin-protein liga	K.TAYEWVNPAAYGLVVVTSSEGR@.N	5.68	2.19	2.59	0.39
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.LISQIQPEVNR@.E	6.87	2.49	2.76	0.36
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.LISQIQPEVNR@.E	29.86	11.18	2.67	0.37
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	R.LVTANTIDQK#.I	35.53	13.00	2.73	0.37
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.M*EQQQLEEQK#.K	8.00	3.05	2.63	0.38
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.QEIFYTAIVNR@.T	10.73	3.71	2.89	0.35
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.SINYSELDQFPSELEK#.L	11.17	6.43	1.74	0.58
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	R.TVVEGNIPIESEVNLK#.L	33.17	10.63	3.12	0.32
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.VISDEDLELLLDR@.S	9.68	13.36	0.72	1.38
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.VISDEDLELLLDR@SDLIDQM*K#.A	11.39	6.63	1.72	0.58
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.FFFDPVR@.K	13.04	4.80	2.72	0.37
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.IDEELVTNSGK#.F	24.67	10.30	2.39	0.42
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	R.IGQTK#PVVVYR@.L	71.20	18.14	3.93	0.25
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	R.LDGSM*SYSER@.E	15.72	4.07	3.86	0.26
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.LISQIQPEVNR@.E	51.83	14.96	3.46	0.29
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.M*EQQQLEEQK#.K	16.76	6.60	2.54	0.39
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.QEIFYTAIVNR@.T	14.73	7.23	2.04	0.49
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	R.QGTLQIHPVVVTSFEIAM*R@.D	13.11	2.88	4.55	0.22
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.SINYSELDQFPSELEK#.L	18.50	6.01	3.08	0.33
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	R.TVVEGNIPIESEVNLK#.L	48.14	13.91	3.46	0.29
Q60848_HELLS_MOUSE	Hells	Lymphocyte-specific heli	K.VISDEDLELLLDR@.S	17.04	6.28	2.71	0.37
E9QAM5_HELZ2_MOUSE	Helz2	Helicase with zinc finger (	K.SVDVLGGLLLR@.R	9.57	4.59	2.08	0.48
F2Z461_HERC6_MOUSE	Herc6	E3 ISG15--protein ligase I	K.VFAWGAGSEGQLGIGEFK.E	2.34	2.52	0.93	1.07
Q8C3I8_HGH1_MOUSE	Hgh1	Protein HGH1 homolog (	R.LLPLTQYTDSSVR@.R	6.88	4.76	1.45	0.69
Q99LI8_HGS_MOUSE	Hgs	Hepatocyte growth facto	K.ESDAM*FAAER@.A	7.32	3.73	1.96	0.51
Q99LI8_HGS_MOUSE	Hgs	Hepatocyte growth facto	K.R@DETALQEEEELQLALALSQSEAEEK#ER@.M	7.96	3.80	2.09	0.48
Q99LI8_HGS_MOUSE	Hgs	Hepatocyte growth facto	K.VVQDTYQIM*K#.V	11.04	4.60	2.40	0.42
Q8R1F6_HID1_MOUSE	Hid1	Protein HID1 OS=Mus mu	R.LLSNPLLQTYLPNSTK#.K	3.09	3.03	1.02	0.98
P70349_HINT1_MOUSE	Hint1	Histidine triad nucleotid	K.AQVAQPGGDTIFGK#.I	18.74	7.64	2.45	0.41
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	K.AINTQEVAVK#.E	11.07	7.45	1.49	0.67
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.EIAASTAQLVAASK#.V	27.05	12.43	2.18	0.46
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.EISGLTGQLDNM*K#.I	6.83	2.63	2.59	0.39
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	K.GSLNLTQLQQASR@.G	18.44	5.77	3.20	0.31
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.LIQIPQLPENPPNFLR@.A	6.45	4.05	1.59	0.63
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.QELQVLHSNLETSAQSEAK#.W	17.67	9.46	1.87	0.54
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	K.TLGEELLPR@.G	18.44	8.43	2.19	0.46
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.VSELEAELAEQQHLGR@.Q	28.73	12.36	2.32	0.43
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.WTEGLISASK#.A	51.69	16.22	3.19	0.31
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	K.AINTQEVAVK#.E	16.53	8.04	2.06	0.49
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.EIAASTAQLVAASK#.V	23.70	8.89	2.67	0.37
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.EISGLTGQLDNM*K#.I	6.73	2.64	2.55	0.39
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	K.GSLNLTQLQQASR@.G	18.63	5.57	3.34	0.30
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.LIQIPQLPENPPNFLR@.A	20.11	8.76	2.29	0.44
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.QELQVLHSNLETSAQSEAK#.W	14.32	6.10	2.34	0.43
Q8VD75_HIP1_MOUSE	Hip1	Huntingtin-interacting p	R.VLELENDLQK#.E	14.28	2.95	4.84	0.21
Q61666_HIRA_MOUSE	Hira	Protein HIRA OS=Mus mu	K.FPEILATLR@.G	8.20	3.48	2.36	0.42
Q61666_HIRA_MOUSE	Hira	Protein HIRA OS=Mus mu	K.ELLPVIGQNLR@.F	16.26	1.18	13.83	0.07
Q61666_HIRA_MOUSE	Hira	Protein HIRA OS=Mus mu	K.FPEILATLR@.G	10.49	3.53	2.98	0.34
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	K.ER@SGVSLAALK#.K	36.49	21.31	1.71	0.58
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	K.ER@SGVSLAALK#K#.S	95.51	51.14	1.87	0.54
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	K.GTGAAGSFK.L	140.36	295.01	0.48	2.10
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	R.K#K#PAGPSVSELIVQAVSSSK#.E	275.92	302.97	0.91	1.10
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	K.K#PAGPSVSELIVQAVSSSK#.E	24.15	39.15	0.62	1.62
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	K.KSLAAAGYDVEK.N	24.95	34.21	0.73	1.37
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	K.KSLAAAGYDVEKNNSR.I	9.28	10.90	0.85	1.17
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	R.SGVSLAALK#.K	2621.99	1428.31	1.84	0.54
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	R.SGVSLAALK#K#.S	2015.59	714.84	2.82	0.35
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	K.SLAAAGYDVEK#.N	260.11	336.60	0.77	1.29
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	K.SLAAAGYDVEK#NNSR@.I	38.04	36.71	1.04	0.96
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	R.K#K#PAGPSVSELIVQAVSSSK#.E	9.59	3.82	2.51	0.40
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	R.SGVSLAALK#.K	38.48	13.55	2.84	0.35
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	R.SGVSLAALK#K#.S	29.47	6.04	4.88	0.21
P43275_H11_MOUSE	Hist1h1a	Histone H1.1 OS=Mus mu	R.SGVSLAALK#.K	11.30	10.41	1.09	0.92
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	K.ALAAGGYDVEK#.N	2495.13	1171.79	2.13	0.47
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	K.ATGPPVSELITK#.A	1907.48	1049.26	1.82	0.55
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	K.ER@GGVSLPALK#.K	95.09	40.04	2.37	0.42
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	K.ERGGVSLPALK.K	40.89	18.15	2.25	0.44
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	K.ERGGVSLPALKK.A	114.24	58.84	1.94	0.52
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	R.GGVSLPALK#.K	963.31	461.24	2.09	0.48
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	R.GGVSLPALK#K#.A	601.50	244.40	2.46	0.41
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	K.K#ALAAGGYDVEK#.N	332.23	180.84	1.84	0.54
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	K.K#ALAAGGYDVEK#NNSR@.I	31.95	19.17	1.67	0.60
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	R.K#ATGPPVSELITK#.A	1575.71	921.97	1.71	0.59
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	R.KATGPPVSELITK.A	350.43	168.67	2.08	0.48
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	K.K#PAGATPK#.K	108.51	57.53	1.89	0.53
P43276_H15_MOUSE	Hist1h1b	Histone H1.5 OS=Mus mu	K.ATGPPVSELITK#.A	7.34	4.91	1.49	0.67
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.AK#K#PAAAAVTK#.K	167.32	107.32	1.56	0.64
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.ALAAAGYDVEK#.N	3581.73	2018.56	1.77	0.56
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.ASGPPVSELITK#.A	3482.80	2082.14	1.67	0.60
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.ATGAATPK#.K	74.64	51.65	1.45	0.69
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.GTGASGSFK#.L	2248.34	1187.46	1.89	0.53
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.K#ALAAAGYDVEK#.N	997.78	407.27	2.45	0.41
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.KALAAAGYDVEKNNSR.I	229.09	106.83	2.14	0.47
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.K#ALAAAGYDVEK#NNSR@.I	12.99	4.33	3.00	0.33
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	R.K#ASGPPVSELITK#.A	2072.08	1179.76	1.76	0.57
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	R.KASGPPVSELITK.A	608.18	343.67	1.77	0.57
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.K#ATGAATPK#.K	496.90	292.44	1.70	0.59
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.K#PAAAAVTK#.K	593.26	471.06	1.26	0.79
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.K#PAAAAVTK#K#.V	19.66	10.64	1.85	0.54
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.ALAAAGYDVEK#.N	45.25	15.44	2.93	0.34
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.ASGPPVSELITK#.A	53.68	17.72	3.03	0.33

P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	R.K#ASGPPVSELITK#.A	25.74	6.15	4.19	0.24
P15864_H12_MOUSE	Hist1h1c	Histone H1.2 OS=Mus mu	K.ALAAAGYDVEK#.N	25.82	13.06	1.98	0.51
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.AASGEAK#PK#.A	87.16	46.79	1.86	0.54
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.GTLVQTK#GTGASGSFK#.L	6.19	2.73	2.27	0.44
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.K#AAGTATAK#.K	103.14	58.53	1.76	0.57
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.K#AASGEAK#PK#.A	15.84	13.27	1.19	0.84
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.K#PAAAAGAK#.K	409.44	248.66	1.65	0.61
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	R.K#TSGPPVSELITK#.A	938.28	548.55	1.71	0.58
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.SLVSK#GTLVQTK#.G	9.34	5.79	1.61	0.62
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.TSGPPVSELITK#.A	2887.23	1521.44	1.90	0.53
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.TSGPPVSELITK#.A	17.49	11.58	1.51	0.66
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.TSGPPVSELITK#.A	11.99	6.21	1.93	0.52
P43274_H14_MOUSE	Hist1h1e	Histone H1.4 OS=Mus mu	K.TSGPPVSELITK#.A	10.23	6.53	1.57	0.64
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.AGLQFPVGR.V	110.47	767.77	0.14	6.95
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.HLQLAIR.N	78.43	484.72	0.16	6.18
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.NDEELNK.L	6.83	54.41	0.13	7.97
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.VTIAQGGVLPNIQAVLLPK.K	75.87	407.07	0.19	5.37
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.AGLQFPVGR.V	1148.77	8657.64	0.13	7.54
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.HLQLAIR.N	547.30	4019.10	0.14	7.34
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.HLQLAIRNDEELNK.L	67.46	553.54	0.12	8.21
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.HLQLAIRNDEELNKLLGR.V	34.85	274.06	0.13	7.87
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.HLQLAIR@NDEELNK#LLGR@.V	4.66	35.25	0.13	7.56
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.KGNYSER.V	44.30	345.07	0.13	7.79
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	K.LLGRVTIAQGGVLPNIQAVLLPK.K	3.48	15.37	0.23	4.42
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.NDEELNK.L	232.03	1807.71	0.13	7.79
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.NDEELNK#LLGR@.V	504.92	4046.77	0.12	8.01
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.NDEELNKLLGRVTIAQGGVLPNIQAVLLPK.K	7.17	39.12	0.18	5.45
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.VTIAQGGVLPNIQAVLLPK.K	1036.63	5130.43	0.20	4.95
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.VTIAQGGVLPNIQAVLLPKK.T	24.96	263.91	0.09	10.57
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.AGLQFPVGR.V	17.56	65.30	0.27	3.72
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.VTIAQGGVLPNIQAVLLPK.K	6.45	25.18	0.26	3.91
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.AGLQFPVGR.V	6.72	75.49	0.09	11.23
Q8CGP5_H2A1F_MOUSE	Hist1h2af	Histone H2A type 1-F OS=	R.VTIAQGGVLPNIQAVLLPK.K	5.82	27.37	0.21	4.71
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	R.EIQTAVR.L	66.52	391.25	0.17	5.88
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	R.LLLPGELAK.H	144.50	976.74	0.15	6.76
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	K.AVTKYTSSK.-	5.94	37.32	0.16	6.28
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	R.EIQTAVR.L	1313.25	9399.08	0.14	7.16
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	K.HAVSEGTK.A	194.85	1400.15	0.14	7.19
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	R.IASEASR.L	324.24	2309.19	0.14	7.12
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	R.LAHYNK.R	14.01	84.14	0.17	6.01
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	R.LAHYNKR.S	36.02	248.70	0.14	6.90
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	R.LLLPGELAK.H	1803.20	10724.40	0.17	5.95
P70696_H2B1A_MOUSE	Hist1h2ba	Histone H2B type 1-A OS=	K.QVHPDTGISSK.A	470.56	2735.54	0.17	5.81
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AM*GIM*NSFVNDIFER.I	25.67	147.77	0.17	5.76
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AMGIM*NSFVNDIFER.I	2.98	6.81	0.44	2.28
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AM*GIMNSFVNDIFER.I	4.60	19.62	0.23	4.27
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AMGIMNSFVNDIFER.I	4.61	22.18	0.21	4.81
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.ESYSVYVYK.V	43.54	234.86	0.19	5.39
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	R.KESYSVYVYK.V	7.14	43.52	0.16	6.10
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AM*GIM*NSFVNDIFER.I	1103.42	7019.56	0.16	6.36
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AMGIM*NSFVNDIFER.I	113.93	695.14	0.16	6.10
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AMGIM*NSFVNDIFER@.I	5.00	35.09	0.14	7.02
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AM*GIMNSFVNDIFER.I	213.58	1353.08	0.16	6.34
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AMGIMNSFVNDIFER.I	38.14	292.05	0.13	7.66
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.ESYSVYVYK.V	1078.45	5325.30	0.20	4.94
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	R.IAGEASR.L	293.13	2029.01	0.14	6.92
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	R.KESYSVYVYK.V	416.61	2002.65	0.21	4.81
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	R.KESYSVYVYKVLK.Q	9.91	73.70	0.13	7.44
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	R.SRKESYSVYVYK.V	89.46	603.27	0.15	6.74
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AM*GIM*NSFVNDIFER.I	3.13	12.17	0.26	3.89
Q6ZWY9_H2B1C_MOUSE	Hist1h2bc	Histone H2B type 1-C/E/	K.AM*GIM*NSFVNDIFER.I	3.45	14.47	0.24	4.19
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.EIAQDFK.T	242.15	945.09	0.26	3.90
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.KLPFQR.L	55.90	292.01	0.19	5.22
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	K.STELLIR.K	349.33	1576.42	0.22	4.51
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.YRPGTVALR.E	213.75	964.45	0.22	4.51
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	K.DIQLAR@.R	2352.33	8003.12	0.29	3.40
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.EIAQDFK.T	1847.47	5349.29	0.35	2.90
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.KLPFQR.L	1081.19	3688.97	0.29	3.41
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.KSAPATGGVK.K	26.30	106.58	0.25	4.05
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	K.RVTIM*PK.D	1183.69	4452.41	0.27	3.76
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	K.RVTIM*PKDIQLAR.R	13.99	45.61	0.31	3.26
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	K.STELLIR.K	2043.81	6073.98	0.34	2.97
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.VTIM*PK.D	1293.78	4151.55	0.31	3.21
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.VTIM*PKDIQLAR.R	14.07	62.02	0.23	4.41
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.YQKSTELLIR.K	25.06	78.40	0.32	3.13
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.YRPGTVALR.E	616.14	2118.24	0.29	3.44
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	K.STELLIR.K	189.05	686.78	0.28	3.63
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.YR@PGTVALR@.E	62.14	255.61	0.24	4.11
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.EIAQDFK.T	44.31	165.16	0.27	3.73
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	K.STELLIR.K	103.29	357.31	0.29	3.46
P68433_H31_MOUSE	Hist1h3a	Histone H3.1 OS=Mus mu	R.YRPGTVALR.E	29.85	105.68	0.28	3.54
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.DAVTYTEHAK.R	4.06	15.00	0.27	3.69
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.ISGLIYEETR.G	13.55	50.80	0.27	3.75
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.DAVTYTEHAK.R	939.77	3400.54	0.28	3.62
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.DAVTYTEHAKR.K	12.08	34.69	0.35	2.87
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.DNIQGITK#PAIR@.R	441.59	1114.67	0.40	2.52
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.DNIQGITK#PAIR@.R	1753.53	4499.89	0.39	2.57
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.GVLK#VFLENVIR@.D	11.66	38.36	0.30	3.29
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.ISGLIYEETR@.G	1884.62	6384.70	0.30	3.39
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.KTVTAM*DVVYALK.R	230.48	810.69	0.28	3.52
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.KTVTAM*DVVYALK.R	32.65	120.60	0.27	3.69
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.KTVTAMDVVYALK.R	58.30	530.64	0.11	9.10
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.KTVTAM*DVVYALKR.Q	348.43	1028.65	0.34	2.95
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.KTVTAMDVVYALKR.Q	80.13	291.96	0.27	3.64
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	K.RISGLIYEETRGVLK.V	7.75	21.25	0.36	2.74
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	K.TVTAM*DVVYALK.R	1312.97	4035.59	0.33	3.07
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	K.TVTAMDVVYALK.R	317.15	1155.57	0.27	3.64
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	K.VFLENVIR.D	2362.66	8442.61	0.28	3.57
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	K.VFLENVIRDAVTYTEHAK.R	30.22	110.94	0.27	3.67
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	K.VLRDNIQGITKPAIR.R	7.85	24.28	0.32	3.09
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.ISGLIYEETR.G	4.02	15.33	0.26	3.81
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	R.ISGLIYEETR.G	3.27	17.15	0.19	5.25
P62806_H4_MOUSE	Hist1h4a	Histone H4 OS=Mus mus	K.VFLENVIR.D	4.63	20.15	0.23	4.35

Q6GSS7_H2A2A_MOUSE	Hist2h2aa1	Histone H2A type 2-A OS	R.NDEELNKLLGK.V	3.09	20.31	0.15	6.57
Q6GSS7_H2A2A_MOUSE	Hist2h2aa1	Histone H2A type 2-A OS	R.HLQLAIRNDEELNKLLGK.V	42.41	208.10	0.20	4.91
Q6GSS7_H2A2A_MOUSE	Hist2h2aa1	Histone H2A type 2-A OS	R.HLQLAIR@NDEELNK#LLGK#.V	4.47	29.79	0.15	6.66
Q6GSS7_H2A2A_MOUSE	Hist2h2aa1	Histone H2A type 2-A OS	R.KGNYAER.V	33.19	210.07	0.16	6.33
Q6GSS7_H2A2A_MOUSE	Hist2h2aa1	Histone H2A type 2-A OS	K.LLGKVTIAQGGVLPNIQAVLLPK.K	8.78	71.88	0.12	8.19
Q6GSS7_H2A2A_MOUSE	Hist2h2aa1	Histone H2A type 2-A OS	R.NDEELNKLLGKVTIAQGGVLPNIQAVLLPK.K	15.97	134.79	0.12	8.44
Q64522_H2A2B_MOUSE	Hist2h2ab	Histone H2A type 2-B OS	R.HLQLAVR.N	7.49	45.36	0.17	6.06
Q64522_H2A2B_MOUSE	Hist2h2ab	Histone H2A type 2-B OS	K.LLGGVTIAQGGVLPNIQAVLLPKK.T	4.68	30.92	0.15	6.61
Q9D8V0_HM13_MOUSE	Hm13	Minor histocompatibilit	K.LVFPQDLLEK#.G	21.44	15.05	1.42	0.70
Q9D8V0_HM13_MOUSE	Hm13	Minor histocompatibilit	R.QYQLLFTQGSGENK#EEIINYEFDTK#.D	3.34	2.09	1.60	0.63
Q9D8V0_HM13_MOUSE	Hm13	Minor histocompatibilit	K.SSSDM*PETITSR@.D	14.96	9.65	1.55	0.65
Q9DC33_HM20A_MOUSE	Hmg20a	High mobility group prot	K.LEVDVIQER@.S	12.53	7.23	1.73	0.58
Q9DC33_HM20A_MOUSE	Hmg20a	High mobility group prot	R.TAVEK#LEVDVIQER@.S	35.44	18.33	1.93	0.52
Q9DC33_HM20A_MOUSE	Hmg20a	High mobility group prot	R.TAVEKLEVDVIQER.S	5.88	2.94	2.00	0.50
P52927_HMGA2_MOUSE	Hmga2	High mobility group prot	R.GEGAGQPSTSAQGQPAAPVPQK.R	2.46	6.48	0.38	2.64
Q00547_HMMR_MOUSE	Hmmr	Hyaluronan mediated m	R.DVTAQLESVQEK#.Y	3.81	9.81	0.39	2.57
P14901_HMOX1_MOUSE	Hmox1	Heme oxygenase 1 OS=M	K.LVM*ASLYHIYTALEEEIER@.N	3.36	2.56	1.31	0.76
P14901_HMOX1_MOUSE	Hmox1	Heme oxygenase 1 OS=M	R.M*NTLEM*TPEVK#.H	4.47	3.59	1.25	0.80
O70252_HMOX2_MOUSE	Hmox2	Heme oxygenase 2 OS=M	K.LPSTGEGTQFYLFEHVDNAQQFK#.Q	5.49	2.69	2.04	0.49
O70252_HMOX2_MOUSE	Hmox2	Heme oxygenase 2 OS=M	K.M*ADLSELLK#.E	15.65	4.86	3.22	0.31
O70252_HMOX2_MOUSE	Hmox2	Heme oxygenase 2 OS=M	R.YM*GDLSGGQVLK#.K	7.61	4.44	1.71	0.58
Q9CX86_ROA0_MOUSE	Hnrnpa0	Heterogeneous nuclear ri	K.LFIGGLNVQTSESGLR.G	52.61	67.12	0.78	1.28
Q9CX86_ROA0_MOUSE	Hnrnpa0	Heterogeneous nuclear ri	K.LFIGGLNVQTSESGLR.G	8.46	7.64	1.11	0.90
P49312_ROA1_MOUSE	Hnrnpa1	Heterogeneous nuclear ri	R.GFGFVTYATVEEVDAAM*NARPHK.V	5.78	8.25	0.70	1.43
P49312_ROA1_MOUSE	Hnrnpa1	Heterogeneous nuclear ri	K.IEVIEIM*TDR.G	23.93	17.98	1.33	0.75
P49312_ROA1_MOUSE	Hnrnpa1	Heterogeneous nuclear ri	R.KLFIGGLSFETTDESLR.S	2.24	6.22	0.36	2.78
P49312_ROA1_MOUSE	Hnrnpa1	Heterogeneous nuclear ri	K.LFIGGLSFETTDESLR.S	12.86	17.95	0.72	1.40
P49312_ROA1_MOUSE	Hnrnpa1	Heterogeneous nuclear ri	R.NQGGYGGSSSSSSYGSGR.R	6.20	8.64	0.72	1.39
P49312_ROA1_MOUSE	Hnrnpa1	Heterogeneous nuclear ri	K.LFIGGLSFETTDESLR.S	3.61	4.52	0.80	1.25
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	R.DYFEEYGK#IDTIEIITDR@.Q	7.34	19.15	0.38	2.61
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	R.GFGFVTFDDHDPVDKIVLQK.Y	13.01	22.87	0.57	1.76
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	R.GGGGNFGPGPGSNFR.G	31.02	71.04	0.44	2.29
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	K.IDTIEIITDR.Q	29.64	49.56	0.60	1.67
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	R.KLFIGGLSFETTEESLR.N	10.66	18.45	0.58	1.73
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	K.LFIGGLSFETTEESLR.N	25.83	48.29	0.53	1.87
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	R.NM*GGPYGGGNYGPGGSGGSGGYGGR.S	7.27	13.73	0.53	1.89
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	R.NYYEQWGK.L	7.10	13.13	0.54	1.85
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	R.QEM*QEVQSSR.S	9.08	16.06	0.57	1.77
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	K.TLETVPLER.K	5.75	16.30	0.35	2.84
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	R.GGGGNFGPGPGSNFR.G	4.09	9.90	0.41	2.42
O88569_ROA2_MOUSE	Hnrnpa2b1	Heterogeneous nuclear ri	K.IDTIEIITDR.Q	2.61	4.75	0.55	1.82
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	R.GFAFVTFDDHDTVDKIVVQK.Y	13.16	18.93	0.69	1.44
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	K.IETIEVM*EDR.Q	22.15	29.51	0.75	1.33
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	K.IETIEVMEDR.Q	5.26	11.29	0.47	2.15
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	K.IFVGGIKEDTEEYNLR.D	60.16	77.27	0.78	1.28
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	K.K#IFVGGIK#EDTEEYNLR@.D	6.02	9.73	0.62	1.61
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	K.LFIGGLSFETTDDSLR.E	12.80	1.99	6.42	0.16
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	R.SSGSPYGGGYGSGGGSGGYGSR.R	9.19	17.74	0.52	1.93
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	K.YGKIETIEVM*EDR.Q	8.82	16.77	0.53	1.90
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	K.IETIEVM*EDR.Q	4.64	6.89	0.67	1.48
Q8BG05_ROA3_MOUSE	Hnrnpa3	Heterogeneous nuclear ri	R.SSGSPYGGGYGSGGGSGGYGSR.R	2.09	2.24	0.94	1.07
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	K.DLKDYFTK.F	14.58	73.84	0.20	5.06
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	K.EVYQQQQYGSGGR@.G	20.30	78.54	0.26	3.87
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	R.EYFGQFGEIEAIELPIDPK.L	39.89	129.20	0.31	3.24
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	R.GFGFILFK.D	64.04	290.62	0.22	4.54
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	R.GFVFITFK.E	3.03	18.80	0.16	6.20
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	R.GFVFITFKEEDPVK.K	3.77	12.17	0.31	3.23
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	R.GFVFITFKEEDPVKK.V	31.77	171.74	0.18	5.41
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	K.IFVGGLNPEATEEK.I	184.51	380.05	0.49	2.06
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	K.IREYFGQFGEIEAIELPIDPK.L	30.77	139.05	0.22	4.52
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	K.M*FVGGLSWDTSK.K	43.05	37.36	1.15	0.87
Q99020_ROAA_MOUSE	Hnrnpab	Heterogeneous nuclear ri	K.IFVGGLNPEATEEK.I	16.61	14.56	1.14	0.88
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.AAVAGEDGR@.M	246.15	181.40	1.36	0.74
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.DDEK#EPEEGEDDR@DSANGEDDS.-	4.72	5.57	0.85	1.18
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.GDDLQAIKK.E	22.81	17.97	1.27	0.79
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.GFAFVQYVNER.N	468.15	347.78	1.35	0.74
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.K#SDVEAIFSK#.Y	557.77	407.68	1.37	0.73
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.LK#GDDLQAIK#.K	108.64	54.43	2.00	0.50
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.LKGDDLQAIK.K	204.45	120.51	1.70	0.59
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.LKGDDLQAIKK.E	1118.55	710.58	1.57	0.64
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.M*ESEAGADDSAEEGDLLDDDDNEDRGDDQLELK.D	5.38	2.48	2.17	0.46
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.M*ESEAGADDSAEEGDLLDDDDNEDRGDDQLELKDDEK.E	7.72	3.87	2.00	0.50
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.M*IAGQVLDINLAAEPK#.V	807.46	610.94	1.32	0.76
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.M*IAGQVLDINLAAEPK.V	172.88	128.44	1.35	0.74
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.MIAGQVLDINLAAEPK#.V	185.31	143.34	1.29	0.77
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.MYSYPAR.V	102.83	69.05	1.49	0.67
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.M*YSYPAR@.V	397.24	315.64	1.26	0.79
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.NEK#SEEEQSSASVK#.K	75.62	61.38	1.23	0.81
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.NEK#SEEEQSSASVK#.K	193.27	159.27	1.21	0.82
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.QADLSFSSPVEM*K#.N	161.61	121.02	1.34	0.75
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.QK#VDSLLESLEK#.I	212.33	160.23	1.33	0.75
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.R@SAAEM*YGSVPEHPSPSPLLSSSFDLDYDFQR@.D	5.31	4.06	1.31	0.77
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.SAAEM*YGSVPEHPSPSPLLSSSFDLDYDFQR@DYYDR@.M	5.12	1.82	2.82	0.36
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.SDVEAIFSK#.Y	443.30	343.62	1.29	0.78
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.SEEEQSSASVK#.K	150.40	121.66	1.24	0.81
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.VDSLLESLEK#.I	122.10	99.51	1.23	0.82
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.VFIGNLNTLVVK#.K	1546.87	980.09	1.58	0.63
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.KSDVEAIFSK.Y	4.98	11.16	0.45	2.24
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.LK#GDDLQAIK#K#.E	86.15	110.69	0.78	1.28
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.M*IAGQVLDINLAAEPK.V	17.78	45.14	0.39	2.54
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.NEK#SEEEQSSASVK#.K	5.00	9.79	0.51	1.96
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.QADLSFSSPVEM*K.N	16.09	26.68	0.60	1.66
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.QKVDSLLESLEK.I	43.57	83.22	0.52	1.91
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.SDVEAIFSK.Y	3.21	6.72	0.48	2.10
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.SEEEQSSASVK#.K	8.64	17.56	0.49	2.03
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.VDSLLESLEK.I	7.60	12.72	0.60	1.67
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.VFIGNLNTLVVK.K	13.38	26.23	0.51	1.96
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.M*IAGQVLDINLAAEPK.V	11.54	16.89	0.68	1.46
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	K.SEEEQSSASVK.K	3.81	4.30	0.89	1.13
Q9Z204_HNRPC_MOUSE	Hnrnpc	Heterogeneous nuclear ri	R.VFIGNLNTLVVK.K	26.41	36.54	0.72	1.38
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	K.DLKDYFSK.F	38.13	125.11	0.30	3.28
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	K.ESESVDKVM*DQK.E	19.97	64.88	0.31	3.25
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	R.EYFGGFGEVESIELPM*DNK.T	20.13	50.46	0.40	2.51

Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	R.GFGFVLFK.D	196.47	452.25	0.43	2.30
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	K.IDASKNEEDEGHSNSSPR.H	16.04	59.37	0.27	3.70
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	K.IFVGGLSPDTPEEK.I	155.29	548.90	0.28	3.53
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	K.IREYFGGFGEVESIELPM*DNK.T	28.51	107.36	0.27	3.77
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	K.IREYFGGFGEVESIELPMDNK.T	7.59	23.05	0.33	3.04
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	K.M*FIGGLSWDTTK.K	7.29	23.87	0.31	3.27
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	K.YHNVGLSK.C	5.90	17.39	0.34	2.95
G3X9W0_G3X9W0_MOUSE	Hnrnpd	Heterogeneous nuclear ri	K.IDASKNEEDEGK.M	3.06	9.35	0.33	3.05
Q60668_HNRPD_MOUSE	Hnrnpd	Heterogeneous nuclear ri	R.GFGFVLFK.D	7.12	21.72	0.33	3.05
D3YTQ3_D3YTQ3_MOUSE	Hnrnpdl	Heterogeneous nuclear ri	K.DAASVDKVLELK.E	7.10	13.37	0.53	1.88
D3YTQ3_D3YTQ3_MOUSE	Hnrnpdl	Heterogeneous nuclear ri	K.DLTEYLSR.F	86.21	113.38	0.76	1.32
D3YTQ3_D3YTQ3_MOUSE	Hnrnpdl	Heterogeneous nuclear ri	R.HVTAQQPSR@.L	5.16	4.46	1.16	0.86
D3YTQ3_D3YTQ3_MOUSE	Hnrnpdl	Heterogeneous nuclear ri	K.VFVGGLSPDTSEEQIK.E	10.52	15.45	0.68	1.47
D3YTQ3_D3YTQ3_MOUSE	Hnrnpdl	Heterogeneous nuclear ri	K.VFVGGLSPDTSEEQIKEYFGAFGEIENIELPM*DTK.T	20.06	26.87	0.75	1.34
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.HSGPNSADSANDGFVR@.L	583.42	325.93	1.79	0.56
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.HSGPNSADSANDGFVR.L	100.11	57.65	1.74	0.58
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.ITGEAFVQFASQELAEK#.A	1224.32	617.43	1.98	0.50
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	-.M*M*LGPEGGEGYVVK.L	125.73	99.80	1.26	0.79
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.QSGEAFVELESEDDVK#.L	335.99	184.02	1.83	0.55
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.QSGEAFVELESEDDVK#LALK#K#.D	23.11	18.29	1.26	0.79
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.SSQEEVR@.S	115.05	58.24	1.98	0.51
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.SYSDPPLK#.F	860.24	470.48	1.83	0.55
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.TEM*DWVLK#.H	393.27	196.76	2.00	0.50
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.TEMDWVLK#.H	207.12	99.31	2.09	0.48
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.VTGEADVEFATHEEAVAAM*SK#.D	325.13	157.43	2.07	0.48
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.VTGEADVEFATHEEAVAAMSK#.D	45.25	27.61	1.64	0.61
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.YIEVFK#.S	1979.36	849.26	2.33	0.43
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.ITGEAFVQFASQELAEK#.A	3.17	3.58	0.89	1.13
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.VTGEADVEFATHEEAVAAM*SK#.D	6.86	2.40	2.85	0.35
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.HSGPNSADSANDGFVR@.L	14.70	6.56	2.24	0.45
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.ITGEAFVQFASQELAEK#.A	121.59	60.10	2.02	0.49
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.ITGEAFVQFASQELAEK#.A	48.01	31.38	1.53	0.65
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.QSGEAFVELESEDDVK#.L	27.83	13.03	2.14	0.47
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.TEM*DWVLK#.H	15.33	6.78	2.26	0.44
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.VTGEADVEFATHEEAVAAM*SK#.D	19.42	9.88	1.96	0.51
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.YIEVFK#.S	152.26	89.03	1.71	0.58
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.HSGPNSADSANDGFVR@.L	29.95	9.22	3.25	0.31
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	K.ITGEAFVQFASQELAEK#.A	68.93	27.41	2.51	0.40
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.QSGEAFVELESEDDVK#.L	17.99	8.17	2.20	0.45
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.VTGEADVEFATHEEAVAAM*SK#.D	21.22	8.35	2.54	0.39
Q9Z2X1_HNRPF_MOUSE	Hnrnpf	Heterogeneous nuclear ri	R.YIEVFK#.S	108.11	38.35	2.82	0.35
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.ATENDIYNFFSPLNPVR@.V	543.00	355.35	1.53	0.65
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.EGR@PSGEAFVELESEDEVK#.L	388.07	267.12	1.45	0.69
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.FIYTR@.E	485.31	317.81	1.53	0.65
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	K.HTGPNSPDTANDGFVR.L	537.60	405.95	1.32	0.76
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	K.HTGPNSPDTANDGFVR.L	77.52	60.30	1.29	0.78
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	K.IQNGAQGIR@.F	61.53	43.36	1.42	0.70
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	K.SNNVEM*DWVLK#.H	89.43	57.12	1.57	0.64
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	K.SNNVEMDWVLK#.H	41.95	40.77	1.03	0.97
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.STGEAFVQFASQEIAEK#.A	672.48	411.01	1.64	0.61
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.VHIEIGPDGR@.V	846.08	497.27	1.70	0.59
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.VHIEIGPDGR.V	512.65	280.91	1.82	0.55
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.VTGEADVEFATHEDAVAAM*SK#.D	139.74	98.80	1.41	0.71
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.YVELFLNSTAGASGGAYEHR.Y	95.68	74.27	1.29	0.78
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.ATENDIYNFFSPLNPVR.V	14.31	9.31	1.54	0.65
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.ATENDIYNFFSPLNPVR@.V	16.30	14.70	1.11	0.90
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.STGEAFVQFASQEIAEK.A	3.93	4.86	0.81	1.24
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.VHIEIGPDGR@.V	13.05	11.55	1.13	0.89
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.ATENDIYNFFSPLNPVR@.V	81.90	45.19	1.81	0.55
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.ATENDIYNFFSPLNPVR.V	49.67	27.66	1.80	0.56
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.EGR@PSGEAFVELESEDEVK#.L	32.19	24.66	1.31	0.77
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	K.HTGPNSPDTANDGFVR@.L	9.79	6.43	1.52	0.66
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.STGEAFVQFASQEIAEK#.A	63.31	39.46	1.60	0.62
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.VHIEIGPDGR.V	49.88	28.76	1.73	0.58
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.VTGEADVEFATHEDAVAAM*SK#.D	9.40	7.90	1.19	0.84
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.ATENDIYNFFSPLNPVR@.V	36.39	17.20	2.12	0.47
O35737_HNRH1_MOUSE	Hnrnph1	Heterogeneous nuclear ri	R.VHIEIGPDGR@.V	19.76	7.83	2.52	0.40
P70333_HNRH2_MOUSE	Hnrnph2	Heterogeneous nuclear ri	R.ATENDIYNFFSPLNPM*R@.V	57.33	32.14	1.78	0.56
P70333_HNRH2_MOUSE	Hnrnph2	Heterogeneous nuclear ri	R.ATENDIYNFFSPLNPMR@.V	20.24	11.11	1.82	0.55
P70333_HNRH2_MOUSE	Hnrnph2	Heterogeneous nuclear ri	R.GAYGGGYGGYDDYGGYNDGYGFGSDR@.F	10.02	3.58	2.80	0.36
P70333_HNRH2_MOUSE	Hnrnph2	Heterogeneous nuclear ri	R.R@GAYGGGYGGYDDYGGYNDGYGFGSDR@.F	2.97	2.28	1.30	0.77
P70333_HNRH2_MOUSE	Hnrnph2	Heterogeneous nuclear ri	K.SNSVEM*DWVLK#.H	39.22	21.97	1.79	0.56
P70333_HNRH2_MOUSE	Hnrnph2	Heterogeneous nuclear ri	R.ATENDIYNFFSPLNPM*R@.V	3.27	3.03	1.08	0.92
D3YWT1_D3YWT1_MOUSE	Hnrnph3	MCG11326, isoform CRA	R.ATENDIANFFSPLNPIR.V	18.92	17.22	1.10	0.91
D3YWT1_D3YWT1_MOUSE	Hnrnph3	MCG11326, isoform CRA	R.ATENDIANFFSPLNPIR@.V	15.60	23.59	0.66	1.51
D3YWT1_D3YWT1_MOUSE	Hnrnph3	MCG11326, isoform CRA	R.DGM*DNQGGYGSVGR.M	17.97	17.22	1.04	0.96
D3YWT1_D3YWT1_MOUSE	Hnrnph3	MCG11326, isoform CRA	R.STGEAFVQFASK.E	21.52	21.63	1.00	1.00
D3YWT1_D3YWT1_MOUSE	Hnrnph3	MCG11326, isoform CRA	R.VHIDIGADGR.A	6.47	6.33	1.02	0.98
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.DLAGSIIGK#.G	434.55	239.96	1.81	0.55
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.DYDDM*SPR@.R	58.97	31.07	1.90	0.53
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.ENTQTTIK#.L	62.86	36.67	1.71	0.58
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.GGDLM*AYDR@.R	114.62	53.47	2.14	0.47
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.GSYGDLGGPIITTQVTIPK#.D	198.52	108.72	1.83	0.55
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IDEPLEGSEDR@.I	203.99	108.81	1.87	0.53
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IDEPLEGSEDR@IITITGTQDQIQNAQYLLQNSVK#.Q	9.60	5.57	1.72	0.58
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IILDLISESPIK#.G	492.22	266.42	1.85	0.54
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.IITITGTQDQIQNAQYLLQNSVK#.Q	405.84	208.62	1.95	0.51
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.LLIHQSLAGGIIGVK#.G	230.48	115.75	1.99	0.50
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.NLPLPPPPPPR@.G	69.89	55.60	1.26	0.80
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.NTDEM*VELR@.I	166.71	75.88	2.20	0.46
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.NTDEMVELR@.I	36.41	16.14	2.26	0.44
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.R@PAEDM*EEEQAFK#.R	14.83	7.28	2.04	0.49
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.R@PAEDMEEEQAFK#R@.S	50.24	24.85	2.02	0.49
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.RPAEDM*EEEQAFKR.S	148.70	84.97	1.75	0.57
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.SR@NTDEM*VELR@.I	27.48	7.21	3.81	0.26
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.TDYNASVSVPDSSGPER@.I	409.66	216.48	1.89	0.53
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.GSYGDLGGPIITTQVTIPK#.D	22.59	18.62	1.21	0.82
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IDEPLEGSEDR@.I	9.23	10.96	0.84	1.19
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK.Q	2.14	2.50	0.86	1.17
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.IITITGTQDQIQNAQYLLQNSVK#.Q	42.59	30.72	1.39	0.72
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.TDYNASVSVPDSSGPER@.I	7.90	6.36	1.24	0.81
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.AQPYDPNFYDETYDYGGFTM*M*FDDR@.R	14.68	6.33	2.32	0.43
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.DLAGSIIGK#.G	701.67	317.05	2.21	0.45

P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.DYDDM*SPR@.R	115.47	61.11	1.89	0.53
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.ENTQTTIK#.L	146.09	90.33	1.62	0.62
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.GGDLM*AYDR@.R	175.67	66.54	2.64	0.38
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.GSYGDLGGPIITTQVTIPK#.D	335.24	143.80	2.33	0.43
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.HESGASIK#.I	65.19	27.78	2.35	0.43
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.HESGASIKIDEPLEGSEDR.I	82.41	30.34	2.72	0.37
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IDEPLEGSEDR@.I	302.97	149.61	2.03	0.49
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK.Q	36.47	14.36	2.54	0.39
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IILDLISESPIK#.G	1059.93	452.65	2.34	0.43
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.IITITGTQDQIQNAQYLLQNSVK#.Q	1142.59	395.50	2.89	0.35
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.LLIHQSLAGGIIGVK#.G	423.74	172.36	2.46	0.41
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.NAGAVIGK#.G	293.43	113.47	2.59	0.39
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.NLPLPPPPPPR.G	134.92	94.96	1.42	0.70
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.NTDEM*VELR@.I	226.41	93.17	2.43	0.41
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.NTDEMVELR@.I	74.04	32.20	2.30	0.43
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.R@PAEDM*EEEQAFK#.R	7.03	4.70	1.50	0.67
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.R@PAEDMEEEQAFK#R@.S	43.06	20.27	2.12	0.47
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.RPAEDM*EEEQAFKR.S	263.63	104.02	2.53	0.39
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.SR@NTDEM*VELR@.I	21.86	8.76	2.50	0.40
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.TDYNASVSVPDSSGPER@.I	492.76	225.53	2.18	0.46
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.DLAGSIIGK#.G	69.35	24.44	2.84	0.35
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.GSYGDLGGPIITTQVTIPK#.D	46.66	18.58	2.51	0.40
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IDEPLEGSEDR@.I	35.61	14.35	2.48	0.40
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	K.IILDLISESPIK#.G	90.02	36.37	2.48	0.40
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.IITITGTQDQIQNAQYLLQNSVK#.Q	87.23	31.54	2.77	0.36
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.LLIHQSLAGGIIGVK#.G	28.90	7.99	3.62	0.28
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.NTDEM*VELR@.I	24.38	11.06	2.20	0.45
P61979_HNRPK_MOUSE	Hnrnpk	Heterogeneous nuclear ri	R.TDYNASVSVPDSSGPER@.I	49.05	16.58	2.96	0.34
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	R.AITHLNNNFM*FGQK.M	18.74	24.23	0.77	1.29
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.ISR@PGDSDDSR@.S	12.97	14.77	0.88	1.14
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	R.LKTENAGDQHGGGGGGGSGAAGGGGGENYDDPHKTPASPVVHIR.G	5.62	4.60	1.22	0.82
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.NDQDTWDYTNPNLSGQGDPGSNPNKR.Q	8.59	16.60	0.52	1.93
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.SKPGAAM*VEM*ADGYAVDR.A	22.18	37.42	0.59	1.69
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	R.YGPQYGHPPPPPPPPDYGPHADSPVLM*VYGLDQSK.M	13.30	8.76	1.52	0.66
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	R.AITHLNNNFM*FGQK#.M	30.52	34.90	0.87	1.14
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.ISR@PGDSDDSR@.S	23.27	19.60	1.19	0.84
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.NDQDTWDYTNPNLSGQGDPGSNPNK#R@.Q	25.75	20.27	1.27	0.79
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.NGVQAM*VEFDSVQSAQR.A	4.45	5.88	0.76	1.32
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.NPNGPYPYTLK.L	15.57	18.65	0.83	1.20
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.SDALETLGFLNHYQM*K#.N	8.07	6.62	1.22	0.82
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.SKPGAAM*VEM*ADGYAVDR.A	54.93	43.42	1.27	0.79
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	R.SSSGLLEWDSK#SDALETLGFLNHYQM*K#.N	2.90	2.71	1.07	0.93
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK#.T	10.01	5.79	1.73	0.58
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	K.TENAGDQHGGGGGGGSGAAGGGGGENYDDPHKTPASPVVHIR.G	1.36	3.05	0.44	2.25
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	R.YGPQYGHPPPPPPPPDYGPHADSPVLM*VYGLDQSK#.M	27.82	13.89	2.00	0.50
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	R.YGPQYGHPPPPPPPPDYGPHADSPVLMVYGLDQSK.M	13.34	8.54	1.56	0.64
Q8R081_HNRPL_MOUSE	Hnrnpl	Heterogeneous nuclear ri	R.YYGGGNEGGR@.A	11.16	7.00	1.60	0.63
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	K.TDAVEALTALNHYQIR@.V	12.84	6.98	1.84	0.54
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	K.TIPGTALVEM*GDEYAVER@.A	11.07	7.55	1.47	0.68
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	R.AVTHLNNVK#.L	25.59	5.77	4.43	0.23
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	R.FTSAGQASK#.N	20.79	7.89	2.63	0.38
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	R.HDGYGSHGPLLPLPSR@.Y	58.19	20.18	2.88	0.35
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	R.ITR@PGNTDDPSGGNK#.V	11.32	3.10	3.65	0.27
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	R.ITRPGNTDDPSGGNK.V	71.87	26.16	2.75	0.36
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	R.LK#TEEGEIVYSAEESENR@.Q	36.55	10.98	3.33	0.30
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	R.QALVEFENIDSAK#.E	21.77	8.98	2.42	0.41
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	K.QHSVVPSQIFELEDGTSSYK#DFAM*SK#.N	37.78	9.68	3.90	0.26
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	K.TDAVEALTALNHYQIR@.V	55.97	17.46	3.21	0.31
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	K.TIPGTALVEM*GDEYAVER@.A	52.32	17.88	2.93	0.34
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	K.TLSGLLEWK#.C	47.27	17.24	2.74	0.36
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	R.HDGYGSHGPLLPLPSR@.Y	12.51	5.60	2.24	0.45
Q921F4_HNRLL_MOUSE	Hnrnpll	Heterogeneous nuclear ri	K.TIPGTALVEM*GDEYAVER@.A	10.37	2.86	3.63	0.28
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.AAEVLNK#.H	214.38	16.22	13.22	0.08
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.ADILEDK#DGK#.S	38.55	36.20	1.06	0.94
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.AFITNIPFDVK#.W	76.65	70.42	1.09	0.92
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.EK#VGEVTYVELLM*DAEGK#.S	8.56	7.52	1.14	0.88
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.EK#VGEVTYVELLMDAEGK#.S	3.20	5.07	0.63	1.58
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.EVFSM*AGVVVR@.A	8.58	8.06	1.06	0.94
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.GIGM*GNLGPAGM*GM*EGIGFGINK.I	10.16	8.08	1.26	0.80
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.IGGM*EGPFGGGM*ENM*GR.F	15.40	14.89	1.03	0.97
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.INEILSNALK#.R	63.89	66.66	0.96	1.04
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.LK#EVFSM*AGVVVR@.A	25.61	22.17	1.15	0.87
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*AAPIDR.V	31.89	87.48	0.36	2.74
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GAGLGHGM*DR@.V	6.06	4.26	1.42	0.70
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GAGM*GFGLER@.M	36.37	28.93	1.26	0.80
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GLAM*GGAGGASFDR@.A	14.03	10.12	1.39	0.72
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GLVM*DR@.M	39.62	29.93	1.32	0.76
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPAIER.M	50.22	41.11	1.22	0.82
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPAM*GPALGAGIER.M	18.91	15.30	1.24	0.81
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*VPTGM*GASLER.M	27.46	27.03	1.02	0.98
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.NLPFDFTWK#.M	20.00	15.16	1.32	0.76
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.QGGGGAGGSVPGIER@.M	56.12	52.02	1.08	0.93
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.VGEVTYVELLMDAEGK#.S	6.99	7.05	0.99	1.01
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.AFITNIPFDVK.W	3.64	4.64	0.79	1.27
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GLAM*GGAGGASFDR@.A	5.84	6.33	0.92	1.08
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPAM*GPALGAGIER.M	5.55	5.45	1.02	0.98
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.AAEVLNK#.H	445.97	310.35	1.44	0.70
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.ADILEDK#DGK#.S	245.61	157.25	1.56	0.64
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.AFITNIPFDVK#.W	940.10	635.74	1.48	0.68
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.EKVGEVTYVELLM*DAEGK.S	86.45	50.17	1.72	0.58
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.EK#VGEVTYVELLMDAEGK#.S	36.73	26.74	1.37	0.73
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.EVFSM*AGVVVR@.A	65.41	60.84	1.08	0.93
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.FESPEVAER@.A	360.37	264.86	1.36	0.73
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.FGSGM*NM*GR.I	129.71	80.68	1.61	0.62
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.GDFFPPER@PQQLPHGLGGIGM*GLGPGGQPIDANHLSK#.G	29.13	16.53	1.76	0.57
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.GEER@PTQNEK#.R	15.45	14.14	1.09	0.91
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.GGNR@FEPYSNPTK#.R	82.39	54.35	1.52	0.66
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.GIGM*GNLGPAGMGM*EGIGFGINK#.I	17.03	9.48	1.80	0.56
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.GIGMGNLGPAGM*GM*EGIGFGINK.I	7.43	5.08	1.46	0.68
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.GIGMGNLGPAGM*GM*EGIGFGINK#.I	23.57	12.69	1.86	0.54
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.GIGM*GNLGPAGM*GMEGIGFGINK#.I	5.90	4.68	1.26	0.79
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.IGGM*EGPFGGGM*ENM*GR.F	178.49	121.06	1.47	0.68
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.IGGM*EGPFGGGM*ENMGR@.F	9.89	5.32	1.86	0.54

Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.IGGM*EGPFGGGMENM*GR@.F	4.99	6.36	0.79	1.27
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.IGGMEGPFGGGM*ENM*GR@.F	13.76	9.76	1.41	0.71
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.IGSGVER@.M	295.38	191.68	1.54	0.65
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.INEILSNALK#.R	615.78	383.48	1.61	0.62
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.ISGAGM*ER.M	123.23	78.89	1.56	0.64
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.ISGAGMER@.M	32.90	22.57	1.46	0.69
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.LGSTVFVANLDYK#.V	387.64	242.63	1.60	0.63
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.LKEVFSM*AGVVVR.A	291.09	158.64	1.83	0.54
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.LK#EVFSMAGVVVR@.A	49.05	29.68	1.65	0.61
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MAAPIDR@.V	87.25	62.77	1.39	0.72
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*AAPIDR.V	436.86	321.32	1.36	0.74
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GAGLGHGM*DR.V	50.93	28.07	1.81	0.55
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GAGLGHGMDR@.V	7.41	5.58	1.33	0.75
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GAGM*GFGLER@.M	311.22	200.93	1.55	0.65
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MGAGM*GFGLER@.M	34.22	21.22	1.61	0.62
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GAGMGFGLER@.M	20.75	14.70	1.41	0.71
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GANNLER.M	158.05	103.74	1.52	0.66
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MGANNLER@.M	40.85	27.61	1.48	0.68
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GANSLER@.M	348.15	219.53	1.59	0.63
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MGANSLER@.M	74.12	46.75	1.59	0.63
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GLAM*GGAGGASFDR@.A	436.11	274.77	1.59	0.63
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MGLAM*GGAGGASFDR@.A	28.46	19.76	1.44	0.69
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GLAMGGAGGASFDR@.A	15.40	7.38	2.09	0.48
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MGLAMGGAGGASFDR@.A	8.79	5.01	1.75	0.57
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GLSM*DR@.M	109.09	69.94	1.56	0.64
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MGLVM*DR@.M	32.61	18.35	1.78	0.56
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GLVMDR@.M	18.20	10.85	1.68	0.60
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GLVM*DR.M	195.03	127.22	1.53	0.65
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPAIER@.M	436.86	321.32	1.36	0.74
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPAM*GPALGAGIER@.M	406.36	282.03	1.44	0.69
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MGPAM*GPALGAGIER@.M	26.65	20.31	1.31	0.76
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPAMGPALGAGIER@.M	27.23	14.25	1.91	0.52
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MGPAMGPALGAGIER@.M	15.61	8.00	1.95	0.51
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MGPGIDR@.I	36.80	26.11	1.41	0.71
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPGIDR@.I	325.28	233.04	1.40	0.72
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPLGLDHM*ASSIER@.M	464.22	311.26	1.49	0.67
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPLGLDHM*ASSIER.M	24.07	15.56	1.55	0.65
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPLGLDHMASSIER@.M	62.34	42.98	1.45	0.69
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPVM*DR.M	123.79	72.68	1.70	0.59
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GPVMDR@.M	28.76	24.17	1.19	0.84
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GSSIER@.M	96.42	70.42	1.37	0.73
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*VPTGM*GASLER@.M	209.87	130.79	1.60	0.62
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.MVPTGMGASLER@.M	15.43	13.91	1.11	0.90
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.NLPFDFTWK#.M	396.12	275.20	1.44	0.69
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.QGGGGAGGSVPGIER@.M	548.06	358.48	1.53	0.65
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.VGEVTYVELLM*DAEGK#.S	151.08	90.87	1.66	0.60
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.VGEVTYVELLM*DAEGK#.S	32.24	24.93	1.29	0.77
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.VGEVTYVELLMDAEGK#.S	68.83	43.00	1.60	0.62
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.VGQTIER@.M	227.61	138.21	1.65	0.61
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.VGSEIER@.M	447.39	331.50	1.35	0.74
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.VK#EDPDGEHAR@.R	13.13	9.32	1.41	0.71
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.VKEDPDGEHAR.R	117.84	93.06	1.27	0.79
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.ADILEDK#DGK#.S	15.69	11.79	1.33	0.75
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.AFITNIPFDVK#.W	38.73	23.39	1.66	0.60
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.IGGM*EGPFGGGM*ENM*GR.F	12.05	6.03	2.00	0.50
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.INEILSNALK#.R	57.13	29.20	1.96	0.51
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.LGSTVFVANLDYK#.V	21.20	12.10	1.75	0.57
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GAGLGHGM*DR@.V	9.86	3.95	2.50	0.40
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GAGM*GFGLER.M	17.43	7.56	2.31	0.43
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GANSLER@.M	26.07	14.44	1.81	0.55
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*GLAM*GGAGGASFDR@.A	26.55	13.04	2.04	0.49
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.M*VPTGM*GASLER@.M	16.11	6.64	2.43	0.41
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	K.QGGGGAGGSVPGIER@.M	26.59	15.63	1.70	0.59
Q9D0E1_HNRPM_MOUSE	Hnrnpm	Heterogeneous nuclear ri	R.VGQTIER@.M	22.98	12.22	1.88	0.53
F7B5B5_F7B5B5_MOUSE	Hnrnpr	Protein Hnrnpr OS=Mus	R.NLATTVTEEILEK.S	1.67	6.23	0.27	3.72
F7B5B5_F7B5B5_MOUSE	Hnrnpr	Protein Hnrnpr OS=Mus	R.DLYEDELVPLFEK.A	16.90	26.28	0.64	1.55
F7B5B5_F7B5B5_MOUSE	Hnrnpr	Protein Hnrnpr OS=Mus	R.LM*M*DPLSGQNR@.G	5.80	5.34	1.09	0.92
F7B5B5_F7B5B5_MOUSE	Hnrnpr	Protein Hnrnpr OS=Mus	R.NLATTVTEEILEK.S	22.25	38.54	0.58	1.73
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.DIDIHEVR@.I	18.30	8.35	2.19	0.46
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.DR@LSASSLTM*ESFAFLWAGGR@.A	11.08	3.22	3.44	0.29
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.FIEIAAR@.K	61.14	34.68	1.76	0.57
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.LSASSLTM*ESFAFLWAGGR@.A	7.45	2.88	2.59	0.39
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.NFILDQTNVSAAAQR@.R	37.13	21.62	1.72	0.58
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.NGQDLGVAFK#.I	14.92	8.19	1.82	0.55
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.YNILGTNTIM*DK.M	17.01	9.19	1.85	0.54
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.DIDIHEVR@.I	302.42	93.73	3.23	0.31
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.DLPEHAVLK#.M	359.61	95.75	3.76	0.27
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.DR@LSASSLTM*ESFAFLWAGGR@.A	71.47	15.90	4.50	0.22
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.FIEIAAR@.K	569.96	176.72	3.23	0.31
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.GYFEYIEENK#.Y	80.22	24.04	3.34	0.30
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.HAAENPGK#.Y	17.00	10.05	1.69	0.59
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.HAAENPGK#YNILGTNTIM*DK#.M	10.88	3.85	2.83	0.35
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.IGWSLTTSGM*LLGEEEFSYGYSLK#.G	12.51	5.01	2.50	0.40
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.LK#VSELK#EELK#.K	33.76	6.89	4.90	0.20
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.LNTLLQR@.A	264.81	87.98	3.01	0.33
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.LQAALDNEAGGR@PAM*EPGNGSLDLGGDAAGR@.S	58.38	13.45	4.34	0.23
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.LQAALDNEAGGR@PAMEPGNGSLDLGGDAAGR@.S	10.05	3.69	2.72	0.37
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.LSASSLTM*ESFAFLWAGGR@.A	40.86	9.13	4.48	0.22
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.LSASSLTM*ESFAFLWAGGR.A	78.22	20.59	3.80	0.26
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.M*M*VAGFK#.K	73.28	30.85	2.38	0.42
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.NFILDQTNVSAAAQR@.R	406.47	128.66	3.16	0.32
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.NGQDLGVAFK#.I	146.35	37.84	3.87	0.26
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.QM*ADTGK#LNTLLQR@.A	52.30	13.00	4.02	0.25
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.RNFILDQTNVSAAAQR.R	30.88	8.73	3.54	0.28
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.SSGPTSLFAVTVAPPGAR@.Q	321.73	107.34	3.00	0.33
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.TTWVTK#.H	61.75	24.48	2.52	0.40
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.VSELK#EELK#.K	59.53	20.68	2.88	0.35
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.VTEK#IPVR@.H	37.57	11.92	3.15	0.32
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.YNILGTNTIM*DK#.M	189.62	58.79	3.23	0.31
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.YNILGTNTIMDK#.M	28.77	8.76	3.28	0.30
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.DLPEHAVLK#.M	68.13	22.23	3.07	0.33
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.FIEIAAR@.K	111.92	31.74	3.53	0.28
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.LNTLLQR@.A	62.45	17.24	3.62	0.28

Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.LQAALDNEAGGR@PAM*EPGNGSLDLGGDAAGR@.S	10.34	5.91	1.75	0.57
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	R.NFILDQTNVSAAAQR.R	87.34	22.31	3.92	0.26
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.NGQDLGVAFK#.I	28.99	7.00	4.14	0.24
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.SSGPTSLFAVTVAPPGAR@.Q	65.38	17.87	3.66	0.27
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.VSELK#EELK#.K	25.82	7.17	3.60	0.28
Q8VEK3_HNRPU_MOUSE	Hnrnpu	Heterogeneous nuclear ri	K.YNILGTNTIM*DK#.M	37.26	16.02	2.33	0.43
Q8VDM6_HNRL1_MOUSE	Hnrnpul1	Heterogeneous nuclear ri	R.NYILDQTNVYGSAQR@.R	6.82	4.96	1.37	0.73
Q8VDM6_HNRL1_MOUSE	Hnrnpul1	Heterogeneous nuclear ri	K.HLPSTEPDPHVVR@.I	42.70	27.50	1.55	0.64
Q8VDM6_HNRL1_MOUSE	Hnrnpul1	Heterogeneous nuclear ri	K.INEEISVK#.H	43.71	25.11	1.74	0.57
Q8VDM6_HNRL1_MOUSE	Hnrnpul1	Heterogeneous nuclear ri	K.M*R@PFEGFQR@.K	61.37	13.54	4.53	0.22
Q8VDM6_HNRL1_MOUSE	Hnrnpul1	Heterogeneous nuclear ri	R.NYILDQTNVYGSAQR@.R	30.45	15.09	2.02	0.50
Q8VDM6_HNRL1_MOUSE	Hnrnpul1	Heterogeneous nuclear ri	R.QNQFYETPVIK#.Q	14.21	5.37	2.64	0.38
Q8VDM6_HNRL1_MOUSE	Hnrnpul1	Heterogeneous nuclear ri	K.TEM*K#QEAPPSFLPPEASQLK#.T	12.92	8.48	1.52	0.66
Q8VDM6_HNRL1_MOUSE	Hnrnpul1	Heterogeneous nuclear ri	K.YNILGTNAIM*DK#.M	32.34	18.09	1.79	0.56
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.NYYGYQGYR@.-	8.34	4.38	1.90	0.53
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.ANFSLPEK#.C	37.16	22.13	1.68	0.60
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.AVEEQGDDQDSEK#.S	21.00	12.74	1.65	0.61
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.AYYEFR@.E	105.58	47.83	2.21	0.45
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.DEEEDQTLVNLDTYTSDLHFQISK#.D	14.12	4.61	3.07	0.33
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.EVEGDDVPESIM*LEM*K#.A	29.46	165.35	0.18	5.61
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.FPTLWSGAR@.S	141.93	88.10	1.61	0.62
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.GLEEPEM*DPK#.S	40.70	25.36	1.61	0.62
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.KEVEGDDVPESIM*LEM*K.A	18.26	8.62	2.12	0.47
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.K#LLLFK#.T	32.94	14.72	2.24	0.45
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.K#VVVVVPNEEDWK#R@.R	114.44	51.37	2.23	0.45
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.LK#VTELR@.S	41.56	14.87	2.79	0.36
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.LVQIASR@.S	290.38	143.01	2.03	0.49
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.M*KGLEEPEM*DPK.S	19.13	10.81	1.77	0.57
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.NGEDLGVAFR@.I	70.76	28.42	2.49	0.40
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.NYYGYQGYR@.-	73.57	31.20	2.36	0.42
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.R@YNVLGAETVLTQM*R@.M	24.16	14.79	1.63	0.61
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.SGDETPGSEAPGDK#.A	35.99	20.31	1.77	0.56
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.SGDETPGSEAPGDK#AVEEQGDDQDSEK#.S	95.02	44.02	2.16	0.46
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.TQWALK#.Y	77.69	40.97	1.90	0.53
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.VTQNLPM*K#.E	45.99	23.97	1.92	0.52
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.VVVVVPNEEDWK#.R	9.45	4.74	1.99	0.50
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.YGGQPLFSEK#.F	59.55	35.60	1.67	0.60
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.YNVLGAETVLTQM*R@.M	115.69	53.86	2.15	0.47
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.YNVLGAETVLTQMR.M	19.45	8.81	2.21	0.45
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.AVEEQGDDQDSEK#.S	9.53	2.40	3.97	0.25
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.EVEGDDVPESIM*LEM*K#.A	6.37	1.59	4.01	0.25
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.FPTLWSGAR@.S	33.36	11.84	2.82	0.36
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.K#VVVVVPNEEDWK#R@.R	29.08	11.27	2.58	0.39
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.NYYGYQGYR@.-	14.85	4.77	3.11	0.32
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.SGDETPGSEAPGDK#.A	18.66	7.52	2.48	0.40
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.SGDETPGSEAPGDK#AVEEQGDDQDSEK#.S	11.76	5.34	2.20	0.45
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	K.VVVVVPNEEDWK#.R	13.84	3.94	3.51	0.29
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.YGGQPLFSEK#.F	17.09	5.22	3.27	0.31
Q00PI9_HNRL2_MOUSE	Hnrnpul2	Heterogeneous nuclear ri	R.YNVLGAETVLTQM*R.M	47.00	15.43	3.05	0.33
Q99JP6_HOME3_MOUSE	Homer3	Homer protein homolog	R.EANAAATQWR@.Q	5.53	3.16	1.75	0.57
Q99JP6_HOME3_MOUSE	Homer3	Homer protein homolog	R.EAPDTAER@EETQQQVQDLETR@.N	10.84	3.30	3.29	0.30
Q99JP6_HOME3_MOUSE	Homer3	Homer protein homolog	K.EATSQSVEQLEAR@.V	11.13	7.15	1.56	0.64
Q99JP6_HOME3_MOUSE	Homer3	Homer protein homolog	R.NAELEQQLR@.S	9.21	22.71	0.41	2.47
Q7TMK6_HOOK2_MOUSE	Hook2	Protein Hook homolog 2	R.LNQQQLSELR@.A	5.54	4.20	1.32	0.76
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	R.HLQLQTQLEQLQEETFR@.L	19.91	7.92	2.51	0.40
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	K.IALLQSLLDDANLR@.K	12.90	6.17	2.09	0.48
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	K.IDPVYFDDNWLNR@.I	9.49	3.70	2.56	0.39
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	R.IEELQEALR.K	18.96	8.47	2.24	0.45
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	R.LASTGSGQSFLAR@.Q	14.03	5.06	2.77	0.36
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	R.LLEVQSQVEELQK#.S	23.77	8.88	2.68	0.37
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	K.LNQEDSDNEK#IALLQSLLDDANLR@.K	8.14	3.54	2.30	0.43
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	R.LNQSDSIEDPNSPAGR@.R	8.84	3.83	2.31	0.43
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	K.QNQGAAPEIQALK#.N	13.39	4.69	2.86	0.35
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	R.QQNDELTTLADEAQSLK#DEIDVLR@.H	12.63	8.45	1.50	0.67
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	K.SSLLAENQILM*ER@.L	11.40	5.40	2.11	0.47
Q8BUK6_HOOK3_MOUSE	Hook3	Protein Hook homolog 3	R.LASTGSGQSFLAR@.Q	6.05	2.13	2.84	0.35
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.EASYSLIR@.K	22.66	20.30	1.12	0.90
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.GASGSFVVVQK#.S	16.88	12.96	1.30	0.77
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	R.GQLEQITGK#.G	36.91	23.39	1.58	0.63
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	R.KYVSQYYPK.L	6.23	8.21	0.76	1.32
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.LEDVLPLAFTR@.L	34.08	22.84	1.49	0.67
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.M*DAILTEAIK#.A	13.53	14.33	0.94	1.06
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.TGASVVAIR@.K	23.85	16.05	1.49	0.67
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	R.VDIRPQLLK.N	43.98	33.62	1.31	0.76
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.YPSLGLER@.R	15.29	8.44	1.81	0.55
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.AEDTTM*PIR@.R	9.03	5.74	1.57	0.64
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.ARPSPSVIK.K	74.61	30.93	2.41	0.41
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.EASYSLIR@.K	93.12	43.52	2.14	0.47
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.GASGSFVVVQK#.S	94.40	42.26	2.23	0.45
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.GASGTFQLK#.K	90.88	51.37	1.77	0.57
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.GKGASGSFVVVQK.S	48.36	23.50	2.06	0.49
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	R.GQLEQITGK#.G	184.58	86.04	2.15	0.47
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	R.K#VPAAQR@.G	42.63	29.71	1.44	0.70
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	R.K#YVSQYYPK#.L	39.94	17.17	2.33	0.43
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.LEDVLPLAFTR@.L	252.10	114.59	2.20	0.45
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.M*DAILTEAIK#.A	90.98	41.31	2.20	0.45
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.MDAILTEAIK#.A	16.55	7.79	2.13	0.47
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.NGWLEQISGK#.G	20.79	10.34	2.01	0.50
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.SGEKPLLGGSLM*EYAILSAIAAM*NEPK.T	39.04	19.84	1.97	0.51
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.TGASVVAIR@.K	137.80	61.21	2.25	0.44
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.YPSLGLER@.R	99.11	47.19	2.10	0.48
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.YVSQYYPK#.L	34.82	17.44	2.00	0.50
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	R.GQLEQITGK#.G	27.59	9.78	2.82	0.35
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.K#ESGGSDDEDEDDDDDESSEDSEDEEPPPK#R@.S	3.57	2.45	1.46	0.69
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.LEDVLPLAFTR@.L	38.53	17.82	2.16	0.46
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.M*DAILTEAIK#.A	18.46	6.53	2.83	0.35
Q3TEA8_HP1B3_MOUSE	Hp1bp3	Heterochromatin protei	K.YPSLGLER@.R	17.05	6.50	2.62	0.38
P62748_HPCL1_MOUSE	Hpcal1	Hippocalcin-like protein	K.LSLEEFIK#.G	13.74	6.51	2.11	0.47
P62748_HPCL1_MOUSE	Hpcal1	Hippocalcin-like protein	R.TFDTNSDGTIDFR@.E	10.59	3.65	2.90	0.34
Q8R3H7_HS2ST_MOUSE	Hs2st1	Heparan sulfate 2-O-sulfc	R.EK#DGDLYILAQNFFYEK#.I	13.12	3.14	4.18	0.24
Q99N15_Q99N15_MOUSE	Hsd17b10	17beta-hydroxysteroid d	K.GGIVGM*TLPIAR@.D	13.85	4.20	3.30	0.30
Q99N15_Q99N15_MOUSE	Hsd17b10	17beta-hydroxysteroid d	R.LVAGEM*GQNEPDQGGQR@.G	7.08	1.59	4.45	0.22
Q99N15_Q99N15_MOUSE	Hsd17b10	17beta-hydroxysteroid d	R.DLAPTGIR@.V	16.39	7.51	2.18	0.46

Q99N15_Q99N15_MOUSE	Hsd17b10	17beta-hydroxysteroid d	K.GGIVGM*TLPIAR@.D	17.78	7.02	2.53	0.39
Q99N15_Q99N15_MOUSE	Hsd17b10	17beta-hydroxysteroid d	K.GLVAVVTGGASGLGLATAK#.R	15.03	5.24	2.87	0.35
Q99N15_Q99N15_MOUSE	Hsd17b10	17beta-hydroxysteroid d	R.LVAGEM*GQNEPDQGGQR@.G	7.35	3.69	1.99	0.50
Q99N15_Q99N15_MOUSE	Hsd17b10	17beta-hydroxysteroid d	R.LVGQGATAVLLDVPDSEGEAQAK#.K	14.83	4.35	3.41	0.29
Q99N15_Q99N15_MOUSE	Hsd17b10	17beta-hydroxysteroid d	R.NFLASQVPFPSR@.L	29.70	11.90	2.50	0.40
Q99N15_Q99N15_MOUSE	Hsd17b10	17beta-hydroxysteroid d	R.VINVNLIGTFNVIR@.L	4.35	3.22	1.35	0.74
P51660_DHB4_MOUSE	Hsd17b4	Peroxisomal multifuncti	R.VVLVTGAGGGLGR@.A	9.12	6.45	1.41	0.71
P51660_DHB4_MOUSE	Hsd17b4	Peroxisomal multifuncti	R.IDVVVNNAGILR@.D	7.41	2.48	2.98	0.34
P51660_DHB4_MOUSE	Hsd17b4	Peroxisomal multifuncti	R.VVLVTGAGGGLGR@.A	13.88	2.26	6.14	0.16
P51660_DHB4_MOUSE	Hsd17b4	Peroxisomal multifuncti	R.GALVIVNDLGGDFK#.G	8.10	11.55	0.70	1.42
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.ADLINNLGTIAK#.S	29.03	10.99	2.64	0.38
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.EDQTEYLEER@.R	6.56	2.24	2.92	0.34
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HNDDEQYAWESSAGGSFTVR@.T	6.67	4.76	1.40	0.71
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.ADLINNLGTIAK#.S	9.33	4.74	1.97	0.51
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	R.GVVDSEDLPLNISR.E	2.79	2.86	0.98	1.02
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	R.TLTIVDTGIGM*TK#.A	9.50	4.05	2.35	0.43
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.ADLINNLGTIAK#.S	374.87	172.16	2.18	0.46
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	R.ALLFVPR@.R	67.03	22.25	3.01	0.33
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.DQVANSAFVER@.L	64.10	24.46	2.62	0.38
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.EDQTEYLEER@.R	54.43	31.40	1.73	0.58
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.EGLELPEDEEEK#.K	12.35	6.20	1.99	0.50
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.FYEQFSK#.N	34.28	14.28	2.40	0.42
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HFSVEGQLEFR@.A	109.48	51.36	2.13	0.47
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HFSVEGQLEFR.A	41.01	23.10	1.78	0.56
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HIYFITGETK#.D	45.44	17.04	2.67	0.37
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HLEINPDHSIIETLR@.Q	46.81	23.37	2.00	0.50
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HNDDEQYAWESSAGGSFTVR@.T	54.50	21.74	2.51	0.40
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HSQFIGYPITLFVEK#.E	37.54	13.66	2.75	0.36
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	R.NPDDITNEEYGEFYK#.S	38.58	14.92	2.59	0.39
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	R.R@APFDLFENR@.K	23.26	11.12	2.09	0.48
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.TLVSVTK#.E	84.96	32.02	2.65	0.38
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.VILHLK#EDQTEYLEER@.R	88.51	34.60	2.56	0.39
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	R.YESLTDPSK#.L	40.53	26.52	1.53	0.65
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.YIDQEELNK#.T	254.25	106.13	2.40	0.42
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.ADLINNLGTIAK#.S	196.15	55.17	3.56	0.28
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	R.ALLFVPR@.R	17.37	5.38	3.23	0.31
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.DQVANSAFVER@.L	22.01	30.16	0.73	1.37
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.EDQTEYLEER@.R	47.82	11.57	4.13	0.24
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.EGLELPEDEEEK#.K	22.26	8.32	2.68	0.37
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HFSVEGQLEFR@.A	24.77	10.20	2.43	0.41
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HLEINPDHSIIETLR@.Q	24.19	5.67	4.27	0.23
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.HNDDEQYAWESSAGGSFTVR@.T	30.25	10.52	2.88	0.35
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	R.NPDDITNEEYGEFYK#.S	12.96	4.18	3.10	0.32
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.VILHLK#EDQTEYLEER@.R	50.63	12.87	3.93	0.25
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	R.YESLTDPSK#.L	41.85	10.17	4.11	0.24
P07901_HS90A_MOUSE	Hsp90aa1	Heat shock protein HSP 9	K.YIDQEELNK#.T	123.75	39.05	3.17	0.32
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.ALLFIPR.R	11.93	13.41	0.89	1.12
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.EQVANSAFVER@.V	6.43	7.44	0.86	1.16
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.HLEINPDHPIVETLR@.Q	12.40	8.12	1.53	0.66
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.IDIIPNPQER.T	15.22	7.00	2.17	0.46
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.NPDDITQEEYGEFYK.S	11.38	8.77	1.30	0.77
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.SIYYITGESK#.E	10.12	7.97	1.27	0.79
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.YHTSQSGDEM*TSLSEYVSR@.M	10.40	7.81	1.33	0.75
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.ADHGEPIGR@.G	23.11	16.38	1.41	0.71
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.ALLFIPR@.R	318.20	148.82	2.14	0.47
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.EQVANSAFVER@.V	191.77	90.21	2.13	0.47
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.FYEAFSK#.N	194.72	94.91	2.05	0.49
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.HLEINPDHPIVETLR@.Q	165.64	76.99	2.15	0.46
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.HSQFIGYPITLYLEK#.E	157.19	76.39	2.06	0.49
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.HSQFIGYPITLYLEK#ER@.E	11.67	4.44	2.63	0.38
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.IDIIPNPQER@.T	180.24	85.47	2.11	0.47
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.IEDVGSDEEDDSGK#.D	5.71	1.55	3.69	0.27
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.KHLEINPDHPIVETLR.Q	169.60	74.57	2.27	0.44
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.LGIHEDSTNR.R	67.69	30.80	2.20	0.46
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR@.M	17.59	9.27	1.90	0.53
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.NPDDITQEEYGEFYK#.S	163.66	86.02	1.90	0.53
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.R@APFDLFENK#.K	68.85	35.80	1.92	0.52
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.R@APFDLFENK#K#.K	29.54	19.27	1.53	0.65
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.SIYYITGESK#.E	155.84	74.37	2.10	0.48
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.SLVSVTK#.E	182.81	85.63	2.14	0.47
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.YHTSQSGDEM*TSLSEYVSR@.M	135.78	61.08	2.22	0.45
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.YHTSQSGDEMTSLSEYVSR@.M	16.51	7.34	2.25	0.44
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.ALLFIPR@.R	292.19	69.73	4.19	0.24
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.APFDLFENK#.K	28.99	8.54	3.39	0.29
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.EQVANSAFVER@.V	87.51	21.89	4.00	0.25
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.HLEINPDHPIVETLR@.Q	112.32	29.74	3.78	0.26
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.HSQFIGYPITLYLEK#.E	79.79	20.42	3.91	0.26
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.IDIIPNPQER@.T	56.54	14.54	3.89	0.26
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.IEDVGSDEEDDSGK#DK#.K	32.91	9.43	3.49	0.29
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.KHLEINPDHPIVETLR.Q	63.17	18.96	3.33	0.30
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.NPDDITQEEYGEFYK#.S	116.19	31.50	3.69	0.27
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.R@APFDLFENK#.K	46.20	13.71	3.37	0.30
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.R@APFDLFENK#K#.K	15.00	5.35	2.80	0.36
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.SIYYITGESK#.E	94.52	26.37	3.58	0.28
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	K.SLTNDWEDHLAVK#.H	11.65	1.33	8.78	0.11
P11499_HS90B_MOUSE	Hsp90ab1	Heat shock protein HSP 9	R.YHTSQSGDEM*TSLSEYVSR@.M	102.35	30.44	3.36	0.30
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.LISLTDENALAGNEELTVK#.I	5.57	3.65	1.53	0.66
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.EGSR@TDDEVVQR@EEEAIQLDGLNASQIR@.E	5.40	2.40	2.25	0.44
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.ELISNASDALDK#.I	14.12	4.34	3.26	0.31
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.DISTNYYASQK#.K	125.49	63.95	1.96	0.51
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.EAESSPFVER@.L	142.05	75.01	1.89	0.53
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.EEASDYLELDTIK#.N	44.35	20.56	2.16	0.46
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.EEEAIQLDGLNASQIR@.E	10.52	6.07	1.73	0.58
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.EESDDEAAVEEEEEEK#.K	5.79	2.24	2.58	0.39
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.EGSRTDDEVVQREEEAIQLDGLNASQIR.E	93.04	40.46	2.30	0.43
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.EGSR@TDDEVVQR@EEEAIQLDGLNASQIR@.E	9.84	5.77	1.71	0.59
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.EGVKFDESEK.T	23.55	12.38	1.90	0.53
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.ELISNASDALDK#.I	220.10	95.76	2.30	0.44
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.EVEEDEYK#.A	29.07	15.71	1.85	0.54
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.FAFQAEVNR@.M	276.13	142.30	1.94	0.52
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.FQNVAK#.E	128.41	55.56	2.31	0.43
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.GLFDEYGSK#.K	133.25	64.16	2.08	0.48
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.GTTITLVLK#EEASDYLELDTIK#.N	30.56	13.73	2.23	0.45

P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.GVVDSDDLPLNVSR@.E	387.91	188.44	2.06	0.49
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.IYFM*AGSSR@.K	80.43	42.76	1.88	0.53
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.IYFMAGSSR@.K	25.14	13.84	1.82	0.55
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.K#EAESSPFVER@.L	17.88	12.18	1.47	0.68
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.K#TFEINPR@.H	30.46	11.14	2.73	0.37
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.K#YSQFINFPIYVWSSK#.T	32.61	11.54	2.83	0.35
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.LIINSLYK#.N	323.91	174.25	1.86	0.54
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.LISLTDENALAGNEELTVK#.I	81.34	42.11	1.93	0.52
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.NLLHVTDTGVGM*TR@.E	121.16	64.33	1.88	0.53
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.NLLHVTDTGVGM*TR.E	12.19	6.79	1.79	0.56
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.NLLHVTDTGVGM*TREELVK.N	61.07	28.03	2.18	0.46
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.SGTSEFLNK#.M	166.01	83.84	1.98	0.51
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.SGYLLPDTK#.A	141.50	80.52	1.76	0.57
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.SILFVPTSAPR@.G	229.79	112.24	2.05	0.49
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.TETVEEPLEEDEAAK#.E	9.28	5.26	1.76	0.57
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.TETVEEPLEEDEAAK#EEK#.E	96.04	52.57	1.83	0.55
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.TETVEEPLEEDEAAK#EEK#EESDDEAAVEEEEEEK#.K	3.14	2.22	1.41	0.71
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.TFEINPR.H	160.70	83.67	1.92	0.52
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.TLDM*IK#K#.I	5.20	3.35	1.55	0.64
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.YNDTFWK#.E	42.60	19.72	2.16	0.46
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.YSQFINFPIYVWSSK#.T	31.29	17.62	1.78	0.56
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.DISTNYYASQK#.K	20.66	12.52	1.65	0.61
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.EEASDYLELDTIK#.N	15.14	5.05	3.00	0.33
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.EEEAIQLDGLNASQIR@.E	9.38	3.73	2.52	0.40
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.EESDDEAAVEEEEEEK#.K	4.55	1.64	2.78	0.36
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.EGSR@TDDEVVQR@EEEAIQLDGLNASQIR@.E	20.75	8.10	2.56	0.39
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.ELISNASDALDK#.I	107.85	34.00	3.17	0.32
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.FAFQAEVNR@.M	60.32	30.22	2.00	0.50
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.FQSSHHSTDITSLDQYVER@.M	12.57	7.67	1.64	0.61
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.GTTITLVLK#EEASDYLELDTIK#.N	4.34	2.56	1.70	0.59
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.GVVDSDDLPLNVSR@.E	88.71	34.05	2.61	0.38
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.LISLTDENALAGNEELTVK#.I	126.30	15.10	8.36	0.12
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.SGTSEFLNK#.M	35.70	14.94	2.39	0.42
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	R.SGYLLPDTK#.A	37.62	18.95	1.99	0.50
P08113_ENPL_MOUSE	Hsp90b1	Endoplasmin OS=Mus mu	K.SILFVPTSAPR@.G	61.96	25.57	2.42	0.41
Q99M31_HSP7E_MOUSE	Hspa14	Heat shock 70 kDa protei	R.VLSTNTSDNIGGAHFTDTLAQYLASEFQR@.L	2.88	1.75	1.65	0.61
Q61696_HS71A_MOUSE	Hspa1a	Heat shock 70 kDa protei	R.IINEPTAAAIAYGLDR.T	7.94	4.68	1.70	0.59
Q61696_HS71A_MOUSE	Hspa1a	Heat shock 70 kDa protei	K.ITITNDK#GR@.L	60.99	30.28	2.01	0.50
Q61696_HS71A_MOUSE	Hspa1a	Heat shock 70 kDa protei	K.NQVALNPQNTVFDAK#.R	6.85	3.75	1.83	0.55
Q61696_HS71A_MOUSE	Hspa1a	Heat shock 70 kDa protei	K.QTQTFTTYSDNQPGVLIQVYEGER@.A	151.34	66.62	2.27	0.44
Q61696_HS71A_MOUSE	Hspa1a	Heat shock 70 kDa protei	R.TTPSYVAFTDTER@.L	510.86	231.76	2.20	0.45
Q61696_HS71A_MOUSE	Hspa1a	Heat shock 70 kDa protei	K.QTQTFTTYSDNQPGVLIQVYEGER@.A	21.52	7.70	2.79	0.36
Q61696_HS71A_MOUSE	Hspa1a	Heat shock 70 kDa protei	R.TTPSYVAFTDTER@.L	74.67	19.68	3.79	0.26
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.IEIESFFEGEDFSETLTR@.A	3.83	4.85	0.79	1.27
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.VEIIANDQGNR@.I	6.07	6.26	0.97	1.03
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.AK#FEELNM*DLFR@.S	124.86	86.29	1.45	0.69
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.AKFEELNM*DLFR.S	47.80	15.81	3.02	0.33
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.AK#FEELNMDLFR@.S	26.53	10.89	2.44	0.41
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.ALSSQHQAR@.I	9.90	5.36	1.85	0.54
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.DAGTIAGLNVM*R@.I	110.95	92.42	1.20	0.83
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.DAGTIAGLNVMR.I	21.65	16.21	1.34	0.75
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.DNHLLGTFDLTGIPPAPR@.G	42.98	31.81	1.35	0.74
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.ELEEIVQPIISK#.L	72.14	63.21	1.14	0.88
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.IEIESFFEGEDFSETLTR@.A	70.80	47.66	1.49	0.67
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.IEWLESHQDADIEDFK#.A	47.32	37.94	1.25	0.80
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.IEWLESHQDADIEDFK#AK#.K	41.75	33.34	1.25	0.80
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.IINEPTAAAIAYGLDK#.R	128.75	69.02	1.87	0.54
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.IINEPTAAAIAYGLDK#R@.E	224.07	158.24	1.42	0.71
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.ITITNDQNR@.L	120.38	89.49	1.35	0.74
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.ITPSYVAFTPEGER@.L	132.14	100.89	1.31	0.76
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.K#K#ELEEIVQPIISK#.L	123.73	84.74	1.46	0.68
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.K#SDIDEIVLVGGSTR@.I	91.42	70.84	1.29	0.77
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.K#SQIFSTASDNQPTVTIK#.V	15.69	11.22	1.40	0.72
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.K#TK#PYIQVDIGGGQTK#.T	10.68	11.93	0.90	1.12
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.KVTHAVVTVPAYFNDAQR.Q	5.81	9.99	0.58	1.72
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.LYGSGGPPPTGEEDTSEK#DEL.-	36.20	27.85	1.30	0.77
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.M*KETAEAYLGKK.V	40.25	25.14	1.60	0.62
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.NELESYAYSLK#.N	87.98	59.89	1.47	0.68
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.NQLTSNPENTVFDAK#.R	107.64	91.45	1.18	0.85
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.SDIDEIVLVGGSTR@.I	35.18	25.08	1.40	0.71
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.SQIFSTASDNQPTVTIK#.V	87.59	59.85	1.46	0.68
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.TFAPEEISAM*VLTK#.M	22.02	16.51	1.33	0.75
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.TFAPEEISAMVLTK#.M	28.08	20.68	1.36	0.74
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.TK#PYIQVDIGGGQTK#.T	77.04	62.13	1.24	0.81
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.TKPYIQVDIGGGQTK.T	7.95	6.79	1.17	0.85
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.TWNDPSVQQDIK#.F	76.03	59.97	1.27	0.79
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.VEIIANDQGNR@.I	515.96	245.21	2.10	0.48
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.VLEDSDLK#K#.S	22.27	18.46	1.21	0.83
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.VLEDSDLK#K#SDIDEIVLVGGSTR@.I	9.70	9.20	1.05	0.95
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.VTHAVVTVPAYFNDAQR.Q	106.88	70.88	1.51	0.66
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.ELEEIVQPIISK#.L	18.23	11.60	1.57	0.64
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.IEIESFFEGEDFSETLTR@.A	19.26	8.80	2.19	0.46
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.IINEPTAAAIAYGLDK#.R	26.91	11.08	2.43	0.41
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.ITITNDQNR@.L	24.74	17.52	1.41	0.71
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.ITPSYVAFTPEGER@.L	31.43	18.66	1.68	0.59
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.LYGSGGPPPTGEEDTSEK#DEL.-	6.18	4.89	1.27	0.79
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.NQLTSNPENTVFDAK#.R	17.74	15.92	1.11	0.90
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.SQIFSTASDNQPTVTIK#.V	16.26	11.19	1.45	0.69
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.TK#PYIQVDIGGGQTK#.T	15.68	8.67	1.81	0.55
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	R.VEIIANDQGNR@.I	62.92	17.92	3.51	0.28
P20029_GRP78_MOUSE	Hspa5	78 kDa glucose-regulated	K.VTHAVVTVPAYFNDAQR@.Q	26.01	18.37	1.42	0.71
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	R.AR@FEELNADLFR@.G	489.12	169.34	2.89	0.35
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	K.DAGTIAGLNVLR@.I	839.66	348.95	2.41	0.42
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	K.DISENK#R@.A	34.00	16.93	2.01	0.50
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	K.DNNLLGK#.F	235.47	98.97	2.38	0.42
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	K.EIAEAYLGK#.T	51.96	29.16	1.78	0.56
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	R.FDDAVVQSDM*K#.H	27.97	14.72	1.90	0.53
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	R.FEELNADLFR@.G	111.79	53.39	2.09	0.48
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	K.FELTGIPPAPR@.G	20.89	17.30	1.21	0.83
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	K.HWPFMVVNDAGR@PK#.V	33.59	18.87	1.78	0.56
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	K.LLQDFFNGK#.E	168.01	69.02	2.43	0.41
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	R.LSK#EDIER@.M	99.07	43.04	2.30	0.43
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 kD	K.LYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD.-	5.16	5.16	1.00	1.00

P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.M*K#EIAEAYLGK#.T	294.97	171.53	1.72	0.58
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.MK#EIAEAYLGK#.T	91.19	42.04	2.17	0.46
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.M*VNHFIAEFK#.R	270.62	117.66	2.30	0.43
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.M*VNHFIAEFK#R@.K	40.59	14.66	2.77	0.36
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.M*VQEAEK#.Y	34.12	15.64	2.18	0.46
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.M*VQEAEK#YK#.A	6.54	4.70	1.39	0.72
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.NQTAEK#EEFEHQQK#.E	2.60	1.54	1.69	0.59
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.NQVAM*NPTNTVFDAK#.R	397.73	182.81	2.18	0.46
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.NQVAMNPTNTVFDAK#.R	51.63	19.24	2.68	0.37
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.NSLESYAFNM*K#.A	167.21	70.00	2.39	0.42
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.NSLESYAFNMK#.A	77.39	33.44	2.31	0.43
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.R@FDDAVVQSDM*K#.H	179.13	84.01	2.13	0.47
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.R@FDDAVVQSDMK#.H	9.86	2.96	3.33	0.30
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.SFYPEEVSSM*VLTK#.M	97.62	41.30	2.36	0.42
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.SFYPEEVSSMVLTK#.M	46.65	19.99	2.33	0.43
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.SINPDEAVAYGAAVQAAILSGDK#.S	17.91	10.20	1.76	0.57
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.SINPDEAVAYGAAVQAAILSGDK#.S	81.67	35.68	2.29	0.44
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.SQIHDIVLVGGSTR@.I	244.41	110.17	2.22	0.45
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.SQIHDIVLVGGSTR.I	27.94	13.41	2.08	0.48
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.STAGDTHLGGEDFDNR@.M	367.40	148.83	2.47	0.41
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.STAGDTHLGGEDFDNR.M	78.17	31.10	2.51	0.40
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.TVTNAVVTVPAYFNDSQR.Q	174.93	82.50	2.12	0.47
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.TVTNAVVTVPAYFNDSQR@.Q	178.26	83.13	2.14	0.47
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.VQVEYK#.G	198.36	97.86	2.03	0.49
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.VQVEYK#GETK#.S	89.11	40.98	2.17	0.46
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.VQVEYK#GETK#.S	418.34	191.48	2.18	0.46
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.ARFEELNADLFR.G	81.03	20.58	3.94	0.25
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.AR@FEELNADLFR@.G	10.40	5.04	2.06	0.48
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.DAGTIAGLNVLR@.I	124.61	36.76	3.39	0.29
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.DNNLLGK#.F	25.66	3.93	6.53	0.15
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.FDDAVVQSDM*K#.H	10.59	3.31	3.20	0.31
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.FEELNADLFR@.G	18.85	7.03	2.68	0.37
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.GTLDPVEK#.A	90.00	24.19	3.72	0.27
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.LLQDFFNGK#.E	21.12	7.70	2.74	0.36
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.M*K#EIAEAYLGK#.T	36.98	12.41	2.98	0.34
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.M*VNHFIAEFK#.R	32.20	10.34	3.11	0.32
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.NQVAM*NPTNTVFDAK#.R	45.07	14.01	3.22	0.31
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.NQVAMNPTNTVFDAK#.R	6.91	2.71	2.55	0.39
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.NSLESYAFNM*K#.A	24.54	7.19	3.41	0.29
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.NSLESYAFNMK#.A	11.62	2.57	4.53	0.22
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	R.R@FDDAVVQSDM*K#.H	6.77	2.14	3.16	0.32
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.SQIHDIVLVGGSTR@.I	50.32	18.79	2.68	0.37
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.STAGDTHLGGEDFDNR.M	8.23	2.63	3.13	0.32
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.TVTNAVVTVPAYFNDSQR@.Q	18.62	4.71	3.95	0.25
P63017_HSP7C_MOUSE	Hspa8	Heat shock cognate 71 k	K.VQVEYK#.G	56.98	20.04	2.84	0.35
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	R.AQFEGIVTDLIK#.R	30.57	20.71	1.48	0.68
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	K.DAGQISGLNVLR@.V	17.21	9.63	1.79	0.56
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	K.LLGQFTLIGIPPAPR@.G	8.12	6.22	1.31	0.77
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	K.NAVITVPAYFNDSQR@.Q	10.37	6.68	1.55	0.64
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	R.QAVTNPNNTFYATK#.R	18.94	8.14	2.33	0.43
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	K.SDIGEVILVGGM*TR@.M	7.27	5.72	1.27	0.79
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	K.SQVFSTAADGQTQVEIK#.V	6.78	3.55	1.91	0.52
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	R.TTPSVVAFTADGER@.L	21.25	16.74	1.27	0.79
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	R.VINEPTAAALAYGLDK#.S	6.68	5.36	1.25	0.80
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	K.VLENAEGAR@.T	22.29	12.71	1.75	0.57
P38647_GRP75_MOUSE	Hspa9	Stress-70 protein, mitoc	K.VQQTVQDLFGR@.A	25.62	14.41	1.78	0.56
P14602_HSPB1_MOUSE	Hspb1	Heat shock protein beta-	K.AVTQSAEITIPVTFEAR@.A	13.82	17.13	0.81	1.24
P14602_HSPB1_MOUSE	Hspb1	Heat shock protein beta-	R.KYTLPPGVDPTLVSSSLSPEGTLTVEAPLPK.A	3.32	11.00	0.30	3.31
P14602_HSPB1_MOUSE	Hspb1	Heat shock protein beta-	R.LFDQAFGVPR@.L	33.82	51.14	0.66	1.51
P14602_HSPB1_MOUSE	Hspb1	Heat shock protein beta-	K.AVTQSAEITIPVTFEAR.A	14.14	20.32	0.70	1.44
P14602_HSPB1_MOUSE	Hspb1	Heat shock protein beta-	R.KYTLPPGVDPTLVSSSLSPEGTLTVEAPLPK.A	3.22	3.37	0.96	1.05
P14602_HSPB1_MOUSE	Hspb1	Heat shock protein beta-	R.LFDQAFGVPR.L	21.31	33.17	0.64	1.56
P14602_HSPB1_MOUSE	Hspb1	Heat shock protein beta-	R.VSLDVNHFAPEELTVK#.T	24.87	39.10	0.64	1.57
Q9JK92_HSPB8_MOUSE	Hspb8	Heat shock protein beta-	R.FGVPAEGR@.S	14.77	8.54	1.73	0.58
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.ALK#IPAM*TIAK#.N	64.53	16.54	3.90	0.26
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.ALM*LQGVDLLADAVAVTM*GPK#.G	159.08	38.96	4.08	0.24
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.APGFGDNR@.K	33.76	9.26	3.65	0.27
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.APGFGDNR@K#.N	14.41	4.20	3.43	0.29
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.DDAM*LLK#.G	22.53	4.31	5.23	0.19
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.DM*AIATGGAVFGEEGLNLNLEDVQAHDLGK#.V	43.63	6.32	6.90	0.14
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.DMAIATGGAVFGEEGLNLNLEDVQAHDLGK#.V	10.89	2.00	5.43	0.18
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.GANPVEIR@.R	166.68	37.84	4.41	0.23
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.GVM*LAVDAVIAELK#.K	7.38	2.28	3.23	0.31
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.GYISPYFINTSK#.G	115.47	29.39	3.93	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.ILQSSSEVGYDAM*LGDFVNM*VEK#.G	10.01	8.33	1.20	0.83
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.IPAMTIAK#.N	15.95	5.42	2.94	0.34
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.IQEITEQLDITTSEYEK#.E	21.04	5.32	3.96	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.IQEITEQLDITTSEYEK#EK#.L	106.56	21.81	4.88	0.20
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.ISSVQSIVPALEIANAHR@.K	223.12	55.18	4.04	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.K#GVITVK#.D	121.34	32.56	3.73	0.27
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.K#ISSVQSIVPALEIANAHR@.K	16.32	3.26	5.00	0.20
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.K#PLVIIAEDVDGEALSTLVLNR@.L	149.87	37.10	4.04	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.LSDGVAVLK#.V	205.86	52.78	3.90	0.26
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.LVQDVANNTNEEAGDGTTTATVLAR@.S	158.65	41.26	3.85	0.26
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.NAGVEGSLIVEK#.I	201.95	43.69	4.62	0.22
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.NQLK#DM*AIATGGAVFGEEGLNLNLEDVQAHDLGK#.V	30.64	6.83	4.49	0.22
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.TLNDELEIIEGM*K#.F	7.76	2.31	3.37	0.30
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.TLNDELEIIEGMK#.F	20.27	4.44	4.56	0.22
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.TVIIEQSWGSPK#.V	46.63	11.15	4.18	0.24
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGEVIVTK#.D	80.72	25.80	3.13	0.32
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGEVIVTK#DDAM*LLK#.G	87.94	20.45	4.30	0.23
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGEVIVTK#DDAMLLK#.G	41.64	11.06	3.76	0.27
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGGTSDVEVNEK#.K	301.77	83.22	3.63	0.28
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGLQVVAVK#.A	137.60	34.49	3.99	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.VTDALNATR@.A	132.67	29.59	4.48	0.22
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.ALK#IPAM*TIAK#.N	44.82	8.72	5.14	0.19
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.ALM*LQGVDLLADAVAVTM*GPK#.G	184.95	47.61	3.88	0.26
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.APGFGDNR@.K	34.99	5.57	6.29	0.16
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.DDAM*LLK#.G	19.80	4.23	4.68	0.21
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.DM*AIATGGAVFGEEGLNLNLEDVQAHDLGK#.V	51.03	9.94	5.14	0.19
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.DMAIATGGAVFGEEGLNLNLEDVQAHDLGK#.V	8.71	4.07	2.14	0.47
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.GANPVEIR.R	201.57	47.99	4.20	0.24
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.GIIDPTK#.V	136.24	30.91	4.41	0.23

P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.GVM*LAVDAVIAELK#.K	5.90	3.38	1.75	0.57
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.ILQSSSEVGYDAM*LGDFVNM*VEK#.G	13.80	9.57	1.44	0.69
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.ILQSSSEVGYDAM*LGDFVNMVEK#.G	6.61	1.63	4.07	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.IPAM*TIAK#.N	97.46	27.38	3.56	0.28
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.IQEITEQLDITTSEYEK#.E	15.21	5.69	2.67	0.37
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.ISSVQSIVPALEIANAHR@.K	167.39	41.78	4.01	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.ISSVQSIVPALEIANAHR@.K	7.07	1.92	3.69	0.27
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.KPLVIIAEDVDGEALSTLVLNR.L	154.72	36.19	4.28	0.23
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.K#PLVIIAEDVDGEALSTLVLNR@.L	3.85	0.00	#DIV/0!	0.00
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.LSDGVAVLK#.V	188.12	50.74	3.71	0.27
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.LVQDVANNTNEEAGDGTTTATVLAR@.S	211.69	43.31	4.89	0.20
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.NAGVEGSLIVEK#.I	178.46	50.27	3.55	0.28
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.NQLK#DM*AIATGGAVFGEEGLNLNLEDVQAHDLGK#.V	1.84	1.44	1.28	0.78
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.R@IQEITEQLDITTSEYEK#EK#.L	11.18	2.84	3.93	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.TLNDELEIIEGMK#.F	27.80	8.51	3.27	0.31
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.TVIIEQSWGSPK#.V	56.67	15.45	3.67	0.27
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGEVIVTK#.D	122.98	31.69	3.88	0.26
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGEVIVTK#DDAM*LLK#.G	145.92	36.36	4.01	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGEVIVTK#DDAM*LLK#.G	13.54	4.25	3.18	0.31
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGGTSDVEVNEK#.K	219.38	56.94	3.85	0.26
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGLQVVAVK#.A	126.16	28.71	4.39	0.23
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	R.VTDALNATR@.A	176.65	43.29	4.08	0.25
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.ISSVQSIVPALEIANAHR@.K	9.31	5.67	1.64	0.61
P63038_CH60_MOUSE	Hspd1	60 kDa heat shock protei	K.VGGTSDVEVNEK#.K	13.37	3.08	4.33	0.23
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.AASISAVSLEVAQPGPSSGPR.A	2.46	13.42	0.18	5.47
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.AELLVAEAPSKPITVTVEEQR.S	7.15	21.65	0.33	3.03
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	K.AFAYLQVPER.V	7.39	13.88	0.53	1.88
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.AYDGLSLPEDTETVTASR.Y	2.60	9.99	0.26	3.85
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	K.DIIYIGGAPDVATLTR.G	4.71	9.72	0.48	2.06
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.FLVHDAFWALPK.Q	3.18	8.08	0.39	2.54
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.GM*LEPVQKPDVILVGAGYR.L	7.32	23.29	0.31	3.18
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.GM*VFGIPDGVLELVPQR.G	3.73	5.78	0.65	1.55
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.GSIQVDGEDLVTGR.S	3.77	9.25	0.41	2.46
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.LSFDQPNDFK.G	4.82	14.95	0.32	3.11
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.QLISTHFAPGDFQGFALVNPQR.N	4.65	13.76	0.34	2.96
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.SIEYSPQLEDASAK.E	9.45	15.99	0.59	1.69
B1B0C7_B1B0C7_MOUSE	Hspg2	Basement membrane-spe	R.VEGGAVPLESSVLVTIEPAGTAPGVIPPVR.I	1.86	5.57	0.33	2.99
Q9JIY5_HTRA2_MOUSE	Htra2	Serine protease HTRA2, n	K.LAQNAEDVYEAVR@.T	6.03	2.11	2.86	0.35
Q9JKR6_HYOU1_MOUSE	Hyou1	Hypoxia up-regulated pr	R.DAVIYPILVEFTR@.E	7.16	9.14	0.78	1.28
Q9JKR6_HYOU1_MOUSE	Hyou1	Hypoxia up-regulated pr	K.VAIVK#PGVPM*EIVLNK#.E	10.16	6.71	1.51	0.66
Q9JKR6_HYOU1_MOUSE	Hyou1	Hypoxia up-regulated pr	K.VQEVLLK#.A	10.56	7.77	1.36	0.74
Q8BU30_SYIC_MOUSE	Iars	Isoleucine--tRNA ligase, c	K.APLK#PYPVPTSDNILIQEQTQLK#.G	3.30	3.80	0.87	1.15
Q6ZPR6_IBTK_MOUSE	Ibtk	Inhibitor of Bruton tyros	K.TSLYEIPVVSSSSFFEEFGK#.L	4.79	2.61	1.84	0.54
Q9JHJ8_ICOSL_MOUSE	Icoslg	ICOS ligand OS=Mus mus	R.VFM*NTATELVK#.I	4.99	2.88	1.73	0.58
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	K.APIQWEER@.N	60.99	17.01	3.58	0.28
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	R.ENTEGEYSGIEHVIVDGVVQSIK#.L	89.71	35.20	2.55	0.39
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	R.IAEFAFEYAR@.N	121.77	40.78	2.99	0.33
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	K.LITEEASK#R@.I	30.18	11.68	2.58	0.39
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	R.M*SDGLFLQK#.C	60.81	25.14	2.42	0.41
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	R.NVTAIQGPGGK#.W	79.00	28.41	2.78	0.36
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	K.TPIAAGHPSM*NLLLR@.K	91.57	33.19	2.76	0.36
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	K.TPIAAGHPSMNLLLR@.K	12.65	3.65	3.46	0.29
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	K.TPYTDVNIVTIR@.E	75.15	29.40	2.56	0.39
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	K.TPYTDVNIVTIR@.E	8.11	3.45	2.35	0.43
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	R.IAEFAFEYAR@.N	13.16	3.25	4.06	0.25
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	K.TPYTDVNIVTIR@.E	11.00	2.78	3.95	0.25
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	R.ENTEGEYSGIEHVIVDGVVQSIK#.L	20.39	3.67	5.55	0.18
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	R.IAEFAFEYAR@.N	14.76	2.86	5.17	0.19
Q9D6R2_IDH3A_MOUSE	Idh3a	Isocitrate dehydrogenas	K.TPYTDVNIVTIR@.E	12.43	2.15	5.77	0.17
Q91VA7_Q91VA7_MOUSE	Idh3b	Isocitrate dehydrogenas	K.AAAVPVEFK#.E	39.17	19.42	2.02	0.50
Q91VA7_Q91VA7_MOUSE	Idh3b	Isocitrate dehydrogenas	R.DM*GGYSTTTDFIK#.S	25.24	8.57	2.95	0.34
Q91VA7_Q91VA7_MOUSE	Idh3b	Isocitrate dehydrogenas	K.FAFDYATK#.K	27.68	12.06	2.29	0.44
Q91VA7_Q91VA7_MOUSE	Idh3b	Isocitrate dehydrogenas	K.GELASYDM*QLR@.R	11.06	6.52	1.70	0.59
Q91VA7_Q91VA7_MOUSE	Idh3b	Isocitrate dehydrogenas	R.HLNLEYHSSM*IADAVK#.K	9.17	6.96	1.32	0.76
Q91VA7_Q91VA7_MOUSE	Idh3b	Isocitrate dehydrogenas	R.HNNLDLVIIR@.E	22.67	8.49	2.67	0.37
Q91VA7_Q91VA7_MOUSE	Idh3b	Isocitrate dehydrogenas	R.K#LDLFANVVHVK#.S	30.27	19.34	1.57	0.64
Q91VA7_Q91VA7_MOUSE	Idh3b	Isocitrate dehydrogenas	R.VEGAFPVTM*LPGDGVGPELM*HAVK#.E	18.35	9.91	1.85	0.54
P70404_IDHG1_MOUSE	Idh3g	Isocitrate dehydrogenas	R.ENTEGEYSSLEHESVAGVVESLK#.I	29.10	14.08	2.07	0.48
P70404_IDHG1_MOUSE	Idh3g	Isocitrate dehydrogenas	R.HK#DIDILIVR@.E	103.74	37.32	2.78	0.36
Q62293_Q62293_MOUSE	Ifggb5	Interferon-gamma-induc	K.AIAQM*GM*NFYFVR.T	27.22	7.10	3.83	0.26
Q62293_Q62293_MOUSE	Ifggb5	Interferon-gamma-induc	R.DIESAPLHIAVTGETGAGK#.S	24.52	14.84	1.65	0.61
Q62293_Q62293_MOUSE	Ifggb5	Interferon-gamma-induc	K.GAAPTGAIETTM*K#.R	10.14	7.20	1.41	0.71
Q62293_Q62293_MOUSE	Ifggb5	Interferon-gamma-induc	K.STFINTLR@.G	21.70	10.72	2.02	0.49
Q62293_Q62293_MOUSE	Ifggb5	Interferon-gamma-induc	R.TK#IDSDLDNEQK#.F	13.96	10.71	1.30	0.77
Q8CGE8_IFI5A_MOUSE	Ifi205a	Interferon-activable prot	K.GILEINETSSVLEAAPK#.Q	7.95	8.74	0.91	1.10
Q8CGE8_IFI5A_MOUSE	Ifi205a	Interferon-activable prot	K.GILEINETSSVLEAAPK.Q	3.01	3.23	0.93	1.07
Q9D8C4_IN35_MOUSE	Ifi35	Interferon-induced 35 kD	K.IPFSVPEVPLVFQGQTK#.Q	16.30	16.12	1.01	0.99
Q9D8C4_IN35_MOUSE	Ifi35	Interferon-induced 35 kD	R.VLVSGFPAGLR.L	8.27	10.71	0.77	1.29
Q9D8C4_IN35_MOUSE	Ifi35	Interferon-induced 35 kD	R.VQVQPLELPVVTNIQVSSQPDNHR@.V	10.58	9.74	1.09	0.92
Q8BV66_IFI44_MOUSE	Ifi44	Interferon-induced prote	R.VLLLGPIGAGK.S	7.24	6.93	1.04	0.96
Q8BV66_IFI44_MOUSE	Ifi44	Interferon-induced prote	R.VLLLGPIGAGK#.S	13.81	6.66	2.07	0.48
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	K.AISAAENAILEVAVIGQSGTGK#.S	9.57	5.32	1.80	0.56
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	K.EFLPQYSALISK#.A	10.75	4.86	2.21	0.45
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	R.FSLNDALLAQK#.I	58.88	31.07	1.90	0.53
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	K.GASENSFQQLAK#.E	16.23	4.56	3.56	0.28
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	R.TK#VDSDLYNEQK#.A	9.65	2.15	4.50	0.22
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	R.TQFLNIVVDDAK#.H	10.97	4.06	2.71	0.37
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	R.FSLNDALLAQK#.I	11.13	15.69	0.71	1.41
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	K.GASENSFQQLAK#.E	8.96	2.82	3.18	0.31
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	K.SSFINALR@.G	12.46	6.71	1.86	0.54
Q61635_Q61635_MOUSE	Ifi47	GTP-binding protein OS=	R.TQFLNIVVDDAK#.H	7.91	2.25	3.51	0.28
Q8R5F7_IFIH1_MOUSE	Ifih1	Interferon-induced helic	R.IIGLSGDTQLK#.I	12.70	10.72	1.18	0.84
Q8R5F7_IFIH1_MOUSE	Ifih1	Interferon-induced helic	K.QNK#PAIPLPQILGLTASPGVGAAK#.K	8.26	6.40	1.29	0.77
Q8R5F7_IFIH1_MOUSE	Ifih1	Interferon-induced helic	R.ISAAGNSGNESGVR@.E	12.32	6.13	2.01	0.50
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.AITLYLK#.G	48.78	56.38	0.87	1.16
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.ALHLLNR@.A	15.59	15.79	0.99	1.01
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.ALK#VEPENPEYNTGYAVVAYR@.Q	66.76	79.26	0.84	1.19
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.EAEALIQSEQLSK.R	81.57	94.59	0.86	1.16
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.GQQDEALQSLK#.E	32.53	28.06	1.16	0.86
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.GQQDEALQSLKEAEALIQSEQLSK.R	9.20	8.68	1.06	0.94
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.ISEQVQFLDIK#.N	54.06	72.20	0.75	1.34
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.LLFENNDIPDLEVR@.I	88.92	102.12	0.87	1.15
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.LTGEM*NPAF.-	41.95	41.95	1.00	1.00

Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.NPLGM*HNLLAYVR.H	25.52	26.21	0.97	1.03
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.QDLDDNFISLEPLR.K	14.58	16.09	0.91	1.10
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.QDLDDNFISLEPLRK.A	49.50	61.85	0.80	1.25
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.R@QDNVQELAQQAIHEFQETLK#.L	99.96	81.15	1.23	0.81
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.TLVAHIEQDIHLR@.Y	34.19	28.53	1.20	0.83
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.VEPENPEYNTGYAVVAYR@.Q	4.29	7.08	0.61	1.65
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.EAEALIQSEQLSK#.R	75.92	3.35	22.66	0.04
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.LLFENNDIPDLEVR.I	7.11	8.65	0.82	1.22
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.RQDNVQELAQQAIHEFQETLK.L	15.63	13.17	1.19	0.84
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.RQDNVQELAQQAIHEFQETLK.L	9.36	9.87	0.95	1.05
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.AITLYLK#.G	32.96	17.62	1.87	0.53
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.ALK#VEPENPEYNTGYAVVAYR@.Q	36.20	17.30	2.09	0.48
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.EAEALIQSEQLSK#.R	40.95	22.03	1.86	0.54
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.GQQDEALQSLK#.E	29.14	14.97	1.95	0.51
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.GQQDEALQSLK#EAEALIQSEQLSK#.R	5.59	4.38	1.28	0.78
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.HLK#GQQDEALQSLK#.E	16.23	7.21	2.25	0.44
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.ISEQVQFLDIK#.N	49.95	32.17	1.55	0.64
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.LLFENNDIPDLEVR@.I	58.98	29.70	1.99	0.50
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.NPLGM*HNLLAYVR@.H	31.28	10.33	3.03	0.33
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.QDLDDNFISLEPLR@K#.A	50.96	21.73	2.35	0.43
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.R@QDNVQELAQQAIHEFQETLK#.L	54.54	23.29	2.34	0.43
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.VEPENPEYNTGYAVVAYR@.Q	5.78	3.19	1.81	0.55
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.AITLYLK#.G	66.40	24.49	2.71	0.37
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.ALKVEPENPEYNTGYAVVAYR.Q	55.64	22.84	2.44	0.41
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.EAEALIQSEQLSK#.R	78.76	41.56	1.90	0.53
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.GQQDEALQSLK#.E	39.74	20.32	1.96	0.51
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.GQQDEALQSLK#EAEALIQSEQLSK#.R	14.89	4.75	3.14	0.32
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.GSLAEAQIYLDK#VEK#.V	56.83	40.80	1.39	0.72
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.ISEQVQFLDIK#.N	93.33	30.70	3.04	0.33
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.K#LLTALEK#.V	27.79	7.44	3.74	0.27
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.LLFENNDIPDLEVR@.I	161.58	53.07	3.04	0.33
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.LTGEM*NPAF.-	30.02	30.02	1.00	1.00
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.NALFYYEK#.A	49.15	18.57	2.65	0.38
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.NPLGM*HNLLAYVR@.H	52.14	18.27	2.85	0.35
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.QDLDDNFISLEPLR@.K	20.35	9.06	2.25	0.45
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.QDLDDNFISLEPLR@K#.A	56.68	23.82	2.38	0.42
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.QDNVQELAQQAIHEFQETLK#.L	22.00	6.54	3.37	0.30
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	R.R@QDNVQELAQQAIHEFQETLK#.L	116.73	40.32	2.89	0.35
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.TLVAHIEQDIHLR@.Y	58.86	17.67	3.33	0.30
Q64282_IFIT1_MOUSE	Ifit1	Interferon-induced prote	K.VEPENPEYNTGYAVVAYR@.Q	11.88	5.66	2.10	0.48
Q99J93_IFM2_MOUSE	Ifitm2	Interferon-induced trans	K.M*VGDVVGAQAYASTAK#.C	3.56	2.15	1.66	0.60
Q99J93_IFM2_MOUSE	Ifitm2	Interferon-induced trans	R.TTVINMPR@.E	20.04	7.76	2.58	0.39
Q99J93_IFM2_MOUSE	Ifitm2	Interferon-induced trans	R.TTVINM*PR@.E	83.25	48.47	1.72	0.58
Q9CQW9_IFM3_MOUSE	Ifitm3	Interferon-induced trans	R.IK#EEYEVAEM*GAPHGSASVR@.T	81.03	40.27	2.01	0.50
Q9CQW9_IFM3_MOUSE	Ifitm3	Interferon-induced trans	R.IK#EEYEVAEMGAPHGSASVR@.T	6.22	2.90	2.14	0.47
Q9CQW9_IFM3_MOUSE	Ifitm3	Interferon-induced trans	K.M*VGDVTGAQAYASTAK#.C	41.66	22.54	1.85	0.54
Q9CQW9_IFM3_MOUSE	Ifitm3	Interferon-induced trans	K.MVGDVTGAQAYASTAK#.C	4.52	1.63	2.78	0.36
Q9D0P8_IFT27_MOUSE	Ift27	Intraflagellar transport p	R.SQTSGISLPGVLVGTK#.T	9.56	3.39	2.82	0.35
Q8BKE9_IFT74_MOUSE	Ift74	Intraflagellar transport p	R.GGPLGTGGVLSSQIK#.V	8.08	2.67	3.03	0.33
Q8BKE9_IFT74_MOUSE	Ift74	Intraflagellar transport p	K.ISELTTEINK#.L	7.89	5.05	1.56	0.64
Q61249_IGBP1_MOUSE	Igbp1	Immunoglobulin-bindin	R.AAQQQEDQEQK#DEESEEK#.A	8.45	2.63	3.21	0.31
Q61249_IGBP1_MOUSE	Igbp1	Immunoglobulin-bindin	K.LLEDVEVATEPTGSR@.T	12.10	4.30	2.81	0.36
Q61249_IGBP1_MOUSE	Igbp1	Immunoglobulin-bindin	R.NEDLEEIASTDLK#.Y	12.22	5.49	2.23	0.45
Q61249_IGBP1_MOUSE	Igbp1	Immunoglobulin-bindin	K.SAVESGQADDER@.V	4.26	1.58	2.69	0.37
Q61249_IGBP1_MOUSE	Igbp1	Immunoglobulin-bindin	R.WIAVSLEELESIDQEIK#.I	6.86	6.23	1.10	0.91
Q61249_IGBP1_MOUSE	Igbp1	Immunoglobulin-bindin	K.YGVLPDR@.G	10.52	4.36	2.41	0.41
Q61249_IGBP1_MOUSE	Igbp1	Immunoglobulin-bindin	R.NEDLEEIASTDLK#.Y	4.50	3.17	1.42	0.70
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	R.DILAQVK#.Q	14.70	5.08	2.89	0.35
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	R.DQTPDENDQVIVK#.I	23.89	6.44	3.71	0.27
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	R.LLVPTQYVGAIIGK#.E	25.52	15.87	1.61	0.62
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	K.TVNELQNLTAAEVVVPR@.D	8.91	3.25	2.74	0.36
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	R.DQTPDENDQVIVK#.I	71.46	18.80	3.80	0.26
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	K.IIGHFYASQM*AQR@.K	31.97	8.52	3.75	0.27
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	R.M*VVITGPPEAQFK#.A	13.09	3.95	3.31	0.30
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	R.MVVITGPPEAQFK#.A	14.70	39.18	0.38	2.67
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	K.TVNELQNLTAAEVVVPR@.D	42.04	8.83	4.76	0.21
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	R.DQTPDENDQVIVK#.I	11.92	5.36	2.22	0.45
O88477_IF2B1_MOUSE	Igf2bp1	Insulin-like growth facto	R.LLVPTQYVGAIIGK#.E	23.21	15.66	1.48	0.68
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.DQTPDENEEVIVR@.I	77.54	23.93	3.24	0.31
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.EIVQQVK#.Q	85.28	24.06	3.54	0.28
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.IAPAEGPDVSER@.M	191.03	53.47	3.57	0.28
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.IIGHFFASQTAQR@.K	61.22	13.72	4.46	0.22
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.IM*EVDYSVSK#.K	27.20	6.50	4.18	0.24
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.IMEVDYSVSK#.K	7.57	1.89	4.01	0.25
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.ITISSLQDLSIYNPER@.T	48.13	13.64	3.53	0.28
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.K#LPLAGQVLLK#.S	24.28	7.22	3.36	0.30
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.LAEEVPLK#.I	67.87	20.73	3.27	0.31
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.LYIGNLSPAVTADDLR@.Q	46.56	12.70	3.67	0.27
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.MILEIMQK#.E	9.68	2.41	4.02	0.25
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.M*VIITGPPEAQFK#.A	44.96	15.50	2.90	0.34
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.MVIITGPPEAQFK#.A	11.11	5.25	2.12	0.47
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.SGYAFVDYPDQNWAIR@.A	30.69	9.21	3.33	0.30
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.TVNELQNLTSAEVIVPR@.D	66.53	19.56	3.40	0.29
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.YPQGVAPQR@.S	107.08	26.47	4.05	0.25
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.DQTPDENEEVIVR@.I	58.62	20.57	2.85	0.35
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.IAPAEGPDVSER@.M	90.12	31.99	2.82	0.35
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.IIGHFFASQTAQR@.K	17.46	6.61	2.64	0.38
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.M*VIITGPPEAQFK#.A	26.96	10.29	2.62	0.38
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.MVIITGPPEAQFK#.A	16.17	5.28	3.07	0.33
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.TVNELQNLTSAEVIVPR@.D	48.23	19.75	2.44	0.41
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.TVNELQNLTSAEVIVPR.D	52.20	14.76	3.54	0.28
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.YPQGVAPQR@.S	31.15	7.75	4.02	0.25
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	R.DQTPDENEEVIVR.I	7.39	8.81	0.84	1.19
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.IAPAEGPDVSER.M	12.84	11.99	1.07	0.93
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.ITISSLQDLSIYNPER@.T	5.65	4.96	1.14	0.88
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.LYIGNLSPAVTADDLR.Q	6.68	6.27	1.07	0.94
Q5SF07_IF2B2_MOUSE	Igf2bp2	Insulin-like growth facto	K.TVNELQNLTSAEVIVPR.D	3.42	4.15	0.82	1.22
A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	K.APQVYTIPPPK.E	1.28	12.00	0.11	9.35
A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	K.DVLTITLTPK.V	2.38	52.30	0.05	21.97
A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	K.NTQPIM*DTDGSYFVYSK.L	3.25	18.54	0.18	5.71
A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	K.NTQPIM*DTDGSYFVYSK.L	15.96	136.42	0.12	8.55
A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	K.DVLTITLTPK.V	1.55	219.99	0.01	141.87
A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	K.NTQPIM*DTDGSYFVYSK.L	15.67	155.38	0.10	9.91

A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	R.VNSAAFPAPIEK.T	5.72	232.44	0.02	40.60
A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	K.DVLTITLTPK.V	1.18	124.14	0.01	105.37
A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	K.NTQPIM*DTDGSYFVYSK.L	13.30	105.43	0.13	7.93
A0A0A6YWR2_A0A0A6YWR2_MOUSE	Ighg1	Ig gamma-1 chain C regio	R.VNSAAFPAPIEK.T	2.83	173.54	0.02	61.35
Q9DCE9_Q9DCE9_MOUSE	Igtp	Protein Igtp OS=Mus mus	R.ALQFQDLIK#.M	6.13	4.28	1.43	0.70
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	K.EIDSSVLNVAVTGETGSGK#.S	2.90	1.72	1.68	0.59
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	R.K#IISQEILNLIELR@.M	37.12	27.90	1.33	0.75
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	K.LISDLPIYK#.R	19.46	15.58	1.25	0.80
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	K.SDENNDLPSSFTGYFK#.K	9.97	6.23	1.60	0.63
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	K.SPAVFK#PTDEETIQER@.L	23.85	23.21	1.03	0.97
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	K.SSFINTLR@.G	14.90	11.14	1.34	0.75
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	K.TGVVEVTM*ER@.H	14.50	9.87	1.47	0.68
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	R.TVFGVDETSLQR@.L	18.99	26.85	0.71	1.41
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	K.LISDLPIYK#.R	12.98	8.13	1.60	0.63
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	K.SPAVFKPTDEETIQER.L	14.99	14.31	1.05	0.95
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	R.TKVDSDITNEADGKPQTFDKEK.V	9.52	7.05	1.35	0.74
Q9QZ85_IIGP1_MOUSE	Iigp1	Interferon-inducible GTP	R.TVFGVDETSLQR@.L	21.80	11.49	1.90	0.53
Q9Z1M8_RED_MOUSE	Ik	Protein Red OS=Mus mus	K.AAFQYGIK#.M	25.64	18.96	1.35	0.74
Q9Z1M8_RED_MOUSE	Ik	Protein Red OS=Mus mus	R.EYNEDEDPAAR@.R	17.18	14.89	1.15	0.87
Q9Z1M8_RED_MOUSE	Ik	Protein Red OS=Mus mus	K.FAGSAGWEGTESLK#.K	20.31	5.91	3.44	0.29
Q9Z1M8_RED_MOUSE	Ik	Protein Red OS=Mus mus	K.GLDFALLQK#.V	34.91	33.33	1.05	0.95
Q9Z1M8_RED_MOUSE	Ik	Protein Red OS=Mus mus	K.K#PPEADM*NIFEDIGDYVPSTTK#.T	14.28	17.12	0.83	1.20
Q9Z1M8_RED_MOUSE	Ik	Protein Red OS=Mus mus	K.LTQILSYLR@.Q	48.65	36.91	1.32	0.76
Q9Z1M8_RED_MOUSE	Ik	Protein Red OS=Mus mus	R.M*AYVVDLDDEYADTDIPTTLIR@.S	6.73	5.42	1.24	0.81
Q9DBZ1_IKIP_MOUSE	Ikbip	Inhibitor of nuclear facto	R.LLQTESSEFQGLQSK#.I	7.62	7.80	0.98	1.02
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.AFESTLQLM*ER@.A	5.84	3.15	1.85	0.54
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.AAM*EAINPR@.K	14.63	11.64	1.26	0.80
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.AEQGTVLIGSER@.G	15.73	6.47	2.43	0.41
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.IVTVVPQDTK#.L	19.94	12.45	1.60	0.62
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.NYM*DFLDSETATFIR@.H	6.05	2.92	2.08	0.48
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.SLAVQLADGQVLK#.Y	15.20	6.74	2.26	0.44
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.SSGNSANDLANVAVIDGNR@.V	6.38	4.28	1.49	0.67
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.VFLENVETFVK#.Q	35.21	16.09	2.19	0.46
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.VLFLFEFEEQAK#.E	14.11	5.44	2.59	0.39
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.VLVTVFR@.Q	18.29	11.32	1.62	0.62
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.AAM*EAINPR@.K	26.15	6.92	3.78	0.26
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.AEQGTVLIGSER@.G	30.09	8.31	3.62	0.28
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.AFESTLQLM*ER@.A	12.87	3.39	3.80	0.26
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.DFEVIAEEQIHQDDFGEGK#.F	33.89	10.15	3.34	0.30
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.EYLPFLNTLK#.K	42.85	12.21	3.51	0.29
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.IVTVVPQDTK#.L	43.86	13.24	3.31	0.30
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.NSEGIPVR@.F	18.60	8.99	2.07	0.48
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.NYM*DFLDSETATFIR@.H	13.06	3.78	3.45	0.29
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.SLAVQLADGQVLK#.Y	44.50	13.33	3.34	0.30
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.SSGNSANDLANVAVIDGNR@.V	16.82	6.49	2.59	0.39
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.SVQVSTHPDGK#.K	14.44	3.41	4.23	0.24
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.TTPELEIVLQK#.V	21.89	7.77	2.82	0.35
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.VDIIETSVK#PSILEAQK#.N	29.80	15.54	1.92	0.52
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.VFLENVETFVK#.Q	55.36	19.17	2.89	0.35
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	R.VLVTVFR@.Q	45.82	12.72	3.60	0.28
Q7TT37_ELP1_MOUSE	Ikbkap	Elongator complex prote	K.VQELQGNLPFDPESVSVEEALK#.Y	26.99	14.41	1.87	0.53
O88522_NEMO_MOUSE	Ikbkg	NF-kappa-B essential mod	K.AQVTSLLGELQESQSR@.L	12.94	4.15	3.12	0.32
O88522_NEMO_MOUSE	Ikbkg	NF-kappa-B essential mod	K.EYLQEQLEQLQR@.E	11.71	3.78	3.10	0.32
O88522_NEMO_MOUSE	Ikbkg	NF-kappa-B essential mod	K.IVM*ETVPVLK#.A	8.66	3.65	2.37	0.42
O88522_NEMO_MOUSE	Ikbkg	NF-kappa-B essential mod	K.LAQLQAAYHQLFQDYDSHIK#.S	13.60	7.14	1.90	0.53
O88522_NEMO_MOUSE	Ikbkg	NF-kappa-B essential mod	R.M*QNQSVEAALR@.M	13.21	58.58	0.23	4.44
O88522_NEMO_MOUSE	Ikbkg	NF-kappa-B essential mod	R.QQLQQAEEALVAK#.Q	14.39	7.01	2.05	0.49
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.GTM*TTGHNVADLVVILK#.I	54.24	18.41	2.95	0.34
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.ILITTVPPNLR.K	48.52	20.54	2.36	0.42
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.ILPTLEAVAALGNK#.V	137.40	52.91	2.60	0.39
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.INNVIDNLIVAPGTFEVQIEEVR.Q	8.45	1.41	5.98	0.17
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	R.NQDLAPNSAEQASILSLVTK#.I	32.99	11.91	2.77	0.36
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	R.QPLALNVAYR@.R	79.91	31.10	2.57	0.39
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.R@NQDLAPNSAEQASILSLVTK#.I	18.39	7.24	2.54	0.39
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	R.VK#PAPDETSFSEALLK#R@.N	76.08	27.29	2.79	0.36
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.VLQSALAAIR@.H	140.64	56.68	2.48	0.40
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	R.WFEENASQSTVK#.V	667.23	74.25	8.99	0.11
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.GTM*TTGHNVADLVVILK#.I	16.86	7.86	2.14	0.47
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.ILITTVPPNLR@.K	9.22	5.14	1.79	0.56
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.ILPTLEAVAALGNK#.V	42.50	16.97	2.51	0.40
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.INNVIDNLIVAPGTFEVQIEEVR@.Q	21.11	9.07	2.33	0.43
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	R.NQDLAPNSAEQASILSLVTK#.I	7.78	3.24	2.40	0.42
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.VLQSALAAIR@.H	28.75	10.92	2.63	0.38
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.GTM*TTGHNVADLVVILK#.I	19.02	29.51	0.64	1.55
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.ILITTVPPNLR@.K	15.53	6.30	2.46	0.41
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.ILPTLEAVAALGNK#.V	15.22	3.58	4.25	0.24
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.INNVIDNLIVAPGTFEVQIEEVR@.Q	28.87	16.66	1.73	0.58
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	R.NQDLAPNSAEQASILSLVTK#.I	38.18	17.28	2.21	0.45
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	R.QPLALNVAYR@.R	17.64	7.31	2.41	0.41
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	R.VK#PAPDETSFSEALLK#.R	30.92	15.56	1.99	0.50
Q9CXY6_ILF2_MOUSE	Ilf2	Interleukin enhancer-bin	K.VLQSALAAIR.H	40.35	18.25	2.21	0.45
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.AYAALAALEK#.L	5.30	4.30	1.23	0.81
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.GYGHGQGSYSSYSNSYNSPGGGGGSDYSYDSK#.F	6.78	2.48	2.73	0.37
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	R.LNQLK#PGLQYK#.L	14.46	6.50	2.23	0.45
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.ADPPQAM*NALM*R@.L	19.45	8.90	2.18	0.46
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.AYAALAALEK#.L	93.29	36.48	2.56	0.39
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	R.EDITQSAQHALR.L	25.99	9.32	2.79	0.36
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.FNYSGSGGR@.S	44.00	17.27	2.55	0.39
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	R.FVMEVEVDGQK#.F	33.01	16.58	1.99	0.50
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	R.GLK#YELISETGGSHDK#R@.F	33.04	14.14	2.34	0.43
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.GYGHGQGSYSSYSNSYNSPGGGGGSDYSYDSK#.F	3.74	2.08	1.80	0.56
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.HSSVYPTQEELEAVQNM*VSHTER@.A	8.23	4.57	1.80	0.56
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.HSSVYPTQEELEAVQNMVSHTER@.A	5.36	1.84	2.92	0.34
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	R.IFVNDDR@.H	37.86	13.60	2.78	0.36
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	R.LAAFGQLHK#.V	22.47	8.35	2.69	0.37
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.LFPDTPLALEANK#.K	39.30	22.14	1.78	0.56
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.LISQTGPVHAPIFTM*SVEVDGSNFEASGPSK#.K	8.60	2.29	3.75	0.27
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VADNLAIQLTTVTEDK#YEILQSVDDAAIVIK#.N	7.83	4.40	1.78	0.56
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VADNLAIQLTTVTEDKYEILQSVDDAAIVIK.N	7.79	1.96	3.97	0.25
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VLAGETLSVNDPPDVLDR@.Q	53.68	25.17	2.13	0.47
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VLGM*DPLPSK#.M	87.09	42.51	2.05	0.49
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VLGMDPLPSK#.M	8.11	5.46	1.49	0.67
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VLQDM*GLPTGAEGR@.D	92.38	33.50	2.76	0.36

Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VLQDMGLPTGAEGR@.D	18.18	9.44	1.93	0.52
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	R.VPTWGPLR@.G	39.43	18.06	2.18	0.46
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.YELISETGGSHDK#R@.F	32.16	13.24	2.43	0.41
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.ADPPQAM*NALM*R@.L	9.50	3.27	2.91	0.34
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.AYAALAALEK#.L	30.60	9.18	3.34	0.30
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.LFPDTPLALEANK#.K	28.84	7.05	4.09	0.24
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.LISQTGPVHAPIFTM*SVEVDGSNFEASGPSK#.K	4.53	1.67	2.71	0.37
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VLAGETLSVNDPPDVLDR@.Q	21.66	8.38	2.58	0.39
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VLGM*DPLPSK#.M	31.69	13.02	2.43	0.41
Q9Z1X4_ILF3_MOUSE	Ilf3	Interleukin enhancer-bin	K.VLQDM*GLPTGAEGR@.D	16.32	6.16	2.65	0.38
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.EVPFADLSNM*EIGM*K#.V	16.35	8.88	1.84	0.54
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	K.FALDM*AR@.G	22.74	13.16	1.73	0.58
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	K.FDM*IVPILEK#.M	32.41	21.30	1.52	0.66
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	K.FDMIVPILEK#.M	11.26	8.80	1.28	0.78
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.GM*AFLHTLEPLIPR@.H	36.24	27.65	1.31	0.76
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	K.HSGIDFK#.Q	40.91	20.28	2.02	0.50
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.M*YAPAWVAPEALQK#.K	13.37	9.27	1.44	0.69
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.SAVVEM*LIM*R@.G	17.90	12.63	1.42	0.71
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.SAVVEMLIM*R@.G	7.10	4.04	1.76	0.57
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.SVM*IDEDM*TAR.I	24.55	15.60	1.57	0.64
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.SVMIDEDM*TAR@.I	3.51	2.99	1.17	0.85
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	K.FDM*IVPILEK#.M	18.68	6.67	2.80	0.36
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.GM*AFLHTLEPLIPR@.H	24.43	9.23	2.65	0.38
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.M*YAPAWVAPEALQK#.K	6.90	4.17	1.65	0.60
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.SVM*IDEDM*TAR@.I	11.39	4.17	2.73	0.37
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.EVPFADLSNM*EIGM*K#.V	13.12	4.11	3.19	0.31
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	K.FDM*IVPILEK#.M	35.28	8.74	4.04	0.25
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.GM*AFLHTLEPLIPR@.H	39.82	10.80	3.69	0.27
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.ISM*ADVK#.F	39.11	13.01	3.01	0.33
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	R.SVM*IDEDM*TAR@.I	13.13	4.55	2.89	0.35
O55222_ILK_MOUSE	Ilk	Integrin-linked protein ki	K.YGEM*PVDK#.A	26.03	6.12	4.25	0.24
Q921Y2_IMP3_MOUSE	Imp3	U3 small nucleolar ribon	R.ASAALLDK#.L	10.63	9.10	1.17	0.86
Q921Y2_IMP3_MOUSE	Imp3	U3 small nucleolar ribon	K.LYAM*GLVPTR.G	4.33	3.94	1.10	0.91
Q921Y2_IMP3_MOUSE	Imp3	U3 small nucleolar ribon	R.SM*EDFVTWVDSSK#.I	3.94	2.06	1.91	0.52
Q921Y2_IMP3_MOUSE	Imp3	U3 small nucleolar ribon	R.VGPDVVTDPAFLVTR@.S	55.03	39.78	1.38	0.72
Q8VHZ7_IMP4_MOUSE	Imp4	U3 small nucleolar ribon	R.VITFANQDDYISFR@.H	7.50	4.73	1.59	0.63
Q80V26_IMPA3_MOUSE	Impad1	Inositol monophosphata	K.VLALLDVPDM*TQEK#.A	9.46	3.70	2.56	0.39
Q9WU62_INCE_MOUSE	Incenp	Inner centromere protei	K.ISVDDYGM*DLNSDDSTDDESHPR@.K	3.84	6.03	0.64	1.57
Q9WU62_INCE_MOUSE	Incenp	Inner centromere protei	R.LAEQQLQEEQAK.K	22.50	24.33	0.92	1.08
Q9WU62_INCE_MOUSE	Incenp	Inner centromere protei	K.NQM*LM*TPTLASR.S	6.23	10.41	0.60	1.67
Q9WU62_INCE_MOUSE	Incenp	Inner centromere protei	R.VLSPILLNNILPTTAK.S	6.65	12.82	0.52	1.93
Q9WU62_INCE_MOUSE	Incenp	Inner centromere protei	R.VLSPILLNNILPTTAK#.S	5.82	4.25	1.37	0.73
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	K.AEDEEELQR@.I	9.61	3.69	2.60	0.38
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	K.FDVEVLK#.Q	28.56	11.08	2.58	0.39
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.LLQM*PSVVNYSGLR@.K	8.55	2.80	3.05	0.33
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.LQASIEASQELDK#VFDAIEQK#.K	24.29	8.96	2.71	0.37
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.LRDLEDADLLIQLEAFEEAK.A	15.33	5.07	3.02	0.33
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.NQEEFVPDSDDIK#.A	10.87	2.46	4.41	0.23
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.QLSQALDTSNVM*VK#.K	7.60	2.30	3.30	0.30
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.SFSEDAVTDSSGSGTLPR@.V	6.96	2.17	3.21	0.31
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	K.SVQTNSVQNQGSSSQNTTTPTTK#.V	5.19	1.86	2.80	0.36
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	K.VSASIPEVQK#.Q	20.82	6.79	3.06	0.33
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.VTLLHHVLEEVEK#.S	32.53	13.88	2.34	0.43
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	K.AEDEEELQR@.I	6.92	3.34	2.07	0.48
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.AVM*NSQQGIEYILSNQGYVR@.Q	16.50	4.27	3.86	0.26
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.AVMNSQQGIEYILSNQGYVR@.Q	5.34	2.81	1.90	0.53
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	K.FDVEVLK#.Q	45.14	11.20	4.03	0.25
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.LLQM*PSVVNYSGLR@.K	14.24	11.89	1.20	0.83
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.LQASIEASQELDK#VFDAIEQK#.K	40.11	10.01	4.01	0.25
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.NQEEFVPDSDDIK#.A	18.36	4.26	4.31	0.23
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.QLSQALDTSNVM*VK#.K	8.47	4.15	2.04	0.49
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.SFSEDAVTDSSGSGTLPR@.V	7.10	2.33	3.05	0.33
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.TEADSTSEGPEDEAQR@.G	9.22	3.91	2.36	0.42
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	K.VSASIPEVQK#.Q	17.47	5.77	3.03	0.33
E9QLA5_E9QLA5_MOUSE	Inf2	Inverted formin-2 OS=Mu	R.VTLLHHVLEEVEK#.S	29.85	9.55	3.13	0.32
Q8VEK6_ING3_MOUSE	Ing3	Inhibitor of growth prote	K.VQLANQIYDLVDR@.H	10.66	3.89	2.74	0.36
Q8VEK6_ING3_MOUSE	Ing3	Inhibitor of growth prote	K.ALEDADEK#VQLANQIYDLVDR@.H	6.69	2.14	3.13	0.32
Q8C0D7_ING4_MOUSE	Ing4	Inhibitor of growth prote	R.RLDTDLAR.F	56.96	22.89	2.49	0.40
Q9D8Y8_ING5_MOUSE	Ing5	Inhibitor of growth prote	K.K#AEIDILAAEYISTVK#.T	7.99	5.64	1.42	0.71
Q9D8Y8_ING5_MOUSE	Ing5	Inhibitor of growth prote	R.M*DGSDFESTGAR@.S	13.12	6.67	1.97	0.51
Q9D8Y8_ING5_MOUSE	Ing5	Inhibitor of growth prote	R.RLDADLAR.F	81.50	45.29	1.80	0.56
Q6ZPV2_INO80_MOUSE	Ino80	DNA helicase INO80 OS=M	K.SGSGFGESYSLANPSIR@.A	4.86	1.86	2.62	0.38
Q99PT3_IN80B_MOUSE	Ino80b	INO80 complex subunit	R.AAAPAPAPM*VR@.Y	12.81	3.59	3.56	0.28
Q99PT3_IN80B_MOUSE	Ino80b	INO80 complex subunit	K.LGGQVLGTK#.S	19.75	8.05	2.45	0.41
Q8BHA0_IN80C_MOUSE	Ino80c	INO80 complex subunit	R.FSTVEEFSYIR@.R	5.20	3.03	1.72	0.58
Q8BHA0_IN80C_MOUSE	Ino80c	INO80 complex subunit	K.LSASGFAQGVSIEAM*NESK#.M	3.86	1.77	2.19	0.46
Q8BHA0_IN80C_MOUSE	Ino80c	INO80 complex subunit	K.M*ASSELSSGPVEK#.A	8.30	5.34	1.56	0.64
Q8BHA0_IN80C_MOUSE	Ino80c	INO80 complex subunit	R.R@LPSDVVTGYLALR@.K	7.46	5.47	1.37	0.73
Q8BHA0_IN80C_MOUSE	Ino80c	INO80 complex subunit	K.YSDISGLLANYTDPQSK#.L	6.41	2.31	2.78	0.36
D3Z3H2_D3Z3H2_MOUSE	Ino80e	Coiled-coil domain conta	R.GSGASVGAALTPLPPPK#.M	12.53	5.45	2.30	0.43
Q6P549_SHIP2_MOUSE	Inppl1	Phosphatidylinositol 3,4	R.LLQQQSLPQTGEQELESLVLK#.L	14.06	8.09	1.74	0.58
Q6P549_SHIP2_MOUSE	Inppl1	Phosphatidylinositol 3,4	K.SFENDAQSSDNINFLK#.V	5.62	8.32	0.68	1.48
Q6P4S8_INT1_MOUSE	Ints1	Integrator complex subu	R.AVEDVLETLSDIDEM*SR@.R	11.59	2.97	3.90	0.26
Q6P4S8_INT1_MOUSE	Ints1	Integrator complex subu	R.DASASLSGTSALTGLTK#.R	1.72	19.67	0.09	11.43
Q6P4S8_INT1_MOUSE	Ints1	Integrator complex subu	K.LLQYLDQAVAQDPQTLEQNIM*DK#.N	2.07	2.07	1.00	1.00
Q6P4S8_INT1_MOUSE	Ints1	Integrator complex subu	R.TFQNQIAAIQR@.D	5.24	3.33	1.57	0.64
Q6P4S8_INT1_MOUSE	Ints1	Integrator complex subu	R.TFVDNIQTAFNTK#.M	4.85	3.13	1.55	0.65
Q6P4S8_INT1_MOUSE	Ints1	Integrator complex subu	K.TTSTLLK#PAPSGLPSER@.K	6.29	2.58	2.44	0.41
Q6P4S8_INT1_MOUSE	Ints1	Integrator complex subu	K.VLFTEQPETYYK#.W	6.62	2.45	2.70	0.37
Q6P4S8_INT1_MOUSE	Ints1	Integrator complex subu	K.VYIEDSLGER@.I	11.47	3.00	3.82	0.26
Q8K2A7_INT10_MOUSE	Ints10	Integrator complex subu	K.AAEFYINYVTR@.S	13.55	4.28	3.17	0.32
Q8K2A7_INT10_MOUSE	Ints10	Integrator complex subu	K.ADLSNSIEVLESFK#.L	27.68	4.36	6.35	0.16
Q8K2A7_INT10_MOUSE	Ints10	Integrator complex subu	R.EISIITSALR@.N	24.11	6.73	3.58	0.28
Q8K2A7_INT10_MOUSE	Ints10	Integrator complex subu	R.LLYDM*FVNFPDQPVVWR@.E	4.05	2.62	1.55	0.65
Q8K2A7_INT10_MOUSE	Ints10	Integrator complex subu	R.SLFETLPGR@.V	29.45	9.66	3.05	0.33
Q8K2A7_INT10_MOUSE	Ints10	Integrator complex subu	K.YIIEGLTEK#.S	15.71	7.27	2.16	0.46
Q8K2A7_INT10_MOUSE	Ints10	Integrator complex subu	R.EISIITSALR@.N	10.18	3.55	2.86	0.35
Q8K2A7_INT10_MOUSE	Ints10	Integrator complex subu	R.SEM*LLLLLR@.R	8.66	2.44	3.54	0.28
Q9D168_INT12_MOUSE	Ints12	Integrator complex subu	R.GIDSSYR@PTQK#.D	10.29	2.79	3.68	0.27
Q9D168_INT12_MOUSE	Ints12	Integrator complex subu	K.IGSGNSTSPSVPLK#PLPPLTLGK#.T	9.28	1.94	4.77	0.21
Q80UK8_INT2_MOUSE	Ints2	Integrator complex subu	R.LASLSDPELR@.L	17.09	5.35	3.19	0.31
Q80UK8_INT2_MOUSE	Ints2	Integrator complex subu	R.LVLSELLAIM*NK#.V	7.94	2.50	3.17	0.32
Q80UK8_INT2_MOUSE	Ints2	Integrator complex subu	K.YTQNDLM*IDPLIVLR@.C	8.11	2.51	3.23	0.31

Q80UK8_INT2_MOUSE	Ints2	Integrator complex subu	R.LASLSDPELR@.L	18.37	6.23	2.95	0.34
Q80UK8_INT2_MOUSE	Ints2	Integrator complex subu	R.LVLSELLAIM*NK#.V	12.66	2.90	4.37	0.23
Q80UK8_INT2_MOUSE	Ints2	Integrator complex subu	K.YTQNDLM*IDPLIVLR@.C	14.47	5.24	2.76	0.36
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	K.ETVVEEPVDVTPYLDQLDESLR@DK#.V	12.06	4.60	2.62	0.38
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	K.FSDLFSLAEEYEDSSTK#PPK#.S	38.54	16.20	2.38	0.42
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	K.GK#GTVAAAASGAAGGGGGGAGAGAPGGGR@.L	39.10	11.49	3.40	0.29
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	K.IGYHLLYYLR@.A	11.83	6.59	1.80	0.56
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	R.LIVDHHGTAQLQTLR@.Q	14.47	6.06	2.39	0.42
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	R.QYLSTPDSQSLR@.C	13.66	2.84	4.81	0.21
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	R.TQLVWLVR@.E	9.40	4.93	1.90	0.52
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	R.VLAHLAPLFDNPK#.L	35.08	8.99	3.90	0.26
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	R.YQDWFQR@.Q	12.51	5.22	2.40	0.42
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	K.ETVVEEPVDVTPYLDQLDESLR@DK#.V	14.44	5.94	2.43	0.41
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	K.GK#GTVAAAASGAAGGGGGGAGAGAPGGGR@.L	12.84	4.04	3.18	0.31
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	K.QIAGGDVTAK#.N	25.56	7.68	3.33	0.30
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	R.QYLSTPDSQSLR@.C	15.08	2.77	5.44	0.18
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	R.TQLVWLVR@.E	12.60	1.63	7.75	0.13
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	R.VLAHLAPLFDNPK#.L	12.70	7.27	1.75	0.57
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	K.VLQLQK#.G	32.42	8.77	3.70	0.27
Q7TPD0_INT3_MOUSE	Ints3	Integrator complex subu	R.YQDWFQR@.Q	8.32	2.47	3.36	0.30
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.FLQEVDFFQR@.C	9.69	2.79	3.48	0.29
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.IASLLGLLSK#.T	17.06	8.18	2.09	0.48
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.LLSDDYEQVR@.S	11.06	2.75	4.02	0.25
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.LPENQATQVR@.L	17.02	6.36	2.68	0.37
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.VVQQQQEEIATK#.K	10.22	2.96	3.45	0.29
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	R.VYSVQHLDPQGAQELLEFTIR@.D	10.30	2.97	3.47	0.29
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.ALQLIVTAR@.T	14.90	4.14	3.60	0.28
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.ASATIIEPAGESDNPLR.F	18.33	4.27	4.29	0.23
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.ELYSSGEFSSGR@.K	9.04	2.00	4.51	0.22
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.FLQEVDFFQR@.C	23.64	6.72	3.52	0.28
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.IASLLGLLSK#.T	40.24	7.76	5.18	0.19
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	R.K#LVSSTVPSNITPHEDPSQQFLQQSLER@.V	3.93	1.94	2.02	0.49
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	R.K#PVEAESVEGVVR@.I	22.82	4.37	5.22	0.19
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.LLSDDYEQVR@.S	8.78	5.42	1.62	0.62
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	K.VVQQQQEEIATK#.K	19.91	6.32	3.15	0.32
Q8CIM8_INT4_MOUSE	Ints4	Integrator complex subu	R.VYSVQHLDPQGAQELLEFTIR@.D	17.99	7.91	2.28	0.44
Q8CHT3_INT5_MOUSE	Ints5	Integrator complex subu	R.FQAPPPSTLLR@.Q	12.30	5.48	2.24	0.45
Q8CHT3_INT5_MOUSE	Ints5	Integrator complex subu	K.AFLTGVDPILGHQLSAR@.E	45.38	11.77	3.85	0.26
Q8CHT3_INT5_MOUSE	Ints5	Integrator complex subu	K.FIFQSER@.G	17.70	4.23	4.18	0.24
Q8CHT3_INT5_MOUSE	Ints5	Integrator complex subu	R.LSQTSPAGLK#.A	16.25	3.29	4.94	0.20
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	K.GAVETFM*K#.L	18.18	4.18	4.35	0.23
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	K.GQDEDQVHSVPIAQM*GNYQEYLK#.Q	9.67	3.82	2.53	0.40
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.K#GFQVLQGISEDVPHR@.L	11.81	4.55	2.59	0.39
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.LFALVLR@.L	22.02	6.98	3.15	0.32
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.LIFLQNVIK#.E	30.80	8.27	3.72	0.27
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	K.LPFDK#YELEPSPLTQFILER@.K	9.28	3.31	2.80	0.36
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.LVTGIDNYGQGR@.N	22.11	9.26	2.39	0.42
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	K.VQSGVVINFEK#.T	17.95	4.34	4.13	0.24
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	K.VVQETGIK#.V	16.21	9.40	1.72	0.58
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.YM*LVTFEEPPYAIK#.A	7.04	2.12	3.31	0.30
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	K.YNELGHPFGYLK#.A	17.12	6.73	2.54	0.39
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.ANQINHINSN.-	9.38	9.38	1.00	1.00
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.ELDPDQPR@.R	15.03	4.59	3.28	0.31
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	K.GAVETFM*K#.L	12.49	3.00	4.16	0.24
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.LFALVLR@.L	15.69	2.84	5.52	0.18
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	K.NLQAEGLTTLGQSLR@.T	14.44	3.56	4.06	0.25
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.TAFDLLNLNR@.L	23.97	6.64	3.61	0.28
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	K.VVQETGIK#.V	12.77	9.26	1.38	0.73
Q6PCM2_INT6_MOUSE	Ints6	Integrator complex subu	R.YM*LVTFEEPPYAIK#.A	8.86	1.97	4.50	0.22
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	K.ILNVDEFVK#.R	17.25	6.08	2.84	0.35
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.QLLQQLVTSYPSTK#.M	7.97	2.81	2.83	0.35
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	K.SLEDPYSQQIR@.L	14.17	5.31	2.67	0.37
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.SPAEPIAVQNNQQLALK#.V	6.15	2.03	3.03	0.33
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.VLEEVESLNR@.K	12.10	5.10	2.37	0.42
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	K.YPFPILINSAFLK#.L	10.44	5.93	1.76	0.57
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.YR@DLYQASFDADSATLR@.N	9.76	2.88	3.38	0.30
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.DLYQASFDADSATLR@.N	9.22	2.25	4.09	0.24
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	K.ILNVDEFVK#.R	17.69	6.53	2.71	0.37
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	K.IPIDSM*TNEM*EQR@.V	9.01	3.11	2.89	0.35
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.LAVQDLK#.L	16.43	2.84	5.80	0.17
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.QLLQQLVTSYPSTK#.M	11.27	2.99	3.77	0.26
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	K.SLEDPYSQQIR@.L	21.23	8.47	2.51	0.40
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.SPAEPIAVQNNQQLALK#.V	9.29	2.92	3.18	0.31
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.SVVDTLLTQLHSSQDAAR@.I	41.39	10.71	3.86	0.26
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.VLEEVESLNR@.K	12.88	3.47	3.71	0.27
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	K.YPFPILINSAFLK#.L	10.41	3.97	2.62	0.38
Q7TQK1_INT7_MOUSE	Ints7	Integrator complex subu	R.YR@DLYQASFDADSATLR@.N	16.21	3.41	4.76	0.21
Q80V86_INT8_MOUSE	Ints8	Integrator complex subu	R.SELLSFIK#.K	13.64	6.66	2.05	0.49
Q80V86_INT8_MOUSE	Ints8	Integrator complex subu	R.TIVQSSFPVK#.Q	15.98	6.45	2.48	0.40
Q8K114_INT9_MOUSE	Ints9	Integrator complex subu	K.VLK#PLLSGSIPVEQFVQTLEK#.H	7.36	3.67	2.01	0.50
Q8K114_INT9_MOUSE	Ints9	Integrator complex subu	R.LNFIQVSK#.L	9.81	4.03	2.43	0.41
Q8K114_INT9_MOUSE	Ints9	Integrator complex subu	K.VLK#PLLSGSIPVEQFVQTLEK#.H	11.25	3.91	2.88	0.35
Q8VI75_IPO4_MOUSE	Ipo4	Importin-4 OS=Mus mus	K.TEPQVLATLLR@.A	7.35	3.64	2.02	0.49
Q8BKC5_IPO5_MOUSE	Ipo5	Importin-5 OS=Mus mus	K.EGFVEYTEQVVK#.L	9.25	1.27	7.29	0.14
Q8BKC5_IPO5_MOUSE	Ipo5	Importin-5 OS=Mus mus	R.LLSSAFDEVYPALPSDVQTAIK#.S	8.55	4.86	1.76	0.57
Q8BKC5_IPO5_MOUSE	Ipo5	Importin-5 OS=Mus mus	K.SLLIPYLDNLVK#.H	13.68	5.62	2.43	0.41
Q8BKC5_IPO5_MOUSE	Ipo5	Importin-5 OS=Mus mus	K.SLVEIADTVPK#.Y	18.56	6.06	3.06	0.33
Q8BKC5_IPO5_MOUSE	Ipo5	Importin-5 OS=Mus mus	K.VSDILHSIFSSYK#.E	13.40	5.84	2.29	0.44
Q91YE6_IPO9_MOUSE	Ipo9	Importin-9 OS=Mus mus	K.EALVDTLTGILSPVQEVR@.A	8.44	50.13	0.17	5.94
Q91YE6_IPO9_MOUSE	Ipo9	Importin-9 OS=Mus mus	K.LIINELSNVM*EANAAR@.Q	7.37	2.77	2.66	0.38
Q91YE6_IPO9_MOUSE	Ipo9	Importin-9 OS=Mus mus	K.YSNDPVVASLAQDIFK#.E	4.15	2.34	1.77	0.56
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.GVLLEIEDLQANQFK#.N	10.07	10.60	0.95	1.05
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.NVIFEIGPTEEVGDFEVK.A	13.80	10.04	1.37	0.73
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.ALQSLALGLR.G	15.89	13.61	1.17	0.86
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.ATFYGEQVDYYK#.S	23.54	9.83	2.39	0.42
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.DHINDIIK#.I	39.30	17.56	2.24	0.45
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.DSLHEK#FPDAGEDELLK#.I	14.41	8.39	1.72	0.58
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.EEIQSSISGVTAAYNR@.E	6.36	4.59	1.39	0.72
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.EEYLLLR@.L	22.56	5.56	4.06	0.25
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.EK#LEAYQHLFYLLQTNPTYLAK#.L	7.61	3.23	2.35	0.42
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.EQLWLANEGLITK.L	7.51	6.51	1.15	0.87
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.FALGISAINEAVDSGDVGR@.T	9.34	7.94	1.18	0.85
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.FDVPGDENAEM*DAR@.T	7.76	3.76	2.07	0.48

Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.FLSAIVSSVDK#IPYGM*R@.F	14.26	19.54	0.73	1.37
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.FM*DSVIFTLYNYASNQR@.E	9.85	6.71	1.47	0.68
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.FPDAGEDELLK#.I	7.52	3.07	2.44	0.41
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.FVHLLDQSDQDFQEELDLM*K#.M	9.27	6.12	1.51	0.66
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.GVLLEIEDLQANQFK#.N	36.81	17.22	2.14	0.47
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.IIGNLLYYR.Y	28.98	17.71	1.64	0.61
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.ILAIGLINEALDEGDAQK#.T	17.12	11.64	1.47	0.68
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LEGVLAEVAQHYQDTLIR@.A	22.50	18.76	1.20	0.83
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.LFQTALQEEIK#.S	45.56	31.41	1.45	0.69
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LGLAPQIQDLYGK#.V	8.94	5.45	1.64	0.61
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LIFQM*PQNK#.S	43.12	21.32	2.02	0.49
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.LIVDVIR.F	18.15	11.43	1.59	0.63
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LPYDVTPEQALSHEEVK#.T	37.57	25.84	1.45	0.69
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LQQTYSALNSK#.A	13.74	6.79	2.02	0.49
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LTELGTVDPK#.N	24.46	8.92	2.74	0.36
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.M*FLGDNAHLSIINEYLSQSYQK#.F	25.27	8.83	2.86	0.35
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.NVIFEIGPTEEVGDFEVK#.A	25.13	23.66	1.06	0.94
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.QSGQTDPLQK#EEVQAGVDAANSAAQQYQR@.R	4.05	2.02	2.01	0.50
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.R@LIVDVIR@.F	12.17	3.83	3.18	0.31
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.SK#VDQIQEIVTGNPTVIK#.M	24.40	15.31	1.59	0.63
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.SNQQLENDLNLM*DIK#.I	18.77	12.93	1.45	0.69
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.TLINAEDPPM*IVVR@.K	14.56	7.83	1.86	0.54
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.VDQIQEIVTGNPTVIK#.M	17.05	12.10	1.41	0.71
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.VDQIQEIVTGNPTVIK#.M	14.60	6.40	2.28	0.44
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.VLK#DSLHEK#FPDAGEDELLK#.I	12.30	5.60	2.19	0.46
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.YM*NPAIVAPDAFDIIDLSAGGQLTTDQR@.R	17.99	9.25	1.95	0.51
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.ALESGDM*TTVWK#.Q	27.87	14.42	1.93	0.52
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.ALQSLALGLR.G	68.98	33.30	2.07	0.48
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.ATFYGEQVDYYK#.S	56.50	31.84	1.77	0.56
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.DHINDIIK#.I	51.09	20.34	2.51	0.40
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.DSLHEK#FPDAGEDELLK#.I	15.32	10.40	1.47	0.68
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.DVYEELLTQAEIQGNVNK#.V	23.69	24.57	0.96	1.04
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.DVYEELLTQAEIQGNVNK#.V	11.06	6.54	1.69	0.59
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.EEIQSSISGVTAAYNR@.E	48.19	30.76	1.57	0.64
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.EEVITLIR@.S	11.49	7.70	1.49	0.67
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.EEVQAGVDAANSAAQQYQR@.R	6.69	4.20	1.59	0.63
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.EK#AQETQDESAVLWLDEIQGGIWQSNK#DTQEAQR@.F	3.54	2.04	1.74	0.58
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.EK#LEAYQHLFYLLQTNPTYLAK#.L	7.66	3.16	2.42	0.41
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.EQLWLANEGLITK#.L	56.45	30.07	1.88	0.53
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.ER@DVYEELLTQAEIQGNVNK#.V	22.93	15.98	1.43	0.70
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.FALGISAINEAVDSGDVGR@.T	91.38	44.93	2.03	0.49
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.FDVPGDENAEM*DAR@.T	19.65	11.02	1.78	0.56
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.FM*DSVIFTLYNYASNQR@.E	14.57	9.20	1.58	0.63
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.FQPGETLTEILETPATNEQEAEHQR@.A	115.60	63.77	1.81	0.55
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.FVHLLDQSDQDFQEELDLM*K#.M	27.69	15.77	1.76	0.57
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.FVHLLDQSDQDFQEELDLMK#.M	4.50	3.68	1.22	0.82
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.GLQTQNSDWYM*K#.Q	12.19	7.02	1.74	0.58
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.GVLLEIEDLQANQFK#.N	94.12	43.71	2.15	0.46
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.HTDNVIQWLNAM*DEIGLPK#.I	25.05	13.90	1.80	0.56
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.IFYPETTDIYDR@.K	30.21	17.01	1.78	0.56
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.IIGNLLYYR.Y	72.84	33.55	2.17	0.46
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.ILAIGLINEALDEGDAQK#.T	176.42	110.81	1.59	0.63
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.ITLQDVVSHSK#.K	109.97	48.47	2.27	0.44
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.LAAVAAINAAIQK#.G	26.20	14.07	1.86	0.54
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.LAYLHSHK#DEVVK#.I	3.72	3.66	1.02	0.98
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LEGVLAEVAQHYQDTLIR@.A	182.94	92.72	1.97	0.51
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.LFQTALQEEIK#.S	112.48	108.86	1.03	0.97
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LGLAPQIQDLYGK#.V	79.73	40.80	1.95	0.51
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LGNFFSPK#.V	63.49	32.64	1.95	0.51
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LIFQM*PQNK#.S	82.22	56.03	1.47	0.68
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LPYDVTPEQALSHEEVK#.T	87.99	57.21	1.54	0.65
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.LQQTYSALNSK#.A	33.64	14.68	2.29	0.44
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.LTAEEM*DER@.R	43.62	27.60	1.58	0.63
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.M*FLGDNAHLSIINEYLSQSYQK#.F	49.95	22.19	2.25	0.44
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.NVIFEIGPTEEVGDFEVK#.A	101.72	69.09	1.47	0.68
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.QLQSDLQQK#.R	71.67	34.91	2.05	0.49
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.QSGQTDPLQK#EEVQAGVDAANSAAQQYQR@.R	29.33	13.24	2.22	0.45
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.R@LIVDVIR@.F	27.83	11.32	2.46	0.41
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.SK#VDQIQEIVTGNPTVIK#.M	38.52	24.58	1.57	0.64
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.SNQQLENDLNLM*DIK#.I	56.05	28.02	2.00	0.50
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.SWVNQM*ESQTGEASK#.L	6.62	2.59	2.56	0.39
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.SWVNQM*ESQTGEASK#LPYDVTPEQALSHEEVK#.T	8.84	3.67	2.41	0.42
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.TEVSLTLTNK#.F	28.48	11.08	2.57	0.39
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.TEVSLTLTNK#FDVPGDENAEM*DAR@.T	18.67	11.41	1.64	0.61
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.TILLNTK#.R	60.48	33.44	1.81	0.55
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.TLINAEDPPM*IVVR@.K	44.65	24.10	1.85	0.54
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.TLQALQIPAAK#.L	102.86	58.88	1.75	0.57
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.TVLELM*NPEAQLPQVYPFAADLYQK#.E	33.36	19.22	1.74	0.58
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.VAADTFTALK#.N	38.05	21.28	1.79	0.56
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.VDFTEEEINNM*K#.I	12.15	8.44	1.44	0.69
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.VDQIQEIVTGNPTVIK#.M	42.70	26.31	1.62	0.62
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.VLK#DSLHEK#FPDAGEDELLK#.I	26.58	16.43	1.62	0.62
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	K.YGIQM*PAFSK#.I	33.55	13.09	2.56	0.39
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.YLDELM*K#.L	35.44	17.67	2.01	0.50
Q9JKF1_IQGA1_MOUSE	Iqgap1	Ras GTPase-activating-lik	R.YM*NPAIVAPDAFDIIDLSAGGQLTTDQR@.R	48.24	28.07	1.72	0.58
F8VQ29_F8VQ29_MOUSE	Iqgap3	Protein Iqgap3 OS=Mus	K.SYQQALEGAAAK#.K	8.78	5.94	1.48	0.68
F8VQ29_F8VQ29_MOUSE	Iqgap3	Protein Iqgap3 OS=Mus	K.TLSALLLPAAGLEDVSLHVAPR@.Y	16.09	4.73	3.40	0.29
F8VQ29_F8VQ29_MOUSE	Iqgap3	Protein Iqgap3 OS=Mus	R.VTGDPGAVLWLEEIR@.Q	10.16	20.35	0.50	2.00
Q8R3Y8_I2BP1_MOUSE	Irf2bp1	Interferon regulatory fac	R.LALPSPALEYTLGSR@.L	13.61	8.25	1.65	0.61
Q8R3Y8_I2BP1_MOUSE	Irf2bp1	Interferon regulatory fac	R.HWVAPGGPYSSETPGVPSPIAALK#.N	5.17	2.18	2.37	0.42
Q8R3Y8_I2BP1_MOUSE	Irf2bp1	Interferon regulatory fac	R.QLGELLTDGVR@.S	10.29	3.80	2.71	0.37
E9Q1P8_I2BP2_MOUSE	Irf2bp2	Interferon regulatory fac	R.SPADSLSSAAGASELSAEGAGK#.G	12.33	4.09	3.01	0.33
Q8K3X4_I2BPL_MOUSE	Irf2bpl	Interferon regulatory fac	R.LLGDLLPEAVR@.F	14.16	5.83	2.43	0.41
Q8K3X4_I2BPL_MOUSE	Irf2bpl	Interferon regulatory fac	R.VFAFDAVSK#PGM*DYELK#.L	14.58	1.75	8.34	0.12
Q8K3X4_I2BPL_MOUSE	Irf2bpl	Interferon regulatory fac	R.YGLSAAAAAAAAAAAVEQR@.S	7.90	4.45	1.78	0.56
Q60766_IRGM1_MOUSE	Irgm1	Immunity-related GTPas	R.DLSTSVLSEVR@.L	21.03	6.23	3.38	0.30
Q60766_IRGM1_MOUSE	Irgm1	Immunity-related GTPas	R.LLQNIQENIR@.E	23.05	8.84	2.61	0.38
Q60766_IRGM1_MOUSE	Irgm1	Immunity-related GTPas	K.SQNFYTLR@.R	13.90	2.68	5.20	0.19
Q60766_IRGM1_MOUSE	Irgm1	Immunity-related GTPas	R.LLQNIQENIR@.E	17.49	7.51	2.33	0.43
Q60766_IRGM1_MOUSE	Irgm1	Immunity-related GTPas	K.LLELVYGIK#.E	14.70	6.53	2.25	0.44
Q60766_IRGM1_MOUSE	Irgm1	Immunity-related GTPas	R.LLQNIQENIR@.E	24.68	9.35	2.64	0.38
Q60766_IRGM1_MOUSE	Irgm1	Immunity-related GTPas	K.SQNFYTLR@.R	14.83	5.14	2.89	0.35
Q60766_IRGM1_MOUSE	Irgm1	Immunity-related GTPas	R.VIGHDEDASAPTGVVR@.T	37.66	24.52	1.54	0.65

Q9Z1M2_Q9Z1M2_MOUSE	Irgm2	Interferon-g induced GTF	K.SIDEDNLHTEFGISDPGNAIEIR@.K	4.44	3.67	1.21	0.83
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	R.GHSNIYEVFLTQTVDTLK#.K	45.10	25.78	1.75	0.57
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	K.IGVPAFQQR@.L	52.72	48.21	1.09	0.91
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	R.GHSNIYEVFLTQTVDTLK#K#.K	10.64	9.33	1.14	0.88
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	K.IGVPAFQQR@.L	34.58	39.12	0.88	1.13
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	R.GHSNIYEVFLTQTVDTLK#.K	139.08	83.78	1.66	0.60
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	R.GHSNIYEVFLTQTVDTLK#K#.K	56.27	37.53	1.50	0.67
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	K.IGVPAFQQR@.L	129.07	86.27	1.50	0.67
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	K.M*LGGNDFLVSVTNSM*TVSELKK.Q	78.73	59.20	1.33	0.75
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	K.M*LGGNDFLVSVTNSMTVSELK#K#.Q	16.27	13.75	1.18	0.84
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	R.GHSNIYEVFLTQTVDTLK#.K	158.78	92.16	1.72	0.58
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	R.GHSNIYEVFLTQTVDTLK#K#.K	66.80	38.86	1.72	0.58
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	K.IGVPAFQQR@.L	223.43	144.86	1.54	0.65
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	K.M*LGGNDFLVSVTNSM*TVSELK#.K	4.77	3.43	1.39	0.72
Q64339_ISG15_MOUSE	Isg15	Ubiquitin-like protein IS(	K.M*LGGNDFLVSVTNSMTVSELK#K#.Q	13.04	7.51	1.74	0.58
Q9JL16_ISG20_MOUSE	Isg20	Interferon-stimulated ge	R.LEILQLLK.G	29.72	31.59	0.94	1.06
Q9JL16_ISG20_MOUSE	Isg20	Interferon-stimulated ge	K.YIRPEGEITDYR.T	9.11	14.49	0.63	1.59
Q9JL16_ISG20_MOUSE	Isg20	Interferon-stimulated ge	K.YTIYDTSTDR.L	10.62	14.42	0.74	1.36
Q3U1G5_I20L2_MOUSE	Isg20l2	Interferon-stimulated 20	R.DIQVGNTGHSSVEDAQATM*ELYK#.L	7.82	3.87	2.02	0.50
Q3U1G5_I20L2_MOUSE	Isg20l2	Interferon-stimulated 20	K.IATENSTQAQSK#.D	6.58	6.26	1.05	0.95
Q3U1G5_I20L2_MOUSE	Isg20l2	Interferon-stimulated 20	K.IDLLGEFQSALPK#.T	33.18	14.26	2.33	0.43
Q9CX00_IST1_MOUSE	Ist1	IST1 homolog OS=Mus m	K.ELDSGLAESVSTLIWAAPR@.L	12.01	3.48	3.45	0.29
Q9CX00_IST1_MOUSE	Ist1	IST1 homolog OS=Mus m	R.FGLIQSM*K#.E	25.49	13.00	1.96	0.51
Q9CX00_IST1_MOUSE	Ist1	IST1 homolog OS=Mus m	K.LSVEAPPK#.I	16.65	8.39	1.98	0.50
Q9CX00_IST1_MOUSE	Ist1	IST1 homolog OS=Mus m	R.TNQIGTVNDR@.L	109.25	22.13	4.94	0.20
Q69ZQ2_ISY1_MOUSE	Isy1	Pre-mRNA-splicing factor	K.FIAHVPVPSQQEIEEALVR@.R	43.09	26.98	1.60	0.63
Q69ZQ2_ISY1_MOUSE	Isy1	Pre-mRNA-splicing factor	R.IKELGGPDYGK.V	6.97	4.82	1.45	0.69
Q69ZQ2_ISY1_MOUSE	Isy1	Pre-mRNA-splicing factor	R.IR@DLNDEINK#.L	47.55	26.94	1.76	0.57
Q69ZQ2_ISY1_MOUSE	Isy1	Pre-mRNA-splicing factor	K.YASETLQAQSEEAK#.R	8.06	4.90	1.64	0.61
Q62470_ITA3_MOUSE	Itga3	Integrin alpha-3 OS=Mus	R.AAFLSEQLQPLSR@.L	20.95	6.07	3.45	0.29
Q62470_ITA3_MOUSE	Itga3	Integrin alpha-3 OS=Mus	R.K#EEVGGAVYVFM*NQAGASFPDQPSLLLHGPSR@.S	4.93	1.62	3.05	0.33
Q62470_ITA3_MOUSE	Itga3	Integrin alpha-3 OS=Mus	K.LGLPGLATFGYSLSGK#.M	16.48	4.79	3.44	0.29
Q62470_ITA3_MOUSE	Itga3	Integrin alpha-3 OS=Mus	R.LQSFFGGTVM*GEAAM*K#.T	7.47	2.26	3.30	0.30
Q62470_ITA3_MOUSE	Itga3	Integrin alpha-3 OS=Mus	R.VDGWATLFLR@.T	12.98	3.21	4.04	0.25
Q62470_ITA3_MOUSE	Itga3	Integrin alpha-3 OS=Mus	R.YLLLAGAPR@.D	21.65	6.90	3.14	0.32
P11688_ITA5_MOUSE	Itga5	Integrin alpha-5 OS=Mus	R.DGVSVLVGAPK#.A	10.63	6.46	1.65	0.61
P11688_ITA5_MOUSE	Itga5	Integrin alpha-5 OS=Mus	K.SLQWFGATVR@.A	11.45	6.52	1.75	0.57
P11688_ITA5_MOUSE	Itga5	Integrin alpha-5 OS=Mus	R.TPDFFGSALR@.G	16.72	11.54	1.45	0.69
P11688_ITA5_MOUSE	Itga5	Integrin alpha-5 OS=Mus	R.VTAPLEAEYSGLVR@.H	10.78	6.04	1.79	0.56
P11688_ITA5_MOUSE	Itga5	Integrin alpha-5 OS=Mus	R.VYIYLQR@PAGIDPTPTLTLTGQDEFSR@.F	3.27	3.03	1.08	0.93
P43406_ITAV_MOUSE	Itgav	Integrin alpha-V OS=Mus	K.IQSSNSFDNVSPVVSYK#.V	8.37	4.68	1.79	0.56
P43406_ITAV_MOUSE	Itgav	Integrin alpha-V OS=Mus	K.IYIGDDNPLTLTVK#.A	12.71	8.73	1.45	0.69
P43406_ITAV_MOUSE	Itgav	Integrin alpha-V OS=Mus	K.LQEVGQVSVSLQR@.A	5.37	2.54	2.12	0.47
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	R.GEFFNELVGQQR@.I	12.81	6.61	1.94	0.52
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	R.IGFGSFVEK#.T	63.84	30.43	2.10	0.48
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.LR@PEDITQIQPQQLLLK#.L	57.44	30.97	1.85	0.54
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.LSENNIQTIFAVTEEFQPVYK#.E	55.10	31.97	1.72	0.58
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.NVLSLTDR@.G	17.35	11.82	1.47	0.68
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.SAVTTVVNPK#.Y	65.30	31.94	2.04	0.49
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.SLGTDLM*NEM*R@.R	13.82	6.70	2.06	0.48
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.TVM*PYISTTPAK#.L	12.47	15.80	0.79	1.27
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.WDTGENPIYK#.S	12.86	8.66	1.48	0.67
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	R.IGFGSFVEK#.T	18.63	12.75	1.46	0.68
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.LR@PEDITQIQPQQLLLK#.L	18.33	9.73	1.88	0.53
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.LSENNIQTIFAVTEEFQPVYK#.E	14.19	6.79	2.09	0.48
P09055_ITB1_MOUSE	Itgb1	Integrin beta-1 OS=Mus r	K.NVLSLTDRGEFFNELVGQQR.I	18.35	10.17	1.80	0.55
Q9CQ82_CENPR_MOUSE	Itgb3bp	Centromere protein R OS	K.NLSSIQALEGNR@.Q	8.13	4.66	1.75	0.57
Q9Z0R4_ITSN1_MOUSE	Itsn1	Intersectin-1 OS=Mus mu	R.IAEITHLQQQLQESQQM*LGR@.L	6.80	2.85	2.39	0.42
Q9Z0R4_ITSN1_MOUSE	Itsn1	Intersectin-1 OS=Mus mu	K.IPENEVPTPAK#PVTDLTSAPAPK#.L	5.43	2.99	1.82	0.55
Q9Z0R4_ITSN1_MOUSE	Itsn1	Intersectin-1 OS=Mus mu	R.LPEEPSSEDEQQPEK#.K	5.39	1.49	3.62	0.28
Q9Z0R4_ITSN1_MOUSE	Itsn1	Intersectin-1 OS=Mus mu	K.LQEIDVFNNQLK#.E	9.43	20.54	0.46	2.18
Q9Z0R4_ITSN1_MOUSE	Itsn1	Intersectin-1 OS=Mus mu	R.SGSGM*SVISSSSVDQR@.L	7.74	1.66	4.65	0.21
P05627_JUN_MOUSE	Jun	Transcription factor AP-1	K.NVTDEQEGFAEGFVR@.A	9.89	5.21	1.90	0.53
P09450_JUNB_MOUSE	Junb	Transcription factor jun-	K.AENAGLSSAAGLLR@.E	7.54	8.37	0.90	1.11
P09450_JUNB_MOUSE	Junb	Transcription factor jun-	R.GASAFK#EEPQTVPEAR@.S	22.82	21.75	1.05	0.95
P15066_JUND_MOUSE	Jund	Transcription factor jun-	K.DALTLSLAEQGAAGLK#PGSATAPSALR@PDGAPDGLLASPDLGLLK#.L	3.02	3.36	0.90	1.11
P15066_JUND_MOUSE	Jund	Transcription factor jun-	K.SQNTELASTASLLR.E	8.40	10.71	0.79	1.27
P15066_JUND_MOUSE	Jund	Transcription factor jun-	K.VAASEEQEFAEGFVK#.A	10.60	10.69	0.99	1.01
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	K.ALTTSGGPENTLVFR@.S	7.59	4.79	1.58	0.63
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	K.ALTTSGGPENTLVFR@.S	33.54	14.24	2.36	0.42
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	R.AQSLEPYGTGLK#.A	23.49	9.34	2.52	0.40
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	R.DLGIPDGEAALVAK#.V	9.20	4.18	2.20	0.45
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	R.EVEVAASTAAGALAQR.A	22.02	6.86	3.21	0.31
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	R.LDLDFLK#.Y	23.80	9.66	2.46	0.41
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	K.R@K#EDPADPEVNQR@.N	33.03	22.46	1.47	0.68
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	R.RLEDQAAAPSSGGLGSLTPSAAGSTSSLAGVGLLPPTPR.S	3.25	2.42	1.35	0.74
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	K.VAVLETQLK#.K	27.95	12.50	2.24	0.45
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	K.VAYTTVLQEWLR@.L	18.85	9.47	1.99	0.50
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	R.VPAPEVASGPDPEEEIR@.M	5.42	3.66	1.48	0.68
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	K.YLENPNALTER@.E	21.04	8.04	2.62	0.38
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	K.ALTTSGGPENTLVFR@.S	19.54	9.35	2.09	0.48
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	R.DLGIPDGEAALVAK#.V	6.01	3.22	1.86	0.54
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	R.EVEVAASTAAGALAQR@.A	11.20	2.97	3.78	0.26
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	R.LDLDFLK#.Y	16.86	10.02	1.68	0.59
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	K.VAVLETQLK#.K	13.51	6.36	2.13	0.47
Q8BX02_KANK2_MOUSE	Kank2	KN motif and ankyrin rep	K.VAYTTVLQEWLR@.L	11.59	4.89	2.37	0.42
Q8BQR4_KANL2_MOUSE	Kansl2	KAT8 regulatory NSL com	K.TELGSQTPESSR@.S	8.58	3.34	2.57	0.39
Q8BQR4_KANL2_MOUSE	Kansl2	KAT8 regulatory NSL com	K.TELGSQTPESSR@.S	8.13	5.29	1.54	0.65
A2RSY1_KANL3_MOUSE	Kansl3	KAT8 regulatory NSL com	K.TGAAGAEALSLLLK#.R	11.29	2.12	5.32	0.19
A2RSY1_KANL3_MOUSE	Kansl3	KAT8 regulatory NSL com	K.TGAAGAEALSLLLK#.R	15.63	4.21	3.71	0.27
Q99MN1_SYK_MOUSE	Kars	Lysine--tRNA ligase OS=M	K.LIFYDLR@.G	18.07	6.04	2.99	0.33
Q99MN1_SYK_MOUSE	Kars	Lysine--tRNA ligase OS=M	R.YLDLILNDFVR@.Q	109.93	5.01	21.96	0.05
Q8CHK4_KAT5_MOUSE	Kat5	Histone acetyltransferase	R.NQDNEDEWPLAEILSVK#.D	4.58	2.38	1.93	0.52
Q8CHK4_KAT5_MOUSE	Kat5	Histone acetyltransferase	K.TGTPEK#PLSDLGLLSYR@.S	13.73	6.25	2.20	0.46
Q8BZ21_KAT6A_MOUSE	Kat6a	Histone acetyltransferase	R.AFEGLAETGGSTLK#.S	3.27	2.32	1.41	0.71
Q8BZ21_KAT6A_MOUSE	Kat6a	Histone acetyltransferase	R.R@YANPIGR@PK#.N	13.55	1.51	8.95	0.11
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.EPLLENLTSEYDLDLFR@.R	5.37	3.79	1.41	0.71
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.LQGQITEGSNM*IK#.T	29.07	17.09	1.70	0.59
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	K.VGSPER@PLSDLGLISYR@.S	24.69	9.75	2.53	0.39
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.YELDTWYHSPYPEEYAR@.L	5.38	2.64	2.04	0.49
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.EPLLENLTSEYDLDLFR@.R	8.11	3.24	2.50	0.40
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.LQGQITEGSNM*IK#.T	30.56	12.11	2.52	0.40
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.LSQSSQDSSPVR@.N	4.42	2.82	1.57	0.64

Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.NLPSFGTEEPAYSTR@.R	14.26	6.82	2.09	0.48
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.SQQQPTPVTPK#.K	18.49	10.82	1.71	0.59
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	K.VGSPER@PLSDLGLISYR@.S	40.23	18.41	2.18	0.46
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.YELDTWYHSPYPEEYAR@.L	9.08	3.44	2.64	0.38
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.LQGQITEGSNM*IK#.T	9.72	5.29	1.84	0.54
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	R.NLPSFGTEEPAYSTR@.R	5.26	2.65	1.99	0.50
Q5SVQ0_KAT7_MOUSE	Kat7	Histone acetyltransferase	K.VGSPER@PLSDLGLISYR@.S	16.99	12.64	1.34	0.74
Q9WV86_KTNA1_MOUSE	Katna1	Katanin p60 ATPase-cont	K.TTFFNVSSSTLTSK#.Y	4.97	2.96	1.68	0.60
Q9WV86_KTNA1_MOUSE	Katna1	Katanin p60 ATPase-cont	R.WYDIADLVEAK#.K	5.88	3.09	1.90	0.53
D3Z087_D3Z087_MOUSE	Katnal2	Katanin p60 ATPase-cont	R.VSGAQGPR@M*ER@.G	5.24	2.67	1.96	0.51
Q80UY2_KCMF1_MOUSE	Kcmf1	E3 ubiquitin-protein liga	R.DLDESSGVR@.H	17.30	8.44	2.05	0.49
Q80UY2_KCMF1_MOUSE	Kcmf1	E3 ubiquitin-protein liga	R.SAGGQLNSSGPSASQLQQLQM*QLQLER@.Q	6.15	3.36	1.83	0.55
Q922M3_BACD3_MOUSE	Kctd10	BTB/POZ domain-contai	R.EIEELLAEAK#.Y	7.88	7.12	1.11	0.90
Q922M3_BACD3_MOUSE	Kctd10	BTB/POZ domain-contai	R.GPDNALLEATGGAAGR.S	3.41	5.58	0.61	1.64
Q922M3_BACD3_MOUSE	Kctd10	BTB/POZ domain-contai	R.IYEETLNILLYEAQDGR@GPDNALLEATGGAAGR@.S	4.28	3.47	1.24	0.81
Q922M3_BACD3_MOUSE	Kctd10	BTB/POZ domain-contai	R.R@EIEELLAEAK#.Y	15.87	9.83	1.61	0.62
Q922M3_BACD3_MOUSE	Kctd10	BTB/POZ domain-contai	K.YSYTSNSDDNM*LK#.N	11.05	7.32	1.51	0.66
Q99JH8_ERD21_MOUSE	Kdelr1	ER lumen protein-retaini	K.SQVLFAVVFTAR@.Y	7.43	3.11	2.39	0.42
Q99JH8_ERD21_MOUSE	Kdelr1	ER lumen protein-retaini	K.TGEAETITSHYLFALGVYR@.T	58.15	22.08	2.63	0.38
Q9CQM2_ERD22_MOUSE	Kdelr2	ER lumen protein-retaini	R.ALYLVNWIWR@.F	11.37	3.57	3.19	0.31
Q9CQM2_ERD22_MOUSE	Kdelr2	ER lumen protein-retaini	K.TGEAETITTHYLFFLGLYR@.A	5.82	4.09	1.42	0.70
Q8R1L4_ERD23_MOUSE	Kdelr3	ER lumen protein-retaini	R.LLYLANWIR@.R	24.85	11.11	2.24	0.45
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	R.DITAEFLVK#.S	22.74	9.97	2.28	0.44
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	K.GIFGSSAVPQPK#.E	13.08	9.57	1.37	0.73
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	R.HGLINFGIYK#.R	15.80	4.52	3.49	0.29
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	K.HWDQDDDFEFTGSHLTVR@.N	13.69	7.37	1.86	0.54
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	K.IQLTFEATLQQLEAPYNSDTVLVHR@.V	7.40	3.54	2.09	0.48
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	R.QATPGVPAQQSPSM*.-	10.16	10.16	1.00	1.00
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	R.STSQTFIYK#.C	7.48	1.89	3.96	0.25
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	K.VFLFIR@.N	19.55	10.34	1.89	0.53
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	K.VIIIGSGVSGLAAAR@.Q	37.36	15.58	2.40	0.42
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	K.GIFGSSAVPQPK#.E	6.77	3.28	2.06	0.48
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	K.HWDQDDDFEFTGSHLTVR@.N	4.28	1.50	2.85	0.35
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	K.QQPPAVQFVPPLPEWK#.T	2.87	2.11	1.36	0.74
Q6ZQ88_KDM1A_MOUSE	Kdm1a	Lysine-specific histone de	K.VIIIGSGVSGLAAAR@.Q	17.42	5.68	3.07	0.33
B9EKS2_B9EKS2_MOUSE	Kdm3b	Jumonji domain contain	K.LGLGSVVPVEYLVDR@.E	26.09	7.05	3.70	0.27
B9EKS2_B9EKS2_MOUSE	Kdm3b	Jumonji domain contain	R.VPVAQWPALTFTPLVDK#.L	4.02	2.43	1.65	0.60
B9EKS2_B9EKS2_MOUSE	Kdm3b	Jumonji domain contain	R.ISDTGLASGTGPEK#.Q	9.97	33.36	0.30	3.35
B9EKS2_B9EKS2_MOUSE	Kdm3b	Jumonji domain contain	R.SETEEM*GDEEVFSWLK#.C	4.34	1.46	2.97	0.34
Q3UXZ9_KDM5A_MOUSE	Kdm5a	Lysine-specific demethyl	R.AQEAM*M*DETPDSSK#.L	2.34	1.65	1.41	0.71
Q3UXZ9_KDM5A_MOUSE	Kdm5a	Lysine-specific demethyl	R.LDALPQVESQVAAAR@.A	6.02	7.55	0.80	1.25
Q3UXZ9_KDM5A_MOUSE	Kdm5a	Lysine-specific demethyl	K.NIPAFLPNVLSLK#.E	13.50	7.47	1.81	0.55
Q3UXZ9_KDM5A_MOUSE	Kdm5a	Lysine-specific demethyl	R.QALATDELSSALAK#.L	6.51	6.27	1.04	0.96
Q3UXZ9_KDM5A_MOUSE	Kdm5a	Lysine-specific demethyl	R.SLEPPVLELSPGAK#.A	6.61	5.22	1.27	0.79
Q9Z2X8_KEAP1_MOUSE	Keap1	Kelch-like ECH-associate	R.LLYAVGGFDGTNR@.L	8.82	2.51	3.52	0.28
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.FNFVGK#.I	84.69	34.86	2.43	0.41
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.GESKKDDEENYLDLFSHK.N	53.75	27.11	1.98	0.50
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.ILGPQGNTIK#.R	112.21	52.31	2.15	0.47
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	R.DK#AK#EEELR@.K	9.97	6.57	1.52	0.66
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.DPSGAHPSVR@.L	46.83	26.24	1.78	0.56
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.DSLDPSFTHAMQLLSVEIEK#.I	68.46	31.23	2.19	0.46
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.FNFVGK#.I	369.86	132.56	2.79	0.36
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.GESKKDDEENYLDLFSHK.N	289.49	107.09	2.70	0.37
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.ILGPQGNTIK#.R	872.73	373.05	2.34	0.43
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.ILGPQGNTIKR.L	46.04	17.21	2.68	0.37
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.K#DDEENYLDLFSHK#.N	385.92	149.27	2.59	0.39
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.R@LQEETGAK#.I	59.84	25.04	2.39	0.42
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.YLPELM*AEKDSLDPSFTHAM*QLLSVEIEK.I	19.82	6.23	3.18	0.31
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.YLPELMAEK#DSLDPSFTHAM*QLLSVEIEK#.I	3.46	2.45	1.41	0.71
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.DPSGAHPSVR@.L	27.20	11.02	2.47	0.41
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.DSLDPSFTHAMQLLSVEIEK#.I	52.01	10.02	5.19	0.19
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.FNFVGK#.I	152.51	52.13	2.93	0.34
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.GESK#K#DDEENYLDLFSHK#.N	97.65	29.04	3.36	0.30
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.ILGPQGNTIK#.R	282.00	77.20	3.65	0.27
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.K#DDEENYLDLFSHK#.N	189.87	52.89	3.59	0.28
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.RLQEETGAK.I	31.23	10.58	2.95	0.34
Q60749_KHDR1_MOUSE	Khdrbs1	KH domain-containing,	K.YLPELMAEK#DSLDPSFTHAM*QLLSVEIEK#.I	10.01	4.36	2.30	0.44
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	K.AINQQTGAFVEISR.Q	8.22	7.50	1.10	0.91
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	R.IINDLLQSLR.S	15.13	9.63	1.57	0.64
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	R.VGGGIDVPVPR@.H	11.49	9.17	1.25	0.80
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	K.AINQQTGAFVEISR.Q	19.38	10.49	1.85	0.54
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	K.DAFADAVQR@.A	15.43	8.01	1.92	0.52
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	R.HSVGVVIGR.S	35.55	25.00	1.42	0.70
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	R.IINDLLQSLR@.S	38.59	21.35	1.81	0.55
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	R.SVSLTGAPESVQK#.A	28.67	12.19	2.35	0.43
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	R.VGGGIDVPVPR@.H	29.76	22.72	1.31	0.76
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	K.VQISPDSGGLPER@.S	16.53	7.36	2.25	0.45
Q3U0V1_FUBP2_MOUSE	Khsrp	Far upstream element-bi	R.IINDLLQSLR@.S	7.78	4.35	1.79	0.56
Q8BKS9_K0020_MOUSE	Kiaa0020	Pumilio domain-contain	R.DPAHTVPELIELLQK#.G	12.96	6.54	1.98	0.50
Q8BKS9_K0020_MOUSE	Kiaa0020	Pumilio domain-contain	R.SELIEAIR@.E	17.45	7.97	2.19	0.46
Q8BKS9_K0020_MOUSE	Kiaa0020	Pumilio domain-contain	R.DPAHTVPELIELLQK#.G	16.65	4.48	3.71	0.27
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	R.INQANSPDLLSVSQYYSGELVSYVR@.K	9.21	1.64	5.61	0.18
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	K.LASALDLPLLR@.I	27.39	8.70	3.15	0.32
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	R.SFEYIQDYVSIYGLK#.I	5.09	2.36	2.16	0.46
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	K.TALNNTLDLANVK#.E	9.69	4.00	2.42	0.41
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	K.EGYLR@EEVLLDNIPR@.L	20.35	3.33	6.12	0.16
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	K.FAPVDESITFIGR@.L	26.71	13.27	2.01	0.50
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	K.GPEFWESK#.L	10.12	3.58	2.83	0.35
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	K.LASALDLPLLR@.I	29.66	10.62	2.79	0.36
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	K.LEAK#PELQDLDEEFR@ENNIEIVTR@.F	12.74	4.01	3.17	0.32
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	R.SFEYIQDYVSIYGLK#.I	7.99	2.47	3.23	0.31
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	K.TALNNTLDLANVK#.E	21.14	6.64	3.18	0.31
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	K.TTLVGIIK#.V	12.03	4.67	2.58	0.39
Q8C2E7_STRUM_MOUSE	Kiaa0196	WASH complex subunit s	R.VPINETFISM*VIGR@.L	10.53	1.67	6.31	0.16
Q810A5_K895L_MOUSE	Kiaa0895l	Uncharacterized protein	R.QYWLEGM*LR@.H	17.17	3.46	4.96	0.20
Q3UMB9_WASH7_MOUSE	Kiaa1033	WASH complex subunit	R.FLEEYTSQLR@.R	6.37	3.91	1.63	0.61
Q3UMB9_WASH7_MOUSE	Kiaa1033	WASH complex subunit	R.AVFPIYLDDVYENAVDAAR@.L	13.06	4.34	3.01	0.33
Q3UMB9_WASH7_MOUSE	Kiaa1033	WASH complex subunit	K.LGAAFTDDGFAM*GVAYTLK#.L	7.08	2.45	2.89	0.35
Q3UMB9_WASH7_MOUSE	Kiaa1033	WASH complex subunit	K.QQNVQSTSQDEK#.L	2.26	1.47	1.54	0.65
Q3UMB9_WASH7_MOUSE	Kiaa1033	WASH complex subunit	K.TFK#DEELFPLQVVM*K#.K	8.52	3.76	2.27	0.44
A2AIV2_VIR_MOUSE	Kiaa1429	Protein virilizer homolog	K.ALDSVISM*TEGM*EAFLR@.S	4.11	2.76	1.49	0.67
A2AIV2_VIR_MOUSE	Kiaa1429	Protein virilizer homolog	K.EESPESLFLELEK#.L	11.13	9.55	1.17	0.86
A2AIV2_VIR_MOUSE	Kiaa1429	Protein virilizer homolog	R.LLELILLDQTVR@.V	8.83	2.74	3.22	0.31

A2AIV2_VIR_MOUSE	Kiaa1429	Protein virilizer homolog	K.LTELLDLYQEDR@.G	10.14	4.46	2.27	0.44
A2AIV2_VIR_MOUSE	Kiaa1429	Protein virilizer homolog	K.LVLEHSK#DDDSLESLLDNVIGLK#.Q	14.22	3.84	3.70	0.27
A2AIV2_VIR_MOUSE	Kiaa1429	Protein virilizer homolog	K.TSAVPNHSEPDQDTDAVLER@.A	13.24	3.84	3.45	0.29
A2AIV2_VIR_MOUSE	Kiaa1429	Protein virilizer homolog	K.VNTDGLVLR@.G	9.05	2.72	3.33	0.30
A2A7S8_K1522_MOUSE	Kiaa1522	Uncharacterized protein	K.SYM*TESSTAEDALSVR@.S	4.16	3.64	1.14	0.88
Q5DTW7_K1551_MOUSE	Kiaa1551	Uncharacterized protein	K.TSNVSGDSTDQIK#.I	3.13	1.40	2.23	0.45
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.AIDEHNAEAQESFGK#.N	25.84	11.82	2.19	0.46
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.EEYVSSALER@.T	15.16	5.85	2.59	0.39
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.ENTVSSLVESQK#.L	15.80	3.41	4.64	0.22
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.EQLLDQLQK#.K	15.18	10.86	1.40	0.72
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.EYTEEIER@.L	17.56	9.52	1.84	0.54
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.GLEEITVHNK#DEVYQILEK#.G	22.03	8.22	2.68	0.37
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.IAVLEEELSK#.A	26.81	17.68	1.52	0.66
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.ILAESDGLLQELR@.H	22.03	12.30	1.79	0.56
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.ILQDSLGGR@.T	33.86	13.64	2.48	0.40
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.K#ILAESDGLLQELR@.H	15.17	7.97	1.90	0.53
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.K#YENIQK#PLNSIQENTELR@.S	4.91	1.70	2.88	0.35
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.LNLVDLAGSENIGR@.S	28.10	11.65	2.41	0.41
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.NLNSLFNNM*EELIK#.D	10.26	7.63	1.35	0.74
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.SPNEVYTWEEDPLAGIIPR@.T	10.29	3.87	2.66	0.38
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.SPNEVYTWEEDPLAGIIPR.T	7.51	4.99	1.50	0.67
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.TIVAPSVVSILNINK#.Q	17.13	8.52	2.01	0.50
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.TTAATLM*NAYSSR@.S	9.78	20.10	0.49	2.06
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.VITALVER@.T	41.28	19.07	2.16	0.46
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.YLYPTTLVR@.T	19.46	8.83	2.20	0.45
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.AIDEHNAEAQESFGK#.N	16.29	4.18	3.90	0.26
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.IAVLEEELSK#.A	18.49	3.97	4.66	0.21
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.ILAESDGLLQELR@.H	12.70	3.25	3.91	0.26
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.ILQDSLGGR@.T	18.12	1.89	9.58	0.10
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	K.LNLVDLAGSENIGR@.S	20.44	5.07	4.03	0.25
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.SPNEVYTWEEDPLAGIIPR@.T	5.74	2.57	2.23	0.45
Q6P9P6_KIF11_MOUSE	Kif11	Kinesin-like protein KIF1	R.SPNEVYTWEEDPLAGIIPR@.T	7.83	2.70	2.90	0.34
E9Q4K7_E9Q4K7_MOUSE	Kif13b	Kinesin-like protein OS=	R.APLLSEPASAVPTSPFR@.I	8.01	4.01	2.00	0.50
E9Q4K7_E9Q4K7_MOUSE	Kif13b	Kinesin-like protein OS=	R.EATLNNSLM*R@.L	6.41	1.46	4.38	0.23
E9Q4K7_E9Q4K7_MOUSE	Kif13b	Kinesin-like protein OS=	R.GSLLSEPAIQVR@.R	14.66	1.12	13.13	0.08
E9Q4K7_E9Q4K7_MOUSE	Kif13b	Kinesin-like protein OS=	K.HIVNHAVVNEDPNAR@.I	9.27	1.39	6.68	0.15
E9Q4K7_E9Q4K7_MOUSE	Kif13b	Kinesin-like protein OS=	R.ILVQPTFSDTWATR@.T	5.43	1.87	2.90	0.34
E9Q4K7_E9Q4K7_MOUSE	Kif13b	Kinesin-like protein OS=	R.SVLAVENLLTLDR@.L	18.38	4.81	3.82	0.26
E9Q4K7_E9Q4K7_MOUSE	Kif13b	Kinesin-like protein OS=	R.TVAATNM*NEESSR@.S	7.34	2.91	2.52	0.40
E9Q4K7_E9Q4K7_MOUSE	Kif13b	Kinesin-like protein OS=	K.VILNPVNTNLSK#.G	15.92	3.24	4.91	0.20
L0N7N1_KIF14_MOUSE	Kif14	Kinesin-like protein KIF1	K.SLLDSGLETAQDLR@.Q	6.14	4.14	1.49	0.67
L0N7N1_KIF14_MOUSE	Kif14	Kinesin-like protein KIF1	K.TIADSLINNLLR@.L	8.40	3.70	2.27	0.44
Q6P9L6_KIF15_MOUSE	Kif15	Kinesin-like protein KIF1	K.LLETQEQEIEDGR@.A	4.49	2.10	2.14	0.47
Q6P9L6_KIF15_MOUSE	Kif15	Kinesin-like protein KIF1	K.LLETQEQEIEDGR@.A	7.16	2.27	3.15	0.32
Q6P9L6_KIF15_MOUSE	Kif15	Kinesin-like protein KIF1	K.QLEFLAEENGKLVGHQNLHQK.I	1.80	8.81	0.20	4.88
P97329_KI20A_MOUSE	Kif20a	Kinesin-like protein KIF2	R.LAASASTQQFQEVK#.A	12.77	6.38	2.00	0.50
P97329_KI20A_MOUSE	Kif20a	Kinesin-like protein KIF2	R.DEK#IEELETLLQEAK#.Q	5.77	3.05	1.89	0.53
P97329_KI20A_MOUSE	Kif20a	Kinesin-like protein KIF2	K.ESLTTFYQEQIQER@.D	4.68	2.49	1.88	0.53
P97329_KI20A_MOUSE	Kif20a	Kinesin-like protein KIF2	R.LAASASTQQFQEVK#.A	9.20	3.18	2.90	0.35
P97329_KI20A_MOUSE	Kif20a	Kinesin-like protein KIF2	K.LSLLIGGLQEEELSTSVK#.K	3.91	1.39	2.82	0.35
P97329_KI20A_MOUSE	Kif20a	Kinesin-like protein KIF2	R.VFQGFFTGR@.G	10.34	6.06	1.71	0.59
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	R.FPK#PELEIQFTPLQPNK#.M	5.64	1.93	2.92	0.34
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	K.IDLLNLQDLSSGAK#.G	4.97	1.37	3.62	0.28
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	R.LLTIGENELR@.N	5.53	3.87	1.43	0.70
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	R.ADVEQIQASYNSAVAELQTQK#.A	12.39	7.18	1.73	0.58
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	K.IDLLNLQDLSSGAK#.G	18.30	3.91	4.68	0.21
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	R.LLTIGENELR@.N	16.96	4.13	4.10	0.24
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	R.SIESNVSQIK#.Q	7.65	1.95	3.92	0.25
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	R.TLNVLFDSLQER@.L	9.33	1.69	5.51	0.18
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	R.VQVQLVAER@.E	5.98	2.24	2.66	0.38
Q80WE4_KI20B_MOUSE	Kif20b	Kinesin-like protein KIF2	R.VYVPDTLSSSQEK#.S	9.72	2.23	4.36	0.23
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	R.EAGNINQSLM*TLR@.T	6.73	3.44	1.96	0.51
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	K.LLDINDEETLPK#.L	10.82	5.22	2.07	0.48
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	K.LVQAPLDADGDNVLQEK#.E	7.00	3.59	1.95	0.51
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	R.NLQQELESQNQK#.L	6.26	1.43	4.38	0.23
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	K.AEDYEESLQVM*R@.F	5.83	1.99	2.92	0.34
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	R.EAGNINQSLM*TLR@.T	6.77	1.71	3.97	0.25
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	K.ELFDVVANPLVDDLIHGK#.N	23.67	4.76	4.97	0.20
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	K.LLDINDEETLPK#.L	14.09	5.95	2.37	0.42
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	K.LVQAPLDADGDNVLQEK#.E	8.96	2.69	3.33	0.30
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	R.NLQQELESQNQK#.L	4.20	2.41	1.74	0.57
E9Q5G3_KIF23_MOUSE	Kif23	Kinesin-like protein KIF2	R.VAATQLEM*QNK#.L	6.18	1.56	3.95	0.25
P28740_KIF2A_MOUSE	Kif2a	Kinesin-like protein KIF2	K.FSLIDLAGNER@.G	10.22	5.71	1.79	0.56
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.EK#EELVLELQTAK#.K	45.64	3.23	14.11	0.07
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.GLSEAAGQTAQM*LER@.I	7.17	6.17	1.16	0.86
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.GYNATVLAYGQTGSGK#.T	10.18	4.09	2.49	0.40
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.HQNQDNSDAIELNQDSENSFK#.L	4.07	2.16	1.89	0.53
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.ILAQDVAQLK#.E	16.38	8.06	2.03	0.49
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.K#M*TQNDNQLQPIQFQYQDNIK#.N	5.12	3.57	1.44	0.70
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.LQELEGQIADLK#.K	15.93	3.59	4.43	0.23
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.LTLLQVASK#.Q	9.81	4.40	2.23	0.45
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.NLESEVLSLQR@.E	17.17	13.61	1.26	0.79
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.TVASTAM*NSQSSR@.S	12.22	5.46	2.24	0.45
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.TVASTAMNSQSSR@.S	2.79	54.50	0.05	19.55
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.TYSM*GGAYTAEQEHDSAIGVIPR@.V	9.81	3.46	2.84	0.35
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.VIQLLFK#.E	20.59	5.31	3.88	0.26
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.VLYLLSQLQQSQM*TEK#.Q	10.46	2.62	3.99	0.25
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.WESIATILEAK#.C	9.83	3.05	3.22	0.31
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.YLVGELVSSK#.I	20.24	7.28	2.78	0.36
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.GLSEAAGQTAQM*LER@.I	5.04	2.31	2.18	0.46
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.GYNATVLAYGQTGSGK#.T	5.31	1.20	4.44	0.23
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	K.ILAQDVAQLK#.E	10.43	5.31	1.97	0.51
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.TVASTAM*NSQSSR@.S	9.68	2.55	3.80	0.26
P33174_KIF4_MOUSE	Kif4	Chromosome-associated	R.VIQLLFK#.E	14.08	4.11	3.42	0.29
Q61768_KINH_MOUSE	Kif5b	Kinesin-1 heavy chain OS	K.ISFLENNLEQLTK#.V	22.50	6.35	3.54	0.28
Q61768_KINH_MOUSE	Kif5b	Kinesin-1 heavy chain OS	K.LITDLQDQNQK#.M	13.61	5.23	2.60	0.38
Q61768_KINH_MOUSE	Kif5b	Kinesin-1 heavy chain OS	K.LYLVDLAGSEK#.V	13.99	6.54	2.14	0.47
Q61768_KINH_MOUSE	Kif5b	Kinesin-1 heavy chain OS	K.QLDDK#DEEINQQSQLVEK#.L	6.53	9.93	0.66	1.52
Q61768_KINH_MOUSE	Kif5b	Kinesin-1 heavy chain OS	K.SAEVDSDDTGGSAAQK#.Q	6.14	2.75	2.23	0.45
Q61768_KINH_MOUSE	Kif5b	Kinesin-1 heavy chain OS	K.SLTEYLQNVEQK#.K	13.31	4.47	2.98	0.34
Q8CD76_Q8CD76_MOUSE	Klc1	Kinesin light chain 1 OS=	K.DAANLLNDALAIR@.E	15.86	8.71	1.82	0.55
Q8CD76_Q8CD76_MOUSE	Klc1	Kinesin light chain 1 OS=	K.DGSAFGEYGGWYK#.A	7.67	2.05	3.74	0.27
Q8CD76_Q8CD76_MOUSE	Klc1	Kinesin light chain 1 OS=	R.LGPDDPNVAK#.T	13.39	4.61	2.90	0.34

Q8CD76_Q8CD76_MOUSE	Klc1	Kinesin light chain 1 OS=	K.LTQDEIISK#.T	19.29	6.56	2.94	0.34
Q8CD76_Q8CD76_MOUSE	Klc1	Kinesin light chain 1 OS=	R.VAEVLNDPESM*EK#.R	6.82	5.42	1.26	0.79
Q8CD76_Q8CD76_MOUSE	Klc1	Kinesin light chain 1 OS=	K.YEEVEYYYQR@.A	3.56	1.64	2.17	0.46
Q8CD76_Q8CD76_MOUSE	Klc1	Kinesin light chain 1 OS=	K.YK#DAANLLNDALAIR@.E	14.64	5.13	2.85	0.35
Q91W40_KLC3_MOUSE	Klc3	Kinesin light chain 3 OS=	R.ALSIYEALGGPQDPNVAK#.T	7.50	3.99	1.88	0.53
Q91W40_KLC3_MOUSE	Klc3	Kinesin light chain 3 OS=	R.EQTLGPEHPAVAATLNNLAVLYGK#.R	11.38	4.94	2.30	0.43
Q91W40_KLC3_MOUSE	Klc3	Kinesin light chain 3 OS=	R.TQLSQLSTR@.H	8.82	25.31	0.35	2.87
Q9DBS5_KLC4_MOUSE	Klc4	Kinesin light chain 4 OS=	R.DHPAVAATLNNLAVLYGK#.R	17.38	10.68	1.63	0.61
Q9DBS5_KLC4_MOUSE	Klc4	Kinesin light chain 4 OS=	R.GQGAAAAQQGGYEIPAR@.L	8.54	2.13	4.00	0.25
P55200_KMT2A_MOUSE	Kmt2a	Histone-lysine N-methylt	R.IFESVTLPSNR@.T	5.02	3.33	1.51	0.66
P55200_KMT2A_MOUSE	Kmt2a	Histone-lysine N-methylt	K.AQGQESDSSETSVR@.G	5.43	2.88	1.88	0.53
P55200_KMT2A_MOUSE	Kmt2a	Histone-lysine N-methylt	K.IIQAAINSDGGQPEIK#.K	8.54	3.18	2.68	0.37
P55200_KMT2A_MOUSE	Kmt2a	Histone-lysine N-methylt	K.SEEGGAPAPAPAPEPK#.Q	10.73	8.86	1.21	0.83
P55200_KMT2A_MOUSE	Kmt2a	Histone-lysine N-methylt	R.SSVSSVPSLGTATDPEASAK#.A	7.41	3.06	2.42	0.41
P55200_KMT2A_MOUSE	Kmt2a	Histone-lysine N-methylt	R.VFVDFEGISLR@.R	17.49	8.13	2.15	0.46
O08550_KMT2B_MOUSE	Kmt2b	Histone-lysine N-methylt	R.NIDAGEMVIEYSGIVIR@.S	4.27	4.56	0.94	1.07
Q6PDK2_KMT2D_MOUSE	Kmt2d	Histone-lysine N-methylt	K.AGPLAHTPLGAGGFPAALPSGPAGELHAK#.V	7.29	2.57	2.83	0.35
Q6PDK2_KMT2D_MOUSE	Kmt2d	Histone-lysine N-methylt	K.AYQSTFTGETNTPYSK#.Q	5.17	1.82	2.84	0.35
Q6PDK2_KMT2D_MOUSE	Kmt2d	Histone-lysine N-methylt	K.SQLDILSLLK#.Q	26.11	5.05	5.17	0.19
Q6PDK2_KMT2D_MOUSE	Kmt2d	Histone-lysine N-methylt	K.VIEQGLEDLVFTDASPQAVWNR@.I	8.60	2.76	3.11	0.32
Q9Z2Q2_KNOP1_MOUSE	Knop1	Lysine-rich nucleolar pro	K.SEALEFVPIDSPK#.A	5.49	6.27	0.88	1.14
Q9Z2Q2_KNOP1_MOUSE	Knop1	Lysine-rich nucleolar pro	K.SEALEFVPIDSPK#.A	11.94	8.19	1.46	0.69
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.AIGNIVTGTDEQTQK#.V	37.20	24.59	1.51	0.66
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	K.EATWTM*SNITAGR@.Q	10.58	7.13	1.48	0.67
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	K.GINSNNLESQLQATQAAR@.K	8.97	5.71	1.57	0.64
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	K.LLGATELPIVTPALR@.A	49.28	28.85	1.71	0.59
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.NK#NPAPPLDAVEQILPTLVR@.L	32.84	21.64	1.52	0.66
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.NNQGTVNWSVEDIVK#.G	7.92	5.02	1.58	0.63
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.NVSSFPDDATSPLQENR@.N	8.82	6.16	1.43	0.70
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	K.VIDAGALAVFPSLLTNPK#.T	29.99	16.35	1.83	0.55
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.AIGNIVTGTDEQTQK#.V	18.95	6.21	3.05	0.33
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	K.LLGATELPIVTPALR@.A	22.30	14.56	1.53	0.65
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.NK#NPAPPLDAVEQILPTLVR@.L	14.29	6.56	2.18	0.46
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.NVSSFPDDATSPLQENR@.N	4.87	2.26	2.15	0.46
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	K.VIDAGALAVFPSLLTNPK#.T	14.23	6.79	2.10	0.48
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.AIGNIVTGTDEQTQK#.V	20.05	7.17	2.80	0.36
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	K.GINSNNLESQLQATQAAR@.K	5.63	0.00	#DIV/0!	0.00
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	K.LLGATELPIVTPALR@.A	32.99	11.88	2.78	0.36
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.NK#NPAPPLDAVEQILPTLVR@.L	25.71	7.71	3.34	0.30
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	R.NVSSFPDDATSPLQENR@.N	3.84	1.61	2.39	0.42
P52293_IMA1_MOUSE	Kpna2	Importin subunit alpha-1	K.VIDAGALAVFPSLLTNPK#.T	10.07	2.87	3.51	0.29
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	K.DSQVVQVVLDGLK#.N	46.18	21.34	2.16	0.46
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	K.DSQVVQVVLDGLK#.N	4.04	2.94	1.38	0.73
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	R.HR@NEVTVELR@.K	55.70	21.86	2.55	0.39
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	R.NVPQEESLEDSDVDADFK#.A	22.43	11.93	1.88	0.53
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	R.NVPQEESLEDSDVDADFK#.A	8.08	4.44	1.82	0.55
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	K.SGILPILVK#.C	80.58	45.30	1.78	0.56
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	R.HR@NEVTVELR@.K	52.06	17.12	3.04	0.33
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	R.NVPQEESLEDSDVDADFK#.A	11.63	4.97	2.34	0.43
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	K.SGILPILVK#.C	71.16	29.42	2.42	0.41
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	K.DSQVVQVVLDGLK#.N	36.22	14.10	2.57	0.39
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	R.NVPQEESLEDSDVDADFK#.A	10.84	4.65	2.33	0.43
O35344_IMA4_MOUSE	Kpna3	Importin subunit alpha-4	K.SGILPILVK#.C	28.99	13.14	2.21	0.45
O35343_IMA3_MOUSE	Kpna4	Importin subunit alpha-3	K.EAAWAISNLTISGR@.K	62.88	24.32	2.59	0.39
O35343_IMA3_MOUSE	Kpna4	Importin subunit alpha-3	R.K#LLSSDR@NPPIDDLIK#.S	51.22	23.57	2.17	0.46
O35343_IMA3_MOUSE	Kpna4	Importin subunit alpha-3	K.LLSSDR@NPPIDDLIK#.S	92.16	37.72	2.44	0.41
O35343_IMA3_MOUSE	Kpna4	Importin subunit alpha-3	R.NEVVVELR@.K	22.99	10.67	2.15	0.46
O35343_IMA3_MOUSE	Kpna4	Importin subunit alpha-3	R.NPPIDDLIK#.S	32.46	18.33	1.77	0.56
O35343_IMA3_MOUSE	Kpna4	Importin subunit alpha-3	K.IEQLQNHENEDIYK#.L	40.49	14.02	2.89	0.35
O35343_IMA3_MOUSE	Kpna4	Importin subunit alpha-3	R.K#LLSSDR@NPPIDDLIK#.S	19.82	9.47	2.09	0.48
O35343_IMA3_MOUSE	Kpna4	Importin subunit alpha-3	R.NPPIDDLIK#.S	23.81	12.15	1.96	0.51
O35343_IMA3_MOUSE	Kpna4	Importin subunit alpha-3	R.VQNTSLEAIVQNASSDNQGIQLSAVQAAR@.K	18.66	5.91	3.16	0.32
O35345_IMA7_MOUSE	Kpna6	Importin subunit alpha-7	K.EAAWAITNATSGGTPEQIR@.Y	8.26	4.89	1.69	0.59
O35345_IMA7_MOUSE	Kpna6	Importin subunit alpha-7	K.EPSPPIDEVINTPGVVDR@.F	10.08	7.17	1.41	0.71
O35345_IMA7_MOUSE	Kpna6	Importin subunit alpha-7	R.FVEFLK#.R	31.04	13.07	2.38	0.42
O35345_IMA7_MOUSE	Kpna6	Importin subunit alpha-7	K.IVQVALNGLENILR@.L	22.67	9.72	2.33	0.43
O35345_IMA7_MOUSE	Kpna6	Importin subunit alpha-7	K.LLSK#EPSPPIDEVINTPGVVDR@.F	5.26	5.91	0.89	1.12
O35345_IMA7_MOUSE	Kpna6	Importin subunit alpha-7	R.FVEFLK#.R	21.05	13.67	1.54	0.65
O35345_IMA7_MOUSE	Kpna6	Importin subunit alpha-7	K.IVQVALNGLENILR@.L	15.23	8.16	1.87	0.54
O35345_IMA7_MOUSE	Kpna6	Importin subunit alpha-7	K.IVQVALNGLENILR@.L	9.82	3.39	2.89	0.35
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.AAVENLPTFLVELSR@.V	25.49	9.26	2.75	0.36
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	K.LAATNALLNSLEFTK#.A	39.35	18.89	2.08	0.48
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	K.SNEILTAIIQGM*R@.K	19.40	1.26	15.44	0.06
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.SSAYESLM*EIVK#.N	7.25	2.89	2.51	0.40
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.VAALQNLVK#.I	16.81	6.94	2.42	0.41
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.VLANPGNSQVAR@.V	31.17	9.58	3.25	0.31
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.AAVENLPTFLVELSR@.V	41.21	13.44	3.07	0.33
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	K.GDQENVHPDVM*LVQPR@.V	9.53	6.02	1.58	0.63
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	K.LAATNALLNSLEFTK#.A	59.30	18.73	3.17	0.32
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.LQQVLQM*ESHIQSTSDR@.I	23.02	6.81	3.38	0.30
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.SSAYESLM*EIVK#.N	11.17	3.76	2.97	0.34
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.VAAGLQIK#.N	16.78	5.29	3.17	0.32
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.VAALQNLVK#.I	20.84	8.57	2.43	0.41
P70168_IMB1_MOUSE	Kpnb1	Importin subunit beta-1	R.VLANPGNSQVAR@.V	38.26	10.66	3.59	0.28
Q8BGA5_KRR1_MOUSE	Krr1	KRR1 small subunit proc	R.GLLEESSFATLFPK#.Y	21.35	10.52	2.03	0.49
Q8BGA5_KRR1_MOUSE	Krr1	KRR1 small subunit proc	R.SVSFEQAVR@.I	22.89	9.94	2.30	0.43
Q5RL79_KTAP2_MOUSE	Krtcap2	Keratinocyte-associated	K.ISSTLYQATAPVLTPAK#.I	7.24	5.41	1.34	0.75
Q61595_KTN1_MOUSE	Ktn1	Kinectin OS=Mus muscul	K.AHQLSVTSQVQELQNLLR@.G	6.98	4.00	1.75	0.57
Q61595_KTN1_MOUSE	Ktn1	Kinectin OS=Mus muscul	R.ASK#EESLQIQVQDILEQNEALK#.A	6.18	1.65	3.75	0.27
Q61595_KTN1_MOUSE	Ktn1	Kinectin OS=Mus muscul	R.DAVSNTTNQLESK.Q	6.01	7.27	0.83	1.21
Q61595_KTN1_MOUSE	Ktn1	Kinectin OS=Mus muscul	K.QSDQVSFVSLIEDLK#R@.V	6.98	5.97	1.17	0.85
Q61595_KTN1_MOUSE	Ktn1	Kinectin OS=Mus muscul	R.TVEELLETGLIQVATR@.E	10.19	4.29	2.38	0.42
Q9CXA2_T3HPD_MOUSE	L3hypdh	Trans-L-3-hydroxyproline	R.RLVFEPR.G	152.95	64.85	2.36	0.42
Q61292_LAMB2_MOUSE	Lamb2	Laminin subunit beta-2	K.AAQLDGLEAR@.M	11.85	3.57	3.32	0.30
Q61292_LAMB2_MOUSE	Lamb2	Laminin subunit beta-2	R.LQELEGTYEENER@.A	7.77	4.39	1.77	0.56
Q61292_LAMB2_MOUSE	Lamb2	Laminin subunit beta-2	R.VLDISIPASPEQIQR@.L	11.74	3.43	3.42	0.29
Q61292_LAMB2_MOUSE	Lamb2	Laminin subunit beta-2	R.YSEIEPSTEGEVIYR@.V	9.47	3.51	2.70	0.37
Q61087_LAMB3_MOUSE	Lamb3	Laminin subunit beta-3	K.RMQLQDIM*MDFK#.G	4.48	1.69	2.65	0.38
P11438_LAMP1_MOUSE	Lamp1	Lysosome-associated me	K.ALQATVGNSYK#.C	29.67	12.69	2.34	0.43
P11438_LAMP1_MOUSE	Lamp1	Lysosome-associated me	K.EIYTM*DSTTDIK#.A	38.87	16.32	2.38	0.42
P11438_LAMP1_MOUSE	Lamp1	Lysosome-associated me	K.M*LSLNVFSVQVQAFK#.V	8.13	3.54	2.29	0.44
P17047_LAMP2_MOUSE	Lamp2	Lysosome-associated me	R.AFQINTFNLK#.V	64.75	25.63	2.53	0.40
P17047_LAMP2_MOUSE	Lamp2	Lysosome-associated me	K.TITIAVPDK#.A	13.49	9.51	1.42	0.71

P17047_LAMP2_MOUSE	Lamp2	Lysosome-associated me	K.VPLDVIFK#.C	55.90	32.62	1.71	0.58
P17047_LAMP2_MOUSE	Lamp2	Lysosome-associated me	K.YLDFIFAVK#.N	20.93	7.75	2.70	0.37
P17047_LAMP2_MOUSE	Lamp2	Lysosome-associated me	R.AFQINTFNLK#.V	33.27	10.66	3.12	0.32
P17047_LAMP2_MOUSE	Lamp2	Lysosome-associated me	K.VPLDVIFK#.C	22.00	13.71	1.60	0.62
Q9CQ22_LTOR1_MOUSE	Lamtor1	Ragulator complex prote	R.IAAYAYSALSQIR@.V	5.62	3.07	1.83	0.55
Q9CQ22_LTOR1_MOUSE	Lamtor1	Ragulator complex prote	R.LAVLSSSLTHWK#.K	10.19	3.71	2.74	0.36
Q9CQ22_LTOR1_MOUSE	Lamtor1	Ragulator complex prote	R.TDEQALLSSILAK#.T	26.35	12.60	2.09	0.48
Q9JHS3_LTOR2_MOUSE	Lamtor2	Ragulator complex prote	R.VTAAIASNIWAAYDR@.N	4.17	2.38	1.75	0.57
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.LGIGQSQEM*NTLFR@.F	7.35	12.72	0.58	1.73
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.DFQEETVK#DYEAGQLYGLEK#.F	12.23	3.25	3.76	0.27
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.DFVEAPPPK#.V	14.71	3.21	4.58	0.22
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.FQQVPTDALANK#.L	48.69	17.50	2.78	0.36
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.FSHPTALPQQLPSQQLM*SK#.D	43.34	15.99	2.71	0.37
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.FWAFLK#.Y	28.19	7.16	3.94	0.25
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.FWSFFLR@.D	18.17	4.76	3.82	0.26
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.GLSASLPDLDSESWIEVK#.K	11.80	3.75	3.14	0.32
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.HPVVAGGSGEGR@.K	9.30	3.68	2.53	0.40
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.ILIVTQTPPYM*R@.R	20.10	6.85	2.93	0.34
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.K#FDGTEGPR@.T	13.33	4.44	3.00	0.33
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.K#M*DADGFLPITLIASFHR@.V	10.26	5.66	1.81	0.55
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.LDIFK#DFQEETVK#DYEAGQLYGLEK#.F	16.60	6.58	2.52	0.40
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.LFGAPEPSTIAR@.S	69.23	27.16	2.55	0.39
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.LGIGQSQEM*NTLFR@.F	33.26	9.59	3.47	0.29
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.LQEYLGK#.F	41.46	13.84	3.00	0.33
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.M*DADGFLPITLIASFHR@.V	22.55	12.62	1.79	0.56
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.QIEYYFSVDNLER@.D	19.57	7.60	2.57	0.39
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.VGDFGDAVNWPTPGEIAHK#.S	12.01	6.17	1.95	0.51
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.VVEM*VEEK#.V	34.79	8.42	4.13	0.24
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.YYSYGLEK#.K	17.21	23.82	0.72	1.38
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.FQQVPTDALANK#.L	21.83	6.35	3.44	0.29
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.GLSASLPDLDSESWIEVK#.K	6.13	3.58	1.71	0.58
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.HPVVAGGSGEGR@.K	5.56	4.17	1.33	0.75
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.ILIVTQTPPYM*R@.R	8.85	3.06	2.89	0.35
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.LGIGQSQEM*NTLFR@.F	9.82	4.38	2.24	0.45
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	R.QIEYYFSVDNLER@.D	7.06	3.09	2.29	0.44
Q6ZQ58_LARP1_MOUSE	Larp1	La-related protein 1 OS=	K.VGDFGDAVNWPTPGEIAHK#.S	6.65	1.71	3.88	0.26
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	R.EIPETTPVEEVK#.A	19.33	15.39	1.26	0.80
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	K.LTTNTDLILEVLR.S	32.91	21.17	1.55	0.64
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	K.DLYLISQM*DSDQFVPIWTVANM*EEIKK.L	7.89	5.62	1.40	0.71
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	R.EIPETTPVEEVK#.A	17.71	10.17	1.74	0.57
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	K.FDLLATNFPPLPGSSSR@.V	12.40	5.57	2.23	0.45
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	R.HNPTVTGQQEQTYLPK#.E	21.51	8.67	2.48	0.40
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	K.LTTNTDLILEVLR@.S	44.78	20.74	2.16	0.46
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	R.SSSGSEHSTEGSVSLGDGPLSR@.S	18.58	8.25	2.25	0.44
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	R.VPDELGLENR@.M	37.71	14.20	2.66	0.38
Q8BWW4_LARP4_MOUSE	Larp4	La-related protein 4 OS=	K.LTTNTDLILEVLR@.S	5.30	2.75	1.93	0.52
Q6A0A2_LAR4B_MOUSE	Larp4b	La-related protein 4B OS	K.AIAINTFLPK#.N	10.43	3.71	2.81	0.36
Q6A0A2_LAR4B_MOUSE	Larp4b	La-related protein 4B OS	K.AIAINTFLPK#.N	20.12	8.50	2.37	0.42
Q6A0A2_LAR4B_MOUSE	Larp4b	La-related protein 4B OS	R.GPGLLESPSIFNFTADR@.L	11.41	6.64	1.72	0.58
Q6A0A2_LAR4B_MOUSE	Larp4b	La-related protein 4B OS	R.LSSLIIGSSK#.E	13.09	4.75	2.76	0.36
Q6A0A2_LAR4B_MOUSE	Larp4b	La-related protein 4B OS	K.LSTDVDLIVEVLR@.S	9.09	3.35	2.72	0.37
Q6A0A2_LAR4B_MOUSE	Larp4b	La-related protein 4B OS	R.NLSTDASTNTVPVVGPR@.E	9.17	4.99	1.84	0.54
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	K.AIEFLNNPPEEAPR@.K	21.38	18.07	1.18	0.85
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	K.DGVGQAASEVSK#.E	30.32	17.59	1.72	0.58
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	R.DK#VEASSLPEAR@.A	25.05	13.24	1.89	0.53
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	R.FK#TPEDAQAVM*NAQTEIR@.K	13.81	4.88	2.83	0.35
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	K.GFAFVEFETK#.E	26.29	14.84	1.77	0.56
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	K.HSWNLEVLSGDHEQR@.Y	14.54	5.30	2.74	0.36
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	K.IVSGEPLPGR@.K	19.11	11.96	1.60	0.63
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	K.QVLADIAK#.Q	15.29	7.86	1.95	0.51
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	K.SSSVVELDLEGTR@.I	21.35	11.03	1.94	0.52
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	R.TASEGSEAETPEAPK#.Q	5.92	3.65	1.62	0.62
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	R.TVYVELLPK#.N	24.37	12.97	1.88	0.53
Q05CL8_LARP7_MOUSE	Larp7	La-related protein 7 OS=	K.VSAQGPQFVTGVIVK#.I	19.84	9.88	2.01	0.50
Q8BMJ2_SYLC_MOUSE	Lars	Leucine--tRNA ligase, cyt	K.SLGLSDDDIVK#.F	8.09	16.42	0.49	2.03
Q8BMJ2_SYLC_MOUSE	Lars	Leucine--tRNA ligase, cyt	K.VIASELGSLPELK#.K	9.82	3.02	3.25	0.31
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	K.AM*GQVLPDEEQEK#.L	8.21	3.98	2.06	0.48
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.EALQGSAWQVSSEDVR@.W	7.57	4.30	1.76	0.57
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.FVNLISER@.K	19.02	6.29	3.02	0.33
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.LGNELPLAVASTADLVR.C	19.47	10.52	1.85	0.54
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	K.LIDAAGTLGTDELR@.L	27.15	13.11	2.07	0.48
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.LLYGM*ALVR@.F	11.06	18.82	0.59	1.70
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	K.AIEGSSSSSTGK#.A	9.75	1.48	6.61	0.15
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	K.AM*GQVLPDEEQEK#.L	15.52	5.73	2.71	0.37
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.AWDGQSFK#ENQPESPSAR@.G	8.03	2.69	2.99	0.33
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.EALQGSAWQVSSEDVR@.W	12.56	5.04	2.49	0.40
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.ELLVSYEEEQFK#.V	18.32	7.33	2.50	0.40
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.FVNLISER@.K	35.00	11.81	2.96	0.34
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.LGNELPLAVASTADLVR@.C	39.24	11.76	3.34	0.30
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	K.LIDAAGTLGTDELR@.L	31.18	12.96	2.41	0.42
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.LLYGM*ALVR@.F	14.36	7.57	1.90	0.53
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.LPGQTEDPAELM*LDNYDTM*YLLDQPVIEHR@.L	6.74	8.84	0.76	1.31
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	R.WGTFPLGR@.L	13.68	3.16	4.32	0.23
A2BE28_LAS1L_MOUSE	Las1l	Ribosomal biogenesis pr	K.YLAQEVNIPDWIVELR@.H	15.07	8.33	1.81	0.55
Q61792_LASP1_MOUSE	Lasp1	LIM and SH3 domain pro	K.GFSVVADTPELQR@.I	65.93	27.31	2.41	0.41
Q61792_LASP1_MOUSE	Lasp1	LIM and SH3 domain pro	K.GK#GFSVVADTPELQR@.I	18.60	5.18	3.59	0.28
Q61792_LASP1_MOUSE	Lasp1	LIM and SH3 domain pro	R.LK#QQSELQSQVR@.Y	82.00	28.93	2.83	0.35
Q61792_LASP1_MOUSE	Lasp1	LIM and SH3 domain pro	K.QQSELQSQVR.Y	34.66	19.21	1.80	0.55
Q61792_LASP1_MOUSE	Lasp1	LIM and SH3 domain pro	K.QSFTM*VADTPENLR@.L	27.57	13.20	2.09	0.48
Q61792_LASP1_MOUSE	Lasp1	LIM and SH3 domain pro	K.TQDQISNIK#.Y	68.25	17.52	3.90	0.26
Q61792_LASP1_MOUSE	Lasp1	LIM and SH3 domain pro	K.YHEEFEK#.S	58.03	8.01	7.25	0.14
Q61792_LASP1_MOUSE	Lasp1	LIM and SH3 domain pro	R.YK#EEFEK#.N	27.68	9.18	3.01	0.33
Q5XJE5_LEO1_MOUSE	Leo1	RNA polymerase-associat	R.GLSASYLEPDR@YDEEEEGEESVSLAAIK#.N	7.29	5.21	1.40	0.71
Q5XJE5_LEO1_MOUSE	Leo1	RNA polymerase-associat	K.VNTDLGNDLYFVK#.L	14.42	14.49	1.00	1.00
Q3V1T4_P3H1_MOUSE	Lepre1	Prolyl 3-hydroxylase 1 O	R.SPYNYLQVAYFK#.I	8.13	6.37	1.28	0.78
Q8CG70_P3H3_MOUSE	Leprel2	Prolyl 3-hydroxylase 3 O	R.AYSAGAWAPAVALLR@.E	17.75	3.58	4.95	0.20
Q8CG70_P3H3_MOUSE	Leprel2	Prolyl 3-hydroxylase 3 O	R.FEGLTVLK#.A	11.98	8.97	1.34	0.75
Q8CG70_P3H3_MOUSE	Leprel2	Prolyl 3-hydroxylase 3 O	R.SFPVQDFLLSQLR@.R	6.67	4.45	1.50	0.67
Q8K2B0_SC65_MOUSE	Leprel4	Synaptonemal complex	K.AVAAAYTFLQR@.N	19.69	57.93	0.34	2.94
Q8K2B0_SC65_MOUSE	Leprel4	Synaptonemal complex	K.DSVM*QQNLVYYR@.F	10.76	3.10	3.47	0.29
Q8K2B0_SC65_MOUSE	Leprel4	Synaptonemal complex	K.GDEAEAEPEPELT.-	5.98	5.98	1.00	1.00
Q8K2B0_SC65_MOUSE	Leprel4	Synaptonemal complex	R.GM*LDIGDESLTDLEAQPYEAVFLR@.A	12.04	4.89	2.46	0.41
P16045_LEG1_MOUSE	Lgals1	Galectin-1 OS=Mus musc	R.LNM*EAINYM*AADGDFK#.I	9.62	7.24	1.33	0.75

P16045_LEG1_MOUSE	Lgals1	Galectin-1 OS=Mus musc	K.SFVLNLGK#.D	24.96	23.44	1.06	0.94
Q07797_LG3BP_MOUSE	Lgals3bp	Galectin-3-binding prote	K.SELAVSSELDLLK.A	6.24	8.18	0.76	1.31
Q07797_LG3BP_MOUSE	Lgals3bp	Galectin-3-binding prote	R.YNQLYTYGYGSVAR.Y	3.88	4.68	0.83	1.20
Q07797_LG3BP_MOUSE	Lgals3bp	Galectin-3-binding prote	K.SELAVSSELDLLK.A	8.22	7.49	1.10	0.91
O08573_LEG9_MOUSE	Lgals9	Galectin-9 OS=Mus musc	R.FNENAVVR.N	21.03	20.06	1.05	0.95
O08573_LEG9_MOUSE	Lgals9	Galectin-9 OS=Mus musc	R.NTQINNSWGQEER.S	9.39	7.55	1.24	0.80
P37913_DNLI1_MOUSE	Lig1	DNA ligase 1 OS=Mus mu	K.DK#QPEQATTSNQVASLYR@.K	8.61	5.60	1.54	0.65
P37913_DNLI1_MOUSE	Lig1	DNA ligase 1 OS=Mus mu	K.DTEQIAEFLEQSVK#.D	9.88	4.16	2.37	0.42
P37913_DNLI1_MOUSE	Lig1	DNA ligase 1 OS=Mus mu	R.LGPPQQGLELGVGDGVLLK#.A	10.17	5.72	1.78	0.56
P37913_DNLI1_MOUSE	Lig1	DNA ligase 1 OS=Mus mu	K.TLSSFFTPR@.K	10.74	5.14	2.09	0.48
P37913_DNLI1_MOUSE	Lig1	DNA ligase 1 OS=Mus mu	R.IDGAVAPDHWLDPSIVWEVK#.C	4.05	3.13	1.29	0.77
P37913_DNLI1_MOUSE	Lig1	DNA ligase 1 OS=Mus mu	R.LGPPQQGLELGVGDGVLLK#.A	8.35	2.95	2.83	0.35
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.ELSVEEQIK#R@.N	13.15	4.47	2.94	0.34
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.FGSR@PEAVIQSR@.Y	17.40	8.10	2.15	0.47
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.HEAEK#PETSENTETSGK#.I	15.06	11.77	1.28	0.78
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.IAWPPPAELGGSGSALEEGIK#.V	32.89	17.17	1.92	0.52
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.K#GWSESEQSEEFGGGIATM*ER@.K	25.98	11.70	2.22	0.45
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.K#GWSESEQSEEFGGGIATMER@.K	5.54	3.97	1.40	0.72
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.QSSPASYTNELK#.T	16.58	12.24	1.35	0.74
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.SDNEETLGR@PAQPPNAGESPHSPGVEDAPIAK#.V	48.25	40.59	1.19	0.84
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.SQDVGFWEGEVVR@.E	51.03	20.70	2.46	0.41
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.VGVLAASM*EAK#.A	115.30	65.27	1.77	0.57
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.VGVLAASMEAK#.A	28.95	22.99	1.26	0.79
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.WQGEEVPR.S	30.69	15.76	1.95	0.51
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.YNVPLNR.L	22.11	15.01	1.47	0.68
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.SQDVGFWEGEVVR@.E	5.83	1.94	3.01	0.33
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.EFTTQNQK#.S	43.18	20.99	2.06	0.49
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.ELSVEEQIK#.R	21.62	13.61	1.59	0.63
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.ELSVEEQIKR.N	29.42	14.29	2.06	0.49
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.FGSR@PEAVIQSR@.Y	51.74	27.75	1.86	0.54
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.GNYDEGFGHK#.Q	17.36	14.13	1.23	0.81
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.HEAEK#PETSENTETSGK#.I	96.52	55.95	1.73	0.58
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.HEAEKPETSENTETSGK.I	3.54	2.00	1.77	0.57
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.HEAEK#PETSENTETSGK#IEK#.Y	21.03	43.02	0.49	2.05
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.IAWPPPAELGGSGSALEEGIK#.V	58.66	37.43	1.57	0.64
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.K#GWSESEQSEEFGGGIATM*ER@.K	38.32	22.54	1.70	0.59
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.K#GWSESEQSEEFGGGIATMER@.K	5.16	5.18	1.00	1.00
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.QSSPASYTNELK#.T	94.36	58.86	1.60	0.62
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.SEAQQPM*HPK#PLSPDAR@.T	38.52	20.98	1.84	0.54
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.SQDVGFWEGEVVR@.E	117.35	49.64	2.36	0.42
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.SRPFTVAASFR.T	42.20	24.20	1.74	0.57
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.SSAIVEIFSK#.Y	35.82	20.28	1.77	0.57
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.TSSLPESSPSK#.T	161.61	107.70	1.50	0.67
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.VGVLAASM*EAK#.A	296.69	174.72	1.70	0.59
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.VGVLAASMEAK#.A	40.16	23.05	1.74	0.57
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.WQGEEVPR@.S	74.57	38.98	1.91	0.52
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.HEAEK#PETSENTETSGK#.I	26.99	10.50	2.57	0.39
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.HEAEK#PETSENTETSGK#IEK#.Y	15.84	8.11	1.95	0.51
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.IAWPPPAELGGSGSALEEGIK#.V	13.91	5.75	2.42	0.41
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	R.K#GWSESEQSEEFGGGIATM*ER@.K	7.37	1.30	5.69	0.18
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.QSSPASYTNELK#.T	12.78	5.69	2.25	0.45
Q9ERG0_LIMA1_MOUSE	Lima1	LIM domain and actin-bi	K.SDNEETLGR@PAQPPNAGESPHSPGVEDAPIAK#.V	9.19	4.50	2.04	0.49
Q8BGB5_LIMD2_MOUSE	Limd2	LIM domain-containing p	K.GNYDEGFGR@.K	6.33	3.50	1.81	0.55
Q99JW4_LIMS1_MOUSE	Lims1	LIM and senescent cell ar	K.FPLELK#.K	36.36	20.32	1.79	0.56
Q99JW4_LIMS1_MOUSE	Lims1	LIM and senescent cell ar	K.GGFAPAEK#.I	106.34	49.40	2.15	0.46
Q99JW4_LIMS1_MOUSE	Lims1	LIM and senescent cell ar	K.LSETLGR@.K	140.63	50.76	2.77	0.36
Q99JW4_LIMS1_MOUSE	Lims1	LIM and senescent cell ar	R.VIEGDVVSALNK#.A	79.34	39.67	2.00	0.50
Q99JW4_LIMS1_MOUSE	Lims1	LIM and senescent cell ar	R.VIEGDVVSALNK#.A	13.61	16.47	0.83	1.21
Q99JW4_LIMS1_MOUSE	Lims1	LIM and senescent cell ar	R.VIEGDVVSALNK#.A	7.64	3.14	2.44	0.41
Q99JW4_LIMS1_MOUSE	Lims1	LIM and senescent cell ar	R.VIEGDVVSALNK#.A	8.07	5.22	1.54	0.65
Q8CD94_LIN52_MOUSE	Lin52	Protein lin-52 homolog (	R.GLQNLAYQLGLDESR@.E	4.07	3.18	1.28	0.78
O88952_LIN7C_MOUSE	Lin7c	Protein lin-7 homolog C (	R.EVYEHVYETVDISSSPEVR@.A	12.48	4.75	2.63	0.38
O88952_LIN7C_MOUSE	Lin7c	Protein lin-7 homolog C (	R.VVELPK#TEEGLGFNIM*GGK#.E	5.06	5.28	0.96	1.04
Q8C735_LIN9_MOUSE	Lin9	Protein lin-9 homolog OS	R.GIHDGLFTGQIDAVDTLNATYR@.V	5.30	2.31	2.30	0.44
Q9D0F3_LMAN1_MOUSE	Lman1	Protein ERGIC-53 OS=Mu	R.DIDSLAQR.S	544.67	338.03	1.61	0.62
Q9D0F3_LMAN1_MOUSE	Lman1	Protein ERGIC-53 OS=Mu	K.GHPDLQGQPADDIFESIGDR@.E	15.03	6.47	2.32	0.43
Q9D0F3_LMAN1_MOUSE	Lman1	Protein ERGIC-53 OS=Mu	R.R@GAGTPGQPGQVSQQELDTVVK#.S	10.33	5.27	1.96	0.51
Q9D0F3_LMAN1_MOUSE	Lman1	Protein ERGIC-53 OS=Mu	R.YVSSLTEEISR@.R	27.55	12.80	2.15	0.46
Q9DBH5_LMAN2_MOUSE	Lman2	Vesicular integral-memb	K.DNFHGLAIFLDTYPNDETTER@.V	20.79	9.89	2.10	0.48
Q9DBH5_LMAN2_MOUSE	Lman2	Vesicular integral-memb	K.DNVDDPTGNFR@.N	25.77	6.42	4.02	0.25
Q9DBH5_LMAN2_MOUSE	Lman2	Vesicular integral-memb	K.LFQLTVER@.T	29.55	8.79	3.36	0.30
Q9DBH5_LMAN2_MOUSE	Lman2	Vesicular integral-memb	R.LPTGYYFGASAGTGDLSDNHDIISIK#.L	22.90	13.72	1.67	0.60
Q9DBH5_LMAN2_MOUSE	Lman2	Vesicular integral-memb	R.NR@DHDTFLAVR@.Y	24.84	6.63	3.75	0.27
Q9DBH5_LMAN2_MOUSE	Lman2	Vesicular integral-memb	R.TPEEESIDWTK#.I	17.15	6.22	2.76	0.36
Q9DBH5_LMAN2_MOUSE	Lman2	Vesicular integral-memb	K.DNFHGLAIFLDTYPNDETTER@.V	12.81	6.28	2.04	0.49
Q9DBH5_LMAN2_MOUSE	Lman2	Vesicular integral-memb	K.DNVDDPTGNFR@.N	12.37	4.05	3.06	0.33
Q8VEE1_LMCD1_MOUSE	Lmcd1	LIM and cysteine-rich do	K.GAAPVDSPVVYADR@.A	5.93	2.94	2.02	0.50
Q8VEE1_LMCD1_MOUSE	Lmcd1	LIM and cysteine-rich do	K.SEALGVGEVALPGQGGLPK#.E	5.60	2.62	2.14	0.47
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.LADALQELR.A	15.43	17.67	0.87	1.14
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.M*QQQLDEYQELLDIK.L	3.77	5.04	0.75	1.34
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.NSNLVGAAHEELQQSR.I	2.05	2.64	0.78	1.29
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.SLETENAGLR.L	2.73	5.62	0.48	2.06
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.TALINSTGEEVAM*R.K	6.39	10.43	0.61	1.63
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.SLETENAGLR.L	3.11	13.46	0.23	4.33
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.TALINSTGEEVAM*R.K	2.98	8.24	0.36	2.76
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	K.AAGGAGAQVGGSISSGSSASSVTVTR.S	17.57	15.26	1.15	0.87
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	K.AGQVVTIWASGAGATHSPPTDLVWK.A	20.32	21.63	0.94	1.06
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	K.EAALSTALSEK#.R	52.76	67.53	0.78	1.28
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	K.EGDLLAAQAR@.L	54.48	70.29	0.78	1.29
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.IDSLSAQLSQLQK#.Q	44.80	59.36	0.75	1.33
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.IRIDSLSAQLSQLQK.Q	33.57	43.84	0.77	1.31
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.ITESEEVVSR.E	107.19	143.29	0.75	1.34
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.KLLEGEEER.L	8.41	11.66	0.72	1.39
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.LADALQELR.A	116.96	163.14	0.72	1.39
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.LAVYIDR.V	87.97	110.69	0.79	1.26
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.LK#DLEALLNSK#.E	118.75	149.79	0.79	1.26
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	K.LLEGEEER.L	78.67	109.76	0.72	1.40
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.LQEKEDLQELNDR.L	64.82	93.56	0.69	1.44
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.LQEK#EDLQELNDR@.L	14.52	15.31	0.95	1.05
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	K.LRDLEDSLAR.E	82.49	97.90	0.84	1.19
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.LSPSPTSQR.S	38.21	61.61	0.62	1.61
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.M*QQQLDEYQELLDIK.L	32.33	39.79	0.81	1.23
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.MQQQLDEYQELLDIK.L	6.35	8.38	0.76	1.32

P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.NSNLVGAAHEELQQSR@.I	63.86	67.90	0.94	1.06
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.SGAQASSTPLSPTR.I	66.72	91.18	0.73	1.37
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.SLETENAGLR@.L	37.39	56.89	0.66	1.52
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	K.SNEDQSM*GNWQIR.R	17.17	18.52	0.93	1.08
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	K.SNEDQSMGNWQIR.R	4.09	6.85	0.60	1.68
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.SVGGSGGGSFGDNLVTR.S	33.72	36.19	0.93	1.07
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.TALINSTGEEVAM*R.K	39.40	52.19	0.75	1.32
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.TLEGELHDLR.G	30.56	13.30	2.30	0.44
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.VAVEEVDEEGK.F	17.23	28.15	0.61	1.63
P48678_LMNA_MOUSE	Lmna	Prelamin-A/C OS=Mus mu	R.VAVEEVDEEGK#FVR@.L	140.07	176.15	0.80	1.26
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	K.ALYETELADAR.R	10.84	20.91	0.52	1.93
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	K.DAALATALGDKK.S	9.24	29.32	0.32	3.17
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	R.DQM*QQQLSDYEQLLDVK.L	1.53	3.94	0.39	2.57
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	K.FKAEHDQLLLNYAK.K	5.28	14.46	0.37	2.74
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	R.IESLSSQLSNLQK.E	2.87	10.23	0.28	3.57
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	R.IQELEDM*LAK.E	12.71	14.43	0.88	1.14
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	R.LAVYIDK.V	9.27	25.95	0.36	2.80
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	R.LSSEM*NTSTVNSAR.E	4.83	14.43	0.33	2.99
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	R.LVEVDSGR.Q	12.67	19.44	0.65	1.53
P14733_LMNB1_MOUSE	Lmnb1	Lamin-B1 OS=Mus muscu	K.TTIPEEEEEEEEEPIGVAVEEER.F	6.82	14.88	0.46	2.18
P21619_LMNB2_MOUSE	Lmnb2	Lamin-B2 OS=Mus muscu	R.VELEQTYQAK.L	4.06	6.54	0.62	1.61
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.AGEEDR@GQLEDDAVYEDQSQK#.L	14.35	6.78	2.11	0.47
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.ATFSSM*SGLDSVSDSGEGR@.G	5.91	1.83	3.23	0.31
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.ATGPK#PDSSHFISGSASEK#EVIATEDVASLSSPTLPSSSLSHDR@.A	6.33	2.25	2.81	0.36
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.EPVAATWEATWSEGSK#.S	3.75	1.38	2.71	0.37
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.LSTPIAGLDNINVFLR@.A	14.13	17.67	0.80	1.25
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.QASGSSAEPHQAPLLSTEPR@.R	12.92	6.33	2.04	0.49
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.R@SQFFEQGSSDSVAPDLPVPTLSAPSR@.W	2.72	1.89	1.44	0.69
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.SM*SDVSAEDVQNLR@.Q	18.80	10.11	1.86	0.54
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.STTELNDPLIEK#.N	14.08	3.82	3.68	0.27
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.WIDTTSGIYNSDK#.S	9.24	3.69	2.50	0.40
F6TFN2_F6TFN2_MOUSE	Lmo7	Protein Lmo7 (Fragment	R.SWASPVYTETDGTFSR@.S	7.14	2.73	2.62	0.38
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.AGEEDRGQLEDDAVYEDQSQK.L	29.41	7.00	4.20	0.24
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.AQSNPYYNGPYLNLK#.A	10.31	1.75	5.89	0.17
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.ASESISLK#.N	42.24	13.15	3.21	0.31
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.ATFSSM*SGLDSVSDSGEGR@.G	12.82	4.27	3.00	0.33
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.ATGPK#PDSSHFISGSASEK#.E	11.60	4.42	2.63	0.38
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.EAQAWAEAEAK#.A	16.31	4.67	3.49	0.29
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.EDSFESLDSLGSR@.S	11.78	7.31	1.61	0.62
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.EPVAATWEATWSEGSK#.S	5.57	1.70	3.28	0.30
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.EVIATEDVASLSSPTLPSSSLSHDR@.A	17.74	6.76	2.62	0.38
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.ISASLPR@.S	57.46	22.29	2.58	0.39
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.LAPSPSEEPR@.Q	58.59	19.93	2.94	0.34
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.LSTPIAGLDNINVFLR.A	75.90	27.31	2.78	0.36
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.NFETTDFR@.A	17.47	6.07	2.88	0.35
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.NPSSAVPPPAGSVK#.T	11.38	6.06	1.88	0.53
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.QASGSSAEPHQAPLLSTEPR@.R	22.66	10.63	2.13	0.47
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.R@EDDTSGM*LPTDR@.S	5.11	2.42	2.11	0.47
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.R@SQFFEQGSSDSVAPDLPVPTLSAPSR@.W	8.00	1.98	4.04	0.25
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.SLDQFSDM*R@.V	20.13	5.90	3.41	0.29
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.SLDSEGTR@.A	13.56	5.49	2.47	0.40
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.SM*SDVSAEDVQNLR@.Q	44.90	17.65	2.54	0.39
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.SMSDVSAEDVQNLR@.Q	4.68	1.88	2.49	0.40
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.SSSLSVTTDFSESLQSPYTESK#.E	17.35	4.56	3.80	0.26
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.STTELNDPLIEK#.N	28.20	9.97	2.83	0.35
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	R.WAWDQEEER@.R	7.29	2.31	3.15	0.32
E9PYF4_E9PYF4_MOUSE	Lmo7	Protein Lmo7 OS=Mus m	K.WIDTTSGIYNSDK#.S	18.34	5.72	3.20	0.31
F6TFN2_F6TFN2_MOUSE	Lmo7	Protein Lmo7 (Fragment	R.SWASPVYTETDGTFSR@.S	26.81	8.51	3.15	0.32
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	K.AQLSAAVLTLLIK#.Q	9.30	2.30	4.04	0.25
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	K.EVEDELGPK#PQLEM*VTEAATDTSK#.E	10.58	6.28	1.69	0.59
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	R.FSVGGM*TDVAEIK#.G	24.50	10.21	2.40	0.42
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	K.HVM*DVVDEELSK#.L	8.30	2.41	3.45	0.29
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	K.IVSGEAQTVQVTPENLQDFVGK#PVFTVER@.M	17.95	9.77	1.84	0.54
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	R.LAQPYVGVFLK#.R	23.71	9.21	2.57	0.39
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	R.M*EM*INVSGYVAQEK#.L	7.90	3.51	2.25	0.44
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	R.VLEFIAVSQLR@.G	34.44	11.92	2.89	0.35
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	R.VVDNPIYLSDM*GAALTGAESHELQDVLEETNILK#.R	6.72	1.64	4.09	0.24
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	R.DIFPIAFPR@.R	10.05	4.80	2.09	0.48
Q8CGK3_LONM_MOUSE	Lonp1	Lon protease homolog, n	K.EVEDELGPK#PQLEM*VTEAATDTSK#.E	3.97	1.74	2.29	0.44
P28301_LYOX_MOUSE	Lox	Protein-lysine 6-oxidase	R.M*VGDDPYNPYK.Y	3.47	7.36	0.47	2.12
P28301_LYOX_MOUSE	Lox	Protein-lysine 6-oxidase	R.NRPGYGTGYFQYGLPDLVPDPYYIQASTYVQK.M	2.26	2.68	0.84	1.18
P28301_LYOX_MOUSE	Lox	Protein-lysine 6-oxidase	R.TPILLLR.D	18.85	31.15	0.61	1.65
P28301_LYOX_MOUSE	Lox	Protein-lysine 6-oxidase	K.VSVNPSYLVPESDYTNNVVR.C	3.86	9.59	0.40	2.48
P97873_LOXL1_MOUSE	Loxl1	Lysyl oxidase homolog 1	R.VLLAGAPQTSQR@.R	12.02	8.79	1.37	0.73
Q924C6_LOXL4_MOUSE	Loxl4	Lysyl oxidase homolog 4	R.EALFGAQLGQGLGPIHLSEVR.C	11.01	14.39	0.77	1.31
Q924C6_LOXL4_MOUSE	Loxl4	Lysyl oxidase homolog 4	K.VSNALGPQGR.R	5.04	5.60	0.90	1.11
Q91V01_MBOA5_MOUSE	Lpcat3	Lysophospholipid acyltra	K.VWLFETTPR@.F	12.31	6.86	1.79	0.56
Q8BFW7_LPP_MOUSE	Lpp	Lipoma-preferred partne	K.SAQPSPHYM*AGPSSGQIYGPGPR@.G	3.27	2.21	1.48	0.68
Q8BFW7_LPP_MOUSE	Lpp	Lipoma-preferred partne	R.YYEPYYAAGPSYGGR@.S	8.78	3.96	2.22	0.45
Q8BFW7_LPP_MOUSE	Lpp	Lipoma-preferred partne	K.EPIM*PAPGQEETVR@.I	9.97	3.82	2.61	0.38
Q8BFW7_LPP_MOUSE	Lpp	Lipoma-preferred partne	K.M*LYDM*ENPPADDYFGR@.C	4.71	2.15	2.19	0.46
Q8BFW7_LPP_MOUSE	Lpp	Lipoma-preferred partne	K.SAQPSPHYM*AGPSSGQIYGPGPR@.G	23.29	13.85	1.68	0.59
Q8BFW7_LPP_MOUSE	Lpp	Lipoma-preferred partne	R.SEGDTAYGQQVQPNTWK#.R	8.68	3.30	2.63	0.38
Q8BFW7_LPP_MOUSE	Lpp	Lipoma-preferred partne	R.YYEPYYAAGPSYGGR@.S	21.97	7.40	2.97	0.34
Q9ESE1_LRBA_MOUSE	Lrba	Lipopolysaccharide-resp	R.VGVGTSFGLPQTR@.R	11.15	4.92	2.26	0.44
Q3UMG5_LRCH2_MOUSE	Lrch2	Leucine-rich repeat and c	R.NDSHITGSK#PDSQK#DQEVYDFIDPNTEDVAVPEEGDTHIGSFVSFLK#.G	3.29	2.80	1.17	0.85
Q3UMG5_LRCH2_MOUSE	Lrch2	Leucine-rich repeat and c	R.NNLHVLPDELGDLPLVK#.L	15.45	5.10	3.03	0.33
Q3UMG5_LRCH2_MOUSE	Lrch2	Leucine-rich repeat and c	K.YLFDLPLK#.V	13.02	4.88	2.67	0.37
Q8BVU0_LRCH3_MOUSE	Lrch3	Leucine-rich repeat and c	R.ALEEAAVTGVLSLSGR@.K	13.77	3.41	4.03	0.25
Q8BVU0_LRCH3_MOUSE	Lrch3	Leucine-rich repeat and c	R.ASPLLLSSAPATDPTDAITR.Q	5.32	6.36	0.84	1.20
Q8BVU0_LRCH3_MOUSE	Lrch3	Leucine-rich repeat and c	K.IAPDLPDYER@.R	19.17	10.34	1.85	0.54
Q8BVU0_LRCH3_MOUSE	Lrch3	Leucine-rich repeat and c	R.LPEELAEVPLIR.L	24.69	15.81	1.56	0.64
Q8BVU0_LRCH3_MOUSE	Lrch3	Leucine-rich repeat and c	R.WSGNEPTDEFSDLPLR.V	5.99	2.40	2.49	0.40
Q8BVU0_LRCH3_MOUSE	Lrch3	Leucine-rich repeat and c	R.ALEEAAVTGVLSLSGR@.K	20.04	1.66	12.05	0.08
Q8BVU0_LRCH3_MOUSE	Lrch3	Leucine-rich repeat and c	R.LPEELAEVPLIR@.L	19.24	7.84	2.45	0.41
Q8BVU0_LRCH3_MOUSE	Lrch3	Leucine-rich repeat and c	R.LPEELAEVPLIR@.L	14.51	5.88	2.47	0.41
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	R.ETLVQDNIQWPTGLAVDYHNER@.L	6.70	3.01	2.23	0.45
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	K.IETAAM*DGTLR@.E	10.54	3.77	2.79	0.36
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	K.TLISGM*IDEPHAIVVDPLR@.G	14.23	9.57	1.49	0.67
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	R.AALSGANVLTLIEK#.D	21.36	5.77	3.70	0.27
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	K.AVTDEEPFLIFANR@.Y	14.17	6.39	2.22	0.45
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	K.GDYSVLVPGLR@.N	6.81	2.57	2.65	0.38
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	K.GPVGLAIDFPESK#.L	17.12	7.19	2.38	0.42

Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	R.IDLETGENR@.E	12.83	3.28	3.91	0.26
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	K.IVFPHGITLDLVSR@.L	12.24	2.65	4.62	0.22
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	R.M*YDAQQQQVGTNK#.C	15.76	1.60	9.82	0.10
Q91ZX7_LRP1_MOUSE	Lrp1	Prolow-density lipoprot	R.SLDPFK#PFIIFSNR@.H	13.50	6.79	1.99	0.50
P55302_AMRP_MOUSE	Lrpap1	Alpha-2-macroglobulin r	K.IQEYNVLLDTLSR.A	6.69	7.02	0.95	1.05
P55302_AMRP_MOUSE	Lrpap1	Alpha-2-macroglobulin r	K.VSHQGYGSTTEFEEPR.V	5.51	5.07	1.09	0.92
Q6PB66_LPPRC_MOUSE	Lrpprc	Leucine-rich PPR motif-c	K.NVQGIIDILK#.I	7.85	4.99	1.57	0.64
Q6PB66_LPPRC_MOUSE	Lrpprc	Leucine-rich PPR motif-c	K.TLLELIPELR@.D	11.34	4.77	2.38	0.42
Q6PB66_LPPRC_MOUSE	Lrpprc	Leucine-rich PPR motif-c	K.TSQVTSSDLESTLEK#.L	6.76	2.57	2.63	0.38
Q6PB66_LPPRC_MOUSE	Lrpprc	Leucine-rich PPR motif-c	K.TSQVTSSDLESTLEK#.L	3.96	1.96	2.02	0.50
Q6EDY6_LR16A_MOUSE	Lrrc16a	Leucine-rich repeat-cont	K.LTVASFLSDR@.I	9.03	2.52	3.58	0.28
Q6EDY6_LR16A_MOUSE	Lrrc16a	Leucine-rich repeat-cont	R.SNR@LEELVLENAGLR@.I	9.94	2.13	4.66	0.21
O35125_LRC23_MOUSE	Lrrc23	Leucine-rich repeat-cont	R.GNQLESTKGIYLPK#.L	10.37	2.56	4.04	0.25
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.FLALEGNPLR@.T	26.01	14.20	1.83	0.55
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.GTAAVLEYLR@.D	17.94	7.07	2.54	0.39
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.ILPEEITSLK#.N	17.14	8.71	1.97	0.51
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.LLDYSDK#.Q	17.02	8.21	2.07	0.48
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	R.LLPALTVLDIHDNQLTSLPSAIR@.E	37.99	14.25	2.67	0.37
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.LQSLSDDLR@.L	13.56	5.82	2.33	0.43
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.LQTINLSFNR@.F	14.45	5.36	2.70	0.37
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.LTFLDLR@.N	15.61	6.57	2.37	0.42
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	R.SSGQLNLAGR@.N	22.46	15.00	1.50	0.67
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.FLALEGNPLR@.T	24.20	5.03	4.81	0.21
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.GTAAVLEYLR@.D	15.37	3.46	4.45	0.22
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.LQTINLSFNR@.F	15.59	11.82	1.32	0.76
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.LTFLDLR@.N	15.30	2.90	5.28	0.19
Q9CRC8_LRC40_MOUSE	Lrrc40	Leucine-rich repeat-cont	K.TTLITSINFSK#.N	10.58	6.96	1.52	0.66
Q505F5_LRC47_MOUSE	Lrrc47	Leucine-rich repeat-cont	R.ELLLTGPGLEER@.V	8.10	9.29	0.87	1.15
Q505F5_LRC47_MOUSE	Lrrc47	Leucine-rich repeat-cont	R.ESGEGEEEVADSAR@.L	5.82	4.25	1.37	0.73
Q505F5_LRC47_MOUSE	Lrrc47	Leucine-rich repeat-cont	R.NALGPGLSPELGPLPALR@.V	6.66	5.63	1.18	0.84
Q9D1G5_LRC57_MOUSE	Lrrc57	Leucine-rich repeat-cont	R.GLTEFPSELQK#.L	7.54	3.05	2.47	0.40
Q9D1G5_LRC57_MOUSE	Lrrc57	Leucine-rich repeat-cont	R.SIPDTVGELQAIELNLNQNQISQLSVK#.I	1.90	2.47	0.77	1.30
Q922Q8_LRC59_MOUSE	Lrrc59	Leucine-rich repeat-cont	R.DK#LDGNELDLSLSDLNEVPVK#.E	11.16	6.52	1.71	0.58
Q922Q8_LRC59_MOUSE	Lrrc59	Leucine-rich repeat-cont	K.LQQLPADFGR.L	15.89	11.41	1.39	0.72
Q922Q8_LRC59_MOUSE	Lrrc59	Leucine-rich repeat-cont	R.LVNLQHLDLLNNR@.L	18.73	13.66	1.37	0.73
Q922Q8_LRC59_MOUSE	Lrrc59	Leucine-rich repeat-cont	K.WLDLK#DNPLDPVLAK#.V	9.97	6.57	1.52	0.66
Q922Q8_LRC59_MOUSE	Lrrc59	Leucine-rich repeat-cont	R.LVTLPVSFAQLK#.N	8.22	3.46	2.38	0.42
Q3UZ39_LRRF1_MOUSE	Lrrfip1	Leucine-rich repeat flight	R.GTGGNQR@EDEVQAGDTTVEDQVGTVASGPAK#.Q	5.52	1.50	3.68	0.27
E9QN52_E9QN52_MOUSE	Lrrfip2	Leucine-rich repeat flight	R.FSAEDEALSNIAR@.E	4.62	3.04	1.52	0.66
E9QN52_E9QN52_MOUSE	Lrrfip2	Leucine-rich repeat flight	R.NSASATTPLSGNSSR@.R	7.99	3.53	2.26	0.44
Q5S006_LRRK2_MOUSE	Lrrk2	Leucine-rich repeat serin	R.YSANDEVQK#.L	5.37	3.74	1.43	0.70
Q8BUI3_LRWD1_MOUSE	LRWD1	Leucine-rich repeat and \	R.ELDLSNNLLETLPANLGLSHLR@.I	40.41	4.29	9.43	0.11
Q8BUI3_LRWD1_MOUSE	LRWD1	Leucine-rich repeat and \	K.IQSLNLSGLQLLSEHLDPNLLGR@.L	14.92	3.64	4.10	0.24
Q3UM18_LSG1_MOUSE	Lsg1	Large subunit GTPase 1 h	K.LILTPFER@.N	22.25	8.99	2.48	0.40
Q3UM18_LSG1_MOUSE	Lsg1	Large subunit GTPase 1 h	R.TGLLSFEESQR@.I	12.07	4.21	2.87	0.35
Q9D0R8_LSM12_MOUSE	Lsm12	Protein LSM12 homolog	R.LQGEVVAFDYQSK#.M	12.60	9.62	1.31	0.76
Q9D0R8_LSM12_MOUSE	Lsm12	Protein LSM12 homolog	R.TETPPPLASLNVSK#.L	4.69	2.08	2.26	0.44
O35900_LSM2_MOUSE	Lsm2	U6 snRNA-associated Sm	R.YVQLPADEVDTQLLQDAAR@.K	6.38	6.73	0.95	1.05
O35900_LSM2_MOUSE	Lsm2	U6 snRNA-associated Sm	R.YVQLPADEVDTQLLQDAAR.K	6.20	3.83	1.62	0.62
P62311_LSM3_MOUSE	Lsm3	U6 snRNA-associated Sm	R.GDGVVLVAPPLR@.V	31.50	19.55	1.61	0.62
Q9QXA5_LSM4_MOUSE	Lsm4	U6 snRNA-associated Sm	R.IPDEIIDM*VR@.E	7.92	6.33	1.25	0.80
P19973_LSP1_MOUSE	Lsp1	Lymphocyte-specific pro	R.LQQYTQATESSGR@.T	5.47	2.23	2.45	0.41
Q8BLN5_ERG7_MOUSE	Lss	Lanosterol synthase OS=	R.LSASEDPLVQSLR@.Q	8.35	3.32	2.51	0.40
Q8BLN5_ERG7_MOUSE	Lss	Lanosterol synthase OS=	K.STVFGTALNYVALR@.I	11.39	6.87	1.66	0.60
Q8BLN5_ERG7_MOUSE	Lss	Lanosterol synthase OS=	R.LSASEDPLVQSLR@.Q	6.29	3.74	1.68	0.59
Q8BLN5_ERG7_MOUSE	Lss	Lanosterol synthase OS=	K.STVFGTALNYVALR.I	10.46	7.07	1.48	0.68
Q8CG19_LTBP1_MOUSE	Ltbp1	Latent-transforming gro	R.DALVDFSEQYGPETDPYFIQDR.F	4.90	5.72	0.86	1.17
Q8CG19_LTBP1_MOUSE	Ltbp1	Latent-transforming gro	K.EAQPGQSQVSYQGLPVQK.T	3.35	5.29	0.63	1.58
Q8CG19_LTBP1_MOUSE	Ltbp1	Latent-transforming gro	R.SQVQQDAQSAGGSR@.L	3.75	2.36	1.59	0.63
Q8CG19_LTBP1_MOUSE	Ltbp1	Latent-transforming gro	K.VKEAQPGQSQVSYQGLPVQK.T	7.01	9.59	0.73	1.37
Q6NSQ7_LTV1_MOUSE	Ltv1	Protein LTV1 homolog O	R.LQEVLNDYYK#.E	6.72	4.81	1.40	0.72
Q6NSQ7_LTV1_MOUSE	Ltv1	Protein LTV1 homolog O	K.LPSSVFASEFEEDVGLLNK#.A	11.95	4.86	2.46	0.41
Q9CYI4_LUC7L_MOUSE	Luc7l	Putative RNA-binding pr	K.AEQLGAEGNVDESQK#.I	183.65	86.80	2.12	0.47
Q9CYI4_LUC7L_MOUSE	Luc7l	Putative RNA-binding pr	R.ALLDQLM*GTAR@.D	146.53	75.99	1.93	0.52
Q9CYI4_LUC7L_MOUSE	Luc7l	Putative RNA-binding pr	R.ALLDQLMGTAR@.D	15.19	7.70	1.97	0.51
Q9CYI4_LUC7L_MOUSE	Luc7l	Putative RNA-binding pr	K.ILMEVEK#.V	25.22	13.36	1.89	0.53
Q9CYI4_LUC7L_MOUSE	Luc7l	Putative RNA-binding pr	R.LAETQEEISAEVSAK#.A	41.16	17.38	2.37	0.42
Q9CYI4_LUC7L_MOUSE	Luc7l	Putative RNA-binding pr	K.LHLGFIQIR@.E	51.41	17.72	2.90	0.34
Q9CYI4_LUC7L_MOUSE	Luc7l	Putative RNA-binding pr	R.SLR@EESWEYGR@.N	14.80	4.96	2.99	0.33
Q9CYI4_LUC7L_MOUSE	Luc7l	Putative RNA-binding pr	K.AEQLGAEGNVDESQK#.I	7.03	4.10	1.72	0.58
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.ADYEIASK#.E	411.93	180.63	2.28	0.44
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.AM*LDQLM*GTSR.D	218.99	95.99	2.28	0.44
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.AMLDQLM*GTSR.D	16.41	8.31	1.98	0.51
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.AM*LDQLMGTSR@.D	15.98	21.04	0.76	1.32
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.EAEEVYR.N	245.69	98.66	2.49	0.40
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.FR@DQDLASR@.D	91.02	43.41	2.10	0.48
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.LADHFGGK#.L	78.18	40.38	1.94	0.52
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.LAETQEEISAEVAAK#.A	179.57	78.55	2.29	0.44
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	K.LHLGFIEIR.E	36.76	14.92	2.46	0.41
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.NSMPASSFQQQK#.L	53.26	23.75	2.24	0.45
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.NSM*PASSFQQQK#.L	206.29	99.31	2.08	0.48
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	K.R@LAETQEEISAEVAAK#.A	15.24	5.59	2.73	0.37
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	K.VEQLGAEGNVEESQK#.V	332.58	168.25	1.98	0.51
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	K.VEQLGAEGNVEESQK#VM*DEVEK#.A	151.55	73.89	2.05	0.49
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.VHELNEEIGK#.L	611.35	225.91	2.71	0.37
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.AM*LDQLM*GTSR@.D	6.91	3.38	2.04	0.49
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.ADYEIASK#.E	27.37	10.18	2.69	0.37
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.AM*LDQLM*GTSR@.D	27.17	13.73	1.98	0.51
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.LAETQEEISAEVAAK#.A	8.62	5.47	1.58	0.63
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.NSM*PASSFQQQK#.L	11.31	6.57	1.72	0.58
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	K.VEQLGAEGNVEESQK#.V	12.29	5.79	2.12	0.47
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.VHELNEEIGK#.L	16.35	5.05	3.24	0.31
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.LAETQEEISAEVAAK#.A	9.85	4.03	2.44	0.41
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	K.VEQLGAEGNVEESQK#.V	7.29	3.25	2.24	0.45
Q7TNC4_LC7L2_MOUSE	Luc7l2	Putative RNA-binding pr	R.VHELNEEIGK#.L	7.80	3.07	2.54	0.39
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=	R.EK#QSEDTNPESK#.E	3.64	2.55	1.43	0.70
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=	K.ESDTK#NEVNGTSEDIK#SEGDTQSN.-	32.65	15.57	2.10	0.48
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=	K.IK#ATVEELK#EK#.L	45.44	24.01	1.89	0.53
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=	R.LALSQNQQSSGAAGPTGK#.N	103.20	44.70	2.31	0.43
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=	R.STTSTIESFAAQEK#.Q	115.43	56.09	2.06	0.49
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=	R.YLQSLLAEVER@.R	81.45	39.79	2.05	0.49
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=	R.LALSQNQQSSGAAGPTGK#.N	10.20	1.97	5.17	0.19
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=	R.STTSTIESFAAQEK#.Q	6.96	5.52	1.26	0.79

Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	R.YLQSLLAEVER@.R	22.26	11.96	1.86	0.54
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	K.ATVEELK#EK#.L	22.83	10.77	2.12	0.47
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	K.IK#ATVEELK#EK#.L	20.47	6.94	2.95	0.34
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	R.LALSQNQQSSGAAGPTGK#.N	42.76	16.71	2.56	0.39
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	K.QSEDTNPESK#.E	3.46	2.31	1.50	0.67
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	R.STTSTIESFAAQEK#.Q	48.50	18.08	2.68	0.37
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	R.STTSTIESFAAQEK#.Q	33.87	9.31	3.64	0.27
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	R.YLQSLLAEVER@.R	51.29	21.05	2.44	0.41
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	K.ESDTK#NEVNGTSEDIK#SEGDTQSN.-	2.46	1.55	1.59	0.63
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	K.IDVLLQQIEELGSEGK#.V	5.99	1.47	4.06	0.25
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	R.LALSQNQQSSGAAGPTGK#.N	20.22	6.15	3.29	0.30
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	R.STTSTIESFAAQEK#.Q	36.08	9.02	4.00	0.25
Q5SUF2_LC7L3_MOUSE	Luc7l3	Luc7-like protein 3 OS=M	R.YLQSLLAEVER.R	45.26	13.04	3.47	0.29
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	K.NNDLQDNYLTELNR.N	3.86	3.89	0.99	1.01
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	R.R@LDELEEATK#.N	8.42	7.08	1.19	0.84
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	K.VTSSITIYPSDSSGPR@.A	9.62	12.39	0.78	1.29
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	R.AEDELLDLQDK#.V	10.64	2.46	4.33	0.23
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	R.IEDGISSTLSSK#.E	14.71	5.49	2.68	0.37
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	K.NNDLQDNYLTELNR@.N	6.18	3.22	1.92	0.52
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	K.SLTLSFVNER@.K	10.86	3.80	2.86	0.35
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	R.SQENILQGFSLPNK#.E	9.65	4.30	2.25	0.45
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	K.VIQAEGSDSSTLAEIEVLR@.Q	4.53	3.09	1.46	0.68
Q8R4U7_LUZP1_MOUSE	Luzp1	Leucine zipper protein 1	K.VTSSITIYPSDSSGPR@.A	13.42	4.24	3.17	0.32
Q60767_LY75_MOUSE	Ly75	Lymphocyte antigen 75 (	K.LFLEDIVNR@.D	25.32	2.84	8.90	0.11
Q08288_LYAR_MOUSE	Lyar	Cell growth-regulating nu	R.ELLQQISAFDNVPR@.K	12.35	8.79	1.41	0.71
Q08288_LYAR_MOUSE	Lyar	Cell growth-regulating nu	K.K#AQGGQASEEGADR@NGGPGEDAAEGQTK#.T	2.41	1.68	1.43	0.70
Q08288_LYAR_MOUSE	Lyar	Cell growth-regulating nu	R.NGGPGEDAAEGQTK.T	2.56	2.62	0.98	1.02
Q08288_LYAR_MOUSE	Lyar	Cell growth-regulating nu	K.NQEAGHEAAGEEAAEASGPPEK#.K	10.32	5.55	1.86	0.54
Q3UFF7_LYPL1_MOUSE	Lyplal1	Lysophospholipase-like p	K.ASVVYQDLQQGGR@.M	3.37	1.86	1.81	0.55
P17897_LYZ1_MOUSE	Lyz1	Lysozyme C-1 OS=Mus mu	R.STDYGIFQINSR.Y	5.48	13.60	0.40	2.48
Q8K3C3_LZIC_MOUSE	Lzic	Protein LZIC OS=Mus mus	R.TRLAEM*DR@.D	6.49	31.81	0.20	4.90
Q9JHQ5_LZTL1_MOUSE	Lztfl1	Leucine zipper transcript	K.AQDLDDLENTVATLR@.S	11.73	4.37	2.68	0.37
Q9JHQ5_LZTL1_MOUSE	Lztfl1	Leucine zipper transcript	K.TIEIQAVNALDEK#.S	7.48	5.26	1.42	0.70
P24668_MPRD_MOUSE	M6pr	Cation-dependent mann	R.GVGDDQLGEESEER@.D	20.84	5.40	3.86	0.26
P24668_MPRD_MOUSE	M6pr	Cation-dependent mann	K.NEVALLER@.L	38.77	25.49	1.52	0.66
P24668_MPRD_MOUSE	M6pr	Cation-dependent mann	K.SFESTVGQGSDTYSYIFR@.V	26.75	5.77	4.63	0.22
P24668_MPRD_MOUSE	M6pr	Cation-dependent mann	K.SNDK#ETVVGR@.I	9.94	2.24	4.43	0.23
P24668_MPRD_MOUSE	M6pr	Cation-dependent mann	K.NEVALLER@.L	114.72	201.61	0.57	1.76
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	K.AGSELLESSAGDDASSLR.S	14.35	7.01	2.05	0.49
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	R.DQEPIPQNIDR.V	6.87	4.33	1.59	0.63
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	R.DQIIELDQTGNQLK#.F	8.11	3.01	2.70	0.37
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	R.EAEEELAASGGQSPTGEQIPQFQQR@.Q	8.32	3.44	2.42	0.41
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	K.FLDVLELAEK#.F	26.49	12.77	2.07	0.48
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	K.LDNLLGEVR.D	20.18	9.91	2.04	0.49
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	R.LEQDQTTAQLQVQK#.A	6.95	3.36	2.06	0.48
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	R.LLDAEDVDVPSPDEK#.S	4.93	2.39	2.06	0.48
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	K.LVSDANEQYK#.L	12.78	4.83	2.65	0.38
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	K.NSVFSVLDEEITK#.A	3.97	2.09	1.90	0.53
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	K.QFHETAEPISDFLSVTEK#.K	6.92	3.55	1.95	0.51
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	K.QTTGEEVLLIQEK#.L	7.07	4.73	1.49	0.67
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	R.R@GEELIGR@.S	21.51	11.96	1.80	0.56
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	K.TEQSVALLEQK#.W	9.12	3.01	3.03	0.33
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	R.TSLAGDTSNSSSPASTGAK#.A	7.85	3.89	2.02	0.50
E9PVY8_E9PVY8_MOUSE	Macf1	Microtubule-actin cross-	R.VDEIDAAIQR@.S	14.79	6.61	2.24	0.45
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.AILGSYDSELTQTEYSTQLTQR@.L	14.92	8.15	1.83	0.55
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.FVVELQQR@.E	23.68	13.07	1.81	0.55
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.GGPIPADLEAASSLPSSK#.E	17.97	12.40	1.45	0.69
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.IQELQASQDER@.A	17.75	9.56	1.86	0.54
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.LQSWENLDQTM*GLNLR@.T	4.52	3.56	1.27	0.79
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.LTLQGDYNQSR@.T	14.30	8.92	1.60	0.62
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.M*EGTSGLDVSTSASGSLQK#.Q	8.82	5.08	1.74	0.58
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.M*QLLETEFSR@.S	9.55	6.47	1.48	0.68
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.VQQQLQDEVR@.Q	24.34	12.98	1.87	0.53
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.VSELQLSAM*DQK#.V	16.05	9.32	1.72	0.58
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.AILGSYDSELTQTEYSTQLTQR@.L	34.88	7.69	4.54	0.22
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.EM*K#ETNGLLTEELEGLQR@.K	9.33	3.21	2.91	0.34
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.EQEDSLASAR@.E	33.53	11.36	2.95	0.34
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.FVVELQQR@.E	49.51	17.88	2.77	0.36
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.GGPIPADLEAASSLPSSK#.E	42.35	12.88	3.29	0.30
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.IQELQASQDER@.A	36.43	11.14	3.27	0.31
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.LQSWENLDQTM*GLNLR@.T	9.07	4.81	1.89	0.53
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.LTLQGDYNQSR@.T	23.58	7.74	3.05	0.33
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.M*EGTSGLDVSTSASGSLQK#.Q	26.98	7.93	3.40	0.29
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.M*QEALVDLELEK#EK#.L	45.33	15.62	2.90	0.34
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.M*QLLETEFSR@.S	21.88	6.63	3.30	0.30
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.QANAQLLEER@.K	14.55	3.14	4.63	0.22
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.QNLDAVSQQLR@.E	32.55	6.50	5.01	0.20
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.VHAHSSEM*EAQLSQALEELGVQK#.Q	9.35	3.98	2.35	0.43
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	K.VQQQLQDEVR@.Q	55.78	19.30	2.89	0.35
Q9WTX8_MD1L1_MOUSE	Mad1l1	Mitotic spindle assembly	R.VSELQLSAM*DQK#.V	21.67	6.81	3.18	0.31
Q9Z1B5_MD2L1_MOUSE	Mad2l1	Mitotic spindle assembly	R.GIYPSETFTR.V	29.11	13.99	2.08	0.48
Q9Z1B5_MD2L1_MOUSE	Mad2l1	Mitotic spindle assembly	R.SFTTTIHK#.V	27.87	13.40	2.08	0.48
Q9Z1B5_MD2L1_MOUSE	Mad2l1	Mitotic spindle assembly	K.VNSM*VAYK#.T	15.81	9.87	1.60	0.62
Q9Z1B5_MD2L1_MOUSE	Mad2l1	Mitotic spindle assembly	K.YGLTLLTTTDPELIK#.Y	15.65	9.27	1.69	0.59
Q4VC33_MAEA_MOUSE	Maea	Macrophage erythroblast	K.AVESIQAEDESAK#.L	11.19	4.21	2.66	0.38
Q4VC33_MAEA_MOUSE	Maea	Macrophage erythroblast	R.IQEFIELVR@.Q	13.98	11.70	1.19	0.84
O54790_MAFG_MOUSE	Mafg	Transcription factor Maf(	R.GPLAAGLGPLVPGK.V	3.39	8.13	0.42	2.39
O54790_MAFG_MOUSE	Mafg	Transcription factor Maf(	K.VAATSVITIVK.S	2.40	10.10	0.24	4.20
O89012_O89012_MOUSE	Magea8	MCG115467 OS=Mus mu	K.AFPTKAEMLESIGR@.E	2.40	17.65	0.14	7.36
Q9QYH6_MAGD1_MOUSE	Maged1	Melanoma-associated an	R.IPFTFWAR@.Y	9.58	5.25	1.83	0.55
Q9QYH6_MAGD1_MOUSE	Maged1	Melanoma-associated an	K.VPGADAQTQNVNQAK#.M	5.13	3.12	1.65	0.61
Q9CQL1_MGN2_MOUSE	Magohb	Protein mago nashi hom	K.GK#FGHEFLEFEFR@PDGK#.L	80.89	26.21	3.09	0.32
Q9CQL1_MGN2_MOUSE	Magohb	Protein mago nashi hom	K.IGSLIDVNQSK#.D	182.74	81.42	2.24	0.45
Q9CQL1_MGN2_MOUSE	Magohb	Protein mago nashi hom	K.IGSLIDVNQSKDPEGLR.V	98.31	43.31	2.27	0.44
Q9CQL1_MGN2_MOUSE	Magohb	Protein mago nashi hom	K.IGSLIDVNQSK#DPEGLR@.V	5.17	1.47	3.51	0.29
Q9CQL1_MGN2_MOUSE	Magohb	Protein mago nashi hom	K.NDVM*IR.K	85.59	33.63	2.54	0.39
Q9CQL1_MGN2_MOUSE	Magohb	Protein mago nashi hom	R.VFYYLVQDLK#.C	27.27	11.38	2.40	0.42
Q9CQL1_MGN2_MOUSE	Magohb	Protein mago nashi hom	R.VGRQELEIVIGDEHISFTTSK.I	51.06	22.18	2.30	0.43
Q9CQL1_MGN2_MOUSE	Magohb	Protein mago nashi hom	R.YANNSNYK#NDVM*IR@.K	5.02	2.17	2.31	0.43
Q8BGS0_MAK16_MOUSE	Mak16	Protein MAK16 homolog	K.ALEQIDENLIYWPR@.F	8.80	3.14	2.80	0.36
Q8BGS0_MAK16_MOUSE	Mak16	Protein MAK16 homolog	K.ALIAAQLDNAIEK#.E	14.72	8.82	1.67	0.60
Q8BGS0_MAK16_MOUSE	Mak16	Protein MAK16 homolog	K.ALIAAQLDNAIEK#ELLER@.L	14.40	7.87	1.83	0.55
Q8BGS0_MAK16_MOUSE	Mak16	Protein MAK16 homolog	R.AYVEIEYEQETEPM*AK#.V	5.22	2.40	2.18	0.46

Q8BGS0_MAK16_MOUSE	Mak16	Protein MAK16 homolog	R.LK#QDTYGDIYNFPIHAFDK#.A	15.35	8.93	1.72	0.58
E2QJ64_ECOLX	malE	Maltose-binding periplas	K.EFLENYLLTDEGLEAVNK.D	2.79	12.83	0.22	4.60
E2QJ64_ECOLX	malE	Maltose-binding periplas	R.FGGYAQSGLLAEITPDKAFQDK.L	1.56	5.30	0.29	3.40
E2QJ64_ECOLX	malE	Maltose-binding periplas	R.FGGYAQSGLLAEITPDK.A	1.56	15.25	0.10	9.80
E2QJ64_ECOLX	malE	Maltose-binding periplas	K.VNYGVTVLPTFK.G	1.71	40.57	0.04	23.70
E2QJ64_ECOLX	malE	Maltose-binding periplas	K.EFLENYLLTDEGLEAVNK.D	2.50	15.95	0.16	6.39
E2QJ64_ECOLX	malE	Maltose-binding periplas	R.FGGYAQSGLLAEITPDK.A	2.59	34.28	0.08	13.22
E2QJ64_ECOLX	malE	Maltose-binding periplas	R.TAVINAASGR.Q	1.11	130.24	0.01	117.48
E2QJ64_ECOLX	malE	Maltose-binding periplas	K.VNYGVTVLPTFK.G	2.00	110.53	0.02	55.28
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.AVLDALLEGK#.A	43.68	15.88	2.75	0.36
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.ITSFPESESYSYETSTK#.T	3.94	1.92	2.05	0.49
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.SSYYVVSGNDPAAEEPSR@.A	13.50	6.87	1.96	0.51
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.TPEVSGYTYEK#.T	16.25	7.80	2.08	0.48
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.AVLDALLEGK#.A	27.93	15.29	1.83	0.55
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.NVDVEFFK#.R	7.27	3.51	2.07	0.48
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.SSYYVVSGNDPAAEEPSR.A	5.23	3.47	1.51	0.66
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.ESSPLYSPGFSDSTSAAK#.E	4.85	3.27	1.48	0.68
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.ITSFPESESYSYETSTK#.T	11.86	8.52	1.39	0.72
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.THDVGGYYYEK#.T	8.30	5.47	1.52	0.66
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.TPEEGGYSYEISEK#.T	19.48	14.65	1.33	0.75
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.AAEAGVTEEQYGYLGTSAK#.Q	20.84	8.25	2.53	0.40
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.AIGNIELGIR.S	32.32	12.66	2.55	0.39
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.ASAELDIK#.D	12.58	6.24	2.02	0.50
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.ASLSPM*DEPVPDSESPVEK#.V	7.11	4.23	1.68	0.59
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.DIK#PQLELIEDEEK#.L	13.78	10.06	1.37	0.73
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.DLTGQVPTPPVK#.Q	35.01	11.10	3.15	0.32
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.DVM*SDETNNEETESPSQEFVNITK#.Y	18.66	5.49	3.40	0.29
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.EM*SLYASLASEK#.V	14.18	8.32	1.71	0.59
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.ESSPLYSPGFSDSTSAAK#.E	14.08	8.50	1.66	0.60
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.ETQPGEAYVIQK#.E	7.95	5.33	1.49	0.67
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.FSPEVPGQK#.I	29.84	19.80	1.51	0.66
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.GEAEQSEEEGEEEDK#AEDAR@.E	8.39	5.10	1.64	0.61
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.HSPTEDDESAK#AEADVHLK#.E	4.36	2.71	1.61	0.62
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.ITSFPESESYSYETSTK#.T	14.18	9.16	1.55	0.65
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.LEM*YVLNPVK#.S	6.88	38.93	0.18	5.66
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.LGGDVSPTQIDVSQFGSFK#.E	5.90	3.72	1.58	0.63
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.M*SISEGTVSDK#.S	18.00	12.90	1.40	0.72
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.NLISPDLGVVFLNVPENLK#DPEPNIK#.M	45.07	19.65	2.29	0.44
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.SDISPLTPR@.E	19.88	9.64	2.06	0.48
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.SDVLETVVLINPSDEAVSTEVR@.L	24.73	10.53	2.35	0.43
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.SDVLETVVLINPSDEAVSTEVR.L	7.78	3.46	2.25	0.44
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.SPPLLGSESPYEDFLSADSK#.V	13.33	6.78	1.97	0.51
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.SPSLSPSPPSPIEK#.T	9.03	5.39	1.68	0.60
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.SSHLPTEVTEK#PQAVPVSFEFSEAK#DENER@.A	18.85	6.98	2.70	0.37
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.SVGNTIEPVILFQK#.M	29.78	18.45	1.61	0.62
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.SVNFSLTPNEIK#.V	34.42	16.11	2.14	0.47
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.THDVGGYYYEK#.T	5.66	1.85	3.06	0.33
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.TLEVVSPSQSVTGSAGHTPYYQSPTDEK#.S	23.63	9.08	2.60	0.38
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.TPEEGGYSYEISEK#.T	20.69	10.32	2.00	0.50
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.TPEVSGYTYEK#.T	20.60	12.91	1.60	0.63
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.TPQASTYSYETSDR.C	11.28	8.04	1.40	0.71
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.TSDVETM*SSQSALALDER@.K	14.35	6.52	2.20	0.45
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	K.TTEAAATAVGTAATTAAVVAAAGIAASGPVK#.E	31.85	13.31	2.39	0.42
P14873_MAP1B_MOUSE	Map1b	Microtubule-associated	R.VLFPGNSTQYNILEGLEK#.L	21.32	10.45	2.04	0.49
P20357_MTAP2_MOUSE	Map2	Microtubule-associated	K.DVLEDIPR@.W	24.78	4.88	5.08	0.20
P31938_MP2K1_MOUSE	Map2k1	Dual specificity mitogen-	K.LPSGVFSLEFQDFVNK#.C	8.39	5.70	1.47	0.68
Q63932_MP2K2_MOUSE	Map2k2	Dual specificity mitogen-	R.RKPVLPALTINPTIAEGPSPTSEGASEANLVDLQK.K	8.75	7.38	1.19	0.84
Q63932_MP2K2_MOUSE	Map2k2	Dual specificity mitogen-	K.VSIAVLR@.G	6.66	4.57	1.46	0.69
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.ALETM*AEQTTDVVHSPSTDTTPGPDTEAALAK#.D	7.74	3.76	2.06	0.49
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.ALETMAEQTTDVVHSPSTDTTPGPDTEAALAK#.D	4.59	3.12	1.47	0.68
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.ATSPSTLVSTGPSSR@.S	26.10	7.27	3.59	0.28
P27546_MAP4_MOUSE	Map4	Microtubule-associated	R.DFM*AALEAEPYDDIVGETVEK#.T	3.18	1.54	2.06	0.48
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.DMSPSAETEAPLAK#.N	6.94	2.13	3.26	0.31
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.DVTLPLEAERPLVTDM*TPSLETEM*TLGK.E	27.34	6.80	4.02	0.25
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.DVTLPLEAER@PLVTDM*TPSLETEMTLGK#.E	3.82	9.36	0.41	2.45
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.ETAPPTETNLGM*AK#.D	17.16	4.10	4.18	0.24
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.ETETTLPIK#M*DLAPPEDVLLTK#.E	24.23	4.53	5.35	0.19
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.GM*VSLSEIEEALAK#.N	44.50	12.90	3.45	0.29
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.M*DLAPPEDVLLTK#.E	20.45	2.41	8.50	0.12
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.MDLAPPEDVLLTK#.E	13.48	7.25	1.86	0.54
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.NADLHSGTELIVDNSMAPASDLALPLETK#.V	7.69	5.94	1.29	0.77
P27546_MAP4_MOUSE	Map4	Microtubule-associated	R.NTTPTGAAPPAGM*TSTR@.V	20.23	5.06	4.00	0.25
P27546_MAP4_MOUSE	Map4	Microtubule-associated	R.SPATTLPK#.R	35.63	10.04	3.55	0.28
P27546_MAP4_MOUSE	Map4	Microtubule-associated	K.VAEFNNVTPLSEEEVTSVK#.D	14.35	3.56	4.04	0.25
Q61161_M4K2_MOUSE	Map4k2	Mitogen-activated protei	R.SLDTNEVTQEITDETR@.I	6.99	2.10	3.34	0.30
A2AJI0_MA7D1_MOUSE	Map7d1	MAP7 domain-containin	R.SLQLSAWESSIVDR@.L	6.10	5.30	1.15	0.87
A2AJI0_MA7D1_MOUSE	Map7d1	MAP7 domain-containin	R.AAEEKEPAAPASPAPSPVPSPTPAQPQK.E	4.81	5.21	0.92	1.08
A2AJI0_MA7D1_MOUSE	Map7d1	MAP7 domain-containin	K.ETAANNSGPDPVK#.A	8.62	4.68	1.84	0.54
A2AJI0_MA7D1_MOUSE	Map7d1	MAP7 domain-containin	R.LM*TPTLSFLAR.S	17.14	9.50	1.80	0.55
A2AJI0_MA7D1_MOUSE	Map7d1	MAP7 domain-containin	R.TAEGLLPFAEAEAFLK#.K	7.13	5.28	1.35	0.74
A2AJI0_MA7D1_MOUSE	Map7d1	MAP7 domain-containin	R.VEPGPGAPAAVLAR@.I	21.51	16.15	1.33	0.75
Q9ESN9_JIP3_MOUSE	Mapk8ip3	C-Jun-amino-terminal ki	K.RNSRNMEVQVTQEMR@.N	5.65	2.03	2.79	0.36
Q8BKH7_SIN1_MOUSE	Mapkap1	Target of rapamycin com	K.FGFSTLALVEK#.Y	15.52	5.77	2.69	0.37
Q61166_MARE1_MOUSE	Mapre1	Microtubule-associated	K.FFDANYDGK#EYDPVAAR@.Q	6.54	4.16	1.57	0.64
Q61166_MARE1_MOUSE	Mapre1	Microtubule-associated	K.ILQAGFK#.R	18.66	15.31	1.22	0.82
Q61166_MARE1_MOUSE	Mapre1	Microtubule-associated	R.QGQETAVAPSLVAPALSK#PK#.K	11.60	13.48	0.86	1.16
Q8VHJ5_MARK1_MOUSE	Mark1	Serine/threonine-protei	K.IANELK#L.-	13.47	7.03	1.92	0.52
Q8VHJ5_MARK1_MOUSE	Mark1	Serine/threonine-protei	K.LLVLNPIK#.R	12.17	7.85	1.55	0.64
Q8VHJ5_MARK1_MOUSE	Mark1	Serine/threonine-protei	K.LFEVIETEK#.T	11.87	2.90	4.09	0.24
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.DLDELSR@.Y	31.88	44.51	0.72	1.40
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.DLDELSRYPEDKITPENLPQILLQLK.R	144.05	130.67	1.10	0.91
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.DLDELSR@YPEDK#ITPENLPQILLQLK#.R	24.31	27.26	0.89	1.12
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.DSFDDR@GPSLNPVLDYDHGSR@.S	33.17	38.39	0.86	1.16
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.FDSEYER@.M	107.96	123.59	0.87	1.14
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GDTDQASNILASFGLSAR@.D	152.62	176.06	0.87	1.15
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GPGPLQER.S	134.65	170.03	0.79	1.26
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.IGPYQPNVPVGIDYVIPK#.T	10.02	11.00	0.91	1.10
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.INEAFIEM*ATTEDAQAAVDYYTTTPALVFGK#PVR@.V	3.67	2.10	1.75	0.57
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.ITPENLPQILLQLK.R	270.61	353.70	0.77	1.31
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.RTEEGPTLSYGR.D	31.50	36.60	0.86	1.16
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.SFQQSSLGR@.D	268.63	316.86	0.85	1.18
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.SQESGYYDR@.M	22.21	24.00	0.93	1.08
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.TEEGPTLSYGR.D	136.97	173.15	0.79	1.26

Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.YPEDKITPENLPQILLQLK.R	35.77	115.66	0.31	3.23
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GDTDQASNILASFGLSAR.D	13.30	9.55	1.39	0.72
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.IGPYQPNVPVGIDYVIPK#.T	35.78	34.19	1.05	0.96
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.SFQQSSLGR@.D	24.92	13.79	1.81	0.55
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.DLDELSR@.Y	92.19	41.82	2.20	0.45
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.DLDELSRYPEDKITPENLPQILLQLK.R	264.71	117.54	2.25	0.44
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.DLDELSR@YPEDK#ITPENLPQILLQLK#.R	46.05	23.26	1.98	0.51
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.FDSEYER@.M	167.51	77.33	2.17	0.46
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GAPPSSNIEDFHGLLPK#.G	12.77	5.91	2.16	0.46
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GDTDQASNILASFGLSAR@.D	264.61	124.84	2.12	0.47
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GNLGAGNGNLQGPR@.H	83.21	36.30	2.29	0.44
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GPGPLQER@.S	420.05	224.35	1.87	0.53
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GPLPLSSQHR.G	78.58	38.57	2.04	0.49
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.IGPYQPNVPVGIDYVIPK#.T	442.03	201.57	2.19	0.46
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.IKKPEGKPDQK.F	14.40	7.44	1.93	0.52
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.INEAFIEM*ATTEDAQAAVDYYTTTPALVFGKPVR.V	38.76	13.19	2.94	0.34
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.INEAFIEMATTEDAQAAVDYYTTTPALVFGKPVR.V	9.28	5.30	1.75	0.57
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.ITPENLPQILLQLK#.R	659.14	348.50	1.89	0.53
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.K#VDK#IEELDQENEAALENGIK#.N	4.91	3.02	1.62	0.62
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.LASLM*NLGM*SSSLNQQGAHSALSSASTSSHNLQSIFNIGSR@.G	54.98	21.62	2.54	0.39
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.M*KSQAFIEM*ETR.E	37.15	13.89	2.67	0.37
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.NYILMR@.M	15.68	4.86	3.23	0.31
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.R@GAPPSSNIEDFHGLLPK#.G	17.88	11.34	1.58	0.63
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.RRTEEGPTLSYGR.D	65.28	27.70	2.36	0.42
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.SFQQSSLGR@.D	377.01	172.40	2.19	0.46
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.SQAFIEM*ETR@.E	409.13	180.86	2.26	0.44
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.SQAFIEMETR@.E	55.92	24.77	2.26	0.44
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.SQESGYYDR@.M	25.33	12.61	2.01	0.50
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.TDAQK#TESPAEGK#EQEEK#.S	20.87	10.12	2.06	0.49
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.TEEGPTLSYGR@.D	303.70	140.60	2.16	0.46
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.TESPAEGK#EQEEK#.S	54.47	27.53	1.98	0.51
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.VHLSQK#.Y	55.12	29.25	1.88	0.53
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.VVHIM*DFQR@.G	514.68	242.86	2.12	0.47
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.VVHIMDFQR@.G	92.53	40.67	2.28	0.44
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.YPEDKITPENLPQILLQLK.R	61.97	27.79	2.23	0.45
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.DSFDDR@GPSLNPVLDYDHGSR@.S	14.33	10.68	1.34	0.75
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.FDSEYER@.M	42.67	16.24	2.63	0.38
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GDTDQASNILASFGLSAR@.D	66.57	31.74	2.10	0.48
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GNLGAGNGNLQGPR@.H	11.35	5.07	2.24	0.45
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.GPGPLQER@.S	55.95	28.16	1.99	0.50
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.IGPYQPNVPVGIDYVIPK#.T	87.43	40.19	2.18	0.46
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.ITPENLPQILLQLK#.R	108.54	59.34	1.83	0.55
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.LASLM*NLGM*SSSLNQQGAHSALSSASTSSHNLQSIFNIGSR@.G	7.56	4.07	1.86	0.54
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.R@R@TEEGPTLSYGR@.D	12.51	5.27	2.37	0.42
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.R@TEEGPTLSYGR@.D	7.30	4.27	1.71	0.58
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.SQAFIEM*ETR@.E	34.22	16.98	2.02	0.50
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.TDAQK#TESPAEGK#EQEEK#.S	4.00	1.31	3.04	0.33
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.TEEGPTLSYGR@.D	43.27	23.62	1.83	0.55
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	K.TESPAEGK#EQEEK#.S	7.68	2.47	3.11	0.32
Q8K310_MATR3_MOUSE	Matr3	Matrin-3 OS=Mus muscul	R.YPEDKITPENLPQILLQLK.R	14.21	6.58	2.16	0.46
P28574_MAX_MOUSE	Max	Protein max OS=Mus mu:	K.ATEYIQYM*R.R	3.03	6.23	0.49	2.06
P28574_MAX_MOUSE	Max	Protein max OS=Mus mu:	R.QNALLEQQVR.A	2.82	10.31	0.27	3.65
Q8C6L5_CGAS_MOUSE	Mb21d1	Cyclic GMP-AMP synthas	R.IELQEYYETGAFYLVK.F	2.67	3.82	0.70	1.43
Q8C6L5_CGAS_MOUSE	Mb21d1	Cyclic GMP-AMP synthas	R.VPQQQAILDPELPAVR.E	2.66	2.80	0.95	1.05
Q9Z2E1_MBD2_MOUSE	Mbd2	Methyl-CpG-binding don	K.AFIVTDEDIR@.K	37.57	29.05	1.29	0.77
Q9Z2E1_MBD2_MOUSE	Mbd2	Methyl-CpG-binding don	K.GLQGVGPGSNDETLLSAVASALHTSSAPITGQVSAAVEK#.N	6.66	2.33	2.85	0.35
Q9Z2E1_MBD2_MOUSE	Mbd2	Methyl-CpG-binding don	R.LQGLSASDVTEQIIK#.T	25.63	12.08	2.12	0.47
Q9Z2E1_MBD2_MOUSE	Mbd2	Methyl-CpG-binding don	R.LR@NDPLNQNK#.G	7.74	5.32	1.46	0.69
Q9Z2E1_MBD2_MOUSE	Mbd2	Methyl-CpG-binding don	R.YLGNAVDLSSFDFR@.T	16.83	4.05	4.15	0.24
Q9Z2D8_MBD3_MOUSE	Mbd3	Methyl-CpG-binding don	K.AFM*VTDDDIR@.K	62.28	17.59	3.54	0.28
Q9Z2D8_MBD3_MOUSE	Mbd3	Methyl-CpG-binding don	K.K#LSGLSAFDIAEELVR@.T	84.09	19.08	4.41	0.23
Q9Z2D8_MBD3_MOUSE	Mbd3	Methyl-CpG-binding don	R.K#QEELVQQVR@.K	34.04	7.95	4.28	0.23
Q9Z2D8_MBD3_MOUSE	Mbd3	Methyl-CpG-binding don	K.LSGLSAFDIAEELVR@.T	131.92	39.02	3.38	0.30
Q9Z2D8_MBD3_MOUSE	Mbd3	Methyl-CpG-binding don	R.YLGGSM*DLSTFDFR@.T	33.81	10.25	3.30	0.30
Q9Z2D8_MBD3_MOUSE	Mbd3	Methyl-CpG-binding don	K.AFM*VTDDDIR@.K	5.31	3.44	1.54	0.65
Q9Z2D8_MBD3_MOUSE	Mbd3	Methyl-CpG-binding don	K.K#LSGLSAFDIAEELVR@.T	16.33	11.05	1.48	0.68
Q9Z2D8_MBD3_MOUSE	Mbd3	Methyl-CpG-binding don	K.LSGLSAFDIAEELVR@.T	14.11	4.32	3.26	0.31
Q99LQ1_MBIP1_MOUSE	Mbip	MAP3K12-binding inhibi	K.ILELEGISPEYFQSVNFSGK#.R	9.17	1.87	4.91	0.20
Q99LQ1_MBIP1_MOUSE	Mbip	MAP3K12-binding inhibi	K.TQNLFDPEVVQIK#.A	19.46	5.42	3.59	0.28
Q9JKP5_MBNL1_MOUSE	Mbnl1	Muscleblind-like protein	K.AAQYQVNQAAAAQAAATAAAM*GIPQAVLPPLPK#.R	8.31	3.24	2.56	0.39
A0A0A6YWB0_A0A0A6YWB0_MOUSE	Mbnl1	Muscleblind-like protein	K.AAQYQVNQAAAAQAAATAAAM*TQSAVK#.S	13.94	4.89	2.85	0.35
A0A0A6YWB0_A0A0A6YWB0_MOUSE	Mbnl1	Muscleblind-like protein	K.AAQYQVNQAAAAQAAATAAAMTQSAVK#.S	8.32	3.95	2.11	0.47
A0A0A6YWB0_A0A0A6YWB0_MOUSE	Mbnl1	Muscleblind-like protein	K.RPLEATFDLGIPQAVLPPLPK.R	23.03	10.74	2.14	0.47
Q8K5B2_MCFD2_MOUSE	Mcfd2	Multiple coagulation fac	R.DDDK#NNDGYIDYAEFAK#.S	34.94	15.43	2.26	0.44
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.ESM*ATGSIPITVR.H	5.72	4.73	1.21	0.83
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.QLVAEQVTYQR@.N	14.42	6.13	2.35	0.43
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.VM*M*ESFIDTQK.F	3.34	3.33	1.00	1.00
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.AGIVTSLQAR.C	29.48	16.09	1.83	0.55
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.AIFTTGQGASAVGLTAYVQR@.H	12.10	5.42	2.23	0.45
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.ATEDGEEDEEM*IESIENLEDLK#GHSVR@.E	12.99	10.17	1.28	0.78
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.DTVDPVQDEM*LAR@.F	9.21	9.49	0.97	1.03
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.DYVM*EDDVNM*AIR@.V	6.97	5.60	1.24	0.80
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.ESLVVNYEDLAAR@.E	37.68	17.08	2.21	0.45
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.ESM*ATGSIPITVR@.H	23.36	14.29	1.63	0.61
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.EWTLEAGALVLADR.G	11.14	5.85	1.91	0.52
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.FGAQQDTIEIPEK#DLM*DK#.A	16.42	8.04	2.04	0.49
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.GLALALFGGEPK#.N	33.28	17.68	1.88	0.53
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.IFASIAPSIYGHEDIK#R@.G	34.39	19.66	1.75	0.57
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.ISDPLTSSPGR.S	10.14	6.71	1.51	0.66
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.KDEGLTNGGTLEPAM*PNTYGVEPLPQEVLK.K	1.78	2.57	0.69	1.44
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.QINIHNLSAFYDSDLFK#.F	16.20	8.10	2.00	0.50
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.QLVAEQVTYQR@.N	15.05	10.79	1.40	0.72
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.R@ADALTSSPGR@.D	10.11	5.79	1.75	0.57
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.VAVGELTDEDVK#.M	38.93	24.43	1.59	0.63
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.VM*M*ESFIDTQK#.F	9.27	5.50	1.68	0.59
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.YDPSLTFSENVDLTEPIISR@.F	7.49	7.10	1.06	0.95
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.AGIVTSLQAR@.C	11.58	5.31	2.18	0.46
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.ATEDGEEDEEM*IESIENLEDLK#GHSVR@.E	9.06	4.14	2.19	0.46
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.DNNDLLLFILK#.Q	5.45	2.20	2.47	0.40
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.DTVDPVQDEM*LAR@.F	5.20	2.44	2.13	0.47
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.ESLVVNYEDLAAR@.E	19.97	6.29	3.17	0.32
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.ESM*ATGSIPITVR@.H	13.80	5.57	2.48	0.40
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.GLALALFGGEPK#.N	39.40	12.96	3.04	0.33

P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.ISHLPLVEELR@.S	14.15	4.67	3.03	0.33
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	K.VAVGELTDEDVK#.M	19.78	12.87	1.54	0.65
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.VM*M*ESFIDTQK#.F	7.05	2.89	2.44	0.41
P97310_MCM2_MOUSE	Mcm2	DNA replication licensing	R.YDPSLTFSENVDLTEPIISR@.F	4.44	2.65	1.68	0.60
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.ALK#DFVASIDATYAK#.Q	10.68	3.61	2.96	0.34
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.ALKDFVASIDATYAK.Q	29.47	15.78	1.87	0.54
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.DYLDFLDDEEDQGIYQNK#.V	8.51	3.97	2.14	0.47
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.EAQR@DYLDFLDDEEDQGIYQNK#.V	8.77	3.68	2.38	0.42
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.LIVSVNDLR@.R	86.43	37.06	2.33	0.43
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.LLNNAFEELVAFQR@.A	5.27	1.44	3.65	0.27
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.AALLEVFQEAHEQSVGM*LHLTESINR@.N	16.16	7.92	2.04	0.49
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.ALK#DFVASIDATYAK#.Q	25.55	9.87	2.59	0.39
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.DIQPAFSADDIAK#.I	86.89	40.10	2.17	0.46
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.DYLDFLDDEEDQGIYQNK#.V	7.19	3.36	2.14	0.47
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.EAQRDYLDFLDDEEDQGIYQNK.V	13.88	5.72	2.43	0.41
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.ELISDNQYR@.L	39.20	24.61	1.59	0.63
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.GDINILLIGDPSVAK#.S	62.60	34.00	1.84	0.54
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.GSSGVGLTAAVTTDQETGER@.R	36.70	16.55	2.22	0.45
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.IIKPTLTQESAAYIAEEYSR.L	122.60	50.44	2.43	0.41
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.IQVVGTYR@.C	44.88	19.00	2.36	0.42
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.LEAGAM*VLADR@.G	10.16	2.87	3.54	0.28
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.LIVSVNDLR@.R	49.75	31.06	1.60	0.62
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.LLNNAFEELVAFQR@.A	29.25	14.41	2.03	0.49
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.M*VSAAFM*K#.K	14.05	5.68	2.47	0.40
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.SK#DVFEQLAR@.S	84.54	32.34	2.61	0.38
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.SQDSM*SSDTAR@.T	3.59	2.39	1.50	0.66
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.SVDVILDDDLVDK#.V	32.38	13.73	2.36	0.42
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.TAIHEVM*EQGR@.V	17.88	5.96	3.00	0.33
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.TDDSQEK#TDDSQETQDSQK#.V	5.02	2.48	2.02	0.49
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.TLETLIR@.L	80.06	34.78	2.30	0.43
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.TPM*ENIGLQDSLLSR@.F	41.00	20.96	1.96	0.51
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.TVDLQDAEEAVELVQYAYFK#.K	59.33	29.44	2.02	0.50
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.APAGQLPR@.S	17.99	7.11	2.53	0.40
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.DIQPAFSADDIAK#.I	28.75	8.87	3.24	0.31
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.DYLDFLDDEEDQGIYQNK#.V	9.13	2.29	3.99	0.25
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.ELISDNQYR@.L	17.35	5.82	2.98	0.34
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.GSSGVGLTAAVTTDQETGER@.R	14.60	5.68	2.57	0.39
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.IIK#PTLTQESAAYIAEEYSR@.L	40.96	12.41	3.30	0.30
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.LIVSVNDLR@.R	38.67	15.51	2.49	0.40
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.LLNNAFEELVAFQR@.A	17.82	6.27	2.84	0.35
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.SK#DVFEQLAR@.S	25.78	9.74	2.65	0.38
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	R.SVDVILDDDLVDK#.V	18.28	5.12	3.57	0.28
P25206_MCM3_MOUSE	Mcm3	DNA replication licensing	K.TPM*ENIGLQDSLLSR@.F	17.28	6.21	2.78	0.36
Q9WUU9_GANP_MOUSE	Mcm3ap	Germinal-center associat	K.LVLVLPDVEEQTPESPGR@.I	3.30	2.84	1.16	0.86
Q9WUU9_GANP_MOUSE	Mcm3ap	Germinal-center associat	R.STVFPLDGVVR@.M	7.44	5.51	1.35	0.74
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.ALADDDFLTVTGK#.T	36.87	15.61	2.36	0.42
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	K.GSSAVGLTAYVM*K#DPETR@.Q	24.20	68.56	0.35	2.83
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.K#GLQVDLQSDGAAAEDIVPSEQSLGQK#.L	17.37	6.41	2.71	0.37
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.LSEEASQALIEAYVNM*R@.K	3.68	30.05	0.12	8.16
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.NLNPEDIDQLITISGM*VIR@.T	10.93	8.83	1.24	0.81
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	K.R@LHGLDEEAEQK#.L	17.37	11.15	1.56	0.64
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.SVLHEVM*EQQTLSIAK#.A	14.89	15.41	0.97	1.03
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.TGIVDISILTTGM*SATSR@.K	14.22	8.86	1.61	0.62
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.TSVLAAANPIESQWNPK#.K	13.93	6.25	2.23	0.45
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	K.TTIENIQLPHTLLSR@.F	44.25	22.20	1.99	0.50
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.VNVTGIYR@.A	27.41	12.06	2.27	0.44
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.ALADDDFLTVTGK#.T	18.44	7.29	2.53	0.40
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.GM*VSAYPR@.Q	4.38	1.14	3.84	0.26
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.K#GLQVDLQSDGAAAEDIVPSEQSLGQK#.L	7.91	2.10	3.77	0.27
P49717_MCM4_MOUSE	Mcm4	DNA replication licensing	R.LSEEASQALIEAYVNM*R@.K	8.49	2.59	3.28	0.30
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.IPGIIISASAVR@.A	15.58	9.53	1.63	0.61
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.LAALPNIYELISK#.S	30.58	15.43	1.98	0.50
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.LFQVSTLDAALSGNLSGVEGFTTQEDQEM*LSR@.I	9.27	2.07	4.47	0.22
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.LQPFATEADVEEALR@.L	13.57	6.55	2.07	0.48
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.IPGIIISASAVR@.A	4.13	3.15	1.31	0.76
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.LQPFATEADVEEALR@.L	27.57	12.92	2.13	0.47
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.M*K#LQPFATEADVEEALR@.L	9.13	1.31	6.97	0.14
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.VLQLM*LR@.R	10.78	4.41	2.45	0.41
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.AGITTTLNSR@.C	58.11	29.00	2.00	0.50
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.FAIGSQVSEHSIVQDFTK#.Q	9.64	3.53	2.73	0.37
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.FGLNPSK#.G	44.57	23.50	1.90	0.53
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.GSSAAGLTASVIR@.D	19.67	8.58	2.29	0.44
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.GSSAAGLTASVIR@DPSSR@.N	56.22	20.74	2.71	0.37
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.HVM*TLHVSALTQTQAVEGEIDLAK#.M	3.23	1.64	1.97	0.51
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.IPGIIISASAVR@.A	80.03	42.48	1.88	0.53
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.LAALPNIYELISK#.S	164.46	85.97	1.91	0.52
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.LQPFATEADVEEALR@.L	44.92	29.48	1.52	0.66
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.M*K#LQPFATEADVEEALR@.L	8.01	4.44	1.80	0.55
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.QPAEHLQLLEEAAK#.E	29.06	17.62	1.65	0.61
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.R@GDINLLM*LGDPGTAK#.S	42.76	23.24	1.84	0.54
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.VAIHEAM*EQQTISIAK#.A	27.12	15.86	1.71	0.58
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.VLGIQVDTDGSGR@.S	80.58	40.20	2.00	0.50
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.VLQLM*LR@.R	24.17	11.87	2.04	0.49
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.VTIM*GIYSIK#.K	10.72	7.68	1.40	0.72
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.WDETK#GEDNIDFM*PTILSR@.F	13.17	16.03	0.82	1.22
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.AGITTTLNSR@.C	72.76	20.85	3.49	0.29
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.EDDR@VAIHEAM*EQQTISIAK#.A	6.74	3.13	2.16	0.46
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.FAIGSQVSEHSIVQDFTK#.Q	115.36	34.25	3.37	0.30
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.FGLNPSK#.G	46.13	18.02	2.56	0.39
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.GSSAAGLTASVIR@.D	25.03	5.99	4.18	0.24
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.HVM*TLHVSALTQTQAVEGEIDLAK#.M	5.55	2.01	2.76	0.36
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.IPGIIISASAVR@.A	107.05	28.51	3.76	0.27
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.LAALPNIYELISK#.S	298.20	74.91	3.98	0.25
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.LFQVSTLDAALSGNLSGVEGFTTQEDQEM*LSR@.I	51.27	15.45	3.32	0.30
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.LPDGLTR@.R	41.34	11.75	3.52	0.28
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.LQELPDAVPHGEMPR@.H	14.83	4.50	3.30	0.30
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.LQPFATEADVEEALR@.L	94.68	29.93	3.16	0.32
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.LSAEAAEK#.L	67.83	15.57	4.36	0.23
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.M*K#LQPFATEADVEEALR@.L	11.81	2.09	5.64	0.18
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.QLEAIVR.I	52.33	12.17	4.30	0.23
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.R@GDINLLM*LGDPGTAK#.S	59.68	17.93	3.33	0.30
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.R@LPDGLTR@.R	42.79	8.72	4.91	0.20
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.SFAGSVSPQEEEEFR@.R	9.19	3.98	2.31	0.43

P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.SISPSIFGGM*DM*K#.K	18.35	4.40	4.18	0.24
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.VAIHEAM*EQQTISIAK#.A	57.57	66.85	0.86	1.16
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.VLGIQVDTDGSGR@.S	97.75	24.65	3.96	0.25
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	K.VLQLM*LR@.R	38.61	10.65	3.63	0.28
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.VTIM*GIYSIK#.K	11.17	4.92	2.27	0.44
P49718_MCM5_MOUSE	Mcm5	DNA replication licensing	R.WDETK#GEDNIDFM*PTILSR@.F	20.09	5.45	3.69	0.27
P97311_MCM6_MOUSE	Mcm6	DNA replication licensing	K.DFYVAFQDLPTR@.H	15.93	10.05	1.58	0.63
P97311_MCM6_MOUSE	Mcm6	DNA replication licensing	R.FNGSSEDASQETVSK#PSLR@.L	5.43	3.67	1.48	0.67
P97311_MCM6_MOUSE	Mcm6	DNA replication licensing	K.HVDEFSPR@.A	21.12	9.60	2.20	0.45
P97311_MCM6_MOUSE	Mcm6	DNA replication licensing	R.IQETQAELPR@.G	26.56	11.98	2.22	0.45
P97311_MCM6_MOUSE	Mcm6	DNA replication licensing	R.VSGADGYETEGIR@.G	26.63	13.47	1.98	0.51
P97311_MCM6_MOUSE	Mcm6	DNA replication licensing	K.DFYVAFQDLPTR@.H	7.68	4.33	1.77	0.56
P97311_MCM6_MOUSE	Mcm6	DNA replication licensing	K.HVDEFSPR@.A	9.65	3.07	3.14	0.32
P97311_MCM6_MOUSE	Mcm6	DNA replication licensing	R.IQETQAELPR@.G	11.39	3.97	2.87	0.35
P97311_MCM6_MOUSE	Mcm6	DNA replication licensing	R.VSGADGYETEGIR@.G	9.00	4.86	1.85	0.54
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	K.ALLLLLVGGVDQSPQGM*K#.I	18.44	7.36	2.50	0.40
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	K.FLQEFYYENELGK#.K	10.30	6.03	1.71	0.59
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.GSSGVGLTAAVLR@.D	25.29	12.44	2.03	0.49
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.IAQPGDHVSVTGIFLPVLR@.T	40.21	20.95	1.92	0.52
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.LFGDVVQELLPEYK#.E	32.57	15.90	2.05	0.49
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.M*VDIVEK#EDVNEAIR@.L	18.32	8.07	2.27	0.44
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.NPQNQYPSELM*R@.R	11.35	4.55	2.49	0.40
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	K.SDDDVSGAGELSSEELK#.Q	17.22	7.07	2.44	0.41
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.SITVVLEGENTR@.I	23.37	16.91	1.38	0.72
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.SLEQNVQLPAALLSR@.F	12.17	6.65	1.83	0.55
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	K.SQLLSYIDR@.L	19.92	12.71	1.57	0.64
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.TGFQQM*AQGLLSETYLEAHWIVK#.M	11.06	4.18	2.65	0.38
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.TLLAILR@.L	44.61	19.06	2.34	0.43
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	K.ALLLLLVGGVDQSPQGM*K#.I	12.34	2.62	4.72	0.21
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	K.FLQEFYYENELGK#.K	7.40	4.15	1.78	0.56
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.GSSGVGLTAAVLR@.D	14.88	5.98	2.49	0.40
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.IAQPGDHVSVTGIFLPVLR@.T	30.43	10.47	2.91	0.34
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.LFGDVVQELLPEYK#.E	26.80	8.84	3.03	0.33
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.NPQNQYPSELM*R@.R	6.57	2.26	2.90	0.34
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	K.SDDDVSGAGELSSEELK#.Q	11.42	5.09	2.25	0.45
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.SITVVLEGENTR@.I	10.42	20.81	0.50	2.00
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.SLEQNVQLPAALLSR@.F	10.65	3.47	3.07	0.33
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	K.SQLLSYIDR@.L	18.60	4.70	3.96	0.25
Q61881_MCM7_MOUSE	Mcm7	DNA replication licensing	R.TLLAILR@.L	22.64	5.80	3.90	0.26
Q8R3C0_MCMBP_MOUSE	Mcmbp	Mini-chromosome maint	R.SYEDDEDM*DLQPSK#.Q	1.71	1.25	1.37	0.73
Q99L90_MCRS1_MOUSE	Mcrs1	Microspherule protein 1	K.APSTPVPPSPAPTPGLTK#.R	5.19	3.56	1.46	0.69
Q99L90_MCRS1_MOUSE	Mcrs1	Microspherule protein 1	R.LSNNSVVEIASLR@.F	12.93	3.23	4.00	0.25
Q99L90_MCRS1_MOUSE	Mcrs1	Microspherule protein 1	K.WQVLVDSITGM*GSPDFDNQTLAVLR@.G	6.58	2.54	2.59	0.39
Q99L90_MCRS1_MOUSE	Mcrs1	Microspherule protein 1	R.WYALLYDPVISK#.L	8.63	8.25	1.05	0.96
Q99L90_MCRS1_MOUSE	Mcrs1	Microspherule protein 1	R.WYALLYDPVISK#.L	3.37	3.24	1.04	0.96
P08249_MDHM_MOUSE	Mdh2	Malate dehydrogenase, n	K.AGAGSATLSM*AYAGAR.F	4.33	6.42	0.67	1.48
P08249_MDHM_MOUSE	Mdh2	Malate dehydrogenase, n	R.ANTFVAELK.G	4.47	14.19	0.31	3.17
P08249_MDHM_MOUSE	Mdh2	Malate dehydrogenase, n	K.IFGVTTLDIVR.A	5.50	21.01	0.26	3.82
P08249_MDHM_MOUSE	Mdh2	Malate dehydrogenase, n	R.IQEAGTEVVK.A	4.44	19.95	0.22	4.49
P08249_MDHM_MOUSE	Mdh2	Malate dehydrogenase, n	K.M*IAEAIPELK.A	6.05	19.23	0.31	3.18
Q9D967_MGDP1_MOUSE	Mdp1	Magnesium-dependent p	R.DGM*SLQTLTQGLETFAK#.A	6.63	3.85	1.72	0.58
Q9D967_MGDP1_MOUSE	Mdp1	Magnesium-dependent p	R.LQSLGVPVAAASR@.T	13.81	8.86	1.56	0.64
Q2VPQ9_EAF6_MOUSE	Meaf6	Chromatin modification-	R.K#QELAETLANLER@.Q	16.08	10.34	1.56	0.64
Q2VPQ9_EAF6_MOUSE	Meaf6	Chromatin modification-	R.QIYAFEGSYLEDTQM*YGNIIR@.G	3.59	1.86	1.93	0.52
Q2VPQ9_EAF6_MOUSE	Meaf6	Chromatin modification-	K.R@K#QELAETLANLER@.Q	35.21	14.78	2.38	0.42
Q2VPQ9_EAF6_MOUSE	Meaf6	Chromatin modification-	K.SSVTSAAAVSALAGVQDQLIEK#.R	17.03	9.36	1.82	0.55
Q2VPQ9_EAF6_MOUSE	Meaf6	Chromatin modification-	K.SSVTSAAAVSALAGVQDQLIEK#R@.E	9.56	7.15	1.34	0.75
Q2VPQ9_EAF6_MOUSE	Meaf6	Chromatin modification-	K.TAPPQIPDTR@.R	25.81	10.33	2.50	0.40
Q2VPQ9_EAF6_MOUSE	Meaf6	Chromatin modification-	K.SSVTSAAAVSALAGVQDQLIEK#.R	25.63	10.97	2.34	0.43
P14404_EVI1_MOUSE	Mecom	MDS1 and EVI1 complex	R.AAAESSAIQSISHV.-	16.64	16.64	1.00	1.00
P14404_EVI1_MOUSE	Mecom	MDS1 and EVI1 complex	R.APPNTLPENLLR@.K	11.59	6.81	1.70	0.59
P14404_EVI1_MOUSE	Mecom	MDS1 and EVI1 complex	K.YFGSTGLVGLQDK#.K	7.00	5.84	1.20	0.83
P14404_EVI1_MOUSE	Mecom	MDS1 and EVI1 complex	R.AAAESSAIQSISHV.-	8.86	8.86	1.00	1.00
Q9Z2D6_MECP2_MOUSE	Mecp2	Methyl-CpG-binding pro	K.AAASEGVQVK.R	10.49	15.65	0.67	1.49
Q9Z2D6_MECP2_MOUSE	Mecp2	Methyl-CpG-binding pro	R.GRKPGSVVAAAAAEAK.K	2.09	18.11	0.12	8.65
Q9Z2D6_MECP2_MOUSE	Mecp2	Methyl-CpG-binding pro	K.VGDTSLDPNDFDFTVTGR.G	4.29	10.11	0.42	2.35
Q925J9_MED1_MOUSE	Med1	Mediator of RNA polyme	K.DAPLPDGQSLQGTLVSK#.I	7.31	4.43	1.65	0.61
Q925J9_MED1_MOUSE	Med1	Mediator of RNA polyme	K.GLVNLYNLPGDNK#.L	5.54	2.24	2.48	0.40
Q925J9_MED1_MOUSE	Med1	Mediator of RNA polyme	R.VPLILNM*IR@.H	13.44	6.97	1.93	0.52
Q925J9_MED1_MOUSE	Med1	Mediator of RNA polyme	K.DAPLPDGQSLQGTLVSK#.I	8.87	2.25	3.94	0.25
Q925J9_MED1_MOUSE	Med1	Mediator of RNA polyme	K.GLVNLYNLPGDNK#.L	9.20	2.70	3.41	0.29
Q9CXU0_MED10_MOUSE	Med10	Mediator of RNA polyme	R.QLGIIVSDFQPSSQAGLSQK#.L	6.35	2.22	2.86	0.35
Q9D8C6_MED11_MOUSE	Med11	Mediator of RNA polyme	R.EIGAILQNAGTAILELSK#.E	26.24	8.69	3.02	0.33
Q9D8C6_MED11_MOUSE	Med11	Mediator of RNA polyme	R.QAAAFTTSVQHVEAELSAQIR@.Y	21.50	9.31	2.31	0.43
A2AGH6_MED12_MOUSE	Med12	Mediator of RNA polyme	R.IVDGAVFAVLK#.A	15.95	6.72	2.38	0.42
A2AGH6_MED12_MOUSE	Med12	Mediator of RNA polyme	R.LLDNEDGENPQR@.Q	8.21	3.82	2.15	0.47
A2AGH6_MED12_MOUSE	Med12	Mediator of RNA polyme	R.NISVETASLDVYAK#.Y	5.94	3.55	1.67	0.60
A2AGH6_MED12_MOUSE	Med12	Mediator of RNA polyme	K.NTADPFTEWTQIITK#.Y	8.84	2.62	3.38	0.30
A2AGH6_MED12_MOUSE	Med12	Mediator of RNA polyme	R.SGVWLVAPLIAK#.L	16.10	6.80	2.37	0.42
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	K.VSDEIVQQYQIK#.N	5.41	2.37	2.28	0.44
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	K.EYGSVDTAPGGTVLEGNSSSVGTQFR@.I	10.83	2.71	4.00	0.25
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	K.FVTEWFSQAADGNNEAFSK#.L	9.48	1.62	5.84	0.17
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	K.HK#VEDGTSAVTVLSHEEDAM*SLFSPSK#.Q	6.44	2.93	2.20	0.46
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	K.LDLLPSGPSM*PFIK#.E	22.77	4.82	4.73	0.21
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	R.LLSTESHDEVTNILQQPLALGYFVSTAK#.A	20.61	3.07	6.72	0.15
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	R.LYTPPFILAPVK#.D	15.15	4.18	3.62	0.28
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	R.M*LLSLQPVLQDAIQK#.K	15.32	4.85	3.16	0.32
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	K.NQYLSAIASDTEQEPK#.I	9.14	3.31	2.77	0.36
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	K.TLTGFGPGLAM*ETALK#.S	17.75	3.19	5.56	0.18
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	K.VGISSNWVR@.V	8.96	3.87	2.32	0.43
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	K.VSDEIVQQYQIK#.N	20.32	6.12	3.32	0.30
Q5SWW4_MED13_MOUSE	Med13	Mediator of RNA polyme	R.VSVSDEIGM*DTDSASQR@.L	8.43	3.18	2.65	0.38
Q6JPI3_MD13L_MOUSE	Med13l	Mediator of RNA polyme	K.NPER@PSPIQLYSPPFILAPIK#DK#.Q	9.80	4.63	2.12	0.47
Q6JPI3_MD13L_MOUSE	Med13l	Mediator of RNA polyme	K.VDEALVR@.S	23.22	22.00	1.06	0.95
A2ABV5_MED14_MOUSE	Med14	Mediator of RNA polyme	R.AGTSSQTM*PTNM*PPPR@.K	3.42	1.51	2.27	0.44
A2ABV5_MED14_MOUSE	Med14	Mediator of RNA polyme	R.DGAYSLFDNSK#.L	8.44	2.88	2.92	0.34
A2ABV5_MED14_MOUSE	Med14	Mediator of RNA polyme	R.HVYLTYENLLSEPVGGR@.K	11.91	4.48	2.65	0.38
A2ABV5_MED14_MOUSE	Med14	Mediator of RNA polyme	R.IIQQETLQLINSNEPGVIM*FK#.T	13.26	4.60	2.88	0.35
A2ABV5_MED14_MOUSE	Med14	Mediator of RNA polyme	K.TFLNM*FVDSNQDAR@.R	6.08	2.96	2.05	0.49
A2ABV5_MED14_MOUSE	Med14	Mediator of RNA polyme	K.TNQTLQLK#.V	11.46	9.86	1.16	0.86
A2ABV5_MED14_MOUSE	Med14	Mediator of RNA polyme	K.VVEM*FLNDWSSIAR@.L	5.16	1.64	3.14	0.32
Q6PGF3_MED16_MOUSE	Med16	Mediator of RNA polyme	K.LFLM*AITSTLK#.S	5.51	1.68	3.29	0.30
Q6PGF3_MED16_MOUSE	Med16	Mediator of RNA polyme	K.LPISLTNTDLK#.V	14.66	8.19	1.79	0.56

Q6PGF3_MED16_MOUSE	Med16	Mediator of RNA polyme	R.NLIAFTTDLR@.N	10.18	3.77	2.70	0.37
Q6PGF3_MED16_MOUSE	Med16	Mediator of RNA polyme	R.APTLPSSTSTLQLDGLTR@.A	8.03	3.54	2.27	0.44
Q6PGF3_MED16_MOUSE	Med16	Mediator of RNA polyme	K.LPISLTNTDLK#.V	14.20	7.19	1.98	0.51
Q6PGF3_MED16_MOUSE	Med16	Mediator of RNA polyme	R.NLIAFTTDLR@.N	11.65	1.60	7.29	0.14
Q8VCD5_MED17_MOUSE	Med17	Mediator of RNA polyme	R.LSGPQAFDK#NEINSIQSTEGLLEK#.I	12.79	7.09	1.80	0.55
Q8VCD5_MED17_MOUSE	Med17	Mediator of RNA polyme	R.TAATIDSLASR@.I	11.67	10.44	1.12	0.89
Q8VCD5_MED17_MOUSE	Med17	Mediator of RNA polyme	R.TAATIDSLASR@.I	14.73	2.21	6.65	0.15
Q9CZ82_MED18_MOUSE	Med18	Mediator of RNA polyme	K.GQQASPFVLR@.A	16.23	8.23	1.97	0.51
Q8C1S0_MED19_MOUSE	Med19	Mediator of RNA polyme	R.SLIEKPPILGGSFNPITGTM*LSGFR.L	6.92	7.61	0.91	1.10
Q8C1S0_MED19_MOUSE	Med19	Mediator of RNA polyme	R.SLIEKPPILGGSFNPITGTM*LSGFR.L	4.25	3.72	1.14	0.88
Q9R0X0_MED20_MOUSE	Med20	Mediator of RNA polyme	K.SLQQTVELLTK#.K	36.46	12.54	2.91	0.34
Q9R0X0_MED20_MOUSE	Med20	Mediator of RNA polyme	K.VGTVTM*GPSAR@.G	18.37	3.89	4.72	0.21
Q9CQ39_MED21_MOUSE	Med21	Mediator of RNA polyme	K.IQSALADIAQSQLK#.T	33.94	15.72	2.16	0.46
Q62276_MED22_MOUSE	Med22	Mediator of RNA polyme	K.IEDETQVSR@.A	38.02	12.59	3.02	0.33
Q62276_MED22_MOUSE	Med22	Mediator of RNA polyme	K.QFLILNDFPSVNEAIDQR.N	8.91	2.89	3.08	0.32
Q80YQ2_MED23_MOUSE	Med23	Mediator of RNA polyme	K.DVGNALLNVVLK#.S	16.62	6.37	2.61	0.38
Q80YQ2_MED23_MOUSE	Med23	Mediator of RNA polyme	K.FLTEALLPVVK#.T	15.33	4.97	3.09	0.32
Q80YQ2_MED23_MOUSE	Med23	Mediator of RNA polyme	K.GLLPYDK#DLFEPQTALLR@.Y	18.09	6.66	2.72	0.37
Q80YQ2_MED23_MOUSE	Med23	Mediator of RNA polyme	R.LITALGSSEVQPQFTR@.F	10.97	5.31	2.07	0.48
Q80YQ2_MED23_MOUSE	Med23	Mediator of RNA polyme	K.SSVALAPALVETYSR@.L	8.59	3.78	2.27	0.44
Q80YQ2_MED23_MOUSE	Med23	Mediator of RNA polyme	K.TVLSAESEELNR@.A	13.11	3.89	3.37	0.30
Q99K74_MED24_MOUSE	Med24	Mediator of RNA polyme	R.LLSSSDDDANILSSPTDR@.S	7.14	3.20	2.23	0.45
Q99K74_MED24_MOUSE	Med24	Mediator of RNA polyme	R.LQEGLEAGTPAPGEK#.Q	15.08	5.94	2.54	0.39
Q99K74_MED24_MOUSE	Med24	Mediator of RNA polyme	K.SLDLLLAAAAATGK#.L	11.95	7.23	1.65	0.61
Q99K74_MED24_MOUSE	Med24	Mediator of RNA polyme	K.SPEGLLGVLGHM*LSGK#.S	5.95	4.32	1.38	0.73
Q99K74_MED24_MOUSE	Med24	Mediator of RNA polyme	K.SSENANIQPNPGLILR@.A	7.24	1.97	3.68	0.27
Q99K74_MED24_MOUSE	Med24	Mediator of RNA polyme	K.VVLAITDLSLPLGR@.Q	15.08	4.45	3.39	0.29
Q99K74_MED24_MOUSE	Med24	Mediator of RNA polyme	R.LQEGLEAGTPAPGEK#.Q	9.07	4.54	2.00	0.50
Q99K74_MED24_MOUSE	Med24	Mediator of RNA polyme	K.VVLAITDLSLPLGR@.Q	19.43	8.22	2.36	0.42
Q920D3_MED28_MOUSE	Med28	Mediator of RNA polyme	K.K#PADM*PQGSLAFLEQASANIPAPLK#.Q	8.07	2.05	3.93	0.25
Q920D3_MED28_MOUSE	Med28	Mediator of RNA polyme	K.K#PADM*PQGSLAFLEQASANIPAPLK#QT.-	10.96	2.86	3.84	0.26
Q9CQI9_MED30_MOUSE	Med30	Mediator of RNA polyme	R.IGQETVQDIVYR@.T	32.46	10.96	2.96	0.34
Q9CQI9_MED30_MOUSE	Med30	Mediator of RNA polyme	R.TM*EIFQLLR@.N	73.79	21.49	3.43	0.29
Q9CQI9_MED30_MOUSE	Med30	Mediator of RNA polyme	R.TMEIFQLLR@.N	5.36	3.48	1.54	0.65
Q9CXU1_MED31_MOUSE	Med31	Mediator of RNA polyme	R.LQQALAEQQQQNNTAGK#.-	7.39	3.69	2.00	0.50
Q9CXU1_MED31_MOUSE	Med31	Mediator of RNA polyme	R.LQQALAEQQQQNNTAGK#.-	7.29	4.43	1.64	0.61
Q9CQA5_MED4_MOUSE	Med4	Mediator of RNA polyme	R.DSDIQQLQK#.Q	13.96	7.35	1.90	0.53
Q9CQA5_MED4_MOUSE	Med4	Mediator of RNA polyme	K.EAEQILATAVYQAK#.E	16.92	4.71	3.59	0.28
Q9CQA5_MED4_MOUSE	Med4	Mediator of RNA polyme	R.ELIEM*LAISR@.N	11.45	3.50	3.27	0.31
Q9CQA5_MED4_MOUSE	Med4	Mediator of RNA polyme	R.K#GAISSEEIIK#.Y	9.53	1.38	6.89	0.15
Q9CQA5_MED4_MOUSE	Med4	Mediator of RNA polyme	K.LLQLEEENQVLELLIHR@.D	36.27	10.48	3.46	0.29
Q9CQA5_MED4_MOUSE	Med4	Mediator of RNA polyme	R.LLSALEDLEVLSR@.E	21.76	6.85	3.18	0.31
Q9CQA5_MED4_MOUSE	Med4	Mediator of RNA polyme	R.M*GGVSGM*AGLGSTR@.E	21.05	6.63	3.18	0.31
Q9CQA5_MED4_MOUSE	Med4	Mediator of RNA polyme	R.R@PYPTDLEM*R@.S	7.85	2.77	2.84	0.35
Q921D4_MED6_MOUSE	Med6	Mediator of RNA polyme	K.R@K#EEPSSIFQR@.Q	23.86	11.40	2.09	0.48
Q9CZB6_MED7_MOUSE	Med7	Mediator of RNA polyme	K.EYTDENIQEGLAPK#PPPPIK#.D	12.23	8.53	1.43	0.70
Q9D7W5_MED8_MOUSE	Med8	Mediator of RNA polyme	K.QTFNPGDTNALVAAVAFGK#.G	16.36	5.75	2.85	0.35
P97367_MEIS2_MOUSE	Meis2	Homeobox protein Meis	R.IVQPM*IDQSNR@.A	8.48	6.71	1.26	0.79
P97367_MEIS2_MOUSE	Meis2	Homeobox protein Meis	K.M*PIDLVIDER@.D	8.26	2.47	3.34	0.30
O88559_MEN1_MOUSE	Men1	Menin OS=Mus musculus	R.GQTVNAGVAER@.S	3.89	2.85	1.37	0.73
Q8K3A9_MEPCE_MOUSE	Mepce	7SK snRNA methylphosp	R.LQAQTSEGDPGTEGEEGTITVR@.K	8.16	2.70	3.02	0.33
Q76I26_Q76I26_MOUSE	Methig1	Protein Methig1 OS=Mus	R.ELFSNLQEFAGPSGK#.L	3.42	1.06	3.24	0.31
Q9CQG2_MET16_MOUSE	Mettl16	Methyltransferase-like pr	R.EDFGLSIDIPLER@.L	4.21	3.01	1.40	0.71
Q8C3P7_MTA70_MOUSE	Mettl3	N6-adenosine-methyltra	K.K#VSQEILELLNTTTAK#.E	4.98	3.24	1.53	0.65
Q8C3P7_MTA70_MOUSE	Mettl3	N6-adenosine-methyltra	R.NPEAALSPTFR@.S	8.02	2.37	3.38	0.30
G3UYU0_G3UYU0_MOUSE	Mex3a	Protein Mex3a OS=Mus	R.DR@DPVFEITGAPGNVER@.A	5.99	3.54	1.69	0.59
G3UYU0_G3UYU0_MOUSE	Mex3a	Protein Mex3a OS=Mus	R.IQQQTNTYIITPSR@.D	5.90	2.38	2.48	0.40
G3UYU0_G3UYU0_MOUSE	Mex3a	Protein Mex3a OS=Mus	K.SGAAFGVAPALPGQVTIR@.V	6.96	2.48	2.80	0.36
G3UYU0_G3UYU0_MOUSE	Mex3a	Protein Mex3a OS=Mus	R.VVGLVVGPK#.G	10.28	7.26	1.42	0.71
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	R.LER@EDSSEEEEEEIDDEEIER@.R	10.84	5.90	1.84	0.54
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	R.DFSAPTLEDHFNK#.T	5.95	4.34	1.37	0.73
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	R.DVFER@PSAK#.K	34.42	20.66	1.67	0.60
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	R.EDSSEEEEEEIDDEEIER@.R	6.68	3.48	1.92	0.52
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	R.ISEDVEER@.L	75.99	49.35	1.54	0.65
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	K.IVEPEVVGESDSEVEGDAWR@.L	9.37	5.49	1.71	0.59
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	R.K#IVEPEVVGESDSEVEGDAWR@.L	5.09	3.69	1.38	0.72
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	R.LER@EDSSEEEEEEIDDEEIER@.R	18.42	5.22	3.53	0.28
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	K.QPPIQSTAGAVPVR.N	26.52	20.30	1.31	0.77
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	R.TK#YTHLVDQDTTSFDSAWGQESAQNTK#.F	8.87	3.84	2.31	0.43
Q9CQU1_MFAP1_MOUSE	Mfap1	Microfibrillar-associated	K.YTHLVDQDTTSFDSAWGQESAQNTK#.F	7.27	5.04	1.44	0.69
P21956_MFGM_MOUSE	Mfge8	Lactadherin OS=Mus mu	K.INAWTAQSNSAK#.E	11.43	5.42	2.11	0.47
P21956_MFGM_MOUSE	Mfge8	Lactadherin OS=Mus mu	R.K#FEFIQDESGGDK#EFLGNLDNNSLK#.V	7.04	3.66	1.92	0.52
P21956_MFGM_MOUSE	Mfge8	Lactadherin OS=Mus mu	R.QVTGIITQGAR@.D	30.58	15.65	1.95	0.51
P21956_MFGM_MOUSE	Mfge8	Lactadherin OS=Mus mu	R.TGIVNAWTASNYDSK#PWIQVNLLR@.K	4.56	1.38	3.31	0.30
P21956_MFGM_MOUSE	Mfge8	Lactadherin OS=Mus mu	K.VAYSLDGR@.K	60.38	27.08	2.23	0.45
P21956_MFGM_MOUSE	Mfge8	Lactadherin OS=Mus mu	K.VNM*FNPTLEAQYIK#.L	11.94	7.32	1.63	0.61
P21956_MFGM_MOUSE	Mfge8	Lactadherin OS=Mus mu	R.VSGVM*TQGASR@.A	27.31	363.07	0.08	13.29
P26187_MGMT_MOUSE	Mgmt	Methylated-DNA--protei	K.FGETVSYQQLAALAGNPK#.A	4.19	1.87	2.24	0.45
P19788_MGP_MOUSE	Mgp	Matrix Gla protein OS=M	R.NANTFM*SPQQR@.W	14.75	8.32	1.77	0.56
P19788_MGP_MOUSE	Mgp	Matrix Gla protein OS=M	R.YAM*VYGYNAAYNR@.Y	23.23	10.58	2.19	0.46
Q3TN34_MILK2_MOUSE	Micall2	MICAL-like protein 2 OS=	R.HR@PDLINFSALR@.K	10.66	7.25	1.47	0.68
Q3TN34_MILK2_MOUSE	Micall2	MICAL-like protein 2 OS=	K.VPNVVTAPTSK#.V	5.07	4.01	1.26	0.79
Q3TN34_MILK2_MOUSE	Micall2	MICAL-like protein 2 OS=	K.VPTVVTVPTSK#.V	12.50	6.93	1.80	0.55
Q3TN34_MILK2_MOUSE	Micall2	MICAL-like protein 2 OS=	K.VSPVVDAPAQESSR@.E	11.66	3.22	3.63	0.28
Q8VE19_MIO_MOUSE	Mios	WD repeat-containing pr	K.EAGNLEGILLTGLTK#.D	6.09	1.83	3.32	0.30
Q8VE19_MIO_MOUSE	Mios	WD repeat-containing pr	R.VASFYEGQVAIWDLR@.K	3.97	1.77	2.24	0.45
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	K.SPQVTTENITTNTK#PQTSTSGK#.K	4.76	3.67	1.30	0.77
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	K.TEAVLAENTTAR@.H	6.97	2.60	2.68	0.37
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	R.APGTPAPVQEENDSTAFM*ETPK#.Q	11.27	3.51	3.21	0.31
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	R.AQPLEDLDGFQELFQTPAGANDSVTVEESAK#.M	5.45	3.07	1.77	0.56
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	K.DITGFQDSFQIPDHANGPLVVVK#.T	12.42	2.81	4.42	0.23
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	K.ESTPQTLDSSASR@.T	10.49	5.21	2.01	0.50
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	R.GGM*VPVQTSTETAK#.M	9.07	3.57	2.54	0.39
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	K.GLSADSPASDGSK#.N	7.41	2.58	2.88	0.35
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	K.HENTVQTPK#.N	19.88	5.57	3.57	0.28
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	R.HSVNLDEGESAQAVHK#.T	21.51	16.10	1.34	0.75
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	R.HTLVETM*NEK#.T	6.28	1.56	4.02	0.25
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	K.ISLASSQAEPVR@.T	7.96	4.95	1.61	0.62
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	R.K#VDFSEDLSGLTEM*FK#.T	10.56	4.47	2.36	0.42
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	K.LPSSSPPLEPTDTSVTSR@.R	3.50	1.91	1.83	0.54
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	R.SGASEANLIVAK#.S	30.21	9.30	3.25	0.31
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	K.SPQVTTENITTNTK#PQTSTSGK#.K	9.65	2.87	3.36	0.30
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus	R.SQPLEDLDGFQELFQTPAGASDSVTVEESAK#.I	5.30	1.77	3.00	0.33

E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus m	K.SSGSTPVTAASSPK#.V	19.92	7.73	2.58	0.39
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus m	K.TEAVLAENTTAR@.H	15.42	2.91	5.30	0.19
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus m	K.TSVGNIAVR@.E	12.10	6.63	1.83	0.55
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus m	R.HSVNLDEGESAQAVHK#.T	11.14	4.20	2.65	0.38
E9PVX6_E9PVX6_MOUSE	Mki67	Protein Mki67 OS=Mus m	K.SSGSTPVTAASSPK#.V	7.07	3.27	2.16	0.46
Q6ZQI3_MLEC_MOUSE	Mlec	Malectin OS=Mus muscul	K.K#EEEEEEEEYDEGSNLK#R@.Q	8.49	3.70	2.30	0.44
Q6ZQI3_MLEC_MOUSE	Mlec	Malectin OS=Mus muscul	K.LYIEFVK#.G	10.69	6.39	1.67	0.60
Q6ZQI3_MLEC_MOUSE	Mlec	Malectin OS=Mus muscul	R.STPEDQILYQTER@.Y	23.85	12.87	1.85	0.54
Q6ZQI3_MLEC_MOUSE	Mlec	Malectin OS=Mus muscul	R.YNEETFGYEVPVK#EEGDYVLVLK#.F	11.46	6.51	1.76	0.57
Q9JK91_MLH1_MOUSE	Mlh1	DNA mismatch repair pro	R.TLPNATTVDNIR@.S	11.34	2.69	4.21	0.24
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	R.IVQATTLLTM*DK#.Y	5.09	11.15	0.46	2.19
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	R.ELQPQQQPR@.T	15.01	4.95	3.04	0.33
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	K.GILVFQLK#.R	12.57	5.89	2.13	0.47
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	K.IDDVLHTLTGAM*SLLR@.R	11.07	13.72	0.81	1.24
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	R.ISETTM*LQSGM*R@.L	5.38	1.37	3.92	0.26
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	R.IVQATTLLTM*DK#.Y	9.28	4.80	1.93	0.52
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	K.LPYLVELSPDGSDSR@.D	10.35	1.49	6.96	0.14
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	R.SM*DAETYVDGQR@.I	8.87	4.82	1.84	0.54
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	R.SQDADLPGSSGAPENLTFK#.E	5.30	1.65	3.20	0.31
E9Q852_E9Q852_MOUSE	Mllt4	Afadin OS=Mus musculus	K.TQVLSPDSLFTAK#.F	11.63	2.59	4.49	0.22
Q61391_NEP_MOUSE	Mme	Neprilysin OS=Mus musc	R.IGYPDDIISNENK#.L	5.67	4.01	1.41	0.71
Q61391_NEP_MOUSE	Mme	Neprilysin OS=Mus musc	K.ALYGTTSETATWR@.R	7.59	41.05	0.18	5.41
Q61391_NEP_MOUSE	Mme	Neprilysin OS=Mus musc	R.EDEYFENIIQNLK#.F	3.79	1.57	2.41	0.41
Q61391_NEP_MOUSE	Mme	Neprilysin OS=Mus musc	R.FIM*DLVSSLSR@.N	13.48	5.69	2.37	0.42
Q61391_NEP_MOUSE	Mme	Neprilysin OS=Mus musc	R.IGYPDDIISNENK#.L	10.05	4.24	2.37	0.42
Q61391_NEP_MOUSE	Mme	Neprilysin OS=Mus musc	R.LYVEAAFAGESK#.H	7.50	3.31	2.27	0.44
Q61391_NEP_MOUSE	Mme	Neprilysin OS=Mus musc	K.TEDIVAVQK#.A	19.20	8.29	2.32	0.43
Q8K273_MMGT1_MOUSE	Mmgt1	Membrane magnesium tr	R.VLFR@PSDATNSSNLDALSSNTSLK#.L	14.89	5.68	2.62	0.38
Q9D071_MMS19_MOUSE	Mms19	MMS19 nucleotide excisi	R.LPTSVLLPYK#.S	9.07	3.36	2.70	0.37
Q99LX5_MMTA2_MOUSE	Mmtag2	Multiple myeloma tumor	R.EALLAALGYK#.N	10.42	5.66	1.84	0.54
Q99LX5_MMTA2_MOUSE	Mmtag2	Multiple myeloma tumor	R.VDSEGPSTAPTAPR@.K	18.90	8.51	2.22	0.45
P51949_MAT1_MOUSE	Mnat1	CDK-activating kinase ass	R.EEDFPSLR@.E	25.49	13.06	1.95	0.51
P51949_MAT1_MOUSE	Mnat1	CDK-activating kinase ass	R.SM*K#PVTFSTGIK#.M	13.75	13.06	1.05	0.95
Q921Y0_MOB1A_MOUSE	Mob1a	MOB kinase activator 1A	R.ELAPLQELIEK#.L	22.96	9.01	2.55	0.39
Q921Y0_MOB1A_MOUSE	Mob1a	MOB kinase activator 1A	K.IGVPFPK#.N	11.61	6.64	1.75	0.57
Q921Y0_MOB1A_MOUSE	Mob1a	MOB kinase activator 1A	R.ELAPLQELIEK#.L	200.48	89.30	2.25	0.45
Q921Y0_MOB1A_MOUSE	Mob1a	MOB kinase activator 1A	K.HAEATLGSGNLR@.Q	37.87	16.45	2.30	0.43
Q921Y0_MOB1A_MOUSE	Mob1a	MOB kinase activator 1A	K.IGVPFPK#.N	117.46	48.42	2.43	0.41
Q921Y0_MOB1A_MOUSE	Mob1a	MOB kinase activator 1A	K.K#NIPEGSHQYELLK#.H	10.87	5.47	1.99	0.50
Q6PEB6_PHOCN_MOUSE	Mob4	MOB-like protein phocei	K.DNLIVPILEEEVQNSVSGESEA.-	5.29	5.29	1.00	1.00
A2BDX3_MOCS3_MOUSE	Mocs3	Adenylyltransferase and s	R.VPPPPLAPR@.A	503.86	479.10	1.05	0.95
A2BDX3_MOCS3_MOUSE	Mocs3	Adenylyltransferase and s	R.VPPPPLAPR.A	6.10	10.62	0.57	1.74
Q80UM7_MOGS_MOUSE	Mogs	Mannosyl-oligosaccharid	R.LGPLLDVLADSR@.H	10.55	3.68	2.87	0.35
Q8BMD7_MORC4_MOUSE	Morc4	MORC family CW-type zir	K.LNAYWK#.E	17.11	1.24	13.84	0.07
P60762_MO4L1_MOUSE	Morf4l1	Mortality factor 4-like pr	K.ANQEQYAEGK#.M	5.19	1.50	3.46	0.29
P60762_MO4L1_MOUSE	Morf4l1	Mortality factor 4-like pr	R.AR@VDPTVENEETFM*NR@.V	8.83	3.66	2.41	0.41
P60762_MO4L1_MOUSE	Morf4l1	Mortality factor 4-like pr	R.GNTDNK#EYAVNEVVAGIK#.E	9.23	2.56	3.61	0.28
P60762_MO4L1_MOUSE	Morf4l1	Mortality factor 4-like pr	K.NSATLFSASDYEVAPPEYHR@.K	8.55	4.33	1.97	0.51
P60762_MO4L1_MOUSE	Morf4l1	Mortality factor 4-like pr	K.VK#IPEELK#PWLVDDWDLITR@.Q	9.11	2.88	3.16	0.32
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.QVEKIR@YCITK.L	17.79	2.16	8.23	0.12
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.AQLETTLK#.S	39.86	21.36	1.87	0.54
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.EGEGGLPLQVEPEWR@.N	11.89	6.81	1.75	0.57
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.EGNSPSFFNPEEAATVTSYLK#.Q	18.08	7.34	2.46	0.41
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.ETGNPGGQLVLAGDPR@.Q	36.49	14.30	2.55	0.39
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.FESFLAER@.G	37.13	14.95	2.48	0.40
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.FNVAVTR@.A	22.34	7.55	2.96	0.34
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.FVDGLTFK#.V	25.75	11.81	2.18	0.46
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.GDHLFALLSSETQQDDPVTYK#.G	28.82	13.36	2.16	0.46
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.GVSLLPSDVK#.F	38.74	13.55	2.86	0.35
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.HGLGYSLLER@.L	24.54	7.87	3.12	0.32
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.HGVDVEVQGPHEAR@.D	46.82	12.23	3.83	0.26
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.HYDLDSVPM*TWDPVDQNPR@.L	6.17	2.92	2.12	0.47
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.IANLAFVTK#.T	42.45	18.70	2.27	0.44
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.LDLQQGQDLLQGLSK#.L	42.04	14.69	2.86	0.35
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.LLAYNSLYK#.K	39.78	14.45	2.75	0.36
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.LSFSTSLLSR@.F	30.61	9.40	3.26	0.31
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.QLLPTLLQGPSIFTAPK#.E	33.82	15.21	2.22	0.45
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.SLESNPEQLQAM*K#.H	27.13	14.89	1.82	0.55
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.SVILISTVR@.S	36.38	13.55	2.68	0.37
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.VGSVEEFQGQER@.S	42.81	17.35	2.47	0.41
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.VLITTLITASR@.L	44.11	16.88	2.61	0.38
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.VNFTFNR@.Q	22.83	9.59	2.38	0.42
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.WEGLPQQGFPIIFHGVM*GK#.D	13.25	7.02	1.89	0.53
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.EGEGGLPLQVEPEWR@.N	16.37	5.82	2.81	0.36
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.EGNSPSFFNPEEAATVTSYLK#.Q	16.14	7.72	2.09	0.48
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.ETGNPGGQLVLAGDPR@.Q	31.38	15.34	2.05	0.49
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.FESFLAER@.G	31.24	12.39	2.52	0.40
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.GDHLFALLSSETQQDDPVTYK#.G	28.91	11.94	2.42	0.41
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.GVSLLPSDVK#.F	37.65	10.59	3.55	0.28
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.HGLGYSLLER@.L	17.80	9.62	1.85	0.54
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.HGVDVEVQGPHEAR@.D	45.84	17.95	2.55	0.39
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.IANLAFVTK#.T	51.52	23.77	2.17	0.46
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.LDLQQGQDLLQGLSK#.L	40.85	15.17	2.69	0.37
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.LSFSTSLLSR@.F	21.59	9.94	2.17	0.46
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.NVGVISPYR@.K	21.10	5.55	3.80	0.26
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.QLLPTLLQGPSIFTAPK#.E	34.78	18.34	1.90	0.53
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.SLESNPEQLQAM*K#.H	20.93	9.24	2.26	0.44
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.SVILISTVR@.S	41.82	20.78	2.01	0.50
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	K.VGSVEEFQGQER.S	41.39	15.84	2.61	0.38
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.VLITTLITASR@.L	36.28	13.68	2.65	0.38
P23249_MOV10_MOUSE	Mov10	Putative helicase MOV-1(	R.WADVQLPEK#.R	6.72	6.75	0.99	1.01
Q8VBX6_MPDZ_MOUSE	Mpdz	Multiple PDZ domain pro	R.HATQEAVAALLK#.C	5.85	3.20	1.83	0.55
Q8VBX6_MPDZ_MOUSE	Mpdz	Multiple PDZ domain pro	R.IQIGDQIIAVDGTNLQGFTNQQAVEVLR@.H	5.39	8.56	0.63	1.59
Q8VBX6_MPDZ_MOUSE	Mpdz	Multiple PDZ domain pro	K.SLGISIVGGR@.G	9.94	5.68	1.75	0.57
I7HJS5_I7HJS5_MOUSE	Mpdz	Multiple PDZ domain pro	R.IGVAK#PLPIDTPDAESIAESR@.F	8.63	5.38	1.60	0.62
Q810V0_MPP10_MOUSE	Mphosph10	U3 small nucleolar ribon	K.RPENSLLEETLHFDHAVR.M	15.32	10.80	1.42	0.71
Q810V0_MPP10_MOUSE	Mphosph10	U3 small nucleolar ribon	R.VTFALPDDEAEDTSPLAVK.Q	8.44	6.36	1.33	0.75
Q9D1Q1_MPH6_MOUSE	Mphosph6	M-phase phosphoprotein	R.ANYEEDENGTIK#.A	4.67	2.53	1.84	0.54
Q9JLB0_MPP6_MOUSE	Mpp6	MAGUK p55 subfamily m	R.FIVLNPAR@.F	7.65	3.25	2.36	0.42
Q9JLB0_MPP6_MOUSE	Mpp6	MAGUK p55 subfamily m	K.GEILQIVNR@.E	6.62	3.98	1.66	0.60
Q9JLB0_MPP6_MOUSE	Mpp6	MAGUK p55 subfamily m	R.VENNDLVIAR@.I	10.54	3.47	3.04	0.33
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.EGEFTLSAM*TSGIR@.R	9.01	8.93	1.01	0.99
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.ELEVLSEQYSQK#.C	11.53	12.58	0.92	1.09

P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.FGM*LDTIDGPGM*EDTALR@.M	4.41	4.44	0.99	1.01
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.LLAEETAATISAIEAM*K#.N	18.05	17.15	1.05	0.95
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.M*AVTSSSGGSSGSSSSIPSAEK#VPTTK#.S	15.13	8.94	1.69	0.59
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.QEISSLK#DELQTALR@.D	19.39	18.01	1.08	0.93
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.QYLEELQSVQR@.E	7.85	6.65	1.18	0.85
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.SPEGTTVSGYDIM*K#.S	17.83	12.44	1.43	0.70
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.TFDWAEFR@PIQQALAQER@.A	14.32	12.87	1.11	0.90
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.TLLTGDGGGESTGLPLTQGK#.D	12.50	11.56	1.08	0.92
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.AATEALGEK#SPEGTTVSGYDIM*K#.S	17.32	6.04	2.87	0.35
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.AEEQLPPLLSPPSPSTPHSR@.R	11.14	5.31	2.10	0.48
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.DAYELEVLLR@.V	42.82	16.76	2.56	0.39
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.DIYTELSIAK#.A	23.29	6.02	3.87	0.26
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.EASDLLEQNR@.L	49.59	17.69	2.80	0.36
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.EGEFTLSAM*TSGIR@.R	41.71	12.41	3.36	0.30
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.FGM*LDTIDGPGM*EDTALR@.M	20.69	6.96	2.97	0.34
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.GFAAM*EETHQK#.K	13.56	4.22	3.21	0.31
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.HVLPASAPDVTSSLPEGK#.N	57.05	20.78	2.75	0.36
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.LLAEETAATISAIEAM*K#.N	120.06	35.93	3.34	0.30
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.LLAEETAATISAIEAMK#.N	18.97	8.80	2.16	0.46
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.LSTHELTSLLEK#.E	60.62	17.94	3.38	0.30
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.M*AVTSSSGGSSGSSSSIPSAEK#VPTTK#.S	23.57	7.22	3.26	0.31
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.MAVTSSSGGSSGSSSSIPSAEK#VPTTK#.S	8.99	6.91	1.30	0.77
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.NYGFQIHTK#.E	12.00	6.93	1.73	0.58
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.QEISSLK#DELQTALR@.D	67.77	20.10	3.37	0.30
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.QYLEELQSVQR@.E	27.54	10.57	2.61	0.38
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.SPEGTTVSGYDIM*K#.S	40.60	16.51	2.46	0.41
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.SPEGTTVSGYDIMK#.S	6.05	2.03	2.98	0.34
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.SPGLLGTPDLK#.T	64.14	24.74	2.59	0.39
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.SQISSINSDIEALR@.R	6.45	2.14	3.02	0.33
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.STEK#QEAEPGEPDPEQK#K#.S	25.58	9.01	2.84	0.35
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.STESSM*TPDLLNFK#.K	25.82	10.78	2.40	0.42
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.SVIEQVSWDN.-	9.67	9.67	1.00	1.00
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	K.TFDWAEFR@PIQQALAQER@.A	55.07	19.30	2.85	0.35
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.TLLTGDGGGESTGLPLTQGK#.D	47.24	8.19	5.77	0.17
P97434_MPRIP_MOUSE	Mprip	Myosin phosphatase Rho	R.VESGYFSLEK#.A	41.36	14.69	2.82	0.36
Q5SWZ5_Q5SWZ5_MOUSE	Mprip	Myosin phosphatase Rho	K.ASAYEDQLQGHVQQVEALQK#.E	8.00	4.17	1.92	0.52
Q5SWZ5_Q5SWZ5_MOUSE	Mprip	Myosin phosphatase Rho	R.ASLLQASALASQLEQER@.Q	6.06	3.67	1.65	0.61
Q5SWZ5_Q5SWZ5_MOUSE	Mprip	Myosin phosphatase Rho	K.DAK#EPLSTTEPTEEGSGILPLGSVTR@.V	8.16	7.59	1.08	0.93
Q5SWZ5_Q5SWZ5_MOUSE	Mprip	Myosin phosphatase Rho	R.DLETQQALQR@.D	9.72	5.82	1.67	0.60
Q5SWZ5_Q5SWZ5_MOUSE	Mprip	Myosin phosphatase Rho	R.LESQQGQSQEALLALHQQWAGTEAQLR@.E	4.47	2.62	1.71	0.59
Q5SWZ5_Q5SWZ5_MOUSE	Mprip	Myosin phosphatase Rho	R.VATSDGDVAELQEK#.L	11.73	5.27	2.23	0.45
Q5SWZ5_Q5SWZ5_MOUSE	Mprip	Myosin phosphatase Rho	R.VFPGFPHSQPEDEDPSAGLGEEGSSGSLSR@.E	3.34	7.30	0.46	2.19
Q5SWZ5_Q5SWZ5_MOUSE	Mprip	Myosin phosphatase Rho	R.VIQQILETLR.H	11.78	11.88	0.99	1.01
Q64449_MRC2_MOUSE	Mrc2	C-type mannose receptor	R.TLGDQLSLLLGAR.A	55.21	10.45	5.28	0.19
Q61216_MRE11_MOUSE	Mre11a	Double-strand break repa	K.EDENSWFNLFVIHQNR@.S	13.36	4.60	2.90	0.34
Q61216_MRE11_MOUSE	Mre11a	Double-strand break repa	R.FFIEDVVLANHPNLFNPDNPK#.V	24.21	5.85	4.14	0.24
Q61216_MRE11_MOUSE	Mre11a	Double-strand break repa	R.GNDTFVTFDEILR@.L	20.92	5.78	3.62	0.28
Q61216_MRE11_MOUSE	Mre11a	Double-strand break repa	R.HIDALEDK#IDEEVR@R@.F	37.55	15.50	2.42	0.41
Q61216_MRE11_MOUSE	Mre11a	Double-strand break repa	K.IGPIK#NEQQLFYVSQPGSSVVTSLSPGEAVK#.K	9.67	3.01	3.21	0.31
Q61216_MRE11_MOUSE	Mre11a	Double-strand break repa	K.LALYGLGSIPDER@.L	21.19	7.34	2.89	0.35
Q61216_MRE11_MOUSE	Mre11a	Double-strand break repa	K.NVQLSLLTER@.G	25.80	11.08	2.33	0.43
Q61216_MRE11_MOUSE	Mre11a	Double-strand break repa	K.VDISPVLLQK#.G	32.66	11.20	2.92	0.34
Q9CQT1_MTNA_MOUSE	Mri1	Methylthioribose-1-phos	R.AGAGGPGLAALVAFVR@.D	9.38	4.44	2.11	0.47
Q9CQT1_MTNA_MOUSE	Mri1	Methylthioribose-1-phos	R.DLGQVAAQEAER@EGATEETVR@.E	7.14	2.58	2.77	0.36
P58059_RT21_MOUSE	Mrps21	28S ribosomal protein S2	R.ILTTDGLTEVISR@.R	8.96	2.72	3.29	0.30
Q8VE22_RT23_MOUSE	Mrps23	28S ribosomal protein S2	K.ALLAEGIILR@.R	12.00	3.41	3.52	0.28
Q80ZS3_RT26_MOUSE	Mrps26	28S ribosomal protein S2	R.LQLEAQAQEVQK#.A	9.63	4.60	2.09	0.48
Q80X85_RT07_MOUSE	Mrps7	28S ribosomal protein S7	K.AAAATETSSVFADPVISK#.F	3.61	2.04	1.77	0.56
Q9D7N3_RT09_MOUSE	Mrps9	28S ribosomal protein S9	R.AIAYLFPSGLFEK#.R	7.61	4.28	1.78	0.56
Q9D0I8_MRT4_MOUSE	Mrto4	mRNA turnover protein 4	R.GEVGLLFTNR@.T	26.73	15.37	1.74	0.58
Q9D0I8_MRT4_MOUSE	Mrto4	mRNA turnover protein 4	K.LFGYEM*AEFK#.V	30.32	11.59	2.62	0.38
Q9D0I8_MRT4_MOUSE	Mrto4	mRNA turnover protein 4	R.SPSDEYK#DNLHQVSK#.K	35.08	14.52	2.42	0.41
Q9D0I8_MRT4_MOUSE	Mrto4	mRNA turnover protein 4	R.TK#EEVNEWFTK#.Y	21.21	15.28	1.39	0.72
Q9D0I8_MRT4_MOUSE	Mrto4	mRNA turnover protein 4	K.YTEM*DFAR@.A	28.45	13.82	2.06	0.49
Q9D0I8_MRT4_MOUSE	Mrto4	mRNA turnover protein 4	K.ATLTVSLDPGPLK.Q	9.43	10.88	0.87	1.15
Q9D0I8_MRT4_MOUSE	Mrto4	mRNA turnover protein 4	R.GEVGLLFTNR.T	6.74	5.48	1.23	0.81
Q9D0I8_MRT4_MOUSE	Mrto4	mRNA turnover protein 4	K.LFGYEM*AEFK#.V	9.52	5.97	1.59	0.63
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.ALNLFQGSVEDTTGSQSLAALLNK#.C	23.94	11.80	2.03	0.49
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.ASPGNLSQFEDILFGNNDM*SASVGVM*GIK#.M	6.74	4.52	1.49	0.67
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.DSLIIIDELGR@.G	34.17	16.69	2.05	0.49
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.ETLQLEGAAEAGFVR@.F	15.68	23.38	0.67	1.49
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.FTNSELSSLNEEYTK#.N	23.77	7.66	3.10	0.32
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.GDFYTAHGEDALLAAR@.E	16.37	7.62	2.15	0.47
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.HVGVGYVDSTQR@.K	12.02	4.44	2.71	0.37
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.IILEFLSK#.V	29.71	15.45	1.92	0.52
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.K#GEQINSAALPEM*ENQVAVSSLSAVIK#.F	14.36	5.37	2.68	0.37
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.LNLVEAFVEDSELR@.Q	20.66	10.11	2.04	0.49
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.LYQGINQLPSVIQALEK#.Y	8.73	3.43	2.55	0.39
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.M*QSTLINAAR@.G	13.55	6.54	2.07	0.48
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.NK#GEYEEAQDAIVK#.E	6.40	3.61	1.77	0.56
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.NNSFVNEIISR@.I	13.18	8.94	1.47	0.68
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.TLQSVVLSK#.M	29.09	15.99	1.82	0.55
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.DIYQDLNR@.L	24.12	8.31	2.90	0.34
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.DSLIIIDELGR@.G	54.16	12.49	4.34	0.23
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.ETLQLEGAAEAGFVR@.F	25.11	8.69	2.89	0.35
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.FTNSELSSLNEEYTK#.N	23.01	5.27	4.37	0.23
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.GDFYTAHGEDALLAAR@.E	24.52	7.38	3.32	0.30
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.GGILITER@.K	41.50	9.13	4.55	0.22
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.GVSTFM*AEM*LETASILR@.S	6.93	2.77	2.50	0.40
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.HVGVGYVDSTQR@.K	10.63	340.90	0.03	32.08
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.IILEFLSK#.V	28.34	10.41	2.72	0.37
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.K#GEQINSAALPEM*ENQVAVSSLSAVIK#.F	21.95	5.51	3.99	0.25
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.LDSSAQFGYYFR@.V	18.25	5.24	3.48	0.29
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.LNLVEAFVEDSELR@.Q	41.41	14.58	2.84	0.35
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.LYQGINQLPSVIQALEK#.Y	11.77	4.12	2.85	0.35
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	K.NK#GEYEEAQDAIVK#.E	18.65	8.58	2.17	0.46
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.QSLQEDLLR@.R	22.33	8.29	2.69	0.37
P43247_MSH2_MOUSE	Msh2	DNA mismatch repair pro	R.VGAGDSQLK#.G	35.60	13.42	2.65	0.38
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	R.LANLPEEVIQK.G	10.31	13.17	0.78	1.28
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	K.GR@FPDLTAELQR@.W	20.81	8.78	2.37	0.42
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	R.GTATFDGTAIANAVVK#.E	22.13	7.87	2.81	0.36
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	K.GTQTYSVLDGDPSENYSR@.Y	11.62	4.98	2.33	0.43
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	R.LANLPEEVIQK#.G	28.84	21.37	1.35	0.74

P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	R.M*NQSLQLFR@.E	10.17	6.33	1.61	0.62
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	R.SAAVSASSPEAK#.D	14.17	7.22	1.96	0.51
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	K.SIVYWGIGR@.N	9.34	4.54	2.06	0.49
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	R.TLVAHYPPVQILFEK#.G	12.78	9.16	1.39	0.72
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	R.VEQTETPEM*M*EAR@.C	9.31	6.88	1.35	0.74
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	R.VISDSESDIGGSDVEFK#PDTK#.Q	8.41	5.34	1.57	0.64
P54276_MSH6_MOUSE	Msh6	DNA mismatch repair pro	K.VSGLLEEVAGGFTSK#.T	33.88	15.75	2.15	0.47
Q61474_MSI1H_MOUSE	Msi1	RNA-binding protein Mus	R.GFGFVTFM*DQAGVDK#.V	11.13	4.24	2.63	0.38
Q61474_MSI1H_MOUSE	Msi1	RNA-binding protein Mus	K.HYFEQFGK#.V	11.02	5.70	1.94	0.52
Q61474_MSI1H_MOUSE	Msi1	RNA-binding protein Mus	R.SYTGLAPGYTYQFPEFR@.V	16.15	5.40	2.99	0.33
Q920Q6_MSI2H_MOUSE	Msi2	RNA-binding protein Mus	R.GFGFVTFADPASVDK.V	48.68	35.93	1.35	0.74
Q920Q6_MSI2H_MOUSE	Msi2	RNA-binding protein Mus	R.GFGFVTFENEDVVEK#.V	10.91	9.11	1.20	0.84
Q920Q6_MSI2H_MOUSE	Msi2	RNA-binding protein Mus	K.IFVGGLSANTVVEDVK#.Q	39.73	28.94	1.37	0.73
Q920Q6_MSI2H_MOUSE	Msi2	RNA-binding protein Mus	K.M*FIGGLSWQTSPDSLR@.D	8.93	5.62	1.59	0.63
Q920Q6_MSI2H_MOUSE	Msi2	RNA-binding protein Mus	K.VEDAM*LM*FDK#.T	5.09	4.38	1.16	0.86
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	K.GAAVQSIPVFGALR.S	14.84	12.80	1.16	0.86
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	R.GVLTWGLLPGPYSLGEPQK#.N	6.75	3.47	1.95	0.51
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	K.NPNLQGLLSAEGVR@.S	9.78	8.45	1.16	0.86
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	K.TAELLQDEYAGR.G	9.17	7.66	1.20	0.84
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	R.TLGDLAEELSR@.L	12.64	8.14	1.55	0.64
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	R.YLEELEDR@.L	7.51	6.15	1.22	0.82
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	K.NPNLQGLLSAEGVR@.S	6.05	4.36	1.39	0.72
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	K.GAAVQSIPVFGALR@.S	16.71	1.32	12.63	0.08
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	R.GVLTWGLLPGPYSLGEPQK#.N	7.46	2.25	3.32	0.30
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	K.NPNLQGLLSAEGVR@.S	12.68	24.71	0.51	1.95
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	K.TAELLQDEYAGR@.G	10.09	5.60	1.80	0.56
Q2YDW2_MSTO1_MOUSE	Msto1	Protein misato homolog	R.TLGDLAEELSR@.L	18.89	5.00	3.78	0.26
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	R.DISSSLIALADK.H	5.84	5.87	0.99	1.01
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	R.DISSSLIALADK#.H	30.38	10.57	2.87	0.35
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	R.EVEEEVENPEM*VDLPEK#.L	7.42	3.72	2.00	0.50
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	R.K#PLEAVLR@.Y	15.19	16.21	0.94	1.07
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	R.LPEASQSPLVLK#.Q	43.37	14.62	2.97	0.34
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	K.SSSSVLSSLTPAK#.S	18.27	8.28	2.21	0.45
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	K.SYLER@EDFFFYSLVYDPQQK#.T	5.01	2.80	1.79	0.56
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	K.YGK#DFTDIQQDFLPWK#.S	14.28	4.61	3.10	0.32
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	R.YQADITDLLK#.E	20.01	8.88	2.25	0.44
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	R.DISSSLIALADK#.H	16.12	3.44	4.68	0.21
F8WHY8_F8WHY8_MOUSE	Mta1	Metastasis-associated pro	R.LPEASQSPLVLK#.Q	12.39	3.53	3.51	0.28
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.DISSSLNSLADSNAR@.E	24.06	9.52	2.53	0.40
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.EFEEESK#QPGVSEQQR@.H	25.46	12.65	2.01	0.50
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.LPLATIVK#.D	19.64	8.74	2.25	0.45
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	K.TPTQLEGAAR@.G	35.96	9.07	3.96	0.25
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.VGDYVYFENSSSNPYLVR@.R	20.81	7.25	2.87	0.35
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	K.VWDPDNPLTDR@.Q	14.43	7.53	1.92	0.52
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.DISSSLNSLADSNAR@.E	40.12	10.83	3.70	0.27
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	K.DLVAQAPLK#PK#.T	32.45	9.28	3.50	0.29
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.EFEEESK#QPGVSEQQR@.H	60.03	9.71	6.18	0.16
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	K.FQAEIPDR@.L	35.04	11.54	3.04	0.33
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.GHLSR@PEAQSLSPYTTSANR@.A	20.24	3.19	6.35	0.16
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.GLGGIM*VK#.R	30.19	7.41	4.07	0.25
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	K.LNPADAPNPVVFVATK#.D	32.85	10.89	3.02	0.33
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.LPLATIVK#.D	51.13	13.10	3.90	0.26
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.QK#LNPADAPNPVVFVATK#.D	20.52	3.98	5.15	0.19
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	K.TPTQLEGAAR@.G	81.77	22.71	3.60	0.28
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.VGDYVYFENSSSNPYLVR@.R	24.56	6.33	3.88	0.26
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	K.VWDPDNPLTDR@.Q	30.29	7.36	4.11	0.24
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	R.DISSSLNSLADSNAR@.E	6.96	2.13	3.27	0.31
Q9R190_MTA2_MOUSE	Mta2	Metastasis-associated pro	K.TPTQLEGAAR@.G	11.46	14.36	0.80	1.25
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	K.QIDQFLVVAR.S	37.77	12.62	2.99	0.33
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	R.VGDYVYFENSSSNPYLIR@.R	6.57	3.39	1.94	0.52
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	K.DFNDIR@QDFLPWK#.S	17.69	3.95	4.48	0.22
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	K.ETEEESETPVEADLTEK#.Q	7.23	3.11	2.33	0.43
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	R.HR@ELFLSR@.Q	23.82	9.75	2.44	0.41
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	K.QIDQFLVVAR@.S	71.03	22.42	3.17	0.32
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	R.VGDYVYFENSSSNPYLIR@.R	13.04	3.27	3.99	0.25
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	K.ETEEESETPVEADLTEK#.Q	9.32	2.31	4.03	0.25
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	K.QIDQFLVVAR@.S	30.60	2.89	10.59	0.09
Q924K8_MTA3_MOUSE	Mta3	Metastasis-associated pro	R.VGDYVYFENSSSNPYLIR@.R	9.40	3.86	2.43	0.41
Q9CQ65_MTAP_MOUSE	Mtap	S-methyl-5'-thioadenosin	K.IGIIGGTGLDDPEILEGR.T	2.16	3.35	0.65	1.55
Q791V5_MTCH2_MOUSE	Mtch2	Mitochondrial carrier ho	R.GLFTGLTPR@.L	13.42	1.74	7.72	0.13
Q791V5_MTCH2_MOUSE	Mtch2	Mitochondrial carrier ho	K.VLQYYQESEK#PEELGSVTVQK#.E	10.30	2.42	4.26	0.23
Q3UHU5_MTCL1_MOUSE	Mtcl1	Microtubule cross-linkin	R.AGPAEPLSR@.V	9.82	4.83	2.03	0.49
Q3UHU5_MTCL1_MOUSE	Mtcl1	Microtubule cross-linkin	K.GPAASVPLQEELK#.S	13.25	2.90	4.57	0.22
Q3UHU5_MTCL1_MOUSE	Mtcl1	Microtubule cross-linkin	R.IVDGLSPLSHLTESSSFLSTVTSVSR@.D	11.97	3.94	3.04	0.33
Q3UHU5_MTCL1_MOUSE	Mtcl1	Microtubule cross-linkin	K.IVELEVENR@.G	9.65	3.02	3.19	0.31
Q3UHU5_MTCL1_MOUSE	Mtcl1	Microtubule cross-linkin	R.LQIDELSGK#.V	14.23	1.64	8.66	0.12
Q3UHU5_MTCL1_MOUSE	Mtcl1	Microtubule cross-linkin	R.QELGPGQETGTSSR@.G	2.98	1.61	1.85	0.54
Q3UHU5_MTCL1_MOUSE	Mtcl1	Microtubule cross-linkin	K.SLGELDSSAEGK#.G	13.34	4.18	3.19	0.31
P00405_COX2_MOUSE	Mtco2	Cytochrome c oxidase su	R.ILYM*M*DEINNPVLTVK#.T	6.61	2.25	2.94	0.34
Q8BKY8_MTEF2_MOUSE	Mterf2	Transcription terminatio	R.AVGETLK#.C	1137.64	519.76	2.19	0.46
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	K.AYTEEDLDLVEK#.G	18.38	7.42	2.48	0.40
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	R.EIGLLTEEVELYGETK#.A	10.78	3.77	2.86	0.35
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	K.GVPTGFVLPIR@.D	21.81	12.32	1.77	0.57
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	R.M*FGVPVVVAVNVFK#.T	16.55	2.93	5.64	0.18
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	K.STTTIGLVQALGAHLR@.Q	15.42	4.83	3.19	0.31
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	K.TDPTTLTDDEINR@.F	19.29	9.32	2.07	0.48
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	K.TPVPSDIAISR@.S	21.81	9.18	2.38	0.42
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	K.VVGDVAYDEAK#.E	7.82	4.24	1.85	0.54
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	R.ASQAPSSFQLLYDLK#.L	5.06	2.19	2.31	0.43
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	R.EIGLLTEEVELYGETK#.A	6.29	1.82	3.46	0.29
Q922D8_C1TC_MOUSE	Mthfd1	C-1-tetrahydrofolate syn	K.GVPTGFVLPIR@.D	7.88	1.48	5.33	0.19
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	K.AAVELVEK#.S	20.74	8.71	2.38	0.42
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	R.FQFLYDVQLPIVEK#.I	17.67	4.24	4.17	0.24
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	K.LIAEESVSLLAAALR@.I	22.80	7.42	3.07	0.33
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	R.LNIDPATITWQR@.V	11.34	7.31	1.55	0.64
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	K.LSGGSPGVPVDK#.L	15.81	5.70	2.77	0.36
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	K.M*HGGGPSVTAGVPLK#K#.E	8.26	4.27	1.94	0.52
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	R.VHGLTLQISEDSLSNK#.V	12.49	6.73	1.86	0.54
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	R.VIAQTVYGAK#.D	26.60	7.81	3.40	0.29
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	K.VQLSLLER@.L	17.21	10.08	1.71	0.59
Q3V3R1_C1TM_MOUSE	Mthfd1l	Monofunctional C1-tetra	K.YVLVAGITPTPLGEGK#.S	14.24	4.77	2.98	0.34
Q6DID5_MUM1_MOUSE	Mum1	PWWP domain-containi	R.VALDVLNER@.T	13.24	5.15	2.57	0.39
A2AMM0_MURC_MOUSE	Murc	Muscle-related coiled-co	K.GGYSPQEGGDPPTPEPLK#.V	10.80	7.22	1.50	0.67

A2AMM0_MURC_MOUSE	Murc	Muscle-related coiled-co	K.LSQSHSNTGYVVNK#.L	67.06	28.22	2.38	0.42
A2AMM0_MURC_MOUSE	Murc	Muscle-related coiled-co	R.LSSVTEDEDQDAALTIVTVLDR@.V	22.62	11.80	1.92	0.52
A2AMM0_MURC_MOUSE	Murc	Muscle-related coiled-co	K.SVQIDLLK#.L	13.15	5.56	2.37	0.42
A2AMM0_MURC_MOUSE	Murc	Muscle-related coiled-co	R.VASVVDSVQASQK#.R	60.53	18.13	3.34	0.30
A2AMM0_MURC_MOUSE	Murc	Muscle-related coiled-co	K.VTFK#PQVR@.V	9.58	3.66	2.62	0.38
Q9EQK5_MVP_MOUSE	Mvp	Major vault protein OS=	K.ALQPLEEGEGEEK#.V	6.78	4.20	1.61	0.62
Q9EQK5_MVP_MOUSE	Mvp	Major vault protein OS=	R.GIQDVYVLSEQQGLLLK#.A	8.65	0.00	#DIV/0!	0.00
Q9EQK5_MVP_MOUSE	Mvp	Major vault protein OS=	R.IEGEGSVLQAK#.L	9.76	7.70	1.27	0.79
Q9EQK5_MVP_MOUSE	Mvp	Major vault protein OS=	K.ILDQSEAEK#.A	7.73	6.47	1.19	0.84
Q9EQK5_MVP_MOUSE	Mvp	Major vault protein OS=	K.SFFLQPGER@.L	12.10	6.28	1.93	0.52
Q9EQK5_MVP_MOUSE	Mvp	Major vault protein OS=	R.VVFGPELVSLDPEEQFTVLSLSAGR@PK#.R	14.37	7.45	1.93	0.52
Q9CZH7_MXRA7_MOUSE	Mxra7	Matrix-remodeling-assoc	R.VAEPEESEAEEPAAEGR@.Q	8.82	4.77	1.85	0.54
O35682_MYADM_MOUSE	Myadm	Myeloid-associated differ	R.TTITTTTSSSTTVGSAR@.A	12.73	5.85	2.17	0.46
O35682_MYADM_MOUSE	Myadm	Myeloid-associated differ	R.ALTQPLGLLR@.L	83.68	46.65	1.79	0.56
O35682_MYADM_MOUSE	Myadm	Myeloid-associated differ	R.ARPGEITGYM*ATVPGLLK.V	23.71	12.56	1.89	0.53
O35682_MYADM_MOUSE	Myadm	Myeloid-associated differ	R.TTITTTTSSSTTVGSAR@.A	118.91	61.69	1.93	0.52
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.AEPATPAEAAQSDR@.H	29.20	8.98	3.25	0.31
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.ALDLIEVLVTK#.Q	9.75	5.05	1.93	0.52
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.ATQTLQTLGEAQSK#.G	10.97	1.79	6.13	0.16
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.FELFWK#.K	10.72	4.37	2.46	0.41
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LLGASLPLLSEEQLQLVM*R@.G	18.37	3.34	5.49	0.18
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LPNVALDLLR@.L	28.28	6.74	4.19	0.24
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LSVDLTAPLGVLQSK#.Q	7.96	4.31	1.84	0.54
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.NAASQQDAVTEGAM*PAATGK#.D	6.79	5.87	1.16	0.86
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.NVTSVTSLTTQQR@.Q	10.99	3.53	3.11	0.32
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.SPAPSNPTLSPSTPAK#.T	19.83	14.91	1.33	0.75
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.TK#K#ATPQIPETK#.Q	35.66	125.78	0.28	3.53
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.YLELFLLAK#.Q	23.68	3.70	6.40	0.16
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.AEPATPAEAAQSDR@.H	25.35	14.61	1.73	0.58
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.AQDASLNVPER@.A	18.13	14.71	1.23	0.81
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LLGASLPLLSEEQLQLVM*R@.G	18.55	1.84	10.09	0.10
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LPNVALDLLR@.L	25.30	4.08	6.20	0.16
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.VLEEGLLK#.N	9.04	1.51	5.99	0.17
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.AEPATPAEAAQSDR@.H	40.11	23.77	1.69	0.59
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.ALDLIEVLVTK#.Q	68.56	38.33	1.79	0.56
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.ATQTLQTLGEAQSK#.G	47.63	23.98	1.99	0.50
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.DM*FLQPDLNSLVDFSTANQK#.R	17.72	10.02	1.77	0.57
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.DM*FLQPDLNSLVDFSTANQK#.R	7.89	3.88	2.04	0.49
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.EFLDFFWDIAK#PDQETR@.L	32.23	19.28	1.67	0.60
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.ELSILELLNTLLR@.T	42.11	26.16	1.61	0.62
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.FLNAEALQSYVAWLR@.D	6.65	3.40	1.96	0.51
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.GFLPETK#.K	29.81	15.14	1.97	0.51
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LITGLGVGR@.E	70.33	38.64	1.82	0.55
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LK#SEGTTPEK#.N	5.68	3.40	1.67	0.60
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LLEYLR@.T	52.30	25.35	2.06	0.48
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LLGASLPLLSEEQLQLVM*R@.G	11.76	5.13	2.29	0.44
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LPNVALDLLR@.L	90.90	49.29	1.84	0.54
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LQQSLQQGNHSSGSNR@.L	6.56	3.39	1.93	0.52
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LSVDLTAPLGVLQSK#.Q	84.92	51.66	1.64	0.61
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.NAASQQDAVTEGAM*PAATGK#.D	11.71	7.83	1.50	0.67
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.NVTSVTSLTTQQR@.Q	67.44	33.39	2.02	0.50
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.QAWDQM*M*STLK#.E	7.12	5.81	1.23	0.82
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.SPAPSNPTLSPSTPAK#.T	36.64	19.73	1.86	0.54
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.SPSLLQSGVK#.K	33.30	16.18	2.06	0.49
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.VLEEGLLK#.N	38.95	23.66	1.65	0.61
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.VYSASLESLLTK#.R	68.77	28.12	2.45	0.41
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.YLELFLLAK#.Q	58.20	29.29	1.99	0.50
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.AEPATPAEAAQSDR@.H	102.86	43.24	2.38	0.42
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.ALDLIEVLVTK#.Q	177.92	78.97	2.25	0.44
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.ALVDILSEVPESM*FQEILPK#.V	21.95	12.99	1.69	0.59
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.AQDASLNVPER@.A	191.91	85.37	2.25	0.44
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.ATQTLQTLGEAQSK#.G	100.21	40.81	2.46	0.41
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.DEAVVEQIAR@.F	9.42	17.09	0.55	1.81
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.DIPSDTQSPVSTK#.R	61.76	29.13	2.12	0.47
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.DIPSDTQSPVSTK#R@.K	8.27	3.32	2.49	0.40
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.DM*FLQPDLNSLVDFSTANQK#.R	69.31	28.08	2.47	0.41
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.EHK#LPNVALDLLR@.L	70.18	25.60	2.74	0.36
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.FELFWK#.K	35.19	23.78	1.48	0.68
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.FLNAEALQSYVAWLR@.D	12.68	5.74	2.21	0.45
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.GFLPETK#.K	79.80	38.91	2.05	0.49
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.HFGENM*VISK#PQNLFK#.I	46.34	18.26	2.54	0.39
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.K#ATPQIPETK#.Q	38.97	18.27	2.13	0.47
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.K#GFLPETK#.K	30.82	9.13	3.38	0.30
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LITGLGVGR@.E	197.93	81.36	2.43	0.41
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LLEYLR@.T	128.62	47.75	2.69	0.37
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LLGASLPLLSEEQLQLVM*R@.G	133.30	51.02	2.61	0.38
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LLGASLPLLSEEQLQLVM*R.G	43.69	15.92	2.74	0.36
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LPNVALDLLR@.L	184.68	83.75	2.21	0.45
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LQQSLQQGNHSSGSNR.L	11.82	6.53	1.81	0.55
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LSQVNGATPVSPIEPESK#.K	10.45	3.19	3.28	0.31
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.LSVDLTAPLGVLQSK#.Q	299.87	120.64	2.49	0.40
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LVQLADM*LLNHNR.N	16.58	6.16	2.69	0.37
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LYDLYWQAM*R@.M	14.77	6.32	2.34	0.43
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.LYDLYWQAMR@.M	9.66	4.47	2.16	0.46
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.M*LGVQR@PK#.S	19.88	10.87	1.83	0.55
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.NAASQQDAVTEGAM*PAATGK#.D	37.75	14.86	2.54	0.39
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.NAASQQDAVTEGAM*PAATGK#.D	26.56	15.27	1.74	0.57
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.NAASQQDAVTEGAMPAATGK#.D	6.38	4.01	1.59	0.63
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.NAASQQDAVTEGAM*PAATGK#DQPPSTGK#.K	10.26	5.68	1.80	0.55
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.NVTSVTSLTTQQR@.Q	158.40	62.21	2.55	0.39
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.QAWDQM*M*STLK#.E	19.26	5.24	3.67	0.27
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.QHFSFPLDDR@.N	53.46	15.51	3.45	0.29
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.SPAPSNPTLSPSTPAK#.T	119.78	44.33	2.70	0.37
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.SPSLLQSGVK#.K	103.55	32.60	3.18	0.31
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.SPTK#AEPATPAEAAQSDR@.H	11.48	4.03	2.85	0.35
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.VLEEGLLK#.N	85.86	31.26	2.75	0.36
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	R.VYSASLESLLTK#.R	152.61	56.22	2.71	0.37
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.YLELFLLAK#.Q	43.93	19.06	2.30	0.43
Q7TPV4_MBB1A_MOUSE	Mybbp1a	Myb-binding protein 1A	K.YSLQAM*NK#.A	59.75	23.30	2.56	0.39
Q9EQS3_MYCBP_MOUSE	Mycbp	C-Myc-binding protein O	K.LVQYEPPQEEK#.R	38.63	21.33	1.81	0.55
Q9EQS3_MYCBP_MOUSE	Mycbp	C-Myc-binding protein O	K.SGVLDTLTK#.V	29.51	15.77	1.87	0.53
Q9EQS3_MYCBP_MOUSE	Mycbp	C-Myc-binding protein O	K.VLVALYEEPEK#PTSALDFLK#.H	27.13	12.81	2.12	0.47
Q7TPH6_MYCB2_MOUSE	Mycbp2	E3 ubiquitin-protein liga	K.NAIAETIIALTK#.M	10.19	2.84	3.60	0.28

Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.EVFSIAGTVK.R	18.85	21.07	0.89	1.12
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.FESAESAEK.A	22.49	31.31	0.72	1.39
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.GFGDSFGR@.L	52.17	62.66	0.83	1.20
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.GFLSGPM*GSGM*R.D	22.47	19.96	1.13	0.89
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.LGSAM*IGGFAGR@.I	29.33	33.63	0.87	1.15
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.LGSTIFVANLDFK#.V	39.27	36.45	1.08	0.93
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.M*GPGIGAILER.S	41.50	47.29	0.88	1.14
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.MGPGIGAILER.S	3.94	6.23	0.63	1.58
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.NLPFDLTWQK#.L	54.69	48.46	1.13	0.89
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.VFISNIPYDM*K#.W	38.94	51.92	0.75	1.33
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.VFISNIPYDMK.W	8.64	13.64	0.63	1.58
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.VGEVTYVELFK#.D	32.17	43.36	0.74	1.35
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.VGEVTYVELFK#DAEGK#.S	26.04	29.57	0.88	1.14
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.YDLSGRPLNIKEDPDGENAR.R	6.06	7.17	0.85	1.18
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.GFLSGPM*GSGM*R.D	4.91	6.99	0.70	1.42
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.LGSAM*IGGFAGR@.I	9.49	9.60	0.99	1.01
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.M*GPGIGAILER.S	25.49	32.79	0.78	1.29
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.NLPFDLTWQK#.L	15.45	27.99	0.55	1.81
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.EK#VGEVTYVELFK#.D	18.55	11.65	1.59	0.63
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.EK#VGEVTYVELFK#DAEGK#.S	8.48	2.37	3.58	0.28
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.EVFSIAGTVK#.R	40.20	26.23	1.53	0.65
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.FESAESAEK#.A	24.07	18.05	1.33	0.75
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.GFGDSFGR.L	61.23	54.27	1.13	0.89
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.GFLSGPM*GSGM*R@.D	26.67	19.45	1.37	0.73
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.GNQIFVR@.N	74.14	59.13	1.25	0.80
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.LGSAM*IGGFAGR@.I	33.56	24.51	1.37	0.73
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.LGSTIFVANLDFK#.V	59.14	38.67	1.53	0.65
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.LKEVFSIAGTVK.R	46.30	34.71	1.33	0.75
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.M*ENDESVK#EEK#.S	4.10	2.53	1.62	0.62
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.M*GPGIGAILER@.S	76.30	58.80	1.30	0.77
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.NLPFDLTWQK#.L	73.53	59.27	1.24	0.81
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.RDTHPGEPEKPPR.S	25.70	21.55	1.19	0.84
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	R.VFISNIPYDM*K#.W	50.46	37.18	1.36	0.74
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.VGEVTYVELFK#.D	59.08	47.26	1.25	0.80
Q8C854_MYEF2_MOUSE	Myef2	Myelin expression factor	K.YDLSGRPLNIKEDPDGENAR.R	8.61	7.98	1.08	0.93
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ELDDATEANEGLSR@.E	6.94	5.08	1.37	0.73
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ALEEALEAK#EEFER@.Q	19.22	11.51	1.67	0.60
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.DAAGLESQLQDTQELLQEETR.Q	5.80	8.22	0.71	1.42
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ELDDATEANEGLSR@.E	16.10	12.70	1.27	0.79
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.FDQLLAEEK#.G	10.92	6.85	1.59	0.63
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.HAEQER@DELADEIANSASGK#.S	6.06	4.25	1.42	0.70
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.IGQLEEQLEQEAK#.E	21.78	16.82	1.30	0.77
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.KFDQLLAEEK.G	17.45	21.30	0.82	1.22
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.LDPHLVLDQLR.C	10.16	12.09	0.84	1.19
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.LQQLFNHTM*FILEQEEYQR.E	5.86	4.65	1.26	0.79
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.NILAEQLQAETELFAEAEEM*R@.A	12.12	7.06	1.72	0.58
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.QLEEAEEEATR@.A	5.11	7.24	0.70	1.42
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.QVLALQSQLADTK.K	5.39	6.20	0.87	1.15
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.TQLEELEDELQATEDAK#.L	9.53	7.91	1.20	0.83
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.TTLQVDTLNTELAAER@.S	7.78	4.99	1.56	0.64
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.ADEWLM*K#.N	69.60	43.37	1.60	0.62
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ADM*EDLM*SSK#.D	49.62	30.33	1.64	0.61
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.AGK#LDPHLVLDQLR@.C	112.73	81.93	1.38	0.73
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.AGVLAHLEEER@.D	653.49	370.46	1.76	0.57
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.AGVLAHLEEER.D	151.01	88.75	1.70	0.59
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.AGVLAHLEEER@DLK#.I	363.90	185.45	1.96	0.51
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.AK#LQELEGAVK#.S	69.36	63.25	1.10	0.91
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ALEEALEAK#.E	95.19	81.05	1.17	0.85
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ALEEALEAK#EEFER@.Q	576.75	375.35	1.54	0.65
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ALELDPNLYR@.I	551.26	379.96	1.45	0.69
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ALEQQVEEM*R@.T	158.33	113.20	1.40	0.71
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ALEQQVEEMR@.T	49.45	33.73	1.47	0.68
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ALEQQVEEM*R@TQLEELEDELQATEDAK#.L	79.42	50.09	1.59	0.63
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.AM*VNKDDIQK.M	56.16	40.78	1.38	0.73
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.ANKLQNELDNVSTLLEEAEK.K	20.20	12.84	1.57	0.64
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.ATDK#TFVEK#.L	25.96	18.39	1.41	0.71
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.ATISALEAK#.I	535.64	356.51	1.50	0.67
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.AVIYNPATQADWTAK#.K	188.85	131.90	1.43	0.70
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.DAAGLESQLQDTQELLQEETR@.Q	592.61	382.01	1.55	0.64
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.DAAGLESQLQDTQELLQEETR.Q	78.78	53.53	1.47	0.68
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.DDVGK#NVHELEK#.S	65.26	39.56	1.65	0.61
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.DDVGK#NVHELEK#.S	5.69	2.54	2.24	0.45
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.DEIFAQSK#.E	84.19	73.55	1.14	0.87
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.DELADEIANSASGK#.S	53.77	41.02	1.31	0.76
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.DHNIPGELER.Q	35.02	28.45	1.23	0.81
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.DLEAQIEAANK#.A	105.24	83.65	1.26	0.79
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.DLSEELEALK#.T	33.35	27.58	1.21	0.83
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.DR@AEAEAR@.E	25.03	14.47	1.73	0.58
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.DVDR@IVGLDQVTGM*TETAFGSAYK#.T	4.62	3.75	1.23	0.81
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.DVEALSQR@.L	151.49	114.99	1.32	0.76
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.EEELQGALAR@.G	41.45	29.83	1.39	0.72
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.EIFM*QVEDER@.R	10.93	10.57	1.03	0.97
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ELDDATEANEGLSR@.E	434.90	312.13	1.39	0.72
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ELEAELEDER@.K	147.79	110.40	1.34	0.75
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.ELQAQIAELQEDFESEK#.A	355.94	216.53	1.64	0.61
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.EQADFAVEALAK#.A	442.19	279.50	1.58	0.63
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.EQEVAELK#.K	44.10	34.01	1.30	0.77
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.ER@NTDQASM*PENTVAQK#.L	18.15	8.74	2.08	0.48
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.FDQLLAEEK#.G	241.49	160.23	1.51	0.66
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.FK#ATISALEAK#.I	52.75	24.30	2.17	0.46
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.FLSNGYIPIPGQQDK#.D	28.79	16.41	1.75	0.57
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.GDDETLHK#.N	43.96	32.77	1.34	0.75
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.GGPISFSSSR@.S	128.76	95.49	1.35	0.74
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.HAEQER@DELADEIANSASGK#.S	144.84	92.34	1.57	0.64
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.HATALEELSEQLEQAK#.R	199.27	138.22	1.44	0.69
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.HATALEELSEQLEQAK#.R	13.17	8.34	1.58	0.63
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.HATALEELSEQLEQAK#R@.F	119.51	66.18	1.81	0.55
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.HATALEELSEQLEQAKR.F	373.99	205.40	1.82	0.55
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.HEM*PPHIYAISESAYR@.C	51.23	32.88	1.56	0.64
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.HGFEAASIK#.E	59.33	52.46	1.13	0.88
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.HGFEAASIK#EER@.G	223.83	161.16	1.39	0.72
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	K.HQQLLEEK#.N	151.94	119.95	1.27	0.79
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc	R.IAQLEEELEEEQSNM*ELLNDR@.F	172.89	133.24	1.30	0.77

Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.IAQLEEELEEEQSNM*ELLNDR.F	11.17	11.01	1.01	0.99
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.IAQLEEELEEEQSNMELLNDR@.F	38.10	30.57	1.25	0.80
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.IAQLEEELEEEQSNM*ELLNDR@FR@.K	18.47	13.54	1.36	0.73
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.IGQLEEQLEQEAK#.E	665.04	426.15	1.56	0.64
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.IKKM*EEEVLLLEDQNSK.F	34.97	23.09	1.51	0.66
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.IVFQEFR@.Q	470.76	333.70	1.41	0.71
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.IVGLDQVTGM*TETAFGSAYK#.T	252.52	153.22	1.65	0.61
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.IVGLDQVTGMTETAFGSAYK#.T	29.36	15.53	1.89	0.53
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.K#DHNIPGELER@.Q	65.66	52.77	1.24	0.80
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.KEEELQGALAR.G	268.22	169.88	1.58	0.63
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#EEELQGALAR@.G	73.92	62.51	1.18	0.85
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#FDQLLAEEK#.G	490.12	310.35	1.58	0.63
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.KHQQLLEEK.N	338.66	227.75	1.49	0.67
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.KKLDAQVQELHAK.V	59.67	36.94	1.62	0.62
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.KKVDDDLGTIESLEEAK.K	177.85	135.25	1.31	0.76
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#LDAQVQELHAK#.V	199.93	163.51	1.22	0.82
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.KLDAQVQELHAK.V	15.20	8.49	1.79	0.56
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.K#LDGETTDLQDQIAELQAQVDELK#.V	429.05	284.00	1.51	0.66
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.K#LDGETTDLQDQIAELQAQVDELK#VQLTK#.K	85.83	39.46	2.18	0.46
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.K#LQAQM*K#.D	19.92	13.54	1.47	0.68
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.KLVWIPSER.H	52.85	35.73	1.48	0.68
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.KM*EEEVLLLEDQNSK.F	62.94	48.74	1.29	0.77
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#MEEEVLLLEDQNSK#.F	23.24	14.33	1.62	0.62
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#M*QAHIQDLEEQLDEEEGAR@.Q	50.15	27.52	1.82	0.55
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.KM*QAHIQDLEEQLDEEEGAR.Q	15.11	9.81	1.54	0.65
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#MQAHIQDLEEQLDEEEGAR@.Q	8.72	7.37	1.18	0.84
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#QELEEILHDLESR@.V	359.14	239.49	1.50	0.67
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#QQQLSALK#.V	151.44	106.75	1.42	0.70
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.KTTLQVDTLNTELAAER.S	182.70	112.65	1.62	0.62
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.K#TTLQVDTLNTELAAER@.S	6.00	5.07	1.18	0.84
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#VDDDLGTIESLEEAK#.K	186.57	137.85	1.35	0.74
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.K#VDDDLGTIESLEEAK#K#.K	177.85	135.25	1.31	0.76
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LDGETTDLQDQIAELQAQVDELK#.V	51.22	37.39	1.37	0.73
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LDPHLVLDQLR.C	914.74	591.74	1.55	0.65
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.LEVNM*QAM*K#.A	98.17	64.53	1.52	0.66
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LLKDVEALSQR.L	203.94	159.64	1.28	0.78
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LLK#DVEALSQR@.L	53.98	35.79	1.51	0.66
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LM*ATLR@.N	531.06	282.69	1.88	0.53
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LQNELDNVSTLLEEAEK#.K	172.58	116.58	1.48	0.68
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LQNELDNVSTLLEEAEKK.G	732.09	525.23	1.39	0.72
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.LQQELDDLTVDLDHQR@.Q	545.03	342.30	1.59	0.63
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.LQQELDDLTVDLDHQR.Q	18.18	11.83	1.54	0.65
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LQQLFNHTM*FILEQEEYQR@.E	251.03	125.52	2.00	0.50
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LQQLFNHTMFILEQEEYQR@.E	45.56	25.24	1.80	0.55
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LRLEVNM*QAM*K.A	85.67	48.71	1.76	0.57
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.LRVELAEK.A	88.48	56.37	1.57	0.64
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LVQEQGSHSK.F	42.60	29.85	1.43	0.70
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.LVWIPSER.H	225.14	153.67	1.47	0.68
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.M*EEEVLLLEDQNSK#.F	92.13	58.33	1.58	0.63
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.MEEEVLLLEDQNSK#.F	13.15	10.08	1.30	0.77
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.M*EIDLKDLEAQIEAANK.A	46.72	32.05	1.46	0.69
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.MEIDLK#DLEAQIEAANK#.A	21.90	15.20	1.44	0.69
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.M*QAHIQDLEEQLDEEEGAR@.Q	152.41	110.01	1.39	0.72
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.MQAHIQDLEEQLDEEEGAR@.Q	65.59	42.98	1.53	0.66
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NHEAQIQDM*R@.Q	21.02	16.01	1.31	0.76
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NHEAQIQDMR@.Q	4.72	5.01	0.94	1.06
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NILAEQLQAETELFAEAEEM*R@.A	336.66	188.46	1.79	0.56
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NILAEQLQAETELFAEAEEM*R.A	57.27	42.29	1.35	0.74
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NILAEQLQAETELFAEAEEMR@.A	17.15	12.83	1.34	0.75
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NILAEQLQAETELFAEAEEM*RAR.L	70.74	36.17	1.96	0.51
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.NKQEVM*ISDLEER.L	80.50	61.36	1.31	0.76
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.NK#QEVM*ISDLEER@.L	17.27	10.54	1.64	0.61
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.NKQEVMISDLEER.L	18.30	14.41	1.27	0.79
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NLPIYSENIIEM*YR@.G	151.92	101.84	1.49	0.67
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NLPIYSENIIEM*YR@.G	12.80	6.81	1.88	0.53
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NM*DPLNDNVATLLHQSSDR@.F	247.09	201.33	1.23	0.81
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.NQILQNEK#.K	152.94	108.71	1.41	0.71
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.NQILQNEK#K#.K	5.83	4.20	1.39	0.72
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.NSLQEQQEEEEEAR.K	58.69	34.12	1.72	0.58
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.NTDQASMPENTVAQK#.L	14.27	9.00	1.59	0.63
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.NTDQASM*PENTVAQK#.L	77.26	62.14	1.24	0.80
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.NTNPNFVR@.C	589.82	376.81	1.57	0.64
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.QEEELQAK#DEELLK#.V	313.94	217.55	1.44	0.69
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.QEVM*ISDLEER@.L	15.98	11.47	1.39	0.72
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.QLEEAEEEATR@.A	287.15	215.99	1.33	0.75
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.QLEEEK#NSLQEQQEEEEEAR@.K	44.00	32.57	1.35	0.74
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.QLEEEKNSLQEQQEEEEEARK.N	137.41	81.18	1.69	0.59
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.QLHIEGASLELSDDDTESK#.T	70.69	49.45	1.43	0.70
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.QLLQANPILESFGNAK#.T	351.77	241.12	1.46	0.69
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.QR@YEILTPNAIPK#.G	110.49	78.13	1.41	0.71
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.QVLALQSQLADTK#.K	271.42	193.85	1.40	0.71
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.QVLALQSQLADTKK.K	97.45	64.86	1.50	0.67
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.R@GGPISFSSSR@.S	63.73	43.84	1.45	0.69
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.R@HAEQER@DELADEIANSASGK#.S	11.46	8.70	1.32	0.76
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.R@K#LDGETTDLQDQIAELQAQVDELK#.V	42.60	30.05	1.42	0.71
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.RQLEEAEEEATR.A	41.53	27.00	1.54	0.65
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.R@QLEEAEEEATR@.A	11.95	10.42	1.15	0.87
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.SALLDEK#.R	207.88	120.72	1.72	0.58
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.SALLDEK#R@.R	68.08	49.00	1.39	0.72
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.SDLLLEGFNNYR@.F	296.36	206.29	1.44	0.70
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.SLEAEILQLQEELASSER@.A	741.62	471.05	1.57	0.64
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.SLEAEILQLQEELASSER.A	300.35	207.48	1.45	0.69
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.TELEDTLDTTAAQQELR@.T	24.49	20.57	1.19	0.84
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.TFHIFYQLLSGAGEHLK#.S	12.18	9.73	1.25	0.80
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.TGLEDPER@.Y	440.41	315.21	1.40	0.72
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.TQLEELEDELQATEDAK#.L	310.63	194.02	1.60	0.62
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.TQLEELEDELQATEDAK#.L	309.94	202.55	1.53	0.65
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.TTLQVDTLNTELAAER@.S	204.60	137.78	1.48	0.67
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.VDDDLGTIESLEEAK#.K	71.74	50.33	1.43	0.70
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.VDYK#ADEWLM*K#.N	112.72	68.69	1.64	0.61
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.VEEEEER@.N	35.98	21.40	1.68	0.59
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.VEEEEER@NQILQNEK#.K	212.81	125.91	1.69	0.59
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.VEEEEER@NQILQNEK#K#.K	30.64	20.00	1.53	0.65

Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.VEGELEEMER@.K	27.00	16.28	1.66	0.60
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.VEGELEEM*ER@.K	324.16	228.00	1.42	0.70
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.VIQYLAHVASSHK.G	399.31	270.03	1.48	0.68
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.VKPLLQVTR.Q	227.14	151.51	1.50	0.67
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.VLAYDK#LEK#.T	68.12	48.13	1.42	0.71
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc K.VVSSVLQFGNISFK#.K	338.89	261.07	1.30	0.77
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.YEILTPNAIPK#.G	122.67	86.20	1.42	0.70
Q61879_MYH10_MOUSE	Myh10	Myosin-10 OS=Mus musc R.YLFVDR@.A	379.16	235.74	1.61	0.62
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ELEDATETADAM*NR.E	8.29	8.43	0.98	1.02
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.IAQLEEQLDNETK#.E	8.19	9.01	0.91	1.10
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.QLEEAEEEAQR@.A	9.63	26.92	0.36	2.80
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.RGDLPFVVTR.R	11.33	4.26	2.66	0.38
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ELEDATETADAM*NR.E	2.04	4.07	0.50	2.00
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEEAM*EQK#.A	6.66	4.62	1.44	0.69
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEQQVEEM*K#TQLEELEDELQATEDAK#.L	5.47	8.84	0.62	1.62
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEQQVEEMKTQLEELEDELQATEDAK.L	4.87	7.11	0.68	1.46
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.ASIAALEAK#.I	24.87	24.32	1.02	0.98
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DFSALESQLQDTQELLQEENR@.Q	13.16	12.05	1.09	0.92
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DLEAHIDTANK#.N	5.38	5.17	1.04	0.96
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DLEGLSQR.L	22.14	26.68	0.83	1.20
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ELEDATETADAM*NR.E	27.22	26.56	1.03	0.98
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.HSQAVEELADQLEQTKR.V	5.92	9.03	0.66	1.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.IAQLEEELEEEQGNTELINDR@.L	31.20	27.24	1.15	0.87
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.IAQLEEQLDNETK#.E	24.06	30.17	0.80	1.25
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.IIGLDQVAGM*SETALPGAFK.T	14.64	10.32	1.42	0.70
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.IRELETQISELQEDLESER.A	9.62	7.78	1.24	0.81
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.K#ANLQIDQINTDLNLER@.S	22.94	19.39	1.18	0.85
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.KLEGDSTDLSDQIAELQAQIAELK.M	8.81	9.85	0.89	1.12
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.LQEM*ESAVK.S	27.74	25.25	1.10	0.91
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.NAEQFKDQADK.A	10.86	7.63	1.42	0.70
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.NLPIYSEEIVEM*YK.G	7.17	8.67	0.83	1.21
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.NTDQASM*PDNTAAQK#.V	5.56	6.13	0.91	1.10
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.QAQQER@DELADEIANSSGK#.G	21.11	28.70	0.74	1.36
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.QLEEAEEEAQR@.A	30.46	28.76	1.06	0.94
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.QLLQANPILEAFGNAK#.T	12.46	12.59	0.99	1.01
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.R@GDLPFVVTR@.R	20.80	27.87	0.75	1.34
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.R@K#LEGDSTDLSDQIAELQAQIAELK#.M	7.48	6.54	1.14	0.87
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.SM*EAEM*IQLQEELAAAER@.A	4.40	4.97	0.89	1.13
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.SM*EAEM*IQLQEELAAAER.A	2.94	3.24	0.91	1.10
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.SMEAEMIQLQEELAAAER@.A	1.76	2.49	0.71	1.41
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.TDLLLEPYNK.Y	7.25	11.27	0.64	1.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.VISGVLQLGNIAFK.K	9.93	8.68	1.14	0.87
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.VSHLLGINVTDFTR.G	14.73	16.50	0.89	1.12
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.VVFQEFR.Q	11.47	12.23	0.94	1.07
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.AK#LQEM*ESAVK#.S	73.65	36.00	2.05	0.49
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.AKQTLENERGELANEVK.A	125.40	65.75	1.91	0.52
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEEAMEQK#.A	40.58	21.54	1.88	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEEAM*EQK#.A	272.22	187.81	1.45	0.69
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEEAMEQK#AELER@.L	17.97	9.54	1.88	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.ALELDSNLYR@.I	854.80	444.63	1.92	0.52
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEQQVEEMK#.T	49.47	36.16	1.37	0.73
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEQQVEEM*K#.T	136.73	70.68	1.93	0.52
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEQQVEEM*K#TQLEELEDELQATEDAK#.L	173.70	120.26	1.44	0.69
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ALEQQVEEMK#TQLEELEDELQATEDAK#.L	90.24	53.11	1.70	0.59
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.ANLQIDQINTDLNLER@.S	159.47	93.40	1.71	0.59
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.ANLQIDQINTDLNLER.S	471.15	257.05	1.83	0.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.ASIAALEAK#.I	870.92	449.04	1.94	0.52
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.ATDK#SFVEK#.L	15.72	9.21	1.71	0.59
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.DELADEIANSSGK#.G	121.11	90.64	1.34	0.75
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DFSALESQLQDTQELLQEENR@.Q	925.03	489.20	1.89	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DFSALESQLQDTQELLQEENR.Q	112.94	61.70	1.83	0.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DFSALESQLQDTQELLQEENR@QK#.L	76.22	37.75	2.02	0.50
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DLEAHIDTANK#NR@EEAIK#.Q	10.25	5.29	1.94	0.52
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DLEGLSQR@.L	544.67	338.03	1.61	0.62
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.DLGEELEALK#.T	48.44	29.59	1.64	0.61
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.DLQGR@DEQSEEK#.K	57.47	35.48	1.62	0.62
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DQGELER@.Q	137.55	78.92	1.74	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.DVLLQVEDER@.R	38.93	18.57	2.10	0.48
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.EEILAQAK#.E	249.97	117.95	2.12	0.47
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.EEVGEEAIVELVENGK#.K	35.41	19.60	1.81	0.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ELEDATETADAMNR@.E	84.76	44.88	1.89	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ELEDATETADAM*NR.E	451.13	263.81	1.71	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ELETQISELQEDLESER@.A	282.88	137.39	2.06	0.49
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.ELETQISELQEDLESER@.A	170.45	87.18	1.96	0.51
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.EMEAELEDER@.K	25.90	9.82	2.64	0.38
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.EM*EAELEDER@.K	243.13	138.30	1.76	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.EM*EAELEDERK.Q	58.54	35.72	1.64	0.61
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.EQEVSILK#K#.T	72.69	40.40	1.80	0.56
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.EQLEEEEEAK#R@.N	162.73	82.89	1.96	0.51
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.ERNTDQASM*PDNTAAQK.V	37.04	21.96	1.69	0.59
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.FVSELWK#.D	161.61	97.28	1.66	0.60
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.GALALEEK#.R	580.32	390.94	1.48	0.67
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.GALALEEK#R@.R	114.68	52.60	2.18	0.46
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.GDLPFVVTR@.R	126.02	71.31	1.77	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.HEAM*ITDLEER@.L	48.94	21.67	2.26	0.44
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.HEAMITDLEER@.L	13.31	8.48	1.57	0.64
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.HEDELLAK#.E	455.16	226.59	2.01	0.50
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.HEM*PPHIYAITDTAYR@.S	70.21	45.81	1.53	0.65
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.HLAAENR.L	84.83	46.71	1.82	0.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.HSQAVEELADQLEQTK#.R	151.73	97.07	1.56	0.64
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.HSQAVEELADQLEQTK#R@.V	568.49	236.51	2.40	0.42
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.IAQLEEELEEEQGNTELINDR@.L	459.47	283.61	1.62	0.62
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.IAQLEEQLDNETK#.E	475.38	268.94	1.77	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.IIGLDQVAGM*SETALPGAFK#.T	425.25	226.40	1.88	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.IIGLDQVAGMSETALPGAFK#.T	29.75	16.94	1.76	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.IM*GIPEDEQM*GLLR@.V	319.42	181.44	1.76	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.IM*GIPEDEQMGLLR@.V	30.75	19.75	1.56	0.64
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu R.IMGIPEDEQM*GLLR.V	30.75	19.75	1.56	0.64
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.IRELETQISELQEDLESER.A	368.19	163.15	2.26	0.44
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.IR@ELETQISELQEDLESER@.A	6.40	2.75	2.33	0.43
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.KANLQIDQINTDLNLER.S	410.59	221.57	1.85	0.54
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.K#ANLQIDQINTDLNLER@.S	14.76	7.80	1.89	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu K.K#EEELQAALAR@.L	259.26	141.75	1.83	0.55

Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.KKM*QQNIQELEEQLEEEESAR.Q	8.86	4.25	2.08	0.48
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.K#K#VEAQLQELQVK#.F	355.00	140.78	2.52	0.40
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.K#LEGDSTDLSDQIAELQAQIAELK#.M	335.76	176.99	1.90	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.K#LVWVPSSK#.N	176.24	76.58	2.30	0.43
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.KM*QQNIQELEEQLEEEESAR.Q	111.55	53.06	2.10	0.48
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.KMQQNIQELEEQLEEEESAR.Q	28.53	13.43	2.12	0.47
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.K#TLEDEAK#.T	18.39	10.98	1.68	0.60
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.K#VEAQLQELQVK#.F	154.60	81.51	1.90	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LEGDSTDLSDQIAELQAQIAELK#.M	122.18	59.70	2.05	0.49
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.LEVNLQAM*K#.A	202.15	118.03	1.71	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.LEVNLQAMK#.A	56.12	36.07	1.56	0.64
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LK#DVLLQVEDER@.R	63.88	32.84	1.95	0.51
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LK#DVLLQVEDER@R@.N	353.65	185.51	1.91	0.52
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LKQM*EDEKNSFR.E	86.78	46.64	1.86	0.54
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LKSM*EAEM*IQLQEELAAAER.A	56.71	30.12	1.88	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LQEMESAVK#.S	106.95	51.16	2.09	0.48
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LQEM*ESAVK#.S	610.60	355.58	1.72	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.LQQELDDLLVDLDHQR@.Q	1164.94	705.59	1.65	0.61
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.LQQELDDLLVDLDHQR.Q	43.08	21.40	2.01	0.50
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LQVELDSVTGLLSQSDSK#.S	609.17	302.91	2.01	0.50
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LR@LEVNLQAM*K#.A	30.16	22.34	1.35	0.74
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.LTEM*ETM*QSQLMAEK#.L	26.51	12.15	2.18	0.46
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.LTEMETM*QSQLMAEK#.L	5.54	3.75	1.48	0.68
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.LVWVPSSK#.N	159.13	100.75	1.58	0.63
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.M*QQNIQELEEQLEEEESAR@.Q	246.05	131.67	1.87	0.54
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.M*QQNIQELEEQLEEEESAR.Q	33.59	18.60	1.81	0.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.MQQNIQELEEQLEEEESAR@.Q	94.00	50.20	1.87	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.MQQNIQELEEQLEEEESAR.Q	10.60	5.15	2.06	0.49
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.NAEQFK#DQADK#.A	145.51	89.65	1.62	0.62
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.NAEQFK#DQADK#ASTR@.L	63.86	34.69	1.84	0.54
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NFINNPLAQADWAAK#.K	248.05	138.60	1.79	0.56
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NGFEPASLKEEVGEEAIVELVENGK.K	8.96	7.20	1.24	0.80
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NGFEPASLKEEVGEEAIVELVENGKK.V	6.75	2.89	2.34	0.43
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NK#HEAM*ITDLEER@.L	158.33	65.27	2.43	0.41
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NK#HEAMITDLEER@.L	28.43	12.08	2.35	0.42
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NLPIYSEEIVEM*YK#.G	274.73	147.40	1.86	0.54
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NLPIYSEEIVEMYK#.G	63.40	34.06	1.86	0.54
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NM*DPLNDNIATLLHQSSDK#.F	177.64	91.99	1.93	0.52
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NM*DPLNDNIATLLHQSSDKFVSELWK.D	21.51	10.55	2.04	0.49
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NR@EEAIK#.Q	105.02	63.56	1.65	0.61
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.NSFR@EQLEEEEEAK#R@.N	41.24	25.21	1.64	0.61
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.NTDQASM*PDNTAAQK#.V	328.17	186.72	1.76	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.NTDQASMPDNTAAQK#.V	16.88	11.86	1.42	0.70
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.NWQWWR.L	28.82	14.73	1.96	0.51
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.QAQQERDELADEIANSSGK.G	502.16	304.21	1.65	0.61
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.QK#HSQAVEELADQLEQTK#.R	10.96	5.14	2.13	0.47
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.QLEEAEEEAQR@.A	416.27	242.89	1.71	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.QLLQANPILEAFGNAK#.T	764.71	421.81	1.81	0.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.QQQLTAM*K#.V	134.90	74.10	1.82	0.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.QRYEILTPNSIPK.G	177.26	106.26	1.67	0.60
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.QR@YEILTPNSIPK#.G	14.20	9.05	1.57	0.64
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.QSVSNLEK#.K	176.62	97.46	1.81	0.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.QTLENER@GELANEVK#.A	24.93	10.45	2.39	0.42
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.R@EQEVSILK#K#.T	15.86	7.42	2.14	0.47
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.R@GDLPFVVTR@.R	478.39	277.07	1.73	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.RKLEGDSTDLSDQIAELQAQIAELK.M	247.26	116.13	2.13	0.47
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.R@QAQQER@DELADEIANSSGK#.G	16.73	12.86	1.30	0.77
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.R@QQQLTAM*K#.V	70.91	47.31	1.50	0.67
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.SM*EAEM*IQLQEELAAAER@.A	124.11	71.82	1.73	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.SM*EAEM*IQLQEELAAAER.A	72.23	42.91	1.68	0.59
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.SMEAEM*IQLQEELAAAER@.A	9.74	4.26	2.29	0.44
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.SM*EAEMIQLQEELAAAER@.A	44.61	25.75	1.73	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.SM*EAEMIQLQEELAAAER.A	17.35	9.86	1.76	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.SMEAEMIQLQEELAAAER@.A	32.62	15.97	2.04	0.49
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.TDLLLEPYNK#.Y	448.39	233.17	1.92	0.52
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.TELADK#VTK#.L	102.56	41.90	2.45	0.41
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.TELEDTLDSTAAQQELR@.S	45.28	26.40	1.72	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.TELEDTLDSTAAQQELR.S	59.17	28.76	2.06	0.49
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.TEMEDLMSSK#.D	6.12	3.67	1.67	0.60
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.TEM*EDLM*SSK#.D	96.04	66.39	1.45	0.69
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.TEMEDLMSSK#DDVGK#.S	27.50	17.73	1.55	0.64
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.THEAQIQEM*R@.Q	93.11	53.58	1.74	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.THEAQIQEMR@.Q	14.97	8.65	1.73	0.58
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.THEAQIQEMR@.Q	47.81	25.31	1.89	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.TLEDEAK#.T	151.35	110.59	1.37	0.73
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.TLEDEAK#THEAQIQEMR@.Q	26.90	11.30	2.38	0.42
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.TR@LQQELDDLLVDLDHQR@.Q	27.40	10.14	2.70	0.37
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.VAAYDK#LEK#.T	177.67	77.31	2.30	0.44
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.VAEFTTNLM*EEEEK#.S	223.56	119.25	1.87	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.VAEFTTNLMEEEEK#.S	53.43	30.31	1.76	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.VEAQLQELQVK#.F	124.01	78.16	1.59	0.63
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.VEEEAAQK#.N	76.80	41.25	1.86	0.54
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.VISGVLQLGNIAFK#.K	529.34	301.46	1.76	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.VK#VNK#DDIQK#.M	332.67	181.71	1.83	0.55
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.VNK#DDIQK#.M	86.51	57.03	1.52	0.66
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.VR@TELADK#.V	64.16	31.86	2.01	0.50
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.VSHLLGINVTDFTR@.G	977.68	459.62	2.13	0.47
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.VSHLLGINVTDFTR.G	128.65	61.94	2.08	0.48
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.VVFQEFR.Q	712.94	376.61	1.89	0.53
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	R.YEILTPNSIPK#.G	203.72	117.09	1.74	0.57
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.YK#ASIAALEAK#.I	26.37	9.38	2.81	0.36
Q8VDD5_MYH9_MOUSE	Myh9	Myosin-9 OS=Mus muscu	K.YLYVDK#NFINNPLAQADWAAK#.K	72.39	26.88	2.69	0.37
E9QNY3_E9QNY3_MOUSE	Myl10	Myosin regulatory light c	-.M*FDQSQIQEFK.E	6.07	3.80	1.60	0.63
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.ELLTTM*GDR@FTDEEVDELYR@.E	82.08	49.71	1.65	0.61
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.FTDEEVDELYR@.E	154.49	102.97	1.50	0.67
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	K.GNFNYIEFTR@.I	236.27	147.16	1.61	0.62
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.DGFIDK#EDLHDM*LASMGK#.N	19.30	9.61	2.01	0.50
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.DGFIDK#EDLHDMLASM*GK#.N	63.49	37.83	1.68	0.60
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.DGFIDK#EDLHDMLASM*GK#.N	2.02	1.50	1.34	0.74
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.ELLTTM*GDRFTDEEVDELYR.E	464.31	232.53	2.00	0.50
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.ELLTTM*GDR@FTDEEVDELYR@.E	21.27	7.33	2.90	0.34
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.ELLTTMGDR@FTDEEVDELYR@.E	174.20	96.15	1.81	0.55
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.FTDEEVDELYR@.E	1704.44	984.19	1.73	0.58

Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.FTDEEVDELYR@EAPIDK#K#.G	10.82	3.22	3.36	0.30
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	K.GNFNYIEFTR@.I	2695.10	1438.48	1.87	0.53
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	K.K#GNFNYIEFTR@.I	138.80	63.77	2.18	0.46
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	K.K#GNFNYIEFTR@.I	34.57	20.97	1.65	0.61
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.ELLTTM*GDR@FTDEEVDELYR@.E	24.55	13.57	1.81	0.55
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.FTDEEVDELYR.E	56.82	30.10	1.89	0.53
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	K.GNFNYIEFTR@.I	93.96	56.10	1.67	0.60
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.ELLTTM*GDR@FTDEEVDELYR@.E	13.87	7.60	1.83	0.55
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	R.FTDEEVDELYR@.E	23.34	12.88	1.81	0.55
Q6ZWQ9_Q6ZWQ9_MOUSE	Myl12a	MCG5400 OS=Mus musc	K.GNFNYIEFTR.I	53.94	28.55	1.89	0.53
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.DQGTYEDYVEGLR@.V	12.03	5.87	2.05	0.49
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.EAFQLFDR@.T	177.75	131.97	1.35	0.74
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	R.HVLVTLGEK#.M	198.11	134.90	1.47	0.68
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.NKDQGTYEDYVEGLR.V	158.68	112.67	1.41	0.71
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.NK#DQGTYEDYVEGLR@.V	15.17	11.23	1.35	0.74
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPM*LQTVAK#.N	145.04	110.81	1.31	0.76
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPM*LQTVAK.N	9.28	8.45	1.10	0.91
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPMLQTVAK#.N	55.19	37.06	1.49	0.67
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.DQGTYEDYVEGLR@.V	238.64	131.54	1.81	0.55
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.EAFQLFDR@.T	2824.08	1526.49	1.85	0.54
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	R.HVLVTLGEK#.M	1157.10	580.61	1.99	0.50
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.NK#DQGTYEDYVEGLR@.V	1759.80	925.43	1.90	0.53
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.NK#DQGTYEDYVEGLR@.V	178.05	96.22	1.85	0.54
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.SDEM*NVK#.V	112.12	70.61	1.59	0.63
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.SDEMNVK#.V	63.86	40.52	1.58	0.63
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPM*LQTVAK#.N	2876.61	1487.08	1.93	0.52
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPM*LQTVAK#.N	208.52	112.79	1.85	0.54
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPMLQTVAK#.N	487.31	278.37	1.75	0.57
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.EAFQLFDR@.T	50.80	30.05	1.69	0.59
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	R.HVLVTLGEK.M	81.94	46.01	1.78	0.56
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.NK#DQGTYEDYVEGLR@.V	76.72	41.58	1.85	0.54
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPM*LQTVAK#.N	82.56	45.03	1.83	0.55
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPMLQTVAK#.N	43.35	21.97	1.97	0.51
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.EAFQLFDR@.T	38.12	18.15	2.10	0.48
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	R.HVLVTLGEK#.M	32.86	19.21	1.71	0.58
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.NKDQGTYEDYVEGLR.V	39.80	17.14	2.32	0.43
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPM*LQTVAK#.N	65.95	24.40	2.70	0.37
Q60605_MYL6_MOUSE	Myl6	Myosin light polypeptide	K.VLDFEHFLPMLQTVAK#.N	8.72	10.54	0.83	1.21
Q8CI43_MYL6B_MOUSE	Myl6b	Myosin light chain 6B OS	R.ALGQNPTNAEVLK#.V	278.05	192.98	1.44	0.69
Q8CI43_MYL6B_MOUSE	Myl6b	Myosin light chain 6B OS	R.ALGQNPTNAEVLK#.V	3061.13	1456.61	2.10	0.48
Q8CI43_MYL6B_MOUSE	Myl6b	Myosin light chain 6B OS	R.DQGTYEDYLEGLR@.V	7.19	4.04	1.78	0.56
Q8CI43_MYL6B_MOUSE	Myl6b	Myosin light chain 6B OS	K.ILYSQCGDLM*R.A	11.93	4.40	2.72	0.37
Q8CI43_MYL6B_MOUSE	Myl6b	Myosin light chain 6B OS	K.NRDQGTYEDYLEGLR.V	9.85	5.01	1.97	0.51
Q8CI43_MYL6B_MOUSE	Myl6b	Myosin light chain 6B OS	R.R@VDFETFLPM*LQAVAK#.N	16.17	9.89	1.63	0.61
Q8CI43_MYL6B_MOUSE	Myl6b	Myosin light chain 6B OS	K.SQEPPVDLSK#.V	8.93	7.27	1.23	0.81
Q8CI43_MYL6B_MOUSE	Myl6b	Myosin light chain 6B OS	R.ALGQNPTNAEVLK#.V	95.24	55.59	1.71	0.58
Q8CI43_MYL6B_MOUSE	Myl6b	Myosin light chain 6B OS	R.ALGQNPTNAEVLK#.V	63.96	31.98	2.00	0.50
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAM*FDQSQIQEFK#.E	51.64	33.77	1.53	0.65
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAM*FDQSQIQEFK#.E	67.93	45.08	1.51	0.66
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAMFDQSQIQEFK#.E	10.47	9.41	1.11	0.90
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.EAFNM*IDQNR@.D	128.76	90.90	1.42	0.71
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.EAFNMIDQNR@.D	18.74	17.82	1.05	0.95
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ELLTTM*GDR.F	153.16	92.25	1.66	0.60
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ELLTTMGDR@.F	10.85	7.60	1.43	0.70
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.LNGTDPEDVIR@.N	84.95	65.72	1.29	0.77
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAM*FDQSQIQEFK#.E	972.83	495.46	1.96	0.51
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAM*FDQSQIQEFK#.E	820.18	418.17	1.96	0.51
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAMFDQSQIQEFK#.E	86.09	45.10	1.91	0.52
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAMFDQSQIQEFK#.E	89.18	53.12	1.68	0.60
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAM*FDQSQIQEFKEAFNM*IDQNR.D	59.97	29.76	2.01	0.50
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAMFDQSQIQEFK#EAFNM*IDQNR@.D	2.73	1.83	1.50	0.67
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.DGFIDK#EDLHDM*LASLGK#.N	109.27	46.31	2.36	0.42
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.DGFIDK#EDLHDMLASLGK#.N	15.11	6.58	2.30	0.44
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.EAFNM*IDQNR@.D	919.02	505.96	1.82	0.55
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.EAFNMIDQNR@.D	140.94	76.63	1.84	0.54
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.EAFNM*IDQNRDGFIDKEDLHDM*LASLGK.N	30.50	6.85	4.45	0.22
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.EAPIDKK.G	111.08	71.74	1.55	0.65
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ELLTTM*GDR.F	1237.75	680.64	1.82	0.55
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ELLTTMGDR.F	86.86	61.19	1.42	0.70
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.FTDEEVDEM*YR@.E	34.35	13.25	2.59	0.39
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.FTDEEVDEMYR@.E	4.63	2.12	2.18	0.46
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.GNFNYVEFTR@.I	72.77	36.70	1.98	0.50
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.LNGTDPEDVIR@.N	700.37	395.39	1.77	0.56
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAM*FDQSQIQEFK#.E	30.71	22.28	1.38	0.73
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.EAFNM*IDQNR.D	32.74	22.71	1.44	0.69
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.EAFNMIDQNR@.D	8.06	3.51	2.30	0.44
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ELLTTM*GDR@.F	40.05	26.35	1.52	0.66
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.LNGTDPEDVIR.N	31.22	19.12	1.63	0.61
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	R.ATSNVFAM*FDQSQIQEFK#.E	23.17	8.66	2.68	0.37
Q9CQ19_MYL9_MOUSE	Myl9	Myosin regulatory light p	K.EAFNM*IDQNR@.D	10.17	6.97	1.46	0.69
Q6PDN3_MYLK_MOUSE	Mylk	Myosin light chain kinase	R.SK#PIAPIFLQGLSDLK#.V	13.05	4.04	3.23	0.31
Q6PDN3_MYLK_MOUSE	Mylk	Myosin light chain kinase	R.SK#PIAPIFLQGLSDLK#.V	7.75	2.88	2.69	0.37
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.AAEINGEVDDDDAGGEWR@.L	12.43	11.70	1.06	0.94
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.AGSATVLSGSIAGLEGGSQLALR@.R	42.25	27.75	1.52	0.66
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.AGSATVLSGSIAGLEGGSQLALR.R	18.04	12.89	1.40	0.71
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.AM*EVEM*EDLHLQIDDIAK#.A	7.56	7.95	0.95	1.05
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.APEGQAYR@.R	14.94	13.04	1.15	0.87
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.AVEELLESLDLEK#.S	53.54	36.76	1.46	0.69
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.DFESEK#R@.L	7.18	5.63	1.28	0.78
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.DGFSLASQLK#.S	47.87	28.07	1.71	0.59
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.DLALGLVPGDR@.L	46.29	35.77	1.29	0.77
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.DLDIAGFTQK#.V	16.64	11.43	1.46	0.69
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.DTKEEM*SELAR.K	12.33	8.26	1.49	0.67
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.EK#DM*LLAEAFSLK#.Q	49.39	29.30	1.69	0.59
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.GFFNLNR@.S	35.99	17.77	2.03	0.49
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.GSIILDSGHLSTASSSDDLK#GEEGSFR@.G	9.05	8.54	1.06	0.94
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.IISNLFLGR.A	62.10	41.12	1.51	0.66
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.ISELTSELTDERNTGESASQLLDAETAER.L	26.93	15.20	1.77	0.56
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.LDHDGAILDVDEDDIEK#.A	11.23	6.36	1.77	0.57
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LEDLASLVYLNESSVLHTLR.Q	16.62	19.05	0.87	1.15
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LEEDQEDM*NELM*K#.K	5.66	5.03	1.13	0.89
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LEEQRDEQTSR.H	4.69	2.58	1.82	0.55
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LEISNPIPIK#.V	14.04	9.07	1.55	0.65

Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.LFTTVR@PLIQVQLSEEQIR@.N	19.87	15.41	1.29	0.78
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LGDLQADSDESQR@.A	20.60	15.74	1.31	0.76
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.LHLEGQQVR.N	18.52	23.56	0.79	1.27
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LK#VQPIPELSELSR@.S	23.47	16.44	1.43	0.70
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LPALVPPPPPALR.E	74.44	60.15	1.24	0.81
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.LQALQSQVEFLEQSMVDK.S	10.95	16.14	0.68	1.47
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LQQELEDKM*EVEQQSR.R	39.03	25.49	1.53	0.65
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.LQVDALIDTIK#.R	16.03	9.47	1.69	0.59
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.LQVDALIDTIKR.S	60.36	43.39	1.39	0.72
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.LSTLSDQVNQR@.D	50.50	32.86	1.54	0.65
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LTAELQDTK#.L	53.20	37.96	1.40	0.71
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.LVEINGQNVENK#.S	17.60	11.39	1.54	0.65
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.NK#DEEIQQLR@.S	18.65	12.63	1.48	0.68
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.NK#LEGDSDVDSELEDR@VDGVK#.S	5.71	5.05	1.13	0.89
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.NTGESASQLLDAETAER@.L	28.55	17.10	1.67	0.60
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.NYIVVDEK#.R	15.28	16.10	0.95	1.05
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.QDQSIVLLGSSGSGK#.T	19.10	10.74	1.78	0.56
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.QGPEESGLGEGTK#.L	35.65	24.35	1.46	0.68
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.QM*EVQLEEEYEDKQK.A	15.41	8.96	1.72	0.58
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.QNPATQNAPR@.L	24.52	17.60	1.39	0.72
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.R@EDM*APHIYAVAQTAYR@.A	4.87	5.08	0.96	1.04
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.RFDSELSQAHEETQR.E	39.54	23.71	1.67	0.60
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.R@FDVLAPHLTK#.K	33.18	19.49	1.70	0.59
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.R@LENLASR@.L	54.77	34.04	1.61	0.62
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.R@PTGDFGFSLR@.R	24.26	18.73	1.29	0.77
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.SEELSLPEGK#.A	40.77	32.03	1.27	0.79
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.SLAHADEAR.G	15.93	8.12	1.96	0.51
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.SR@VPELVTK#.R	22.82	12.35	1.85	0.54
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.TALEEQLSR@.L	65.99	42.45	1.55	0.64
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.TEEQIAAEEAWYETEK#.V	14.49	6.65	2.18	0.46
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.TFLQELER@.Y	20.92	15.37	1.36	0.73
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.TR@LEISNPIPIK#.V	49.46	35.44	1.40	0.72
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.VK#DQEEELDEQAGSIQM*LEQAK#.L	31.92	21.29	1.50	0.67
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.VK#DQEEELDEQAGSIQMLEQAK#.L	9.03	5.91	1.53	0.65
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.VK#LDHDGAILDVDEDDIEK#.A	13.73	14.82	0.93	1.08
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.VLAISPEEQK#.T	31.03	20.31	1.53	0.65
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.VVHFAEPGAGTK#.D	10.03	6.73	1.49	0.67
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.VVSLEAELQDISSQESK#.D	7.76	5.99	1.30	0.77
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	K.VVSLEAELQDISSQESK#DEASLAK#.V	72.66	58.34	1.25	0.80
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.YGASLLHTYAGPSLLVLSTR@.G	30.41	26.92	1.13	0.89
Q9JMH9_MY18A_MOUSE	Myo18a	Unconventional myosin-	R.YK#EDNIELAFDDLEPVADDSVAAVDQASHLVR@.S	59.86	39.88	1.50	0.67
P46735_MYO1B_MOUSE	Myo1b	Unconventional myosin-	R.IFLLTNNNLLLADQK#.S	14.29	11.92	1.20	0.83
P46735_MYO1B_MOUSE	Myo1b	Unconventional myosin-	K.IIIAEVVNK#.I	16.99	7.76	2.19	0.46
P46735_MYO1B_MOUSE	Myo1b	Unconventional myosin-	R.SGVEVLFNELEIPVEEHSFGR@.S	22.47	8.51	2.64	0.38
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.ASFLLNLR@.R	19.92	13.51	1.47	0.68
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.DGIIDFTSGSELLITK#.A	31.08	20.91	1.49	0.67
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.DNYPQSVPR@.L	16.90	11.94	1.42	0.71
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.DQAVM*ISGESGAGK#.T	11.09	7.93	1.40	0.72
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.GAPVGGHILSYLLEK#.S	6.74	4.28	1.57	0.63
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.GEELLSPLNLEQAAYAR.D	16.37	14.63	1.12	0.89
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.LGTEEISPR@.V	36.52	30.00	1.22	0.82
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.LLGVEGTTLR@.E	50.25	33.16	1.52	0.66
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.NFHVFYQLLEGGEEETLR@.R	13.19	7.51	1.76	0.57
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.NPQSYLYLVK#.G	18.48	10.82	1.71	0.59
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.NVLDTSWPTPPPALR@.E	8.89	5.76	1.54	0.65
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.QLLLTPSAVVIVEDAK#.V	25.48	18.77	1.36	0.74
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.TFTWLVR@.K	21.52	12.90	1.67	0.60
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.TLFATEDSLEVR.R	24.14	17.71	1.36	0.73
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.VLQSLGSEPIQYAVPVVK#.Y	27.62	18.14	1.52	0.66
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.VNNININQGSITFAGGPGR@.D	9.39	7.55	1.24	0.80
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.YLGLM*ENLR.V	49.17	6.80	7.23	0.14
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.YM*DVQFDFK#.G	15.52	11.80	1.32	0.76
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.ASFLLNLR@.R	150.56	64.30	2.34	0.43
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.DAESPSWR.S	18.85	8.01	2.35	0.42
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.DGIIDFTSGSELLITK#.A	132.37	63.01	2.10	0.48
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.DLQIYSR@.Q	41.68	20.22	2.06	0.49
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.DNYPQSVPR.L	77.28	47.75	1.62	0.62
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.DQAVM*ISGESGAGK#.T	38.74	17.32	2.24	0.45
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.GAPVGGHILSYLLEK#.S	17.95	9.91	1.81	0.55
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.GEELLSPLNLEQAAYAR.D	88.59	46.55	1.90	0.53
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.GEELLSPLNLEQAAYAR@.D	38.50	19.30	2.00	0.50
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.GVSFYEVPPHLFAVADTVYR@.A	84.34	46.86	1.80	0.56
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.HLGYK#PEEYK#.M	46.80	26.02	1.80	0.56
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.IIAK#GEELLSPLNLEQAAYAR@.D	15.88	8.71	1.82	0.55
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.IQAAWR@.G	51.53	18.75	2.75	0.36
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.K#YEAFLQR@.Y	27.65	21.20	1.30	0.77
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.LGTEEISPR@.V	130.58	69.25	1.89	0.53
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.LLGVEGTTLR@.E	142.38	74.56	1.91	0.52
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.LLQSNPVLEAFGNAK#.T	106.87	54.98	1.94	0.51
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.NFHVFYQLLEGGEEETLR@.R	19.83	10.97	1.81	0.55
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.NNDLLFR@.D	18.71	12.51	1.49	0.67
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.NPQSYLYLVK#.G	41.56	23.58	1.76	0.57
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.NVLDTSWPTPPPALR@.E	45.68	31.05	1.47	0.68
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.QK#GDVVLQSDHVIETLTK#.T	17.44	7.91	2.20	0.45
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.QLLLTPSAVVIVEDAK#.V	114.11	54.81	2.08	0.48
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.SEQEEYEAEGIAWEPVQYFNNK#.I	18.46	11.06	1.67	0.60
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.TFTWLVR@.K	62.73	29.66	2.11	0.47
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.TLFATEDSLEVR.R	96.57	44.08	2.19	0.46
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.VLQSLGSEPIQYAVPVVK#.Y	146.79	75.28	1.95	0.51
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.VNNININQGSITFAGGPGR.D	44.20	19.97	2.21	0.45
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	R.VTM*ESALTAR@.D	33.19	15.71	2.11	0.47
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.YLGLM*ENLR.V	61.92	23.67	2.62	0.38
Q9WTI7_MYO1C_MOUSE	Myo1c	Unconventional myosin-	K.YM*DVQFDFK#.G	56.80	35.72	1.59	0.63
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	R.IGELVGVLVNHFK#.S	8.37	9.35	0.89	1.12
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	R.TLFTLEELR@.A	9.83	7.43	1.32	0.76
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	R.VIVQQPGER@.S	8.45	9.39	0.90	1.11
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	R.AWEGNYLASK#PDTPQTSGTFVPVANELK#.R	2.99	3.54	0.84	1.18
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	K.HIDYFNNQIIVDLVEQQHK#.G	5.74	3.29	1.74	0.57
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	R.IGELVGVLVNHFK#.S	14.19	9.44	1.50	0.67
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	R.TLFTLEELR@.A	14.99	7.77	1.93	0.52
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	R.VIVQQPGER@.S	24.88	14.17	1.76	0.57
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	K.VTDGM*FLEALNSK#.L	6.17	3.47	1.78	0.56
Q5SYD0_MYO1D_MOUSE	Myo1d	Unconventional myosin-	K.VVSVIAELLSTK#.A	39.83	25.10	1.59	0.63

E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	K.DIILQSNPLLEAFGNAK.T	14.04	12.73	1.10	0.91
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	K.TEFLSLLAK#.R	12.61	8.70	1.45	0.69
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	R.VFDFLVDSINK#.A	18.41	16.55	1.11	0.90
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	K.YFEIQFSPGGEPDGGK#.I	4.24	4.28	0.99	1.01
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	K.AEQEEYVQEGIR@.W	14.43	6.19	2.33	0.43
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	K.DIILQSNPLLEAFGNAK#.T	38.50	17.31	2.22	0.45
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	K.ISNFLLEK#.S	27.43	11.13	2.47	0.41
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	R.SFHIFYQLIEGASPEQK#.Q	8.91	6.72	1.33	0.75
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	R.VFDFLVDSINK#.A	38.87	17.50	2.22	0.45
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	K.VLQVSIGPGLPK#.N	22.03	13.91	1.58	0.63
E9Q634_MYO1E_MOUSE	Myo1e	Unconventional myosin-	K.YFEIQFSPGGEPDGGK#.I	9.81	4.86	2.02	0.49
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	R.YNVSQLEEWLR@.D	6.02	2.06	2.93	0.34
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	K.ETLEPLIQAAQLLQVK#.K	10.93	4.14	2.64	0.38
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	K.VLNLYTPVNEFEER@.V	9.42	3.90	2.41	0.41
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	K.AISPTSATSSGR@.T	10.75	3.43	3.14	0.32
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	K.LTNLEGVYNSETEK#.L	8.76	4.77	1.84	0.54
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	R.NQSIIVSGESGAGK#.T	13.20	5.47	2.41	0.41
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	K.SAPEVTAPGAPAYR@.V	6.65	4.17	1.60	0.63
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	K.VLNLYTPVNEFEER@.V	11.09	6.39	1.73	0.58
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	R.YFATVSGSASEANVEEK#.V	7.76	2.24	3.47	0.29
Q99104_MYO5A_MOUSE	Myo5a	Unconventional myosin-	R.YQNLLNEFSR@.L	9.00	4.99	1.80	0.55
Q64331_MYO6_MOUSE	Myo6	Unconventional myosin-	R.IVEANPLLEAFGNAK#.T	7.72	5.16	1.50	0.67
P97479_MYO7A_MOUSE	Myo7a	Unconventional myosin-	K.SGQEFDVPIGAVVK#.L	8.97	6.40	1.40	0.71
P97479_MYO7A_MOUSE	Myo7a	Unconventional myosin-	K.TLLTDSATTAR.E	11.27	8.27	1.36	0.73
P97479_MYO7A_MOUSE	Myo7a	Unconventional myosin-	R.VDSQEYANIR@.S	4.67	2.87	1.62	0.62
P97479_MYO7A_MOUSE	Myo7a	Unconventional myosin-	K.VYFPDDTDEAFEVESSTK#.A	4.85	2.29	2.12	0.47
Q9QY06_MYO9B_MOUSE	Myo9b	Unconventional myosin-	K.FLDEFLLNK#.V	9.54	3.40	2.81	0.36
Q9QY06_MYO9B_MOUSE	Myo9b	Unconventional myosin-	K.LILPYSLSEAITAR@.D	9.65	4.81	2.01	0.50
Q9QY06_MYO9B_MOUSE	Myo9b	Unconventional myosin-	R.TILGAGPVLEAFGNAK#.T	9.85	4.67	2.11	0.47
Q9QY06_MYO9B_MOUSE	Myo9b	Unconventional myosin-	K.TPIESLFIEATER@.F	29.35	11.96	2.46	0.41
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	R.AEDIPQM*DDAFSQTVK#.E	9.08	3.16	2.87	0.35
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.ANVTVLDTQIR@.K	11.60	2.56	4.52	0.22
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.DLTQTASSTAR@.A	12.34	5.40	2.28	0.44
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.GPSGTVSEAQLAR@.R	17.05	6.03	2.83	0.35
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	R.IFVELNTFLEK#.K	13.54	1.93	7.01	0.14
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.IPANQLAEVWLK#.L	28.53	10.60	2.69	0.37
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	R.IYPLPDDPSVPAPPR@.Q	5.32	2.39	2.23	0.45
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.K#LEPISSDDLLVVEK#.Y	17.08	3.66	4.67	0.21
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.LIDEVIEDTR@.Y	14.39	3.45	4.18	0.24
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.LIDEVIEDTR@YTLPVTEGK#.A	11.93	2.45	4.88	0.21
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.LNSETDITPK#.L	19.78	2.99	6.61	0.15
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.NLVDPFVEVSFAGK#.M	20.18	8.77	2.30	0.43
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	R.SLLTEADAGHTEFTDEVYQNENR@.Y	11.94	3.73	3.20	0.31
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	R.VIVESATNIPK#.T	17.42	4.35	4.01	0.25
Q69ZN7_MYOF_MOUSE	Myof	Myoferlin OS=Mus musc	K.WLLLNDPEDTSSGAK#.G	6.01	5.28	1.14	0.88
P12979_MYOG_MOUSE	Myog	Myogenin OS=Mus musc	K.VNEAFEALK#.R	32.77	15.77	2.08	0.48
Q9CQ25_MZT2_MOUSE	Mzt2	Mitotic-spindle organizir	R.GGPILGNVTISAER@.G	22.79	35.80	0.64	1.57
Q9CQ25_MZT2_MOUSE	Mzt2	Mitotic-spindle organizir	R.LASDPQDSVPISLSTSTSETR@.G	6.93	2.67	2.60	0.39
Q8CES0_NAA30_MOUSE	Naa30	N-alpha-acetyltransferas	K.VLSAAEAAAPDGASK#.V	3.67	1.29	2.85	0.35
Q6PHQ8_NAA35_MOUSE	Naa35	N-alpha-acetyltransferas	K.FELDSEQVR@.Y	7.73	3.17	2.44	0.41
Q8VE10_NAA40_MOUSE	Naa40	N-alpha-acetyltransferas	R.LGDPLEAFPVFK.K	3.21	13.16	0.24	4.09
Q8VE10_NAA40_MOUSE	Naa40	N-alpha-acetyltransferas	R.VSGLEPATVDWAFDLTK.T	3.06	6.50	0.47	2.13
Q8VE10_NAA40_MOUSE	Naa40	N-alpha-acetyltransferas	R.LGDPLEAFPVFK.K	4.06	22.36	0.18	5.51
Q8VE10_NAA40_MOUSE	Naa40	N-alpha-acetyltransferas	R.VSGLEPATVDWAFDLTK.T	1.46	4.76	0.31	3.26
Q61122_NAB1_MOUSE	Nab1	NGFI-A-binding protein 1	R.R@LTAGLYR@.Q	13.61	3.87	3.52	0.28
Q61122_NAB1_MOUSE	Nab1	NGFI-A-binding protein 1	K.SEVGSLALQSVSDSR@.L	21.28	5.77	3.69	0.27
Q61122_NAB1_MOUSE	Nab1	NGFI-A-binding protein 1	R.IK#IEDGFPDFQESVPTLFQQAR@.A	8.83	2.30	3.84	0.26
Q61122_NAB1_MOUSE	Nab1	NGFI-A-binding protein 1	R.TLGELQLYR@.I	79.79	15.54	5.13	0.19
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.DNTLLLR@.R	41.54	10.89	3.81	0.26
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.ESTYLSSLK#.G	23.08	9.63	2.40	0.42
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.M*VVESVER@.I	44.33	11.41	3.88	0.26
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	K.SPLELGEK#.L	15.98	4.96	3.22	0.31
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.DNTLLLR@.R	36.79	8.23	4.47	0.22
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.ESTYLSSLK#.G	31.05	5.01	6.20	0.16
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.GDTGEIASLLK#.L	50.30	9.26	5.43	0.18
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.HILQQTLM*DEGLR@.L	10.56	2.17	4.85	0.21
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	K.LSPLPGGPGAGDPR@.I	22.26	6.22	3.58	0.28
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.M*VVESVER@.I	59.51	9.62	6.19	0.16
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.R@VELFSLSR@.Q	62.40	7.36	8.48	0.12
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.TPQPR@FK.A	6.46	2.86	2.26	0.44
Q61127_NAB2_MOUSE	Nab2	NGFI-A-binding protein 2	R.VELFSLSR@.Q	14.84	2.59	5.72	0.17
P70670_NACAM_MOUSE	Naca	Nascent polypeptide-ass	K.DIELVM*SQANVSR@.A	10.89	5.78	1.88	0.53
P70670_NACAM_MOUSE	Naca	Nascent polypeptide-ass	K.DIELVMSQANVSR@.A	8.46	4.66	1.82	0.55
P70670_NACAM_MOUSE	Naca	Nascent polypeptide-ass	K.IEDLSQQAQLAAAEK#.F	38.97	19.25	2.03	0.49
P70670_NACAM_MOUSE	Naca	Nascent polypeptide-ass	K.SPASDTYIVFGEAK#.I	42.63	27.45	1.55	0.64
Q7TSZ8_NACC1_MOUSE	Nacc1	Nucleus accumbens-asso	R.AVLAASSSYFR@.D	10.16	6.23	1.63	0.61
Q7TSZ8_NACC1_MOUSE	Nacc1	Nucleus accumbens-asso	R.AVLAASSSYFR@.D	12.62	3.63	3.47	0.29
Q7TSZ8_NACC1_MOUSE	Nacc1	Nucleus accumbens-asso	R.AVLAASSSYFR@.D	12.75	4.64	2.75	0.36
Q7TSZ8_NACC1_MOUSE	Nacc1	Nucleus accumbens-asso	R.LLASFFDR@.N	5.96	6.03	0.99	1.01
Q7TSZ8_NACC1_MOUSE	Nacc1	Nucleus accumbens-asso	K.GTEFFLK#.V	10.71	4.20	2.55	0.39
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.GVSSQETAGIGASAHLVNFK#.G	76.54	60.41	1.27	0.79
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.GWNYILEK#.Y	38.32	13.38	2.86	0.35
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.LHDFGYR@.G	22.16	8.77	2.53	0.40
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.NAQLNIEQDVAPH.-	65.42	65.42	1.00	1.00
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.STEAPLIIR@PDSGNPLDTVLK#.V	126.99	58.25	2.18	0.46
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.VIQGDGVDINTLQEIVEGM*K#.Q	17.44	9.77	1.78	0.56
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.VIQGDGVDINTLQEIVEGM*K#.Q	39.43	14.92	2.64	0.38
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.VIQGDGVDINTLQEIVEGMK#.Q	3.87	1.75	2.21	0.45
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.VK#YEETVFYGLQYILNK#.Y	22.35	12.09	1.85	0.54
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.VLDILGK#.K	64.05	29.90	2.14	0.47
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.WSIENVSFGSGGALLQK#.L	16.24	7.82	2.08	0.48
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.YDGHLPIEVK#.A	56.04	24.64	2.27	0.44
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.YEETVFYGLQYILNK#.Y	28.55	9.69	2.95	0.34
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.YLLETSGNLDGLEYK#.L	67.99	27.14	2.51	0.40
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.STEAPLIIRPDSGNPLDTVLK.V	85.46	29.84	2.86	0.35
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.SYSFDEVR@K#.N	9.85	1.33	7.39	0.14
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.TPAGNFVTLEEGK#GDLEEYGHDLLHTVFK#.N	14.96	6.88	2.17	0.46
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.VIQGDGVDINTLQEIVEGM*K#.Q	27.24	7.00	3.89	0.26
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.NAQLNIEQDVAPH.-	11.21	11.21	1.00	1.00
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.STEAPLIIR@PDSGNPLDTVLK#.V	29.20	10.86	2.69	0.37
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.VIQGDGVDINTLQEIVEGM*K#.Q	7.41	7.76	0.95	1.05
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.WSIENVSFGSGGALLQK#.L	5.87	2.33	2.52	0.40
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.YLLETSGNLDGLEYK#.L	9.42	5.79	1.63	0.62

Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.NAQLNIEQDVAPH.-	17.87	17.87	1.00	1.00
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.STEAPLIIR@PDSGNPLDTVLK#.V	36.34	8.07	4.50	0.22
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	R.VIQGDGVDINTLQEIVEGM*K#.Q	21.23	5.30	4.00	0.25
Q99KQ4_NAMPT_MOUSE	Nampt	Nicotinamide phosphori	K.YDGHLPIEVK#.A	24.63	7.31	3.37	0.30
P28656_NP1L1_MOUSE	Nap1l1	Nucleosome assembly pr	R.LDGLVDTPTGYIESLPK#.V	14.18	10.09	1.41	0.71
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	K.AIDIYEQVGTSAM*DSPLLK#.Y	5.95	4.92	1.21	0.83
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	R.AIEIYTDM*GR@.F	21.44	14.80	1.45	0.69
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	K.HHISIAEIYETELVDVEK#.A	8.44	21.49	0.39	2.55
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	K.K#LLEAHEEQNVDSYTEAVK#EYDSISR@.L	2.42	3.63	0.67	1.50
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	R.LDQWLTTM*LLR@.I	13.75	7.91	1.74	0.58
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	R.LDQWLTTMLLR@.I	6.05	4.15	1.46	0.69
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	K.LLEAHEEQNVDSYTEAVK#.E	8.74	9.08	0.96	1.04
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	K.QAEAM*ALLAEAER.K	10.51	5.99	1.75	0.57
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	K.TIQGDEEDLR.-	59.10	42.25	1.40	0.71
Q9DB05_SNAA_MOUSE	Napa	Alpha-soluble NSF attach	K.VAGYAAQLEQYQK#.A	29.21	13.77	2.12	0.47
Q99MD9_NASP_MOUSE	Nasp	Nuclear autoantigenic sp	K.IAANEETPERDEQM*K#.E	1.67	9.79	0.17	5.86
Q8K224_NAT10_MOUSE	Nat10	N-acetyltransferase 10 OS	K.FIEGISEK#.T	4.99	2.07	2.41	0.41
Q8K224_NAT10_MOUSE	Nat10	N-acetyltransferase 10 OS	R.QQSAQSQVSTTAENK#.T	6.66	3.17	2.10	0.48
Q9R207_NBN_MOUSE	Nbn	Nibrin OS=Mus musculus	K.LLPAAGAAPGEPYR@.L	4.68	3.97	1.18	0.85
P97432_NBR1_MOUSE	Nbr1	Next to BRCA1 gene 1 pro	K.FMWGNLTLASTEK.K	1.90	4.95	0.38	2.60
P13595_NCAM1_MOUSE	Ncam1	Neural cell adhesion mol	R.FIVLSNNYLQIR@.G	5.81	5.78	1.00	1.00
P13595_NCAM1_MOUSE	Ncam1	Neural cell adhesion mol	K.GLGEISAATEFK#.T	10.44	8.26	1.26	0.79
P13595_NCAM1_MOUSE	Ncam1	Neural cell adhesion mol	K.LEGQM*GEDGNSIK#.V	7.94	6.18	1.29	0.78
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.AIIDEFEQK#.L	11.05	5.59	1.98	0.51
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.DQFLDILQAHGHDVNSFVR@.S	6.37	1.95	3.26	0.31
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.EAVLNAYR@.Q	18.36	5.26	3.49	0.29
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.GFAAFLTELAER@.I	14.75	4.46	3.31	0.30
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.GK#PEIVGSNLDALVR@.V	9.78	8.93	1.10	0.91
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.GM*DGIEEFETGQGGSQR@.A	5.65	2.17	2.60	0.38
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.GNAIYNLLPDIISR@.L	11.27	4.95	2.27	0.44
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.ITEAIGIISK#.M	13.87	5.85	2.37	0.42
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.LPQEEGDHQIADAETAEEVK#.G	8.05	2.76	2.91	0.34
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.VLQLFAR@.I	11.59	4.21	2.75	0.36
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.AIIDEFEQK#.L	36.95	19.15	1.93	0.52
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.DK#QTESLVEK#.L	16.07	9.13	1.76	0.57
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.DQFLDILQAHGHDVNSFVR@.S	19.78	10.51	1.88	0.53
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.DSPSVPEPEGSQSNDELVK#.Q	8.95	4.51	1.99	0.50
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.EAIAHLLGVALVR@.Y	38.76	16.50	2.35	0.43
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.EAVLNAYR@.Q	35.17	13.65	2.58	0.39
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.FPNLVDPWTPHLYAR@.L	20.25	13.63	1.49	0.67
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.GFAAFLTELAER@.I	46.22	19.14	2.41	0.41
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.GFAHPDPLWIPFK#.E	11.38	7.41	1.54	0.65
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.GK#PEIVGSNLDALVR@.V	46.59	24.85	1.87	0.53
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.GM*DGIEEFETGQGGSQR@.A	16.12	7.02	2.30	0.44
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.GNAIYNLLPDIISR@.L	42.29	22.76	1.86	0.54
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.ITEAIGIISK#.M	46.71	17.47	2.67	0.37
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.LLESFENM*TSQTSLIDLDIGGK#.G	15.00	5.79	2.59	0.39
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.LLFTM*LEK#.S	29.38	10.98	2.67	0.37
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.LPQEEGDHQIADAETAEEVK#.G	41.61	20.56	2.02	0.49
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.M*LPLIWSK#.E	20.00	7.44	2.69	0.37
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.QLLSYITK#.D	23.88	10.78	2.22	0.45
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.SAAATAALDPEEEWDAM*LPELK#.S	4.18	2.24	1.86	0.54
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.SGGVNQYVVR.E	34.25	14.53	2.36	0.42
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.SIEPGLK#EDTLEFLK#.K	19.00	9.57	1.99	0.50
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.STLQQLLK#.L	47.71	21.79	2.19	0.46
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	K.VK#GQVSEM*AVLLIDPVPQIAALAK#.N	12.92	4.44	2.91	0.34
Q8K2Z4_CND1_MOUSE	Ncapd2	Condensin complex subu	R.VLQLFAR@.I	39.81	18.21	2.19	0.46
Q6ZQK0_CNDD3_MOUSE	Ncapd3	Condensin-2 complex sub	K.DLLEEDDVALANVVMQEAQM*K#.I	8.15	4.42	1.84	0.54
Q6ZQK0_CNDD3_MOUSE	Ncapd3	Condensin-2 complex sub	R.ELEVSEDVAVR@.N	11.26	4.56	2.47	0.41
Q6ZQK0_CNDD3_MOUSE	Ncapd3	Condensin-2 complex sub	K.FFVQEIIFDR@.C	6.75	1.38	4.90	0.20
Q6ZQK0_CNDD3_MOUSE	Ncapd3	Condensin-2 complex sub	K.TVLEEQGLLK#.Q	21.60	4.01	5.39	0.19
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.ALSLVELSSNVTK#.D	17.63	7.55	2.34	0.43
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.APIVNVVVDPSDTR@.K	33.87	12.99	2.61	0.38
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.EFIGQQLILIM*K#.S	17.89	7.53	2.38	0.42
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.IQIVTEIISEIR@.A	34.99	12.17	2.88	0.35
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.K#LAYQVLAEK#.V	3.56	19.10	0.19	5.36
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.LAYQVLAEK#.V	17.00	8.61	1.97	0.51
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.LILLWYNPVTEEDVR@.L	18.70	10.97	1.70	0.59
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.LLSDFLDSEVSELR@.T	55.28	19.36	2.86	0.35
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.LNLAEFLNEDTS.-	10.19	10.19	1.00	1.00
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.LVVALSR@.T	35.76	14.66	2.44	0.41
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.SK#LNLAEFLNEDTS.-	16.21	8.21	1.97	0.51
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.SLDTSEEGGR.K	20.21	5.94	3.40	0.29
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.AIIDQLM*M*FGIEPFK#.T	8.48	4.24	2.00	0.50
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.ALSLVELSSNVTK#.D	15.46	7.76	1.99	0.50
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.APIVNVVVDPSDTR@.K	36.01	11.33	3.18	0.31
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.EFIGQQLILIM*K#.S	16.72	5.29	3.16	0.32
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.ESDPGVVTQDVNTTTAVLQNENEYM*TPVR@.D	6.88	2.39	2.87	0.35
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.FTEGNILEFLHR@.L	35.90	13.66	2.63	0.38
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.HLLQGWLR@.F	9.77	4.20	2.33	0.43
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.IQIVTEIISEIR@.A	20.08	7.03	2.86	0.35
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.K#LAYQVLAEK#.V	8.89	2.73	3.26	0.31
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.LAYQVLAEK#.V	16.22	6.03	2.69	0.37
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.LLSDFLDSEVSELR@.T	74.73	24.65	3.03	0.33
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.LNLAEFLNEDTS.-	13.18	13.18	1.00	1.00
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.LVVALSR@.T	37.88	10.82	3.50	0.29
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.SK#LNLAEFLNEDTS.-	18.07	5.69	3.18	0.31
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	K.SLDTSEEGGR@.K	14.14	4.03	3.51	0.29
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.TGAAEGLAK#.L	14.29	6.97	2.05	0.49
E9PWG6_E9PWG6_MOUSE	Ncapg	Protein Ncapg OS=Mus m	R.VLLLQQGLNDR.S	64.86	21.94	2.96	0.34
Q6DFV1_CNDG2_MOUSE	Ncapg2	Condensin-2 complex sub	K.FAAVLPEYLK#.V	13.87	6.89	2.01	0.50
Q6DFV1_CNDG2_MOUSE	Ncapg2	Condensin-2 complex sub	R.LK#DLLTETLLESPVDR@.W	13.22	4.36	3.03	0.33
Q6DFV1_CNDG2_MOUSE	Ncapg2	Condensin-2 complex sub	R.VAFVDLLLK#.I	25.22	8.12	3.11	0.32
Q6DFV1_CNDG2_MOUSE	Ncapg2	Condensin-2 complex sub	R.EAFIQAVSK#.E	15.44	3.46	4.46	0.22
Q6DFV1_CNDG2_MOUSE	Ncapg2	Condensin-2 complex sub	K.FAAVLPEYLK#.V	15.26	13.37	1.14	0.88
Q6DFV1_CNDG2_MOUSE	Ncapg2	Condensin-2 complex sub	R.LK#DLLTETLLESPVDR@.W	13.80	3.59	3.84	0.26
Q6DFV1_CNDG2_MOUSE	Ncapg2	Condensin-2 complex sub	R.VAFVDLLLK#.I	30.55	9.36	3.26	0.31
Q6DFV1_CNDG2_MOUSE	Ncapg2	Condensin-2 complex sub	K.VLPLLEDQEEEYLK#.L	10.57	2.30	4.60	0.22
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	R.GQQDVLSSPLER@.V	13.22	8.16	1.62	0.62
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	R.NIDVSTTISK#.F	16.27	12.50	1.30	0.77
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.TIEQNLSNINVSEADGK#.C	8.54	1.68	5.08	0.20
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.TPVLEDFPQNDDEK#ER@.M	14.09	8.64	1.63	0.61
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.VAAGTLDASTK#.I	32.87	13.32	2.47	0.41

Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	R.VFDLQFSTDSIHLASPNR@.N	8.66	5.97	1.45	0.69
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	R.GQQDVLSSPLER@.V	5.69	2.78	2.04	0.49
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.TPVLEDFPQNDDEK#ER@.M	7.83	3.19	2.46	0.41
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	R.VFDLQFSTDSIHLASPNR@.N	16.71	5.63	2.97	0.34
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.EADTEANHTESGQEGAPEEVADEK#.K	11.02	5.55	1.99	0.50
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	R.GQQDVLSSPLER@.V	42.89	20.03	2.14	0.47
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.K#DFEINFDDDIDFDAYFQK#.T	4.39	4.76	0.92	1.09
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.LEGTEDLSDVLVM*QGD.-	10.47	10.47	1.00	1.00
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.NAFGLHLIDFM*SEILK#.Q	22.57	5.04	4.48	0.22
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	R.NIDVSTTISK#.F	36.21	38.71	0.94	1.07
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.TIEQNLSNINVSEADGK#.C	22.03	10.94	2.01	0.50
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.TPVLEDFPQNDDEK#ER@.M	37.01	18.56	1.99	0.50
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.VAAGTLDASTK#.I	56.27	24.21	2.32	0.43
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	R.VFDLQFSTDSIHLASPNR@.N	49.26	21.57	2.28	0.44
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	R.GQQDVLSSPLER@.V	7.48	11.81	0.63	1.58
Q8C156_CND2_MOUSE	Ncaph	Condensin complex subu	K.TPVLEDFPQNDDEK#ER@.M	11.17	41.07	0.27	3.68
Q8BSP2_CNDH2_MOUSE	Ncaph2	Condensin-2 complex sul	R.LQETPDPWQSLDPFDSLESK#.V	5.68	1.25	4.56	0.22
Q8BSP2_CNDH2_MOUSE	Ncaph2	Condensin-2 complex sul	R.SQK#DPEDAEEQPM*EVSR@.N	7.67	3.10	2.47	0.40
Q8BSP2_CNDH2_MOUSE	Ncaph2	Condensin-2 complex sul	R.TSQQSAILPR@.R	10.53	3.09	3.40	0.29
Q8BSP2_CNDH2_MOUSE	Ncaph2	Condensin-2 complex sul	K.FIQETELSQR@.I	20.17	5.21	3.87	0.26
Q8BSP2_CNDH2_MOUSE	Ncaph2	Condensin-2 complex sul	R.LQETPDPWQSLDPFDSLESK#.V	6.83	4.58	1.49	0.67
Q8BSP2_CNDH2_MOUSE	Ncaph2	Condensin-2 complex sul	R.LQETPDPWQSLDPFDSLESK#.V	12.08	3.75	3.22	0.31
Q8BSP2_CNDH2_MOUSE	Ncaph2	Condensin-2 complex sul	R.SQK#DPEDAEEQPM*EVSR@.N	8.92	3.01	2.96	0.34
Q8BSP2_CNDH2_MOUSE	Ncaph2	Condensin-2 complex sul	R.TSQQSAILPR@.R	33.46	10.29	3.25	0.31
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	K.ANNYNEAVYLVR.F	20.77	13.78	1.51	0.66
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	K.ATNDEIFSILK#.D	50.26	33.57	1.50	0.67
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	K.DGALEEQIER.L	22.71	12.58	1.80	0.55
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	K.DVPNPNQVDDDDEGFR@.F	11.26	7.77	1.45	0.69
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	R.FIM*ILTEHLVR@.C	12.00	5.83	2.06	0.49
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	R.IFSTTESYLK#.R	37.53	26.63	1.41	0.71
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	R.M*FDYTDDPEGPVM*PGSHSVER.F	7.04	6.26	1.12	0.89
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	K.NLFLVIFQR@.F	18.67	9.83	1.90	0.53
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	K.ANNYNEAVYLVR@.F	10.23	6.03	1.70	0.59
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	K.ATNDEIFSILK#.D	34.25	24.57	1.39	0.72
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	K.DGALEEQIER@.L	12.84	9.45	1.36	0.74
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	K.DVPNPNQVDDDDEGFR@.F	9.46	3.55	2.66	0.38
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	R.IFSTTESYLK#.R	21.40	14.77	1.45	0.69
Q3UYV9_NCBP1_MOUSE	Ncbp1	Nuclear cap-binding prot	R.M*FDYTDDPEGPVM*PGSHSVER@.F	6.17	4.21	1.46	0.68
Q9CQ49_NCBP2_MOUSE	Ncbp2	Nuclear cap-binding prot	R.SDSYVELSEYR.D	147.19	30.61	4.81	0.21
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.FAISELFAK#.N	10.81	4.88	2.22	0.45
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.GFGFVDFNSEEDAK#.A	4.42	1.79	2.47	0.40
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.ALELTGLK#.V	100.70	23.70	4.25	0.24
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.ETLEEVFEK#.A	122.92	33.62	3.66	0.27
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.EVFEDAM*EIR@.L	26.21	6.50	4.03	0.25
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.FAISELFAK#.N	233.74	63.60	3.67	0.27
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.FGYVDFESAEDLEK#.A	86.12	21.55	4.00	0.25
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.GFGFVDFNSEEDAK#.A	103.09	24.71	4.17	0.24
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.GLSEDTTEETLK#.E	14.30	4.16	3.44	0.29
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.GLSEDTTEETLK#ESFEGSVR@.A	157.16	31.19	5.04	0.20
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.GYAFIEFASFEDAK#.E	57.16	15.07	3.79	0.26
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	R.IVTDR@ETGSSK#.G	12.54	3.85	3.26	0.31
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	R.K#FGYVDFESAEDLEK#.A	57.89	9.53	6.07	0.16
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	R.LELQGSNSR@.S	137.66	29.49	4.67	0.21
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.NDLAVVDVR@.T	143.52	39.10	3.67	0.27
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.NLSFNITEDELK#.E	43.85	16.97	2.58	0.39
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.NLSFNITEDELK#EVFEDAM*EIR@.L	62.96	15.26	4.13	0.24
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.QK#VEGSEPTTPFNLFIGNLNPNK#.S	25.24	6.17	4.09	0.24
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	R.SVSLYYTGEK#.G	92.28	21.53	4.29	0.23
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.TLVLSNLSYSATK#.E	72.34	22.11	3.27	0.31
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.VEGSEPTTPFNLFIGNLNPNK#.S	56.78	19.09	2.97	0.34
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.VFGNEIK#.L	140.79	34.14	4.12	0.24
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.FAISELFAK#.N	14.49	6.17	2.35	0.43
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.FGYVDFESAEDLEK#.A	9.29	3.48	2.67	0.38
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.GFGFVDFNSEEDAK#.A	8.39	2.94	2.85	0.35
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.GLSEDTTEETLK#ESFEGSVR@.A	14.89	3.65	4.08	0.25
P09405_NUCL_MOUSE	Ncl	Nucleolin OS=Mus muscu	K.NDLAVVDVR@.T	8.54	3.77	2.26	0.44
O09000_NCOA3_MOUSE	Ncoa3	Nuclear receptor coactiv	R.FSLADGTIVSAQTK#.S	103.83	87.95	1.18	0.85
O09000_NCOA3_MOUSE	Ncoa3	Nuclear receptor coactiv	K.VVNIDTNSLR@.S	8.53	4.89	1.74	0.57
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.GGHPPAIQSLINLLADNR@.Y	57.16	39.63	1.44	0.69
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.GPPGPESQSR.A	19.54	13.19	1.48	0.67
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.LAPASTM*ASQRPVSSTGINFDNPSVQK.A	5.79	5.79	1.00	1.00
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	K.M*ANDAILQER@.D	27.00	13.19	2.05	0.49
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.SSADSLPGPISR@.Q	20.91	20.26	1.03	0.97
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.YFEEIQR.R	22.72	12.34	1.84	0.54
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.YLTAEETDKIINYLR.E	42.22	26.94	1.57	0.64
B7ZC24_B7ZC24_MOUSE	Ncoa5	Nuclear receptor coactiv	R.SSADSLPGELR@.G	11.45	5.34	2.14	0.47
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.DPYSFGDSR@.D	26.10	9.08	2.88	0.35
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.DSFDGR@GPPGPESQSR@.A	7.56	2.45	3.09	0.32
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	K.DYAESVGR.K	43.31	19.37	2.24	0.45
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.GGHPPAIQSLINLLADNR@.Y	115.77	65.49	1.77	0.57
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.GPPGPESQSR@.A	33.89	20.04	1.69	0.59
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.K#DDSYFDR@.Y	6.43	4.00	1.61	0.62
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.LAPASTM*ASQR@PVSSTGINFDNPSVQK#.A	30.63	18.34	1.67	0.60
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	K.M*ANDAILQER@.D	61.41	28.92	2.12	0.47
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.NM*GPR@PGAPSQGLFGQPSSR@.L	22.37	10.19	2.19	0.46
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.NM*PQADAM*VLVAR@.N	21.97	10.04	2.19	0.46
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.QPLGAASGSSLK#.S	55.35	32.96	1.68	0.60
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.R@DPYSFGDSR@.D	11.12	7.23	1.54	0.65
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.RYFEEIQR.R	16.41	11.41	1.44	0.70
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	K.SQPSSQPLQSGQVLPSATPTPAAPPTSQQELQAK#.I	16.09	11.00	1.46	0.68
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.SSADSLPGPISR@.Q	69.47	40.88	1.70	0.59
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.YFEEIQR@.R	72.78	41.15	1.77	0.57
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.YLTAEETDK#IINYLR@.E	88.27	42.78	2.06	0.48
Q91W39_NCOA5_MOUSE	Ncoa5	Nuclear receptor coactiv	R.GGHPPAIQSLINLLADNR.Y	7.86	7.70	1.02	0.98
Q60974_NCOR1_MOUSE	Ncor1	Nuclear receptor corepre	R.SAAVSEQQQLEQK#.N	6.20	2.98	2.08	0.48
Q60974_NCOR1_MOUSE	Ncor1	Nuclear receptor corepre	R.GSITQGTPALPQAGIPTEALVK#.G	4.00	2.99	1.34	0.75
Q60974_NCOR1_MOUSE	Ncor1	Nuclear receptor corepre	R.SAAVSEQQQLEQK#.N	8.76	3.51	2.49	0.40
Q60974_NCOR1_MOUSE	Ncor1	Nuclear receptor corepre	R.SQNSQPEGLLVR@.A	8.63	6.95	1.24	0.81
Q60974_NCOR1_MOUSE	Ncor1	Nuclear receptor corepre	R.SYEAVEGSIK#.Q	8.22	1.57	5.24	0.19
Q60974_NCOR1_MOUSE	Ncor1	Nuclear receptor corepre	R.TVLSGSIM*QGTPR@.A	3.46	2.73	1.26	0.79
Q60974_NCOR1_MOUSE	Ncor1	Nuclear receptor corepre	R.YNTAADALAALVDAAASAPQM*DVSK#.T	9.39	1.58	5.93	0.17
E9PY55_E9PY55_MOUSE	Ncor2	Nuclear receptor corepre	R.QLGAISQGM*SVQLR@.V	8.21	3.38	2.43	0.41
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	K.APM*GPLTM*GLPLAVDPK#.K	8.64	6.17	1.40	0.71

F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	K.EAEK#PAFFPAFPTEGPK#.L	23.35	12.57	1.86	0.54
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.ESSLALNYAAGPR@.G	10.81	3.71	2.91	0.34
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.GHIPLAFDPTSIPR@.G	26.24	16.44	1.60	0.63
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.GQAGPPESLGVPTAQETSVLR@.G	8.17	4.69	1.74	0.57
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	K.GTEAIETVSEAPLKVEEAGSK.A	39.56	23.59	1.68	0.60
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	K.GVVTSVEPGTPTVLR@.W	18.79	7.81	2.41	0.42
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.GYPDTAALENR@.Q	18.77	12.62	1.49	0.67
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.HSSSPLSPGGPTHLAK#PTATSSSER@.E	14.31	7.81	1.83	0.55
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.ILEGLGPQVELPLYNQPSDTR@.Q	14.55	5.53	2.63	0.38
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.LAYLPTAPPPFSSR@.H	17.57	10.56	1.66	0.60
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.LELLPDTLLR@PSPLLATGQPSGSEDLTK#.D	5.30	3.34	1.58	0.63
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	K.LTESNSAM*VK#.S	10.31	4.95	2.09	0.48
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	K.NFGLIASFLER@.K	11.08	2.69	4.12	0.24
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.QLGAISQQGM*SVQLR@.V	5.88	3.14	1.87	0.53
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	K.SEAEEIDVGK#PEEPEASEEPPESVK#.S	3.56	3.30	1.08	0.93
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.SGTSSGAGGSITR@.G	15.87	8.43	1.88	0.53
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.TVTSASIEGLM*GR@.A	12.84	5.22	2.46	0.41
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	R.VVTLAQHISEVITQDYTR@.H	25.31	14.38	1.76	0.57
F8VQL9_F8VQL9_MOUSE	Ncor2	Nuclear receptor corepre	K.YDSGAPSTGTK#.K	9.27	4.25	2.18	0.46
Q8BNY6_NCS1_MOUSE	Ncs1	Neuronal calcium sensor	K.LYDLDNDGYITR@.N	10.00	4.68	2.13	0.47
P57716_NICA_MOUSE	Ncstn	Nicastrin OS=Mus muscu	K.ADVLFVAPR@.E	8.77	1.50	5.87	0.17
P57716_NICA_MOUSE	Ncstn	Nicastrin OS=Mus muscu	R.LENIDSFVELGQVALR@.T	9.00	5.87	1.53	0.65
P57716_NICA_MOUSE	Ncstn	Nicastrin OS=Mus muscu	R.LLYGFLVR@.A	14.21	9.00	1.58	0.63
P57716_NICA_MOUSE	Ncstn	Nicastrin OS=Mus muscu	K.NQVEDLLATLEK#.S	9.97	5.84	1.71	0.59
Q9CZA6_NDE1_MOUSE	Nde1	Nuclear distribution pro	R.ELEQANDDLER@.A	16.40	8.66	1.89	0.53
Q9CZA6_NDE1_MOUSE	Nde1	Nuclear distribution pro	R.GLDSSTSGTPLTPAAR@.I	5.99	4.00	1.50	0.67
Q9CZA6_NDE1_MOUSE	Nde1	Nuclear distribution pro	R.ISALNIVGDLLR@.K	24.48	10.48	2.34	0.43
Q9CPR8_MAGG1_MOUSE	Ndnl2	Melanoma-associated an	K.VAELVQFLLIK#.D	8.81	5.45	1.62	0.62
Q62433_NDRG1_MOUSE	Ndrg1	Protein NDRG1 OS=Mus r	R.LNITPNSGATGNNAGPK.S	6.54	8.76	0.75	1.34
Q62433_NDRG1_MOUSE	Ndrg1	Protein NDRG1 OS=Mus r	K.SVIGM*GTGAGAYILTR@.F	8.61	2.95	2.92	0.34
Q62433_NDRG1_MOUSE	Ndrg1	Protein NDRG1 OS=Mus r	R.TASGSSVTSLEGTR.S	20.62	10.00	2.06	0.48
Q9QYF9_NDRG3_MOUSE	Ndrg3	Protein NDRG3 OS=Mus r	K.YFLQGM*GYIPSASM*TR@.L	3.33	1.90	1.75	0.57
Q9D1J1_NECP2_MOUSE	Necap2	Adaptin ear-binding coat	R.ASEWQLDQPSWSGR@.L	5.63	2.92	1.93	0.52
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	R.DDFLGQVDVPLYPLPTENPR@.M	5.69	4.44	1.28	0.78
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	K.R@PSPDDDLTDEDNDDM*QLQAQR@.A	12.23	5.52	2.21	0.45
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	K.WNEEILFR.V	8.08	5.81	1.39	0.72
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	R.DDFLGQVDVPLYPLPTENPR@.M	6.93	4.03	1.72	0.58
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	R.DDFLGQVDVPLYPLPTENPR@.M	10.76	5.79	1.86	0.54
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	K.EGFFELIPQDLIK#.I	22.59	8.71	2.59	0.39
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	R.LQNVAITGPAVPYSR@.D	11.14	4.88	2.28	0.44
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	K.R@PSPDDDLTDEDNDDM*QLQAQR@.A	11.21	4.07	2.75	0.36
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	K.TGGSEIVVTNK#.N	8.76	4.83	1.81	0.55
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	R.DDFLGQVDVPLYPLPTENPR@.M	5.74	3.74	1.54	0.65
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	K.EGFFELIPQDLIK#.I	15.28	5.95	2.57	0.39
P46935_NEDD4_MOUSE	Nedd4	E3 ubiquitin-protein liga	R.LLQFVTGTSR@.V	13.68	18.23	0.75	1.33
Q8BG30_NELFA_MOUSE	Nelfa	Negative elongation fact	K.LLDISELNTVGAGR@.E	9.82	8.66	1.13	0.88
Q8BG30_NELFA_MOUSE	Nelfa	Negative elongation fact	K.ALILGFM*AGSR@.E	6.64	1.63	4.07	0.25
Q8BG30_NELFA_MOUSE	Nelfa	Negative elongation fact	R.EASR@PPEEPSAPSPTLPTQFK#.Q	16.56	9.07	1.83	0.55
Q8BG30_NELFA_MOUSE	Nelfa	Negative elongation fact	R.EQM*FAAQEM*FK#.T	7.26	0.00	#DIV/0!	0.00
Q8BG30_NELFA_MOUSE	Nelfa	Negative elongation fact	K.LLDISELNTVGAGR@.E	40.08	11.00	3.65	0.27
Q8BG30_NELFA_MOUSE	Nelfa	Negative elongation fact	K.NALTTLAGPLTPPVK#.H	10.95	3.28	3.33	0.30
Q8BG30_NELFA_MOUSE	Nelfa	Negative elongation fact	K.SFPDTGSLNLDLEEQNPNVQDILGELR@.E	5.82	2.61	2.23	0.45
Q8BG30_NELFA_MOUSE	Nelfa	Negative elongation fact	K.TLDTEVVEK#PTK#EETVVENATPDYAAGLVSTQK#.L	15.61	5.19	3.01	0.33
Q8BG30_NELFA_MOUSE	Nelfa	Negative elongation fact	K.LLDISELNTVGAGR@.E	6.99	2.08	3.36	0.30
Q8C4Y3_NELFB_MOUSE	Nelfb	Negative elongation fact	R.DSPDLLLLLR@.L	31.18	6.33	4.93	0.20
Q8C4Y3_NELFB_MOUSE	Nelfb	Negative elongation fact	K.ALEPTGQSGEAVK#.E	15.59	4.90	3.18	0.31
Q8C4Y3_NELFB_MOUSE	Nelfb	Negative elongation fact	K.ASVTYPNTLPESFTK#.F	17.05	6.95	2.45	0.41
Q8C4Y3_NELFB_MOUSE	Nelfb	Negative elongation fact	R.DSPDLLLLLR@.L	48.42	12.57	3.85	0.26
Q8C4Y3_NELFB_MOUSE	Nelfb	Negative elongation fact	R.VSAIASEGK#.A	10.96	5.13	2.14	0.47
Q8C4Y3_NELFB_MOUSE	Nelfb	Negative elongation fact	K.ALEPTGQSGEAVK#.E	18.78	5.53	3.39	0.29
Q8C4Y3_NELFB_MOUSE	Nelfb	Negative elongation fact	K.ASVTYPNTLPESFTK#.F	15.35	2.97	5.18	0.19
Q8C4Y3_NELFB_MOUSE	Nelfb	Negative elongation fact	R.DSPDLLLLLR@.L	19.27	7.25	2.66	0.38
Q922L6_NELFD_MOUSE	Nelfcd	Negative elongation fact	R.GALNPADITVLFK#.M	8.26	4.08	2.03	0.49
Q922L6_NELFD_MOUSE	Nelfcd	Negative elongation fact	R.GALNPADITVLFK#.M	18.50	8.90	2.08	0.48
Q922L6_NELFD_MOUSE	Nelfcd	Negative elongation fact	R.GYVLPVVSYIR@.K	10.96	5.59	1.96	0.51
Q922L6_NELFD_MOUSE	Nelfcd	Negative elongation fact	R.TSLATILDGGEENLEK#.N	11.58	5.55	2.09	0.48
Q922L6_NELFD_MOUSE	Nelfcd	Negative elongation fact	R.GALNPADITVLFK#.M	32.69	9.73	3.36	0.30
Q922L6_NELFD_MOUSE	Nelfcd	Negative elongation fact	R.GYVLPVVSYIR@.K	9.49	3.11	3.05	0.33
Q922L6_NELFD_MOUSE	Nelfcd	Negative elongation fact	R.TSLATILDGGEENLEK#.N	21.66	28.50	0.76	1.32
P19426_NELFE_MOUSE	Nelfe	Negative elongation fact	R.GAFSPFGNIIDLSM*DPPR@.N	4.07	13.82	0.29	3.39
P19426_NELFE_MOUSE	Nelfe	Negative elongation fact	K.SLYESFVSSSDR@.L	7.58	2.73	2.77	0.36
P19426_NELFE_MOUSE	Nelfe	Negative elongation fact	R.SM*SADEDLQEPSR@.R	15.92	3.91	4.07	0.25
Q7TPW1_NEXN_MOUSE	Nexn	Nexilin OS=Mus musculu	K.LEINFEQLLR@.Q	8.13	6.85	1.19	0.84
Q7TPW1_NEXN_MOUSE	Nexn	Nexilin OS=Mus musculu	R.NTSVVDSEPVR@.F	20.58	12.77	1.61	0.62
Q7TPW1_NEXN_MOUSE	Nexn	Nexilin OS=Mus musculu	R.SM*VLDDDSPEIYK#.T	9.80	5.73	1.71	0.58
Q7TPW1_NEXN_MOUSE	Nexn	Nexilin OS=Mus musculu	K.TVSQESLTPGK#LEINFEQLLR@.Q	16.71	12.86	1.30	0.77
Q9WV30_NFAT5_MOUSE	Nfat5	Nuclear factor of activate	R.SGDSQPQVNLFSSTK#.N	7.19	5.49	1.31	0.76
Q9WV30_NFAT5_MOUSE	Nfat5	Nuclear factor of activate	R.SHDVQPFTYTPDPAAGALNVNVK.K	1.86	11.68	0.16	6.29
Q9WV30_NFAT5_MOUSE	Nfat5	Nuclear factor of activate	K.VIFQENVSDENSWK#.S	7.81	2.13	3.66	0.27
O09130_NF2IP_MOUSE	Nfatc2ip	NFATC2-interacting prot	R.ILLLFGESELSPTATPSTLK#.L	12.86	4.83	2.66	0.38
O09130_NF2IP_MOUSE	Nfatc2ip	NFATC2-interacting prot	R.LLDPGEAPVVPVYSGK#.V	3.82	2.20	1.73	0.58
Q8K120_NFAC4_MOUSE	Nfatc4	Nuclear factor of activate	R.FGLSSPLPSPR@.A	8.34	7.73	1.08	0.93
P97863_NFIB_MOUSE	Nfib	Nuclear factor 1 B-type O	K.SGVFNVSELVR.V	5.07	6.93	0.73	1.37
P97863_NFIB_MOUSE	Nfib	Nuclear factor 1 B-type O	K.NPPGYLEDSFVK.S	4.03	5.49	0.73	1.36
P97863_NFIB_MOUSE	Nfib	Nuclear factor 1 B-type O	K.SGVFNVSELVR.V	11.18	14.57	0.77	1.30
P97863_NFIB_MOUSE	Nfib	Nuclear factor 1 B-type O	K.SGVFNVSELVR.V	7.19	12.34	0.58	1.72
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	R.EDFVLAVTGK#.K	11.06	5.64	1.96	0.51
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	K.GIPLESTDGER@.L	58.25	44.03	1.32	0.76
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	R.LDLVM*VILFK#.G	8.39	6.00	1.40	0.72
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	K.TEM*DK#SPFNSPSPQDSPR@.L	10.66	5.70	1.87	0.53
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	R.AFAYTWFNLQAR@.K	7.08	4.73	1.50	0.67
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	R.AVK#DELLGEK#.A	18.35	8.68	2.11	0.47
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	K.GIPLESTDGER.L	92.49	65.83	1.41	0.71
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	R.LDLVM*VILFK#.G	19.69	13.39	1.47	0.68
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	K.TEM*DKSPFNSPSPQDSPR.L	7.19	8.35	0.86	1.16
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	R.TPVVTGTGPNFSLGELQGHLAYDLNPASAGM*R@.R	14.59	10.50	1.39	0.72
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	K.GIPLESTDGER.L	84.62	65.18	1.30	0.77
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	R.LDLVM*VILFK#.G	9.97	6.64	1.50	0.67
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	K.TEM*DK#SPFNSPSPQDSPR@.L	14.59	4.93	2.96	0.34
P70255_NFIC_MOUSE	Nfic	Nuclear factor 1 C-type O	R.TPVVTGTGPNFSLGELQGHLAYDLNPASAGM*R@.R	19.19	8.71	2.20	0.45
O08750_NFIL3_MOUSE	Nfil3	Nuclear factor interleuki	R.FIATQPISASDSR@.-	10.11	5.65	1.79	0.56
O08750_NFIL3_MOUSE	Nfil3	Nuclear factor interleuki	K.LSNSTAVYFQDYQTSK#.A	4.91	1.82	2.69	0.37
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.AFSYTWFNLQAR@.K	7.06	3.38	2.09	0.48

P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.AVK#DELLGEK#PEIK#.Q	29.26	19.91	1.47	0.68
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	K.SIDDSEM*ESPVDDVFYPGTGR.S	6.03	5.64	1.07	0.94
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.VSQTPVATASGPNFSLADLESPSYYNINQVTLGR@.R	7.11	4.66	1.53	0.66
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.AFSYTWFNLQAR@.K	10.68	8.43	1.27	0.79
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.AVK#DELLGEK#PEIK#.Q	40.60	37.66	1.08	0.93
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.AVKDELLGEKPEIK.Q	53.70	37.07	1.45	0.69
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	K.SIDDSEM*ESPVDDVFYPGTGR.S	8.10	4.63	1.75	0.57
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.SPAAGSSQSSGWPNDVDAGPASLK#K#.S	6.24	4.47	1.40	0.72
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.ATASALHFPSTSIIQQSSPYFTHPTIR@.Y	20.00	12.60	1.59	0.63
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.EDFVLTITGK#.K	15.46	11.56	1.34	0.75
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	K.SIDDSEM*ESPVDDVFYPGTGR@.S	9.06	3.91	2.32	0.43
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	K.SIDDSEM*ESPVDDVFYPGTGR.S	6.41	5.16	1.24	0.80
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.SITSPPSTSSTK#.R	19.96	11.36	1.76	0.57
P70257_NFIX_MOUSE	Nfix	Nuclear factor 1 X-type O	R.SPAAGSSQSSGWPNDVDAGPASLK#K#.S	4.52	4.17	1.08	0.92
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	K.DM*VVGFANLGILHVTK#.K	14.35	8.20	1.75	0.57
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	K.EM*DLSVVR@.L	21.67	7.69	2.82	0.35
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	R.GYNPGLLVHSDLAYLQAEGGGDR@.Q	23.65	7.69	3.08	0.33
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	R.LM*FTAFLPDSTGSFTR@.R	9.41	3.56	2.64	0.38
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	R.R@LEPVVSDAIYDSK#.A	20.84	9.52	2.19	0.46
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	K.VFETLEAR@.M	19.31	7.44	2.60	0.39
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	R.FYEEEENGGVWEGFGDFSPTDVHR@.Q	3.27	2.10	1.55	0.64
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	R.ILSILLK#.S	17.62	5.26	3.35	0.30
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	K.LGLGILNNAFR@.L	18.52	8.59	2.16	0.46
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	K.TLM*DNYEVSGGTIK#.E	5.01	2.05	2.44	0.41
P25799_NFKB1_MOUSE	Nfkb1	Nuclear factor NF-kappa-	K.LGLGILNNAFR@.L	12.58	2.00	6.29	0.16
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	K.DPAPETADGPYLVIVEQPK#.Q	6.80	3.16	2.15	0.46
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	K.QFTYYPLVEDK#EEVQR@.K	15.11	8.18	1.85	0.54
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.AGAAAPELLQALLR.S	96.31	31.25	3.08	0.32
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.ALLDYGVTADAR.A	30.62	9.92	3.09	0.32
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	K.DM*TAQFNNLGVLHVTK#.K	13.44	9.04	1.49	0.67
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	K.DPAPETADGPYLVIVEQPK#.Q	12.21	3.46	3.52	0.28
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.DTDAGEGAEEPR@.T	9.75	2.89	3.37	0.30
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.HGDSALHLALR@.A	30.55	10.65	2.87	0.35
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	K.QFTYYPLVEDK#EEVQR@.K	21.76	8.69	2.50	0.40
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.TALHLATEM*EELGLVTHLVTK#.L	14.29	7.52	1.90	0.53
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.TALHLATEM*EELGLVTHLVTK#.L	3.60	2.32	1.55	0.65
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.TALHLATEMEELGLVTHLVTK#.L	8.23	4.57	1.80	0.56
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.TFAGNTPLHLAAGLGSPTLTR@.L	31.82	9.12	3.49	0.29
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.TPPEAPQGEPQALDTLQR@.A	16.19	3.50	4.63	0.22
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	K.VM*DLSIVR@.L	18.54	4.53	4.10	0.24
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.AGAAAPELLQALLR@.S	69.62	16.83	4.14	0.24
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.ALLDYGVTADAR@.A	20.59	5.45	3.78	0.26
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	K.DPAPETADGPYLVIVEQPK#.Q	9.96	2.24	4.45	0.22
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.DTDAGEGAEEPR@.T	7.23	1.68	4.30	0.23
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.HGDSALHLALR@.A	20.11	4.38	4.59	0.22
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.TALHLATEM*EELGLVTHLVTK#.L	9.25	3.61	2.56	0.39
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.TALHLATEM*EELGLVTHLVTK#.L	3.60	2.12	1.70	0.59
Q9WTK5_NFKB2_MOUSE	Nfkb2	Nuclear factor NF-kappa-	R.TFAGNTPLHLAAGLGSPTLTR@.L	22.88	7.66	2.99	0.33
Q6PIJ4_NFRKB_MOUSE	Nfrkb	Nuclear factor related to	K.APSASVPSSAPAGTTVVK#.V	9.01	3.25	2.77	0.36
Q6PIJ4_NFRKB_MOUSE	Nfrkb	Nuclear factor related to	R.AVPSSFSPFVEFK#.E	31.49	6.94	4.54	0.22
Q6PIJ4_NFRKB_MOUSE	Nfrkb	Nuclear factor related to	R.SDR@PAYVTILSLVR@.D	15.32	4.07	3.76	0.27
Q6PIJ4_NFRKB_MOUSE	Nfrkb	Nuclear factor related to	K.TADK#IELGDSDLK#.L	12.64	6.26	2.02	0.50
Q6PIJ4_NFRKB_MOUSE	Nfrkb	Nuclear factor related to	K.APSASVPSSAPAGTTVVK#.V	3.85	1.20	3.20	0.31
Q9Z1J3_NFS1_MOUSE	Nfs1	Cysteine desulfurase, mit	R.FTTEEEVDYTAEK#.C	5.20	3.98	1.31	0.77
Q9QZ23_NFU1_MOUSE	Nfu1	NFU1 iron-sulfur cluster	R.IR@PTVQEDGGDVIYR@.G	10.78	10.81	1.00	1.00
Q9QZ23_NFU1_MOUSE	Nfu1	NFU1 iron-sulfur cluster	K.SVFFGPDFITVTK#.E	10.26	7.33	1.40	0.71
P70353_NFYC_MOUSE	Nfyc	Nuclear transcription fac	K.AAQIFITELTLR@.A	12.99	6.44	2.02	0.50
Q9CRB2_NHP2_MOUSE	Nhp2	H/ACA ribonucleoprotei	K.ELLVNLNPIAQPLASR.R	13.28	17.28	0.77	1.30
Q9CRB2_NHP2_MOUSE	Nhp2	H/ACA ribonucleoprotei	R.TYK#ELLVNLNPIAQPLASR@.R	10.75	13.45	0.80	1.25
Q9D0T1_NH2L1_MOUSE	Nhp2l1	NHP2-like protein 1 OS=	K.QQIQSIQQSIER@.L	212.24	93.92	2.26	0.44
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	R.AFALYSEDEGVLR@.F	134.50	9.41	14.30	0.07
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	R.ASLEAGAEPETIITSGLISPEGLAIDHFR@.R	22.27	13.98	1.59	0.63
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	K.DIGLPNGLTFDPFSK.L	6.72	7.44	0.90	1.11
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	K.DSGQFTDEFLPEQR@.S	11.09	8.83	1.26	0.80
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	R.ITQTAEGLDPENYLSIK.T	9.04	6.82	1.33	0.75
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	K.ADPGLVDVGTSSPGSDR@.A	7.05	3.74	1.88	0.53
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	R.AFALYSEDEGVLR@.F	447.08	9.14	48.92	0.02
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	K.DIGLPNGLTFDPFSK#.L	10.62	5.48	1.94	0.52
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	K.DSGQFTDEFLPEQR@.S	9.78	4.95	1.97	0.51
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	R.EALYFSLTNTEQSVK#.N	9.22	5.53	1.67	0.60
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	K.ESYNVQLQLPAR@.V	15.25	6.27	2.43	0.41
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	R.ETESASLDPQTK#.Q	7.93	6.84	1.16	0.86
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	R.FALDNVR@PATVGGDPSTAR@.S	16.15	5.46	2.96	0.34
O88322_NID2_MOUSE	Nid2	Nidogen-2 OS=Mus musc	R.ITQTAEGLDPENYLSIK#.T	14.76	7.54	1.96	0.51
Q91VE6_MK67I_MOUSE	Nifk	MKI67 FHA domain-inter	K.GIDYSFPSLVLPKPK.N	17.62	6.56	2.69	0.37
Q91VE6_MK67I_MOUSE	Nifk	MKI67 FHA domain-inter	K.GYAFVEFESEDVAK#.I	8.57	7.31	1.17	0.85
Q91VE6_MK67I_MOUSE	Nifk	MKI67 FHA domain-inter	K.IVAETM*DNYLFGER@.L	12.28	5.31	2.31	0.43
Q9CXK8_NIP7_MOUSE	Nip7	60S ribosome subunit bi	R.K#VDPM*AIVVFHQADIGEYVR@.H	8.50	4.06	2.09	0.48
Q9CXK8_NIP7_MOUSE	Nip7	60S ribosome subunit bi	R.LHVTALDYLAPYAK#.Y	22.24	19.76	1.13	0.89
Q9CXK8_NIP7_MOUSE	Nip7	60S ribosome subunit bi	R.LHVTALDYLAPYAK.Y	4.06	2.66	1.53	0.65
Q6KCD5_NIPBL_MOUSE	Nipbl	Nipped-B-like protein OS	K.ALLDYLDENTETDPSLVFSR@.K	6.46	4.56	1.42	0.71
Q6KCD5_NIPBL_MOUSE	Nipbl	Nipped-B-like protein OS	K.LLM*EHLDPDEEEEEGEVSASTNAR@.N	6.27	3.18	1.97	0.51
Q6KCD5_NIPBL_MOUSE	Nipbl	Nipped-B-like protein OS	R.LM*DNSTSVR@.E	8.30	5.02	1.65	0.60
Q6KCD5_NIPBL_MOUSE	Nipbl	Nipped-B-like protein OS	K.NLQTYLQEEDTR@.M	9.90	5.99	1.65	0.60
Q80TM9_NISCH_MOUSE	Nisch	Nischarin OS=Mus muscu	R.EEAHGEQGEEEEEEEEEDVAENR@.Y	11.35	3.16	3.59	0.28
Q80TM9_NISCH_MOUSE	Nisch	Nischarin OS=Mus muscu	R.FVTAIFVLPHEK#.F	6.26	2.92	2.14	0.47
Q80TM9_NISCH_MOUSE	Nisch	Nischarin OS=Mus muscu	R.GPAPAGGPAPAEALAQAEVPAQYPSER@.L	12.89	7.26	1.78	0.56
Q80TM9_NISCH_MOUSE	Nisch	Nischarin OS=Mus muscu	K.LSDLQSVNVGLFDQYFR@.L	8.07	2.40	3.37	0.30
Q80TM9_NISCH_MOUSE	Nisch	Nischarin OS=Mus muscu	R.VPLSTVLLDPTR@.S	23.40	7.78	3.01	0.33
Q9D0F4_NKAP_MOUSE	Nkap	NF-kappa-B-activating pr	R.ALASFNQEER@.R	19.87	11.96	1.66	0.60
Q9D0F4_NKAP_MOUSE	Nkap	NF-kappa-B-activating pr	R.ALASFNQEER@.R	21.75	11.69	1.86	0.54
Q9D0F4_NKAP_MOUSE	Nkap	NF-kappa-B-activating pr	R.SK#AEEPSDLIGPEAPK#.T	15.32	3.85	3.98	0.25
Q9D0F4_NKAP_MOUSE	Nkap	NF-kappa-B-activating pr	K.TLASQDDK#PLNYGHALLPGEGAAM*AEYVK#.A	14.46	6.13	2.36	0.42
P30415_NKTR_MOUSE	Nktr	NK-tumor recognition pr	K.TTHLLPVQSTYSLTNIK#.A	5.96	4.06	1.47	0.68
P30415_NKTR_MOUSE	Nktr	NK-tumor recognition pr	K.TTHLLPVQSTYSLTNIK#.A	21.97	6.42	3.42	0.29
Q8VEJ4_NLE1_MOUSE	Nle1	Notchless protein homol	K.IVDIIYQPQAVFR@.V	5.90	2.59	2.28	0.44
Q8BYM5_NLGN3_MOUSE	Nlgn3	Neuroligin-3 OS=Mus mu	K.FIHTKANR@FEEVAWSK#.Y	1.03	3.24	0.32	3.15
Q99L48_NMD3_MOUSE	Nmd3	60S ribosomal export pr	R.DATIPVESDTDDEGAPR@.I	7.12	3.62	1.97	0.51
Q99L48_NMD3_MOUSE	Nmd3	60S ribosomal export pr	R.DATIPVESDTDDEGAPR@.I	8.40	3.79	2.22	0.45
O88425_NDK6_MOUSE	Nme6	Nucleoside diphosphate	R.EIAAFFPDFSEQR@.W	3.46	2.27	1.52	0.66
O35309_NMI_MOUSE	Nmi	N-myc-interactor OS=Mu	K.INVTGIPDELSEEQTR@.D	7.24	4.83	1.50	0.67
O35309_NMI_MOUSE	Nmi	N-myc-interactor OS=Mu	R.SAVITFVETGVVDK#.I	20.23	18.02	1.12	0.89
O35309_NMI_MOUSE	Nmi	N-myc-interactor OS=Mu	K.VSAHPVPLNTGVR@.F	20.69	15.40	1.34	0.74

O35309_NMI_MOUSE	Nmi	N-myc-interactor OS=Mu	K.YQVFSAVSK#.K	12.21	14.39	0.85	1.18
Q9EPA7_NMNA1_MOUSE	Nmnat1	Nicotinamide/nicotinic	K.FIYESDVLWR@.H	9.57	4.77	2.01	0.50
Q9EPA7_NMNA1_MOUSE	Nmnat1	Nicotinamide/nicotinic	R.NAGVTLAPLQR@.N	15.19	11.79	1.29	0.78
Q8BW10_NOB1_MOUSE	Nob1	RNA-binding protein NO	R.QK#TDVFAPDYIAGVSPFAENDISSR@.S	8.46	2.27	3.73	0.27
Q8BW10_NOB1_MOUSE	Nob1	RNA-binding protein NO	R.TPLPNIDR@.E	15.05	9.75	1.54	0.65
Q8BW10_NOB1_MOUSE	Nob1	RNA-binding protein NO	R.YSLPTPK#.G	19.54	9.39	2.08	0.48
Q8BW10_NOB1_MOUSE	Nob1	RNA-binding protein NO	R.DAPLQDIGK#.N	10.92	3.94	2.77	0.36
Q8BW10_NOB1_MOUSE	Nob1	RNA-binding protein NO	R.LAVLPYQLR@.F	28.15	17.92	1.57	0.64
Q9WV70_NOC2L_MOUSE	Noc2l	Nucleolar complex prote	K.FTSPSTLPLISFM*QR@.T	4.42	2.08	2.13	0.47
Q9WV70_NOC2L_MOUSE	Noc2l	Nucleolar complex prote	R.LFHEVVQAFR@.A	28.56	11.48	2.49	0.40
Q9WV70_NOC2L_MOUSE	Noc2l	Nucleolar complex prote	R.DR@EIQLEISGK#.E	6.13	2.88	2.13	0.47
Q9WV70_NOC2L_MOUSE	Noc2l	Nucleolar complex prote	K.FTSPSTLPLISFM*QR@.T	6.57	5.00	1.31	0.76
Q9WV70_NOC2L_MOUSE	Noc2l	Nucleolar complex prote	R.LEDLNFPEIK#.R	17.12	8.42	2.03	0.49
Q9WV70_NOC2L_MOUSE	Noc2l	Nucleolar complex prote	R.LFHEVVQAFR@.A	32.44	17.49	1.85	0.54
Q9WV70_NOC2L_MOUSE	Noc2l	Nucleolar complex prote	R.M*SSK#PINFSVILK#.L	25.28	12.55	2.01	0.50
Q8VI84_NOC3L_MOUSE	Noc3l	Nucleolar complex prote	K.SPLLPAVLEGLAK#.F	22.54	8.49	2.65	0.38
Q8BG17_NOL12_MOUSE	Nol12	Nucleolar protein 12 OS=	R.EEALEEADELER@.L	6.63	2.42	2.74	0.37
Q8BG17_NOL12_MOUSE	Nol12	Nucleolar protein 12 OS=	K.M*LAER@EEALEEADELER@.L	11.06	6.36	1.74	0.58
Q8R5K4_NOL6_MOUSE	Nol6	Nucleolar protein 6 OS=	R.EAVVWEAESLFEK#.R	12.57	5.89	2.13	0.47
Q8R5K4_NOL6_MOUSE	Nol6	Nucleolar protein 6 OS=	R.GLLAEPGPSSLM*PVLGYDPPQLYLAQLR@.E	10.03	2.66	3.77	0.27
Q8R5K4_NOL6_MOUSE	Nol6	Nucleolar protein 6 OS=	R.LLWGLEGLPLTVSAVQGAHPVLR@.Y	9.31	6.38	1.46	0.68
Q8R5K4_NOL6_MOUSE	Nol6	Nucleolar protein 6 OS=	R.LQVEELLK#.E	23.05	12.50	1.84	0.54
Q8R5K4_NOL6_MOUSE	Nol6	Nucleolar protein 6 OS=	R.SPEGM*VSLR@.D	14.30	5.29	2.70	0.37
Q8R5K4_NOL6_MOUSE	Nol6	Nucleolar protein 6 OS=	R.TEPPAEGLLQPVNLSR@.E	11.27	5.02	2.24	0.45
Q8R5K4_NOL6_MOUSE	Nol6	Nucleolar protein 6 OS=	R.LQVEELLK#.E	18.75	12.25	1.53	0.65
Q8R5K4_NOL6_MOUSE	Nol6	Nucleolar protein 6 OS=	R.TEPPAEGLLQPVNLSR@.E	9.56	4.25	2.25	0.44
Q9D7Z3_NOL7_MOUSE	Nol7	Nucleolar protein 7 OS=	K.AAAQFLTSTWGAQK#.Q	3.93	2.75	1.43	0.70
Q9D7Z3_NOL7_MOUSE	Nol7	Nucleolar protein 7 OS=	K.LLPDAVLEQLTTASEADIK#.K	9.10	3.96	2.30	0.43
Q9D7Z3_NOL7_MOUSE	Nol7	Nucleolar protein 7 OS=	K.VQSVGQIESYM*AVR@.L	10.15	3.40	2.98	0.34
Q3UHX0_NOL8_MOUSE	Nol8	Nucleolar protein 8 OS=	R.GSNLFWSGM*GGSISR@.N	3.94	2.20	1.80	0.56
Q3UHX0_NOL8_MOUSE	Nol8	Nucleolar protein 8 OS=	K.LM*DLQSQFGSDER@.F	6.54	2.04	3.20	0.31
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	K.FTPTLTSEYVELTDGLYTK#.S	7.32	8.99	0.81	1.23
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	R.FVDFLK#.T	16.00	4.95	3.24	0.31
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	R.VLSPNYVVQLYSDR@.C	13.35	4.17	3.20	0.31
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	K.VSPNVTQPVR@.D	11.52	4.30	2.68	0.37
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	K.FTPTLTSEYVELTDGLYTK#.S	10.72	4.28	2.51	0.40
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	K.FTPTLTSEYVELTDGLYTK#.S	5.66	1.24	4.58	0.22
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	R.FVDFLK#.T	23.56	5.32	4.42	0.23
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	R.VLSPNYVVQLYSDR@.C	12.16	2.76	4.40	0.23
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	R.VNSEFTTLK#.K	8.07	1.96	4.12	0.24
Q3TZX8_NOL9_MOUSE	Nol9	Polynucleotide 5'-hydro	K.VSPNVTQPVR@.D	14.56	3.96	3.68	0.27
Q3UFM5_NOM1_MOUSE	Nom1	Nucleolar MIF4G domain	K.ELITEAQTQASGAGNK#.F	10.16	4.35	2.33	0.43
Q3UFM5_NOM1_MOUSE	Nom1	Nucleolar MIF4G domain	K.TYNPFYAFLASK#.F	10.34	4.85	2.13	0.47
Q3UFM5_NOM1_MOUSE	Nom1	Nucleolar MIF4G domain	K.ELITEAQTQASGAGNK#.F	7.33	2.19	3.34	0.30
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	K.AFNLEK#.Q	46.16	14.88	3.10	0.32
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.AVVIVDDR@.G	139.18	73.10	1.90	0.53
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.FAQPGSFEYEYAM*R@.W	54.75	30.60	1.79	0.56
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.FAQPGSFEYEYAMR@.W	15.09	7.20	2.09	0.48
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.FGQAATM*EGIGAIGGTPPAFNR@PAPGAEFAPNK#.R	3.94	1.39	2.83	0.35
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.FGQAATMEGIGAIGGTPPAFNR@PAPGAEFAPNK#R@.R	3.71	2.74	1.36	0.74
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.LFVGNLPPDITEEEM*R@.K	19.52	8.95	2.18	0.46
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.LFVGNLPPDITEEEMR@.K	6.16	4.21	1.47	0.68
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.RM*EELHNQEVQK.R	83.28	47.02	1.77	0.56
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.R@M*EELHNQEVQK#.R	2.88	1.45	1.99	0.50
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	K.VELDNM*PLR.G	79.37	45.45	1.75	0.57
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	K.VELDNMPLR@.G	12.60	7.67	1.64	0.61
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	K.AFNLEK#.Q	29.31	9.75	3.01	0.33
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.AVVIVDDR@.G	166.89	79.65	2.10	0.48
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.FAQPGSFEYEYAM*R@.W	14.85	6.24	2.38	0.42
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	R.LFVGNLPPDITEEEM*R@.K	7.23	1.84	3.94	0.25
Q99K48_NONO_MOUSE	Nono	Non-POU domain-contai	K.VELDNM*PLR.G	26.08	11.65	2.24	0.45
Q9CQS2_NOP10_MOUSE	Nop10	H/ACA ribonucleoprotei	-.M*FLQYYLNEQGDR.V	2.18	7.39	0.30	3.38
Q9CQS2_NOP10_MOUSE	Nop10	H/ACA ribonucleoprotei	K.VLM*TQQPRPVL.-	5.45	6.37	0.86	1.17
Q8R3N1_NOP14_MOUSE	Nop14	Nucleolar protein 14 OS=	K.AVAAELPYVFAAPESFEELK#.F	16.98	10.27	1.65	0.60
Q8R3N1_NOP14_MOUSE	Nop14	Nucleolar protein 14 OS=	K.ELIEELIAK#.S	14.70	5.44	2.70	0.37
Q9CPT5_NOP16_MOUSE	Nop16	Nucleolar protein 16 OS=	R.DLIDYVR@.Y	41.09	12.88	3.19	0.31
Q9CPT5_NOP16_MOUSE	Nop16	Nucleolar protein 16 OS=	K.FGYNVNR@.K	22.59	7.12	3.17	0.32
Q9CPT5_NOP16_MOUSE	Nop16	Nucleolar protein 16 OS=	R.K#PYVVNDLEAEASLPEK#K#.G	21.23	6.60	3.22	0.31
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	K.AQDATAGVLWNEEDTDEDEDDDGVSPESHPR@.K	5.48	3.96	1.38	0.72
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	R.DLAQALINR@.G	55.72	32.72	1.70	0.59
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	K.DLATYYSYGDFLLSK#.L	14.45	10.54	1.37	0.73
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	K.ELLLSAIDSVNAASK#.T	63.88	34.80	1.84	0.54
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	R.GVNLDPLGK#.W	24.20	12.67	1.91	0.52
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	R.LVPTGLDFGQEGFTR@.F	55.58	28.31	1.96	0.51
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	K.NTGVILANDANADR@.L	39.85	23.90	1.67	0.60
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	R.DLAQALINR@.G	25.63	6.28	4.08	0.25
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	K.DLATYYSYGDFLLSK#.L	6.55	2.49	2.63	0.38
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	K.ELLLSAIDSVNAASK#.T	13.12	4.24	3.10	0.32
E9QN31_E9QN31_MOUSE	Nop2	Probable 28S rRNA (cyto	R.LGVTNTIISHYDGR@.Q	26.83	4.39	6.11	0.16
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.EAVVQAEEAAAEITR@.K	17.53	9.67	1.81	0.55
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LSFYETGEIPR@.K	9.40	14.62	0.64	1.56
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.M*SQVAPSLSALIGEAVGAR@.L	10.56	5.13	2.06	0.49
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.VVSLSEYR.Q	21.86	12.25	1.79	0.56
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.YPASTVQILGAEK#.A	11.14	7.33	1.52	0.66
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.EAVVQAEEAAAEITR@.K	37.61	20.85	1.80	0.55
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LAQFIGNR@.R	29.87	12.09	2.47	0.40
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.LEEITM*DGAK#.A	20.09	12.73	1.58	0.63
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LLLETYLPSK#.K	31.14	16.06	1.94	0.52
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LLLETYLPSK#K#.K	38.51	16.62	2.32	0.43
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LSFYETGEIPR@.K	29.09	11.97	2.43	0.41
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.M*SQVAPSLSALIGEAVGAR@.L	37.92	17.15	2.21	0.45
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.NLDVM*K#EAVVQAEEAAAEITR@.K	8.28	4.78	1.73	0.58
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.SSM*GM*DISAIDLINIESFSSR@.V	15.65	3.25	4.81	0.21
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.SSPK#EEVASEPEEAASPTTPK#.K	9.18	5.16	1.78	0.56
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.VR@EWYGYHFPELVK#.I	13.69	2.29	5.97	0.17
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.VVSLSEYR@.Q	51.59	23.73	2.17	0.46
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.YGLIFHSTFIGR@.A	13.83	5.99	2.31	0.43
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.YPASTVQILGAEK#.A	32.98	18.97	1.74	0.58
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.EAVVQAEEAAAEITR@.K	31.94	14.47	2.21	0.45
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.EELASDLEEM*ATSSAK#.R	8.53	3.84	2.22	0.45
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.FSEEPEVAANFTK#.S	21.71	6.54	3.32	0.30
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LAQFIGNR@.R	42.73	27.36	1.56	0.64
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.LEEITM*DGAK#.A	36.90	11.04	3.34	0.30

Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LIAHAGSLTNLAK#.Y	102.49	38.07	2.69	0.37
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.LK#PQENGM*EDPPVSLPK#.S	9.92	4.46	2.23	0.45
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LLLETYLPSK#.K	56.04	18.73	2.99	0.33
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LLLETYLPSK#K#.K	49.58	15.18	3.27	0.31
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.LSFYETGEIPR@.K	49.28	22.09	2.23	0.45
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.M*SQVAPSLSALIGEAVGAR@.L	52.19	22.53	2.32	0.43
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.NLDVM*K#EAVVQAEEAAAEITR@.K	12.32	5.26	2.34	0.43
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.SK#M*SQVAPSLSALIGEAVGAR@.L	6.61	5.61	1.18	0.85
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.SSM*GM*DISAIDLINIESFSSR@.V	31.12	7.85	3.97	0.25
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.SSPK#EEVASEPEEAASPTTPK#.K	21.00	7.36	2.85	0.35
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.VLLGVGDPK#.I	66.01	28.11	2.35	0.43
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	R.VVSLSEYR@.Q	71.38	24.26	2.94	0.34
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.YGLIFHSTFIGR@.A	11.90	7.89	1.51	0.66
Q9D6Z1_NOP56_MOUSE	Nop56	Nucleolar protein 56 OS=	K.YPASTVQILGAEK#.A	63.62	34.29	1.86	0.54
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.FQDTAEALAAFTALM*EGK#.I	11.23	9.35	1.20	0.83
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.IK#AEVEEEM*EEEEAEEEQVVEEEPTVK#.K	5.47	3.59	1.52	0.66
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.LIAHAGSLLNLAK#.H	9.23	6.92	1.33	0.75
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.NYASASLSEFLSEEVEAEVK#.A	10.76	5.08	2.12	0.47
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.NYASASLSEFLSEEVEAEVK.A	4.44	3.83	1.16	0.86
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.SQM*DGLIPGVEPR@.E	23.39	16.82	1.39	0.72
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.TQLYEYLQNR@.M	30.39	15.02	2.02	0.49
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.YDAFGEDSSSAM*GIENR@.A	18.14	11.44	1.59	0.63
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.YGLIYHASLVGQSSPK#.H	14.42	11.35	1.27	0.79
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.EAHEPLAVADAK#.L	71.32	34.41	2.07	0.48
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.FQDTAEALAAFTALM*EGK#.I	28.78	13.77	2.09	0.48
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.HAASTVQILGAEK#.A	30.84	9.27	3.33	0.30
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.IK#AEVEEEM*EEEEAEEEQVVEEEPTVK#.K	11.95	4.34	2.75	0.36
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.K#IEEVDK#EDEITEK#.K	49.42	28.34	1.74	0.57
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.LIAHAGSLLNLAK#.H	60.86	36.24	1.68	0.60
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	-.M*LVLFETSVGYAIFK#.V	13.04	4.78	2.73	0.37
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.M*M*AIAPNVTVMVGELVGAR@.L	6.38	5.96	1.07	0.93
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.NYASASLSEFLSEEVEAEVK#.A	12.08	5.30	2.28	0.44
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.SQM*DGLIPGVEPR@.E	46.28	21.24	2.18	0.46
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.TQLYEYLQNR@.M	42.67	20.79	2.05	0.49
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.YDAFGEDSSSAM*GIENR@.A	40.76	19.29	2.11	0.47
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.YDAFGEDSSSAMGIENR@.A	4.29	2.78	1.54	0.65
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.YGLIYHASLVGQSSPK#.H	34.63	13.45	2.58	0.39
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.FQDTAEALAAFTALM*EGK#.I	22.25	9.61	2.32	0.43
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.IK#AEVEEEM*EEEEAEEEQVVEEEPTVK#.K	3.34	2.13	1.57	0.64
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.K#IEEVDK#EDEITEK#.K	41.68	11.11	3.75	0.27
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.LIAHAGSLLNLAK#.H	36.57	12.03	3.04	0.33
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.NYASASLSEFLSEEVEAEVK#.A	16.47	4.02	4.10	0.24
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.TQLYEYLQNR@.M	29.38	11.75	2.50	0.40
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	R.YDAFGEDSSSAM*GIENR@.A	28.52	7.55	3.78	0.26
Q6DFW4_NOP58_MOUSE	Nop58	Nucleolar protein 58 OS=	K.YGLIYHASLVGQSSPK#.H	18.18	4.44	4.10	0.24
Q8BMC4_NOP9_MOUSE	Nop9	Nucleolar protein 9 OS=	R.TLLQVLGGTLLESER@.G	14.64	6.35	2.30	0.43
Q8BMC4_NOP9_MOUSE	Nop9	Nucleolar protein 9 OS=	R.AEQAPEALPHLSPEALGYFR@.R	13.39	8.15	1.64	0.61
Q8BMC4_NOP9_MOUSE	Nop9	Nucleolar protein 9 OS=	K.NQELIQDPFGHHVAR@.N	11.32	4.88	2.32	0.43
Q8BMC4_NOP9_MOUSE	Nop9	Nucleolar protein 9 OS=	R.NVALTTFLK#.R	17.86	6.41	2.79	0.36
Q8BMC4_NOP9_MOUSE	Nop9	Nucleolar protein 9 OS=	R.TLLQVLGGTLLESER@.G	23.83	7.35	3.24	0.31
Q8BMC4_NOP9_MOUSE	Nop9	Nucleolar protein 9 OS=	R.VLDAIWSGAALGAR@.K	11.83	3.44	3.44	0.29
Q9D6T0_NOSIP_MOUSE	Nosip	Nitric oxide synthase-int	K.AATLPNTEGEQPGPSVGPVGK#.D	12.61	8.43	1.50	0.67
Q9D6T0_NOSIP_MOUSE	Nosip	Nitric oxide synthase-int	R.FTQLDDSVDR@.V	15.72	8.19	1.92	0.52
P60670_NPL4_MOUSE	Nploc4	Nuclear protein localizat	K.AFGAPNVVEDEIDQYLSK#.Q	14.61	7.93	1.84	0.54
P60670_NPL4_MOUSE	Nploc4	Nuclear protein localizat	K.ESSSEQYVPDVFYK#.D	12.21	6.46	1.89	0.53
P60670_NPL4_MOUSE	Nploc4	Nuclear protein localizat	K.HGDLLFLFPSSLAGPSSEM*ETSTSVGLK#.A	8.85	2.70	3.28	0.31
P60670_NPL4_MOUSE	Nploc4	Nuclear protein localizat	K.VGWIFTDLVSEDTR@.K	14.33	4.86	2.95	0.34
P60670_NPL4_MOUSE	Nploc4	Nuclear protein localizat	K.AFGAPNVVEDEIDQYLSK#.Q	13.45	4.41	3.05	0.33
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.DELHIVEAEAM*NYEGSPIK#.V	14.74	4.55	3.24	0.31
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.DELHIVEAEAMNYEGSPIK#.V	9.31	1.32	7.03	0.14
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.GPSSVEDIK#.A	244.37	65.85	3.71	0.27
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.LLGM*SGK#.R	74.32	34.65	2.14	0.47
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.M*SVQPTVSLGGFEITPPVVLR@.L	285.77	125.52	2.28	0.44
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.M*SVQPTVSLGGFEITPPVVLR.L	81.15	29.88	2.72	0.37
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.MSVQPTVSLGGFEITPPVVLR@.L	31.57	12.78	2.47	0.40
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	R.M*TDQEAIQDLWQWR@.K	23.67	6.45	3.67	0.27
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	R.MTDQEAIQDLWQWR@.K	13.72	5.78	2.37	0.42
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	R.SAPGGGNK#VPQK#K#.V	7.75	4.29	1.81	0.55
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	R.TVSLGAGAK#DELHIVEAEAM*NYEGSPIK#.V	87.98	33.52	2.63	0.38
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	R.TVSLGAGAK#DELHIVEAEAM*NYEGSPIK#.V	23.32	6.35	3.68	0.27
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	R.TVSLGAGAK#DELHIVEAEAMNYEGSPIK#.V	29.06	12.54	2.32	0.43
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.VDNDENEHQLSLR.T	21.14	9.05	2.34	0.43
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.VK#LDEDDEDDDEDDEDDEDDDDDDFDEEETEEK#VPVK#.K	3.66	2.00	1.83	0.55
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.VTLATLK#.M	402.99	117.42	3.43	0.29
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.DELHIVEAEAM*NYEGSPIK.V	2.65	2.78	0.95	1.05
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.M*SVQPTVSLGGFEITPPVVLR.L	92.27	79.60	1.16	0.86
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.M*SVQPTVSLGGFEITPPVVLR@.L	36.60	31.75	1.15	0.87
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	R.TVSLGAGAKDELHIVEAEAM*NYEGSPIK.V	10.05	9.09	1.11	0.90
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	R.TVSLGAGAK#DELHIVEAEAMNYEGSPIK#.V	2.08	2.15	0.97	1.03
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.VDNDENEHQLSLR@.T	7.98	4.27	1.87	0.54
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.GPSSVEDIK#.A	17.96	7.47	2.40	0.42
Q61937_NPM_MOUSE	Npm1	Nucleophosmin OS=Mus	K.M*SVQPTVSLGGFEITPPVVLR@.L	12.11	11.39	1.06	0.94
Q99J85_NPTXR_MOUSE	Nptxr	Neuronal pentraxin rece	R.IERIEQELPAR.G	4.83	74.26	0.07	15.36
Q505F1_NR2C1_MOUSE	Nr2c1	Nuclear receptor subfam	R.SPLAATPTFVTDSETAR@.S	4.93	2.67	1.85	0.54
P49117_NR2C2_MOUSE	Nr2c2	Nuclear receptor subfam	R.IQIISTDSAVASPQR@.I	10.49	4.91	2.14	0.47
P49117_NR2C2_MOUSE	Nr2c2	Nuclear receptor subfam	K.QQFILTSPDGAGTGK#.V	8.51	3.98	2.14	0.47
P49117_NR2C2_MOUSE	Nr2c2	Nuclear receptor subfam	K.VILASPETSSAK#.Q	14.80	6.42	2.30	0.43
P49117_NR2C2_MOUSE	Nr2c2	Nuclear receptor subfam	R.IQIVTDSASVER@.L	6.88	3.46	1.99	0.50
P49117_NR2C2_MOUSE	Nr2c2	Nuclear receptor subfam	R.IQIISTDSAVASPQR@.I	3.50	1.78	1.96	0.51
P43135_COT2_MOUSE	Nr2f2	COUP transcription fact	K.TPIETLIR@.D	18.24	6.75	2.70	0.37
P43135_COT2_MOUSE	Nr2f2	COUP transcription fact	R.TVSSSVIEQLFFVR@.L	15.10	8.01	1.89	0.53
P43135_COT2_MOUSE	Nr2f2	COUP transcription fact	K.TPIETLIR@.D	21.35	9.73	2.19	0.46
P43135_COT2_MOUSE	Nr2f2	COUP transcription fact	R.TVSSSVIEQLFFVR@.L	25.70	12.69	2.03	0.49
P43135_COT2_MOUSE	Nr2f2	COUP transcription fact	R.IFQEQVEK#.L	32.68	13.83	2.36	0.42
P43135_COT2_MOUSE	Nr2f2	COUP transcription fact	R.SQYPNQPTR.F	17.34	11.37	1.53	0.66
P43135_COT2_MOUSE	Nr2f2	COUP transcription fact	K.TPIETLIR@.D	43.82	16.49	2.66	0.38
P43135_COT2_MOUSE	Nr2f2	COUP transcription fact	R.TVSSSVIEQLFFVR@.L	36.12	18.04	2.00	0.50
P43136_NR2F6_MOUSE	Nr2f6	Nuclear receptor subfam	R.HAPFFPELPAADQVALLR@.L	12.53	4.03	3.11	0.32
P43136_NR2F6_MOUSE	Nr2f6	Nuclear receptor subfam	R.HAPFFPELPAADQVALLR@.L	7.10	4.16	1.70	0.59
P43136_NR2F6_MOUSE	Nr2f6	Nuclear receptor subfam	R.LLFSTVEWAR@.H	9.91	1.30	7.63	0.13
P43136_NR2F6_MOUSE	Nr2f6	Nuclear receptor subfam	K.AQVALTEYVR@.A	13.69	3.90	3.51	0.28
P43136_NR2F6_MOUSE	Nr2f6	Nuclear receptor subfam	R.HAPFFPELPAADQVALLR@.L	15.05	10.64	1.41	0.71
P08556_RASN_MOUSE	Nras	GTPase NRas OS=Mus mu	K.SFADINLYR@.E	4.52	2.70	1.67	0.60

Q9WU00_NRF1_MOUSE	Nrf1	Nuclear respiratory facto	R.ISDSAVTM*DGQAVEVVTLEQ.-	3.92	3.92	1.00	1.00
Q9WU00_NRF1_MOUSE	Nrf1	Nuclear respiratory facto	K.VFGAAPLENVVR@.K	39.25	12.99	3.02	0.33
Q9WU00_NRF1_MOUSE	Nrf1	Nuclear respiratory facto	R.VSWTQALR@.T	19.56	7.62	2.57	0.39
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.AESLQVTR@.G	61.79	7.75	7.97	0.13
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.DIEAM*DPSILK#.G	46.04	8.20	5.61	0.18
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.ELAVETK#.N	46.24	11.68	3.96	0.25
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.IEVGLVVGNSQVAFEK#.A	8.87	6.31	1.40	0.71
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.K#LFADAEEEQR@.R	28.05	5.18	5.41	0.18
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.LFADAEEEQR@.R	21.61	6.53	3.31	0.30
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.LFGLLVK#.D	24.08	4.39	5.49	0.18
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.M*GIGGLDKEFSDIFR.R	56.93	13.57	4.20	0.24
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.M*GIGGLDK#EFSDIFR@.R	4.94	3.71	1.33	0.75
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.MGIGGLDK#EFSDIFR@.R	7.00	2.53	2.77	0.36
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.NFSGAELEGLVR@.A	91.52	17.32	5.28	0.19
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.NIDSNPYDTDK#.M	32.43	8.80	3.69	0.27
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.VEVDM*EK#.A	65.95	250.77	0.26	3.80
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.VEVDM*EK#AESLQVTR@.G	9.50	4.81	1.97	0.51
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.VVNGPEILNK#.Y	42.42	9.56	4.44	0.23
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.YIFTLR@.T	48.45	7.53	6.43	0.16
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.YVGESEANIR@.K	131.13	31.11	4.21	0.24
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.IAEESNFPFIK#.I	22.35	7.44	3.00	0.33
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.LLDYVPIGPR@.F	54.55	11.15	4.89	0.20
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.AESLQVTR@.G	30.18	9.20	3.28	0.30
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.GSM*AGSTGVHDTVVNQLLSK#.I	37.12	10.76	3.45	0.29
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.IAEESNFPFIK#.I	45.65	15.94	2.86	0.35
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.LFGLLVK#.D	24.15	8.47	2.85	0.35
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.LLDYVPIGPR@.F	64.44	26.07	2.47	0.40
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.M*GIGGLDK#EFSDIFR@.R	32.83	8.15	4.03	0.25
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.NFSGAELEGLVR@.A	56.34	20.31	2.77	0.36
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.NIDSNPYDTDK#.M	12.06	5.04	2.39	0.42
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.TPLVSVLLEGPPHSGK#.T	23.92	9.07	2.64	0.38
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.VLDDGELLVQQTK#.N	85.39	37.31	2.29	0.44
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.VVNGPEILNK#.Y	21.24	9.26	2.29	0.44
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.YIFTLR@.T	40.35	14.42	2.80	0.36
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.YVGESEANIR@.K	48.36	18.73	2.58	0.39
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.GSM*AGSTGVHDTVVNQLLSK#.I	17.21	4.89	3.52	0.28
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.IAEESNFPFIK#.I	15.74	7.36	2.14	0.47
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.LLDYVPIGPR@.F	28.01	10.11	2.77	0.36
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.NFSGAELEGLVR@.A	19.26	6.09	3.16	0.32
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.TPLVSVLLEGPPHSGK#.T	16.07	4.87	3.30	0.30
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	R.VLDDGELLVQQTK#.N	25.69	7.80	3.29	0.30
P46460_NSF_MOUSE	Nsf	Vesicle-fusing ATPase OS=	K.YVGESEANIR@.K	15.52	3.88	3.99	0.25
Q8K305_NSL1_MOUSE	Nsl1	Kinetochore-associated p	K.ALPVLIEQGEGFSQVLK#.M	16.57	4.89	3.39	0.30
Q91VT1_NSE2_MOUSE	Nsmce2	E3 SUMO-protein ligase N	R.M*SDLIPDEALR@.R	16.91	8.99	1.88	0.53
Q91VT1_NSE2_MOUSE	Nsmce2	E3 SUMO-protein ligase N	R.YISFSGIESALSSLK#.N	33.57	21.90	1.53	0.65
G3XA30_G3XA30_MOUSE	Nsmce4a	MCG1618, isoform CRA_	R.EAVLDAQFLVLASDLGK#.E	6.95	4.06	1.71	0.58
G3XA30_G3XA30_MOUSE	Nsmce4a	MCG1618, isoform CRA_	R.ILGLLQTYFR.E	10.02	6.06	1.65	0.60
Q5NCR9_NSRP1_MOUSE	Nsrp1	Nuclear speckle splicing r	R.VLQK#PSVFGSDSDDDETSVSESLQR@.E	4.88	1.49	3.26	0.31
Q8R2U4_NTM1A_MOUSE	Ntmt1	N-terminal Xaa-Pro-Lys N	R.TAGLSLLAEER@.Q	7.20	4.11	1.75	0.57
Q8R2U4_NTM1A_MOUSE	Ntmt1	N-terminal Xaa-Pro-Lys N	R.VVDM*VDVTEDFLAK#.A	7.02	3.26	2.15	0.46
Q9R061_NUBP2_MOUSE	Nubp2	Cytosolic Fe-S cluster ass	R.LAGVPFLGSVPLDSQLTR@.S	18.37	9.87	1.86	0.54
Q9R061_NUBP2_MOUSE	Nubp2	Cytosolic Fe-S cluster ass	R.SLEEGR@DFIQEFPK#.S	10.28	5.50	1.87	0.54
P81117_NUCB2_MOUSE	Nucb2	Nucleobindin-2 OS=Mus	K.LHDVNNDGFLDEQELEALFTR@.E	5.24	6.84	0.77	1.31
P81117_NUCB2_MOUSE	Nucb2	Nucleobindin-2 OS=Mus	R.LVTLEEFLR@.A	13.37	9.41	1.42	0.70
Q6PIP5_NUDC1_MOUSE	Nudcd1	NudC domain-containing	R.LYVIGTGDR@.G	13.28	3.98	3.34	0.30
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.ALFAVPK#.N	33.79	12.10	2.79	0.36
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.LFLVQLQEK#.A	35.70	16.05	2.22	0.45
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.LPGGELNPGEDEVEGLK#.R	5.06	3.36	1.51	0.66
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.LPGGELNPGEDEVEGLK#R@.L	50.90	12.13	4.20	0.24
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	R.TINLYPLTNYTFGTK#.E	18.27	7.59	2.41	0.42
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.YIQQTK#PLTLER@.T	40.34	14.12	2.86	0.35
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.ALFAVPK#.N	75.08	22.23	3.38	0.30
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.K#LFLVQLQEK#.A	12.85	4.20	3.06	0.33
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.LFLVQLQEK#.A	86.88	25.46	3.41	0.29
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	R.LM*TEILGR@.Q	60.24	19.68	3.06	0.33
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.LPGGELNPGEDEVEGLK#R@.L	103.99	43.88	2.37	0.42
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	R.TINLYPLTNYTFGTK#.E	99.64	32.96	3.02	0.33
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	R.TINLYPLTNYTFGTK#.E	8.61	4.69	1.83	0.55
Q9CQF3_CPSF5_MOUSE	Nudt21	Cleavage and polyadenyl	K.YIQQTK#PLTLER@.T	8.15	2.04	4.00	0.25
Q9JKX6_NUDT5_MOUSE	Nudt5	ADP-sugar pyrophosphat	K.SADAVSVIPVLQR@.T	29.10	11.87	2.45	0.41
Q5F2E7_NUFP2_MOUSE	Nufip2	Nuclear fragile X mental r	K.IM*QETSVPALK#.Q	19.82	7.12	2.79	0.36
Q5F2E7_NUFP2_MOUSE	Nufip2	Nuclear fragile X mental r	K.SLSSDEATNPISR@.V	33.51	10.14	3.30	0.30
Q5F2E7_NUFP2_MOUSE	Nufip2	Nuclear fragile X mental r	K.SLSSDEATNPISR@.V	15.68	8.25	1.90	0.53
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.ASM*QPAQIAEGVGITTR@.Q	5.95	4.52	1.32	0.76
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.IATTTTGTATVATTPR@.A	17.15	9.72	1.76	0.57
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.K#LELEEPDSANSSFYSTQSAPASQANLR@.A	5.49	1.57	3.50	0.29
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.VIEGSEM*ELAK#.M	23.86	7.87	3.03	0.33
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.AEELGQELK#.A	66.08	21.19	3.12	0.32
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.AEQDK#ALETLQGQLEEK#.A	10.83	3.09	3.51	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.AGEQQETASLELLKEPPR.A	50.26	14.49	3.47	0.29
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.AHGLLAEENR@.G	18.11	132.11	0.14	7.30
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.ALETLQGQLEEK#.A	118.71	41.69	2.85	0.35
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.AQLQEQLR@.A	72.28	22.07	3.28	0.31
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.ASM*QPAQIAEGVGITTR@.Q	17.31	4.62	3.75	0.27
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.ASQEWAEK#.Q	22.97	9.37	2.45	0.41
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.ASYAEQLSM*LK#.K	14.77	5.23	2.82	0.35
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.DAK#LESLQQQLQAANDAR@.D	14.97	4.61	3.25	0.31
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.DNAQTSVTQAQQEK#.A	70.24	26.55	2.65	0.38
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.DQELASLK#EQAK#.K	12.22	7.73	1.58	0.63
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.EAEQMGGELER@.L	11.05	3.35	3.30	0.30
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.EAEQM*GGELER@.L	68.54	21.08	3.25	0.31
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.EFANHLQQLQGAFNDLIEEHSK#.A	14.17	3.85	3.68	0.27
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.EGQQILQQPLPER@.L	19.75	5.72	3.46	0.29
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.EHPAGGASGEDASGPGTQSETAGK#.T	23.93	10.00	2.39	0.42
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.EK#EHPAGGASGEDASGPGTQSETAGK#.T	25.92	11.56	2.24	0.45
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.ELGELGSLR.Q	89.51	31.77	2.82	0.35
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.ELGHNQAASASAQR@.E	19.01	6.92	2.75	0.36
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.ELQQAGLK#.T	77.83	32.67	2.38	0.42
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.ELQQTLEQLK#.I	73.75	24.91	2.96	0.34
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	K.FM*LDHEESLNLTEDLESFLEK#.V	30.26	9.73	3.11	0.32
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.FREELEQSK.Q	107.80	35.48	3.04	0.33
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.GESQQEVQR@.L	17.55	5.17	3.40	0.29
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus r	R.GK#QEAQLLAER@.S	22.79	8.59	2.65	0.38

E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.GQAPLETSLDSLGDAFPDSGR@.K	10.07	4.58	2.20	0.45
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.GQAPLETSLDSLGDAFPDSGR@.K	10.90	3.78	2.88	0.35
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.GQAQADLAQEK#.A	90.22	32.85	2.75	0.36
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.HELAEATASQHR@.A	18.53	6.89	2.69	0.37
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IAELQQR@.N	58.58	14.92	3.93	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IASSSSENNFLSGSPSSPM*GDILQTPQFQM*R@.R	9.95	2.41	4.13	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IATTTTGTATVATTPR@.A	31.46	9.83	3.20	0.31
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IDHLALLNEK#.Q	76.20	23.86	3.19	0.31
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IQQLEEAHQAETEALR@HELAEATASQHR@.A	11.13	4.51	2.47	0.41
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.ISQLSEENGDLSFK#.V	18.60	5.64	3.30	0.30
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.K#EQAQMLQTMQEQEQAAQGLR@.Q	6.60	2.45	2.69	0.37
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.KLELEEPDSANSSFYSTQSAPASQANLR.A	49.38	10.21	4.84	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.K#SSLISSLEEEVSILNR@.Q	31.83	7.89	4.03	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LATDNTQLQTR@.V	81.79	23.73	3.45	0.29
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LENELSTALQDK#.K	13.16	5.56	2.37	0.42
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LESLQQQLQAANDAR@.D	40.55	10.15	3.99	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LK#EQQLEEAAK#.E	7.23	2.46	2.94	0.34
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LK#EQQLEEAAK#EQEATR@.Q	38.04	12.90	2.95	0.34
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LLQVETASNSAR@.A	107.51	34.99	3.07	0.33
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LPPKVESLESLYFTPTPAR.G	47.40	19.57	2.42	0.41
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LQEQLQDLEELQK#.E	34.31	11.68	2.94	0.34
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LQEQLQDLEELQK#ENK#.E	99.09	31.73	3.12	0.32
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LQESPAPEK#GEVLGDALQLDTLK#.Q	24.40	11.62	2.10	0.48
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LQESPAPEK#GEVLGDALQLDTLK#QEAAK#.L	86.52	20.56	4.21	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LQNTLNEQR@.V	88.71	27.77	3.19	0.31
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LQTQLNELQAQLSQK#.E	40.62	11.62	3.50	0.29
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LSQLEDQATR@.L	75.53	21.49	3.51	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LVDDLSALQEK#.M	100.35	34.86	2.88	0.35
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.QAAGGLQAELM*R@.A	31.01	10.50	2.95	0.34
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.QAAGGLQAELMR@.A	11.97	2.78	4.31	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.QAASSQEPSELEELR@.G	19.60	5.56	3.53	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.QAASSQEPSELEELR@GK#.N	17.34	6.97	2.49	0.40
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.QDHAQQLAIVAEAR@.E	44.53	15.75	2.83	0.35
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.QFLEVELDQAR.E	53.02	18.66	2.84	0.35
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.QQVEQLSSSLK#.L	54.85	18.18	3.02	0.33
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.QSM*AFSILNTPK#.K	14.35	4.77	3.01	0.33
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.SLEAQVAHADQQLR.D	23.80	8.08	2.95	0.34
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.SNR@DDLELELSESLK#.L	26.30	9.08	2.89	0.35
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.TDAETHLAEM*R@.Q	16.36	5.40	3.03	0.33
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.TDAPGPELQALR@.A	75.47	30.63	2.46	0.41
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.TELK#ELQQTLEQLK#.I	36.44	11.99	3.04	0.33
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.TQPDGTSVPGEPASPISQR@.L	22.61	8.94	2.53	0.40
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.TTQIINITM*TK#.K	27.21	8.59	3.17	0.32
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.VEFAALQEALAHALTEK#.E	161.25	59.52	2.71	0.37
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.VESLESLYFTPTPAR@.G	9.86	3.32	2.97	0.34
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.VIEGSEM*ELAK#.M	57.03	15.90	3.59	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.VSSETHQGPGTPESK#.K	6.50	3.39	1.92	0.52
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.YGAM*FQEQLM*ALK#.G	7.07	2.38	2.98	0.34
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.YVQELAAVR@.T	82.17	28.99	2.83	0.35
F6ZQA3_F6ZQA3_MOUSE	Numa1	Protein Numa1 (Fragmen	K.LTAQVEQLEVFQR@.E	61.33	16.98	3.61	0.28
F6ZQA3_F6ZQA3_MOUSE	Numa1	Protein Numa1 (Fragmen	R.QK#LTAQVEQLEVFQR@.E	10.64	4.71	2.26	0.44
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.AEELGQELK#.A	123.89	34.25	3.62	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.AEQDK#ALETLQGQLEEK#.A	31.84	5.60	5.68	0.18
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.AGEQQETASLELLK#.E	57.51	13.04	4.41	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.AGEQQETASLELLK#EPPR@.A	228.33	54.45	4.19	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.AHGLLAEENR@.G	47.49	46.15	1.03	0.97
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.AIQQVQEK#.E	218.57	55.93	3.91	0.26
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.ALETLQGQLEEK#.A	281.23	66.42	4.23	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.AQDHSK#AEEEWK#.A	27.97	10.18	2.75	0.36
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.AQLQEQLR@.A	320.48	74.26	4.32	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.ASDQLGEQQGRPFSSTHAAVK.A	76.26	14.44	5.28	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.ASM*QPAQIAEGVGITTR@.Q	41.43	9.54	4.34	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.ASM*QPAQIAEGVGITTR@.Q	21.61	4.98	4.34	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.ASYAEQLSM*LK#.K	50.09	9.61	5.21	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.ASYAEQLSMLK#.K	11.27	3.30	3.41	0.29
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.ATEM*EAESR@.S	19.01	6.11	3.11	0.32
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.ATSSTQSLAR@.L	92.29	25.04	3.69	0.27
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.DAK#LESLQQQLQAANDAR@.D	77.93	16.11	4.84	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.DAQIAM*M*QQR@.I	86.01	21.19	4.06	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.DNAQTSVTQAQQEK#.A	373.67	79.98	4.67	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.DNAQTSVTQAQQEK#AELSQK#.I	7.56	2.02	3.74	0.27
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.DQELASLK#.E	119.29	24.68	4.83	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.DQELASLK#EQAK#.K	47.31	10.73	4.41	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.EAEQMGGELER@.L	26.52	6.26	4.23	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.EAEQM*GGELER@.L	216.03	42.11	5.13	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EELEQASQAQGAQLTAQLTSM*TGLNATLQQR@.D	6.20	1.76	3.53	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.EFANHLQQLQGAFNDLIEEHSK#.A	60.71	19.14	3.17	0.32
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EGQQILQQPLPER@.L	81.36	19.15	4.25	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EGTDQELAK#.L	58.77	16.32	3.60	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EHPAGGASGEDASGPGTQSETAGK#.T	125.16	27.28	4.59	0.22
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EHPAGGASGEDASGPGTQSETAGK#TDAPGPELQALR@.A	5.33	2.71	1.96	0.51
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EKEHPAGGASGEDASGPGTQSETAGK.T	61.23	12.98	4.72	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.EK#YVQELAAVR@.T	11.30	3.59	3.15	0.32
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.ELEVMTAK#.Y	16.28	5.17	3.15	0.32
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.ELGELGSLR.Q	216.88	50.57	4.29	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.ELGHNQAASASAQR.E	53.32	12.98	4.11	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.ELQQAGLK#.T	313.04	83.27	3.76	0.27
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.ELQQTLEQLK#.I	200.87	42.24	4.76	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EQALSALQLEHTSTQALVSELLPAK#.H	287.54	63.45	4.53	0.22
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EQAQM*LQTM*QEQEQAAQGLR@.Q	32.46	17.25	1.88	0.53
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EQAQMLQTMQEQEQAAQGLR@.Q	15.22	3.94	3.87	0.26
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.EQQLEEAAK#EQEATR@.Q	23.16	5.98	3.87	0.26
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.FM*LDHEESLNLTEDLESFLEK#.V	142.08	28.45	4.99	0.20
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.FQVATDALK#.S	343.88	64.17	5.36	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.GESQQEVQR@.L	58.35	13.25	4.40	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.GEVLGDALQLDTLK#.Q	25.34	4.85	5.22	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.GK#QEAQLLAER@.S	196.07	38.02	5.16	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.GQAPLETSLDSLGDAFPDSGR@.K	43.99	9.46	4.65	0.22
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.GQAPLETSLDSLGDAFPDSGR@.K	28.83	6.31	4.57	0.22
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.GQAQADLAQEK#.A	186.81	34.64	5.39	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.HELAEATASQHR@.A	88.71	21.14	4.20	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.HLTAQVR@.S	203.88	43.61	4.67	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IAELQQR@.N	112.15	25.69	4.37	0.23

E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IASSSSENNFLSGSPSSPM*GDILQTPQFQM*R@.R	23.81	6.33	3.76	0.27
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IATTTTGTATVATTPR@.A	62.21	10.61	5.86	0.17
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IDHLALLNEK#.Q	368.17	86.59	4.25	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.IQQLEEAHQAETEALR@HELAEATASQHR@.A	32.62	6.29	5.19	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.ISQLSEENGDLSFK#.V	74.73	13.40	5.58	0.18
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.IVEQER@.A	97.73	22.82	4.28	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.KEQAQM*LQTM*QEQEQAAQGLR.Q	54.73	10.68	5.12	0.20
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.K#EQAQM*LQTMQEQEQAAQGLR@.Q	5.99	2.54	2.36	0.42
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.KEQAQMLQTMQEQEQAAQGLR.Q	23.17	5.25	4.41	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.K#ISQLSEENGDLSFK#.V	30.12	6.33	4.75	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.KLELEEPDSANSSFYSTQSAPASQANLR.A	98.93	21.81	4.54	0.22
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.K#SSLISSLEEEVSILNR@.Q	113.99	20.89	5.46	0.18
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LATDNTQLQTR@.V	452.14	103.41	4.37	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LENELSTALQDK#.K	45.17	13.34	3.39	0.30
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LENELSTALQDK#K#.C	255.19	56.95	4.48	0.22
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LESLQQQLQAANDAR@.D	138.67	30.32	4.57	0.22
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LGSPDDGNSALLSLPGYR@PTTR@.S	220.16	50.26	4.38	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LK#EQQLEEAAK#.E	118.51	25.37	4.67	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LK#EQQLEEAAK#EQEATR@.Q	150.83	27.95	5.40	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LLQVETASNSAR@.A	325.68	72.82	4.47	0.22
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LLTEKDAQIAM*M*QQR.I	100.57	16.75	6.00	0.17
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LPPK#VESLESLYFTPTPAR@.G	107.63	27.42	3.93	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LQEQLQDLEELQK#.E	120.86	24.63	4.91	0.20
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LQEQLQDLEELQK#ENK#.E	285.01	70.86	4.02	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LQESPAPEK#GEVLGDALQLDTLK#.Q	116.50	32.48	3.59	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LQNTLNEQR@.V	285.25	61.22	4.66	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LQNTLNEQR@VEFAALQEALAHALTEK#EGTDQELAK#.L	6.61	2.00	3.31	0.30
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LQTQLNELQAQLSQK#.E	141.09	32.46	4.35	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LSQLEDQATR@.L	301.29	71.64	4.21	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.LVDDLSALQEK#.M	427.77	118.25	3.62	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.LVVAESEK#.S	168.34	33.00	5.10	0.20
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.QAAGGLQAELM*R@.A	94.27	20.21	4.66	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.QAASSQEPSELEELR@.G	83.91	23.39	3.59	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.QAASSQEPSELEELR@GK#.N	76.03	21.05	3.61	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.QDHAQQLAIVAEAR@.E	197.94	47.36	4.18	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.QELASQAER@.A	137.26	34.89	3.93	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.QFLEVELDQAR@.E	168.68	34.81	4.85	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.QQLASLIADLQSSVSNLSQAK#.E	45.81	9.48	4.83	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.QQVEQLSSSLK#.L	149.43	38.00	3.93	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.QSM*AFSILNTPK#.K	45.39	12.51	3.63	0.28
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.R@LVVAESEK#.S	70.26	16.20	4.34	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.R@VSSETHQGPGTPESK#.K	16.32	4.19	3.90	0.26
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.SLEAQVAHADQQLR.D	51.94	10.77	4.82	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.SNR@DDLELELSESLK#.L	153.26	32.29	4.75	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.SQGQQQEER@.G	6.68	2.23	2.99	0.33
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.SR@FEDEK#QQLASLIADLQSSVSNLSQAK#.E	5.09	2.22	2.29	0.44
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.SSALR@EEVQSLR@.E	27.76	5.67	4.90	0.20
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.SSLISSLEEEVSILNR@.Q	95.49	24.16	3.95	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.TDAETHLAEM*R.Q	52.19	13.22	3.95	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.TDAETHLAEM*R@QEAQSTSR@.E	18.47	5.08	3.64	0.27
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.TDAPGPELQALR@.A	211.38	50.28	4.20	0.24
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.TELK#ELQQTLEQLK#.I	142.73	23.29	6.13	0.16
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.TQPDGTSVPGEPASPISQR@.L	94.26	30.69	3.07	0.33
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.TTQIINITM*TK#.K	82.08	17.33	4.74	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.VEFAALQEALAHALTEK#.E	428.75	98.70	4.34	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.VEFAALQEALAHALTEKEGTDQELAK.L	45.43	8.59	5.29	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.VESLESLYFTPTPAR@.G	55.83	11.46	4.87	0.21
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.VIEGSEM*ELAK#.M	210.64	52.55	4.01	0.25
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.VIEGSEMELAK#.M	19.19	4.33	4.43	0.23
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.VPYTHASTLSEELSPPSHQTK#.R	14.90	2.76	5.40	0.19
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.VTELEAQLK#.A	194.99	38.65	5.05	0.20
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.YGAM*FQEQLM*ALK#.G	27.91	7.25	3.85	0.26
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.YGAM*FQEQLMALK#.G	11.75	15.48	0.76	1.32
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	R.YGAMFQEQLMALK#.G	7.62	1.68	4.55	0.22
E9Q7G0_E9Q7G0_MOUSE	Numa1	Protein Numa1 OS=Mus	K.YVQELAAVR@.T	204.15	47.29	4.32	0.23
F6ZQA3_F6ZQA3_MOUSE	Numa1	Protein Numa1 (Fragmen	K.LTAQVEQLEVFQR@.E	189.76	40.62	4.67	0.21
F6ZQA3_F6ZQA3_MOUSE	Numa1	Protein Numa1 (Fragmen	R.QK#LTAQVEQLEVFQR@.E	56.24	9.97	5.64	0.18
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	R.VLIQANQEDNFGTATPR@.S	7.27	2.03	3.58	0.28
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	K.EADLDVATITK#.T	10.23	7.50	1.36	0.73
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	K.FLILGDVDGLM*DEFSK#.W	7.45	4.01	1.86	0.54
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	K.M*VVETLFQR@.D	11.48	6.70	1.71	0.58
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	R.VM*VDSLVEQEIR@.T	6.45	3.25	1.98	0.50
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	K.YLFTLIR@.A	12.28	4.77	2.58	0.39
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	R.AGM*TEEAQR@.L	71.50	32.43	2.20	0.45
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	K.FLILGDVDGLM*DEFSK#.W	7.49	4.15	1.80	0.55
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	K.VFEELQATDK#.K	7.23	4.49	1.61	0.62
Q8BH74_NU107_MOUSE	Nup107	Nuclear pore complex pr	K.YLFTLIR@.A	11.75	5.26	2.23	0.45
Q8R0G9_NU133_MOUSE	Nup133	Nuclear pore complex pr	R.FLLHQETLPEQLLTER@.Q	11.34	9.88	1.15	0.87
Q8R0G9_NU133_MOUSE	Nup133	Nuclear pore complex pr	R.ENVSLLAEDLEESLTSSVGGR@.G	13.84	4.61	3.00	0.33
Q8R0G9_NU133_MOUSE	Nup133	Nuclear pore complex pr	R.FLLHQETLPEQLLTER@.Q	34.48	9.47	3.64	0.27
Q8R0G9_NU133_MOUSE	Nup133	Nuclear pore complex pr	R.FLTAVQGGSFILSSVGSQLVR@.L	17.57	6.65	2.64	0.38
Q8R0G9_NU133_MOUSE	Nup133	Nuclear pore complex pr	R.YSSLEVEYLQK#.R	10.03	2.66	3.78	0.26
E9Q3G8_E9Q3G8_MOUSE	Nup153	Protein Nup153 OS=Mus	K.TTYGGAAAAVR@.Q	8.60	5.75	1.49	0.67
E9Q3G8_E9Q3G8_MOUSE	Nup153	Protein Nup153 OS=Mus	K.FGIPSSSSGLSQTLTSTGNFK#.F	10.84	5.81	1.87	0.54
E9Q3G8_E9Q3G8_MOUSE	Nup153	Protein Nup153 OS=Mus	K.GFGTSSSLNPAPSAFK#.F	17.15	6.00	2.86	0.35
E9Q3G8_E9Q3G8_MOUSE	Nup153	Protein Nup153 OS=Mus	K.LGTSSDSGSTNTM*NTNFK#.F	6.76	3.24	2.08	0.48
E9Q3G8_E9Q3G8_MOUSE	Nup153	Protein Nup153 OS=Mus	R.LM*TPK#PVSIATNR@.T	14.96	6.75	2.22	0.45
E9Q3G8_E9Q3G8_MOUSE	Nup153	Protein Nup153 OS=Mus	K.QLNAQSYGVTSSTAR@.R	7.24	2.90	2.50	0.40
E9Q3G8_E9Q3G8_MOUSE	Nup153	Protein Nup153 OS=Mus	K.TEFSGSNSSSETVLSSSAQDITAVNSSSYK#.K	5.75	2.28	2.52	0.40
E9Q3G8_E9Q3G8_MOUSE	Nup153	Protein Nup153 OS=Mus	K.VGSSSLPSSSM*FVLGR@.T	7.87	2.97	2.65	0.38
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	K.GLQEFLDR@.N	21.27	6.29	3.38	0.30
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	R.HLLVSNVGGDGEEIER@.F	16.13	10.57	1.53	0.65
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	K.ISLQAIQQLVR@.K	24.56	9.00	2.73	0.37
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	R.K#FQEAQLSEK#.I	8.64	3.03	2.85	0.35
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	R.NSQFSGGPLGNPNTTAR@.V	8.75	3.94	2.22	0.45
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	R.VASVSQNAIVSAAGNIAR@.T	10.90	5.78	1.89	0.53
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	K.GLQEFLDR@.N	13.38	4.83	2.77	0.36
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	K.HGEPEEDVVGLQTFQER@.L	9.95	3.93	2.53	0.39
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	R.HLLVSNVGGDGEEIER@.F	15.08	5.41	2.79	0.36
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	K.ISLQAIQQLVR@.K	26.64	12.45	2.14	0.47
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	R.NSQFSGGPLGNPNTTAR@.V	9.01	6.04	1.49	0.67
Q99P88_NU155_MOUSE	Nup155	Nuclear pore complex pr	R.VASVSQNAIVSAAGNIAR@.T	14.56	5.22	2.79	0.36
Q9Z0W3_NU160_MOUSE	Nup160	Nuclear pore complex pr	R.EM*DYETEVEM*EK#.G	2.76	1.75	1.58	0.63

Q9Z0W3_NU160_MOUSE	Nup160	Nuclear pore complex pr	K.GFDPAQPLNVR@.M	10.18	4.86	2.10	0.48
Q9Z0W3_NU160_MOUSE	Nup160	Nuclear pore complex pr	R.LGDAVILGAGQLFQAQQDLLHR@.T	19.66	7.31	2.69	0.37
Q9Z0W3_NU160_MOUSE	Nup160	Nuclear pore complex pr	R.QIEILELEDLEK#EYSLAR@.I	14.47	5.97	2.42	0.41
Q9Z0W3_NU160_MOUSE	Nup160	Nuclear pore complex pr	R.SELVTESQM*QSIFTDIGK#.V	5.46	1.88	2.90	0.34
Q9Z0W3_NU160_MOUSE	Nup160	Nuclear pore complex pr	R.SFVELSGAER@.E	13.87	4.84	2.86	0.35
Q9Z0W3_NU160_MOUSE	Nup160	Nuclear pore complex pr	R.TAPLLLSYYLIK#.W	15.38	5.72	2.69	0.37
B9EJ54_B9EJ54_MOUSE	Nup205	MCG21756, isoform CRA	K.ASSEGVAIQGQQGTR@.L	16.35	7.86	2.08	0.48
B9EJ54_B9EJ54_MOUSE	Nup205	MCG21756, isoform CRA	K.DLPSADSVQYR@.H	5.18	2.92	1.77	0.56
B9EJ54_B9EJ54_MOUSE	Nup205	MCG21756, isoform CRA	R.FTDELM*EQGLTYK#.V	6.61	1.12	5.91	0.17
B9EJ54_B9EJ54_MOUSE	Nup205	MCG21756, isoform CRA	K.LLDIEGLYSK#.V	8.56	3.43	2.49	0.40
B9EJ54_B9EJ54_MOUSE	Nup205	MCG21756, isoform CRA	R.SGLSQVNQHDIDQLQSDAVNAFGESLQK#.K	8.43	3.21	2.62	0.38
Q9D2F7_P210L_MOUSE	Nup210l	Nuclear pore membrane	R.DVQNPSR@SGDIK#.V	25.60	2.36	10.84	0.09
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	R.AAPGSGTSTFSFAPPSK#.G	5.49	2.68	2.05	0.49
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	K.TTLLEGFAGVEEAR@.E	7.66	2.11	3.63	0.28
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	K.TVPQVVNVQELR@.S	7.36	3.04	2.42	0.41
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	R.AAPGSGTSTFSFAPPSK#.G	13.54	4.85	2.79	0.36
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	K.ALQPPVTEK#.Q	16.18	4.27	3.79	0.26
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	R.IFDSPEELPK#.E	13.26	4.16	3.19	0.31
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	K.SSVSPSPAAGR@.S	21.82	16.82	1.30	0.77
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	K.STEEAAPPAVPDK#.S	4.40	2.65	1.66	0.60
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	R.STQTAPSSAPSTGQK#.S	28.26	9.89	2.86	0.35
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	K.TLELISTEGER@.Q	13.12	3.82	3.44	0.29
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	K.TTLLEGFAGVEEAR@.E	28.39	8.68	3.27	0.31
Q80U93_NU214_MOUSE	Nup214	Nuclear pore complex pr	K.VSNDASGM*VNDM*K#.W	6.45	4.09	1.58	0.63
Q8R4R6_NUP53_MOUSE	Nup35	Nucleoporin NUP53 OS=	K.ASTSDYQVISDR@.Q	8.12	4.24	1.92	0.52
Q8R4R6_NUP53_MOUSE	Nup35	Nucleoporin NUP53 OS=	R.SIYDDISSPGLGSTPLTSR.R	5.67	6.50	0.87	1.15
Q8R4R6_NUP53_MOUSE	Nup35	Nucleoporin NUP53 OS=	K.TGANAQFLPGFLM*GDLPAPVTPQPR@.S	15.01	4.03	3.73	0.27
Q8R4R6_NUP53_MOUSE	Nup35	Nucleoporin NUP53 OS=	R.TLGTPTQSGSTPR.V	10.22	12.63	0.81	1.24
Q8R4R6_NUP53_MOUSE	Nup35	Nucleoporin NUP53 OS=	K.ASTSDYQVISDR@.Q	6.42	4.18	1.54	0.65
Q8R4R6_NUP53_MOUSE	Nup35	Nucleoporin NUP53 OS=	R.GVLSSPSLAFTTPIR@.T	9.02	3.40	2.65	0.38
Q8R4R6_NUP53_MOUSE	Nup35	Nucleoporin NUP53 OS=	R.TLGTPTQSGSTPR@.V	7.86	8.08	0.97	1.03
Q9CWU9_NUP37_MOUSE	Nup37	Nucleoporin Nup37 OS=	R.VDGIAWSPETK#.L	8.78	6.01	1.46	0.69
Q9CWU9_NUP37_MOUSE	Nup37	Nucleoporin Nup37 OS=	K.VGAVAGNDWIIWDITR.S	18.96	12.91	1.47	0.68
Q9CWU9_NUP37_MOUSE	Nup37	Nucleoporin Nup37 OS=	K.VLEGHSDFINDLVFHPK#.E	8.11	7.36	1.10	0.91
Q9CWU9_NUP37_MOUSE	Nup37	Nucleoporin Nup37 OS=	R.WSAISENLFATTGYPGK#.M	4.36	2.38	1.84	0.54
Q9JIH2_NUP50_MOUSE	Nup50	Nuclear pore complex pr	R.ATAGM*EPPSLFGSTK#.L	9.52	9.03	1.05	0.95
Q8BTS4_NUP54_MOUSE	Nup54	Nuclear pore complex pr	R.LDIISEDISELQK#.N	18.96	8.36	2.27	0.44
Q8BTS4_NUP54_MOUSE	Nup54	Nuclear pore complex pr	R.LNELM*SQIR@.M	8.90	6.44	1.38	0.72
Q8BTS4_NUP54_MOUSE	Nup54	Nuclear pore complex pr	K.VLGGNQTLTVNVEGIK#.T	7.95	3.62	2.19	0.46
Q8BTS4_NUP54_MOUSE	Nup54	Nuclear pore complex pr	R.VQLDTIQGELNAPTQFK#.G	9.10	4.07	2.23	0.45
Q8BTS4_NUP54_MOUSE	Nup54	Nuclear pore complex pr	K.VLGGNQTLTVNVEGIK#.T	4.28	2.26	1.89	0.53
Q8BTS4_NUP54_MOUSE	Nup54	Nuclear pore complex pr	R.VQLDTIQGELNAPTQFK#.G	9.89	3.49	2.84	0.35
Q63850_NUP62_MOUSE	Nup62	Nuclear pore glycoprotei	K.ELEDLLSPLEESVK#.E	9.45	3.47	2.72	0.37
Q63850_NUP62_MOUSE	Nup62	Nuclear pore glycoprotei	K.R@LDQELDFILSQQK#.E	8.09	6.05	1.34	0.75
Q8CEC0_NUP88_MOUSE	Nup88	Nuclear pore complex pr	K.FLGSDEEDK#DSLQELTAEQK#.C	11.30	4.62	2.44	0.41
Q8CEC0_NUP88_MOUSE	Nup88	Nuclear pore complex pr	R.ILAETPDSFEK#.H	12.41	6.25	1.99	0.50
Q8CEC0_NUP88_MOUSE	Nup88	Nuclear pore complex pr	K.VIVLSEAEEESLILNK#.G	12.78	3.24	3.95	0.25
Q8CEC0_NUP88_MOUSE	Nup88	Nuclear pore complex pr	K.VLSPQK#PTITLSAYQR@.K	9.08	3.06	2.97	0.34
Q8CEC0_NUP88_MOUSE	Nup88	Nuclear pore complex pr	R.ILAETPDSFEK#.H	7.90	3.15	2.51	0.40
Q8CEC0_NUP88_MOUSE	Nup88	Nuclear pore complex pr	K.VIVLSEAEEESLILNK#.G	7.06	2.77	2.55	0.39
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.AFDIIDR@.L	22.53	5.74	3.93	0.25
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.AQHQLGEFK#.T	7.41	4.22	1.76	0.57
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	K.ASVLLGSR@.G	20.66	5.97	3.46	0.29
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.EALQYFYFLR@.D	27.27	10.99	2.48	0.40
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.LESLSAATTFEPLEPVK#DTDIQGFLK#.N	34.50	13.42	2.57	0.39
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.LLM*LYTR@.K	11.13	4.15	2.68	0.37
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	K.LLSPVVPQISAPQSNK#.E	10.92	4.86	2.25	0.44
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	K.LVPLNQESVEER@.V	36.60	15.15	2.42	0.41
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	K.NEKDNALLSAIEESR.K	17.19	8.27	2.08	0.48
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.NLQEIQQAGER@.L	21.89	8.72	2.51	0.40
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	K.QM*TDVVLTPATDALK#.S	14.18	3.80	3.73	0.27
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.SSLDSIEMAYAR@.Q	1.78	1.96	0.91	1.10
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	K.DNALLSAIEESR@.K	13.64	7.82	1.74	0.57
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.EALQYFYFLR@.D	18.00	6.30	2.86	0.35
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.ILHTLLASGEDALDFTQESEPSYIGDVNPPGR@.S	5.83	3.11	1.88	0.53
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	K.LLSPVVPQISAPQSNK#.E	9.91	4.19	2.37	0.42
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.LTLSQFQK#.Q	18.22	10.82	1.68	0.59
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	K.LVPLNQESVEER@.V	25.02	12.23	2.05	0.49
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.NLQEIQQAGER@.L	24.43	9.89	2.47	0.40
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	K.QM*TDVVLTPATDALK#.S	9.75	6.67	1.46	0.68
Q8BJ71_NUP93_MOUSE	Nup93	Nuclear pore complex pr	R.SSLDSIEM*AYAR@.Q	9.40	4.25	2.21	0.45
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	K.DSPGDFLELPIVK#.H	9.83	7.17	1.37	0.73
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	K.EVIVYVDDNQK#PPVGEGLNR@.K	8.82	8.37	1.05	0.95
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	R.FSFLSK#PVDENNQQDGEDDSLVSR@.F	13.78	7.76	1.78	0.56
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	R.IFALLAGK#PVWQLSEQK#.Q	8.03	1.64	4.90	0.20
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	R.LALLLSQLVGSQSVR@.E	12.97	8.59	1.51	0.66
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	R.SITADPLDYR@.L	10.09	5.03	2.01	0.50
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	K.SLEELRLEDYQANR.K	21.16	11.58	1.83	0.55
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	K.DSPGDFLELPIVK#.H	14.73	6.10	2.42	0.41
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	R.LALLLSQLVGSQSVR@.E	8.08	8.43	0.96	1.04
Q6PFD9_NUP98_MOUSE	Nup98	Nuclear pore complex pr	R.SITADPLDYR@.L	8.42	2.73	3.09	0.32
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	K.AVANESGLNFISVK#.G	30.83	12.35	2.50	0.40
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	K.DQVM*YEALQR@.S	6.89	6.32	1.09	0.92
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	K.ESLPLDLSDDQSNSK#.K	6.43	3.58	1.80	0.56
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	K.GPELLNM*YVGESER@.A	10.09	7.05	1.43	0.70
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	R.KTENLQEVDGEIEALLQK.K	16.71	13.55	1.23	0.81
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	R.LGAEPTSETQDELQR@.L	41.99	24.20	1.74	0.58
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	R.LYSVDYGR@.R	12.88	6.91	1.86	0.54
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	R.STELQISNVK#.F	20.41	13.34	1.53	0.65
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	K.TLFVGLPPPADR@.V	10.16	6.73	1.51	0.66
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	K.TLLAHAIAGELDLPILK#.V	44.24	20.52	2.16	0.46
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	K.VAAPEIVSGVSGESEQK#.L	27.95	15.13	1.85	0.54
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	R.VIQYLSSNR@.C	12.86	6.08	2.12	0.47
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	K.VKPSISIKDQVM*YEALQR.S	10.23	7.07	1.45	0.69
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	R.VLVIGATNR@PDSLDPALR@.R	24.18	15.65	1.54	0.65
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	R.VVNQLLTEM*DGLETR@.Q	16.30	6.70	2.43	0.41
Q9DBY8_NVL_MOUSE	Nvl	Nuclear valosin-containi	K.VAAPEIVSGVSGESEQK#.L	4.93	2.45	2.01	0.50
Q99JX7_NXF1_MOUSE	Nxf1	Nuclear RNA export fact	R.LNVVAFLNELPK#.T	7.97	3.94	2.02	0.49
Q99JX7_NXF1_MOUSE	Nxf1	Nuclear RNA export fact	K.TLNLSGNELK#.T	7.98	6.85	1.16	0.86
Q99JX7_NXF1_MOUSE	Nxf1	Nuclear RNA export fact	R.LNVVAFLNELPK#.T	6.99	3.04	2.30	0.44
P11928_OAS1A_MOUSE	Oas1a	2'-5'-oligoadenylate synt	K.AR@PVILDPADPTGNVAGGNPEGWR@.R	26.59	17.02	1.56	0.64
P11928_OAS1A_MOUSE	Oas1a	2'-5'-oligoadenylate synt	K.AR@PVILDPADPTGNVAGGNPEGWR@.R	28.80	34.76	0.83	1.21
P11928_OAS1A_MOUSE	Oas1a	2'-5'-oligoadenylate synt	K.FIEDYLLPDTTFGADVK#.S	28.19	20.56	1.37	0.73

Q8VI94_OASL1_MOUSE	Oasl1	2'-5'-oligoadenylate synt	K.IQLSQGYLGLQR.L	3.32	12.21	0.27	3.67
Q8VI94_OASL1_MOUSE	Oasl1	2'-5'-oligoadenylate synt	K.LDSFVAQWLQPTR.E	4.04	9.65	0.42	2.39
Q8VI94_OASL1_MOUSE	Oasl1	2'-5'-oligoadenylate synt	R.LEFQGHILEDWFDFK.S	3.80	6.28	0.60	1.65
Q8VI94_OASL1_MOUSE	Oasl1	2'-5'-oligoadenylate synt	R.SHAYAIHPLDYVLNLK.Q	2.48	7.97	0.31	3.21
Q8VI94_OASL1_MOUSE	Oasl1	2'-5'-oligoadenylate synt	K.LDSFVAQWLQPTR.E	3.23	6.97	0.46	2.15
Q8VI94_OASL1_MOUSE	Oasl1	2'-5'-oligoadenylate synt	K.IQLSQGYLGLQR.L	2.98	12.68	0.23	4.26
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.DSK#PAPAIYETLIR@.S	75.10	68.96	1.09	0.92
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.DWK#EEGQDAWER@.I	9.89	12.75	0.78	1.29
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.EVVISFIK#.K	39.21	31.55	1.24	0.80
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.GDR@PIILDPADPTNNLGR@.R	29.50	30.24	0.98	1.03
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.GYPGDFSPSFTELQR@.H	30.61	30.77	0.99	1.01
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.KTDDIIWM*DILPAYDALGPISR.D	23.29	14.92	1.56	0.64
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.KTLADYGIFSK.V	12.29	10.72	1.15	0.87
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.NR@EVVISFIK#.K	15.50	6.64	2.33	0.43
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.QTGTVDWTLWTNPYSPIR.K	5.56	4.78	1.16	0.86
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.SKGYPGDFSPSFTELQR.H	19.68	18.06	1.09	0.92
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.YPGGQSK#PFTIDPDDTILDLK#.E	39.20	40.41	0.97	1.03
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.YPGGQSK#PFTIDPDDTILDLK#EK#.I	17.71	19.99	0.89	1.13
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.YYNFQNEVVR@.N	52.70	39.55	1.33	0.75
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.DSK#PAPAIYETLIR@.S	59.16	56.76	1.04	0.96
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.EVVISFIK#.K	44.77	34.98	1.28	0.78
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.GDR@PIILDPADPTNNLGR@.R	30.73	34.68	0.89	1.13
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.GYPGDFSPSFTELQR@.H	31.89	21.99	1.45	0.69
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.K#TDDIIWM*DILPAYDALGPISR@.D	22.03	16.88	1.31	0.77
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.QTGTVDWTLWTNPYSPIR.K	6.73	4.57	1.47	0.68
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.YPGGQSK#PFTIDPDDTILDLK#.E	34.73	28.11	1.24	0.81
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.YYNFQNEVVR@.N	53.94	30.02	1.80	0.56
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.DSK#PAPAIYETLIR@.S	36.02	31.24	1.15	0.87
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.GDR@PIILDPADPTNNLGR@.R	27.86	25.78	1.08	0.93
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	R.KTDDIIWM*DILPAYDALGPISR.D	11.87	12.32	0.96	1.04
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.QTGTVDWTLWTNPYSPIR@.K	4.85	4.52	1.07	0.93
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.YPGGQSK#PFTIDPDDTILDLK#.E	22.52	16.75	1.34	0.74
Q9Z2F2_OASL2_MOUSE	Oasl2	2'-5'-oligoadenylate synt	K.YYNFQNEVVR@.N	28.93	20.22	1.43	0.70
Q8K2X3_STN1_MOUSE	Obfc1	CST complex subunit STN	R.IGIGDIIR@.V	24.40	8.82	2.77	0.36
Q8K2X3_STN1_MOUSE	Obfc1	CST complex subunit STN	K.LSNAESSSDPAILSTAR@.E	9.70	3.95	2.45	0.41
Q8K2X3_STN1_MOUSE	Obfc1	CST complex subunit STN	K.VYDQPFR@.N	12.30	4.85	2.54	0.39
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	K.AFLDSLPDVK#.I	17.95	7.87	2.28	0.44
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	K.ALEVFPEFAAAHSNLASVLQQQGK#.L	15.70	3.58	4.39	0.23
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	R.EQGNIEEAVR@.L	24.43	10.04	2.43	0.41
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	R.FPAVGEPNIQQYAQNM*GLPQNR@.I	7.72	4.62	1.67	0.60
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	K.IDPSTLQM*WANILK#.R	6.65	4.68	1.42	0.70
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	R.ISPTFADAYSNM*GNTLK#.E	11.43	4.21	2.71	0.37
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	K.LVSIVAEQLEK#.N	18.35	8.10	2.27	0.44
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	K.SR@QEYEDIAVK#.L	7.28	2.56	2.84	0.35
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	K.AFLDSLPDVK#.I	11.65	4.91	2.37	0.42
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	R.AIQINPAFADAHSNLASIHK#.D	9.60	2.68	3.58	0.28
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	K.ALEVFPEFAAAHSNLASVLQQQGK#.L	14.33	4.41	3.25	0.31
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	R.EQGNIEEAVR@.L	10.92	2.90	3.77	0.27
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	R.ISPTFADAYSNM*GNTLK#.E	8.12	1.87	4.35	0.23
Q8CGY8_OGT1_MOUSE	Ogt	UDP-N-acetylglucosamin	K.LVSIVAEQLEK#.N	14.88	5.52	2.70	0.37
Q8VGJ0_Q8VGJ0_MOUSE	Olfr791	Olfactory receptor 791 O	K.QAFSDSVK#.R	20.79	5.37	3.87	0.26
Q8K3K8_OPTN_MOUSE	Optn	Optineurin OS=Mus musc	K.ADLLGIVSELQLK#.L	10.60	2.18	4.86	0.21
Q8K3K8_OPTN_MOUSE	Optn	Optineurin OS=Mus musc	K.M*LLQELSEK#LELAEQALASK#.Q	9.41	2.56	3.67	0.27
Q9Z1N2_ORC1_MOUSE	Orc1	Origin recognition comp	R.NLAVQEPASALEEAR@.L	4.91	2.40	2.04	0.49
Q60862_ORC2_MOUSE	Orc2	Origin recognition comp	R.DK#ASDLVEEYFEAHSSSK#.V	6.81	4.51	1.51	0.66
Q60862_ORC2_MOUSE	Orc2	Origin recognition comp	R.DK#ASDLVEEYFEAHSSSK#.V	8.53	2.72	3.14	0.32
Q60862_ORC2_MOUSE	Orc2	Origin recognition comp	K.VPSVQFVGDDDVLSHILDR@.E	14.74	4.03	3.66	0.27
Q9JK30_ORC3_MOUSE	Orc3	Origin recognition comp	R.SPPVVLILK#.S	11.77	5.29	2.23	0.45
Q9WUJ8_ORC6_MOUSE	Orc6	Origin recognition comp	R.LGLAEPSVLR@.K	26.15	7.99	3.27	0.31
Q9WUJ8_ORC6_MOUSE	Orc6	Origin recognition comp	R.LGLAEPSVLR@.K	12.95	6.06	2.14	0.47
Q9ERY9_ERG28_MOUSE	ORF11	Probable ergosterol bios	R.YLEAEPVSR@.Q	12.67	17.30	0.73	1.37
Q8CI95_OSB11_MOUSE	Osbpl11	Oxysterol-binding protei	R.VVLPTFILEK#.R	15.22	6.59	2.31	0.43
Q8CI95_OSB11_MOUSE	Osbpl11	Oxysterol-binding protei	R.VVLPTFILEK#.R	19.92	6.59	3.02	0.33
Q7TQI3_OTUB1_MOUSE	Otub1	Ubiquitin thioesterase O	R.IQQEIAVQNPLVSER@.L	6.61	2.64	2.50	0.40
Q7TQI3_OTUB1_MOUSE	Otub1	Ubiquitin thioesterase O	R.LLTSGYLQR@.E	14.51	9.92	1.46	0.68
Q7TQI3_OTUB1_MOUSE	Otub1	Ubiquitin thioesterase O	R.IQQEIAVQNPLVSER@.L	5.93	2.36	2.51	0.40
Q3UU35_OVOS_MOUSE	Ovos	Ovostatin homolog OS=M	K.SNSSDEFQTK#.F	15.81	5.84	2.71	0.37
Q6P9R2_OXSR1_MOUSE	Oxsr1	Serine/threonine-protei	K.IPISLVLR@.L	16.15	9.58	1.68	0.59
Q6P9R2_OXSR1_MOUSE	Oxsr1	Serine/threonine-protei	K.LLSGGSVLDIIK#.H	10.76	8.12	1.33	0.75
Q6P9R2_OXSR1_MOUSE	Oxsr1	Serine/threonine-protei	K.SGVLDEPTIATILR@.E	15.66	6.85	2.29	0.44
Q6P9R2_OXSR1_MOUSE	Oxsr1	Serine/threonine-protei	K.IPISLVLR@.L	21.54	11.97	1.80	0.56
Q6P9R2_OXSR1_MOUSE	Oxsr1	Serine/threonine-protei	K.LLSGGSVLDIIK#.H	13.56	6.66	2.04	0.49
Q6P9R2_OXSR1_MOUSE	Oxsr1	Serine/threonine-protei	K.IPISLVLR@.L	14.46	4.04	3.58	0.28
Q6P9R2_OXSR1_MOUSE	Oxsr1	Serine/threonine-protei	K.IVEEPQSNR@.S	9.83	3.55	2.77	0.36
Q6P9R2_OXSR1_MOUSE	Oxsr1	Serine/threonine-protei	K.LLSGGSVLDIIK#.H	10.02	4.01	2.50	0.40
Q9CPV9_P2Y12_MOUSE	P2ry12	P2Y purinoceptor 12 OS=	K.K#GQEGGEPSEETPM.-	12.15	1.96	6.20	0.16
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.FHDIISDAEIEIVK.D	19.35	22.03	0.88	1.14
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	K.GIAVDYLPER.Q	40.85	26.84	1.52	0.66
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.IQDLTGLDVSTAEELQVANYGVGGQYEPHFDFAR@.K	5.24	3.25	1.61	0.62
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.K#DEPDAFR@.E	7.13	9.56	0.75	1.34
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.LNTEWSELENLILK#.D	19.80	19.23	1.03	0.97
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.LQDTYNLDTNTISK#.G	41.89	33.06	1.27	0.79
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.QYFPNDEDQVGAAK#.A	12.13	9.23	1.31	0.76
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	K.VSVLDYLSYAVYQQGDLDK#.A	17.72	15.22	1.16	0.86
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	K.DPEGFVGHPVNAFK#.L	18.81	14.78	1.27	0.79
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.FHDIISDAEIEIVK#.D	28.11	26.32	1.07	0.94
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	K.GIAVDYLPER@.Q	61.49	38.63	1.59	0.63
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.IQDLTGLDVSTAEELQVANYGVGGQYEPHFDFAR@.K	10.05	5.69	1.77	0.57
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.KDEPDAFR.E	24.28	34.56	0.70	1.42
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	K.K#LLELDPEHQR@.A	23.47	21.97	1.07	0.94
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.LNTEWSELENLILK#.D	30.28	23.39	1.29	0.77
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.LQDTYNLDTNTISK#.G	50.43	39.11	1.29	0.78
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.LTSTATKDPEGFVGHPVNAFK.L	7.67	7.30	1.05	0.95
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.QYFPNDEDQVGAAK#.A	14.10	10.75	1.31	0.76
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	K.RLNTEWSELENLILK.D	8.03	9.57	0.84	1.19
Q60715_P4HA1_MOUSE	P4ha1	Prolyl 4-hydroxylase sub	R.LQDTYNLDTNTISK#.G	6.70	7.11	0.94	1.06
Q60716_P4HA2_MOUSE	P4ha2	Prolyl 4-hydroxylase sub	R.QFFPTDEDESGAAR@.A	6.29	4.55	1.38	0.72
Q60716_P4HA2_MOUSE	P4ha2	Prolyl 4-hydroxylase sub	K.QLDAGEEATVTK#.S	8.57	7.56	1.13	0.88
Q60716_P4HA2_MOUSE	P4ha2	Prolyl 4-hydroxylase sub	K.SSWLEEDDDPVVAR@.V	3.36	3.15	1.07	0.94
Q60716_P4HA2_MOUSE	P4ha2	Prolyl 4-hydroxylase sub	K.TAELLQVANYGM*GGQYEPHFDFSR@.S	3.49	3.06	1.14	0.88
Q60716_P4HA2_MOUSE	P4ha2	Prolyl 4-hydroxylase sub	K.TGVLTVASYR@.V	7.94	7.87	1.01	0.99
Q60716_P4HA2_MOUSE	P4ha2	Prolyl 4-hydroxylase sub	R.YYDVM*SDEEIER@.I	5.02	3.81	1.32	0.76
Q60716_P4HA2_MOUSE	P4ha2	Prolyl 4-hydroxylase sub	K.TAELLQVANYGM*GGQYEPHFDFSR@.S	4.82	1.49	3.23	0.31

P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.EADDIVNWLK#.K	85.87	59.30	1.45	0.69
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.HNQLPLVIEFTEQTAPK#.I	106.05	76.45	1.39	0.72
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.IKPHLM*SQEVPEDWDKQPVK.V	40.59	37.10	1.09	0.91
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.ILEFFGLK#.K	186.11	132.90	1.40	0.71
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.LGETYKDHENIIIAK.M	67.99	51.93	1.31	0.76
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.LITLEEEM*TK#.Y	180.10	140.56	1.28	0.78
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.LITLEEEMTK#.Y	23.43	15.57	1.50	0.66
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.M*DSTANEVEAVK#.V	96.37	72.12	1.34	0.75
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.MDSTANEVEAVK#.V	10.45	5.74	1.82	0.55
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.NNFEGEITK#.E	75.79	60.19	1.26	0.79
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.SNFEEALAAHK#.Y	69.11	43.14	1.60	0.62
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.THILLFLPK.S	33.84	33.64	1.01	0.99
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.TLDGFKK.F	37.11	35.73	1.04	0.96
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.VDATEESDLAQQYGVR@.G	83.55	64.84	1.29	0.78
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.VLVGANFEEVAFDEK#.K	80.02	60.90	1.31	0.76
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.YK#PESDELTAEK#.I	64.94	55.20	1.18	0.85
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.YQLDKDGVVLFK.K	115.09	91.94	1.25	0.80
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.EADDIVNWLK#.K	30.18	25.39	1.19	0.84
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.HNQLPLVIEFTEQTAPK#.I	26.76	27.04	0.99	1.01
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.ILEFFGLK#.K	96.53	75.79	1.27	0.79
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.LITLEEEM*TK#.Y	46.09	35.81	1.29	0.78
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.M*DSTANEVEAVK#.V	30.80	23.04	1.34	0.75
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.NNFEGEITK#.E	30.77	20.86	1.48	0.68
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.TVIDYNGER.T	17.17	10.54	1.63	0.61
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.VDATEESDLAQQYGVR@.G	32.38	23.90	1.35	0.74
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.YK#PESDELTAEK#.I	57.39	40.86	1.40	0.71
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	K.YQLDKDGVVLFK.K	55.02	52.00	1.06	0.95
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.ILEFFGLK#.K	9.77	6.24	1.57	0.64
P09103_PDIA1_MOUSE	P4hb	Protein disulfide-isomera	R.LITLEEEM*TK#.Y	7.29	6.07	1.20	0.83
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.AK#EFTNVYIK#.N	77.57	37.70	2.06	0.49
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.ALDTM*NFDVIK#.G	82.12	46.08	1.78	0.56
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.ALDTMNFDVIK#.G	10.59	3.83	2.77	0.36
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.EFSPFGTITSAK#.V	43.87	24.31	1.80	0.55
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.EFTNVYIK#.N	27.69	13.68	2.02	0.49
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.FGPALSVK#.V	82.84	44.08	1.88	0.53
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.FSPAGPILSIR.V	106.73	53.83	1.98	0.50
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.GFGFVSFER.H	85.22	33.03	2.58	0.39
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.GYGFVHFETQEAAER@.A	88.16	41.06	2.15	0.47
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.GYGFVHFETQEAAER.A	11.57	5.54	2.09	0.48
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.IVATK#PLYVALAQR@.K	80.98	44.25	1.83	0.55
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.K#EFSPFGTITSAK#.V	49.48	22.65	2.18	0.46
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.KVFVGR.F	347.87	351.11	0.99	1.01
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.NFGEDM*DDER@.L	19.68	10.35	1.90	0.53
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.NFGEDM*DDER@LK#.E	8.16	3.14	2.60	0.38
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.R@SLGYAYVNFQQPADAER@.A	11.03	5.55	1.99	0.50
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.SGVGNIFIK#.N	81.17	31.49	2.58	0.39
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.SLGYAYVNFQQPADAER.A	56.75	30.84	1.84	0.54
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.YQGVNLYVK#.N	85.44	45.86	1.86	0.54
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.AK#EFTNVYIK#.N	173.58	65.19	2.66	0.38
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.ALDTM*NFDVIK#.G	406.61	144.30	2.82	0.35
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.ALDTMNFDVIK#.G	28.27	12.82	2.21	0.45
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.EFSPFGTITSAK#.V	133.37	60.93	2.19	0.46
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.FGPALSVK#.V	204.41	92.33	2.21	0.45
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.FSPAGPILSIR@.V	280.52	116.30	2.41	0.41
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.GFGFVSFER@.H	245.86	102.97	2.39	0.42
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.GYGFVHFETQEAAER@.A	215.35	83.35	2.58	0.39
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.GYGFVHFETQEAAER.A	21.16	8.26	2.56	0.39
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.ITGM*LLEIDNSELLHM*LESPESLR@.S	71.74	26.07	2.75	0.36
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.ITGMLLEIDNSELLHM*LESPESLR@.S	50.43	18.86	2.67	0.37
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.ITGM*LLEIDNSELLHMLESPESLR@.S	63.66	29.01	2.19	0.46
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.IVATK#PLYVALAQR@.K	188.66	91.15	2.07	0.48
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.KEFSPFGTITSAK.V	30.90	17.36	1.78	0.56
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.NFGEDM*DDER@.L	48.03	20.49	2.34	0.43
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.NLDDGIDDER.L	94.86	42.16	2.25	0.44
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.R@SLGYAYVNFQQPADAER@.A	32.01	11.45	2.80	0.36
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.SGVGNIFIK#.N	266.73	100.05	2.67	0.38
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.SK#VDEAVAVLQAHQAK#.E	244.02	88.84	2.75	0.36
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.SLGYAYVNFQQPADAER@.A	155.50	66.26	2.35	0.43
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.VDEAVAVLQAHQAK#.E	30.76	14.61	2.10	0.48
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.YQGVNLYVK#.N	226.89	81.45	2.79	0.36
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.FGPALSVK#.V	61.25	21.53	2.84	0.35
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.GFGFVSFER@.H	14.58	5.42	2.69	0.37
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	K.NLDDGIDDER@.L	9.02	1.51	5.99	0.17
P29341_PABP1_MOUSE	Pabpc1	Polyadenylate-binding p	R.SLGYAYVNFQQPADAER@.A	10.75	2.95	3.64	0.27
Q6PHQ9_Q6PHQ9_MOUSE	Pabpc4	MCG5546, isoform CRA_	R.EFSPFGSITSAK#.V	12.56	9.83	1.28	0.78
Q6PHQ9_Q6PHQ9_MOUSE	Pabpc4	MCG5546, isoform CRA_	K.FSPAGPVLSIR.V	18.52	19.62	0.94	1.06
Q6PHQ9_Q6PHQ9_MOUSE	Pabpc4	MCG5546, isoform CRA_	R.IVGSKPLYVALAQR.K	13.02	9.34	1.39	0.72
Q6PHQ9_Q6PHQ9_MOUSE	Pabpc4	MCG5546, isoform CRA_	K.FSPAGPVLSIR@.V	29.70	18.92	1.57	0.64
Q6PHQ9_Q6PHQ9_MOUSE	Pabpc4	MCG5546, isoform CRA_	K.GFGFVSYEK#.H	12.58	7.97	1.58	0.63
Q6PHQ9_Q6PHQ9_MOUSE	Pabpc4	MCG5546, isoform CRA_	R.IVGSK#PLYVALAQR@.K	19.78	11.22	1.76	0.57
Q6PHQ9_Q6PHQ9_MOUSE	Pabpc4	MCG5546, isoform CRA_	R.YQGVNLYIK#.N	18.35	11.36	1.61	0.62
Q8CCS6_PABP2_MOUSE	Pabpn1	Polyadenylate-binding p	K.ELQNEVEK#.Q	142.20	67.47	2.11	0.47
Q8CCS6_PABP2_MOUSE	Pabpn1	Polyadenylate-binding p	R.EMEEEAEK#LK#ELQNEVEK#.Q	6.42	2.53	2.54	0.39
Q8CCS6_PABP2_MOUSE	Pabpn1	Polyadenylate-binding p	K.GFAYIEFSDK#.E	52.61	23.07	2.28	0.44
Q8CCS6_PABP2_MOUSE	Pabpn1	Polyadenylate-binding p	R.TSLALDESLFR@.G	374.32	159.73	2.34	0.43
Q8CCS6_PABP2_MOUSE	Pabpn1	Polyadenylate-binding p	R.TSLALDESLFR@.G	67.11	27.66	2.43	0.41
Q8CCS6_PABP2_MOUSE	Pabpn1	Polyadenylate-binding p	K.GFAYIEFSDK#ESVR@.T	17.11	8.08	2.12	0.47
Q8CCS6_PABP2_MOUSE	Pabpn1	Polyadenylate-binding p	R.TSLALDESLFR@.G	16.51	9.71	1.70	0.59
Q8K212_PACS1_MOUSE	Pacs1	Phosphofurin acidic clus	K.DTTSPM*ELAALEK#.V	6.56	2.33	2.81	0.36
Q8K212_PACS1_MOUSE	Pacs1	Phosphofurin acidic clus	R.FLIIPLGSHPVAK#.Y	12.70	4.31	2.95	0.34
Q8K212_PACS1_MOUSE	Pacs1	Phosphofurin acidic clus	K.VAAVGSQSYLSSILR@.F	12.61	2.70	4.68	0.21
Q8K212_PACS1_MOUSE	Pacs1	Phosphofurin acidic clus	K.LK#PFFEGM*SQSSSQTEIGSLNSK#.G	10.97	1.10	9.93	0.10
Q8K212_PACS1_MOUSE	Pacs1	Phosphofurin acidic clus	K.VAAVGSQSYLSSILR@.F	9.11	3.10	2.94	0.34
Q8K2T8_PAF1_MOUSE	Paf1	RNA polymerase II-associ	K.AGVQSGTNALLVVK#.H	9.85	4.84	2.04	0.49
Q8K2T8_PAF1_MOUSE	Paf1	RNA polymerase II-associ	R.EGDGVYYNELETR@.V	6.73	5.70	1.18	0.85
Q8K2T8_PAF1_MOUSE	Paf1	RNA polymerase II-associ	K.GYEENYFFIFR@.E	6.78	5.12	1.32	0.75
Q8K2T8_PAF1_MOUSE	Paf1	RNA polymerase II-associ	R.IDPNVLLDPADEK#LLEEEIQAPTSSK#.R	5.53	3.72	1.49	0.67
Q8K2T8_PAF1_MOUSE	Paf1	RNA polymerase II-associ	R.VTPVEVM*PVFPDFK#.M	5.00	4.51	1.11	0.90
Q9DCL9_PUR6_MOUSE	Paics	Multifunctional protein	K.EIVLADVIDNDSWR@.L	11.40	6.94	1.64	0.61
Q9DCL9_PUR6_MOUSE	Paics	Multifunctional protein	K.EVTPEGLQM*VK#.K	7.90	6.13	1.29	0.78
Q9DCL9_PUR6_MOUSE	Paics	Multifunctional protein	R.IK#AEYEGDGIPTVFVSVAGR@.S	12.88	7.77	1.66	0.60
Q9DCL9_PUR6_MOUSE	Paics	Multifunctional protein	K.EIVLADVIDNDSWR@.L	5.65	2.29	2.47	0.41
Q8VE62_PAIP1_MOUSE	Paip1	Polyadenylate-binding p	R.ADILQVGLR@.E	9.68	6.00	1.61	0.62

Q640Q5_PAN3_MOUSE	Pan3	PAB-dependent poly(A)-s	K.NLILYLLTDQNR@.M	5.97	1.11	5.36	0.19
Q61183_PAPOA_MOUSE	Papola	Poly(A) polymerase alpha	K.LFEAPNFFQK#.Y	5.43	1.53	3.54	0.28
Q61183_PAPOA_MOUSE	Papola	Poly(A) polymerase alpha	R.VTDEILHLVPNIDNFR@.L	4.24	8.18	0.52	1.93
Q99NH2_PARD3_MOUSE	Pard3	Partitioning defective 3 h	R.DVTIGGSAPIYVK#.N	3.79	3.66	1.04	0.97
Q99NH2_PARD3_MOUSE	Pard3	Partitioning defective 3 h	R.EM*NAEPSQM*QTPK#.E	3.64	1.73	2.10	0.48
Q9CSB4_PAR3L_MOUSE	Pard3b	Partitioning defective 3 h	R.AVEISGEGDPLGIHVVPFFSSLSGR@.I	6.64	29.63	0.22	4.46
Q99LX0_PARK7_MOUSE	Park7	Protein deglycase DJ-1 O	K.APLVLK#D.-	4.92	2.63	1.87	0.53
Q8VDG3_PARN_MOUSE	Parn	Poly(A)-specific ribonucl	K.EQEELNDAVGFSR@.V	10.88	2.74	3.97	0.25
Q8VDG3_PARN_MOUSE	Parn	Poly(A)-specific ribonucl	K.EQEELNDAVGFSR@.V	10.67	1.87	5.70	0.18
Q8VDG3_PARN_MOUSE	Parn	Poly(A)-specific ribonucl	R.VM*DIPYLNLEGPDLQPK#.R	6.46	3.56	1.81	0.55
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.ELLIFNQQQVPSGESAILDR.V	3.13	9.42	0.33	3.01
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.TLGDFLAEYAK.S	8.25	29.18	0.28	3.54
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.ALVEYEIDLQK.M	10.32	33.01	0.31	3.20
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.ELLIFNQQQVPSGESAILDR.V	8.97	35.22	0.25	3.93
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	R.GGSDDSSKDPIDVNYEK.L	14.69	75.47	0.19	5.14
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.GIYFADM*VSK.S	4.43	16.24	0.27	3.67
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.KFYPLEIDYGQDEEAVK.K	6.84	16.66	0.41	2.44
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.KFYPLEIDYGQDEEAVKK.L	6.77	18.71	0.36	2.76
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.KPPLLNNADSVQAK.V	7.76	37.96	0.20	4.89
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	R.M*AIM*VQSPM*FDGK.V	2.78	7.07	0.39	2.54
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.SLQELLSAHSLSSWGAEVK.A	28.83	42.40	0.68	1.47
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.TLGDFLAEYAK.S	25.67	94.33	0.27	3.67
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	R.TTNFAGILSQGLR.I	15.36	45.10	0.34	2.94
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.VFSATLGLVDIVK.G	31.16	101.92	0.31	3.27
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.VVDRDSEEAEVIR.K	10.80	40.95	0.26	3.79
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.ELLIFNQQQVPSGESAILDR.V	5.71	10.51	0.54	1.84
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	R.GGSDDSSKDPIDVNYEK.L	7.48	13.67	0.55	1.83
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.KFYPLEIDYGQDEEAVKK.L	3.40	7.17	0.47	2.11
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.SLQELLSAHSLSSWGAEVK.A	5.02	9.35	0.54	1.86
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	K.TLGDFLAEYAK.S	10.05	27.26	0.37	2.71
Q921K2_Q921K2_MOUSE	Parp1	Poly (ADP-ribose) polyme	R.TTNFAGILSQGLR@.I	7.27	26.31	0.28	3.62
Q8CIE4_Q8CIE4_MOUSE	Parp10	Plec1 protein OS=Mus m	R.AGPVGAPGQALPVDSGSIR@.I	8.82	5.92	1.49	0.67
Q8CIE4_Q8CIE4_MOUSE	Parp10	Plec1 protein OS=Mus m	K.AVFVAQVLTGDYGQGSR@.G	6.40	4.52	1.42	0.71
Q8CIE4_Q8CIE4_MOUSE	Parp10	Plec1 protein OS=Mus m	K.EK#PGGPGETVVEQQEEIPTLEAEEEPVALSTGAR@.G	4.51	2.48	1.81	0.55
Q8CIE4_Q8CIE4_MOUSE	Parp10	Plec1 protein OS=Mus m	R.LEALEENSQEFQDVVR@.A	6.40	2.59	2.47	0.40
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	K.SIPDYWDPAALPDLGFK.K	3.86	2.82	1.37	0.73
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	K.VSPSPAGPQGSSER@.K	11.59	8.28	1.40	0.71
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	K.YVSPQDVQM*K#.Q	6.78	4.95	1.37	0.73
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	R.LGLSSDLVSR@.L	28.48	5.82	4.90	0.20
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	R.LVLAVSSLR@.L	12.01	3.87	3.11	0.32
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	R.QGSGHPVTTISSSDVER@.A	22.69	14.61	1.55	0.64
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	R.SHEFTNSESLEQLER@.L	11.72	5.53	2.12	0.47
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	K.SIPDYWDPAALPDLGFK#.K	7.21	3.56	2.02	0.49
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	R.TSLGTDALER@.L	16.91	9.12	1.85	0.54
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	R.VLVGDFVR@.G	31.50	10.20	3.09	0.32
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	K.VSPSPAGPQGSSER@.K	26.47	13.64	1.94	0.52
Q8BZ20_PAR12_MOUSE	Parp12	Poly [ADP-ribose] polyme	R.WQFLDGGK#.W	12.45	5.49	2.27	0.44
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.AIIDAIEEFVQK#.K	12.88	15.01	0.86	1.17
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	R.DASAVLSGIK#.S	15.89	13.27	1.20	0.83
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.DHENIQAFSDEFDKR.N	9.17	9.94	0.92	1.08
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.DVQVSSEVFEFLQQVDSQR@.L	23.64	16.53	1.43	0.70
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.EGGVVLPGNAVISK#.A	18.49	15.28	1.21	0.83
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	R.FPVDVVVNAANENLK.H	13.73	6.55	2.10	0.48
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.GPLSQAFLEK.A	16.27	13.35	1.22	0.82
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.GTALFLVGSSFK.D	18.27	18.51	0.99	1.01
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.HISGLAQALSK.A	8.67	12.96	0.67	1.49
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.IKPSLIVDYLR.T	19.97	22.22	0.90	1.11
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.IYLVGLPAK#.V	16.79	15.46	1.09	0.92
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	R.LLETTNVVR@.V	19.89	16.31	1.22	0.82
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.LLLVNLQTSDPEYNM*VASAFR.Q	5.96	6.21	0.96	1.04
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.LPASFQESLDLPLWK#.F	9.39	7.69	1.22	0.82
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.LQVYFQSR@.K	11.49	9.01	1.28	0.78
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.M*PLSVFPYYPSLGTALYGEEK#PLIK#.L	15.30	19.09	0.80	1.25
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.SLFEAQNILAIYELK.G	17.06	15.44	1.11	0.90
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	R.SNQQLQLAPR.L	16.42	14.48	1.13	0.88
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.TLQEVQFLLHPK.D	16.68	14.48	1.15	0.87
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.TSIQVSGISR.D	12.21	14.01	0.87	1.15
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	K.TTENLSLQSIAFPAIGTGNLR.F	9.66	9.52	1.01	0.99
Q2EMV9_PAR14_MOUSE	Parp14	Poly [ADP-ribose] polyme	R.VLFSPEDVR.Q	14.81	12.74	1.16	0.86
E9PYK3_E9PYK3_MOUSE	Parp4	Protein Parp4 OS=Mus m	R.SEQPVDILQIFR@.V	4.68	2.91	1.61	0.62
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.DLSSWGGPETDPASTM*TLR@.I	11.58	3.32	3.48	0.29
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.EIHLVSNEDPTVASFK#.S	6.40	4.04	1.58	0.63
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.GGLEAGSPAINLM*GVK#.V	22.51	10.71	2.10	0.48
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.GPQADLIDAVM*R@.I	23.85	10.48	2.28	0.44
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.HNVFEILK#.S	42.86	25.37	1.69	0.59
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.HVVDAVVNAANENLLHGSGLAGSLVK#.T	27.43	10.81	2.54	0.39
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.IFYAEM*TK#.R	9.55	8.05	1.19	0.84
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.ISVGGIAITGAGR@.L	34.36	15.69	2.19	0.46
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.IVIFPVDVETYK#.I	94.33	54.88	1.72	0.58
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.M*YSTSYNPVYGAGIYFTK#.S	9.98	6.50	1.54	0.65
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.SASESILGR@.D	67.58	36.01	1.88	0.53
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.VAQSILR@.Q	68.96	33.70	2.05	0.49
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.VLLAAFQEK#.K	53.56	35.57	1.51	0.66
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.VSISETVSPR@.T	62.78	26.53	2.37	0.42
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.WTVTNSQTAIELLK#.F	30.10	10.23	2.94	0.34
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.YPASLTQELQDR@.K	40.86	18.68	2.19	0.46
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.DLSSWGGPETDPASTM*TLR@.I	7.63	2.14	3.57	0.28
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.HNVFEILK#.S	35.14	20.05	1.75	0.57
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.HVVDAVVNAANENLLHGSGLAGSLVK#.T	21.60	5.97	3.62	0.28
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.ISVGGIAITGAGR@.L	24.66	10.27	2.40	0.42
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.IVIFPVDVETYK#.I	61.66	24.86	2.48	0.40
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.M*YSTSYNPVYGAGIYFTK#.S	6.63	3.51	1.89	0.53
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.NILDYVTK#.Y	33.42	10.85	3.08	0.32
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.TGGFEIQEESK#R@.I	6.58	2.89	2.27	0.44
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.VAQSILR@.Q	37.30	18.29	2.04	0.49
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	K.VLLAAFQEK#.K	66.02	22.98	2.87	0.35
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.WTVTNSQTAIELLK#.F	15.89	7.59	2.09	0.48
Q8CAS9_PARP9_MOUSE	Parp9	Poly [ADP-ribose] polyme	R.YPASLTQELQDR@.K	20.60	9.85	2.09	0.48
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	R.DAFDTLFDHAPDK#LNVVK#.K	43.82	15.57	2.81	0.36
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	K.DLAEDLYDGQVLQK#.L	67.25	26.06	2.58	0.39
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	R.IIVK#DLAEDLYDGQVLQK#.L	23.91	5.07	4.72	0.21
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	K.K#TLITFVNK#.H	10.20	3.83	2.66	0.38
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	K.LESEK#LNVAEVTQSEIAQK#.Q	71.25	25.77	2.77	0.36

Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	K.LFEK#LESEK#LNVAEVTQSEIAQK#.Q	10.56	5.53	1.91	0.52
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	K.LNVAEVTQSEIAQK#.Q	66.86	20.81	3.21	0.31
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	R.QIQEEITGNTEALSGR@.H	52.48	16.53	3.18	0.31
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	K.TLITFVNK#.H	63.86	19.84	3.22	0.31
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	R.TM*VDPNSR@.N	25.29	9.62	2.63	0.38
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	K.VLIDWINDVLVGER@.I	76.45	26.84	2.85	0.35
Q9EPC1_PARVA_MOUSE	Parva	Alpha-parvin OS=Mus mu	R.VLYNLFTK#.Y	81.29	31.05	2.62	0.38
Q9ES46_PARVB_MOUSE	Parvb	Beta-parvin OS=Mus mus	K.LNVAEVTQSEIGQK#.Q	5.15	1.48	3.49	0.29
Q9ES46_PARVB_MOUSE	Parvb	Beta-parvin OS=Mus mus	K.SAINSPM*APALVDIHPEDTQLEENEER@.T	4.39	1.47	2.99	0.33
Q925B0_PAWR_MOUSE	Pawr	PRKC apoptosis WT1 reg	R.DANAPASFSSSSTLEK#.R	13.40	9.11	1.47	0.68
Q00288_PAX8_MOUSE	Pax8	Paired box protein Pax-8	K.ATLTSSNTPLGR@.N	16.52	9.04	1.83	0.55
Q00288_PAX8_MOUSE	Pax8	Paired box protein Pax-8	R.LSIDSQSSSSGPR@.K	20.41	15.15	1.35	0.74
P58501_PAXB1_MOUSE	Paxbp1	PAX3- and PAX7-binding	K.AGGAFSNALSSLNVLRPGEIPDAAFIHAAR.K	18.73	9.89	1.89	0.53
P58501_PAXB1_MOUSE	Paxbp1	PAX3- and PAX7-binding	R.ASLLSFQDEEEENEEVFK#.V	6.98	3.11	2.24	0.45
P58501_PAXB1_MOUSE	Paxbp1	PAX3- and PAX7-binding	K.LFNPLIR@.L	17.93	8.09	2.21	0.45
P58501_PAXB1_MOUSE	Paxbp1	PAX3- and PAX7-binding	R.YLVHLADTIYR@.N	13.30	4.03	3.30	0.30
P58501_PAXB1_MOUSE	Paxbp1	PAX3- and PAX7-binding	K.AGGAFSNALSSLNVLRPGEIPDAAFIHAAR.K	15.70	6.43	2.44	0.41
P58501_PAXB1_MOUSE	Paxbp1	PAX3- and PAX7-binding	K.LFNPLIR@.L	10.83	5.87	1.85	0.54
P58501_PAXB1_MOUSE	Paxbp1	PAX3- and PAX7-binding	R.LQLLTWTPLEAK#.C	19.42	8.06	2.41	0.41
P58501_PAXB1_MOUSE	Paxbp1	PAX3- and PAX7-binding	K.NSGPYLFFQR@.Q	13.10	4.10	3.19	0.31
P58501_PAXB1_MOUSE	Paxbp1	PAX3- and PAX7-binding	K.TLQELSIDGLLNR@.Y	16.20	3.05	5.32	0.19
Q6NZQ4_PAXI1_MOUSE	Paxip1	PAX-interacting protein	R.QTFIDEQNYILR@.D	7.13	2.80	2.55	0.39
Q9D0B6_PBDC1_MOUSE	Pbdc1	Protein PBDC1 OS=Mus	K.FEGIVEDYNYGTLLR.L	9.03	4.55	1.98	0.50
Q9D0B6_PBDC1_MOUSE	Pbdc1	Protein PBDC1 OS=Mus	R.IQFFAIEIAR@.N	23.58	8.29	2.84	0.35
Q9D0B6_PBDC1_MOUSE	Pbdc1	Protein PBDC1 OS=Mus	K.LISSVDPQFLK#.L	30.55	13.10	2.33	0.43
Q9D0B6_PBDC1_MOUSE	Pbdc1	Protein PBDC1 OS=Mus	K.VDDQIYSEFR@.E	22.64	6.86	3.30	0.30
Q9D0B6_PBDC1_MOUSE	Pbdc1	Protein PBDC1 OS=Mus	R.IQFFAIEIAR.N	15.53	8.00	1.94	0.51
Q9D0B6_PBDC1_MOUSE	Pbdc1	Protein PBDC1 OS=Mus	K.LISSVDPQFLK#.L	10.11	5.30	1.91	0.52
Q9D0B6_PBDC1_MOUSE	Pbdc1	Protein PBDC1 OS=Mus	K.VDDQIYSEFR@.E	9.46	5.08	1.86	0.54
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.IILEPM*DLK#.I	10.76	2.73	3.94	0.25
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.ILFNVVLEAR@.E	12.55	4.37	2.87	0.35
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.K#PIIPQK#EPSPLLEK#.K	17.13	4.88	3.51	0.28
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.LNEVYEAVK#.N	17.12	3.91	4.38	0.23
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.LSAIFLR@.L	17.51	6.20	2.82	0.35
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.LWTM*PISSVR@.F	7.69	6.04	1.27	0.79
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.R@DDIEDGDSM*ISSATSDTGSAK#.R	8.39	4.52	1.86	0.54
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.TDSEIYEDAVELQQFFIR@.I	15.44	4.41	3.50	0.29
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.VVDDEIYYFR@.K	21.85	5.86	3.73	0.27
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.YEEGESEAESITSFM*DVSNPFHQLYDTVR@.S	4.09	1.83	2.24	0.45
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.YIEGLSAESNSISK#.W	12.22	2.22	5.51	0.18
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.AAQQQQPSASPR@.A	18.17	4.63	3.92	0.26
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.AQHPDYSFGELSR@.L	83.18	23.48	3.54	0.28
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.EAEK#SEDSSGTTGLSGLHR@.T	67.51	11.44	5.90	0.17
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.EAEKSEDSSGTTGLSGLHR.T	37.37	9.57	3.90	0.26
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.EILEQLLEAIVVATNPSGR@.L	45.81	8.50	5.39	0.19
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.ELGPLPDDDDM*ASPK#.L	87.07	22.48	3.87	0.26
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.ELGPLPDDDDMASPK#.L	6.24	2.43	2.57	0.39
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.HYNEEGSQVYNDAHILEK#.L	136.62	23.01	5.94	0.17
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.IILEPM*DLK#.I	91.95	19.68	4.67	0.21
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.IILEPMDLK#.I	15.51	5.58	2.78	0.36
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.ILFNVVLEAR@.E	35.75	9.39	3.81	0.26
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.INM*SGYILFSSEM*R@.A	9.69	2.97	3.26	0.31
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.K#DYPDYYK#.I	6.34	2.65	2.40	0.42
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.K#K#YPDYYQQIK#.M	16.26	4.48	3.63	0.28
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.K#PIIPQK#EPSPLLEK#.K	60.08	19.58	3.07	0.33
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.LISELFQK#.L	64.54	12.73	5.07	0.20
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.LLHSEAYLK#.Y	82.31	28.27	2.91	0.34
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.LNEVYEAVK#.N	135.26	35.17	3.85	0.26
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.LSAIFLR@.L	85.13	13.84	6.15	0.16
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.LSAITM*ALQYGSESEEDAALAAAR@.Y	81.16	17.26	4.70	0.21
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.LWDLYLR@.T	38.11	8.63	4.42	0.23
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.LWTM*PISSVR@.F	58.42	25.21	2.32	0.43
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.LWTMPISSVR@.F	15.72	2.58	6.09	0.16
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.M*PISLQQIR@.T	134.84	31.49	4.28	0.23
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.NGEILLSPALSYTTK#.H	26.62	7.57	3.52	0.28
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.NHQGQLIAEPFFHLPSK#.K	76.21	18.68	4.08	0.25
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.NQPDYYEVVSQPIDLM*K#.I	28.94	6.76	4.28	0.23
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.R@ATSPSSSVSGDFDDGHHSVPTPGPSR@.K	20.82	3.85	5.41	0.18
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.R@DDIEDGDSM*ISSATSDTGSAK#.R	99.57	19.50	5.11	0.20
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.R@LSAIFLR@.L	45.07	8.40	5.37	0.19
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.SDYYNK#VPVSK#.I	51.97	12.69	4.09	0.24
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.SELPDYYLTIK#.K	123.93	29.87	4.15	0.24
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.SSLGEER@NPTSK#.Y	12.64	2.43	5.21	0.19
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.TDSEIYEDAVELQQFFIR@.I	107.09	31.34	3.42	0.29
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.TYNEPGSQVFK#.D	86.34	22.72	3.80	0.26
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.VLLETR@.R	157.46	38.80	4.06	0.25
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.VQYPDYYAIIK#.E	18.80	3.67	5.12	0.20
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.VVDDEIYYFR@.K	148.79	32.22	4.62	0.22
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.WDQTLAAR@.R	44.75	10.36	4.32	0.23
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.YEEGESEAESITSFM*DVSNPFHQLYDTVR@.S	17.75	5.25	3.38	0.30
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.YIEGLSAESNSISK#.W	86.82	21.80	3.98	0.25
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.YNDM*WLK#.V	18.25	5.55	3.29	0.30
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	R.YNVPNSAIYK#.R	35.18	9.04	3.89	0.26
F8VQD1_F8VQD1_MOUSE	Pbrm1	Protein polybromo-1 OS	K.YPDYYQQIK#.M	11.58	5.15	2.25	0.44
P41778_PBX1_MOUSE	Pbx1	Pre-B-cell leukemia trans	K.GGGSAAAAAAAAASGGAGSDNSVEHSDYR@.A	17.13	3.52	4.87	0.21
P41778_PBX1_MOUSE	Pbx1	Pre-B-cell leukemia trans	R.K#QDIGDILQQIM*TITDQSLDEAQAR@.K	2.88	2.74	1.05	0.95
O35984_PBX2_MOUSE	Pbx2	Pre-B-cell leukemia trans	K.GGGSAAAAAAAAASGGGVSPDNSIEHSDYR@.S	5.25	3.02	1.74	0.57
O35984_PBX2_MOUSE	Pbx2	Pre-B-cell leukemia trans	R.LDNM*LLAEGVAGPEK#.G	12.33	3.34	3.69	0.27
O35317_PBX3_MOUSE	Pbx3	Pre-B-cell leukemia trans	K.GGGSAAAAAAAAASGGSSDNSIEHSDYR@.A	6.83	3.95	1.73	0.58
Q05920_PYC_MOUSE	Pc	Pyruvate carboxylase, mi	R.LDNASAFQGAVISPHYDSLLVK#.V	9.81	4.47	2.20	0.46
Q05920_PYC_MOUSE	Pc	Pyruvate carboxylase, mi	R.SVVEFLQGYIGIPHGGFPEPFR@.S	6.25	4.07	1.54	0.65
Q05920_PYC_MOUSE	Pc	Pyruvate carboxylase, mi	R.VVHSYEELEENYTR@.A	4.19	3.64	1.15	0.87
Q05920_PYC_MOUSE	Pc	Pyruvate carboxylase, mi	K.DFTATFGPLDSLNTR@.L	4.87	3.15	1.55	0.65
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.AFAM*IIDKLEEDINSSM*TNSTAASRPPVTLR.L	326.79	82.81	3.95	0.25
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.AFAMIIDKLEEDINSSM*TNSTAASRPPVTLR.L	76.41	20.74	3.68	0.27
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.AFAMIIDK#LEEDINSSMTNSTAASR@PPVTLR@.L	5.11	3.27	1.56	0.64
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.ESTGAQVQVAGDM*LPNSTER@.A	473.95	178.93	2.65	0.38
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.ESTGAQVQVAGDM*LPNSTER.A	264.72	92.19	2.87	0.35
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.ESTGAQVQVAGDMLPNSTER.A	35.12	11.46	3.06	0.33
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.IANPVEGSSGR@.Q	463.19	168.47	2.75	0.36
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.IITLTGPTNAIFK#.A	723.55	243.66	2.97	0.34
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.IR@EESGAR@.I	23.83	8.27	2.88	0.35
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.LEEDINSSM*TNSTAASR@PPVTLR@.L	12.15	3.44	3.53	0.28

P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QGANINEIR@.Q	461.81	168.94	2.73	0.37
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QM*SGAQIK#.I	115.53	41.83	2.76	0.36
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QMSGAQIK#.I	63.87	22.60	2.83	0.35
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QVTITGSAASISLAQYLINAR@.L	24.28	8.55	2.84	0.35
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QVTITGSAASISLAQYLINAR@.L	145.09	48.56	2.99	0.33
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.ESTGAQVQVAGDM*LPNSTER@.A	27.70	13.15	2.11	0.47
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.ESTGAQVQVAGDM*LPNSTER.A	15.74	7.69	2.05	0.49
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.IANPVEGSSGR@.Q	17.00	7.52	2.26	0.44
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.IITLTGPTNAIFK#.A	98.03	48.28	2.03	0.49
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QVTITGSAASISLAQYLINAR@.L	9.29	2.64	3.52	0.28
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.AFAM*IIDKLEEDINSSM*TNSTAASRPPVTLR.L	64.43	14.38	4.48	0.22
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.ESTGAQVQVAGDM*LPNSTER@.A	115.33	25.18	4.58	0.22
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.ESTGAQVQVAGDM*LPNSTER.A	63.38	15.32	4.14	0.24
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.EVGSIIGK#.K	213.75	48.75	4.38	0.23
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.IANPVEGSSGR@.Q	155.49	44.02	3.53	0.28
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.IITLTGPTNAIFK#.A	274.91	72.69	3.78	0.26
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QGANINEIR@.Q	169.46	38.91	4.35	0.23
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QVTITGSAASISLAQYLINAR@.L	52.98	18.10	2.93	0.34
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.AFAM*IIDK#.L	11.55	3.88	2.98	0.34
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.AFAM*IIDKLEEDINSSM*TNSTAASRPPVTLR.L	33.27	4.95	6.73	0.15
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.ESTGAQVQVAGDM*LPNSTER@.A	60.51	15.50	3.90	0.26
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.ESTGAQVQVAGDM*LPNSTER.A	29.18	6.43	4.54	0.22
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.IANPVEGSSGR@.Q	56.86	12.88	4.41	0.23
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.IITLTGPTNAIFK#.A	130.63	29.82	4.38	0.23
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	K.LEEDINSSM*TNSTAASR@PPVTLR@.L	8.69	2.41	3.60	0.28
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QGANINEIR@.Q	67.95	19.32	3.52	0.28
P60335_PCBP1_MOUSE	Pcbp1	Poly(rC)-binding protein	R.QVTITGSAASISLAQYLINAR@.L	27.48	9.17	3.00	0.33
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.AFAM*IIDKLEEDISSSM*TNSTAASRPPVTLR.L	105.34	32.73	3.22	0.31
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.AFAMIIDK#LEEDISSSMTNSTAASR@PPVTLR@.L	29.36	5.80	5.06	0.20
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.GVTIPYR@PK#PSSSPVIFAGGQDR@.Y	13.34	4.20	3.18	0.31
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.IANPVEGSTDR@.Q	588.12	230.59	2.55	0.39
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	R.IITLAGPTNAIFK#.A	610.73	215.54	2.83	0.35
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.LEEDISSSM*TNSTAASR@PPVTLR@.L	10.97	4.04	2.72	0.37
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.LHQLAM*QQSHFPM*THGNTGFSGIESSSPEVK#.G	47.60	16.82	2.83	0.35
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.LHQLAM*QQSHFPMTHGNTGFSGIESSSPEVK#.G	6.96	2.12	3.28	0.30
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	R.LSSETGGM*GSS.-	27.75	27.75	1.00	1.00
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	R.QVTITGSAASISLAQYLINVR@.L	83.48	22.30	3.74	0.27
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	R.QVTITGSAASISLAQYLINVR.L	12.89	6.10	2.11	0.47
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.IANPVEGSTDR@.Q	44.56	20.91	2.13	0.47
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	R.IITLAGPTNAIFK#.A	52.79	20.06	2.63	0.38
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.IANPVEGSTDR@.Q	106.30	31.38	3.39	0.30
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	R.IITLAGPTNAIFK#.A	185.43	42.43	4.37	0.23
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	R.QVTITGSAASISLAQYLINVR@.L	14.71	7.59	1.94	0.52
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.IANPVEGSTDR@.Q	133.39	31.36	4.25	0.24
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	R.IITLAGPTNAIFK#.A	212.92	48.28	4.41	0.23
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	K.LEEDISSSM*TNSTAASR@PPVTLR@.L	16.26	2.64	6.16	0.16
Q61990_PCBP2_MOUSE	Pcbp2	Poly(rC)-binding protein	R.QVTITGSAASISLAQYLINVR@.L	22.76	3.60	6.31	0.16
P57724_PCBP4_MOUSE	Pcbp4	Poly(rC)-binding protein	K.IGNQAEGAGER@.H	15.12	3.98	3.80	0.26
P57724_PCBP4_MOUSE	Pcbp4	Poly(rC)-binding protein	R.ETTGAQVQVAGDLLPNSTER@.A	3.95	2.40	1.64	0.61
Q9R0L6_PCM1_MOUSE	Pcm1	Pericentriolar material 1	R.ALYALQDIVSR@.H	16.78	7.67	2.19	0.46
Q9R0L6_PCM1_MOUSE	Pcm1	Pericentriolar material 1	K.LM*QDLDNNSIAVK#.Q	3.86	2.23	1.73	0.58
Q9R0L6_PCM1_MOUSE	Pcm1	Pericentriolar material 1	R.M*LQQQEQLR@.A	5.43	1.57	3.46	0.29
Q9R0L6_PCM1_MOUSE	Pcm1	Pericentriolar material 1	K.TPESTNVPSDQEPTSK#.N	2.56	1.80	1.43	0.70
P17918_PCNA_MOUSE	Pcna	Proliferating cell nuclear	R.AEDNADTLALVFEAPNQEK.V	3.58	20.68	0.17	5.78
P17918_PCNA_MOUSE	Pcna	Proliferating cell nuclear	K.ATPLSPTVTLSM*SADVPLVVEYK.I	5.56	19.88	0.28	3.58
P17918_PCNA_MOUSE	Pcna	Proliferating cell nuclear	K.LSQTSNVDKEEEAVTIEM*NEPVHLTFALR.Y	4.37	16.97	0.26	3.88
P17918_PCNA_MOUSE	Pcna	Proliferating cell nuclear	R.NLAM*GVNLTSM*SK.I	5.24	4.42	1.19	0.84
P17918_PCNA_MOUSE	Pcna	Proliferating cell nuclear	R.YLNFFTK.A	8.30	41.81	0.20	5.04
P17918_PCNA_MOUSE	Pcna	Proliferating cell nuclear	K.YYLAPK.I	15.28	58.81	0.26	3.85
Q61398_PCOC1_MOUSE	Pcolce	Procollagen C-endopepti	R.SNQDQILNNLSK#.R	7.70	4.26	1.81	0.55
Q61398_PCOC1_MOUSE	Pcolce	Procollagen C-endopepti	R.YDALEVFAGSGTSGQR.L	4.20	4.99	0.84	1.19
Q9CQF9_PCYOX_MOUSE	Pcyox1	Prenylcysteine oxidase O	K.AGFSETFLNEM*IAPVM*K#.V	3.20	2.15	1.49	0.67
Q9CQF9_PCYOX_MOUSE	Pcyox1	Prenylcysteine oxidase O	K.IDVFER@.E	14.28	5.94	2.40	0.42
Q8C7K6_PCYXL_MOUSE	Pcyox1l	Prenylcysteine oxidase-li	R.FIDDVVSAVLR@.A	23.80	12.53	1.90	0.53
P49586_PCY1A_MOUSE	Pcyt1a	Choline-phosphate cytid	K.EAPGPNGATEEDGIPSK#.V	5.62	1.87	3.01	0.33
P49586_PCY1A_MOUSE	Pcyt1a	Choline-phosphate cytid	R.EFIGSFLEM*FGPEGALK#.H	11.36	6.78	1.67	0.60
P49586_PCY1A_MOUSE	Pcyt1a	Choline-phosphate cytid	R.TEGISTSDIITR@.I	35.30	11.91	2.96	0.34
Q8VE70_PDC10_MOUSE	Pdcd10	Programmed cell death p	K.IPDEINDR.V	33.24	16.14	2.06	0.49
Q8VE70_PDC10_MOUSE	Pdcd10	Programmed cell death p	K.SFSDTLK#.T	19.51	8.23	2.37	0.42
Q8VE70_PDC10_MOUSE	Pdcd10	Programmed cell death p	K.SVEVNFTESLLR@.M	13.87	6.71	2.07	0.48
Q8VE70_PDC10_MOUSE	Pdcd10	Programmed cell death p	R.VNLSAAQTLR@.A	37.26	17.08	2.18	0.46
Q8VE70_PDC10_MOUSE	Pdcd10	Programmed cell death p	K.IPDEINDR@.V	12.51	5.13	2.44	0.41
Q8VE70_PDC10_MOUSE	Pdcd10	Programmed cell death p	K.SVEVNFTESLLR@.M	8.36	5.42	1.54	0.65
Q8VE70_PDC10_MOUSE	Pdcd10	Programmed cell death p	R.VNLSAAQTLR@.A	10.93	1.49	7.33	0.14
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.AIFENTLSTYPK#.R	28.48	11.09	2.57	0.39
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.ALEYVEAK#.S	18.49	9.39	1.97	0.51
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.AVQYNEPLK#.V	21.53	10.18	2.12	0.47
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.ER@QESESEQELVNK#.R	9.51	6.09	1.56	0.64
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.FAQLEFQLGDVER@.A	23.75	14.41	1.65	0.61
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.FYNDVQGLVPK#.H	16.08	7.90	2.04	0.49
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.GLTVSFPFGK#.I	24.22	14.05	1.72	0.58
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.IEDPEINSIEDVK#.E	7.16	3.10	2.31	0.43
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.ILDDVPVGTSPTTTLK#.A	50.28	25.56	1.97	0.51
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.IPLLLTSLSFK#.V	14.66	8.29	1.77	0.57
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.K#PALVSTVEGGQDPK#.S	26.48	10.79	2.45	0.41
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.LEEGEVAM*GR@.V	16.54	7.04	2.35	0.43
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.LNEQVAQEEPLEDLLR.L	11.72	4.62	2.53	0.39
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.LPELFSPGM*LVR.C	6.49	5.21	1.25	0.80
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.NLIELSLLPSDTGR@PDVFSPAPEPK#.Q	24.43	19.05	1.28	0.78
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.SGAAEEDDSGVEVYYR@.E	6.05	1.64	3.70	0.27
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.SIIAAPFLR@.Y	32.33	13.91	2.32	0.43
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.SSQQVVEQDNLFDVSTEEGPIK#R@.K	20.45	10.20	2.01	0.50
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.TTEPGVTGLILAVEGPASK#.R	23.77	11.92	1.99	0.50
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	K.VFLHLADIYTK#.S	38.90	15.62	2.49	0.40
Q6NS46_RRP5_MOUSE	Pdcd11	Protein RRP5 homolog O	R.VLALSLR@.S	34.82	20.10	1.73	0.58
P46718_PDCD2_MOUSE	Pdcd2	Programmed cell death p	K.IALEPEQILR@.Y	13.60	10.24	1.33	0.75
Q61823_PDCD4_MOUSE	Pdcd4	Programmed cell death p	R.APQLVGQFIAR@.A	24.84	3.80	6.53	0.15
Q61823_PDCD4_MOUSE	Pdcd4	Programmed cell death p	K.SGVPVLAVSLALEGK#.A	14.28	1.19	11.97	0.08
Q61823_PDCD4_MOUSE	Pdcd4	Programmed cell death p	R.APQLVGQFIAR@.A	12.86	2.55	5.05	0.20
Q61823_PDCD4_MOUSE	Pdcd4	Programmed cell death p	K.SGVPVLAVSLALEGK#.A	10.65	1.78	5.97	0.17
P12815_PDCD6_MOUSE	Pdcd6	Programmed cell death p	K.AGVNFSEFTGVWK#.Y	13.90	5.13	2.71	0.37
P12815_PDCD6_MOUSE	Pdcd6	Programmed cell death p	K.YITDWQNVFR@.T	14.02	7.20	1.95	0.51
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.ATLVK#PTPVNVPVSQK#.F	20.71	10.06	2.06	0.49

Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.ELPELLQR@.N	14.08	8.71	1.62	0.62
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.FLTALAQDGVINEEALSVTELDR@.I	11.25	8.43	1.33	0.75
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.LANQAADYFGDAFK#.Q	10.62	5.44	1.95	0.51
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	R.LLDEEEATDNDLR@.A	21.83	14.40	1.52	0.66
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.NIQVSHQEFSK#.M	7.67	4.11	1.87	0.54
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.STSVVEQGGIQTVDQLIK#.E	10.41	5.07	2.06	0.49
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.TM*QGSEVVSVLK#.S	12.36	9.16	1.35	0.74
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.FLTALAQDGVINEEALSVTELDR@.I	13.17	12.75	1.03	0.97
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.FYNELTEILVR@.F	142.91	44.39	3.22	0.31
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	R.LLDEEEATDNDLR@.A	10.49	4.84	2.17	0.46
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.STSVVEQGGIQTVDQLIK#.E	9.38	3.54	2.65	0.38
Q9WU78_PDC6I_MOUSE	Pdcd6ip	Programmed cell death 6	K.TM*QGSEVVSVLK#.S	7.93	3.09	2.57	0.39
Q8BVF2_PDCL3_MOUSE	Pdcl3	Phosducin-like protein 3	K.ELEEEEAEK#EEQLLQQSVVK#.T	8.91	3.98	2.24	0.45
Q8BVF2_PDCL3_MOUSE	Pdcl3	Phosducin-like protein 3	K.ESLK#ELEEEEAEK#EEQLLQQSVVK#.T	20.38	9.13	2.23	0.45
Q8BVF2_PDCL3_MOUSE	Pdcl3	Phosducin-like protein 3	K.FGEVLEISGK#.D	12.44	7.12	1.75	0.57
Q8BVF2_PDCL3_MOUSE	Pdcl3	Phosducin-like protein 3	R.NLPTVFVYR@.E	25.63	16.17	1.58	0.63
B2KF84_B2KF84_MOUSE	Pde4d	cAMP-specific 3',5'-cyclic	K.ITTCNIGDEENINDGR.A	3.48	8.30	0.42	2.39
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.ALEQFLQEYFDGNLK.R	16.00	27.39	0.58	1.71
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.ALEQFLQEYFDGNLK#R@.Y	59.65	92.57	0.64	1.55
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.DGEEAGAYDGPR.T	17.50	28.88	0.61	1.65
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.DLLTAYYDVDYEK.N	43.97	79.62	0.55	1.81
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.ELNDFISYLQR.E	37.53	61.07	0.61	1.63
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.FISDKDASVVGFFR.D	46.95	90.97	0.52	1.94
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.FVM*QEEFSR.D	46.91	66.99	0.70	1.43
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.FVMQEEFSR.D	8.47	13.37	0.63	1.58
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.IFRDGEEAGAYDGPR.T	27.22	41.60	0.65	1.53
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.KTFSHELSDFGLESTTGEVPVVAIR.T	6.24	10.50	0.59	1.68
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.LAPEYEAAATR.L	73.70	128.51	0.57	1.74
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.LKGIVPLAK.V	6.73	10.25	0.66	1.52
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.LNFAVASR@.K	39.69	63.39	0.63	1.60
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.LSK#DPNIVIAK#.M	49.23	113.26	0.43	2.30
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.M*DATANDVPSPYEVK.G	20.26	30.18	0.67	1.49
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.MDATANDVPSPYEVK.G	4.57	7.24	0.63	1.58
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.TFSHELSDFGLESTTGEVPVVAIR.T	20.09	42.53	0.47	2.12
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.YGVSGYPTLK.I	47.81	80.82	0.59	1.69
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.ALEQFLQEYFDGNLK.R	6.62	8.88	0.75	1.34
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.ALEQFLQEYFDGNLK.R	5.94	6.76	0.88	1.14
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.DLLTAYYDVDYEK.N	22.54	28.76	0.78	1.28
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.ELNDFISYLQR.E	39.11	45.41	0.86	1.16
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.FAHTNIESLVK.E	23.37	28.40	0.82	1.22
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.FISDK#DASVVGFFR@.D	39.89	46.42	0.86	1.16
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.FVM*QEEFSR.D	24.15	31.47	0.77	1.30
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.IFRDGEEAGAYDGPR.T	16.04	16.84	0.95	1.05
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.K#TFSHELSDFGLESTTGEVPVVAIR@.T	4.74	4.58	1.03	0.97
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.LSK#DPNIVIAK#.M	34.69	35.40	0.98	1.02
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.M*DATANDVPSPYEVK.G	13.62	15.04	0.91	1.10
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.MDATANDVPSPYEVK.G	3.12	5.43	0.58	1.74
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.YGVSGYPTLK#.I	23.85	34.56	0.69	1.45
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.ELNDFISYLQR@.E	16.47	9.96	1.65	0.60
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.FISDK#DASVVGFFR@.D	23.74	13.35	1.78	0.56
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.FVM*QEEFSR@.D	11.94	8.87	1.35	0.74
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	R.LAPEYEAAATR@.L	28.26	11.47	2.46	0.41
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.M*DATANDVPSPYEVK#.G	9.46	6.71	1.41	0.71
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.SEPIPESNEGPVK#.V	23.11	12.52	1.85	0.54
P27773_PDIA3_MOUSE	Pdia3	Protein disulfide-isomera	K.TFSHELSDFGLESTTGEVPVVAIR@.T	12.89	8.80	1.46	0.68
P08003_PDIA4_MOUSE	Pdia4	Protein disulfide-isomera	K.FAM*EPEEFDSDTLR.E	5.05	5.61	0.90	1.11
P08003_PDIA4_MOUSE	Pdia4	Protein disulfide-isomera	K.M*DATANDITNDQYK.V	2.47	4.37	0.56	1.77
P08003_PDIA4_MOUSE	Pdia4	Protein disulfide-isomera	K.VDATEQTDLAK.R	7.57	27.94	0.27	3.69
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.AATALK#DVVK#.V	44.21	27.48	1.61	0.62
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.DVVELTDDTFDK#.N	12.68	6.69	1.89	0.53
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	R.EPWDGKDGELPVEDDIDLSDVELDDLEK.D	6.12	4.61	1.33	0.75
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	R.EPWDGKDGELPVEDDIDLSDVELDDLEKDEL.-	26.61	17.06	1.56	0.64
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.GESPVDYDGGR@.T	122.03	73.14	1.67	0.60
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.GSFSEQGINEFLR@.E	183.09	89.82	2.04	0.49
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	R.GSTAPVGGGSFPTITPR@.E	179.83	93.76	1.92	0.52
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.IFQK#GESPVDYDGGR@.T	35.29	15.02	2.35	0.43
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.LAAVDATM*NQVLASR@.Y	111.54	58.30	1.91	0.52
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.LAAVDATMNQVLASR@.Y	44.41	19.04	2.33	0.43
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.NLEPEWAAAATEVK#.E	57.97	38.73	1.50	0.67
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	R.NSYLEVLLK#.L	137.77	79.71	1.73	0.58
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	R.TGEAIVDAALSALR@.Q	273.93	132.83	2.06	0.48
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	R.TGEAIVDAALSALR@.Q	111.08	56.86	1.95	0.51
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.VGAVNADK#HQSLGGQYGVQGFPTIK#.I	26.06	15.93	1.64	0.61
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	R.GSTAPVGGGSFPTITPR@.E	10.47	8.31	1.26	0.79
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	K.LAAVDATM*NQVLASR@.Y	4.62	3.50	1.32	0.76
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	R.NSYLEVLLK#.L	7.93	4.98	1.59	0.63
Q3TML0_Q3TML0_MOUSE	Pdia6	Protein disulfide-isomera	R.TGEAIVDAALSALR@.Q	4.84	3.57	1.35	0.74
O70400_PDLI1_MOUSE	Pdlim1	PDZ and LIM domain pro	R.SAM*PFTASPAPSTR@.V	8.66	10.09	0.86	1.16
O70400_PDLI1_MOUSE	Pdlim1	PDZ and LIM domain pro	R.VTPPEGYDVVTVFR@E.-	37.16	20.84	1.78	0.56
Q8R1G6_PDLI2_MOUSE	Pdlim2	PDZ and LIM domain pro	R.FSSLDLEEDSEVFK#.M	10.87	3.98	2.73	0.37
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.DFSAPLTISR.V	42.07	13.71	3.07	0.33
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.EPAEPTASEPK#.Q	4.07	3.36	1.21	0.83
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.GPSPWGFR@.L	24.59	8.73	2.82	0.36
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.GYFFLDER@.L	21.87	6.36	3.44	0.29
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.M*LR@EPAEPTASEPK#.Q	34.41	12.53	2.75	0.36
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.SGLGSPYGQPPR@.L	31.81	15.92	2.00	0.50
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.SSVSGISLEDNR@.S	67.98	20.52	3.31	0.30
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.VDLGSEVYR@.M	78.70	37.55	2.10	0.48
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.VK#PPEGYDVVAVYPNAK#.V	30.47	11.99	2.54	0.39
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.YLQGM*LEAGEGGDRPGSGGPR.N	34.66	11.95	2.90	0.34
P70271_PDLI4_MOUSE	Pdlim4	PDZ and LIM domain pro	R.VDLGSEVYR@.M	8.35	7.81	1.07	0.93
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.GPFLVALGK#.S	73.65	39.61	1.86	0.54
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.ILGEVINALK#.Q	39.07	13.58	2.88	0.35
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.K#ANSTQEPSQQPASSGASPLSASEGPESPGSSR@PSVAGLR@.S	17.49	10.02	1.75	0.57
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.K#ILGEVINALK#.Q	6.27	3.56	1.76	0.57
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.NTM*AYIGFVEEK#.G	17.25	9.79	1.76	0.57
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.SPSWQR@PNQAAPSTGR@.I	32.44	10.58	3.07	0.33
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.SSGTGASVGPPQPSDQDTLVQR@.A	17.25	9.07	1.90	0.53
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.GPFLVALGK#.S	31.37	21.65	1.45	0.69
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.ILGEVINALK#.Q	13.46	9.07	1.48	0.67
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.NTM*AYIGFVEEK#.G	6.89	4.46	1.54	0.65
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.SSGTGASVGPPQPSDQDTLVQR.A	4.29	5.01	0.86	1.17
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.EVVK#PVPITSPAVSK#.V	33.06	8.98	3.68	0.27

Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.GPFLVALGK#.S	57.28	20.76	2.76	0.36
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.IGDVVLSIDGISAQGM*THLEAQNK#.I	14.28	2.53	5.65	0.18
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.IGDVVLSIDGISAQGMTHLEAQNK#.I	5.33	2.68	1.99	0.50
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.KANSTQEPSQQPASSGASPLSASEGPESPGSSRPSVAGLR.S	17.28	5.35	3.23	0.31
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.K#ILGEVINALK#.Q	9.39	2.09	4.50	0.22
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.SPSWQR@PNQAAPSTGR@.I	13.34	4.08	3.27	0.31
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.SSGTGASVGPPQPSDQDTLVQR@.A	13.90	3.36	4.14	0.24
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.GPFLVALGK#.S	40.31	13.59	2.96	0.34
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	R.ILAQITGTEHLTESENDNTK#.K	21.77	4.76	4.58	0.22
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.ILGEVINALK#.Q	25.77	9.02	2.86	0.35
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.K#ANSTQEPSQQPASSGASPLSASEGPESPGSSR@PSVAGLR@.S	11.62	3.43	3.39	0.30
Q8CI51_PDLI5_MOUSE	Pdlim5	PDZ and LIM domain pro	K.NTM*AYIGFVEEK#.G	10.86	3.46	3.14	0.32
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.DFNVPLSISR@.L	47.62	30.74	1.55	0.65
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	R.HSQPATPTPLQNR@.T	10.98	8.77	1.25	0.80
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.ITGEIM*HALK#.M	10.73	5.56	1.93	0.52
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	R.LSLGLSR@.A	55.14	34.72	1.59	0.63
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	R.TSIVQAAAGGGTGGGSNNGK#.T	9.67	5.43	1.78	0.56
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.VLEEGGFFEEK#.G	93.59	47.13	1.99	0.50
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.VVLEGPAPWGFR@.L	63.79	31.15	2.05	0.49
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	R.YAPDK#TSTVLTR@.H	11.11	5.34	2.08	0.48
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	R.YTFAPSASLNK#.T	72.29	36.71	1.97	0.51
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.VLEEGGFFEEK#.G	15.25	16.48	0.93	1.08
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.AAQAGVAVGDWVLNIDGENAGSLTHIEAQNK#.I	8.66	3.27	2.65	0.38
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	R.HSQPATPTPLQNR@.T	6.80	3.69	1.84	0.54
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	R.LSLGLSR@.A	28.08	11.72	2.40	0.42
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.VLEEGGFFEEK#.G	45.48	19.71	2.31	0.43
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.VVLEGPAPWGFR@.L	29.95	12.41	2.41	0.41
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	R.YTFAPSASLNK#.T	29.61	11.36	2.61	0.38
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	R.LSLGLSR@.A	20.94	10.13	2.07	0.48
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.TAR@PFGAPPPTDSTLR@.Q	11.37	6.12	1.86	0.54
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.VLEEGGFFEEK#.G	48.23	17.05	2.83	0.35
Q3TJD7_PDLI7_MOUSE	Pdlim7	PDZ and LIM domain pro	K.VVLEGPAPWGFR@.L	22.32	9.29	2.40	0.42
Q62011_PDPN_MOUSE	Pdpn	Podoplanin OS=Mus mus	R.EHESTTTVK#VVTSHSVDK.K	16.28	43.81	0.37	2.69
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	R.DLALVNDQLLGFVR@.E	18.13	6.72	2.70	0.37
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	K.LWSPDEEVSPEVLAK#.V	4.49	2.49	1.80	0.55
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	K.SIEGTADDEEEGVSPDSAIR@.S	7.23	4.26	1.70	0.59
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	R.DLALVNDQLLGFVR@.E	40.02	18.05	2.22	0.45
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	K.LWSPDEEVSPEVLAK#.V	7.97	3.27	2.44	0.41
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	K.NK#EINSDQSTQGNISSDR@.G	10.20	2.34	4.36	0.23
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	R.SGLELLK#.V	17.04	5.66	3.01	0.33
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	R.SR@EQSSEASETGVSENEENPVR@.I	3.97	2.78	1.43	0.70
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	K.SVVANFIVK#.D	18.40	5.24	3.51	0.28
Q6A026_PDS5A_MOUSE	Pds5a	Sister chromatid cohesio	K.SYISEETR@.V	6.90	3.05	2.26	0.44
Q4VA53_PDS5B_MOUSE	Pds5b	Sister chromatid cohesio	K.SIDGTADDEDEGVPTDQAIR@.A	7.99	6.60	1.21	0.83
Q4VA53_PDS5B_MOUSE	Pds5b	Sister chromatid cohesio	K.YSLQSAAGK#.D	12.35	5.76	2.14	0.47
Q99K01_PDXD1_MOUSE	Pdxdc1	Pyridoxal-dependent de	K.ILVEDELSSPVVVFR@.F	8.29	5.59	1.48	0.67
Q99K01_PDXD1_MOUSE	Pdxdc1	Pyridoxal-dependent de	R.SFNLTAGSLESTEYTYVHK#.V	7.86	4.45	1.77	0.57
Q99K01_PDXD1_MOUSE	Pdxdc1	Pyridoxal-dependent de	K.ILVEDELSSPVVVFR@.F	5.96	2.86	2.09	0.48
Q9CZG9_PDZ11_MOUSE	Pdzd11	PDZ domain-containing	R.AGLQEGDQVLAVNDVDFQDIEHSK#.A	5.62	6.92	0.81	1.23
Q9CZG9_PDZ11_MOUSE	Pdzd11	PDZ domain-containing	K.ASQLGIFISK#.V	8.25	3.18	2.60	0.38
B9EJ80_B9EJ80_MOUSE	Pdzd8	PDZ domain containing	R.DVFLGDTVPFIK#.T	11.33	4.82	2.35	0.43
Q8BFY6_PEF1_MOUSE	Pef1	Peflin OS=Mus musculus	R.IDVAGFSALWK#.F	9.23	4.91	1.88	0.53
Q8BFY6_PEF1_MOUSE	Pef1	Peflin OS=Mus musculus	R.SGSISSTELQQALSQM*GYNLSPQFTQLLVSR@.Y	5.00	2.27	2.21	0.45
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	R.FGALISR@.L	18.61	4.73	3.94	0.25
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	K.LASFFLSR@.L	11.07	6.11	1.81	0.55
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	K.LDM*GEALAPPSQR@.K	14.86	6.61	2.25	0.44
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	R.LLPQVLNAWSTGR@.D	10.94	5.82	1.88	0.53
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	K.NINLLGDGPLR.L	21.51	10.76	2.00	0.50
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	R.SIQQVLQSQDSPSTM*ELAVAVLR@.D	7.88	6.43	1.23	0.82
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	R.FGALISR@.L	45.19	13.17	3.43	0.29
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	R.HASQLPTLFR@.D	23.15	11.79	1.96	0.51
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	K.LASFFLSR@.L	28.83	10.16	2.84	0.35
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	R.LLPQVLNAWSTGR@.D	32.05	15.00	2.14	0.47
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	R.LPSLGAGFSQGLK#.H	32.03	8.73	3.67	0.27
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	K.NINLLGDGPLR@.L	52.67	18.26	2.88	0.35
Q9DBD5_PELP1_MOUSE	Pelp1	Proline-, glutamic acid- a	R.SIQQVLQSQDSPSTM*ELAVAVLR@.D	20.96	7.59	2.76	0.36
Q8VCI5_PEX19_MOUSE	Pex19	Peroxisomal biogenesis f	K.FFQELFDSELASQATAEFEK#.A	5.33	2.34	2.27	0.44
O09012_PEX5_MOUSE	Pex5	Peroxisomal targeting si	K.IAALQVEFER@.A	12.56	5.33	2.36	0.42
O09012_PEX5_MOUSE	Pex5	Peroxisomal targeting si	R.ILGSLLSDSLFLEVK#.D	7.01	1.68	4.17	0.24
O70591_PFD2_MOUSE	Pfdn2	Prefoldin subunit 2 OS=	K.GAVSAEQVIAGFNR.L	6.65	4.42	1.50	0.66
O70591_PFD2_MOUSE	Pfdn2	Prefoldin subunit 2 OS=	K.IIETLSQQLQAK#.G	3.65	3.22	1.13	0.88
Q3UWL8_Q3UWL8_MOUSE	Pfdn4	Protein Pfdn4 OS=Mus m	K.AAAEDVNVTFEDQQK#.I	8.41	5.03	1.67	0.60
Q3UWL8_Q3UWL8_MOUSE	Pfdn4	Protein Pfdn4 OS=Mus m	K.TLQEEIDALESR@.V	8.70	5.83	1.49	0.67
Q9WU28_PFD5_MOUSE	Pfdn5	Prefoldin subunit 5 OS=	K.IQQLTALGAAQATVK#.A	5.66	2.64	2.14	0.47
Q9WU28_PFD5_MOUSE	Pfdn5	Prefoldin subunit 5 OS=	K.NQLDQEVEFLSTSIAQLK#.V	4.16	3.52	1.18	0.84
P12382_PFKAL_MOUSE	Pfkl	ATP-dependent 6-phosp	K.AIGVLTSGGDAQGM*NAAVR@.A	6.05	3.47	1.74	0.57
P12382_PFKAL_MOUSE	Pfkl	ATP-dependent 6-phosp	K.AIGVLTSGGDAQGM*NAAVR@.A	5.16	5.66	0.91	1.10
Q8BX10_PGAM5_MOUSE	Pgam5	Serine/threonine-protei	R.AVETTDIISK#.H	29.44	15.60	1.89	0.53
Q8BX10_PGAM5_MOUSE	Pgam5	Serine/threonine-protei	R.EPLSLINLK#.K	19.28	9.92	1.94	0.51
Q8BX10_PGAM5_MOUSE	Pgam5	Serine/threonine-protei	R.NVESGEDELTSR@.L	36.96	24.12	1.53	0.65
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	K.FYGPEGPYGVFAGR@.D	12.13	3.35	3.62	0.28
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	R.DFTPAELR.R	72.29	37.06	1.95	0.51
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	K.EGEEPTVYSDDEEPK#DETAR@.K	7.48	3.09	2.42	0.41
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	R.FDGVQDPR@.I	31.43	18.79	1.67	0.60
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	K.FYGPEGPYGVFAGR.D	90.68	38.70	2.34	0.43
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	R.GDQPGASGDNDDDEPPPLPR@.L	12.20	5.79	2.11	0.47
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	R.GDQPGASGDNDDDEPPPLPR@.L	11.38	7.05	1.61	0.62
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	K.IVR@GDQPGASGDNDDDEPPPLPR@.L	25.97	12.41	2.09	0.48
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	R.K#FYGPEGPYGVFAGR@.D	63.48	28.25	2.25	0.45
O55022_PGRC1_MOUSE	Pgrmc1	Membrane-associated pr	R.R@DFTPAELR@.R	12.33	5.47	2.25	0.44
Q80UU9_PGRC2_MOUSE	Pgrmc2	Membrane-associated pr	K.LSTLGSGGESGGDGSPGGAGATAAR@.S	11.75	7.12	1.65	0.61
Q80UU9_PGRC2_MOUSE	Pgrmc2	Membrane-associated pr	R.DFSLEQLR@.Q	32.48	13.50	2.41	0.42
Q80UU9_PGRC2_MOUSE	Pgrmc2	Membrane-associated pr	K.FYGPAGPYGIFAGR@.D	32.14	16.48	1.95	0.51
Q80UU9_PGRC2_MOUSE	Pgrmc2	Membrane-associated pr	K.LSTLGSGGESGGDGSPGGAGATAAR.S	11.91	3.28	3.63	0.28
Q9JJT9_PHAX_MOUSE	Phax	Phosphorylated adapter	R.TPGGVFLNLLK#.N	12.39	5.61	2.21	0.45
P67778_PHB_MOUSE	Phb	Prohibitin OS=Mus musc	K.AAELIANSLATAGDGLIELR@.K	4.07	3.32	1.22	0.82
P67778_PHB_MOUSE	Phb	Prohibitin OS=Mus musc	K.EFTEAVEAK#.Q	12.65	13.93	0.91	1.10
P67778_PHB_MOUSE	Phb	Prohibitin OS=Mus musc	R.FDAGELITQR@.E	12.52	18.88	0.66	1.51
P67778_PHB_MOUSE	Phb	Prohibitin OS=Mus musc	R.ILFRPVASQLPR.I	19.93	19.24	1.04	0.97
P67778_PHB_MOUSE	Phb	Prohibitin OS=Mus musc	R.IYTSIGEDYDER@.V	9.11	9.30	0.98	1.02
P67778_PHB_MOUSE	Phb	Prohibitin OS=Mus musc	R.VLPSITTEILK.S	12.87	14.69	0.88	1.14
O35129_PHB2_MOUSE	Phb2	Prohibitin-2 OS=Mus mu	K.FNASQLITQR@.A	6.63	7.66	0.87	1.16
O35129_PHB2_MOUSE	Phb2	Prohibitin-2 OS=Mus mu	R.IGGVQQDTILAEGLHFR@.I	17.20	16.03	1.07	0.93

O35129_PHB2_MOUSE	Phb2	Prohibitin-2 OS=Mus mu	R.IPWFQYPIIYDIR@.A	16.62	8.02	2.07	0.48
O35129_PHB2_MOUSE	Phb2	Prohibitin-2 OS=Mus mu	K.IVQAEGEAEAAK#.M	38.84	36.36	1.07	0.94
O35129_PHB2_MOUSE	Phb2	Prohibitin-2 OS=Mus mu	R.IYLTADNLVLNLQDESFTR.G	7.55	5.45	1.39	0.72
O35129_PHB2_MOUSE	Phb2	Prohibitin-2 OS=Mus mu	R.LGLDYEER@.V	11.20	10.62	1.05	0.95
O35129_PHB2_MOUSE	Phb2	Prohibitin-2 OS=Mus mu	K.LLLGAGAVAYGVR@.E	11.42	12.86	0.89	1.13
O35129_PHB2_MOUSE	Phb2	Prohibitin-2 OS=Mus mu	R.VLSRPNAQELPSM*YQR.L	15.78	12.33	1.28	0.78
Q64028_PHC1_MOUSE	Phc1	Polyhomeotic-like protei	R.K#GTGVVQPLPAAQTVTVSQGSQTEAESAAAK#.K	6.30	2.35	2.68	0.37
Q9QWH1_PHC2_MOUSE	Phc2	Polyhomeotic-like protei	R.AQEIDGQALLLLK#.E	31.96	11.35	2.82	0.35
Q9QWH1_PHC2_MOUSE	Phc2	Polyhomeotic-like protei	R.DLVGVGHHFLPSEPTK#.W	36.77	12.49	2.94	0.34
Q9QWH1_PHC2_MOUSE	Phc2	Polyhomeotic-like protei	R.DLVGVGHHFLPSEPTK#WNVEDVYEFIR@.S	9.90	3.86	2.57	0.39
Q9QWH1_PHC2_MOUSE	Phc2	Polyhomeotic-like protei	R.SSLLVGNLK#.K	24.53	13.82	1.77	0.56
Q9QWH1_PHC2_MOUSE	Phc2	Polyhomeotic-like protei	R.VDFAYK#.F	32.13	10.75	2.99	0.33
Q9QWH1_PHC2_MOUSE	Phc2	Polyhomeotic-like protei	K.WNVEDVYEFIR@.S	38.66	15.20	2.54	0.39
Q9QWH1_PHC2_MOUSE	Phc2	Polyhomeotic-like protei	K.YAQGFLPEK#PPQQDHTTTTDSEM*EEPYLQESK#.E	4.15	2.65	1.57	0.64
Q8CHP6_PHC3_MOUSE	Phc3	Polyhomeotic-like protei	R.GEDLTSEHPLLEQVELPAVASVSASVIK#.S	5.57	1.73	3.22	0.31
Q9D8M7_PHF10_MOUSE	Phf10	PHD finger protein 10 OS	R.AYFDLQTHVIQVPQGK#.Y	23.99	2.66	9.03	0.11
Q9D8M7_PHF10_MOUSE	Phf10	PHD finger protein 10 OS	K.HAEYSVILQEK#.E	9.78	7.34	1.33	0.75
Q9D8M7_PHF10_MOUSE	Phf10	PHD finger protein 10 OS	R.SDEVIDLM*IK#.E	9.97	2.62	3.80	0.26
Q9D8M7_PHF10_MOUSE	Phf10	PHD finger protein 10 OS	K.VSSYPVALIPGQFQEYYK#.R	10.77	2.90	3.71	0.27
Q9D8M7_PHF10_MOUSE	Phf10	PHD finger protein 10 OS	K.AAEFNSNLNR@.E	13.38	2.92	4.58	0.22
Q9D8M7_PHF10_MOUSE	Phf10	PHD finger protein 10 OS	K.HAEYSVILQEK#.E	12.64	3.05	4.15	0.24
Q9D8M7_PHF10_MOUSE	Phf10	PHD finger protein 10 OS	K.VSSYPVALIPGQFQEYYK#.R	8.46	3.82	2.21	0.45
A6H5X4_PHF11_MOUSE	Phf11	PHD finger protein 11 OS	K.KDQAILQVDGNHGTYK.L	11.25	17.23	0.65	1.53
A6H5X4_PHF11_MOUSE	Phf11	PHD finger protein 11 OS	R.K#FQEVIK#.S	28.02	31.43	0.89	1.12
A6H5X4_PHF11_MOUSE	Phf11	PHD finger protein 11 OS	R.LSSGPPAQPK.T	27.05	57.64	0.47	2.13
A6H5X4_PHF11_MOUSE	Phf11	PHD finger protein 11 OS	R.LSSGPPAQPK.T	7.85	16.71	0.47	2.13
Q9D4H9_PHF14_MOUSE	Phf14	PHD finger protein 14 OS	R.K#AELM*GISTDIFPVDNSDTSSSVDGR@.R	15.28	8.92	1.71	0.58
Q9D4H9_PHF14_MOUSE	Phf14	PHD finger protein 14 OS	K.LNVPAILR@.A	23.44	13.21	1.77	0.56
Q9D4H9_PHF14_MOUSE	Phf14	PHD finger protein 14 OS	K.NSTEEIM*PSDK#.Q	13.33	5.08	2.62	0.38
Q9D4H9_PHF14_MOUSE	Phf14	PHD finger protein 14 OS	R.SEGQGIWALLGR@.I	31.03	21.95	1.41	0.71
Q9D4H9_PHF14_MOUSE	Phf14	PHD finger protein 14 OS	K.LNVPAILR@.A	10.72	5.57	1.93	0.52
Q9WTU0_PHF2_MOUSE	Phf2	Lysine-specific demethyl	R.VASIETGLAAAAAK#.L	7.47	4.03	1.85	0.54
Q9WTU0_PHF2_MOUSE	Phf2	Lysine-specific demethyl	R.VLNVTNLEFSDTR.M	171.56	8.01	21.42	0.05
Q9WTU0_PHF2_MOUSE	Phf2	Lysine-specific demethyl	R.VPGSQLTVGYM*EEHGFTEPILVPK#.K	8.07	4.53	1.78	0.56
Q9WTU0_PHF2_MOUSE	Phf2	Lysine-specific demethyl	R.VPGSQLTVGYM*EEHGFTEPILVPK#.K	5.48	3.99	1.37	0.73
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	R.APQFINLK#.R	9.74	4.62	2.11	0.47
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.AYPVSGSPEYLTEDLPDSIQVGGR@.I	10.06	3.93	2.56	0.39
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.ELFSFFR@.D	13.85	3.78	3.67	0.27
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	R.LLLQDQENSLQDNR@.T	7.30	2.42	3.02	0.33
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	R.M*APPIDDLSPK#.T	10.07	3.73	2.70	0.37
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	R.NK#PSQPLQEDLPTAAEPLM*EVTK#.Q	5.74	5.42	1.06	0.95
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.NSGEETSSVGSSSISPGPLASLSLR@.G	3.15	1.89	1.67	0.60
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	R.SFSLDEPPLFIPDNIATVK#.K	8.20	3.24	2.53	0.40
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.STFSPTPR@PEM*PGTVEVESTFLAR@.L	10.09	4.27	2.36	0.42
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	R.APQFINLK#.R	12.31	4.72	2.61	0.38
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.AYPVSGSPEYLTEDLPDSIQVGGR@.I	8.46	4.04	2.09	0.48
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.EGSDQTTSIESK#.Y	11.01	4.74	2.32	0.43
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.ELFSFFR@.D	16.11	4.30	3.75	0.27
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.ESTALASTGER@.V	21.28	5.02	4.23	0.24
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.GGPNVHPPAATSK#PSADQIR@.Q	4.64	5.80	0.80	1.25
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	R.LLLQDQENSLQDNR@.T	11.29	4.77	2.36	0.42
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	R.NK#PSQPLQEDLPTAAEPLM*EVTK#.Q	12.04	3.48	3.46	0.29
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.NSGEETSSVGSSSISPGPLASLSLR@.G	5.66	2.39	2.36	0.42
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.STFSPTPRPEM*PGTVEVESTFLAR.L	13.95	4.48	3.11	0.32
B2RQG2_B2RQG2_MOUSE	Phf3	PHD finger protein 3 OS=	K.TDILDTEIFEAQAPIEAHSEDK#R@.M	8.54	2.11	4.05	0.25
P83870_PHF5A_MOUSE	Phf5a	PHD finger-like domain-c	K.IVNLGSSK.T	106.75	70.00	1.52	0.66
P83870_PHF5A_MOUSE	Phf5a	PHD finger-like domain-c	K.TDLFYER@.K	85.92	63.89	1.34	0.74
Q9D4J7_PHF6_MOUSE	Phf6	PHD finger protein 6 OS=	R.AEFGDFDIK#.T	40.88	21.05	1.94	0.51
Q9D4J7_PHF6_MOUSE	Phf6	PHD finger protein 6 OS=	K.TAHNSEADLEESFNEHELEPSSPK#.T	10.32	7.71	1.34	0.75
Q9D4J7_PHF6_MOUSE	Phf6	PHD finger protein 6 OS=	R.VAIDQQLTQQQLNGN.-	9.48	9.48	1.00	1.00
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	R.AGTGVDNVDLEAATR@.K	237.15	92.11	2.57	0.39
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	R.GQPLLVFR@.A	144.69	65.27	2.22	0.45
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.GTIQVVTQGTSLK#.N	233.20	88.10	2.65	0.38
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.ILQDGGLQVVEK#.Q	209.54	95.15	2.20	0.45
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.QADVNLVNAK#.L	117.31	52.96	2.22	0.45
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	R.QIPQATASM*K#.D	49.54	21.64	2.29	0.44
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.TLGILGLGR@.I	276.28	124.65	2.22	0.45
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.VTADVINAAEK#.L	314.97	128.42	2.45	0.41
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	R.AGTGVDNVDLEAATR@.K	44.31	14.75	3.00	0.33
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	R.GGIVDEGALLR@.A	45.00	1.32	34.14	0.03
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.GTIQVVTQGTSLK#.N	53.12	12.48	4.26	0.23
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.ILQDGGLQVVEK#.Q	31.62	13.36	2.37	0.42
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.QADVNLVNAK#.L	30.12	7.29	4.13	0.24
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.TLGILGLGR.I	42.26	14.66	2.88	0.35
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.VTADVINAAEK#.L	41.86	14.60	2.87	0.35
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	R.AGTGVDNVDLEAATR@.K	43.48	7.50	5.80	0.17
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	R.GGIVDEGALLR@.A	64.47	13.28	4.85	0.21
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	R.GQPLLVFR@.A	33.32	5.44	6.12	0.16
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.GTIQVVTQGTSLK#.N	52.53	11.18	4.70	0.21
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.ILQDGGLQVVEK#.Q	31.84	9.08	3.51	0.29
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.QADVNLVNAK#.L	23.47	2.83	8.29	0.12
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.TLGILGLGR@.I	47.44	8.36	5.68	0.18
Q61753_SERA_MOUSE	Phgdh	D-3-phosphoglycerate de	K.VTADVINAAEK#.L	49.46	12.11	4.09	0.24
Q8VDD9_PHIP_MOUSE	Phip	PH-interacting protein O	K.SEVSTSPFSIPTR.S	5.42	11.69	0.46	2.16
Q8VDD9_PHIP_MOUSE	Phip	PH-interacting protein O	R.VAVDPVVTEQPSTSSATK.A	4.29	6.36	0.67	1.48
Q8VDD9_PHIP_MOUSE	Phip	PH-interacting protein O	R.YHDM*PDVIDFLVLR.Q	7.79	14.45	0.54	1.85
Q8VDD9_PHIP_MOUSE	Phip	PH-interacting protein O	R.DIIDTPM*DFATVR.E	5.08	6.31	0.80	1.24
Q8VDD9_PHIP_MOUSE	Phip	PH-interacting protein O	K.SEVSTSPFSIPTR@.S	12.20	25.49	0.48	2.09
Q8VDD9_PHIP_MOUSE	Phip	PH-interacting protein O	R.VAVDPVVTEQPSTSSATK#.A	10.43	11.71	0.89	1.12
Q8VDD9_PHIP_MOUSE	Phip	PH-interacting protein O	R.VVVPELSAGVASR@.Q	7.69	2.86	2.69	0.37
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.ADGGPETGELPSIGEATAALALAGR@.R	28.30	10.76	2.63	0.38
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.ADGGPETGELPSIGEATAALALAGR.R	6.53	2.50	2.61	0.38
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.AQAVQESER@.L	10.25	6.20	1.65	0.60
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.DK#EADALETETK#.L	4.79	3.21	1.49	0.67
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.DR@DK#EADALETETK#.L	28.52	12.44	2.29	0.44
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.ELAGQGLLR@.S	17.05	4.41	3.86	0.26
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.ELEQQLQEAAR@.E	6.28	3.48	1.81	0.55
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.GLAGAIVVSGR@.C	40.72	9.38	4.34	0.23
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.GPLDLIETGQGLK#.V	14.56	8.08	1.80	0.55
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.HQGEVLAVEEER@.A	30.27	13.15	2.30	0.43
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.HQGEVLAVEEER.A	10.56	4.94	2.14	0.47
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.LAVLDSQAGQIR@.A	47.53	16.89	2.81	0.36
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.LFEDLEFQQLER@.E	39.45	14.33	2.75	0.36

Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.LGGQLPVVAISLSEYPSSGAR@.S	12.95	5.61	2.31	0.43
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.LSPAYSLGSLTGASPR@.Q	20.54	9.32	2.20	0.45
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.LSTAITLLPLEEGR@.T	19.79	4.13	4.79	0.21
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.LVALETGIQK#.D	45.70	16.24	2.81	0.36
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.LYYM*VAPSAEAM*R@.I	7.29	2.77	2.63	0.38
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.NLAATLQDIETK#R@.Q	6.06	1.81	3.36	0.30
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.QLALQQK#.G	20.64	8.73	2.36	0.42
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.TLQPPESPR@.L	9.46	5.17	1.83	0.55
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.VEEER@ELAGQGLLR@.S	36.24	11.16	3.25	0.31
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.WAAHGTSPEDFSLTLGAR@.G	9.53	18.54	0.51	1.94
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.ADGGPETGELPSIGEATAALALAGR@.R	15.94	7.25	2.20	0.45
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.AQAVQESER@.L	5.45	7.04	0.77	1.29
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.GLAGAIVVSGR@.C	17.96	2.84	6.32	0.16
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.LFEDLEFQQLER@.E	19.06	7.89	2.42	0.41
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.LGGQLPVVAISLSEYPSSGAR@.S	11.73	2.93	4.00	0.25
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.LSPAYSLGSLTGASPR@.Q	9.95	4.40	2.26	0.44
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.LSTAITLLPLEEGR@.T	20.77	6.02	3.45	0.29
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.LVALETGIQK#.D	25.12	11.20	2.24	0.45
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	K.NAALQLLQK#.E	10.45	2.96	3.53	0.28
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.SPSPTLGESLAPR@.K	6.23	1.56	3.99	0.25
Q6PDH0_PHLB1_MOUSE	Phldb1	Pleckstrin homology-like	R.VEEER@ELAGQGLLR@.S	15.68	4.76	3.29	0.30
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.SPNPLLTFSVK#.T	15.53	10.38	1.50	0.67
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.ASYSGTSPSHSFISGEPDR@.V	17.85	12.25	1.46	0.69
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.ATNESSYLSILPK#.T	22.99	14.42	1.59	0.63
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.DADLLDVESK#.H	28.09	12.27	2.29	0.44
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.DLPHSLVDSDNYLNFSSLSSGASPYK#.T	24.03	11.20	2.15	0.47
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.EGLYLSDTLPR@.K	30.65	14.08	2.18	0.46
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.GFPINPNTLK#.E	33.77	21.31	1.58	0.63
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.HFEDLEFQQLEHESR@.L	31.33	22.07	1.42	0.70
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.HFEDLEFQQLEHESR@LDEEK#ENLTQQLLR@.E	10.62	4.27	2.49	0.40
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.IKDINDQM*DESSR@.E	2.35	10.91	0.22	4.65
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.IWM*DVIVTGAEGYTHFLL.-	6.85	6.85	1.00	1.00
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.IYYM*VAPSPEAM*R@.I	7.94	4.28	1.86	0.54
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.K#GSLQDVDVAGFGNLGHSASFLAPR@.G	15.59	10.44	1.49	0.67
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.LDEEK#ENLTQQLLR@.E	2.60	2.40	1.08	0.92
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.LDEEK#ENLTQQLLR@.E	41.58	17.77	2.34	0.43
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.LQELYSEQK#.T	30.79	11.27	2.73	0.37
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.LSAGTTVADVQK#.I	17.32	9.91	1.75	0.57
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.M*VILNNLEELEQK#.I	21.97	12.46	1.76	0.57
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.QSSETPQPVLR@.E	30.33	18.00	1.69	0.59
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.SDELLGDLTR.T	30.80	17.17	1.79	0.56
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.SPNPLLTFSVK#.T	31.55	19.17	1.65	0.61
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.TPEDIGEEQR.T	35.08	23.14	1.52	0.66
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.TPEDIGEEQR@TQELAAM*EDAR@.M	10.86	7.54	1.44	0.69
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.TQELAAMEDAR@.M	8.86	4.62	1.92	0.52
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.TQELAAM*EDAR@.M	13.07	7.07	1.85	0.54
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.ASYSGTSPSHSFISGEPDR@.V	15.10	6.27	2.41	0.42
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.DADLLDVESK.H	9.52	9.11	1.04	0.96
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.EGLYLSDTLPR.K	23.34	11.39	2.05	0.49
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.HFEDLEFQQLEHESR@.L	17.42	9.95	1.75	0.57
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.HK#EPASENVSVR@.T	46.33	17.67	2.62	0.38
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.IYYM*VAPSPEAM*R@.I	7.22	5.32	1.36	0.74
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.LDEEKENLTQQLLR.E	33.85	15.36	2.20	0.45
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.LSAGTTVADVQK#.I	7.76	6.76	1.15	0.87
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.SDELLGDLTR@.T	26.73	15.52	1.72	0.58
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.SETAELM*K#EK#.E	5.02	4.00	1.26	0.80
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.SPNPLLTFSVK#.T	29.99	18.67	1.61	0.62
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.TPEDIGEEQR@.T	22.82	16.80	1.36	0.74
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	K.TPEDIGEEQR@TQELAAM*EDAR@.M	7.98	3.67	2.18	0.46
Q8K1N2_PHLB2_MOUSE	Phldb2	Pleckstrin homology-like	R.TQELAAM*EDAR@.M	140.60	85.99	1.64	0.61
Q2TBE6_P4K2A_MOUSE	Pi4k2a	Phosphatidylinositol 4-k	R.LVVLDYIIR@.N	9.81	1.68	5.85	0.17
Q9JM05_PIAS4_MOUSE	Pias4	E3 SUMO-protein ligase F	R.TPLSGPTVDYPVLYGK#.Y	6.37	3.04	2.10	0.48
Q9JM05_PIAS4_MOUSE	Pias4	E3 SUMO-protein ligase F	R.LSVPCR@.A	25.13	9.33	2.69	0.37
Q9JM05_PIAS4_MOUSE	Pias4	E3 SUMO-protein ligase F	R.TPLSGPTVDYPVLYGK#.Y	7.14	2.06	3.46	0.29
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.ITAAQHSVTGSAVSK#.T	26.78	19.53	1.37	0.73
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.LFAAYNEGIINLLEK#.Y	14.17	9.73	1.46	0.69
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.NTLFNLSNFLDK#.S	19.30	12.38	1.56	0.64
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	K.QAALEEEQAR@.L	9.58	5.79	1.65	0.60
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	K.SGLQGYDM*STFIR@.R	7.28	2.96	2.46	0.41
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.TTNSSWVVVFK#.S	9.96	6.83	1.46	0.69
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.ATTLSNAVSSLASTGLSLTK#.V	26.76	99.83	0.27	3.73
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.FIQYLASR@.N	25.76	14.67	1.76	0.57
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.LFAAYNEGIINLLEK#.Y	24.11	11.11	2.17	0.46
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	K.LVSDDLDSSLANLVGNLGIGNGTTK#.N	3.27	2.22	1.47	0.68
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.NTLFNLSNFLDK#.S	35.61	22.95	1.55	0.64
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	K.QAALEEEQAR@.L	19.87	13.16	1.51	0.66
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	K.SGLQGYDM*STFIR@.R	10.76	8.82	1.22	0.82
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	K.STNVAVDSGGFDELGGLLK#PTVASQNQSLPVAK#.L	4.13	1.98	2.08	0.48
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.TTNSSWVVVFK#.S	10.78	6.51	1.66	0.60
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.LFAAYNEGIINLLEK#.Y	7.42	4.94	1.50	0.66
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	R.NTLFNLSNFLDK#.S	19.87	9.47	2.10	0.48
Q7M6Y3_PICAL_MOUSE	Picalm	Phosphatidylinositol-bir	K.SGLQGYDM*STFIR@.R	7.88	2.71	2.91	0.34
Q9CQJ2_PIHD1_MOUSE	Pih1d1	PIH1 domain-containing	R.EGLEDK#YGLQLNPEWR@.M	6.57	5.69	1.16	0.87
Q9CQJ2_PIHD1_MOUSE	Pih1d1	PIH1 domain-containing	R.FQELLLK#.A	24.60	13.11	1.88	0.53
Q9CQJ2_PIHD1_MOUSE	Pih1d1	PIH1 domain-containing	R.SFLGSISQQNIR@.S	20.20	7.80	2.59	0.39
Q61194_P3C2A_MOUSE	Pik3c2a	Phosphatidylinositol 4-p	R.LIESSLGSIATK#.F	7.19	1.31	5.50	0.18
P26450_P85A_MOUSE	Pik3r1	Phosphatidylinositol 3-k	R.VLSEIFSPVLFR@.F	6.22	2.63	2.36	0.42
Q8VD65_PI3R4_MOUSE	Pik3r4	Phosphoinositide 3-kina:	K.GVIDLAALGITGR@.Q	14.53	7.63	1.91	0.52
Q8VD65_PI3R4_MOUSE	Pik3r4	Phosphoinositide 3-kina:	K.VVTLLSDPENIVK#.Q	14.55	5.88	2.48	0.40
Q9QUR7_PIN1_MOUSE	Pin1	Peptidyl-prolyl cis-trans i	R.GQM*QK#PFEDASFALR@.T	40.39	17.29	2.34	0.43
Q9QUR7_PIN1_MOUSE	Pin1	Peptidyl-prolyl cis-trans i	R.TGEM*SGPVFTDSGIHIILR@.T	9.93	6.32	1.57	0.64
Q9CZX5_PINX1_MOUSE	Pinx1	PIN2/TERF1-interacting t	K.NK#PQASAPGSDLSETPVER@.K	10.91	7.36	1.48	0.67
P70314_PITX1_MOUSE	Pitx1	Pituitary homeobox 1 OS	R.THFTSQQLQELEATFQR@.N	13.70	34.72	0.39	2.54
P52480_KPYM_MOUSE	Pkm	Pyruvate kinase PKM OS=	R.LAPITSDPTEAAAVGAVEASFK.C	3.96	4.58	0.86	1.16
P52480_KPYM_MOUSE	Pkm	Pyruvate kinase PKM OS=	R.APIIAVTR.N	13.41	14.32	0.94	1.07
P70268_PKN1_MOUSE	Pkn1	Serine/threonine-proteir	R.SLAPVELLLR@.G	10.53	3.56	2.96	0.34
Q8BWW9_PKN2_MOUSE	Pkn2	Serine/threonine-proteir	R.ASSLGETDESSELR@.V	12.49	2.37	5.27	0.19
Q8BWW9_PKN2_MOUSE	Pkn2	Serine/threonine-proteir	R.DLK#LDNLLLDTEGFVK#.I	13.18	4.35	3.03	0.33
Q8BWW9_PKN2_MOUSE	Pkn2	Serine/threonine-proteir	K.SSVVIEELSLVASPTLSPR@.Q	12.42	4.21	2.95	0.34
P47713_PA24A_MOUSE	Pla2g4a	Cytosolic phospholipase	R.DVPVVAILGSGGGFR@.A	7.88	5.79	1.36	0.73
P47713_PA24A_MOUSE	Pla2g4a	Cytosolic phospholipase	R.DVPVVAILGSGGGFR@.A	14.25	4.50	3.17	0.32
Q4KWH5_PLCH1_MOUSE	Plch1	1-phosphatidylinositol 4	K.ILIDSIYK#.V	35.36	16.28	2.17	0.46
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.GLLSAEVAR.L	24.00	9.22	2.60	0.38

Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.AAEEAEEAR@EQAER@.E	8.59	4.26	2.02	0.50
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.AALAHSEIATTQAASTK#.A	53.42	18.63	2.87	0.35
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.AELELELGR@.I	26.20	8.84	2.96	0.34
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.AEM*EVLLASK#.A	10.28	4.83	2.13	0.47
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.AGLVGPELHEK#.L	29.74	11.03	2.69	0.37
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.AGTLSITEFADM*LSGNAGGFR@.S	4.79	1.84	2.61	0.38
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.AGTLSITEFADM*LSGNAGGFR@.S	7.54	2.01	3.75	0.27
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.AGVGAPVTQVTLQSTQR@.R	23.12	9.11	2.54	0.39
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.AK#LEQLFQDEVAK#.A	13.42	5.82	2.31	0.43
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.AKLEQLFQDEVAK.A	32.58	12.70	2.56	0.39
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.ALLEEIER@.H	28.52	9.26	3.08	0.32
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.ALQALDELR@.L	40.71	15.58	2.61	0.38
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.AQAELEAQELQR@.R	33.89	11.68	2.90	0.34
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.AQAEVEGLGK#.G	32.56	13.33	2.44	0.41
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.AQLEPVASPAK#.K	39.46	18.19	2.17	0.46
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.AQQVEAAER@.S	17.41	14.83	1.17	0.85
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.AQVEQELTTLR@.L	41.65	16.27	2.56	0.39
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.ATVSAPFGK#.F	26.50	11.67	2.27	0.44
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.AVTGYK#DPYTGEQISLFQAM*K#.K	6.22	7.53	0.83	1.21
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.DAPDGPSVEAEPEYTFEGLR@.Q	13.60	5.61	2.42	0.41
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.DLLQPEVAVALLEAQAGTGHIIDPATSAR@.L	17.91	5.55	3.23	0.31
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.DLLQQFR@.T	42.75	18.48	2.31	0.43
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.DSQDAGGFGPEDR@.L	18.37	11.16	1.65	0.61
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.EAIAELER@.E	17.20	6.75	2.55	0.39
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.EAQAVPATLQELEATK#.A	27.48	9.09	3.02	0.33
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.EEELQQTLQQEQNM*LDR@.L	9.56	2.75	3.47	0.29
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.ELAEQELEK#.Q	16.95	5.90	2.87	0.35
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.ELIPAEEALR@.L	30.02	15.97	1.88	0.53
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.ELSEVGSVR@.T	24.36	13.48	1.81	0.55
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.ESADPLSAWLQDAK#.R	19.13	11.75	1.63	0.61
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.EVAEADSVR@.Q	21.40	11.26	1.90	0.53
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.FLEVQYLTGGLIEPDTPGR@.V	25.65	12.08	2.12	0.47
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.FR@ELAEEAAR@.L	26.33	10.56	2.49	0.40
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.FR@ELAEEAAR@.L	6.22	2.76	2.26	0.44
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.GFFDPNTEENLTYLQLM*ER@.C	5.97	3.09	1.93	0.52
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.GFFDPNTHENLTYLQLLER@.C	56.16	23.00	2.44	0.41
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.GGAEGELQALR@.A	27.59	12.94	2.13	0.47
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.GGELVYTDTEAR@.D	32.45	11.76	2.76	0.36
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.GIIR@PGTAFELLEAQAATGYVIDPIK#.G	23.36	11.15	2.09	0.48
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.GLFDEEM*NEILTDPSDDTK#.G	7.84	4.75	1.65	0.61
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.GLLSAEVAR@.L	23.03	5.67	4.07	0.25
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.GLVEDTLR@.Q	26.74	11.16	2.40	0.42
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.GTNVIAGVWLEEAGQK#.L	14.92	5.71	2.61	0.38
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.GYFDEEM*NR@.I	24.34	12.60	1.93	0.52
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.GYYSPYSVSGSGSTAGSR@.T	10.51	4.69	2.24	0.45
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.HYQQLLQSLEQGEQEESR@.C	18.53	7.29	2.54	0.39
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.IDSAEWGVDLPSVEAQLGSHR@.G	12.65	6.86	1.84	0.54
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.IISLETYNLFR@.E	43.21	20.53	2.10	0.48
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.IK#EIQNTGDR@.L	5.13	1.68	3.06	0.33
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.ILSDPSDDTK#.G	36.24	19.43	1.87	0.54
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LAAEQELIR@.L	57.93	21.90	2.64	0.38
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.LAAISEATR@.L	24.90	11.25	2.21	0.45
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LAEDEAFQR@.R	23.54	8.97	2.62	0.38
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LAEVEAALEK#.Q	56.17	21.74	2.58	0.39
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LAQGHTTVAELTQR@.E	21.14	6.56	3.22	0.31
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LEDLLQDAQDEK#EQLNEYK#.G	27.85	17.93	1.55	0.64
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LEDLLQDAQDEK#EQLNEYK#GHLSGLAK#.R	8.83	2.70	3.27	0.31
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LGFHLPLEVAYQR@.G	39.00	16.43	2.37	0.42
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.LISLFQAM*K#.K	13.24	5.78	2.29	0.44
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LK#AEAELLQQQK#.E	7.90	4.08	1.94	0.52
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LK#QSAEEQAQAQAQAQAAAEK#.L	15.72	6.84	2.30	0.43
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.LLAEENQR.L	42.70	15.49	2.76	0.36
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LLDAQLATGGIVDPR@.L	14.95	6.29	2.38	0.42
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LLDAQLSTGGIVDPSK#.S	53.35	20.26	2.63	0.38
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LLDPEDVDVPQPDEK#.S	35.14	18.39	1.91	0.52
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LLEAQIATGGIIDPEESHR@.L	14.26	4.13	3.46	0.29
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.LLLWSQR@.M	16.08	8.29	1.94	0.52
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LM*ADFQAGR@.V	13.32	8.11	1.64	0.61
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LPVDVAYQR@.G	37.46	15.51	2.41	0.41
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LQAEEVAQQK#.S	54.01	20.12	2.68	0.37
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LQEDKEQM*AQQLVEETQGFQR.T	9.58	2.39	4.02	0.25
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LQHEATAATQK#.R	9.71	5.82	1.67	0.60
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LQLETTER@.Q	29.39	12.09	2.43	0.41
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.LQNVQIALDYLR@.H	19.27	6.38	3.02	0.33
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LR@AETEQGEQQR@.Q	22.72	80.13	0.28	3.53
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LSFSGLR@.A	33.83	14.52	2.33	0.43
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LSVAAQEAAR@.L	42.34	17.06	2.48	0.40
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LSYTQLLK#.R	23.15	12.82	1.81	0.55
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LTAEDLYEAR@.I	35.67	13.63	2.62	0.38
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LTVDEAVR@.A	96.70	44.65	2.17	0.46
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LTVEEAVR@.H	25.74	19.62	1.31	0.76
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.LTVNEAVK#.E	31.77	17.30	1.84	0.54
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.M*GIVGPEFK#.D	17.23	7.42	2.32	0.43
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.M*QAVQEATR@.L	17.02	10.11	1.68	0.59
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.NDESQLSPATR@.G	22.62	25.58	0.88	1.13
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.NLVDNITGQR@.L	39.24	7.83	5.01	0.20
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.QAEAELALR@.V	26.59	10.80	2.46	0.41
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.QITVEELVR@.S	19.69	7.95	2.48	0.40
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.QLAEEDAAR@.Q	22.22	8.66	2.57	0.39
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.QLAEEDLAQQR@.A	32.09	12.78	2.51	0.40
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.QLEM*SAEAER@.L	28.54	9.94	2.87	0.35
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.QQNLASYDYVR@.R	17.64	7.58	2.33	0.43
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.QSAEEQAQAQAQAQAAAEK#.L	14.34	5.67	2.53	0.40
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.QSSEAEIQAK#.A	23.81	6.57	3.62	0.28
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.QVQVALETAQR@.S	24.27	8.01	3.03	0.33
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.QYDIDDAITK#.N	19.09	9.57	1.99	0.50
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.QYINAIK#DYELQLITYK#.A	10.47	4.67	2.24	0.45
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.R@AAEEAEEAR@EQAER@.E	22.31	6.35	3.51	0.28
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.R@DDPSGQM*LLLLSDAR@.K	7.15	4.83	1.48	0.67
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.R@EEAAVDAQQQK#.R	6.94	2.47	2.81	0.36
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.R@PELEDSTLR@.Y	24.48	7.62	3.21	0.31
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.SDQLTGLSLLPLSEK#.A	29.36	12.97	2.26	0.44
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.SEEM*QTVQQEQILQETQALQK#.S	25.46	9.41	2.70	0.37

Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.SIITYVSSLYDAM*PR@.V	13.04	3.82	3.41	0.29
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.SILDEELQR@.L	38.74	14.18	2.73	0.37
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.SLAAEEEAAR@.Q	45.41	19.21	2.36	0.42
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.SLAQADAEK#QK#EEAER@.E	28.64	14.94	1.92	0.52
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.SM*VEEGTGLR@.L	17.92	8.37	2.14	0.47
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.SQVEEELFSVR@.V	32.79	13.20	2.48	0.40
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.SSSVGSSSSYPISSAGPR@.T	19.57	12.36	1.58	0.63
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.STQGAEEVLK#.T	20.25	12.38	1.64	0.61
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.SWSLVTFR@.T	21.56	12.99	1.66	0.60
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.SYVDPSTDER@.L	23.79	9.60	2.48	0.40
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.TELATQEK#.V	17.08	8.83	1.94	0.52
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.TQLASWSDPTEETGPVAGILDTETLEK#.V	16.70	43.28	0.39	2.59
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.VALEEVER@.L	16.45	6.91	2.38	0.42
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.VIYQSLEGAVQAGQLK#.I	20.58	7.88	2.61	0.38
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.VLALPEPSPAAPTLR@.S	52.28	23.94	2.18	0.46
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.VPAQQLQEAGILSQEELQR@.L	21.33	9.13	2.34	0.43
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.VPGAQDGVR@.A	34.09	14.41	2.37	0.42
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.VPLDVAYAR@.G	30.83	12.10	2.55	0.39
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.VPVDVAYK#.R	19.91	11.72	1.70	0.59
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	K.VQSGSESVIQEYVDLR.T	35.30	9.70	3.64	0.27
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.VTQLLER@.W	33.27	14.70	2.26	0.44
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.VYHDPSTQEPVTYSQLQQR@.C	20.81	8.19	2.54	0.39
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.WQAVLAQTDVR@.Q	20.56	8.49	2.42	0.41
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.YLQDLLAWVEENQR@.R	18.97	6.75	2.81	0.36
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.YLYGTGAVAGVYLPGSR@.Q	16.65	7.64	2.18	0.46
Q9QXS1_PLEC_MOUSE	Plec	Plectin OS=Mus musculu	R.YSELTTLTSQYIK#.F	26.85	14.17	1.89	0.53
E9Q6H8_E9Q6H8_MOUSE	Plekha5	Protein Plekha5 OS=Mus	K.AM*VQVSDQTM*HSIPTSPSHGSAAAYQGFSPQR@.T	4.24	2.84	1.49	0.67
E9Q6H8_E9Q6H8_MOUSE	Plekha5	Protein Plekha5 OS=Mus	K.AVNVSLADVR@.G	13.74	2.06	6.67	0.15
E9Q6H8_E9Q6H8_MOUSE	Plekha5	Protein Plekha5 OS=Mus	R.GVISYQTLPR@.N	17.46	3.39	5.16	0.19
E9Q6H8_E9Q6H8_MOUSE	Plekha5	Protein Plekha5 OS=Mus	K.YR@PEEAGIDAK#.L	4.99	8.36	0.60	1.67
Q4VAC9_PKHG3_MOUSE	Plekhg3	Pleckstrin homology dor	K.VTPDQEEQVPSISGLPEEAGELSGGK.A	3.59	4.08	0.88	1.14
Q66T02_PKHG5_MOUSE	Plekhg5	Pleckstrin homology dor	R.ALLQPSDFLK#.G	11.66	7.51	1.55	0.64
Q66T02_PKHG5_MOUSE	Plekhg5	Pleckstrin homology dor	R.FSGFFSSSPSTSAFSR@.E	6.51	3.09	2.11	0.47
Q66T02_PKHG5_MOUSE	Plekhg5	Pleckstrin homology dor	R.IDAYEVVEGSNDEVDK#LLK#.E	7.65	3.95	1.93	0.52
Q66T02_PKHG5_MOUSE	Plekhg5	Pleckstrin homology dor	K.SLGEVLLPVFER@.K	13.51	8.90	1.52	0.66
Q66T02_PKHG5_MOUSE	Plekhg5	Pleckstrin homology dor	K.SLGEVLLPVFER@.K	10.87	9.73	1.12	0.90
Q9DBG5_PLIN3_MOUSE	Plin3	Perilipin-3 OS=Mus musc	R.LQESLPILQQPTEK#.V	12.47	4.77	2.62	0.38
Q9DBG5_PLIN3_MOUSE	Plin3	Perilipin-3 OS=Mus musc	R.SQVNDLQATFSGIHSFQDLSAGVLAQTR@.E	8.78	4.11	2.13	0.47
Q9DBG5_PLIN3_MOUSE	Plin3	Perilipin-3 OS=Mus musc	K.TLTTAAVSTAQPILSK#.L	25.67	6.60	3.89	0.26
Q9DBG5_PLIN3_MOUSE	Plin3	Perilipin-3 OS=Mus musc	R.VAGLPLISSTYGM*VSAAYTSTK#.E	6.51	1.07	6.09	0.16
Q9DBG5_PLIN3_MOUSE	Plin3	Perilipin-3 OS=Mus musc	R.SQVNDLQATFSGIHSFQDLSAGVLAQTR@.E	3.93	1.63	2.42	0.41
Q9R0E1_PLOD3_MOUSE	Plod3	Procollagen-lysine,2-oxo	K.LVGPEEALSAGEAR.D	4.67	6.38	0.73	1.37
Q9R0E1_PLOD3_MOUSE	Plod3	Procollagen-lysine,2-oxo	R.VGVWNVPYISQAYVIR.G	2.06	3.36	0.61	1.63
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	R.AVVLHPLLYTFASGSPDNIK#.Q	63.25	49.00	1.29	0.77
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	K.IWDLASGK#.L	37.58	24.44	1.54	0.65
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	R.LWDLVAGK#.T	64.66	30.22	2.14	0.47
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	R.M*PSESAAQSLAVALPSQTR.V	19.39	10.19	1.90	0.53
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	R.MPSESAAQSLAVALPSQTR@.V	6.04	3.23	1.87	0.53
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	K.QYPANQGQDVEYLVTGTHPYPAGPGVALTADTK#.I	18.41	9.32	1.97	0.51
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	R.SQPTAM*NSIM*ETGNTK#.N	20.78	14.36	1.45	0.69
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	R.TGPAGSEYR@.H	19.07	12.34	1.55	0.65
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	R.TGYNFQR@.V	49.29	26.85	1.84	0.54
Q922V4_PLRG1_MOUSE	Plrg1	Pleiotropic regulator 1 O	K.VYR@EDETATEETHPVSWK#PEIIK#.R	11.39	8.54	1.33	0.75
Q9JJ00_PLS1_MOUSE	Plscr1	Phospholipid scramblase	K.SLDEESVVGK#.I	12.96	3.04	4.26	0.23
Q9JIZ9_PLS3_MOUSE	Plscr3	Phospholipid scramblase	R.EALTDADDFGLQFPVDLDVK#.V	5.39	3.23	1.67	0.60
Q9CPV5_PMF1_MOUSE	Pmf1	Polyamine-modulated fa	K.LLDAIVDTFLQK#.L	22.14	9.34	2.37	0.42
Q9CPV5_PMF1_MOUSE	Pmf1	Polyamine-modulated fa	K.NQELADAVLAGR@.R	10.42	4.89	2.13	0.47
Q9CPV5_PMF1_MOUSE	Pmf1	Polyamine-modulated fa	K.LLDAIVDTFLQK#.L	14.80	3.73	3.96	0.25
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.ALDESLAEPHLEDR@.T	58.30	13.01	4.48	0.22
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.APGQADANGEALDNVFFESLQR@.R	23.73	8.71	2.72	0.37
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.AVSLEAGLR@.H	24.00	9.22	2.60	0.38
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.DNSVSSFLDSTR@.K	29.63	10.28	2.88	0.35
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.ELLEAVNDR@.Y	45.19	10.65	4.24	0.24
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.EVQSVQAQALELSK#.T	16.49	6.57	2.51	0.40
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.LLALHNVSFVELLNAYR@.T	13.50	7.10	1.90	0.53
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.SALASVLAM*R@.D	9.66	3.47	2.79	0.36
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.TLVFFDLK#.I	40.58	10.93	3.71	0.27
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.VLIQPEAFSVYSK#.A	49.04	15.38	3.19	0.31
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.APGQADANGEALDNVFFESLQR@.R	24.69	10.01	2.47	0.41
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.AVSLEAGLR.H	30.53	10.12	3.02	0.33
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.EEASQTVGSM*K#.R	8.84	6.65	1.33	0.75
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.ELLEAVNDR@.Y	62.88	26.87	2.34	0.43
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.EVQSVQAQALELSK#.T	50.95	20.78	2.45	0.41
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.INAAVASPEAASNQPEAASTHPVTTSTPEDLEQPK#.E	12.69	5.53	2.29	0.44
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.ISQLAAVNR@.E	65.24	20.44	3.19	0.31
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.LLALHNVSFVELLNAYR@.T	40.49	16.50	2.45	0.41
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.LYASDQEVLDM*HSFLR@.K	55.91	18.49	3.02	0.33
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.QVVDYVQAQER@.E	51.03	18.05	2.83	0.35
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.SALASVLAM*R@.D	15.45	5.36	2.88	0.35
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.TLVFFDLK#.I	91.18	22.80	4.00	0.25
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.TVPGAHPVPVYAFSM*QGPTYR@.E	25.74	14.50	1.78	0.56
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.VLIQPEAFSVYSK#.A	54.98	17.83	3.08	0.32
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.VQLLTR@.G	68.30	18.47	3.70	0.27
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.ALDESLAEPHLEDR@.T	116.98	41.70	2.80	0.36
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.APGQADANGEALDNVFFESLQR@.R	30.75	10.88	2.83	0.35
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.AVSLEAGLR@.H	50.80	14.80	3.43	0.29
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.EEASQTVGSM*K#.R	11.19	3.16	3.54	0.28
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.ELLEAVNDR@.Y	56.13	19.77	2.84	0.35
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.EVQSVQAQALELSK#.T	50.04	15.86	3.15	0.32
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	K.ISQLAAVNR@.E	93.48	29.57	3.16	0.32
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.LLALHNVSFVELLNAYR@.T	31.64	9.03	3.50	0.29
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.QVVDYVQAQER@.E	32.44	7.62	4.26	0.24
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.SALASVLAM*R@.D	31.92	9.18	3.48	0.29
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.TLVFFDLK#.I	115.69	32.02	3.61	0.28
Q60953_PML_MOUSE	Pml	Protein PML OS=Mus mu	R.VLIQPEAFSVYSK#.A	114.04	32.93	3.46	0.29
D6RG76_D6RG76_MOUSE	Pmm1	Phosphomannomutase 1	R.SRLHPGGEDR@.V	4.91	3.45	1.42	0.70
Q9D1G2_PMVK_MOUSE	Pmvk	Phosphomevalonate kina	K.IVEGVSQPIWLVSDTR@.R	4.63	4.64	1.00	1.00
Q9D1G2_PMVK_MOUSE	Pmvk	Phosphomevalonate kina	R.LVLLFSGK#.R	9.44	7.77	1.21	0.82
A2AJT4_PNISR_MOUSE	Pnisr	Arginine/serine-rich prot	R.SK#FDSDEEDEDAENLEAVSSGK#.V	6.53	3.06	2.13	0.47
A2AJT4_PNISR_MOUSE	Pnisr	Arginine/serine-rich prot	R.TPNEAPSVLEPK#.R	15.57	11.90	1.31	0.76
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.ALQEQLEK#.A	17.00	15.30	1.11	0.90
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.DLIQDQNM*DEK#.G	8.07	7.62	1.06	0.94
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.GFSDSGGGPPAK#.Q	8.74	7.08	1.23	0.81

O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.IFGLLM*GTLQK#.F	6.24	5.19	1.20	0.83
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.LEVQAEEER@.K	12.81	7.66	1.67	0.60
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.TK#PHLFYIPGR@.M	8.48	7.53	1.13	0.89
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.ALQEQLEK#.A	177.52	91.75	1.93	0.52
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.DLEGAVSR@.L	154.43	62.14	2.49	0.40
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.DLIQDQNM*DEK#.G	101.43	38.39	2.64	0.38
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.DLIQDQNMDEK#.G	16.07	8.26	1.94	0.51
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.DLIQDQNM*DEKGK.Q	14.28	6.00	2.38	0.42
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.FK#QESTVATER@.Q	81.13	33.19	2.44	0.41
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.GFSDSGGGPPAK#.Q	72.26	27.44	2.63	0.38
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.HVIAEQEVM*ETNQVESIEPSENETSK#.E	14.79	6.82	2.17	0.46
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.IEFAEQINK#.M	33.53	12.60	2.66	0.38
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.IFGLLM*GTLQK#.F	137.18	53.73	2.55	0.39
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.IFGLLMGTLQK#.F	27.48	10.99	2.50	0.40
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.K#DFPLESIK#LPEVSVEPVLTVHSENK#.S	7.68	56.27	0.14	7.32
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.K#M*NALFEGR@.R	27.69	9.67	2.86	0.35
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.LEVQAEEER@.K	259.47	104.44	2.48	0.40
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.LLALSGPGGGR@.G	108.23	54.74	1.98	0.51
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.LPEVSVEPVLTVHSENK#.S	60.17	22.56	2.67	0.37
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.M*NALFEGR@.R	55.39	30.10	1.84	0.54
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.NEEQK#AEQEEGK#.V	15.19	7.36	2.06	0.48
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.QESDPEDDDVKKPALQSSVVATSK.E	10.66	2.50	4.26	0.23
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.QQDSQPEEVM*DVLEM*VESVK#.H	21.48	7.70	2.79	0.36
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.QQDSQPEEVM*DVLEM*VESVK#.H	6.11	2.74	2.23	0.45
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.QQDSQPEEVM*DVLEMVESVK#.H	7.65	4.72	1.62	0.62
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.QQDSQPEEVMDVLEMVESVK#.H	4.79	2.90	1.65	0.61
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.R@IEFAEQINK#.M	129.55	55.75	2.32	0.43
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.TEEEAEVR@.E	45.33	17.31	2.62	0.38
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.TK#PHLFYIPGR@.M	131.72	51.18	2.57	0.39
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.VELAQLQEEWNEHNAK#.I	8.46	3.84	2.20	0.45
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.ALQEQLEK#.A	68.00	26.73	2.54	0.39
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.DLEGAVSR@.L	50.73	22.87	2.22	0.45
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.DLIQDQNM*DEK#.G	24.49	12.75	1.92	0.52
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.DLIQDQNM*DEK#GK#.Q	3.82	2.68	1.43	0.70
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.FK#QESTVATER@.Q	56.46	21.17	2.67	0.37
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.GFSDSGGGPPAK#.Q	20.06	9.20	2.18	0.46
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.HVIAEQEVM*ETNQVESIEPSENETSK#.E	12.79	3.91	3.27	0.31
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.IEFAEQINK#.M	9.00	4.75	1.90	0.53
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.IFGLLM*GTLQK#.F	24.67	13.26	1.86	0.54
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.IFGLLMGTLQK#.F	8.21	5.25	1.57	0.64
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.LEVQAEEER@.K	76.76	30.54	2.51	0.40
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.LLALSGPGGGR@.G	29.95	20.88	1.43	0.70
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.LPEVSVEPVLTVHSENK#.S	34.14	5.13	6.65	0.15
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.M*NALFEGR@.R	23.63	9.45	2.50	0.40
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	R.R@GFSDSGGGPPAK#.Q	7.78	2.67	2.91	0.34
O35691_PININ_MOUSE	Pnn	Pinin OS=Mus musculus (	K.TK#PHLFYIPGR@.M	32.22	9.87	3.27	0.31
Q8BZH4_POGZ_MOUSE	Pogz	Pogo transposable eleme	R.FANVPDSILLEAK.D	7.98	10.86	0.74	1.36
Q8BZH4_POGZ_MOUSE	Pogz	Pogo transposable eleme	R.FQASQGENLEGK.Y	12.41	8.16	1.52	0.66
Q8BZH4_POGZ_MOUSE	Pogz	Pogo transposable eleme	R.FANVPDSILLEAK#.D	12.18	12.69	0.96	1.04
Q8BZH4_POGZ_MOUSE	Pogz	Pogo transposable eleme	R.FQASQGENLEGK#.Y	10.09	6.05	1.67	0.60
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.ATYAGGLVLDPK#.V	19.34	5.28	3.66	0.27
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.DTGNFVIGQILSDQSR@.D	29.90	7.43	4.03	0.25
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	R.DTIVENIQK#.R	20.78	2.60	7.98	0.13
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	R.FYAK#PLAALVTYK#.G	23.29	1.96	11.89	0.08
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.GETFSHVFGTNTSSLELFLM*NR@.K	13.28	3.74	3.56	0.28
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.LDNLAIDTQYYLAQQIHPVVAR@.I	40.69	8.38	4.86	0.21
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.LGDEDEEIDGDTNK#.Y	22.57	7.34	3.08	0.33
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	R.NEPLLTPIPLK#.R	11.55	2.08	5.56	0.18
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.NIAEQFLSWSGYSEVNLSK#.L	4.12	0.00	#DIV/0!	0.00
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.NYAFEIPDVPEK#SEYLEVR@.Y	23.34	3.79	6.17	0.16
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.QQDLNPDLVLQYDIR@.Q	12.09	3.39	3.56	0.28
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.SYHLSELVQQILK#.T	19.84	4.65	4.27	0.23
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	R.TLIGFFLAK#.V	26.88	6.91	3.89	0.26
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	R.TLYFLPR@.E	17.76	3.33	5.34	0.19
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.TWDQETEPVER@.V	5.55	15.93	0.35	2.87
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.VEIAATER@.T	24.25	15.49	1.57	0.64
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	K.YAALVVEPTSDGNYITK#.Q	30.51	8.55	3.57	0.28
P33609_DPOLA_MOUSE	Pola1	DNA polymerase alpha ca	R.YSAEVPQLPQNLK#.G	27.45	7.20	3.81	0.26
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	K.AM*FQQLM*GVR@.E	8.44	2.35	3.59	0.28
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	R.DVHHEPVYPQPPFTFSELSR@.E	11.72	2.43	4.83	0.21
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	K.LTSPFEDVFK#.Q	11.45	11.44	1.00	1.00
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	R.QGLSVAAQVVR@.I	15.80	4.09	3.87	0.26
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	R.QLLSPSSFSPSATPSQK#.Y	9.26	4.68	1.98	0.51
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	R.SSGSHLVFVPSLR@.D	26.58	7.90	3.36	0.30
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	K.SVILEGDQEHSYGAQIPVDLSELK#.E	18.84	5.01	3.76	0.27
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	R.VSSTPETPLTK#.R	49.68	11.27	4.41	0.23
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	K.VVGDPEPLTGSYK#.A	26.33	6.31	4.17	0.24
P33611_DPOA2_MOUSE	Pola2	DNA polymerase alpha su	K.VVGDPEPLTGSYK#.A	6.60	1.32	5.01	0.20
P52431_DPOD1_MOUSE	Pold1	DNA polymerase delta ca	R.VTGVPLGYLLTR@.G	11.97	9.76	1.23	0.82
P52431_DPOD1_MOUSE	Pold1	DNA polymerase delta ca	R.IDISQLVITK#.E	23.04	12.96	1.78	0.56
P52431_DPOD1_MOUSE	Pold1	DNA polymerase delta ca	R.IFEPILGEGR@.A	10.17	4.31	2.36	0.42
P52431_DPOD1_MOUSE	Pold1	DNA polymerase delta ca	K.TPTGDEFVK#.S	12.43	2.48	5.01	0.20
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	K.IGLSDAR@.L	62.23	19.88	3.13	0.32
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	K.K#DDAITAYK#.K	15.20	6.79	2.24	0.45
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	R.LVHPGVAEVVFVK#.K	32.24	14.27	2.26	0.44
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	K.QNLYDLDEDDDIVVPVPPK#.Q	3.41	2.27	1.50	0.66
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	R.R@GNPASSNPPAEVDPDTVLR@.A	33.02	11.31	2.92	0.34
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	R.R@SPAAFTSPPIGTVTPALK#.L	22.73	8.94	2.54	0.39
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	K.SSGASVTTQPTEFK#.I	35.02	14.70	2.38	0.42
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	K.TIQVPQQK#.A	50.92	17.81	2.86	0.35
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	R.VGIQHSLVNQPAR@.T	81.65	25.57	3.19	0.31
Q8BG81_PDIP3_MOUSE	Poldip3	Polymerase delta-interac	K.VVQNDAYTAPVLPSSVR@.T	22.17	9.81	2.26	0.44
Q9JKP7_DPOE3_MOUSE	Pole3	DNA polymerase epsilon	K.EALPDGVNISK#.E	38.32	18.28	2.10	0.48
Q9JKP7_DPOE3_MOUSE	Pole3	DNA polymerase epsilon	K.TLNASDVLSAM*EEM*EFQR@.F	3.28	1.82	1.80	0.56
O35134_RPA1_MOUSE	Polr1a	DNA-directed RNA polym	R.TALSSVDAAQR@.E	7.37	2.97	2.49	0.40
O35134_RPA1_MOUSE	Polr1a	DNA-directed RNA polym	R.VLEVGALQAVYELER@.I	6.05	3.02	2.01	0.50
P52432_RPAC1_MOUSE	Polr1c	DNA-directed RNA polym	R.ILLAEVPTM*AVEK#.V	17.03	4.93	3.45	0.29
P52432_RPAC1_MOUSE	Polr1c	DNA-directed RNA polym	R.LGLIPILADPR@.L	45.39	14.29	3.18	0.31
P52432_RPAC1_MOUSE	Polr1c	DNA-directed RNA polym	R.NQGEEEGTEIDTLQFR@.L	22.85	3.11	7.35	0.14
P52432_RPAC1_MOUSE	Polr1c	DNA-directed RNA polym	R.VVLGEFGVR@.N	26.26	38.64	0.68	1.47
P97304_RPAC2_MOUSE	Polr1d	DNA-directed RNA polym	K.TALEM*VQAAGTDR@.Q	2.82	1.32	2.13	0.47
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	R.AEIQELAM*VPR.M	15.73	20.04	0.78	1.27
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.AK#QDVIEVIEK#.A	8.03	15.77	0.51	1.96

P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.ALQEWILETDGVSLM*R.V	8.60	10.61	0.81	1.23
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	R.EGLIDTAVK.T	92.24	21.26	4.34	0.23
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.FGVEQPEGDEDLTK#.E	7.36	11.01	0.67	1.50
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.IIITEDGEFK.A	27.42	32.51	0.84	1.19
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.INISQVIAVVGQQNVEGK#.R	43.22	51.83	0.83	1.20
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.INISQVIAVVGQQNVEGK.R	9.09	12.13	0.75	1.33
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	R.KLTM*EQIAEK.I	7.87	9.98	0.79	1.27
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.LLVDSNNPK.I	16.88	18.81	0.90	1.11
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	R.NSINQVVQLR@.Y	20.87	24.61	0.85	1.18
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	R.QTFENQVNR.I	27.42	43.04	0.64	1.57
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.RVDFSAR.T	15.89	21.53	0.74	1.35
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	R.SIAANM*TFAEIVTPFNIDR@.L	7.34	29.73	0.25	4.05
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.SM*ESVM*VK.Y	7.93	13.38	0.59	1.69
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.TAETGYIQR.R	30.84	40.03	0.77	1.30
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.TPSLTVFLLGQSAR.D	17.61	22.84	0.77	1.30
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	R.TVITPDPNLSIDQVGVPR.S	23.06	36.13	0.64	1.57
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	R.YGEDGLAGESVEFQNLATLKPSNK.A	22.94	30.74	0.75	1.34
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.YSPTSPTYSPTSPK.Y	16.91	24.23	0.70	1.43
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	K.YSPTSPTYSPTTPK#.Y	9.54	12.46	0.77	1.31
P08775_RPB1_MOUSE	Polr2a	DNA-directed RNA polym	R.YTPQSPTYTPSSPSYSPSSPSYSPTSPK.Y	4.11	5.41	0.76	1.32
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.AGVSQVLNR.L	18.66	18.46	1.01	0.99
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.DGAPSPM*M*PNEAR@.L	5.79	7.84	0.74	1.35
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.GPIQILNR.Q	19.56	17.54	1.12	0.90
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.ISNLLSDYGYHLR@.G	22.18	18.70	1.19	0.84
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.IVATLPYIK#.Q	11.90	15.67	0.76	1.32
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.LLLAALGR@.R	14.40	10.97	1.31	0.76
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.NLTYSAPLYVDITK#.T	12.41	12.08	1.03	0.97
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.QEVPIIIVFR@.A	23.76	21.95	1.08	0.92
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.TVTLPENEDELESTNR.R	4.65	4.75	0.98	1.02
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.VSANK#GEIGDATPFNDAVNVQK#.I	11.07	9.81	1.13	0.89
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.VSGDDVIIGK#.T	10.96	10.95	1.00	1.00
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.AGVSQVLNR.L	28.79	20.55	1.40	0.71
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.ELPAGINSIVAIASYTGYNQEDSVIM*NR@.S	6.36	3.15	2.02	0.50
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.GEIGDATPFNDAVNVQK#.I	10.07	7.20	1.40	0.71
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.GPIQILNR@.Q	16.43	15.39	1.07	0.94
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.ISNLLSDYGYHLR@.G	35.33	25.69	1.38	0.73
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.IVATLPYIK.Q	13.43	13.37	1.00	1.00
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.K#GFDQEEVFEK#PTR@.E	8.04	8.11	0.99	1.01
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.LDDDGLIAPGVR@.V	14.18	13.81	1.03	0.97
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.LLLAALGR@.R	11.84	6.21	1.91	0.52
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	R.NLTYSAPLYVDITK#.T	18.37	18.21	1.01	0.99
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.QEVPIIIVFR@.A	21.99	19.72	1.12	0.90
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.TVTLPENEDELESTNR@.R	10.91	10.02	1.09	0.92
Q8CFI7_RPB2_MOUSE	Polr2b	DNA-directed RNA polym	K.VSANK#GEIGDATPFNDAVNVQK#.I	14.61	9.89	1.48	0.68
Q99M46_Q99M46_MOUSE	Polr2c	DNA-directed RNA polym	K.FIIENTDLAVANSIR@.R	40.32	31.55	1.28	0.78
Q99M46_Q99M46_MOUSE	Polr2c	DNA-directed RNA polym	R.ITELTEENVK#.F	80.27	74.81	1.07	0.93
Q99M46_Q99M46_MOUSE	Polr2c	DNA-directed RNA polym	R.LGLIPLTSDDIVDK#.L	22.71	13.49	1.68	0.59
Q99M46_Q99M46_MOUSE	Polr2c	DNA-directed RNA polym	R.NR@DNDPNDYVEQDDILIVK#.L	25.58	19.19	1.33	0.75
Q99M46_Q99M46_MOUSE	Polr2c	DNA-directed RNA polym	K.SEYSELDEDESQAPYDPNGK#PER@.F	12.61	13.53	0.93	1.07
Q99M46_Q99M46_MOUSE	Polr2c	DNA-directed RNA polym	K.WNPTAGVAFEYDPDNALR.H	15.93	15.75	1.01	0.99
Q9D7M8_RPB4_MOUSE	Polr2d	DNA-directed RNA polym	R.AGDVEEDASQLIFPK#.E	62.42	60.98	1.02	0.98
Q9D7M8_RPB4_MOUSE	Polr2d	DNA-directed RNA polym	K.ALIPSLEGR@.F	17.57	16.54	1.06	0.94
Q9D7M8_RPB4_MOUSE	Polr2d	DNA-directed RNA polym	K.ALIPSLEGR@FEDEELQQILDDIQTK#.R	21.57	20.41	1.06	0.95
Q9D7M8_RPB4_MOUSE	Polr2d	DNA-directed RNA polym	R.FEDEELQQILDDIQTK#.R	13.17	7.58	1.74	0.58
Q9D7M8_RPB4_MOUSE	Polr2d	DNA-directed RNA polym	R.K#QQNESAEDEQELSEVFM*K#.T	13.23	14.84	0.89	1.12
Q9D7M8_RPB4_MOUSE	Polr2d	DNA-directed RNA polym	K.QQNESAEDEQELSEVFM*K#.T	4.11	3.72	1.10	0.91
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	R.ALIVVQQGM*TPSAK#.Q	13.42	6.31	2.13	0.47
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	K.EEVTELLAR@.Y	10.47	8.35	1.25	0.80
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	R.ALIVVQQGM*TPSAK#.Q	54.81	42.78	1.28	0.78
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	R.ALIVVQQGMTPSAK#.Q	8.68	5.42	1.60	0.62
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	K.EEVTELLAR@.Y	47.13	29.38	1.60	0.62
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	R.GYLVTQDELDQTLEEFK#.A	19.70	19.68	1.00	1.00
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	K.IIR@PSETAGR@.Y	18.25	13.83	1.32	0.76
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	K.IIRPSETAGR.Y	126.59	86.11	1.47	0.68
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	R.IQAGDPVAR@.Y	73.28	45.27	1.62	0.62
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	R.M*QEENITR@.A	28.43	30.81	0.92	1.08
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	R.RTDLTVLVAHNDDPTDQM*FVFFPEEPK.V	22.03	16.08	1.37	0.73
Q80UW8_RPAB1_MOUSE	Polr2e	DNA-directed RNA polym	R.RTDLTVLVAHNDDPTDQM*FVFFPEEPK.V	2.35	1.89	1.24	0.81
P62488_RPB7_MOUSE	Polr2g	DNA-directed RNA polym	K.AIVFR@PFK#GEVVDAVVTQVNK#.V	7.98	8.16	0.98	1.02
P62488_RPB7_MOUSE	Polr2g	DNA-directed RNA polym	R.GFVLYPVK#.Y	41.39	43.01	0.96	1.04
P62488_RPB7_MOUSE	Polr2g	DNA-directed RNA polym	K.TM*DEDIVIQQDDEIR.L	10.48	9.46	1.11	0.90
P62488_RPB7_MOUSE	Polr2g	DNA-directed RNA polym	R.YFGPNLLNTVK#.Q	55.50	63.76	0.87	1.15
P62488_RPB7_MOUSE	Polr2g	DNA-directed RNA polym	K.TM*DEDIVIQQDDEIR@.L	4.13	3.31	1.25	0.80
Q923G2_RPAB3_MOUSE	Polr2h	DNA-directed RNA polym	R.IEGDETSTEAATR@.L	16.22	9.40	1.73	0.58
Q923G2_RPAB3_MOUSE	Polr2h	DNA-directed RNA polym	R.LSAYVSYGGLLM*R@.L	17.71	10.84	1.63	0.61
Q923G2_RPAB3_MOUSE	Polr2h	DNA-directed RNA polym	R.LVIASTLYEDGTLDDGEYNPTDDR@PSR@.A	13.65	8.53	1.60	0.63
Q923G2_RPAB3_MOUSE	Polr2h	DNA-directed RNA polym	K.VYR@IEGDETSTEAATR@.L	30.30	15.03	2.02	0.50
Q923G2_RPAB3_MOUSE	Polr2h	DNA-directed RNA polym	K.VYRIEGDETSTEAATR.L	2.67	1.55	1.72	0.58
P60898_RPB9_MOUSE	Polr2i	DNA-directed RNA polym	K.EAVFFQSHSAR@.A	4.18	3.45	1.21	0.83
P60898_RPB9_MOUSE	Polr2i	DNA-directed RNA polym	K.ITHEVDELTQIIADVSQDPTLPR@.T	67.73	54.04	1.25	0.80
Q6PI63_Q6PI63_MOUSE	Polr2j	DNA-directed RNA polym	K.SQLLK#DPQVLFAGYK#.V	61.35	37.57	1.63	0.61
Q6PI63_Q6PI63_MOUSE	Polr2j	DNA-directed RNA polym	R.VAIKDKQEGIE.-	16.41	10.68	1.54	0.65
Q63871_RPAB4_MOUSE	Polr2k	DNA-directed RNA polym	R.LVVFDAR@.-	53.62	44.06	1.22	0.82
B2RXC6_B2RXC6_MOUSE	Polr3a	Polymerase (RNA) III (DN/	R.IPAEDVPLLLM*NPESGK#PSDLILTR@.L	4.37	3.18	1.37	0.73
Q8K205_Q8K205_MOUSE	Pop1	Blood vessel epicardial su	K.IPILLIQQPGK#.V	9.58	6.22	1.54	0.65
Q8K205_Q8K205_MOUSE	Pop1	Blood vessel epicardial su	K.IPILLIQQPGK#.V	9.59	3.36	2.85	0.35
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	K.FAVFGLGNK#.T	15.01	7.60	1.98	0.51
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	R.LEQLGAQR@.I	14.26	7.89	1.81	0.55
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	R.NIIVFYGSQTGTAEEFANR@.L	5.78	2.79	2.07	0.48
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	K.NPFLAAVTTNR@.K	20.47	11.84	1.73	0.58
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	R.TNVLYELAQYASEPSEQEHLHK#.M	14.46	9.18	1.57	0.64
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	K.FAVFGLGNK#.T	25.80	10.92	2.36	0.42
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	R.GM*SADPEEYDLADLSSLPEIDK#.S	4.75	2.28	2.09	0.48
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	R.LEQLGAQR@.I	23.97	10.26	2.34	0.43
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	R.LPFKPTTPVIM*VGPGTGVAPFM*GFIQER.A	12.38	3.18	3.90	0.26
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	K.NPFLAAVTTNR@.K	23.07	12.06	1.91	0.52
P37040_NCPR_MOUSE	Por	NADPH--cytochrome P45	R.TNVLYELAQYASEPSEQEHLHK#.M	24.91	24.25	1.03	0.97
Q91YU8_SSF1_MOUSE	Ppan	Suppressor of SWI4 1 hor	R.GNM*QAQQSAVR@.L	4.21	3.85	1.09	0.91
Q91YU8_SSF1_MOUSE	Ppan	Suppressor of SWI4 1 hor	R.QAVGEEPDEDLFPTAAK#.R	8.48	2.65	3.20	0.31
Q91YU8_SSF1_MOUSE	Ppan	Suppressor of SWI4 1 hor	R.QNQQAENLQR@.K	8.20	3.80	2.16	0.46
Q91YU8_SSF1_MOUSE	Ppan	Suppressor of SWI4 1 hor	R.QNQQAENLQR@.K	7.77	2.44	3.18	0.31
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.GLASGSAETLPANFR@.V	4.69	1.65	2.85	0.35
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.K#AETLPEVEAELAQR@.I	8.01	3.61	2.22	0.45

B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.QLNTALPQEFAALTK#.E	5.29	2.56	2.07	0.48
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.VTSSM*SSPSM*QPK#.K	3.56	1.71	2.09	0.48
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.EFNNLLITGTDR@.R	9.01	3.18	2.83	0.35
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	K.ESPGQVGVSETENSSQDALGLSK#.L	6.97	1.97	3.54	0.28
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.ETQETLALTQGK#.L	7.80	2.39	3.26	0.31
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.GLASGSAETLPANFR@.V	7.57	2.47	3.07	0.33
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.NSTGSQDGPVSNPSSSNSSQDSLHK#.A	3.70	2.30	1.61	0.62
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.QLNTALPQEFAALTK#.E	6.50	1.95	3.34	0.30
B2RXW8_B2RXW8_MOUSE	Ppfia1	Ppfia1 protein OS=Mus m	R.VTSSM*SSPSM*QPK#.K	5.36	1.49	3.60	0.28
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.DAM*ELPDYVLLTATAK#.V	3.70	2.36	1.57	0.64
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.FRDTEGLIQEINDLR.L	16.86	7.76	2.17	0.46
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.LENDK#ESLVLQVSVLTDQVEAQGEK#.I	5.42	2.23	2.44	0.41
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.LYEEDDLDR@LEQM*EDSEGTVR@.Q	2.85	3.06	0.93	1.07
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.STSSTPGM*GSPSR@.D	4.02	2.62	1.53	0.65
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.AILGAAAEVSLSDGVSTSSLQK#.S	4.07	1.87	2.17	0.46
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.ALHLVEDLR@.G	30.83	16.12	1.91	0.52
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	K.AVESLM*AANEEK#.E	12.41	8.16	1.52	0.66
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.DLGQSNSDLDM*PFAK#.W	15.31	8.99	1.70	0.59
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.FRDTEGLIQEINDLR.L	22.84	11.47	1.99	0.50
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	K.K#LTFSNFGNLR@.K	11.90	4.15	2.87	0.35
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.LENDK#ESLVLQVSVLTDQVEAQGEK#.I	13.03	4.64	2.81	0.36
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	K.LNATEEM*LQQELLSR.T	15.51	9.96	1.56	0.64
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	K.LPTK#PETSFEEGDGR@.A	31.28	15.55	2.01	0.50
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	K.LQLALQALGSEEETNYGK#.L	4.72	3.08	1.53	0.65
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.LYEEDDLDR@LEQM*EDSEGTVR@.Q	9.13	5.06	1.80	0.55
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.SPSASITDEDSNV.-	10.36	10.36	1.00	1.00
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.STSSTPGM*GSPSR@.D	12.46	8.27	1.51	0.66
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.SVDLAEYAPNLR@.G	53.02	18.66	2.84	0.35
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.TSLETQK#LELM*AEISNLK#.L	15.56	7.41	2.10	0.48
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	K.VPGHEASVDDNPFGTR@.K	10.05	5.86	1.71	0.58
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.WLDDIGLPQYK#.T	16.30	7.78	2.09	0.48
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.ALHLVEDLR@.G	28.42	7.36	3.86	0.26
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.DLGQSNSDLDM*PFAK#.W	11.31	4.27	2.65	0.38
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.FR@DTEGLIQEINDLR@.L	30.20	12.31	2.45	0.41
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.LENDK#ESLVLQVSVLTDQVEAQGEK#.I	16.50	5.56	2.97	0.34
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	K.LNATEEM*LQQELLSR@.T	10.57	3.30	3.21	0.31
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.LYEEDDLDR@LEQM*EDSEGTVR@.Q	7.08	3.10	2.28	0.44
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.SPSASITDEDSNV.-	8.11	8.11	1.00	1.00
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.STSSTPGM*GSPSR@.D	14.58	3.08	4.74	0.21
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.TSLETQK#LELM*AEISNLK#.L	12.85	2.00	6.44	0.16
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	K.VPGHEASVDDNPFGTR@.K	8.22	3.85	2.14	0.47
Q8C8U0_LIPB1_MOUSE	Ppfibp1	Liprin-beta-1 OS=Mus mu	R.WLDDIGLPQYK#.T	17.75	7.05	2.52	0.40
G3X959_G3X959_MOUSE	Pphln1	Periphilin 1, isoform CRA	R.DASPSSSSAVASSK#.A	17.84	13.06	1.37	0.73
G3X959_G3X959_MOUSE	Pphln1	Periphilin 1, isoform CRA	R.FITEYDNSAQDFGDPF.-	25.27	25.27	1.00	1.00
G3X959_G3X959_MOUSE	Pphln1	Periphilin 1, isoform CRA	K.M*LIEK#DPSLEK#.S	46.71	26.21	1.78	0.56
G3X959_G3X959_MOUSE	Pphln1	Periphilin 1, isoform CRA	K.RPPLLDK.R	24.58	27.46	0.90	1.12
G3X959_G3X959_MOUSE	Pphln1	Periphilin 1, isoform CRA	K.SVQFALR@.Q	37.00	27.74	1.33	0.75
P24369_PPIB_MOUSE	Ppib	Peptidyl-prolyl cis-trans i	K.TVDNFVALATGEK#.G	20.29	25.08	0.81	1.24
P24369_PPIB_MOUSE	Ppib	Peptidyl-prolyl cis-trans i	R.VIKDFM*IQGGDFTR.G	14.75	16.90	0.87	1.15
P24369_PPIB_MOUSE	Ppib	Peptidyl-prolyl cis-trans i	K.VLEGM*DVVR.K	37.03	33.73	1.10	0.91
P24369_PPIB_MOUSE	Ppib	Peptidyl-prolyl cis-trans i	K.VYFDLQIGDESVGR@.V	9.91	10.37	0.96	1.05
P30412_PPIC_MOUSE	Ppic	Peptidyl-prolyl cis-trans i	R.IVIGLFGNVVPK#.T	9.68	8.92	1.08	0.92
P30412_PPIC_MOUSE	Ppic	Peptidyl-prolyl cis-trans i	K.TVENFVALATGEK#.G	10.92	10.56	1.03	0.97
Q9QZH3_PPIE_MOUSE	Ppie	Peptidyl-prolyl cis-trans i	K.HVVFGEVTEGLDVLR@.Q	13.36	5.98	2.23	0.45
Q9QZH3_PPIE_MOUSE	Ppie	Peptidyl-prolyl cis-trans i	K.K#FDDENFILK#.H	31.83	20.56	1.55	0.65
Q9QZH3_PPIE_MOUSE	Ppie	Peptidyl-prolyl cis-trans i	R.SDVVPMTAENFR@.C	8.37	5.68	1.47	0.68
Q9QZH3_PPIE_MOUSE	Ppie	Peptidyl-prolyl cis-trans i	R.SNPQVYM*DIK#.I	10.36	105.62	0.10	10.19
Q9QZH3_PPIE_MOUSE	Ppie	Peptidyl-prolyl cis-trans i	K.TLEENK#EEEGPEPPK#AEAQEGEPTAK#.K	51.54	41.71	1.24	0.81
Q9QZH3_PPIE_MOUSE	Ppie	Peptidyl-prolyl cis-trans i	R.VLYVGGLAEEVDDK#.V	21.21	11.54	1.84	0.54
A2AR02_PPIG_MOUSE	Ppig	Peptidyl-prolyl cis-trans i	R.GGESIYGGFFEDESFAVK#.H	31.47	11.00	2.86	0.35
Q9D868_PPIH_MOUSE	Ppih	Peptidyl-prolyl cis-trans i	R.GPFADENFK#.L	13.26	15.44	0.86	1.16
Q9D868_PPIH_MOUSE	Ppih	Peptidyl-prolyl cis-trans i	K.IIDGLLVM*R@.K	22.39	15.19	1.47	0.68
Q9D868_PPIH_MOUSE	Ppih	Peptidyl-prolyl cis-trans i	R.M*K#IELFADVVPK#.T	13.42	10.81	1.24	0.81
Q9D0W5_PPIL1_MOUSE	Ppil1	Peptidyl-prolyl cis-trans i	K.DFM*IQGGDPTGTGR@.G	11.99	8.52	1.41	0.71
Q9D0W5_PPIL1_MOUSE	Ppil1	Peptidyl-prolyl cis-trans i	R.GGASIYGK#.Q	112.51	63.01	1.79	0.56
Q9D0W5_PPIL1_MOUSE	Ppil1	Peptidyl-prolyl cis-trans i	R.IIKDFM*IQGGDPTGTGR.G	20.55	15.54	1.32	0.76
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.DLLTDEPFSR@.Q	13.62	7.73	1.76	0.57
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.QDIITLQDPTNLDK#FNVSNFFHVK#.N	11.80	5.23	2.26	0.44
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.SAEEEPSTSTATPTAK#.K	4.90	3.37	1.46	0.69
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	K.SQFFITFR@.S	9.32	5.31	1.75	0.57
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.TTGNVYTYEAVEQLNIK#.A	5.29	2.78	1.90	0.53
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.DLLTDEPFSR@.Q	13.29	7.78	1.71	0.58
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.ETLQELYK#.E	13.33	5.60	2.38	0.42
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.GVLSM*ANSGPNTNK#.S	5.95	3.23	1.84	0.54
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	K.M*SQPQPGNQGPQTYR@.Q	5.73	2.48	2.31	0.43
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.QDIITLQDPTNLDK#FNVSNFFHVK#.N	5.16	3.47	1.49	0.67
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.QDIITLQDPTNLDK#FNVSNFFHVK#.N	17.95	7.94	2.26	0.44
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.SAEEEPSTSTATPTAK#.K	10.72	6.00	1.79	0.56
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	K.VSASFTSTAM*VPETTHEAAVIDEDVLR@.Y	8.99	4.06	2.22	0.45
Q9D787_PPIL2_MOUSE	Ppil2	Peptidyl-prolyl cis-trans i	R.VVGGFDTLTAM*ENVESDPK#.T	5.20	3.11	1.67	0.60
Q9D6L8_PPIL3_MOUSE	Ppil3	Peptidyl-prolyl cis-trans i	K.GFM*VQTGDPTGTGR@.G	7.36	3.90	1.89	0.53
Q9CXG3_PPIL4_MOUSE	Ppil4	Peptidyl-prolyl cis-trans i	R.IGADEEIDDFK#GR@.S	16.48	10.39	1.59	0.63
Q9CXG3_PPIL4_MOUSE	Ppil4	Peptidyl-prolyl cis-trans i	K.LNPVTTDEDLEIIFSR@.F	7.17	4.27	1.68	0.60
Q9CXG3_PPIL4_MOUSE	Ppil4	Peptidyl-prolyl cis-trans i	K.YDLILDEQGEDSK#.S	6.42	2.33	2.75	0.36
P62137_PP1A_MOUSE	Ppp1ca	Serine/threonine-protei	R.AHQVVEDGYEFFAK#.R	48.57	34.84	1.39	0.72
P62137_PP1A_MOUSE	Ppp1ca	Serine/threonine-protei	K.IRYPENFFLLR.G	22.79	14.37	1.59	0.63
P62137_PP1A_MOUSE	Ppp1ca	Serine/threonine-protei	R.LFEYGGFPPESNYLFLGDYVDR@.G	3.93	3.71	1.06	0.94
P62137_PP1A_MOUSE	Ppp1ca	Serine/threonine-protei	R.LLEVQGSR@PGK#.N	9.06	5.18	1.75	0.57
P62137_PP1A_MOUSE	Ppp1ca	Serine/threonine-protei	K.LNLDSIIGR@.L	19.71	10.57	1.87	0.54
P62137_PP1A_MOUSE	Ppp1ca	Serine/threonine-protei	R.YPENFFLLR@.G	12.61	11.30	1.12	0.90
P62137_PP1A_MOUSE	Ppp1ca	Serine/threonine-protei	R.AHQVVEDGYEFFAK#.R	17.60	6.36	2.77	0.36
P62137_PP1A_MOUSE	Ppp1ca	Serine/threonine-protei	R.AHQVVEDGYEFFAK#.R	35.83	4.83	7.42	0.13
P62137_PP1A_MOUSE	Ppp1ca	Serine/threonine-protei	R.YPENFFLLR@.G	8.70	3.08	2.82	0.35
P62141_PP1B_MOUSE	Ppp1cb	Serine/threonine-protei	K.IK#YPENFFLLR@.G	49.57	31.08	1.60	0.63
P62141_PP1B_MOUSE	Ppp1cb	Serine/threonine-protei	K.IVQM*TEAEVR@.G	36.91	27.47	1.34	0.74
P62141_PP1B_MOUSE	Ppp1cb	Serine/threonine-protei	K.IK#YPENFFLLR@.G	19.28	5.71	3.37	0.30
P62141_PP1B_MOUSE	Ppp1cb	Serine/threonine-protei	K.IK#YPENFFLLR@.G	20.36	4.33	4.70	0.21
P63087_PP1G_MOUSE	Ppp1cc	Serine/threonine-protei	K.NVQLQENEIR@.G	15.97	8.10	1.97	0.51
P63087_PP1G_MOUSE	Ppp1cc	Serine/threonine-protei	K.NVQLQENEIR@.G	10.19	3.87	2.63	0.38
P63087_PP1G_MOUSE	Ppp1cc	Serine/threonine-protei	K.NVQLQENEIR@.G	11.58	2.94	3.94	0.25
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-protei	R.QSATAAPGDAAPPAEK#.K	2.20	1.62	1.36	0.74
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-protei	R.APEVLVK#.F	53.44	11.99	4.46	0.22
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-protei	K.ESPHEPDPEPYEPIPPK#.L	8.80	2.86	3.08	0.32

Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	R.GGDPFWDGPGDPM*R@.G	7.64	5.02	1.52	0.66
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	K.GILQELFLNK#.E	54.31	15.43	3.52	0.28
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	K.GLDSFLTR@.D	46.75	12.74	3.67	0.27
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	K.IIPPQPM*EGLGFLDALNSAPVPGIK#.I	34.40	9.75	3.53	0.28
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	K.LASVLVSDWM*AVIR@.S	13.03	4.34	3.00	0.33
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	K.LLNNWLTYSK#.T	25.73	6.60	3.90	0.26
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	K.LPPVLANLM*GSM*GAGK#.S	12.69	5.15	2.47	0.41
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	R.QSATAAPGDAAPPAEK#.K	11.24	3.38	3.32	0.30
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	R.STGLELDTPSLVPVK#.K	7.36	3.24	2.27	0.44
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	R.STGLELDTPSLVPVK#K#.N	67.99	19.49	3.49	0.29
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	R.APEVLVK#.F	6.93	7.18	0.97	1.04
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	K.IIPPQPM*EGLGFLDALNSAPVPGIK#.I	8.02	1.80	4.46	0.22
Q80W00_PP1RA_MOUSE	Ppp1r10	Serine/threonine-proteir	R.STGLELDTPSLVPVK#K#.N	16.92	3.02	5.60	0.18
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.SASYSYLEDR@.K	18.86	22.21	0.85	1.18
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.TYDETYTR@.Y	8.85	4.90	1.81	0.55
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.AQLHDTNM*ELTDLK#.L	9.36	3.33	2.81	0.36
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.ETLIIEPEK#.N	12.70	6.93	1.83	0.55
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.ETQTDSVSR@.Y	24.56	12.11	2.03	0.49
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.K#FPISTTK#.I	34.92	16.94	2.06	0.49
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.K#SPLIESTANM*ENNQPQK#.A	6.69	2.63	2.54	0.39
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.K#TGSYGALAEISASK#.E	16.75	10.40	1.61	0.62
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.LAYVTPTIPR@.R	145.76	67.91	2.15	0.47
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.LEK#DDSTDFK#K#.L	72.42	25.00	2.90	0.35
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.LK#DENGALIR@.V	14.95	7.36	2.03	0.49
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.LSSSLDNK#.E	28.82	14.75	1.95	0.51
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.QGVDIEAAR@.K	64.00	20.63	3.10	0.32
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.RLASTSDIEEKENR.E	75.29	34.18	2.20	0.45
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.R@LASTSDIEEK#ENR@.E	5.11	2.66	1.92	0.52
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.SASYSYLEDR@.K	130.43	64.81	2.01	0.50
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.SGGTALHVAAAK#.G	42.10	17.00	2.48	0.40
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.SPLIESTANM*ENNQPQK#.A	25.08	10.74	2.34	0.43
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.SPLIESTANM*ENNQPQK#.A	14.78	6.27	2.36	0.42
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.SPLIESTANMENNQPQK#.A	3.97	1.16	3.41	0.29
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.SQLEM*EK#R@.E	16.93	12.39	1.37	0.73
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.STGVSFWTQDSDENEQER@.Q	9.72	4.07	2.39	0.42
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.SYLTPVR@DEESESQR@K#.A	23.09	8.50	2.72	0.37
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.TGSYGALAEISASK#.E	60.97	27.60	2.21	0.45
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.TPPGSSSAGTQSSTSNR@.L	20.36	11.02	1.85	0.54
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.TYDETYTR@.Y	80.36	37.90	2.12	0.47
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.WIGSETDLEPPVVK#.R	17.41	6.62	2.63	0.38
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.LAYVTPTIPR@.R	24.98	9.98	2.50	0.40
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	R.SASYSYLEDR@.K	9.69	14.84	0.65	1.53
Q9DBR7_MYPT1_MOUSE	Ppp1r12a	Protein phosphatase 1 re	K.TGSYGALAEISASK#.E	14.15	4.68	3.02	0.33
Q8BG95_MYPT2_MOUSE	Ppp1r12b	Protein phosphatase 1 re	R.LESGGTNPTSSDSYSDR@.A	4.68	1.39	3.38	0.30
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	K.AQLEQSVEENK#ER@.M	12.09	6.42	1.88	0.53
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	K.DSEGLGISIIGM*GAGADM*GLEK#.L	4.11	2.84	1.45	0.69
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.ER@PGEQSEVAQLIQQTLEQER@.W	49.52	25.75	1.92	0.52
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.ETQAQYQALER@.K	28.01	12.63	2.22	0.45
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.FDSK#PAPSAQPAPPPHPPSR@.L	17.91	17.26	1.04	0.96
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.GPGGQQPPQHR@.V	3.74	1.72	2.17	0.46
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	K.HAVTEAEIQQLKR.K	59.02	29.29	2.01	0.50
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	K.ISELEGNLQTLR@.N	22.91	13.20	1.74	0.58
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.K#LQSLEQEK#.G	22.31	11.16	2.00	0.50
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.LELFPVELEK#.D	29.14	23.34	1.25	0.80
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.NEDVDPM*AASAEYELEK#.R	10.93	8.11	1.35	0.74
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.SAYEAGIQALKPPDAPGPDEAPK.A	12.41	6.54	1.90	0.53
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.SVPAASGGDK#EAVAR@.R	9.41	7.56	1.25	0.80
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.VLEESELAR@.K	43.89	27.30	1.61	0.62
Q6R891_NEB2_MOUSE	Ppp1r9b	Neurabin-2 OS=Mus musc	R.ER@PGEQSEVAQLIQQTLEQER@.W	12.31	6.09	2.02	0.49
P63330_PP2AA_MOUSE	Ppp2ca	Serine/threonine-proteir	K.YSFLQFDPAPR@.R	13.53	8.47	1.60	0.63
P63330_PP2AA_MOUSE	Ppp2ca	Serine/threonine-proteir	K.SPDTNYLFM*GDYVDR@.G	6.12	2.04	3.00	0.33
P63330_PP2AA_MOUSE	Ppp2ca	Serine/threonine-proteir	K.YSFLQFDPAPR@.R	10.58	6.38	1.66	0.60
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.IGPILDNSTLQSEVKPILEK.L	27.69	17.62	1.57	0.64
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	R.LAGGDWFTSR@.T	18.35	8.21	2.24	0.45
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.LSTIALALGVER@.T	12.93	7.14	1.81	0.55
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.LTQDQDVDVK#.Y	52.13	35.29	1.48	0.68
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	R.NEDVQLR@.L	26.60	9.77	2.72	0.37
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.SALASVIM*GLSPILGK#.D	16.46	9.83	1.67	0.60
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.SEIIPM*FSNLASDEQDSVR.L	7.19	5.37	1.34	0.75
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.IGPILDNSTLQSEVK#PILEK#.L	33.60	18.27	1.84	0.54
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	R.LAGGDWFTSR@.T	16.24	6.87	2.37	0.42
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.LSTIALALGVER@.T	8.98	5.61	1.60	0.62
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	R.M*AGDPVANVR@.F	15.70	8.80	1.78	0.56
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.SALASVIM*GLSPILGK#.D	10.67	5.37	1.99	0.50
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.SEIIPM*FSNLASDEQDSVR@.L	5.29	3.31	1.60	0.63
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.IGPILDNSTLQSEVK#PILEK#.L	43.26	13.10	3.30	0.30
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	R.LAGGDWFTSR@.T	11.36	3.41	3.33	0.30
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.LSTIALALGVER@.T	9.46	3.02	3.13	0.32
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.LTQDQDVDVK#.Y	35.09	8.35	4.20	0.24
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	R.M*AGDPVANVR@.F	18.36	12.22	1.50	0.67
Q76MZ3_2AAA_MOUSE	Ppp2r1a	Serine/threonine-proteir	K.SALASVIM*GLSPILGK#.D	18.32	3.84	4.77	0.21
Q6P1F6_2ABA_MOUSE	Ppp2r2a	Serine/threonine-proteir	R.VVIFQQEQENK#.I	7.72	4.01	1.93	0.52
Q91V89_Q91V89_MOUSE	Ppp2r5d	Protein Ppp2r5d OS=Mus	K.ESSLTEPVIVGLLK#.F	5.95	3.74	1.59	0.63
Q91V89_Q91V89_MOUSE	Ppp2r5d	Protein Ppp2r5d OS=Mus	R.FLESPDFQPNIAK#.K	8.35	5.66	1.48	0.68
Q61151_2A5E_MOUSE	Ppp2r5e	Serine/threonine-proteir	R.FLESQEFQPSIAK#.K	6.76	6.54	1.03	0.97
Q91VJ5_PQBP1_MOUSE	Pqbp1	Polyglutamine-binding p	K.HLEPEPEEEIIAEDYDDDPVDYEATR.I	4.83	4.43	1.09	0.92
Q91VJ5_PQBP1_MOUSE	Pqbp1	Polyglutamine-binding p	K.TGADTTAAGPLFQQRPYPSPGAVLR.A	6.00	4.85	1.24	0.81
Q9JIG8_PRAF2_MOUSE	Praf2	PRA1 family protein 2 OS	R.ALDDFVLGSAR@.L	41.32	12.49	3.31	0.30
Q9JIG8_PRAF2_MOUSE	Praf2	PRA1 family protein 2 OS	K.R@TPM*GLLLEALGQEQEAGS.-	4.39	2.32	1.89	0.53
Q9EQC8_Q9EQC8_MOUSE	Prcc	Papillary renal cell carcir	K.TK#PASLAPVLGTTTTTPSPSAIK#.A	9.20	3.88	2.37	0.42
P35700_PRDX1_MOUSE	Prdx1	Peroxiredoxin-1 OS=Mus	K.ADEGISFR.G	12.36	10.35	1.19	0.84
P35700_PRDX1_MOUSE	Prdx1	Peroxiredoxin-1 OS=Mus	K.ATAVM*PDGQFK#.D	11.23	11.87	0.95	1.06
P35700_PRDX1_MOUSE	Prdx1	Peroxiredoxin-1 OS=Mus	R.GLFIIDDK#.G	15.79	15.50	1.02	0.98
P35700_PRDX1_MOUSE	Prdx1	Peroxiredoxin-1 OS=Mus	R.SVDEIIR.L	12.93	8.94	1.45	0.69
P35700_PRDX1_MOUSE	Prdx1	Peroxiredoxin-1 OS=Mus	R.TIAQDYGVLK.A	8.55	10.79	0.79	1.26
Q61171_PRDX2_MOUSE	Prdx2	Peroxiredoxin-2 OS=Mus	K.SAPDFTATAVVDGAFK#.E	7.39	4.00	1.85	0.54
P20108_PRDX3_MOUSE	Prdx3	Thioredoxin-dependent p	R.DYGVLLESAGIALR.G	26.66	13.97	1.91	0.52
P20108_PRDX3_MOUSE	Prdx3	Thioredoxin-dependent p	R.GLFIIDPNGVVK#.H	18.15	12.98	1.40	0.72
P20664_PRI1_MOUSE	Prim1	DNA primase small subur	K.VFEQFLENLDK#.S	8.19	1.99	4.11	0.24
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	K.DSHLHFEAISDEEK#.T	12.51	2.83	4.42	0.23
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	R.ENLEDEYEPR@.R	11.71	1.18	9.95	0.10
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	K.IPASGISQILDLVK#.G	36.65	12.29	2.98	0.34
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	R.SLPAVQSDER@.L	10.64	4.91	2.17	0.46

P33610_PRI2_MOUSE	Prim2	DNA primase large subun	K.VPFADALDLFR@.G	30.72	11.39	2.70	0.37
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	R.EQDIM*ASSPSLSGIK#.L	5.93	1.62	3.67	0.27
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	K.IPASGISQILDLVK#.G	32.38	7.56	4.28	0.23
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	K.VPFADALDLFR@.G	24.27	5.79	4.19	0.24
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	K.AIENLGVSYVK#.G	16.58	5.09	3.26	0.31
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	K.IPASGISQILDLVK#.G	29.56	4.60	6.42	0.16
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	R.SLPAVQSDER@.L	7.21	6.39	1.13	0.89
P33610_PRI2_MOUSE	Prim2	DNA primase large subun	K.VPFADALDLFR@.G	20.96	5.06	4.14	0.24
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	K.IADFGLSNM*M*SDGEFLR@.T	4.42	4.42	1.00	1.00
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	K.IGHYILGDTLGVGTFGK#.V	16.58	15.80	1.05	0.95
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	K.M*SLQLYQVDSR@.T	8.93	2.53	3.53	0.28
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	R.NHQDPLAVAYHLIIDNR@.R	6.16	2.53	2.43	0.41
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	R.TYLLDFR@.S	9.70	4.99	1.94	0.51
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	R.VPFLVAETPR.A	39.82	25.82	1.54	0.65
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	R.HTLDELNPQK#.S	9.70	4.99	1.94	0.51
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	K.IADFGLSNM*M*SDGEFLR@.T	9.57	4.16	2.30	0.44
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	K.IGHYILGDTLGVGTFGK#.V	18.81	7.46	2.52	0.40
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	R.TYLLDFR@.S	11.91	4.24	2.81	0.36
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	R.VPFLVAETPR@.A	36.63	18.04	2.03	0.49
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	K.IADFGLSNM*M*SDGEFLR@.T	7.42	3.09	2.41	0.42
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	K.IGHYILGDTLGVGTFGK#.V	20.71	4.78	4.33	0.23
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	R.TYLLDFR@.S	13.22	4.48	2.95	0.34
Q5EG47_AAPK1_MOUSE	Prkaa1	5'-AMP-activated protein	R.VPFLVAETPR@.A	28.47	10.23	2.78	0.36
Q9R078_AAKB1_MOUSE	Prkab1	5'-AMP-activated protein	K.FFVDGQWTHDPSEPIVTSQLGTVNNIIQVK#.K	9.60	3.47	2.77	0.36
Q9R078_AAKB1_MOUSE	Prkab1	5'-AMP-activated protein	K.K#TDFEVFDALM*VDSQK#.C	12.91	4.59	2.81	0.36
Q9R078_AAKB1_MOUSE	Prkab1	5'-AMP-activated protein	R.SQNNFVAILDLPEGEHQYK#.F	8.12	4.04	2.01	0.50
Q9R078_AAKB1_MOUSE	Prkab1	5'-AMP-activated protein	K.YVTTLLYK#PI.-	26.67	9.52	2.80	0.36
P05132_KAPCA_MOUSE	Prkaca	cAMP-dependent protein	R.ILQAVNFPFLVK#.L	9.58	6.36	1.51	0.66
P68181_KAPCB_MOUSE	Prkacb	cAMP-dependent protein	R.ILQAVEFPFLVR@.L	15.12	2.36	6.40	0.16
O54950_AAKG1_MOUSE	Prkag1	5'-AMP-activated protein	K.FDVINLAAEK#.T	58.69	26.74	2.19	0.46
O54950_AAKG1_MOUSE	Prkag1	5'-AMP-activated protein	R.LPVIDPESGNTLYILTHK#.R	27.81	12.46	2.23	0.45
O54950_AAKG1_MOUSE	Prkag1	5'-AMP-activated protein	K.LVVFDTSLQVK#.K	14.22	8.66	1.64	0.61
O54950_AAKG1_MOUSE	Prkag1	5'-AMP-activated protein	K.TYNNLDVSVTK#.A	28.39	12.03	2.36	0.42
O54950_AAKG1_MOUSE	Prkag1	5'-AMP-activated protein	R.VVDIYSK#.F	69.37	30.96	2.24	0.45
O54950_AAKG1_MOUSE	Prkag1	5'-AMP-activated protein	K.FDVINLAAEK#.T	11.06	4.64	2.38	0.42
O54950_AAKG1_MOUSE	Prkag1	5'-AMP-activated protein	R.LPVIDPESGNTLYILTHK#.R	11.52	4.60	2.50	0.40
O54950_AAKG1_MOUSE	Prkag1	5'-AMP-activated protein	R.VSALPVVDEK#.G	10.52	3.53	2.98	0.34
O54950_AAKG1_MOUSE	Prkag1	5'-AMP-activated protein	R.LPVIDPESGNTLYILTHK#.R	15.21	7.31	2.08	0.48
Q9DBC7_KAP0_MOUSE	Prkar1a	cAMP-dependent protein	K.HNIQALLK#.D	9.84	7.14	1.38	0.73
Q9DBC7_KAP0_MOUSE	Prkar1a	cAMP-dependent protein	R.LTVADALEPVQFEDGQK#.I	15.12	6.18	2.44	0.41
Q9DBC7_KAP0_MOUSE	Prkar1a	cAMP-dependent protein	R.R@SENEEFVEVGR@.L	7.80	6.37	1.22	0.82
Q9DBC7_KAP0_MOUSE	Prkar1a	cAMP-dependent protein	R.SENEEFVEVGR@.L	8.20	4.26	1.92	0.52
P12367_KAP2_MOUSE	Prkar2a	cAMP-dependent protein	R.GSFGELALM*YNTPR@.A	13.50	7.12	1.90	0.53
P12367_KAP2_MOUSE	Prkar2a	cAMP-dependent protein	K.M*FESFIESVPLFK#.S	10.33	3.89	2.66	0.38
P12367_KAP2_MOUSE	Prkar2a	cAMP-dependent protein	K.NLDQEQLSQVLDAM*FEK#.I	4.94	2.19	2.26	0.44
P12367_KAP2_MOUSE	Prkar2a	cAMP-dependent protein	K.TDEHVIDQGDDGDNFYVIER@.G	19.20	4.99	3.85	0.26
P31324_KAP3_MOUSE	Prkar2b	cAMP-dependent protein	K.EGEHVIDQGDDGDNFYVIDR@.G	14.33	3.08	4.65	0.22
P31324_KAP3_MOUSE	Prkar2b	cAMP-dependent protein	R.HQPADLLEFALQHFTR@.L	6.98	1.47	4.75	0.21
P31324_KAP3_MOUSE	Prkar2b	cAMP-dependent protein	R.K#M*YESFIESLPFLK#.S	7.40	1.77	4.18	0.24
P31324_KAP3_MOUSE	Prkar2b	cAMP-dependent protein	K.M*YESFIESLPFLK#.S	8.80	7.46	1.18	0.85
P31324_KAP3_MOUSE	Prkar2b	cAMP-dependent protein	R.TWGDAGAAAGGGIPSK#.G	5.88	2.15	2.73	0.37
P31324_KAP3_MOUSE	Prkar2b	cAMP-dependent protein	K.VYNDGEQIIAQGDLADSFFIVESGEVK#.I	8.11	2.65	3.06	0.33
Q91VJ2_PRDBP_MOUSE	Prkcdbp	Protein kinase C delta-bi	K.LATM*LEALR@.E	9.92	2.39	4.15	0.24
Q62074_KPCI_MOUSE	Prkci	Protein kinase C iota type	K.ASSSLGLQDFDLLR@.V	18.99	7.88	2.41	0.42
Q62074_KPCI_MOUSE	Prkci	Protein kinase C iota type	R.DLK#LDNVLLDSEGHIK#.L	21.75	9.50	2.29	0.44
Q62074_KPCI_MOUSE	Prkci	Protein kinase C iota type	R.DLK#LDNVLLDSEGHIK#.L	11.02	6.15	1.79	0.56
Q62074_KPCI_MOUSE	Prkci	Protein kinase C iota type	K.ELVNDDEDIDWVQTEK#.H	5.18	1.82	2.84	0.35
Q8BZ03_KPCD2_MOUSE	Prkd2	Serine/threonine-protein	R.SVVGTPAYLAPEVLLNQGYNR@.S	14.06	3.52	4.00	0.25
Q9WTX2_PRKRA_MOUSE	Prkra	Interferon-inducible dou	R.EDSGTFSLGK#.M	20.35	7.59	2.68	0.37
Q9WTX2_PRKRA_MOUSE	Prkra	Interferon-inducible dou	R.SDVQVHVPTFTFR@.V	17.28	8.67	1.99	0.50
Q9WTX2_PRKRA_MOUSE	Prkra	Interferon-inducible dou	K.TPIQVLHEYGM*K#.T	32.33	12.75	2.54	0.39
Q9JIF0_ANM1_MOUSE	Prmt1	Protein arginine N-methy	R.ATLYVTAIEDR@.Q	15.45	3.80	4.06	0.25
Q8CIG8_ANM5_MOUSE	Prmt5	Protein arginine N-methy	K.AAILPTSIFLTNK#.K	12.56	12.04	1.04	0.96
Q8CIG8_ANM5_MOUSE	Prmt5	Protein arginine N-methy	R.GPLVNASLR@.A	15.55	11.51	1.35	0.74
Q8CIG8_ANM5_MOUSE	Prmt5	Protein arginine N-methy	R.SDLLLSGR@.D	10.27	10.60	0.97	1.03
Q8CIG8_ANM5_MOUSE	Prmt5	Protein arginine N-methy	R.VPLVAPEDLR@.D	29.20	16.72	1.75	0.57
Q8CIG8_ANM5_MOUSE	Prmt5	Protein arginine N-methy	K.YSQYQQAIYK#.C	5.43	3.47	1.57	0.64
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.ALQDEWDAVM*LHSFTLR@.Q	44.47	29.16	1.53	0.66
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.ALQDEWDAVMLHSFTLR@.Q	86.79	48.59	1.79	0.56
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.ATVLTTER@.K	212.48	124.43	1.71	0.59
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	R.EALATLK#PQAGLIVPQAVPSSQPSVVGAGEPMDLGELVGM*TPEIIQK#.L	8.09	4.82	1.68	0.60
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.FIASTGM*DR@.S	182.13	105.66	1.72	0.58
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.ILTGGADK#NVVVFDK#.S	173.62	107.27	1.62	0.62
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.K#VTSVVFHPSQELVFSASPDATIR@.I	28.58	15.29	1.87	0.54
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.STEQILATLK#.G	250.77	126.38	1.98	0.50
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.TLQLDNNFEVK#.S	106.86	64.16	1.67	0.60
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.ATVLTTER@.K	57.63	20.76	2.78	0.36
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.FIASTGM*DR@.S	32.34	14.18	2.28	0.44
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.ILTGGADK#NVVVFDK#.S	35.64	11.75	3.03	0.33
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	K.STEQILATLK#.G	58.76	15.10	3.89	0.26
Q99KP6_PRP19_MOUSE	Prpf19	Pre-mRNA-processing fac	R.TNVANFPGHSGPITSIAFSENGYYLATAADDSSVK#.L	8.63	2.68	3.22	0.31
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	K.DQTK#PTPLILDEQGR@.T	19.25	9.66	1.99	0.50
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	R.LGLTPPPEPK#.V	33.81	30.13	1.12	0.89
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	K.LQAEISQAAR@.K	42.15	23.46	1.80	0.56
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	K.REDYFGITNLVEHPAQLNPPVDNDTPVTLGVYLTK.K	8.26	4.62	1.79	0.56
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	R.VLGTEAVQDPTK#.V	9.35	6.78	1.38	0.73
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	K.DQTKPTPLILDEQGR.T	15.83	8.39	1.89	0.53
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	R.FVDK#LFEAVEEGR@.S	15.74	6.94	2.27	0.44
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	R.LGLTPPPEPK#.V	26.35	14.43	1.83	0.55
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	K.LQAEISQAAR@.K	25.98	15.12	1.72	0.58
Q922U1_PRPF3_MOUSE	Prpf3	U4/U6 small nuclear ribc	K.QLSFISPPAPQPK#.T	9.22	6.74	1.37	0.73
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.IEEYISK#.Q	82.99	23.98	3.46	0.29
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.IM*GVAGGLTNLSK#.M	51.91	20.11	2.58	0.39
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.IYEYVESR@.M	70.74	25.75	2.75	0.36
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.LGLTEIR@.K	40.09	17.59	2.28	0.44
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.LGLTEIR@K#.Q	16.21	4.63	3.50	0.29
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.M*SFGEIEEDAYQEDLGFSLGHLGK#.S	43.20	11.65	3.71	0.27
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.M*SFIAPNLSIIIGASTAAK#.I	7.70	3.55	2.17	0.46
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.M*SFIAPNLSIIIGASTAAK#.I	7.94	3.45	2.30	0.43
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.QANVSEVM*GPVEAAPEYR@.V	21.58	8.05	2.68	0.37
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.QSVVYGGK#.S	21.22	5.64	3.76	0.27
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.R@FPELESLVPNALDYIR@.T	69.19	24.53	2.82	0.35
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.SSGTASSVAFTPLQGLEIVNPQAAEK#.K	30.45	8.86	3.44	0.29

Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.SSGTASSVAFTPLQGLEIVNPQAAEK#K#.V	17.36	4.63	3.75	0.27
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.VGYELK#DEIER@.K	114.51	39.78	2.88	0.35
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.VIVDANNLTVEIENELNIIHK#.F	85.77	27.91	3.07	0.33
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.IEEYISK#.Q	42.02	12.94	3.25	0.31
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.IM*GVAGGLTNLSK#.M	36.49	15.72	2.32	0.43
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.IYEYVESR@.M	42.09	11.27	3.73	0.27
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.M*SFGEIEEDAYQEDLGFSLGHLGK#.S	57.06	13.31	4.29	0.23
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.M*SFIAPNLSIIIGASTAAK#.I	11.37	3.65	3.11	0.32
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.QANVSEVM*GPVEAAPEYR@.V	17.28	5.77	3.00	0.33
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.RFPELESLVPNALDYIR.T	78.85	18.74	4.21	0.24
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.SSGTASSVAFTPLQGLEIVNPQAAEK#.K	26.51	6.61	4.01	0.25
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.SSGTASSVAFTPLQGLEIVNPQAAEK#K#.V	15.24	5.28	2.89	0.35
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.VGYELK#DEIER@.K	88.11	22.69	3.88	0.26
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.VIVDANNLTVEIENELNIIHK#.F	81.22	25.67	3.16	0.32
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.IYEYVESR@.M	14.86	3.29	4.52	0.22
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	R.M*SFGEIEEDAYQEDLGFSLGHLGK#.S	25.13	1.96	12.85	0.08
Q8CCF0_PRP31_MOUSE	Prpf31	U4/U6 small nuclear ribc	K.VGYELK#DEIER@.K	27.08	8.59	3.15	0.32
Q4FK66_PR38A_MOUSE	Prpf38a	Pre-mRNA-splicing factor	K.DAHSIHGTNPQYLVEK#.I	27.69	23.12	1.20	0.84
Q4FK66_PR38A_MOUSE	Prpf38a	Pre-mRNA-splicing factor	R.M*LGALYM*R@.L	21.16	15.11	1.40	0.71
Q4FK66_PR38A_MOUSE	Prpf38a	Pre-mRNA-splicing factor	K.M*LQIQPEK#DIIVEFIK#.N	7.50	6.77	1.11	0.90
Q4FK66_PR38A_MOUSE	Prpf38a	Pre-mRNA-splicing factor	K.YLEPLYNDYR@.K	8.79	7.26	1.21	0.83
Q4FK66_PR38A_MOUSE	Prpf38a	Pre-mRNA-splicing factor	K.DAHSIHGTNPQYLVEK#.I	21.83	8.26	2.64	0.38
Q4FK66_PR38A_MOUSE	Prpf38a	Pre-mRNA-splicing factor	R.YVLEEAEQLEPR@.V	19.70	5.96	3.31	0.30
Q80SY5_PR38B_MOUSE	Prpf38b	Pre-mRNA-splicing factor	K.LEWFSTLFPR@.I	15.35	6.88	2.23	0.45
Q80SY5_PR38B_MOUSE	Prpf38b	Pre-mRNA-splicing factor	K.TYHEVVDEIYFK#.V	40.11	12.68	3.16	0.32
Q9DAW6_PRP4_MOUSE	Prpf4	U4/U6 small nuclear ribc	K.AGIEAGNINITSGEVFEIEEHISER@.Q	14.21	13.66	1.04	0.96
Q9DAW6_PRP4_MOUSE	Prpf4	U4/U6 small nuclear ribc	R.ALGEPITLFGEGPAER@.R	32.35	23.55	1.37	0.73
Q9DAW6_PRP4_MOUSE	Prpf4	U4/U6 small nuclear ribc	K.FEPIHGDFLLTGAYDNTAK#.I	28.87	22.08	1.31	0.76
Q9DAW6_PRP4_MOUSE	Prpf4	U4/U6 small nuclear ribc	R.GHNTNVGAIVFHPK#.S	19.30	12.71	1.52	0.66
Q9DAW6_PRP4_MOUSE	Prpf4	U4/U6 small nuclear ribc	R.LWIANYSLPR@.A	17.01	16.56	1.03	0.97
Q9DAW6_PRP4_MOUSE	Prpf4	U4/U6 small nuclear ribc	K.TK#APDDLVAPVVK#.K	35.42	29.71	1.19	0.84
Q9DAW6_PRP4_MOUSE	Prpf4	U4/U6 small nuclear ribc	R.ALGEPITLFGEGPAER.R	14.21	5.34	2.66	0.38
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.ELEDLEGYQNTIVAGGLITK.S	5.35	2.71	1.98	0.51
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.AEQM*FGEM*EVWNAISER@.D	13.99	7.26	1.93	0.52
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.ALEK#EEEEEK#QK#.T	156.22	63.42	2.46	0.41
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.ELEDLEGYQNTIVAGGLITK#.S	63.32	19.52	3.24	0.31
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.EPAFEDITLESER@.K	59.96	23.98	2.50	0.40
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.FLENHEK#.M	20.55	6.01	3.42	0.29
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.FTNM*LGQPGSTALDLFK#.F	111.20	47.76	2.33	0.43
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.FTNMLGQPGSTALDLFK#.F	14.70	6.48	2.27	0.44
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.FVKEPAFEDITLESER.K	271.38	94.68	2.87	0.35
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.FYVEDLK#.A	183.80	68.79	2.67	0.37
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.GGLM*VSEM*ESQPPSR@.G	8.57	4.08	2.10	0.48
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.K#AEQMFGEMEVWNAISER@.D	7.31	2.64	2.76	0.36
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.K#QAFNAYK#.V	16.31	6.35	2.57	0.39
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.LAFNSLLEK#.A	324.33	114.83	2.82	0.35
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.MIINDPR@.Y	23.06	6.34	3.63	0.28
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.QAFNAYK#.V	50.60	22.81	2.22	0.45
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.QATPPIELDAVWEDIR@.E	31.50	11.48	2.74	0.36
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.QSTWEK#PDDLK#TPAEQLLSK#.C	15.87	6.89	2.30	0.43
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.QSTWEK#PDDLK#TPAEQLLSK#.C	54.75	26.98	2.03	0.49
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.R@TLLEQLDDDQ.-	23.00	7.72	2.98	0.34
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.SDSGK#PYYYNSQTK#.E	17.53	4.14	4.23	0.24
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.SNLHAM*IK#.A	27.77	12.31	2.26	0.44
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.STTLDAGNIK#.L	180.21	70.99	2.54	0.39
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.TLLEQLDDDQ.-	120.08	120.08	1.00	1.00
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.TPAEQLLSK#.C	35.19	13.98	2.52	0.40
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.VPSNASWEQAMK#.M	24.76	6.27	3.95	0.25
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.VQTEK#EEK#EEAR@.S	43.46	16.14	2.69	0.37
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.ELEDLEGYQNTIVAGGLITK#.S	27.86	8.53	3.27	0.31
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.EPAFEDITLESER@.K	29.34	7.99	3.67	0.27
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.FTNM*LGQPGSTALDLFK#.F	62.27	21.69	2.87	0.35
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.FVK#EPAFEDITLESER@.K	116.87	27.40	4.27	0.23
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.FYVEDLK#.A	74.15	20.88	3.55	0.28
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.LAFNSLLEK#.A	103.09	34.12	3.02	0.33
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.QATPPIELDAVWEDIR@.E	8.20	3.30	2.48	0.40
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.R@TLLEQLDDDQ.-	11.21	2.54	4.41	0.23
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.STTLDAGNIK#.L	65.68	25.88	2.54	0.39
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.TLLEQLDDDQ.-	53.65	53.65	1.00	1.00
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	K.TPAEQLLSK#.C	14.49	3.91	3.70	0.27
Q9R1C7_PR40A_MOUSE	Prpf40a	Pre-mRNA-processing fac	R.TYYYNTETK#.Q	42.18	15.09	2.80	0.36
Q61136_PRP4B_MOUSE	Prpf4b	Serine/threonine-proteir	R.APEIIIGK#.S	16.82	12.01	1.40	0.71
Q61136_PRP4B_MOUSE	Prpf4b	Serine/threonine-proteir	R.ANQEVAVK#.I	13.12	4.97	2.64	0.38
Q61136_PRP4B_MOUSE	Prpf4b	Serine/threonine-proteir	R.ISINQALQHAFIQEK#.I	21.21	6.18	3.43	0.29
Q61136_PRP4B_MOUSE	Prpf4b	Serine/threonine-proteir	R.SYSQQLFLALK#.L	14.66	3.46	4.24	0.24
Q61136_PRP4B_MOUSE	Prpf4b	Serine/threonine-proteir	R.TK#LDDLALLEDLEK#.Q	12.35	6.87	1.80	0.56
Q61136_PRP4B_MOUSE	Prpf4b	Serine/threonine-proteir	K.VQSGM*GLILQGYESGSEEEGEIHEK#.A	8.76	2.35	3.73	0.27
Q61136_PRP4B_MOUSE	Prpf4b	Serine/threonine-proteir	R.YNVYGYTGQGVFSNVVR@.A	13.13	7.25	1.81	0.55
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.AAELETDIR@.A	44.64	19.04	2.34	0.43
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.AAVELEEPEDAR@.I	56.29	16.18	3.48	0.29
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.AEVLWLMGAK#.S	8.95	1.63	5.48	0.18
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.ESLEALLQR@.A	44.92	17.86	2.52	0.40
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.FELQHGTEEQQEEVR@.K	40.80	14.59	2.80	0.36
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.GQIEEQGELM*EK#.A	22.55	8.13	2.77	0.36
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.HIWITAAK#.L	20.26	5.72	3.54	0.28
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.IDSDLGDAWAFFYK#.F	20.79	9.67	2.15	0.47
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.IGEILVLVAAR@.I	11.95	3.58	3.33	0.30
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.K#IGEILVLVAAR@.I	13.45	6.65	2.02	0.49
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.K#LAEVTEEEWLSIPEVGDAR@.N	8.26	4.06	2.03	0.49
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.LEEANGNTQM*VEK#.I	5.37	1.40	3.85	0.26
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.LEEVTGK#.L	48.63	12.72	3.82	0.26
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.LESENNEYER@.A	27.13	8.50	3.19	0.31
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.LETYENAR@.K	37.87	11.75	3.22	0.31
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.LSQVSDSVSGQTVVDPK#.G	27.76	10.06	2.76	0.36
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.NIANTLM*AK#.A	31.89	9.80	3.25	0.31
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.NPGLWLESVR@.L	34.36	15.11	2.27	0.44
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.SEDVWLEAAR@.L	11.80	6.59	1.79	0.56
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.AAELETDIR@.A	31.67	11.50	2.75	0.36
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.AAVELEEPEDAR@.I	34.41	8.61	4.00	0.25
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.AVVAQAVR@.H	46.86	15.15	3.09	0.32
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.ESLEALLQR@.A	35.02	8.16	4.29	0.23
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.FELQHGTEEQQEEVR@.K	22.98	3.98	5.78	0.17
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.GQIEEQGELM*EK#.A	17.52	4.62	3.79	0.26

Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.HIWITAAK#.L	16.48	8.66	1.90	0.53
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.HYEDFPK#.L	17.81	5.33	3.34	0.30
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.IDSDLGDAWAFFYK#.F	23.81	7.29	3.27	0.31
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.LEEANGNTQM*VEK#.I	7.47	2.63	2.84	0.35
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.LESENNEYER.A	28.28	7.34	3.85	0.26
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	R.LSQVSDSVSGQTVVDPK#.G	27.45	9.78	2.81	0.36
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.NPGLWLESVR@.L	20.91	10.20	2.05	0.49
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.SEDVWLEAAR@.L	11.50	3.90	2.95	0.34
Q91YR7_PRP6_MOUSE	Prpf6	Pre-mRNA-processing fac	K.WLAGDVPAAR@.S	15.30	8.86	1.73	0.58
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.ALDIPLVK#.N	76.78	40.83	1.88	0.53
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.ALNM*AIPGGPK#.F	24.10	12.76	1.89	0.53
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.ANPALYVLR@.E	66.02	28.35	2.33	0.43
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.AQIAGYLYGVSPPDNPQVK#.E	14.31	9.74	1.47	0.68
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.ASEM*AGPPQM*PNDFLSFQDIATEAAHPIR@.L	36.61	20.52	1.78	0.56
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.AVFWDIK#.N	38.27	16.33	2.34	0.43
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.DGVWNLQNEVTK#.E	30.93	16.44	1.88	0.53
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.DIILGM*EISAPSQQR@.Q	30.05	14.77	2.03	0.49
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.DINLQDEDWNEFNDINK#.I	18.48	8.99	2.06	0.49
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.DVM*DSTTTQK#.Y	9.43	5.06	1.86	0.54
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.EAVVNTQELLDLLVK#.C	16.32	8.37	1.95	0.51
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.EELGLIEQAYDNPHEALSR@.I	62.65	29.75	2.11	0.47
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.ELGGLGM*LSM*GHVLIPQSDLR@.W	48.98	20.34	2.41	0.42
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.EQSQLTATQTR@.T	38.28	17.98	2.13	0.47
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.ETGYTYILPK#.N	32.49	20.94	1.55	0.64
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.EVGIEFM*DLYSHLVPVYDVEPLEK#.I	24.19	13.55	1.79	0.56
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.FGDLILK#.A	71.49	24.59	2.91	0.34
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.FNTGPVGK#.G	55.38	29.81	1.86	0.54
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.FPPVVFYTPK#.E	17.55	11.42	1.54	0.65
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.FSPIPFPPLSYK#.H	32.38	22.44	1.44	0.69
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.FTLWWSPTINR@.A	16.74	9.96	1.68	0.59
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.GPGNPVPGPLAPLPDYM*SEEK#.L	6.74	4.02	1.67	0.60
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.GPGNPVPGPLAPLPDYM*SEEKLQEK.A	19.17	13.27	1.44	0.69
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.GTYFPTWEGLFWEK#.A	14.73	12.21	1.21	0.83
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.HDVNLGR@.A	48.32	23.17	2.08	0.48
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.HGDEIITSTTSNYETQTFSSK#.T	50.35	23.68	2.13	0.47
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.HLIYYR@.F	25.46	10.88	2.34	0.43
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.IDLTLLNR@.L	81.64	43.14	1.89	0.53
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.IIHTSVWAGQK#.R	14.96	5.61	2.67	0.37
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.IM*ADNPSWDGEK#.T	12.82	5.69	2.25	0.44
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.ISLIQIFR@.A	47.31	21.13	2.24	0.45
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.ITDAYLDQYLWYEADK#.R	5.13	3.47	1.48	0.68
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.K#GM*LDPLEVHLLDFPNIVIK#.G	28.36	12.81	2.21	0.45
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.LIVDHNIADYM*TAK#.N	72.69	34.86	2.09	0.48
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.LLENM*PM*PWEQIR@.D	9.72	5.89	1.65	0.61
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.LLILALER@.L	74.15	40.98	1.81	0.55
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.LNQSQR@EELGLIEQAYDNPHEALSR@.I	20.02	11.20	1.79	0.56
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.LTPSGYEWGR@.Q	19.23	6.75	2.85	0.35
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.LWNLNNYR@.T	27.08	11.87	2.28	0.44
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.NNVNVASLTQSEIR@.D	25.12	14.82	1.69	0.59
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.NNVNVASLTQSEIR@DIILGM*EISAPSQQR@.Q	8.06	4.43	1.82	0.55
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.QILM*ASGSTTFTK#.I	20.90	14.45	1.45	0.69
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.QQIAEIEK#.Q	56.16	29.73	1.89	0.53
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.R@ALDIPLVK#.N	14.39	11.04	1.30	0.77
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.R@LTLEDLEDSWDR@.G	17.44	6.74	2.59	0.39
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.SVTTVQWENSFVSVYSK#.D	15.55	7.29	2.13	0.47
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.TAEEVAALIR@.S	70.05	34.74	2.02	0.50
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.TEDPDLPAFYFDPLINPISHR@.H	112.60	67.90	1.66	0.60
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.TFEGNLTTK#PINGAIFIFNPR@.T	6.86	4.40	1.56	0.64
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.TGQLFLK#.I	37.11	19.64	1.89	0.53
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.TILQHLSEAWR.C	14.73	7.23	2.04	0.49
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.TVNK#HGDEIITSTTSNYETQTFSSK#.T	11.29	3.39	3.33	0.30
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.VILK#PDK#.T	25.54	11.67	2.19	0.46
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.VPGLPTPIENM*ILR.Y	27.38	15.44	1.77	0.56
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.VPGLPTPIENMILR@.Y	7.71	4.95	1.56	0.64
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.VWAEYALK#.R	38.46	17.17	2.24	0.45
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.VYLGALK#.Y	58.49	25.58	2.29	0.44
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.WLGNLLAR@.Q	25.37	14.63	1.73	0.58
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.WQFTLPM*M*STLYR@.L	17.38	8.00	2.17	0.46
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.YIQPWESEFIDSQR@.V	26.03	17.80	1.46	0.68
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	R.YLTEHPDPNNENIVGYNNK#.K	18.64	9.05	2.06	0.49
Q99PV0_PRP8_MOUSE	Prpf8	Pre-mRNA-processing-spl	K.YYVLNALK#.H	55.07	28.79	1.91	0.52
E9PYL2_E9PYL2_MOUSE	Prr12	Protein Prr12 OS=Mus m	R.ATGPETAGGGAAGGGGGYR@PIIQSPGYK#.T	3.62	3.79	0.95	1.05
E9PYL2_E9PYL2_MOUSE	Prr12	Protein Prr12 OS=Mus m	K.GLGGSGGAGGAPGTPYELAK#.E	6.11	4.43	1.38	0.72
E9PYL2_E9PYL2_MOUSE	Prr12	Protein Prr12 OS=Mus m	R.IR@PLEGPAM*AGPASITTDGAK#.K	6.35	3.87	1.64	0.61
E9PYL2_E9PYL2_MOUSE	Prr12	Protein Prr12 OS=Mus m	R.TSGADGLVGEDGPADAAK#.G	4.14	3.97	1.04	0.96
Q3UPH1_PRRC1_MOUSE	Prrc1	Protein PRRC1 OS=Mus n	K.SGGELDIVVTSNK#.E	22.86	4.63	4.93	0.20
Q3UPH1_PRRC1_MOUSE	Prrc1	Protein PRRC1 OS=Mus n	R.WSGLLVTVGEVLEK#.S	17.67	6.70	2.64	0.38
Q3UPH1_PRRC1_MOUSE	Prrc1	Protein PRRC1 OS=Mus n	R.WSGLLVTVGEVLEK#.S	5.31	3.51	1.51	0.66
F8WHT3_F8WHT3_MOUSE	Prrc2b	Protein PRRC2B OS=Mus	K.FIQSEM*SEAVER@.A	8.51	2.93	2.90	0.34
F8WHT3_F8WHT3_MOUSE	Prrc2b	Protein PRRC2B OS=Mus	R.LLSFSPEEFPTLK#.A	15.42	4.24	3.64	0.28
F8WHT3_F8WHT3_MOUSE	Prrc2b	Protein PRRC2B OS=Mus	R.SPDEALPGGLGSHSPYALER@.T	7.25	3.62	2.00	0.50
F8WHT3_F8WHT3_MOUSE	Prrc2b	Protein PRRC2B OS=Mus	R.TAVTAFSSTEPGTSEGFK#.S	6.48	2.84	2.28	0.44
F8WHT3_F8WHT3_MOUSE	Prrc2b	Protein PRRC2B OS=Mus	R.TYTEDQGGIDTR@.S	7.26	1.86	3.89	0.26
Q3TLH4_PRC2C_MOUSE	Prrc2c	Protein PRRC2C OS=Mus	K.AFGSGIDIK#PGTPPIGGR@.S	9.22	1.94	4.76	0.21
P49769_PSN1_MOUSE	Psen1	Presenilin-1 OS=Mus mus	R.AAVQELSGSILTSEDPEER@.G	5.97	1.76	3.40	0.29
P49722_PSA2_MOUSE	Psma2	Proteasome subunit alph	R.YNEDLELEDAIHTAILTLK#.E	6.56	9.53	0.69	1.45
Q9Z2U1_PSA5_MOUSE	Psma5	Proteasome subunit alph	R.AIGSASEGAQSSLQEVYHK#.S	22.86	8.46	2.70	0.37
Q9Z2U1_PSA5_MOUSE	Psma5	Proteasome subunit alph	R.LFQVEYAIEAIK#.L	12.68	5.89	2.15	0.46
Q9Z2U1_PSA5_MOUSE	Psma5	Proteasome subunit alph	R.GVNTFSPEGR@.L	17.64	10.94	1.61	0.62
Q9Z2U1_PSA5_MOUSE	Psma5	Proteasome subunit alph	R.LFQVEYAIEAIK#.L	31.58	13.56	2.33	0.43
Q9Z2U1_PSA5_MOUSE	Psma5	Proteasome subunit alph	K.SSLIILK#.Q	19.00	12.09	1.57	0.64
O35955_PSB10_MOUSE	Psmb10	Proteasome subunit beta	R.ALSTPTEPVQR@.A	11.69	7.79	1.50	0.67
O35955_PSB10_MOUSE	Psmb10	Proteasome subunit beta	R.LPFTALGSGQGAAVALLEDR@.F	12.55	4.65	2.70	0.37
Q9R1P1_PSB3_MOUSE	Psmb3	Proteasome subunit beta	R.FGPYYTEPVIAGLDPK#.T	2.79	6.16	0.45	2.21
P62192_PRS4_MOUSE	Psmc1	26S protease regulatory s	K.APQETYADIGGLDNQIQEIK#.E	5.11	2.47	2.07	0.48
P62192_PRS4_MOUSE	Psmc1	26S protease regulatory s	K.AVANQTSATFLR@.V	22.93	7.65	3.00	0.33
P62192_PRS4_MOUSE	Psmc1	26S protease regulatory s	K.K#QEGTPEGLYL.-	8.76	3.75	2.34	0.43
P62192_PRS4_MOUSE	Psmc1	26S protease regulatory s	R.M*TLADDVTLDDLIM*AK#.D	10.53	2.93	3.59	0.28
P62192_PRS4_MOUSE	Psmc1	26S protease regulatory s	R.NQEQM*KPLEEKQEEER.S	8.24	2.71	3.05	0.33
P62192_PRS4_MOUSE	Psmc1	26S protease regulatory s	R.VAEEHAPSIVFIDEIDAIGTK#.R	26.40	8.59	3.07	0.33
P62192_PRS4_MOUSE	Psmc1	26S protease regulatory s	K.AVANQTSATFLR@.V	10.10	4.14	2.44	0.41
P62192_PRS4_MOUSE	Psmc1	26S protease regulatory s	R.VAEEHAPSIVFIDEIDAIGTK#.R	8.20	3.11	2.64	0.38
P46471_PRS7_MOUSE	Psmc2	26S protease regulatory s	R.FDDGAGGDNEVQR@.T	38.90	15.50	2.51	0.40

P46471_PRS7_MOUSE	Psmc2	26S protease regulatory s	R.FVNLGIEPPK#GVLLFGPPGTGK#.T	7.85	4.75	1.65	0.61
P46471_PRS7_MOUSE	Psmc2	26S protease regulatory s	K.FVVDLSDQVAPTDIEEGM*R@.V	5.40	2.70	2.00	0.50
P46471_PRS7_MOUSE	Psmc2	26S protease regulatory s	K.IATEK#DFLEAVNK#.V	19.16	9.82	1.95	0.51
P46471_PRS7_MOUSE	Psmc2	26S protease regulatory s	R.KIEFSLPDLEGR.T	22.06	10.73	2.06	0.49
P46471_PRS7_MOUSE	Psmc2	26S protease regulatory s	K.QVEDDIQQLLK#.K	6.38	3.19	2.00	0.50
P46471_PRS7_MOUSE	Psmc2	26S protease regulatory s	R.FDDGAGGDNEVQR@.T	2.59	1.55	1.67	0.60
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	K.AM*EVDER@PTEQYSDIGGLDK#.Q	15.99	4.81	3.32	0.30
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	K.DSYLILETLPTEYDSR@.V	17.23	8.53	2.02	0.49
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	K.EK#APSIIFIDELDAIGTK#.R	23.13	9.76	2.37	0.42
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	R.GATELTHEDYM*EGILEVQAK#.K	8.23	5.19	1.59	0.63
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	K.GVLM*YGPPGTGK#.T	12.79	4.06	3.15	0.32
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	R.K#M*NVSPDVNYEELAR@.C	12.59	6.66	1.89	0.53
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	R.LLDSEIK#.I	29.65	11.72	2.53	0.40
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	K.M*STEEIVQR@.T	18.26	4.12	4.43	0.23
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	R.TM*LELLNQLDGFQPNTQVK#.V	9.49	2.80	3.38	0.30
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	R.VDILDPALLR@.S	35.45	10.29	3.44	0.29
O88685_PRS6A_MOUSE	Psmc3	26S protease regulatory s	K.VIAATNR@VDILDPALLR@.S	12.50	5.08	2.46	0.41
P54775_PRS6B_MOUSE	Psmc4	26S protease regulatory s	R.ILLELLNQM*DGFDQNVNVK#.V	33.67	8.92	3.77	0.26
P54775_PRS6B_MOUSE	Psmc4	26S protease regulatory s	R.ILLELLNQMDGFDQNVNVK#.V	8.24	2.71	3.05	0.33
P54775_PRS6B_MOUSE	Psmc4	26S protease regulatory s	K.IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR.Y	24.54	5.75	4.27	0.23
P54775_PRS6B_MOUSE	Psmc4	26S protease regulatory s	K.R@FDAQTGADR@.E	11.63	4.21	2.77	0.36
P54775_PRS6B_MOUSE	Psmc4	26S protease regulatory s	K.R@FDAQTGADR@EVQR@.I	11.52	3.92	2.94	0.34
P54775_PRS6B_MOUSE	Psmc4	26S protease regulatory s	R.VVGSEFVQK#.Y	36.87	14.43	2.56	0.39
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	R.EELQLLQEQGSYVGEVVR@.A	2.19	2.26	0.97	1.03
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	R.EHAPSIIFM*DEIDSIGSSR@.L	21.02	8.88	2.37	0.42
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	K.EVIELPVK#HPELFEALGIAQPK#.G	23.82	9.47	2.51	0.40
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	K.IAELM*PGASGAEVK#.G	16.67	5.96	2.80	0.36
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	R.LEGGSGGDSEVQR@.T	53.89	13.66	3.94	0.25
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	R.LLR@EELQLLQEQGSYVGEVVR@.A	48.00	10.44	4.60	0.22
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	R.R@VHVTQEDFEM*AVAK#.V	17.86	5.47	3.26	0.31
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	R.TM*LELLNQLDGFEATK#.N	35.92	12.32	2.91	0.34
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	R.VHVTQEDFEM*AVAK#.V	4.42	2.56	1.73	0.58
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	K.VPDSTYEM*IGGLDK#.Q	23.39	9.03	2.59	0.39
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	R.LEGGSGGDSEVQR@.T	4.63	3.57	1.30	0.77
P62196_PRS8_MOUSE	Psmc5	26S protease regulatory s	R.LLR@EELQLLQEQGSYVGEVVR@.A	6.85	4.10	1.67	0.60
P62334_PRS10_MOUSE	Psmc6	26S protease regulatory s	K.ALQSVGQIVGEVLK#.Q	42.69	18.55	2.30	0.43
P62334_PRS10_MOUSE	Psmc6	26S protease regulatory s	R.EVDPLVYNM*SHEDPGNVSYSEIGGLSEQIR@.E	10.55	4.95	2.13	0.47
P62334_PRS10_MOUSE	Psmc6	26S protease regulatory s	R.EVIELPLTNPELFQR@.V	33.19	17.53	1.89	0.53
P62334_PRS10_MOUSE	Psmc6	26S protease regulatory s	K.IHIDLPNEQAR@.L	16.44	6.60	2.49	0.40
P62334_PRS10_MOUSE	Psmc6	26S protease regulatory s	K.LSDGFNGADLR.N	14.08	9.02	1.56	0.64
P62334_PRS10_MOUSE	Psmc6	26S protease regulatory s	R.VALDM*TTLTIM*R@.Y	9.01	4.61	1.95	0.51
P62334_PRS10_MOUSE	Psmc6	26S protease regulatory s	K.ALQSVGQIVGEVLK#.Q	6.63	1.66	3.99	0.25
Q3TXS7_PSMD1_MOUSE	Psmd1	26S proteasome non-ATF	R.AAVESLGFILFR@.T	24.17	8.73	2.77	0.36
Q3TXS7_PSMD1_MOUSE	Psmd1	26S proteasome non-ATF	K.IEEEEQEPEPPEPFEYIDD.-	3.05	3.05	1.00	1.00
Q3TXS7_PSMD1_MOUSE	Psmd1	26S proteasome non-ATF	K.TNLYQDDAVTGEAAGLALGLVM*LGSK#.N	7.37	2.80	2.63	0.38
Q3TXS7_PSMD1_MOUSE	Psmd1	26S proteasome non-ATF	R.AAVESLGFILFR@.T	13.25	5.87	2.26	0.44
Q3TXS7_PSMD1_MOUSE	Psmd1	26S proteasome non-ATF	K.IEEEEQEPEPPEPFEYIDD.-	3.72	3.72	1.00	1.00
Q3TXS7_PSMD1_MOUSE	Psmd1	26S proteasome non-ATF	K.TNLYQDDAVTGEAAGLALGLVM*LGSK#.N	6.38	1.95	3.27	0.31
Q8BG32_PSD11_MOUSE	Psmd11	26S proteasome non-ATF	K.ALLVEVQLLESK#.T	7.80	2.35	3.32	0.30
Q8BG32_PSD11_MOUSE	Psmd11	26S proteasome non-ATF	R.DIQENDEEAVQVK#.E	23.97	6.77	3.54	0.28
Q8BG32_PSD11_MOUSE	Psmd11	26S proteasome non-ATF	K.EQSILELGSLLAK#.T	38.15	16.78	2.27	0.44
Q8BG32_PSD11_MOUSE	Psmd11	26S proteasome non-ATF	K.IM*LNTPEDVQALVSGK#.L	15.76	4.89	3.22	0.31
Q8BG32_PSD11_MOUSE	Psmd11	26S proteasome non-ATF	R.LVSLYFDTK#.R	21.57	5.05	4.27	0.23
Q8BG32_PSD11_MOUSE	Psmd11	26S proteasome non-ATF	K.TAYSYFYEAFEGYDSIDSPK#.A	3.62	2.50	1.45	0.69
Q8BG32_PSD11_MOUSE	Psmd11	26S proteasome non-ATF	K.TAYSYFYEAFEGYDSIDSPK#.A	3.13	1.55	2.01	0.50
Q8BG32_PSD11_MOUSE	Psmd11	26S proteasome non-ATF	R.VQIEHISSLIK#.L	32.01	6.44	4.97	0.20
Q9D8W5_PSD12_MOUSE	Psmd12	26S proteasome non-ATF	K.FFQEENTENLK#.L	17.05	6.88	2.48	0.40
Q9D8W5_PSD12_MOUSE	Psmd12	26S proteasome non-ATF	K.IYVEIER@.A	20.40	11.47	1.78	0.56
Q9D8W5_PSD12_MOUSE	Psmd12	26S proteasome non-ATF	R.LQEVIETLLSLEK#.Q	24.78	9.91	2.50	0.40
Q9D8W5_PSD12_MOUSE	Psmd12	26S proteasome non-ATF	R.LQEVIETLLSLEK#.Q	11.48	4.41	2.60	0.38
Q9WVJ2_PSD13_MOUSE	Psmd13	26S proteasome non-ATF	K.DLPVSEQQER@.A	14.97	7.01	2.14	0.47
Q9WVJ2_PSD13_MOUSE	Psmd13	26S proteasome non-ATF	K.LNIGDLQATK#.E	12.89	5.30	2.43	0.41
Q9WVJ2_PSD13_MOUSE	Psmd13	26S proteasome non-ATF	R.VLDLQQIK#.G	23.04	9.27	2.48	0.40
O35593_PSDE_MOUSE	Psmd14	26S proteasome non-ATF	R.AVAVVVDPIQSVK#.G	22.30	13.88	1.61	0.62
O35593_PSDE_MOUSE	Psmd14	26S proteasome non-ATF	R.VIDVFAM*PQSGTGVSVEAVDPVFQAK#.M	228.46	13.90	16.44	0.06
O35593_PSDE_MOUSE	Psmd14	26S proteasome non-ATF	R.VIDVFAMPQSGTGVSVEAVDPVFQAK#.M	6.83	2.90	2.36	0.42
Q8VDM4_PSMD2_MOUSE	Psmd2	26S proteasome non-ATF	K.AQR@EPLLTLVK#.E	12.93	5.00	2.59	0.39
Q8VDM4_PSMD2_MOUSE	Psmd2	26S proteasome non-ATF	R.AVPLALALISVSNPR@.L	14.16	4.63	3.06	0.33
Q8VDM4_PSMD2_MOUSE	Psmd2	26S proteasome non-ATF	R.DK#TPVQSQQPSATTPSGADEK#.S	6.01	3.63	1.65	0.60
Q8VDM4_PSMD2_MOUSE	Psmd2	26S proteasome non-ATF	K.EWQELDDAEK#.A	6.20	1.86	3.33	0.30
Q8VDM4_PSMD2_MOUSE	Psmd2	26S proteasome non-ATF	R.FGGSGSQVDSAR@.M	29.34	12.22	2.40	0.42
Q8VDM4_PSMD2_MOUSE	Psmd2	26S proteasome non-ATF	R.LNILDTLSK#.F	18.53	8.34	2.22	0.45
Q8VDM4_PSMD2_MOUSE	Psmd2	26S proteasome non-ATF	K.YLYSSEDYIK#.S	8.38	5.40	1.55	0.65
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	K.FNQVLDQFGEK#.F	6.34	2.69	2.36	0.42
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	R.HDADGQATLLNLLLR@.N	11.50	3.12	3.69	0.27
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	K.AIQLEYSEAR@.R	9.60	2.79	3.44	0.29
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	R.DGVIEASINHEK#.G	7.65	1.35	5.69	0.18
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	K.FNQVLDQFGEK#.F	14.24	6.18	2.30	0.43
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	K.FQTDGTYTLIIR@.L	43.84	196.00	0.22	4.47
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	R.HDADGQATLLNLLLR@.N	16.38	3.90	4.20	0.24
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	R.ISLADIAQK#.L	13.27	5.34	2.49	0.40
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	K.LQLDSPEDAEFIVAK#.A	16.12	7.44	2.17	0.46
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	R.SLM*PYFLLTQAVR@.T	9.47	2.46	3.85	0.26
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	K.SVFPEQANNNEWAR@.Y	5.66	4.49	1.26	0.79
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	R.VYEFLDK#LDVVR@.S	16.42	4.56	3.60	0.28
P14685_PSMD3_MOUSE	Psmd3	26S proteasome non-ATF	R.HDADGQATLLNLLLR@.N	10.62	3.38	3.14	0.32
O35226_PSMD4_MOUSE	Psmd4	26S proteasome non-ATF	R.AAAASAAEAGIATPGTEDSDDALLK#.M	18.41	4.66	3.95	0.25
O35226_PSMD4_MOUSE	Psmd4	26S proteasome non-ATF	K.EK#VNVDIINFGEEEVNTEK#.L	13.53	5.06	2.67	0.37
O35226_PSMD4_MOUSE	Psmd4	26S proteasome non-ATF	K.LTAFVNTLNGK#.D	6.60	4.06	1.62	0.62
O35226_PSMD4_MOUSE	Psmd4	26S proteasome non-ATF	R.SVM*GALASQATK#.D	33.80	9.93	3.40	0.29
O35226_PSMD4_MOUSE	Psmd4	26S proteasome non-ATF	R.SVMGALASQATK#.D	8.14	3.18	2.56	0.39
O35226_PSMD4_MOUSE	Psmd4	26S proteasome non-ATF	K.VNVDIINFGEEEVNTEK#.L	19.58	8.56	2.29	0.44
F7AI87_F7AI87_MOUSE	Psmd4	26S proteasome non-ATF	R.AAAASAAEAGIATPGTEGER@.D	3.04	1.64	1.85	0.54
F7AI87_F7AI87_MOUSE	Psmd4	26S proteasome non-ATF	R.AAAASAAEAGIATPGTEGER@DSDDALLK#.M	11.17	3.81	2.93	0.34
Q99JI4_PSMD6_MOUSE	Psmd6	26S proteasome non-ATF	K.GAEILEVLHSLPAVR@.Q	14.67	4.33	3.39	0.30
Q99JI4_PSMD6_MOUSE	Psmd6	26S proteasome non-ATF	K.GAEILEVLHSLPAVR@.Q	9.46	8.01	1.18	0.85
Q99JI4_PSMD6_MOUSE	Psmd6	26S proteasome non-ATF	R.IGLFYM*DNDLITR@.N	67.42	4.91	13.73	0.07
P26516_PSMD7_MOUSE	Psmd7	26S proteasome non-ATF	K.TFEHVTSEIGAEEAEEVGVEHLLR@.D	19.17	3.39	5.66	0.18
P26516_PSMD7_MOUSE	Psmd7	26S proteasome non-ATF	R.VVGVLLGSWQK#.K	21.01	9.02	2.33	0.43
Q9CX56_PSMD8_MOUSE	Psmd8	26S proteasome non-ATF	R.ILFFSTPK#.K	18.46	7.02	2.63	0.38
Q9CX56_PSMD8_MOUSE	Psmd8	26S proteasome non-ATF	K.LVLLELNFLPTTGTK#.L	7.36	2.25	3.27	0.31
P97371_PSME1_MOUSE	Psme1	Proteasome activator co	K.APLDIPVPDPVK#EK#.E	9.64	7.27	1.33	0.75
P97371_PSME1_MOUSE	Psme1	Proteasome activator co	R.IEDGNNFGVAVQEK#.V	17.43	8.82	1.98	0.51

P97371_PSME1_MOUSE	Psme1	Proteasome activator co	K.ISELDAFLK#EPALNEANLSNLK#.A	10.49	4.52	2.32	0.43
P97371_PSME1_MOUSE	Psme1	Proteasome activator co	K.IVVLLQR@.L	30.29	12.48	2.43	0.41
P97371_PSME1_MOUSE	Psme1	Proteasome activator co	K.K#ISELDAFLK#EPALNEANLSNLK#.A	5.68	2.54	2.23	0.45
P97371_PSME1_MOUSE	Psme1	Proteasome activator co	K.KISELDAFLKEPALNEANLSNLK.A	15.20	8.86	1.72	0.58
P97371_PSME1_MOUSE	Psme1	Proteasome activator co	R.NAYAVLYDIILK#.N	50.01	18.48	2.71	0.37
P97371_PSME1_MOUSE	Psme1	Proteasome activator co	R.QLVHELDEAEYQEIR@.L	17.61	4.16	4.24	0.24
P97372_PSME2_MOUSE	Psme2	Proteasome activator co	K.IEDGNDFGVAIQEK#.V	10.09	5.02	2.01	0.50
P97372_PSME2_MOUSE	Psme2	Proteasome activator co	R.K#IISLSQLLQEDSLNVADLSSLR@.A	12.58	4.47	2.82	0.36
P97372_PSME2_MOUSE	Psme2	Proteasome activator co	R.TK#VEAFQTTISK#.Y	5.82	2.86	2.04	0.49
P61290_PSME3_MOUSE	Psme3	Proteasome activator co	R.ITSEAEDLVANFFPK#.K	10.90	4.94	2.21	0.45
P61290_PSME3_MOUSE	Psme3	Proteasome activator co	K.SNQQLVDIIEK#.V	25.63	10.38	2.47	0.40
Q8R326_PSPC1_MOUSE	Pspc1	Paraspeckle component	R.FAQPGTFEFEYASR@.W	19.81	10.21	1.94	0.52
Q8R326_PSPC1_MOUSE	Pspc1	Paraspeckle component	K.NLSPVVSNELLEQAFSQFGPVEK#.A	39.52	12.73	3.10	0.32
Q8R326_PSPC1_MOUSE	Pspc1	Paraspeckle component	R.YGEPSEVFINR@.D	21.91	1.32	16.56	0.06
Q8R326_PSPC1_MOUSE	Pspc1	Paraspeckle component	K.AELDGTILK#.S	17.81	39.19	0.45	2.20
Q8R326_PSPC1_MOUSE	Pspc1	Paraspeckle component	K.AVVVVDDR@.G	19.70	3.77	5.23	0.19
Q8R326_PSPC1_MOUSE	Pspc1	Paraspeckle component	K.NLSPVVSNELLEQAFSQFGPVEK#.A	25.85	7.11	3.64	0.28
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.AQAALQAVNSVQSGNLALAASAAAVDAGM*AM*AGQSPVLR@.I	45.22	16.06	2.82	0.36
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.AQAALQAVNSVQSGNLALAASAAAVDAGM*AM*AGQSPVLR@.I	16.67	8.42	1.98	0.51
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.DYGSSPLHR@.F	504.76	188.97	2.67	0.37
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.DYTRPDLPSGDSQPSLDQTM*AAAFGLSVPNVHGALAPLAIPSAAAAAAASR.I	63.71	27.87	2.29	0.44
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.ELKTDSSPNQAR.A	21.62	6.56	3.29	0.30
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.ENALVQM*ADGSQAQLAM*SHLNGHK#.L	16.97	4.88	3.48	0.29
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.GKNQAFIEM*NTEEAANTM*VNYYTSVAPVLR.G	16.55	6.63	2.50	0.40
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.GK#NQAFIEMNTEEAANTM*VNYYTSVAPVLR@.G	4.31	1.92	2.25	0.44
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.GK#NQAFIEM*NTEEAANTMVNYYTSVAPVLR@.G	4.97	3.47	1.43	0.70
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.GK#NQAFIEMNTEEAANTMVNYYTSVAPVLR@.G	10.41	3.74	2.78	0.36
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.HQSVQLPR@.E	438.66	167.51	2.62	0.38
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.IAIPGLAGAGNSVLLVSNLNPER@.V	923.32	371.43	2.49	0.40
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.IAIPGLAGAGNSVLLVSNLNPER.V	183.19	72.68	2.52	0.40
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.K#LPSDVTEGEVISLGLPFGK#.V	826.06	334.28	2.47	0.40
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.K#M*ALIQMGSVEEAVQALIELHNHDLGENHHLR@.V	6.39	2.60	2.46	0.41
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.LPSDVTEGEVISLGLPFGK#.V	58.97	22.64	2.60	0.38
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.M*ALIQM*GSVEEAVQALIELHNHDLGENHHLR@.V	10.28	4.04	2.55	0.39
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.NFQNIFPPSATLHLSNIPPSVSEDDLK#.S	119.48	47.80	2.50	0.40
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.NNQFQALLQYADPVSAQHAK#.L	679.78	256.85	2.65	0.38
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.NQAFIEM*NTEEAANTM*VNYYTSVAPVLR@.G	23.54	11.06	2.13	0.47
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.TDSSPNQAR@.A	20.32	7.85	2.59	0.39
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.IAIPGLAGAGNSVLLVSNLNPER@.V	19.56	12.14	1.61	0.62
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.K#LPSDVTEGEVISLGLPFGK#.V	15.22	9.43	1.61	0.62
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.AQAALQAVNSVQSGNLALAASAAAVDAGM*AM*AGQSPVLR@.I	13.98	6.09	2.30	0.44
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.DYGSSPLHR@.F	71.39	21.53	3.32	0.30
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.DYTRPDLPSGDSQPSLDQTM*AAAFGLSVPNVHGALAPLAIPSAAAAAAASR.I	12.15	4.60	2.64	0.38
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.IAIPGLAGAGNSVLLVSNLNPER@.V	178.63	56.37	3.17	0.32
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.IAIPGLAGAGNSVLLVSNLNPER.V	27.02	10.29	2.63	0.38
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.KLPSDVTEGEVISLGLPFGK.V	154.38	62.22	2.48	0.40
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.LPSDVTEGEVISLGLPFGK#.V	13.32	4.84	2.75	0.36
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.M*ALIQM*GSVEEAVQALIELHNHDLGENHHLR@.V	19.15	4.97	3.85	0.26
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.NFQNIFPPSATLHLSNIPPSVSEDDLK#.S	25.74	12.69	2.03	0.49
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.NNQFQALLQYADPVSAQHAK#.L	100.80	34.78	2.90	0.35
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.SLFSSNGGVVK#.G	26.79	5.73	4.68	0.21
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.IAIPGLAGAGNSVLLVSNLNPER@.V	19.84	6.87	2.89	0.35
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	R.KLPSDVTEGEVISLGLPFGK.V	30.08	11.49	2.62	0.38
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.LPSDVTEGEVISLGLPFGK#.V	5.53	3.68	1.50	0.67
Q8BGJ5_Q8BGJ5_MOUSE	Ptbp1	MCG13402, isoform CRA	K.NFQNIFPPSATLHLSNIPPSVSEDDLK#.S	3.42	3.18	1.07	0.93
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.DSALIQM*ADGNQSQLAM*NHLNGQK#.M	7.21	2.82	2.56	0.39
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	R.DYTR@PDLPSGDGQPALDPAIAAAFAK#.E	100.52	29.29	3.43	0.29
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	R.EGLDDQGLTK#.D	199.95	43.78	4.57	0.22
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.ELK#TDNTLNQR@.A	14.08	4.11	3.43	0.29
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.ETSLLAVPGALSPLAIPNAAAAAAAAAAGR@.V	18.13	12.26	1.48	0.68
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.GK#NQAFLELATEEAAITM*VNYYSAVTPHLR@.N	3.84	2.03	1.89	0.53
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.HQTVQLPR@.E	62.15	15.05	4.13	0.24
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	R.K#LPGEVTETEVIALGLPFGK#.V	211.01	50.88	4.15	0.24
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	R.K#LPGEVTETEVIALGLPFGK#.V	7.65	1.96	3.90	0.26
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.LPGEVTETEVIALGLPFGK#.V	10.80	2.97	3.64	0.27
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.LVNLNVK#.Y	174.82	39.76	4.40	0.23
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.NFQNIFPPSATLHLSNIPPSVAEEDLR@.T	24.26	6.66	3.64	0.27
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.NNQFQALLQYGDPVNAQQAK#.L	55.02	11.62	4.73	0.21
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.NQAFLELATEEAAITM*VNYYSAVTPHLR@.N	10.90	3.22	3.38	0.30
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.TDNTLNQR@.A	25.54	57.76	0.44	2.26
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	R.TLFANTGGTVK#.A	120.25	29.75	4.04	0.25
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.VTNLLM*LK#.G	18.80	9.59	1.96	0.51
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	R.DYTR@PDLPSGDGQPALDPAIAAAFAK#.E	33.97	32.48	1.05	0.96
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	R.EGLDDQGLTK#.D	45.04	10.76	4.18	0.24
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.HQTVQLPR@.E	16.17	4.62	3.50	0.29
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	R.K#LPGEVTETEVIALGLPFGK#.V	58.58	10.31	5.68	0.18
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.LVNLNVK#.Y	27.19	5.12	5.31	0.19
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.NFQNIFPPSATLHLSNIPPSVAEEDLR@.T	4.31	1.72	2.51	0.40
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	K.NNQFQALLQYGDPVNAQQAK#.L	19.59	3.55	5.52	0.18
Q91Z31_PTBP2_MOUSE	Ptbp2	Polypyrimidine tract-bin	R.TLFANTGGTVK#.A	27.35	8.41	3.25	0.31
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	K.DFSNSPLHR@.F	50.98	29.26	1.74	0.57
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	R.EGQEDQGLTK#.D	363.07	164.94	2.20	0.45
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	K.ENALVQM*ADASQAQLAMNHLSGQR@.L	4.77	2.71	1.76	0.57
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	K.HQAVQLPR@.E	99.78	70.57	1.41	0.71
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	K.NFQNIFPPSATLHLSNIPPSVTM*DDLK#.N	19.37	12.21	1.59	0.63
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	K.NNQFQALLQYADPVNAQYAK#.M	74.54	34.53	2.16	0.46
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	K.SQAFLEM*ASEEAAVTM*INYYTPVTPHLR@.S	12.58	8.08	1.56	0.64
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	K.SQAFLEM*ASEEAAVTMINYYTPVTPHLR@.S	5.61	4.01	1.40	0.72
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	K.SQAFLEMASEEAAVTMINYYTPVTPHLR.S	4.45	2.05	2.17	0.46
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	R.SQPVYIQYSNHR@.E	13.37	11.52	1.16	0.86
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	K.TDNLPNQAR.A	46.88	31.18	1.50	0.67
Q8BHD7_PTBP3_MOUSE	Ptbp3	Polypyrimidine tract-bin	R.EGQEDQGLTK#.D	84.77	22.68	3.74	0.27
Q8BWM0_PGES2_MOUSE	Ptges2	Prostaglandin E synthase	R.K#VPILVAQEGDSLQQLNDSSVIISALK#.T	7.97	2.30	3.47	0.29
Q8BWM0_PGES2_MOUSE	Ptges2	Prostaglandin E synthase	R.TPAEALASFDYIVR@.E	8.37	2.25	3.71	0.27
Q8BKG3_PTK7_MOUSE	Ptk7	Inactive tyrosine-protein	R.FAQGSSLSFAAVDR@.L	7.20	40.84	0.18	5.67
Q8BKG3_PTK7_MOUSE	Ptk7	Inactive tyrosine-protein	R.VVLAPQDVVVAR@.N	11.56	2.45	4.73	0.21
Q8BKG3_PTK7_MOUSE	Ptk7	Inactive tyrosine-protein	R.VVLAPQDVVVAR@.N	17.28	4.73	3.65	0.27
Q8K2C9_HACD3_MOUSE	ptplad1	Very-long-chain (3R)-3-hy	R.FSFTLPYPVK#.M	6.32	5.31	1.19	0.84
Q8K2C9_HACD3_MOUSE	ptplad1	Very-long-chain (3R)-3-hy	R.VELSDVQNPAISITDNVLHFK#.A	15.03	7.71	1.95	0.51
P35831_PTN12_MOUSE	Ptpn12	Tyrosine-protein phosph	K.TPSQDSDYINANFIK#.G	5.92	2.71	2.19	0.46
P35831_PTN12_MOUSE	Ptpn12	Tyrosine-protein phosph	K.TPSQDSDYINANFIK#.G	2.63	2.43	1.08	0.93
Q64512_PTN13_MOUSE	Ptpn13	Tyrosine-protein phosph	R.ILELPR@.M	10.29	2.33	4.42	0.23
Q64512_PTN13_MOUSE	Ptpn13	Tyrosine-protein phosph	R.NFFGPEFVK#.M	8.45	2.71	3.12	0.32

Q64512_PTN13_MOUSE	Ptpn13	Tyrosine-protein phosph	K.TYHSDIFSISSESPSVISSESDFR@.Q	4.67	2.20	2.12	0.47
Q64512_PTN13_MOUSE	Ptpn13	Tyrosine-protein phosph	K.VDLASLTAASQEEK#PIEEDATQESR@.N	6.47	2.63	2.46	0.41
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.AALPTPALTPEDK#.A	27.54	19.41	1.42	0.70
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.DIR@DLLEEDELQEQK#.L	7.91	2.29	3.45	0.29
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.ELQEAQEHDAR@.G	6.33	1.80	3.51	0.28
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.GAPLVKPLPVNPTDPAVTGPDIFAK.L	33.38	14.39	2.32	0.43
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.GQLGDAGALDAIWR@.E	17.30	5.17	3.35	0.30
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.GQPDTVQDALR@.F	12.67	6.22	2.04	0.49
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.HVEQVLQR@.H	44.78	12.07	3.71	0.27
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.LLSGPLDQVR@.A	31.73	8.22	3.86	0.26
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.LQETLGQAGAGPGPSVAK#.A	16.36	7.25	2.26	0.44
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.LQQLQQELEAFR@.G	33.34	10.99	3.03	0.33
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.NHLPQDSQDLVLGGDVPISSIQATIAK#.L	28.44	7.43	3.83	0.26
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.NLVQSM*QVLSGVFTDVEASLK#.D	12.16	3.02	4.03	0.25
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.NYGENPEAYNEELK#.K	6.86	2.15	3.19	0.31
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.R@EEGEAVEAGDTPEELR@.S	38.61	14.79	2.61	0.38
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.SQEGK#DFYADLESK#.V	16.18	2.70	5.99	0.17
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.VLSLQFR@.D	40.69	12.21	3.33	0.30
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.VPM*GSGQEAAVAVTWTEIFSGK#.S	18.72	6.00	3.12	0.32
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	R.VSLEQQLR@.E	25.65	10.31	2.49	0.40
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.VYLEQNLAAQDNVLR@.A	15.17	4.16	3.65	0.27
Q6PB44_PTN23_MOUSE	Ptpn23	Tyrosine-protein phosph	K.WNSTLQTLVASYEAYEDLM*K#K#.S	6.94	2.50	2.78	0.36
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.AHATTSNTVSK#.L	24.73	11.33	2.18	0.46
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.ATEEPSGTGSDELIK#.S	323.54	152.83	2.12	0.47
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.ATEM*VEVGPEDDEVGAER@.G	52.82	26.29	2.01	0.50
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.ATEMVEVGPEDDEVGAER@.G	11.75	4.83	2.43	0.41
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.ATEM*VEVGPEDDEVGAER@GEATDLLR@.G	127.74	50.63	2.52	0.40
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.EGEVEVLK#.A	114.34	45.67	2.50	0.40
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.GEATDLLR@.G	87.98	37.12	2.37	0.42
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.IIGAVDQIQLTQAQLEER@.Q	542.34	232.66	2.33	0.43
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.IIGAVDQIQLTQAQLEER.Q	130.22	51.27	2.54	0.39
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.IREGEVEVLK.A	232.36	87.60	2.65	0.38
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.K#LEVNEAELLR@.R	475.03	180.44	2.63	0.38
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.K#SFTPDHVVYAR@.S	160.59	76.60	2.10	0.48
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.LEVNEAELLR@.R	47.70	21.14	2.26	0.44
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.QAEM*EGAVQSIQGELSK#.L	101.90	44.67	2.28	0.44
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.QAEMEGAVQSIQGELSK#.L	14.50	5.58	2.60	0.38
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.SDQVNGVLVLSLLDK#.I	187.61	80.93	2.32	0.43
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.VMIYQDEVK#.L	27.03	10.50	2.57	0.39
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.VM*IYQDEVK#LPAK#.L	449.46	215.14	2.09	0.48
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.AHATTSNTVSK#.L	15.09	6.99	2.16	0.46
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.ATEEPSGTGSDELIK#.S	124.83	61.36	2.03	0.49
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.ATEM*VEVGPEDDEVGAER@.G	28.52	10.84	2.63	0.38
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.ATEMVEVGPEDDEVGAER.G	9.33	4.29	2.17	0.46
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.ATEM*VEVGPEDDEVGAERGEATDLLR.G	62.66	29.19	2.15	0.47
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.GEATDLLR@.G	24.85	10.36	2.40	0.42
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.GSSPDVHTLLEITEESDAVLVDK#SDSD.-	5.05	2.26	2.23	0.45
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.IIGAVDQIQLTQAQLEER@.Q	209.79	81.29	2.58	0.39
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.IIGAVDQIQLTQAQLEER.Q	55.09	19.00	2.90	0.34
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.K#LEVNEAELLR@.R	187.90	75.41	2.49	0.40
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.KLEVNEAELLR.R	43.05	17.28	2.49	0.40
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.K#LEVNEAELLR@R@.R	34.85	15.67	2.22	0.45
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.K#SFTPDHVVYAR@.S	71.70	26.12	2.75	0.36
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.LEVNEAELLR@.R	28.60	11.84	2.41	0.41
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.QAEM*EGAVQSIQGELSK#.L	55.98	23.09	2.42	0.41
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	R.QAEMEGAVQSIQGELSK#.L	11.90	5.38	2.21	0.45
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.SDQVNGVLVLSLLDK#.I	71.47	29.98	2.38	0.42
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.VM*IYQDEVK#.L	45.16	73.67	0.61	1.63
O54724_PTRF_MOUSE	Ptrf	Polymerase I and transcri	K.VM*IYQDEVK#LPAK#.L	159.49	55.81	2.86	0.35
Q8R2Y8_PTH2_MOUSE	Ptrh2	Peptidyl-tRNA hydrolase	K.APDEDTLIQLLTHAK#.T	3.04	1.64	1.86	0.54
Q8R2Y8_PTH2_MOUSE	Ptrh2	Peptidyl-tRNA hydrolase	K.APDEDTLIQLLTHAK#.T	29.26	10.92	2.68	0.37
Q8R2Y8_PTH2_MOUSE	Ptrh2	Peptidyl-tRNA hydrolase	R.DTETGTEASILGESGEYK#.M	4.19	1.78	2.35	0.42
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.AVTPPM*PLLTPATPGGLPPAAAVAAAAATAK#.I	51.22	16.89	3.03	0.33
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.GFAFVEYEVPEAAQLALEQM*NSVM*LGGR@.N	9.68	2.66	3.64	0.27
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.GYGFIEYEK#.A	25.75	8.05	3.20	0.31
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	R.K#VVAEVYDQER@.F	9.58	3.28	2.92	0.34
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.LGLPPLTPEQQEALQK#.A	29.45	11.72	2.51	0.40
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	R.QAFAPFGPIK#.S	34.87	9.30	3.75	0.27
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.QGEEEDAEIIVK#.I	46.27	4.82	9.60	0.10
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.SIDM*SWDSVTM*K#.H	7.09	3.27	2.17	0.46
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.VGR@PSNIGQAQPIIDQLAEEAR@.A	48.47	10.77	4.50	0.22
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	R.VYVGSIYYELGEDTIR@.Q	30.17	7.04	4.29	0.23
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.AQSSQDAVSSM*NLFDLGGQYLR@.V	43.15	8.72	4.95	0.20
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.AQSSQDAVSSMNLFDLGGQYLR@.V	11.96	4.33	2.76	0.36
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.AVTPPMPLLTPATPGGLPPAAAVAAAAATAK#.I	30.54	7.89	3.87	0.26
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.GFAFVEYEVPEAAQLALEQM*NSVM*LGGR@.N	18.12	6.30	2.88	0.35
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.GYGFIEYEK#.A	60.78	11.94	5.09	0.20
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.IFVEFSM*ASETHK#.A	5.65	3.78	1.49	0.67
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	R.K#VVAEVYDQER@.F	39.28	8.72	4.50	0.22
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	R.K#VVAEVYDQER@.F	23.11	5.66	4.09	0.24
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.LGLPPLTPEQQEALQK#.A	61.41	19.23	3.19	0.31
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.QGEEEDAEIIVK#.I	64.93	19.65	3.30	0.30
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.SIDM*SWDSVTM*K#.H	13.95	1.73	8.06	0.12
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.VGRPSNIGQAQPIIDQLAEEAR.A	84.50	19.52	4.33	0.23
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.VVAEVYDQER@.F	26.84	5.15	5.21	0.19
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	K.VVAEVYDQER@FDNSDLSA.-	6.85	1.52	4.49	0.22
Q3UEB3_PUF60_MOUSE	Puf60	Poly(U)-binding-splicing	R.VYVGSIYYELGEDTIR@.Q	68.55	21.14	3.24	0.31
E9Q6M7_E9Q6M7_MOUSE	Pum1	Pumilio homolog 1 OS=N	K.ALEFIPSDQQNEM*VR@.E	5.57	4.35	1.28	0.78
E9Q6M7_E9Q6M7_MOUSE	Pum1	Pumilio homolog 1 OS=N	R.SM*DELNHDFQALALEGR@.A	8.37	3.55	2.36	0.42
E9Q6M7_E9Q6M7_MOUSE	Pum1	Pumilio homolog 1 OS=N	K.ALEFIPSDQQNEM*VR@.E	8.64	3.48	2.49	0.40
E9Q6M7_E9Q6M7_MOUSE	Pum1	Pumilio homolog 1 OS=N	R.QHGEQLGGGGSGGGGYNTSK#.H	7.61	1.64	4.65	0.21
Q3UR91_Q3UR91_MOUSE	Pum2	Pumilio homolog 2 OS=N	K.DQYANYVVQK#.M	9.78	13.86	0.71	1.42
Q3UR91_Q3UR91_MOUSE	Pum2	Pumilio homolog 2 OS=N	K.ALESISSDQQSEM*VK#.E	7.08	5.74	1.23	0.81
Q3UR91_Q3UR91_MOUSE	Pum2	Pumilio homolog 2 OS=N	R.DLIGHIVEFSQDQHGSR@.F	25.04	10.16	2.46	0.41
Q3UR91_Q3UR91_MOUSE	Pum2	Pumilio homolog 2 OS=N	K.DQYANYVVQK#.M	27.89	17.69	1.58	0.63
Q3UR91_Q3UR91_MOUSE	Pum2	Pumilio homolog 2 OS=N	K.FASNVVEK#.C	36.49	17.01	2.15	0.47
Q3UR91_Q3UR91_MOUSE	Pum2	Pumilio homolog 2 OS=N	K.DQYANYVVQK#.M	14.14	25.57	0.55	1.81
Q3UR91_Q3UR91_MOUSE	Pum2	Pumilio homolog 2 OS=N	K.FASNVVEK#.C	20.35	8.31	2.45	0.41
P42669_PURA_MOUSE	Pura	Transcriptional activator	R.DYLGDFIEHYAQLGPSQPPDLAQAQDEPR.R	6.87	14.87	0.46	2.16
P42669_PURA_MOUSE	Pura	Transcriptional activator	R.FFFDVGSNK#.Y	16.71	36.05	0.46	2.16
P42669_PURA_MOUSE	Pura	Transcriptional activator	R.GPGLGSTQGQTIALPAQGLIEFR.D	31.35	76.96	0.41	2.45
P42669_PURA_MOUSE	Pura	Transcriptional activator	R.GPGLGSTQGQTIALPAQGLIEFR@.D	5.80	12.71	0.46	2.19
P42669_PURA_MOUSE	Pura	Transcriptional activator	K.IAEVGAGGNK.S	14.68	44.13	0.33	3.01

P42669_PURA_MOUSE	Pura	Transcriptional activator	K.LIDDYGVEEEPAELPEGTSLTVDNKR.F	24.96	76.16	0.33	3.05
P42669_PURA_MOUSE	Pura	Transcriptional activator	R.NSITVPYK.V	18.02	50.65	0.36	2.81
P42669_PURA_MOUSE	Pura	Transcriptional activator	K.SEFLVR.E	40.47	91.75	0.44	2.27
P42669_PURA_MOUSE	Pura	Transcriptional activator	R.VSEVKPTYR.N	5.12	14.71	0.35	2.87
P42669_PURA_MOUSE	Pura	Transcriptional activator	R.GPGLGSTQGQTIALPAQGLIEFR@.D	10.58	15.08	0.70	1.43
P42669_PURA_MOUSE	Pura	Transcriptional activator	K.LIDDYGVEEEPAELPEGTSLTVDNKR.F	7.15	14.83	0.48	2.07
O35295_PURB_MOUSE	Purb	Transcriptional activator	R.DSLGDFIEHYAQLGPSSPEQLAAGAEEGGGPR.R	13.05	21.44	0.61	1.64
O35295_PURB_MOUSE	Purb	Transcriptional activator	R.GGGGFGGGPGPGGLQSGQTIALPAQGLIEFR.D	32.21	82.04	0.39	2.55
O35295_PURB_MOUSE	Purb	Transcriptional activator	R.GGGGGGGGGPGGFQPAPR.G	33.51	103.01	0.33	3.07
O35295_PURB_MOUSE	Purb	Transcriptional activator	R.GGGGGGGGPGGEQETQELASK.R	19.80	59.48	0.33	3.00
O35295_PURB_MOUSE	Purb	Transcriptional activator	R.GGGGGGGGPGGEQETQELASK#R@.L	8.35	17.21	0.49	2.06
O35295_PURB_MOUSE	Purb	Transcriptional activator	K.IAEVGAGGSK.S	47.07	70.69	0.67	1.50
O35295_PURB_MOUSE	Purb	Transcriptional activator	R.NAITVPFK.A	22.15	50.71	0.44	2.29
O35295_PURB_MOUSE	Purb	Transcriptional activator	R.RGGGSGGGDESEGEEVDED.-	6.05	11.80	0.51	1.95
O35295_PURB_MOUSE	Purb	Transcriptional activator	K.YGVFLR.V	15.99	33.16	0.48	2.07
O35295_PURB_MOUSE	Purb	Transcriptional activator	K.YYLDLK.E	12.26	30.42	0.40	2.48
O35295_PURB_MOUSE	Purb	Transcriptional activator	R.GGGGGGGGPGGEQETQELASK.R	2.62	6.52	0.40	2.49
Q99LL5_PWP1_MOUSE	Pwp1	Periodic tryptophan pro	R.VWDISTVSSVNEAFGR@.R	10.08	5.11	1.97	0.51
Q8BU03_PWP2_MOUSE	Pwp2	Periodic tryptophan pro	R.AGQLLPVVQFLQK#.G	12.76	6.44	1.98	0.50
Q8BU03_PWP2_MOUSE	Pwp2	Periodic tryptophan pro	R.AGQLLPVVQFLQK#.G	19.00	8.99	2.11	0.47
Q8VI36_PAXI_MOUSE	Pxn	Paxillin OS=Mus muscul	R.ELDELM*ASLSDFK#.M	13.38	7.95	1.68	0.59
Q922W5_P5CR1_MOUSE	Pycr1	Pyrroline-5-carboxylate	R.LGAQALLGAAK#.M	21.93	13.08	1.68	0.60
Q9DCC4_P5CR3_MOUSE	Pycrl	Pyrroline-5-carboxylate	R.IAAQTLLGTAK#.M	57.96	30.12	1.92	0.52
Q9QYS9_QKI_MOUSE	Qki	Protein quaking OS=Mus	K.EYPDFNFVGR@.I	16.30	8.89	1.83	0.55
Q9QYS9_QKI_MOUSE	Qki	Protein quaking OS=Mus	R.IITGPAPVLPPAALR@.T	8.03	4.30	1.87	0.54
Q9QYS9_QKI_MOUSE	Qki	Protein quaking OS=Mus	R.LLDEEISR@.V	69.60	30.61	2.27	0.44
Q9QYS9_QKI_MOUSE	Qki	Protein quaking OS=Mus	K.LLVPAAEGEDSLK#.K	22.78	143.57	0.16	6.30
Q9QYS9_QKI_MOUSE	Qki	Protein quaking OS=Mus	K.LYVPVK#.E	14.70	5.35	2.75	0.36
Q9QYS9_QKI_MOUSE	Qki	Protein quaking OS=Mus	K.LYVPVK#EYPDFNFVGR@.I	56.55	26.37	2.14	0.47
Q9QYS9_QKI_MOUSE	Qki	Protein quaking OS=Mus	R.SAELPDAVGPIVQLQEK#.L	41.13	15.88	2.59	0.39
Q9QYS9_QKI_MOUSE	Qki	Protein quaking OS=Mus	R.LLDEEISR@.V	8.66	2.77	3.13	0.32
Q9QYS9_QKI_MOUSE	Qki	Protein quaking OS=Mus	R.SAELPDAVGPIVQLQEK#.L	6.04	3.55	1.70	0.59
Q9CYK2_QPCT_MOUSE	Qpct	Glutaminyl-peptide cycl	R.SFSNIISTLNPEAK#.R	13.59	5.68	2.40	0.42
Q3UA37_QRIC1_MOUSE	Qrich1	Glutamine-rich protein 1	K.LYDFYLFK#.C	7.59	1.64	4.63	0.22
Q3UA37_QRIC1_MOUSE	Qrich1	Glutamine-rich protein 1	K.NAELEK#DAQNR@.L	2.78	1.32	2.11	0.47
P61027_RAB10_MOUSE	Rab10	Ras-related protein Rab-1	K.AFLTLAEDILR@.K	134.95	59.83	2.26	0.44
P61027_RAB10_MOUSE	Rab10	Ras-related protein Rab-1	K.LLLIGDSGVGK#.T	195.35	65.91	2.96	0.34
P61027_RAB10_MOUSE	Rab10	Ras-related protein Rab-1	K.LQIWDTAGQER@.F	230.93	79.70	2.90	0.35
P61027_RAB10_MOUSE	Rab10	Ras-related protein Rab-1	R.NIDEHANEDVER@.M	8.36	4.39	1.90	0.53
P61027_RAB10_MOUSE	Rab10	Ras-related protein Rab-1	K.AFLTLAEDILR@.K	17.26	10.95	1.58	0.63
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	K.AQIWDTAGQER@.Y	14.36	5.38	2.67	0.37
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	R.GAVGALLVYDIAK#.H	25.53	9.74	2.62	0.38
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	K.VVLIGDSGVGK#.S	31.10	8.30	3.75	0.27
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	R.AITSAYYR.G	181.11	60.65	2.99	0.33
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	K.AQIWDTAGQER@.Y	47.88	21.11	2.27	0.44
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	R.DDEYDYLFK#.V	8.52	2.78	3.06	0.33
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	R.DHADSNIVIM*LVGNK#.S	23.32	8.49	2.75	0.36
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	R.DHADSNIVIMLVGNK#.S	21.79	9.18	2.37	0.42
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	R.ENDM*SPSNNVVPIHVPPTTENK#PK#.V	4.02	1.86	2.17	0.46
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	R.GAVGALLVYDIAK#.H	244.81	76.17	3.21	0.31
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	K.HLTYENVER@.W	93.17	36.99	2.52	0.40
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	R.NEFNLESK#.S	97.92	28.54	3.43	0.29
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	K.STIGVEFATR@.S	242.76	91.49	2.65	0.38
P62492_RB11A_MOUSE	Rab11a	Ras-related protein Rab-1	K.VVLIGDSGVGK#.S	232.23	82.81	2.80	0.36
P46638_RB11B_MOUSE	Rab11b	Ras-related protein Rab-1	K.NILTEIYR@.I	49.70	16.28	3.05	0.33
P46638_RB11B_MOUSE	Rab11b	Ras-related protein Rab-1	K.NNLSFIETSALDSTNVEEAFK#.N	34.11	11.39	2.99	0.33
Q8R361_RFIP5_MOUSE	Rab11fip5	Rab11 family-interacting	R.ATVALDEVFR@.A	19.64	6.51	3.02	0.33
Q8R361_RFIP5_MOUSE	Rab11fip5	Rab11 family-interacting	K.K#YDLESASAILPSSALEDPELGSLGK#.M	5.29	2.80	1.89	0.53
P35283_RAB12_MOUSE	Rab12	Ras-related protein Rab-1	K.DNFNVDEIFLK#.L	7.93	3.24	2.45	0.41
Q9DD03_RAB13_MOUSE	Rab13	Ras-related protein Rab-1	K.LQVWDTAGQER@.F	4.45	2.80	1.59	0.63
Q9DD03_RAB13_MOUSE	Rab13	Ras-related protein Rab-1	K.SSVNVDEAFSSLAR@.D	17.21	3.89	4.43	0.23
Q9DD03_RAB13_MOUSE	Rab13	Ras-related protein Rab-1	K.TITTAYYR@.G	19.97	7.66	2.61	0.38
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	K.IYQNIQDGSLDLNAAESGVQHK#PSAPQGGR@.L	4.75	2.34	2.03	0.49
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	R.NLTNPNTVIILIGNK#.A	6.93	3.35	2.07	0.48
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	R.GAAGALM*VYDITR@.R	21.72	9.08	2.39	0.42
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	R.GAAGALMVYDITR@.R	4.77	5.48	0.87	1.15
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	R.IIEVSGQK#.I	89.56	33.53	2.67	0.37
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	K.IYQNIQDGSLDLNAAESGVQHK#PSAPQGGR@.L	22.76	9.71	2.34	0.43
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	R.NLTNPNTVIILIGNK#.A	79.26	34.52	2.30	0.44
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	K.QFAEENGLLFLEASAK#.T	6.58	1.92	3.44	0.29
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	K.TGENVEDAFLEAAK#K#.I	75.49	24.30	3.11	0.32
Q91V41_RAB14_MOUSE	Rab14	Ras-related protein Rab-1	K.YIIIGDM*GVGK#.S	27.79	12.71	2.19	0.46
P35293_RAB18_MOUSE	Rab18	Ras-related protein Rab-1	R.FTDDTFDPELAATIGVDFK#.V	7.50	2.76	2.71	0.37
P35293_RAB18_MOUSE	Rab18	Ras-related protein Rab-1	R.GAQGVILVYDVTR@.R	35.28	15.80	2.23	0.45
P35293_RAB18_MOUSE	Rab18	Ras-related protein Rab-1	K.IIQTPGLWESENQNK#.G	17.72	9.19	1.93	0.52
P35293_RAB18_MOUSE	Rab18	Ras-related protein Rab-1	K.ILIIGESGVGK#.S	48.36	22.79	2.12	0.47
P35293_RAB18_MOUSE	Rab18	Ras-related protein Rab-1	K.LAIWDTAGQER.F	25.86	14.24	1.82	0.55
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.EFADSLGIPFLETSAK#.N	22.78	11.52	1.98	0.51
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.FADDTYTESYISTIGVDFK#.I	9.08	2.89	3.15	0.32
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.GAHGIIVVYDVTDQESFNNVK#.Q	11.40	5.49	2.08	0.48
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.NATNVEQSFM*TM*AAEIK#.K	2.41	4.36	0.55	1.81
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.QWLQEIDR@.Y	13.11	5.24	2.50	0.40
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.EFADSLGIPFLETSAK#.N	111.80	46.15	2.42	0.41
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.FADDTYTESYISTIGVDFK#.I	23.79	8.56	2.78	0.36
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.GAHGIIVVYDVTDQESFNNVK#.Q	27.03	9.95	2.72	0.37
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.M*GPGATAGGAEK#.S	20.24	10.57	1.91	0.52
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.NATNVEQSFM*TM*AAEIK#.K	18.61	7.42	2.51	0.40
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.NATNVEQSFM*TM*AAEIK#.K	10.76	5.76	1.87	0.54
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.QWLQEIDR@.Y	39.05	9.27	4.21	0.24
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.QWLQEIDR@YASENVNK#.L	29.99	7.10	4.22	0.24
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.TIELDGK#.T	110.31	40.02	2.76	0.36
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.TITSSYYR@.G	83.47	26.52	3.15	0.32
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.EFADSLGIPFLETSAK#.N	18.14	11.28	1.61	0.62
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.FADDTYTESYISTIGVDFK#.I	7.50	2.78	2.70	0.37
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.GAHGIIVVYDVTDQESFNNVK#.Q	12.44	2.67	4.66	0.21
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	K.EFADSLGIPFLETSAK#.N	25.37	14.98	1.69	0.59
P62821_RAB1A_MOUSE	Rab1A	Ras-related protein Rab-1	R.FADDTYTESYISTIGVDFK#.I	11.96	4.13	2.90	0.34
Q9D1G1_RAB1B_MOUSE	Rab1b	Ras-related protein Rab-1	K.EFADSLGVPFLETSAK#.N	76.22	22.51	3.39	0.30
Q9D1G1_RAB1B_MOUSE	Rab1b	Ras-related protein Rab-1	R.GAHGIIVVYDVTDQESYANVK#.Q	42.88	8.56	5.01	0.20
Q9D1G1_RAB1B_MOUSE	Rab1b	Ras-related protein Rab-1	K.NATNVEQAFM*TM*AAEIK#.K	22.04	6.20	3.55	0.28
Q9D1G1_RAB1B_MOUSE	Rab1b	Ras-related protein Rab-1	K.NATNVEQAFM*TMAAEIK#.K	5.46	1.72	3.17	0.32
P53994_RAB2A_MOUSE	Rab2a	Ras-related protein Rab-2	K.TASNVEEAFINTAK#.E	6.65	5.91	1.13	0.89
P53994_RAB2A_MOUSE	Rab2a	Ras-related protein Rab-2	R.DTFNHLTTWLEDAR@.Q	19.66	12.25	1.61	0.62

P53994_RAB2A_MOUSE	Rab2a	Ras-related protein Rab-2	R.FQPVHDLTIGVEFGAR@.M	22.57	10.77	2.10	0.48
P53994_RAB2A_MOUSE	Rab2a	Ras-related protein Rab-2	R.GAAGALLVYDITR@.R	55.32	27.73	1.99	0.50
P53994_RAB2A_MOUSE	Rab2a	Ras-related protein Rab-2	K.IQEGVFDINNEANGIK#.I	21.44	9.41	2.28	0.44
P53994_RAB2A_MOUSE	Rab2a	Ras-related protein Rab-2	K.LQIWDTAGQESFR@.S	30.20	19.61	1.54	0.65
P53994_RAB2A_MOUSE	Rab2a	Ras-related protein Rab-2	R.M*ITIDGK#.Q	21.64	14.76	1.47	0.68
P53994_RAB2A_MOUSE	Rab2a	Ras-related protein Rab-2	K.TASNVEEAFINTAK#.E	79.01	40.98	1.93	0.52
P53994_RAB2A_MOUSE	Rab2a	Ras-related protein Rab-2	K.YIIIGDTGVGK#.S	13.85	7.33	1.89	0.53
Q6PHN9_RAB35_MOUSE	Rab35	Ras-related protein Rab-3	K.FAGQM*GIQLFETSAK#.E	10.71	4.40	2.43	0.41
Q6PHN9_RAB35_MOUSE	Rab35	Ras-related protein Rab-3	K.FAGQM*GIQLFETSAK#.E	30.15	8.05	3.75	0.27
Q6PHN9_RAB35_MOUSE	Rab35	Ras-related protein Rab-3	K.QQQQQQNDVVK#.L	10.03	2.98	3.37	0.30
Q80UJ7_RB3GP_MOUSE	Rab3gap1	Rab3 GTPase-activating p	R.LAGAFSSDTSFF.-	7.95	7.95	1.00	1.00
Q80UJ7_RB3GP_MOUSE	Rab3gap1	Rab3 GTPase-activating p	R.SDEISFADFR@.F	14.12	3.03	4.65	0.21
Q80UJ7_RB3GP_MOUSE	Rab3gap1	Rab3 GTPase-activating p	R.STFEEEGR@EVADITHALSK#.L	10.64	5.51	1.93	0.52
Q80UJ7_RB3GP_MOUSE	Rab3gap1	Rab3 GTPase-activating p	R.STFEEEGR@EVADITHALSK#.L	8.92	6.11	1.46	0.68
Q80UJ7_RB3GP_MOUSE	Rab3gap1	Rab3 GTPase-activating p	K.TSLSDSTTSAYPGDAGK#.T	10.31	3.27	3.16	0.32
Q8BMG7_RBGPR_MOUSE	Rab3gap2	Rab3 GTPase-activating p	K.GGFSPFGNTQGPSR@.V	8.48	4.86	1.75	0.57
Q8BMG7_RBGPR_MOUSE	Rab3gap2	Rab3 GTPase-activating p	R.VAQFLVIYAPR@.R	10.76	3.99	2.70	0.37
Q8BMG7_RBGPR_MOUSE	Rab3gap2	Rab3 GTPase-activating p	R.VILLDVAR@.G	21.32	9.57	2.23	0.45
Q91ZR1_RAB4B_MOUSE	Rab4b	Ras-related protein Rab-4	R.GAAGALLVYDITSR@.E	7.96	4.67	1.70	0.59
Q91ZR1_RAB4B_MOUSE	Rab4b	Ras-related protein Rab-4	R.M*GSGIQYGDISLR@.Q	2.59	1.88	1.38	0.73
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	K.FEIWDTAGQER@.Y	5.74	3.39	1.69	0.59
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	R.GVDLTEPAQPAR@.S	8.67	4.46	1.95	0.51
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	K.LVLLGESAVGK#.S	41.10	15.53	2.65	0.38
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	K.FEIWDTAGQER@.Y	12.53	5.40	2.32	0.43
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	R.GAQAAIVVYDITNEESFAR@.A	10.63	5.49	1.94	0.52
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	R.GVDLTEPAQPAR@.S	18.58	7.33	2.54	0.39
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	K.LVLLGESAVGK#.S	103.42	38.62	2.68	0.37
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	R.QASPNIVIALSGNK#.A	11.57	6.07	1.91	0.52
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	K.TSM*NVNEIFM*AIAK#.K	8.96	5.02	1.78	0.56
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	K.TSMNVNEIFM*AIAK#.K	49.82	17.73	2.81	0.36
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	R.YHSLAPM*YYR@.G	21.99	4.34	5.07	0.20
Q9CQD1_RAB5A_MOUSE	Rab5a	Ras-related protein Rab-5	K.LVLLGESAVGK#.S	11.45	3.97	2.88	0.35
P61021_RAB5B_MOUSE	Rab5b	Ras-related protein Rab-5	K.SEPQNLGGAAGR@.S	17.11	5.11	3.35	0.30
P61021_RAB5B_MOUSE	Rab5b	Ras-related protein Rab-5	R.GAQAAIVVYDITNQETFAR@.A	8.76	3.17	2.76	0.36
P61021_RAB5B_MOUSE	Rab5b	Ras-related protein Rab-5	R.QASPSIVIALAGNK#.A	6.26	5.45	1.15	0.87
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	R.GAQAAIVVYDITNTDTFAR@.A	7.30	3.08	2.37	0.42
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	R.GVDLQESNPASR@.S	9.75	4.36	2.24	0.45
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	K.NEPQNAAGAPGR.T	8.54	4.70	1.82	0.55
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	R.QASPNIVIALAGNK#.A	11.55	6.16	1.87	0.53
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	R.GAQAAIVVYDITNTDTFAR@.A	21.51	5.75	3.74	0.27
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	R.GAQAAIVVYDITNTDTFAR@.A	14.96	5.75	2.60	0.38
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	R.GVDLQESNPASR@.S	57.96	24.19	2.40	0.42
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	K.NEPQNAAGAPGR@.T	32.70	12.58	2.60	0.38
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	K.TAM*NVNEIFM*AIAK#.K	49.82	17.73	2.81	0.36
P35278_RAB5C_MOUSE	Rab5c	Ras-related protein Rab-5	R.GVDLQESNPASR@.S	3.62	5.27	0.69	1.46
D3YV69_D3YV69_MOUSE	Rab6a	Ras-related protein Rab-6	R.DSAAAVVVYDITNVNSFQQTTK#.W	15.41	6.84	2.25	0.44
D3YV69_D3YV69_MOUSE	Rab6a	Ras-related protein Rab-6	R.DSAAAVVVYDITNVNSFQQTTK#.W	3.17	2.51	1.26	0.79
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	R.DSTVAVVVYDITNVNSFQQTTK#.W	27.11	11.63	2.33	0.43
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	K.ELNVM*FIETSAK#.A	71.76	29.99	2.39	0.42
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	K.ELNVMFIETSAK#.A	15.78	4.78	3.30	0.30
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	K.FK#LVFLGEQSVGK#.T	18.72	7.58	2.47	0.40
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	R.FM*YDSFDNTYQATIGIDFLSK#.T	2.87	2.22	1.30	0.77
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	R.GSDVIIM*LVGNK#.T	46.68	25.28	1.85	0.54
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	R.GSDVIIMLVGNK#.T	63.75	27.19	2.34	0.43
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	K.LVFLGEQSVGK#.T	192.91	102.85	1.88	0.53
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	R.QVSIEEGER.K	65.94	33.78	1.95	0.51
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	R.SLIPSYIR.D	131.98	61.99	2.13	0.47
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	K.TM*YLEDR@.T	36.08	15.88	2.27	0.44
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	R.VAAALPGM*ESTQDR@.S	70.50	38.63	1.83	0.55
P35279_RAB6A_MOUSE	Rab6a	Ras-related protein Rab-6	K.WIDDVR@.T	38.45	19.28	1.99	0.50
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.ATIGADFLTK#.E	15.62	7.37	2.12	0.47
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.FQSLGVAFYR@.G	13.99	5.39	2.59	0.39
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.VIILGDSGVGK#.T	18.24	5.52	3.30	0.30
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.ATIGADFLTK#.E	69.49	23.85	2.91	0.34
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.DEFLIQASPR@.D	5.85	3.77	1.55	0.64
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.DPENFPFVVLGNK#.I	81.81	28.37	2.88	0.35
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.EAINVEQAFQTIAR.N	102.06	28.69	3.56	0.28
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.FQSLGVAFYR@.G	40.20	15.22	2.64	0.38
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.LVTM*QIWDTAGQER@.F	5.46	1.88	2.90	0.35
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.LVTMQIWDTAGQER@.F	12.98	5.29	2.45	0.41
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.NALK#QETEVELYNEFPEPIK#.L	17.24	6.24	2.76	0.36
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.NALK#QETEVELYNEFPEPIK#LDK#.N	20.50	8.68	2.36	0.42
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.NALK#QETEVELYNEFPEPIK#LDK#.N	11.05	4.82	2.29	0.44
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.TLDSWR@DEFLIQASPR@.D	6.13	2.21	2.78	0.36
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.TLDSWRDEFLIQASPR.D	61.59	15.58	3.95	0.25
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.TSLM*NQYVNK#.K	5.87	3.47	1.69	0.59
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.VIILGDSGVGK#.T	96.98	29.03	3.34	0.30
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.ATIGADFLTK#.E	12.53	7.03	1.78	0.56
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.DPENFPFVVLGNK#.I	16.33	7.96	2.05	0.49
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.FQSLGVAFYR@.G	9.26	4.55	2.03	0.49
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.TLDSWR@DEFLIQASPR@.D	12.17	5.35	2.28	0.44
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.ATIGADFLTK#.E	18.72	8.54	2.19	0.46
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.DPENFPFVVLGNK#.I	19.67	14.08	1.40	0.72
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	R.FQSLGVAFYR@.G	9.25	4.15	2.23	0.45
P51150_RAB7A_MOUSE	Rab7a	Ras-related protein Rab-7	K.TLDSWR@DEFLIQASPR@.D	8.41	2.62	3.21	0.31
P55258_RAB8A_MOUSE	Rab8a	Ras-related protein Rab-8	K.ANINVENAFFTLAR@.D	13.50	4.65	2.90	0.34
Q9R0M6_RAB9A_MOUSE	Rab9a	Ras-related protein Rab-9	K.DSTNVAAAFEEAVR@.R	10.38	4.44	2.34	0.43
Q9R0M6_RAB9A_MOUSE	Rab9a	Ras-related protein Rab-9	K.IILLGDGGVGK#.S	15.47	6.94	2.23	0.45
Q9Z0S9_PRAF1_MOUSE	Rabac1	Prenylated Rab acceptor	K.DAEGEGLSATTLLPK#.L	3.62	2.70	1.34	0.75
P63001_RAC1_MOUSE	Rac1	Ras-related C3 botulinun	K.LTPITYPQGLAM*AK#.E	12.19	3.99	3.05	0.33
Q9WVM1_RGAP1_MOUSE	Racgap1	Rac GTPase-activating pr	R.GLTEAGLYR@.I	15.51	5.61	2.77	0.36
Q9WVM1_RGAP1_MOUSE	Racgap1	Rac GTPase-activating pr	R.TDTDNLGTPQNTGGM*R@.L	7.10	2.24	3.17	0.32
Q9WVM1_RGAP1_MOUSE	Racgap1	Rac GTPase-activating pr	K.TPLSSSLSQR@.L	19.35	8.00	2.42	0.41
Q9WVM1_RGAP1_MOUSE	Racgap1	Rac GTPase-activating pr	K.VSLLGPVTTPEFQLVK#.T	12.24	5.01	2.44	0.41
Q9WVM1_RGAP1_MOUSE	Racgap1	Rac GTPase-activating pr	R.GLTEAGLYR@.I	14.85	6.21	2.39	0.42
Q9WVM1_RGAP1_MOUSE	Racgap1	Rac GTPase-activating pr	K.SALAFLNR@.G	30.42	8.17	3.72	0.27
Q9WVM1_RGAP1_MOUSE	Racgap1	Rac GTPase-activating pr	R.TDTDNLGTPQNTGGM*R@.L	11.96	1.48	8.07	0.12
Q9WVM1_RGAP1_MOUSE	Racgap1	Rac GTPase-activating pr	K.TPLSSSLSQR@.L	19.64	4.82	4.08	0.25
Q9WVM1_RGAP1_MOUSE	Racgap1	Rac GTPase-activating pr	K.VSLLGPVTTPEFQLVK#.T	24.30	3.97	6.12	0.16
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	R.AQLSDYSDIVTTLDLAPPTK#.K	7.05	6.58	1.07	0.93
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	R.DVIDEPIIEEPSR@.L	41.28	21.87	1.89	0.53
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.EFENPEVPR@EEQQPQQQQPQPQR@.D	2.55	3.84	0.66	1.51
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.EKEEEEEEEDEDASGGDQDQEER.R	2.08	2.01	1.03	0.97

Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.EK#EEEEEEEDEDASGGDQDQEER@R@.W	2.68	2.34	1.15	0.87
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.EK#EK#EEEEEEEDEDASGGDQDQEER@.R	6.94	2.69	2.58	0.39
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.FYSFLVLK#.K	50.85	14.88	3.42	0.29
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.GGEADNLDEFLK#EFENPEVPR@EEQQPQQQQPQPQR@.D	6.74	4.01	1.68	0.59
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.LFFLPAQPLWNNR@.L	34.64	20.21	1.71	0.58
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	R.LQDSVM*EASR@.T	30.54	14.41	2.12	0.47
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.M*AFR@PGVVDLPEENR@.E	24.80	13.23	1.88	0.53
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.M*NHLEYEDQYK#DDNFGEGNDGGILDDK#.L	14.05	5.17	2.72	0.37
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	R.TSGHLLLGVVR@.I	35.06	14.96	2.34	0.43
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	R.TTIEESAM*PPPPPQGVK#.R	8.68	5.19	1.67	0.60
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	R.AQLSDYSDIVTTLDLAPPTK#.K	6.61	3.08	2.14	0.47
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	R.EAAYNAITLPEEFHDFDQPLPDLDDIDVAQQFSLNQSR@.V	2.72	1.78	1.52	0.66
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.LFFLPAQPLWNNR@.L	15.66	5.40	2.90	0.35
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	R.LQDSVM*EASR@.T	10.10	48.91	0.21	4.84
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	K.M*AFR@PGVVDLPEENR@.E	14.37	6.58	2.18	0.46
Q61550_RAD21_MOUSE	Rad21	Double-strand-break rep	R.TTIEESAM*PPPPPQGVK#.R	5.90	1.74	3.39	0.29
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.DSLIQSLATHLELDGFER@.G	18.55	3.89	4.77	0.21
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.EQISPLETALEK#.L	13.94	7.06	1.98	0.51
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.GQDIEYIEIR@.S	24.09	7.46	3.23	0.31
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.ILELDQELTK#.A	22.32	5.25	4.25	0.24
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.R@QQM*EEQSVELSTEVQSLNR@.E	5.72	2.06	2.77	0.36
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.SDADENVSASDK#.R	5.07	2.60	1.95	0.51
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.SELQQLEGSSDR@.I	17.20	4.39	3.92	0.26
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.VFQTEAELQEVISDLQSK#.L	36.97	9.69	3.81	0.26
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.AELLVEQGR@.L	16.17	7.19	2.25	0.45
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.AEVM*SLQNEK#.A	10.32	3.80	2.72	0.37
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.DLDIYYK#.T	14.59	2.82	5.17	0.19
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.DSLIQSLATHLELDGFER@.G	19.92	8.98	2.22	0.45
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.EAQLASSQEIVR@.S	16.43	4.66	3.52	0.28
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.GNTFVHDPK#.V	10.35	3.35	3.09	0.32
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.GQDIEYIEIR@.S	28.58	10.74	2.66	0.38
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.HSDELTSLLGYFPNK#K#.Q	39.56	11.35	3.49	0.29
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.ILELDQELTK#.A	31.45	79.00	0.40	2.51
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.K#LIQDQQEQIQHLK#.S	11.24	6.81	1.65	0.61
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.LEENIDTIK#R@.N	20.20	8.00	2.52	0.40
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.LK#NDIEEQETLLGTIM*PEEESAK#.V	4.16	1.77	2.34	0.43
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.LQGVDLDR@.T	25.10	7.68	3.27	0.31
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.R@QQM*EEQSVELSTEVQSLNR@.E	12.68	4.03	3.15	0.32
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.SELQQLEGSSDR@.I	24.56	11.04	2.22	0.45
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.SFGIEDK#DK#.Q	5.32	2.99	1.78	0.56
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.TASQLLSDLTDK#EALK#.Q	48.45	41.53	1.17	0.86
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	K.TLDQAIM*K#.F	18.10	4.78	3.79	0.26
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.VFQTEAELQEVISDLQSK#.L	72.66	22.43	3.24	0.31
P70388_RAD50_MOUSE	Rad50	DNA repair protein RAD5	R.VFQTEAELQEVISDLQSK#.L	11.53	5.08	2.27	0.44
Q99NG0_ARIP4_MOUSE	Rad54l2	Helicase ARIP4 OS=Mus n	K.AAQQEELER@.R	7.73	1.19	6.52	0.15
Q99NG0_ARIP4_MOUSE	Rad54l2	Helicase ARIP4 OS=Mus n	R.FLYDNLVESLER@.F	8.86	3.34	2.65	0.38
Q8C570_RAE1L_MOUSE	Rae1	mRNA export factor OS=	R.GLIVYQLENQPSEFR@.R	20.54	17.12	1.20	0.83
Q8C570_RAE1L_MOUSE	Rae1	mRNA export factor OS=	K.M*WDLNSNQAIQIAQHDAPVK#.T	12.90	10.92	1.18	0.85
Q8C570_RAE1L_MOUSE	Rae1	mRNA export factor OS=	R.SSNPM*M*VLQLPER.C	8.00	6.61	1.21	0.83
O08602_RAE1A_MOUSE	Raet1a	Retinoic acid early-induc	R.SANDESGVIM*NK#.W	15.23	4.72	3.23	0.31
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.AK#EQEVTALVQK#.F	31.81	22.02	1.44	0.69
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.SSPPVEHPAGTSTTDNDVIIR@.Q	15.20	11.89	1.28	0.78
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.VLNELTQLK#.Q	23.10	16.24	1.42	0.70
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.YQQAQEEIM*K#.L	17.80	11.88	1.50	0.67
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.AAVSDAM*VPK#.S	33.07	10.96	3.02	0.33
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.AEISSIQENK#DR@.L	9.59	3.24	2.96	0.34
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.AFLFEK#.Y	50.71	14.89	3.41	0.29
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	R.AK#SEEALSEM*K#.S	10.60	3.35	3.17	0.32
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	R.AQEELAGM*R@.R	24.37	6.89	3.54	0.28
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.ASDIPSSDAK#.S	41.53	9.53	4.36	0.23
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.DK#EAEADLSFQSFHSTQTDLAPSPGK#.A	3.66	2.55	1.43	0.70
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	R.EAPADEDIDTLK#.Q	15.78	5.24	3.01	0.33
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	R.EAQAELEDYR@.K	18.54	3.73	4.97	0.20
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.K#GADLSLVDSLGHNALHYSK#.L	30.46	12.04	2.53	0.40
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.LGLLSQESADGYSHLR@.E	139.69	31.70	4.41	0.23
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.LK#EALNSLSQLSYSTSSSK#.R	32.97	8.02	4.11	0.24
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.LQASLESEVNALATK#.L	78.65	21.72	3.62	0.28
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.LSENAGIQNLLLSK#.I	73.81	27.35	2.70	0.37
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.QLQDELQSQR@.T	53.14	13.98	3.80	0.26
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.QVSELSQLYR@.E	42.82	11.30	3.79	0.26
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.SEEALSEM*K#.S	15.65	4.59	3.41	0.29
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.SPAENIDNSGK#.T	37.66	16.58	2.27	0.44
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.SQM*PQEAPDDSGDM*K#.E	4.19	1.42	2.95	0.34
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.SSPPVEHPAGTSTTDNDVIIR@.Q	85.10	25.24	3.37	0.30
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.VASLTLHNK#.E	22.33	5.40	4.14	0.24
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.VLNELTQLK#.Q	72.12	22.14	3.26	0.31
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.YEEAM*K#EVLSVQK#.Q	22.76	10.51	2.16	0.46
Q9EP71_RAI14_MOUSE	Rai14	Ankycorbin OS=Mus mus	K.YQQAQEEIM*K#.L	37.38	11.21	3.33	0.30
P63321_RALA_MOUSE	Rala	Ras-related protein Ral-A	R.ADQWNVNYVETSAK#.T	1.21	10.08	0.12	8.33
P63321_RALA_MOUSE	Rala	Ras-related protein Ral-A	K.VFFDLM*R@.E	16.64	8.27	2.01	0.50
P63321_RALA_MOUSE	Rala	Ras-related protein Ral-A	K.VIM*VGSGGVGK#.S	24.22	12.43	1.95	0.51
P63321_RALA_MOUSE	Rala	Ras-related protein Ral-A	R.VK#EDENVPFLLVGNK#.S	16.13	5.84	2.76	0.36
Q8BQZ4_RLGPB_MOUSE	Ralgapb	Ral GTPase-activating pr	K.ADLSIPDLHEIVTEELEER@.H	5.32	2.69	1.98	0.51
Q8BQZ4_RLGPB_MOUSE	Ralgapb	Ral GTPase-activating pr	R.FLHM*LSNPVDLSNPAVISSTPK#.F	6.72	1.94	3.46	0.29
A2AU61_A2AU61_MOUSE	Raly	RNA-binding protein Ral	R.AATAIYR@.L	146.26	119.23	1.23	0.82
A2AU61_A2AU61_MOUSE	Raly	RNA-binding protein Ral	K.R@AATAIYR@.L	42.04	34.62	1.21	0.82
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.AAVLGENGR@.V	51.81	46.60	1.11	0.90
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.DDGDEEGLLTHSEEELEHSQDTDAEDGALQ.-	141.94	141.94	1.00	1.00
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.GYAFVQYANER@.H	177.37	166.61	1.06	0.94
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.IQTSNVTNK#.N	60.47	70.00	0.86	1.16
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.K#SDVETIFSK#.Y	153.31	134.57	1.14	0.88
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.LEQIAEEQK#.A	299.59	272.74	1.10	0.91
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.LEQIAEEQKANPDGK.K	12.43	10.20	1.22	0.82
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.LFDYR@.G	165.42	149.00	1.11	0.90
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.LPAPQEDTASEAGTPQGEVQTR@.D	49.34	39.34	1.25	0.80
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.SDVETIFSK#.Y	85.95	71.84	1.20	0.84
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.SNIDALLGR@.L	342.28	305.57	1.12	0.89
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.SNIDALLGR@LEQIAEEQK#.A	6.57	4.61	1.43	0.70
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.SSELQTIK#.T	265.18	254.09	1.04	0.96
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.STAVTTGSAK#.I	63.89	61.38	1.04	0.96
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.VFIGNLNTAVVK#.K	455.16	409.86	1.11	0.90
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.VLAGQTLDINM*AGEPKPNRPK.G	130.24	114.02	1.14	0.88
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.VLAGQTLDINMAGEPK#PNR@PK#.G	8.67	7.80	1.11	0.90

Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.VTVPLVR.R	359.33	352.30	1.02	0.98
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.GYAFVQYANER.H	9.88	13.45	0.74	1.36
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.IQTSNVTNK.N	8.90	15.83	0.56	1.78
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.LEQIAEEQK.A	13.67	21.46	0.64	1.57
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.LPAPQEDTASEAGTPQGEVQTR@.D	5.27	2.18	2.41	0.41
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.SDVETIFSK.Y	6.02	8.50	0.71	1.41
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.VFIGNLNTAVVK.K	29.50	53.77	0.55	1.82
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.VLAGQTLDINM*AGEPKPNRPK.G	1.86	3.37	0.55	1.81
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.VTVPLVR.R	47.00	79.41	0.59	1.69
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.GYAFVQYANER.H	17.37	15.49	1.12	0.89
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.LEQIAEEQK#.A	22.09	17.23	1.28	0.78
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.LPAPQEDTASEAGTPQGEVQTR@.D	22.54	14.12	1.60	0.63
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.SNIDALLGR.L	21.72	18.16	1.20	0.84
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	K.TELTQIK#.S	25.75	25.42	1.01	0.99
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.VFIGNLNTAVVK#.K	32.83	25.56	1.28	0.78
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.VLAGQTLDINM*AGEPKPNRPK.G	23.25	23.06	1.01	0.99
Q64012_RALY_MOUSE	Raly	RNA-binding protein Ral	R.LEQIAEEQK#.A	14.07	9.79	1.44	0.70
P62827_RAN_MOUSE	Ran	GTP-binding nuclear pro	K.FNVWDTAGQEK.F	2.46	6.50	0.38	2.65
P62827_RAN_MOUSE	Ran	GTP-binding nuclear pro	K.LVLVGDGGTGK.T	8.24	15.99	0.52	1.94
P62827_RAN_MOUSE	Ran	GTP-binding nuclear pro	K.NLQYYDISAK.S	5.39	9.40	0.57	1.74
P62827_RAN_MOUSE	Ran	GTP-binding nuclear pro	K.SNYNFEKPFLWLAR.K	5.31	17.77	0.30	3.35
Q6VN19_RBP10_MOUSE	Ranbp10	Ran-binding protein 10	R.VGEAIETTQR@.F	10.76	9.20	1.17	0.86
Q6VN19_RBP10_MOUSE	Ranbp10	Ran-binding protein 10	K.VQGTVHGFPISAR@.L	8.53	6.13	1.39	0.72
Q6VN19_RBP10_MOUSE	Ranbp10	Ran-binding protein 10	R.ELQALSEQLGR@.E	5.90	31.88	0.19	5.40
Q6VN19_RBP10_MOUSE	Ranbp10	Ran-binding protein 10	R.M*TETPIQEEQASIK#.N	5.50	2.16	2.55	0.39
Q6VN19_RBP10_MOUSE	Ranbp10	Ran-binding protein 10	R.VGEAIETTQR@.F	9.52	2.88	3.30	0.30
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	R.ELLESFDSALQSVK#.S	9.47	7.52	1.26	0.79
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	R.ILDDSDSNTSVVQK#.L	9.38	6.41	1.46	0.68
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	R.YIASVQGSAPSPR@.E	8.19	5.56	1.47	0.68
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	R.FGESTTGFNFSFK#.S	10.18	3.10	3.29	0.30
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	K.FGQGDLPK#.S	8.77	5.29	1.66	0.60
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	R.FK#TPEEAALFK#.C	11.25	8.27	1.36	0.74
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	K.HLENDPSFQAHDTSGQK#.N	13.96	6.35	2.20	0.46
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	R.ILDDSDSNTSVVQK#.L	14.92	7.30	2.04	0.49
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	K.ILQNYDNK#.Q	10.74	6.21	1.73	0.58
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	K.LPVPLESVK#.E	14.01	10.15	1.38	0.72
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	K.NTLTENM*GPNQQK#.N	9.92	5.78	1.72	0.58
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	K.SASSFVQTSFK#.F	15.37	11.02	1.39	0.72
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	R.SFVWHALDYADELPK#PEQLAIR@.F	3.71	2.96	1.25	0.80
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	R.SFVWHALDYADELPK#PEQLAIR@.F	7.00	4.78	1.47	0.68
Q9ERU9_RBP2_MOUSE	Ranbp2	E3 SUMO-protein ligase	K.SVFTTAASELANK#.S	22.86	10.97	2.08	0.48
P69566_RANB9_MOUSE	Ranbp9	Ran-binding protein 9 O	R.LYPAVDEQETPLPR@.S	4.98	2.11	2.37	0.42
P69566_RANB9_MOUSE	Ranbp9	Ran-binding protein 9 O	R.NPNLLFTLK#.V	11.11	5.56	2.00	0.50
P69566_RANB9_MOUSE	Ranbp9	Ran-binding protein 9 O	R.STDQTVLEELASIK#.N	10.24	6.30	1.63	0.61
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.GAVAIADAVR@.G	25.99	9.15	2.84	0.35
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.LEGNTVGVEAAR.V	12.51	8.39	1.49	0.67
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.TQVAGGQLSFK#.G	32.71	11.82	2.77	0.36
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.VINLNDNTFTEK#.G	47.68	20.19	2.36	0.42
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.TAVLDAIDALM*K#.K	9.57	4.92	1.94	0.51
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.VSVLIVQQTDTSDPEK#VVSAFLK#.V	7.60	5.27	1.44	0.69
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.DAALVVAEAVADK#.A	7.69	6.67	1.15	0.87
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.DAALVVAEAVADK#AELEK#.L	14.63	5.10	2.87	0.35
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.DVIK#EIEEFDGLEALR@LEGNTVGVEAAR@.V	4.01	2.47	1.62	0.62
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.EIEEFDGLEALR@.L	9.87	5.06	1.95	0.51
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.EIEEFDGLEALR@LEGNTVGVEAAR@.V	6.29	3.02	2.08	0.48
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.GAVAIADAVR@.G	64.20	22.66	2.83	0.35
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.GFEALLK#.S	49.68	16.73	2.97	0.34
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.GGVAM*AETLK#.T	43.86	13.05	3.36	0.30
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.GSGEEPATPSR@.K	14.87	9.39	1.58	0.63
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.HNLLQTLYNI.-	64.74	64.74	1.00	1.00
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.LEGNTVGVEAAR@.V	39.96	24.28	1.65	0.61
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.LNTAEDAK#DVIK#EIEEFDGLEALR@.L	14.91	8.23	1.81	0.55
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.TQVAGGQLSFK#.G	67.27	19.31	3.48	0.29
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.VINLNDNTFTEK#.G	99.31	30.63	3.24	0.31
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.VSVLIVQQTDTSDPEK#.V	28.67	10.95	2.62	0.38
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.VSVLIVQQTDTSDPEK#VVSAFLK#.V	38.17	13.22	2.89	0.35
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.VVSAFLK#.V	33.42	10.23	3.27	0.31
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.GAVAIADAVR@.G	12.12	4.28	2.83	0.35
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.HNLLQTLYNI.-	13.55	13.55	1.00	1.00
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.TAVLDAIDALM*K#.K	9.85	4.09	2.41	0.41
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	R.VINLNDNTFTEK#.G	15.87	6.89	2.30	0.43
P46061_RAGP1_MOUSE	Rangap1	Ran GTPase-activating pr	K.VSVLIVQQTDTSDPEK#.V	3.73	5.91	0.63	1.58
P62835_RAP1A_MOUSE	Rap1a	Ras-related protein Rap-1	K.INVNEIFYDLVR@.Q	7.37	4.19	1.76	0.57
P62835_RAP1A_MOUSE	Rap1a	Ras-related protein Rap-1	K.LVVLGSGGVGK#.S	13.61	4.60	2.96	0.34
P62835_RAP1A_MOUSE	Rap1a	Ras-related protein Rap-1	K.INVNEIFYDLVR@.Q	52.41	26.63	1.97	0.51
P62835_RAP1A_MOUSE	Rap1a	Ras-related protein Rap-1	K.LVVLGSGGVGK#.S	53.46	24.01	2.23	0.45
P62835_RAP1A_MOUSE	Rap1a	Ras-related protein Rap-1	K.SK#INVNEIFYDLVR@.Q	24.75	8.15	3.04	0.33
P62835_RAP1A_MOUSE	Rap1a	Ras-related protein Rap-1	K.YDPTIEDSYR@K#.Q	7.53	3.10	2.43	0.41
P62835_RAP1A_MOUSE	Rap1a	Ras-related protein Rap-1	K.INVNEIFYDLVR@.Q	10.14	4.40	2.30	0.43
P62835_RAP1A_MOUSE	Rap1a	Ras-related protein Rap-1	K.LVVLGSGGVGK#.S	13.05	6.09	2.14	0.47
P61226_RAP2B_MOUSE	Rap2b	Ras-related protein Rap-	K.ASVDELFAEIVR@.Q	7.73	2.04	3.78	0.26
Q8CHG7_RPGF2_MOUSE	Rapgef2	Rap guanine nucleotide	R.NIEPTEYIDDLFK#.L	10.98	1.86	5.89	0.17
P18911_RARG_MOUSE	Rarg	Retinoic acid receptor ga	K.EAVRNDRNK.K	1.21	37.08	0.03	30.66
P18911_RARG_MOUSE	Rarg	Retinoic acid receptor ga	K.LQEPLLEALR@.L	11.32	3.90	2.90	0.34
P18911_RARG_MOUSE	Rarg	Retinoic acid receptor ga	R.YTPEQDTM*TFSDGLTLNR@.T	4.41	2.09	2.11	0.47
Q99MK9_RASF1_MOUSE	Rassf1	Ras association domain-	R.ETPDLSQAETEQK#.I	5.78	3.34	1.73	0.58
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	R.ADGQALGDSHLR@.V	34.53	14.77	2.34	0.43
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	R.APEQELPPLDPEEIR@K#.R	9.20	4.12	2.23	0.45
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	K.GFAVLEYETAEM*AEAAQER@.A	7.23	2.73	2.65	0.38
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	K.GFAVLEYETAEM*AEAAQER@.A	22.11	4.73	4.67	0.21
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	K.GFAVLEYETAEMAEAAQER@.A	9.74	2.15	4.52	0.22
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	R.R@APEQELPPLDPEEIR@K#.R	14.75	6.25	2.36	0.42
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	R.SGGGSGGPLSHFYSGSPTSYFTSGLQAGLK#.Q	3.97	3.49	1.14	0.88
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	R.SM*LAALIAAQATALNR@.G	16.68	6.52	2.56	0.39
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	R.TLYVHWTDAGQLTPALLHSR@.C	20.58	4.91	4.19	0.24
Q9CW46_RAVR1_MOUSE	Raver1	Ribonucleoprotein PTB-	R.LPPEPGLPDSYGFDYPTDVGPR.R	2.51	1.82	1.38	0.73
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.GEFGGFGSVSGK#.I	44.35	19.07	2.33	0.43
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.IGEEQSPEDAEDGPPELLFIHGGHTAK#.I	188.39	85.50	2.20	0.45
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.INHEGEVNR@.A	29.33	17.54	1.67	0.60
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.LHSFESHK#DEIFQVQWSPHNETILASSGTDR@.R	15.63	3.17	4.93	0.20
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.LM*IWDTR@.S	81.75	34.83	2.35	0.43
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.LMIWDTR@.S	39.77	15.15	2.62	0.38
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	R.LNVWDLSK#.I	130.76	49.96	2.62	0.38

Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	R.LVLGTHTSDEQNHLVIASVQLPNDDAQFDASHYDSEK#.G	10.48	2.39	4.38	0.23
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	R.R@LNVWDLSK#.I	121.57	45.90	2.65	0.38
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.TIFTGHTAVVEDVSWHLLHESLFGSVADDQK#.L	50.79	15.96	3.18	0.31
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.TPSSDVLVFDYTK#.H	246.53	106.93	2.31	0.43
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.TVALWDLR@.N	273.38	99.82	2.74	0.37
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	R.VINEEYK#.I	210.87	85.60	2.46	0.41
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	R.R@LNVWDLSK#.I	9.11	7.23	1.26	0.79
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.TPSSDVLVFDYTK#.H	134.50	3.87	34.79	0.03
Q60972_RBBP4_MOUSE	Rbbp4	Histone-binding protein	K.TVALWDLR@.N	18.90	6.15	3.07	0.33
Q8BX09_RBBP5_MOUSE	Rbbp5	Retinoblastoma-binding	K.ELDENVEYEER@.E	8.07	3.02	2.67	0.37
Q8BX09_RBBP5_MOUSE	Rbbp5	Retinoblastoma-binding	R.FPSPILK#.V	18.49	5.58	3.31	0.30
Q8BX09_RBBP5_MOUSE	Rbbp5	Retinoblastoma-binding	K.HVVLPVDDDSDLNVVASFDR@.R	21.63	7.90	2.74	0.37
Q8BX09_RBBP5_MOUSE	Rbbp5	Retinoblastoma-binding	R.IVIWDFLTR@.G	58.29	18.10	3.22	0.31
Q8BX09_RBBP5_MOUSE	Rbbp5	Retinoblastoma-binding	R.QSSADGSQPPK#.K	3.74	1.41	2.64	0.38
Q8BX09_RBBP5_MOUSE	Rbbp5	Retinoblastoma-binding	K.SAPVM*LTLSDSK#.H	22.92	4.97	4.61	0.22
Q8BX09_RBBP5_MOUSE	Rbbp5	Retinoblastoma-binding	K.TDSQDLVASFR@.V	27.25	9.43	2.89	0.35
Q8BX09_RBBP5_MOUSE	Rbbp5	Retinoblastoma-binding	K.TTNIELQGVPNDEVHPLLGVK#.G	22.41	6.50	3.45	0.29
Q8BX09_RBBP5_MOUSE	Rbbp5	Retinoblastoma-binding	R.VTTGTSNTTAIK#.S	45.87	12.16	3.77	0.27
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	K.AADSDLQITNAQTK#.E	6.11	3.23	1.89	0.53
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	K.EEYTDDNALIPK#.N	6.19	5.71	1.08	0.92
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	K.GASSIAITALM*EEK#.G	19.98	8.13	2.46	0.41
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	R.K#GEESESFLNPELLETSR@.K	10.51	3.84	2.74	0.37
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	K.LGYLVSPPQQIR@.R	25.92	8.64	3.00	0.33
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	K.YAIPTIDAEAYAIGK#.K	15.88	6.25	2.54	0.39
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	K.AADSDLQITNAQTK#.E	6.71	1.90	3.53	0.28
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	K.AIDDASASISLAQLTK#.T	18.71	6.38	2.93	0.34
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	R.K#GEESESFLNPELLETSR@.K	14.16	3.98	3.56	0.28
P97868_RBBP6_MOUSE	Rbbp6	E3 ubiquitin-protein liga	K.LGYLVSPPQQIR@.R	17.16	5.03	3.41	0.29
Q60973_RBBP7_MOUSE	Rbbp7	Histone-binding protein	K.DYALHWLVLGTHTSDEQNHLVVAR@.V	35.13	10.99	3.20	0.31
Q60973_RBBP7_MOUSE	Rbbp7	Histone-binding protein	K.EM*FEDTVEER@.V	51.67	17.43	2.96	0.34
Q60973_RBBP7_MOUSE	Rbbp7	Histone-binding protein	K.EMFEDTVEER@.V	10.67	2.39	4.46	0.22
Q60973_RBBP7_MOUSE	Rbbp7	Histone-binding protein	K.LHTFESHK#DEIFQVHWSPHNETILASSGTDR@.R	2.61	6.93	0.38	2.66
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	R.ESEVELPVPGAGADGPEPGLSK#.R	7.46	4.95	1.51	0.66
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	K.GFGFVTFENSADADR@.A	113.72	73.51	1.55	0.65
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	K.IEVNNATAR.V	11.91	6.68	1.78	0.56
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	K.ILDVEIIFNER@.G	63.28	35.91	1.76	0.57
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	R.K#IEVNNATAR@.V	69.10	43.67	1.58	0.63
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	K.R@LHVSNIPFR@.F	66.44	38.25	1.74	0.58
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	R.TEEAADGGM*QNEPLTPGYHGFPAR@.D	5.83	2.96	1.97	0.51
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	R.VYTADPYHALAPAASYGVGAVASLYR@.G	17.82	7.36	2.42	0.41
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	R.YAQPATATAATAAAAAAAAYSDGYGR@.V	47.40	30.78	1.54	0.65
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	R.YAQPATATAATAAAAAAAAYSDGYGR@.V	13.74	8.46	1.62	0.62
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	R.ESEVELPVPGAGADGPEPGLSK#.R	6.16	4.69	1.31	0.76
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	K.GFGFVTFENSADADR@.A	17.29	5.06	3.42	0.29
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	K.ILDVEIIFNER@.G	20.16	4.99	4.04	0.25
Q8BP71_RFOX2_MOUSE	Rbfox2	RNA binding protein fox-	R.YAQPATATAATAAAAAAAAYSDGYGR@.V	10.25	8.34	1.23	0.81
Q64701_RBL1_MOUSE	Rbl1	Retinoblastoma-like prot	K.LSLIQFFSK#.M	10.26	6.82	1.50	0.66
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.DGLGSDNIGSR@.M	11.36	5.09	2.23	0.45
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.GFAFVEFSHLQDATR@.W	10.42	6.42	1.62	0.62
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	K.YGGISTASVDFEQPTR@.D	6.77	2.21	3.06	0.33
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.DGLGSDNIGSR@.M	81.44	31.17	2.61	0.38
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.ESATADAGYAILEK#.K	78.42	30.56	2.57	0.39
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	K.GDPAGTGPEASLEAGADSVSLQAFSR@.A	33.66	12.39	2.72	0.37
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.GFAFVEFSHLQDATR@.W	122.07	44.58	2.74	0.37
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.GFAFVEFSHLQDATR.W	20.00	9.26	2.16	0.46
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.GLVAAYSGESDSEEEQER@.G	10.44	6.12	1.71	0.59
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.GQLQSHGVQAR.E	28.07	8.93	3.14	0.32
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.K#YGGISTASVDFEQPTR@.D	32.64	11.62	2.81	0.36
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.LDQQALPLGGR@.E	145.98	63.89	2.29	0.44
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.M*LPQAATEDDIR@.G	10.91	2.31	4.72	0.21
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.NLNPHSTM*DSILGALAPYAVLSSSNVR@.V	52.55	20.27	2.59	0.39
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.NLNPHSTMDSILGALAPYAVLSSSNVR@.V	20.18	5.51	3.66	0.27
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	K.NSFQPISALR@.D	59.85	70.93	0.84	1.19
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	K.QGIVTPIEAQTR@.V	74.15	32.37	2.29	0.44
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.TEQGEEEEEEDEEEEEK#ASNIVM*LR@.M	6.56	3.44	1.91	0.52
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	K.TINVEFAK#.G	117.04	49.99	2.34	0.43
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	K.YGGISTASVDFEQPTR@.D	64.08	21.34	3.00	0.33
Q99KG3_RBM10_MOUSE	Rbm10	RNA-binding protein 10 (	R.ESATADAGYAILEK#.K	11.29	3.04	3.72	0.27
Q8R4X3_RBM12_MOUSE	Rbm12	RNA-binding protein 12 (	R.ELVLNPEGEVSSAK#.V	14.90	4.00	3.72	0.27
Q8R4X3_RBM12_MOUSE	Rbm12	RNA-binding protein 12 (	K.VTLLLSSK#.T	6.37	1.43	4.44	0.23
Q80YR9_R12BA_MOUSE	Rbm12b1	RNA-binding protein 12E	R.LISEEQM*QEFGVK#.S	6.70	4.33	1.55	0.65
Q80YR9_R12BA_MOUSE	Rbm12b1	RNA-binding protein 12E	K.TVLQYR@PVLIDPVSR@.K	17.84	9.97	1.79	0.56
Q80YR9_R12BA_MOUSE	Rbm12b1	RNA-binding protein 12E	K.YSQEGFSGSGQK#.L	5.97	3.98	1.50	0.67
Q66JV4_R12BB_MOUSE	Rbm12b2	RNA-binding protein 12E	R.LISEEQM*QEFGIK#.S	7.90	4.82	1.64	0.61
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.AQPSVSLGAAYR@.A	20.37	52.43	0.39	2.57
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.AQPSVSLGAPYR@.G	27.37	17.78	1.54	0.65
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.LSESQLSFR@.R	35.35	29.88	1.18	0.85
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.TQPMAAQAASYR@.A	6.22	2.45	2.54	0.39
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.TQPM*AAQAASYR@.A	29.28	18.79	1.56	0.64
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.YSGSYNDYLR@.A	19.16	19.03	1.01	0.99
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.AQPSVSLGAAYR@.A	80.04	41.72	1.92	0.52
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.AQPSVSLGAPYR.G	73.27	41.01	1.79	0.56
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.ASYVAPLTAQPATYR@.A	83.56	47.05	1.78	0.56
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.INVELSTK#.G	97.78	56.44	1.73	0.58
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	K.K#GPALAIQSGDK#.T	41.06	19.26	2.13	0.47
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	K.KGPALAIQSGDK.T	65.17	44.60	1.46	0.68
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	K.K#GPALAIQSGDK#TK#.K	27.27	16.90	1.61	0.62
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	K.K#PGAGDTAFPGTGGFSATFDYQQAFGNSTGGFDGQAR@.Q	9.00	4.06	2.22	0.45
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.LAELSDYR.R	24.10	14.62	1.65	0.61
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.LSESQLSFR@.R	155.45	70.78	2.20	0.46
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	K.R@INVELSTK#.G	38.59	19.83	1.95	0.51
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.TQPM*AAQAASYR@.A	54.89	35.99	1.53	0.66
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.TQSSASLAASYAAQQHPQAAASYR@.G	119.23	63.85	1.87	0.54
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.YSGSYNDYLR.A	63.03	26.59	2.37	0.42
Q8C2Q3_RBM14_MOUSE	Rbm14	RNA-binding protein 14 (	R.LSESQLSFR@.R	9.04	3.46	2.61	0.38
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus r	R.EVDEISPEDDQR@.A	26.37	7.01	3.76	0.27
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus r	K.QDGGTAPVAASSPK#.L	10.93	4.08	2.68	0.37
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus r	R.SSGAASSAPGGGDGVEYK#.T	2.62	2.55	1.03	0.97
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus r	R.AATSAVTAYEPLDSLDR@.R	27.55	13.16	2.09	0.48
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus r	R.EVDEISPEDDQR@.A	13.01	7.13	1.82	0.55
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus r	R.FGVITEVDIK#.R	15.56	6.44	2.42	0.41
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus r	K.ISHLSGSGSGDER@.V	3.21	1.40	2.30	0.43
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus r	K.QAAGVISLPVGGNK#.D	16.69	8.11	2.06	0.49

Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus	R.SSGAASSAPGGGDGVEYK#.T	13.38	7.73	1.73	0.58
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus	R.VAFVNFR.R	24.67	14.34	1.72	0.58
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus	R.VGAGAGAAPFR@.E	19.57	10.85	1.80	0.55
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus	R.VGAGAGAAPFR@EVDEISPEDDQR@.A	10.91	5.03	2.17	0.46
Q0VBL3_Q0VBL3_MOUSE	Rbm15	Protein Rbm15 OS=Mus	R.YQQQYLQPLPLTHYELVTDTFGHR@.A	30.61	9.85	3.11	0.32
Q6PHZ5_RB15B_MOUSE	Rbm15b	Putative RNA-binding pr	R.NLVSYLK#.Q	20.32	5.92	3.43	0.29
Q6PHZ5_RB15B_MOUSE	Rbm15b	Putative RNA-binding pr	R.ALDYYGLYDDR@.G	12.34	4.22	2.92	0.34
Q6PHZ5_RB15B_MOUSE	Rbm15b	Putative RNA-binding pr	R.ASPLPPPPPPPGAEPAGPGSTAAPEYK#.T	2.56	2.51	1.02	0.98
Q6PHZ5_RB15B_MOUSE	Rbm15b	Putative RNA-binding pr	R.FGEISLR@.L	15.48	6.68	2.32	0.43
Q6PHZ5_RB15B_MOUSE	Rbm15b	Putative RNA-binding pr	R.LWVGGLGPNTSLAALAR@.E	16.13	5.85	2.76	0.36
Q6PHZ5_RB15B_MOUSE	Rbm15b	Putative RNA-binding pr	R.NLVSYLK#.Q	18.73	6.01	3.12	0.32
Q6PHZ5_RB15B_MOUSE	Rbm15b	Putative RNA-binding pr	K.QAAGVISLPVGGSK#.G	6.77	1.63	4.15	0.24
Q6PHZ5_RB15B_MOUSE	Rbm15b	Putative RNA-binding pr	R.TFLEGDWTSLSK#.S	9.44	3.87	2.44	0.41
Q6PHZ5_RB15B_MOUSE	Rbm15b	Putative RNA-binding pr	K.TLLISSLSPALPAEHLEDR@.L	27.62	15.11	1.83	0.55
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	R.DFPYEEDSR@PR@.S	12.58	5.44	2.31	0.43
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	R.EGQGLGK#HEQGLSTALSVEK#.T	32.42	11.44	2.83	0.35
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	K.LLQSQLQVK#.K	124.88	49.16	2.54	0.39
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	R.NM*VGAGEVDEDLEVETK#.E	4.91	2.99	1.64	0.61
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	K.QSTVLAPVIDLK#.R	78.14	31.99	2.44	0.41
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	K.SDSNPLTEILK#.C	16.25	6.17	2.63	0.38
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	R.SM*GGAAIAPPTSLVEK#.D	38.44	11.36	3.38	0.30
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	R.SM*GGAAIAPPTSLVEK#DK#.E	8.72	5.51	1.58	0.63
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	R.SPTGPSNSFLANM*GGTVAHK#.I	17.51	6.93	2.53	0.40
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	R.TK#QSTVLAPVIDLK#.R	16.87	4.22	4.00	0.25
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	R.VLDLAEQV.-	56.72	56.72	1.00	1.00
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	K.QSTVLAPVIDLK#.R	6.04	3.64	1.66	0.60
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	K.LLQSQLQVK#.K	16.37	4.05	4.04	0.25
Q8JZX4_SPF45_MOUSE	Rbm17	Splicing factor 45 OS=Mu	K.QSTVLAPVIDLK#.R	12.78	5.28	2.42	0.41
Q8R3C6_RBM19_MOUSE	Rbm19	Probable RNA-binding pr	K.ANSSSSHNWNTLFM*GPNAVADAIAQK#.Y	2.71	3.26	0.83	1.20
Q8R3C6_RBM19_MOUSE	Rbm19	Probable RNA-binding pr	R.ELFSTFGELK#.T	16.42	7.46	2.20	0.45
Q8R3C6_RBM19_MOUSE	Rbm19	Probable RNA-binding pr	K.FQEFLSIHQK#.R	14.25	7.50	1.90	0.53
Q8R3C6_RBM19_MOUSE	Rbm19	Probable RNA-binding pr	R.GFGFVDFITK#.Q	25.40	9.59	2.65	0.38
Q8R3C6_RBM19_MOUSE	Rbm19	Probable RNA-binding pr	R.TLGENEEEEDLADSGR@.L	13.28	6.68	1.99	0.50
Q8R3C6_RBM19_MOUSE	Rbm19	Probable RNA-binding pr	R.VALGETQLVQEVR@.S	21.99	7.50	2.93	0.34
Q8BHS3_RBM22_MOUSE	Rbm22	Pre-mRNA-splicing factor	K.ATSTSDM*LLK#.L	43.59	34.74	1.25	0.80
Q8BHS3_RBM22_MOUSE	Rbm22	Pre-mRNA-splicing factor	R.DAGLSFK#DDM*PK#.S	12.51	10.00	1.25	0.80
Q8BHS3_RBM22_MOUSE	Rbm22	Pre-mRNA-splicing factor	R.NHFYQFGEIR@.T	58.00	39.42	1.47	0.68
Q8BHS3_RBM22_MOUSE	Rbm22	Pre-mRNA-splicing factor	K.SDVNKEYYTQNM*ER.E	9.87	6.41	1.54	0.65
Q8BHS3_RBM22_MOUSE	Rbm22	Pre-mRNA-splicing factor	K.TITTLYVGGLGDTITETDLR.N	36.19	27.41	1.32	0.76
Q8BHS3_RBM22_MOUSE	Rbm22	Pre-mRNA-splicing factor	K.TITTLYVGGLGDTITETDLR@.N	30.63	18.27	1.68	0.60
Q8BHS3_RBM22_MOUSE	Rbm22	Pre-mRNA-splicing factor	R.TITVVQR@.Q	104.33	71.77	1.45	0.69
Q8BHS3_RBM22_MOUSE	Rbm22	Pre-mRNA-splicing factor	R.YYGINDPVADK#.L	96.98	70.37	1.38	0.73
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.K#LPVDSVFNK#FEDEDSDDVPR@.K	6.02	2.87	2.10	0.48
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.LLIYETEAK#.K	19.37	11.25	1.72	0.58
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.LPVDSVFNKFEDEDSDDVPR.K	31.37	17.83	1.76	0.57
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.ASDM*LIR@.Q	38.76	13.89	2.79	0.36
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.DR@EEDEEDAYER@.R	21.94	6.29	3.49	0.29
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.EDINAIEM*EEDKR.D	16.56	7.08	2.34	0.43
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.EK#EELEEIR@.Q	56.16	20.51	2.74	0.37
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.FPVAPLIPYPLITK#.E	29.89	11.20	2.67	0.37
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.GAIEVLIR@.E	174.26	58.98	2.95	0.34
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.K#LVPLDYGEDDK#NATK#.G	49.31	14.88	3.31	0.30
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.LGASNSPGQPNSVK#.R	65.81	13.56	4.85	0.21
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.LLHDLQIGEK#.K	154.28	46.55	3.31	0.30
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.LPVDSVFNKFEDEDSDDVPR.K	35.81	7.33	4.88	0.20
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.R@FPVAPLIPYPLITK#.E	292.22	96.75	3.02	0.33
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.ASDM*LIR@.Q	22.97	5.51	4.17	0.24
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.DR@EEDEEDAYER@.R	12.51	3.00	4.17	0.24
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.FPVAPLIPYPLITK#.E	16.12	5.06	3.19	0.31
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.GAIEVLIR@.E	87.89	20.84	4.22	0.24
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.K#LVPLDYGEDDK#NATK#.G	13.57	3.37	4.03	0.25
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	K.LGASNSPGQPNSVK#.R	5.95	1.27	4.70	0.21
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.LK#EFLEDYDDDR@DDPK#.Y	23.59	4.58	5.15	0.19
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.LLAEGHPDPDAELQR@.M	96.44	25.20	3.83	0.26
B2RY56_RBM25_MOUSE	Rbm25	RNA-binding protein 25 (	R.LLHDLQIGEK#.K	72.01	17.20	4.19	0.24
Q6NZN0_RBM26_MOUSE	Rbm26	RNA-binding protein 26 (	R.TIGSGEPGVSTK#.K	6.74	3.28	2.06	0.49
Q6NZN0_RBM26_MOUSE	Rbm26	RNA-binding protein 26 (	K.VIQPLVQQPILPVVK#.Q	8.87	2.48	3.58	0.28
Q5SFM8_RBM27_MOUSE	Rbm27	RNA-binding protein 27 (	R.AISGLEGPLTK#.K	13.58	3.00	4.52	0.22
Q5SFM8_RBM27_MOUSE	Rbm27	RNA-binding protein 27 (	R.AQTQR@PNLIGLTSGDM*DANPR@.A	8.94	2.67	3.35	0.30
Q5SFM8_RBM27_MOUSE	Rbm27	RNA-binding protein 27 (	R.LQLGTPPPLLAAR@.L	17.61	6.57	2.68	0.37
Q5SFM8_RBM27_MOUSE	Rbm27	RNA-binding protein 27 (	R.LSSGEDTTELR@.K	7.74	4.73	1.64	0.61
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	K.AAEGVSAADM*AK#.R	32.89	17.97	1.83	0.55
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	K.AEVEQVELPDGK#.K	29.06	14.67	1.98	0.50
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	K.AVDDKQLR.K	1.18	2.88	0.41	2.44
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	K.AVFTHYGTVLEVNIPK#.K	14.81	6.61	2.24	0.45
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	R.FNQLVEQYK#.Q	24.78	15.95	1.55	0.64
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	R.GFAFVQFK#.N	18.82	11.46	1.64	0.61
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	R.GFGYVTFSM*LEDVQR@.A	11.02	12.47	0.88	1.13
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	K.GQSLGYAFAEFQK#.H	6.20	6.40	0.97	1.03
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	K.QQLASSVQAPK#.R	17.82	10.62	1.68	0.60
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	K.R@PIVEFSLEDR@.R	20.36	15.89	1.28	0.78
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	R.SDQLEELFSQVGPVK#.Q	19.19	8.32	2.31	0.43
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	K.VDLAVTR@.D	25.97	15.01	1.73	0.58
Q8CGC6_RBM28_MOUSE	Rbm28	RNA-binding protein 28 (	K.VVQSATQDQSK#.A	10.50	8.05	1.30	0.77
Q9CXK9_RBM33_MOUSE	Rbm33	RNA-binding protein 33 (	K.AALLEFEER@.E	17.60	8.53	2.06	0.48
Q8C5L7_RBM34_MOUSE	Rbm34	RNA-binding protein 34 (	R.GFGYVLFENTDAVHLALK#.L	12.29	6.72	1.83	0.55
Q8C5L7_RBM34_MOUSE	Rbm34	RNA-binding protein 34 (	R.K#LDDDDDDEEESVSQTK#.K	2.29	2.53	0.91	1.10
Q8C5L7_RBM34_MOUSE	Rbm34	RNA-binding protein 34 (	R.NPLTGVGR@.G	18.89	21.39	0.88	1.13
Q8C5L7_RBM34_MOUSE	Rbm34	RNA-binding protein 34 (	K.VADGEALDVALSLAK#.D	18.16	15.10	1.20	0.83
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.AAAM*ANNLQK#.G	40.64	16.75	2.43	0.41
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.DLEEFFSTVGK#.V	250.08	103.71	2.41	0.41
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.GIFEPFGR@.I	126.51	47.55	2.66	0.38
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.IESIQLM*M*DSETGR@.S	29.31	13.43	2.18	0.46
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.IESIQLM*MDSETGR.S	5.80	3.15	1.84	0.54
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	K.IGLPHSIK#.L	12.32	5.77	2.13	0.47
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	K.NSAQGNVYVK#.C	12.53	7.94	1.58	0.63
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.TDASSASSFLDSDELER@.T	139.56	62.45	2.23	0.45
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.TGIDLGTTGR@.L	118.63	44.57	2.66	0.38
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.VLGVPIIVQASQAEK#.N	200.33	79.15	2.53	0.40
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.DLEEFFSTVGK#.V	7.00	7.76	0.90	1.11
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.GIFEPFGR@.I	11.26	5.17	2.18	0.46
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	K.HGGVIHIYVDK#.N	14.05	6.07	2.32	0.43
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.IESIQLM*M*DSETGR@.S	2.20	2.26	0.97	1.03

Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	K.NSAQGNVYVK#.C	38.21	11.36	3.36	0.30
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.TDASSASSFLDSDELER@.T	23.34	15.80	1.48	0.68
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.TGIDLGTTGR@.L	22.39	8.23	2.72	0.37
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.VLGVPIIVQASQAEK#.N	14.45	11.15	1.30	0.77
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.AAAM*ANNLQK#.G	46.25	18.98	2.44	0.41
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.DLEEFFSTVGK#.V	190.75	76.80	2.48	0.40
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.GIFEPFGR@.I	96.60	39.09	2.47	0.40
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	K.HGGVIHIYVDK#.N	21.81	12.99	1.68	0.60
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.IESIQLM*M*DSETGR@.S	26.24	9.60	2.73	0.37
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.IESIQLM*MDSETGR@.S	7.12	3.00	2.37	0.42
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	K.NSAQGNVYVK#.C	29.88	15.10	1.98	0.51
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.SK#GIAYVEFVDVSSVPLAIGLTGQR@.V	14.31	5.99	2.39	0.42
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.TDASSASSFLDSDELER@.T	100.89	47.59	2.12	0.47
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.TGIDLGTTGR@.L	144.11	54.75	2.63	0.38
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.VLGVPIIVQASQAEK#.N	208.64	88.62	2.35	0.42
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.DLEEFFSTVGK#.V	17.30	7.89	2.19	0.46
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.TDASSASSFLDSDELER@.T	10.84	5.48	1.98	0.51
Q8VH51_RBM39_MOUSE	Rbm39	RNA-binding protein 39 (	R.VLGVPIIVQASQAEK#.N	15.36	8.45	1.82	0.55
Q8C7Q4_RBM4_MOUSE	Rbm4	RNA-binding protein 4 O	R.ATGPVLTVGEGYGYGHDSELSQASAAAR@.N	19.33	11.45	1.69	0.59
Q8C7Q4_RBM4_MOUSE	Rbm4	RNA-binding protein 4 O	R.VADLTEQYNEQYGAVR@.T	25.64	13.18	1.95	0.51
Q91V81_RBM42_MOUSE	Rbm42	RNA-binding protein 42 (	R.ELGLGLGLGLK#.D	9.55	4.36	2.19	0.46
Q91V81_RBM42_MOUSE	Rbm42	RNA-binding protein 42 (	R.ELGLGLGLGLK#.D	10.02	4.37	2.29	0.44
Q8VE92_RBM4B_MOUSE	Rbm4b	RNA-binding protein 4B (	R.AEDAVEAIR@.G	62.68	29.86	2.10	0.48
Q8VE92_RBM4B_MOUSE	Rbm4b	RNA-binding protein 4B (	R.GLDNTEFQGK#.R	24.63	16.36	1.51	0.66
Q8VE92_RBM4B_MOUSE	Rbm4b	RNA-binding protein 4B (	K.LFIGNLPR.E	43.06	26.81	1.61	0.62
Q8VE92_RBM4B_MOUSE	Rbm4b	RNA-binding protein 4B (	K.NYGFVHIEDK#.T	10.67	5.95	1.79	0.56
Q8VE92_RBM4B_MOUSE	Rbm4b	RNA-binding protein 4B (	R.VADFTEQYNEQYGAVR@.T	18.25	6.04	3.02	0.33
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	K.DLVLPDGNR@.V	27.03	12.78	2.11	0.47
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	R.EM*M*ESFEGPQPADVR.L	17.70	9.74	1.82	0.55
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	R.ESAAADAGFALFEK#.K	40.32	19.59	2.06	0.49
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	R.GLPITITESDIR.E	48.65	20.44	2.38	0.42
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	R.GLVAAYSGDSDNEEELVER@.L	4.60	1.97	2.33	0.43
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	R.HQQLSDLHK#.Q	627.21	42.71	14.69	0.07
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	K.M*LQAM*GWR@.E	15.59	5.92	2.63	0.38
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	R.NIAPHTVVDSIM*TALSPYASLAVNNIR@.L	21.10	6.60	3.20	0.31
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	K.QFDAGTVNYEQPTK#.D	22.91	9.27	2.47	0.40
Q91YE7_RBM5_MOUSE	Rbm5	RNA-binding protein 5 O	R.QQLLPELVR.N	52.73	20.03	2.63	0.38
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	R.DAQQDLQDQDYR@.T	17.42	10.06	1.73	0.58
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	R.ETDSDR@NPVDK#EDTDTSSK#.G	10.58	4.73	2.24	0.45
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	K.FQESTSEGK#PPLEDVFK#.K	19.66	8.66	2.27	0.44
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	R.GSATTDLDFR@.N	13.30	5.27	2.53	0.40
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	K.ILQNLDPPFSIDGK#.M	15.56	9.93	1.57	0.64
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	K.LSGGEQQSSDAGLFK#EEGDLDFLGQQDTDYR@.S	8.26	3.51	2.35	0.43
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	K.M*VAVNLATGK#.R	8.23	4.69	1.76	0.57
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	K.QSEQELAYLER@.R	9.38	6.12	1.53	0.65
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	K.VVNPLIGLLGEYGGDSDYEEEEEEEQAPPVQPR@.T	10.68	3.07	3.48	0.29
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	R.DAQQDLQDQDYR@.T	7.28	5.29	1.38	0.73
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	R.ETDSDR@NPVDK#EDTDTSSK#.G	6.08	4.10	1.48	0.67
Q3ULB0_Q3ULB0_MOUSE	Rbm6	Protein Rbm6 OS=Mus m	K.LSGGEQQSSDAGLFK#EEGDLDFLGQQDTDYR@.S	5.44	3.42	1.59	0.63
Q9CQT2_RBM7_MOUSE	Rbm7	RNA-binding protein 7 O	R.EDFYYDDR@.N	7.48	3.44	2.18	0.46
Q9CQT2_RBM7_MOUSE	Rbm7	RNA-binding protein 7 O	R.QAVM*NSVFR@.Q	12.65	5.30	2.39	0.42
Q9CQT2_RBM7_MOUSE	Rbm7	RNA-binding protein 7 O	R.SFSSPEDYQR@.Q	60.90	26.09	2.33	0.43
Q9CQT2_RBM7_MOUSE	Rbm7	RNA-binding protein 7 O	R.TLFVGNLETK#.V	65.94	26.20	2.52	0.40
Q9CQT2_RBM7_MOUSE	Rbm7	RNA-binding protein 7 O	R.TVGNVSPTAQM*VQR@.S	50.64	19.04	2.66	0.38
Q9CQT2_RBM7_MOUSE	Rbm7	RNA-binding protein 7 O	R.TVGNVSPTAQMVQR@.S	2.96	1.84	1.61	0.62
Q9CQT2_RBM7_MOUSE	Rbm7	RNA-binding protein 7 O	K.VTEELLFELFHQAGPVIK#.V	123.15	45.98	2.68	0.37
Q9CQT2_RBM7_MOUSE	Rbm7	RNA-binding protein 7 O	R.TVGNVSPTAQM*VQR@.S	3.32	2.59	1.29	0.78
Q9CWZ3_RBM8A_MOUSE	Rbm8a	RNA-binding protein 8A (	K.GYTLVEYETYK.E	9.09	5.86	1.55	0.64
Q9CWZ3_RBM8A_MOUSE	Rbm8a	RNA-binding protein 8A (	R.M*R@EDYDSVEQDGDEPGPQR@.S	17.23	17.33	0.99	1.01
Q9CWZ3_RBM8A_MOUSE	Rbm8a	RNA-binding protein 8A (	R.MR@EDYDSVEQDGDEPGPQR@.S	9.27	1.84	5.04	0.20
Q9CWZ3_RBM8A_MOUSE	Rbm8a	RNA-binding protein 8A (	K.FAEYGEIK#.N	68.08	36.99	1.84	0.54
Q9CWZ3_RBM8A_MOUSE	Rbm8a	RNA-binding protein 8A (	K.GYTLVEYETYK#.E	168.14	80.73	2.08	0.48
Q9CWZ3_RBM8A_MOUSE	Rbm8a	RNA-binding protein 8A (	R.MREDYDSVEQDGDEPGPQR.S	9.69	4.05	2.39	0.42
Q9CWZ3_RBM8A_MOUSE	Rbm8a	RNA-binding protein 8A (	R.M*R@EDYDSVEQDGDEPGPQR@.S	186.95	100.26	1.86	0.54
Q91W59_RBMS1_MOUSE	Rbms1	RNA-binding motif, singl	K.GYGFVDFDSPAAAQK.A	33.65	46.40	0.73	1.38
Q8VC70_RBMS2_MOUSE	Rbms2	RNA-binding motif, singl	K.ASGVQAQM*AK#.Q	14.71	16.44	0.89	1.12
Q8VC70_RBMS2_MOUSE	Rbms2	RNA-binding motif, singl	K.ASGVQAQMAK#.Q	11.76	8.17	1.44	0.69
Q8VC70_RBMS2_MOUSE	Rbms2	RNA-binding motif, singl	R.GLQPGTTDQDLVK#.L	82.31	107.67	0.76	1.31
Q8VC70_RBMS2_MOUSE	Rbms2	RNA-binding motif, singl	K.GYGFVDFDSPSSAQK.A	57.76	68.22	0.85	1.18
Q8VC70_RBMS2_MOUSE	Rbms2	RNA-binding motif, singl	K.LYVAQQM*APPSPR@.N	9.94	13.63	0.73	1.37
Q8R0F5_RBMX2_MOUSE	Rbmx2	RNA-binding motif prote	R.APQESEDVDDVTR@.E	52.99	35.70	1.48	0.67
Q8R0F5_RBMX2_MOUSE	Rbmx2	RNA-binding motif prote	R.EVQLGVAEK#.V	24.18	14.85	1.63	0.61
Q8R0F5_RBMX2_MOUSE	Rbmx2	RNA-binding motif prote	K.LINELNER@.E	38.78	22.38	1.73	0.58
Q8R0F5_RBMX2_MOUSE	Rbmx2	RNA-binding motif prote	R.STVLAVDNFNGIK#.I	11.95	5.99	1.99	0.50
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	K.AIK#VEQATK#PSFESGR@.R	201.78	142.35	1.42	0.71
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	K.ALEAVFGK#.Y	206.36	167.12	1.23	0.81
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.DR@DYSDHPSGGSYR@.D	136.34	119.45	1.14	0.88
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.DRDYSDHPSGGSYR.D	8.37	6.99	1.20	0.83
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.DSYESYGNSR.S	59.00	51.21	1.15	0.87
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.DVYLSPR@.D	135.33	110.87	1.22	0.82
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.GFAFVTFESPADAK#.D	188.78	163.06	1.16	0.86
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.GGYM*DDGGYSM*NFNM*SSSR.G	25.27	19.21	1.32	0.76
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.GYGDRDGYGR.D	6.91	4.26	1.62	0.62
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.IVEILLM*K#.D	100.45	67.43	1.49	0.67
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.IVEILLMK#.D	31.22	22.94	1.36	0.73
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	K.LFIGGLNTETNEK#.A	314.67	249.13	1.26	0.79
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.REPLPSR.R	101.49	100.56	1.01	0.99
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.RGPPPPPR.S	64.64	88.18	0.73	1.36
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	K.R@STPSGPVR@.S	11.82	7.67	1.54	0.65
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.SDLYSSGR@.D	177.86	154.17	1.15	0.87
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	K.VEQATK#PSFESGR@.R	34.84	27.13	1.28	0.78
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	K.VEQATKPSFESGR.R	232.56	195.52	1.19	0.84
Q91VM5_RMXL1_MOUSE	Rbmxl1	RNA binding motif protei	R.YDDYSSSR@.D	40.68	32.28	1.26	0.79
Q80Y56_RBNS5_MOUSE	Rbsn	Rabenosyn-5 OS=Mus mu	R.EVIPFQLEASR@.G	10.48	3.75	2.79	0.36
Q80Y56_RBNS5_MOUSE	Rbsn	Rabenosyn-5 OS=Mus mu	K.ILTLGLNQDPSPHPNTLR@.L	9.37	3.81	2.46	0.41
Q80Y56_RBNS5_MOUSE	Rbsn	Rabenosyn-5 OS=Mus mu	R.YSATLFVQEK#.L	6.51	1.69	3.84	0.26
Q4VGL6_RC3H1_MOUSE	Rc3h1	Roquin-1 OS=Mus muscu	K.LVLLALEDGSALSR@.K	10.79	4.30	2.51	0.40
Q4VGL6_RC3H1_MOUSE	Rc3h1	Roquin-1 OS=Mus muscu	R.R@PLSASLGQLNEVGLPSAPILSDESAVDLSNR@.K	3.50	1.60	2.18	0.46
Q9JJT0_RCL1_MOUSE	Rcl1	RNA 3'-terminal phospha	R.GVTNDQVDPSVDVLK#.A	5.76	3.22	1.79	0.56
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	K.ASDLDGDLTATR@.E	120.17	59.52	2.02	0.50
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	R.HLVYESDK#.N	11.55	6.46	1.79	0.56
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	R.HWILPQDYDHAQAEAR@.H	42.30	20.79	2.03	0.49
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	R.IDSDGDGLVTTEELK#.L	28.39	13.54	2.10	0.48

Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	K.ISWEEYK#.Q	52.27	25.64	2.04	0.49
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	K.IVDR@IDSDGDGLVTTEELK#.L	81.42	35.35	2.30	0.43
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	K.QATYGYYLGNPAEFHDSSDHHTFK#.K	6.71	5.53	1.21	0.82
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	K.TFDQLSPDESK#.E	14.77	9.18	1.61	0.62
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	R.VVRPDSELGERPPEDNQSFQYDHEAFLGKEDSK.T	3.95	3.08	1.28	0.78
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	K.ASDLDGDLTATR@.E	7.24	4.62	1.57	0.64
Q05186_RCN1_MOUSE	Rcn1	Reticulocalbin-1 OS=Mus	R.IDSDGDGLVTTEELK#.L	4.19	1.57	2.68	0.37
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.ADYDREALLGVQEDVDEYVK.L	91.16	53.35	1.71	0.59
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.DPTANEDPEWILVEK#.D	18.57	12.86	1.44	0.69
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.DPTANEDPEWILVEK#DR@.F	13.40	9.56	1.40	0.71
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.EALLGVQEDVDEYVK#.L	114.51	70.64	1.62	0.62
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.FVNDYDKDNDGR.L	4.55	2.77	1.64	0.61
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	K.HYAM*QEAK#.Q	11.38	9.04	1.26	0.79
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	K.HYAMQEAK#.Q	12.12	6.86	1.77	0.57
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	K.K#IDSDSDGFLTENELSQWIQM*SFK#.H	36.74	22.06	1.67	0.60
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	K.K#LSEEEILENQDLFLTSEATDYGR@.Q	51.75	26.99	1.92	0.52
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	K.LSEEEILENQDLFLTSEATDYGR@.Q	81.48	46.83	1.74	0.57
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	K.QQFVEYDK#NSDGAVTWDEYNIQM*YDR@.V	8.12	3.23	2.51	0.40
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	K.QQFVEYDK#NSDGAVTWDEYNIQMYDR@.V	4.11	2.05	2.00	0.50
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.R@DPTANEDPEWILVEK#.D	63.31	38.21	1.66	0.60
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.R@DPTANEDPEWILVEK#DR@.F	51.05	37.64	1.36	0.74
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.VIDFDENTALDDTEEGSFR@.Q	139.00	80.95	1.72	0.58
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.EALLGVQEDVDEYVK#.L	6.77	3.01	2.25	0.44
Q8BP92_RCN2_MOUSE	Rcn2	Reticulocalbin-2 OS=Mus	R.VIDFDENTALDDTEEGSFR@.Q	2.69	1.73	1.55	0.65
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	K.AEILSNWNM*FVGSQATNYGEDLTR@.H	47.92	22.98	2.09	0.48
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	K.DGYVQVEEYIADLYSEEPGEEEPAWVQTER@.Q	9.00	3.80	2.37	0.42
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	R.DIVVAETLEDLDK#.N	27.39	13.97	1.96	0.51
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	R.DSVSAAWHTYDTDR@DGR@.V	123.81	56.23	2.20	0.45
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	R.DVAK#EFDK#LSPEESQAR@.L	58.75	30.41	1.93	0.52
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	R.IVDR@M*DLAGDSDGWVSLAELR@.A	34.42	20.02	1.72	0.58
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	R.M*DLAGDSDGWVSLAELR@.A	33.87	24.49	1.38	0.72
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	R.MDLAGDSDGWVSLAELR@.A	18.66	9.67	1.93	0.52
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	R.VADQDGDSM*ATR@.E	38.56	23.33	1.65	0.60
Q8BH97_RCN3_MOUSE	Rcn3	Reticulocalbin-3 OS=Mus	R.VGWEELR@.N	197.02	105.40	1.87	0.53
Q8CFE3_RCOR1_MOUSE	Rcor1	REST corepressor 1 OS=M	R.IQQM*LPDK#.V	19.27	10.01	1.92	0.52
Q8CFE3_RCOR1_MOUSE	Rcor1	REST corepressor 1 OS=M	K.SLADLPNFTPFPDEWTVEDK#.V	5.91	3.13	1.89	0.53
Q8CFE3_RCOR1_MOUSE	Rcor1	REST corepressor 1 OS=M	R.VGPQYQAAVPDFDPAK#.L	19.89	13.02	1.53	0.65
Q8CFE3_RCOR1_MOUSE	Rcor1	REST corepressor 1 OS=M	R.WTTEEQLLAVQAIR@.K	6.40	4.57	1.40	0.71
Q8CFE3_RCOR1_MOUSE	Rcor1	REST corepressor 1 OS=M	K.SLADLPNFTPFPDEWTVEDK#.V	4.22	2.95	1.43	0.70
Q8CFE3_RCOR1_MOUSE	Rcor1	REST corepressor 1 OS=M	R.VGPQYQAAVPDFDPAK#.L	8.11	3.38	2.40	0.42
Q9QYF1_RDH11_MOUSE	Rdh11	Retinol dehydrogenase 1	K.VAIVTGANTGIGK#.E	5.37	2.31	2.33	0.43
Q9QYF1_RDH11_MOUSE	Rdh11	Retinol dehydrogenase 1	K.VAIVTGANTGIGK#.E	5.67	1.40	4.03	0.25
Q9Z129_RECQ1_MOUSE	Recql	ATP-dependent DNA heli	K.SM*ENYYQESGR@.A	2.71	1.74	1.56	0.64
Q99KK1_REEP3_MOUSE	Reep3	Receptor expression-enh	R.EIDDYIVQAK#.E	7.62	1.44	5.29	0.19
G3X8R0_G3X8R0_MOUSE	Reep5	Receptor accessory prote	R.HESQVDSVVK#.D	15.28	10.67	1.43	0.70
G3X8R0_G3X8R0_MOUSE	Reep5	Receptor accessory prote	R.HESQVDSVVK#.D	85.08	37.68	2.26	0.44
G3X8R0_G3X8R0_MOUSE	Reep5	Receptor accessory prote	R.IIRPIFLK.H	19.48	10.53	1.85	0.54
G3X8R0_G3X8R0_MOUSE	Reep5	Receptor accessory prote	K.KATVNLLGDEK.K	15.78	8.29	1.90	0.53
G3X8R0_G3X8R0_MOUSE	Reep5	Receptor accessory prote	K.K#ATVNLLGDEK#K#.S	66.29	26.21	2.53	0.40
G3X8R0_G3X8R0_MOUSE	Reep5	Receptor accessory prote	K.KATVNLLGDEKK.S	7.81	2.32	3.37	0.30
G3X8R0_G3X8R0_MOUSE	Reep5	Receptor accessory prote	R.HESQVDSVVK.D	2.68	6.00	0.45	2.24
Q9JM62_REEP6_MOUSE	Reep6	Receptor expression-enh	R.ALDLAAGITR.D	22.57	8.42	2.68	0.37
Q04207_TF65_MOUSE	Rela	Transcription factor p65	R.TPPYADPSLQAPVR@.V	6.66	3.19	2.09	0.48
Q04863_RELB_MOUSE	Relb	Transcription factor RelB	R.SAGSILGESSTEASK#.T	23.98	5.83	4.11	0.24
Q04863_RELB_MOUSE	Relb	Transcription factor RelB	K.TPPYEDLEISEPVTVNVFLQR@.L	7.37	3.19	2.31	0.43
O54916_REPS1_MOUSE	Reps1	RalBP1-associated Eps dc	R.TVASAATANEIR@.R	6.95	2.47	2.81	0.36
Q9CQU3_RER1_MOUSE	Rer1	Protein RER1 OS=Mus mu	R.LGQIYQSWLDK#.S	39.11	20.49	1.91	0.52
Q9CQU3_RER1_MOUSE	Rer1	Protein RER1 OS=Mus mu	K.VDPSLM*EDSDDGPSLPTK#.Q	20.12	12.52	1.61	0.62
Q6PAQ4_REXO4_MOUSE	Rexo4	RNA exonuclease 4 OS=M	K.ATAPVPQPGPIR@.K	9.88	5.94	1.66	0.60
Q6PAQ4_REXO4_MOUSE	Rexo4	RNA exonuclease 4 OS=M	K.VLFLDHPK#.K	9.72	4.22	2.30	0.43
Q6PAQ4_REXO4_MOUSE	Rexo4	RNA exonuclease 4 OS=M	R.VSIVNQYGK#.C	16.02	11.27	1.42	0.70
Q6PAQ4_REXO4_MOUSE	Rexo4	RNA exonuclease 4 OS=M	K.YVK#PTEPVTDYR@.T	15.23	8.82	1.73	0.58
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.DALVR@PLTSQGVEGAQHVIK#.L	10.69	5.53	1.93	0.52
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.EAHLTPYSLQVVK#.T	12.45	9.23	1.35	0.74
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.GGIQELIGLIK#.H	30.34	13.93	2.18	0.46
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.GYM*TQFPSFPSWLGK#.H	8.67	5.20	1.67	0.60
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.ILDEDGLLDLIR@.T	8.92	8.02	1.11	0.90
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.AVVAESLNNTSIK#.G	5.04	2.92	1.73	0.58
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.GGIQELIGLIK#.H	13.37	5.62	2.38	0.42
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.AALLSGPPGVGK#.T	72.64	31.26	2.32	0.43
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.AK#EESSYNETELLAAR@.R	62.28	21.16	2.94	0.34
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.ALTYDQAK#.A	41.21	14.15	2.91	0.34
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.AVVAESLNNTSIK#.G	92.40	32.68	2.83	0.35
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.DALVR@PLTSQGVEGAQHVIK#.L	54.79	19.05	2.88	0.35
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.DSEEGEESFSSVQDDLSK#.A	6.77	1.85	3.66	0.27
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.EAHLTPYSLQVVK#.T	55.57	18.57	2.99	0.33
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.EGLK#IPPPAM*NEIILGANQDVR@.Q	3.32	2.37	1.40	0.71
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.GFYTSGAAPSVSAR@.H	79.46	30.05	2.64	0.38
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.GGIQELIGLIK#.H	157.03	59.78	2.63	0.38
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.GYM*TQFPSFPSWLGK#.H	19.85	8.82	2.25	0.44
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.HALIM*DEVDGM*AGNEDR@.G	11.47	4.28	2.68	0.37
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.ILDEDGLLDLIR.T	139.20	48.73	2.86	0.35
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.IPPPAM*NEIILGANQDVR@.Q	16.51	8.49	1.94	0.51
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.LTPTSVLDYFGTESVQR@.S	35.28	11.36	3.11	0.32
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.QLQLDEDAELER@.Q	41.19	10.15	4.06	0.25
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.SAM*LSIAFK#.E	24.97	21.27	1.17	0.85
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.SAMLSIAFK#.E	7.35	3.82	1.92	0.52
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.TLALLDEEPK#.I	60.93	20.83	2.93	0.34
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.AALLSGPPGVGK#.T	42.39	12.63	3.36	0.30
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.AK#EESSYNETELLAAR@.R	28.59	6.10	4.69	0.21
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.AVVAESLNNTSIK#.G	46.98	10.35	4.54	0.22
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.DALVR@PLTSQGVEGAQHVIK#.L	17.57	4.37	4.02	0.25
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.EAHLTPYSLQVVK#.T	27.47	6.06	4.53	0.22
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.GFYTSGAAPSVSAR@.H	40.06	10.12	3.96	0.25
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.GGIQELIGLIK#.H	83.28	20.88	3.99	0.25
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.GYM*TQFPSFPSWLGK#.H	15.06	3.80	3.96	0.25
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.ILDEDGLLDLIR@.T	92.56	24.83	3.73	0.27
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.LTPTSVLDYFGTESVQR@.S	23.11	9.05	2.55	0.39
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.QLQLDEDAELER@.Q	19.14	6.45	2.97	0.34
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	K.SAM*LSIAFK#.E	10.74	13.38	0.80	1.24
P35601_RFC1_MOUSE	Rfc1	Replication factor C subu	R.TLALLDEEPK#.I	24.62	7.45	3.30	0.30
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	R.ALLGPALK#.D	82.90	32.66	2.54	0.39
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	R.ALLGPALK#DAVLELNASNDR@.G	11.86	3.22	3.69	0.27

Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.DAVLELNASNDR.G	65.87	23.54	2.80	0.36
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	R.EGNVPNIIIAGPPGTGK#.T	91.11	38.88	2.34	0.43
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.EK#VPYTDDGLEAIIFTAQGDM*R@.Q	40.66	10.56	3.85	0.26
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.EK#VPYTDDGLEAIIFTAQGDMR@.Q	10.35	3.67	2.82	0.35
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.IIILDEADSM*TDGAQQALR@.R	24.21	7.31	3.31	0.30
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.IIILDEADSM*TDGAQQALR@.R	33.13	10.79	3.07	0.33
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	R.LM*NVIEK#.E	33.55	10.61	3.16	0.32
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.LNEIVGNEDTVSR@.L	145.20	42.89	3.39	0.30
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.LTDAQVLTR.L	179.58	60.03	2.99	0.33
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	R.QALNNLQSTFSGFGYINSENVFK#.V	11.63	6.10	1.91	0.52
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.TAGHYELPWVEK#.Y	39.53	16.75	2.36	0.42
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.VAEGVNSLLQM*AGLLAR@.L	20.57	8.13	2.53	0.40
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.VPYTDDGLEAIIFTAQGDM*R@.Q	16.75	8.49	1.97	0.51
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.VPYTDDGLEAIIFTAQGDMR@.Q	6.19	3.72	1.67	0.60
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	R.EGNVPNIIIAGPPGTGK#.T	7.77	2.55	3.05	0.33
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.LNEIVGNEDTVSR@.L	12.09	2.58	4.69	0.21
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	R.EGNVPNIIIAGPPGTGK#.T	12.85	4.64	2.77	0.36
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.EK#VPYTDDGLEAIIFTAQGDM*R@.Q	8.22	1.78	4.61	0.22
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.LNEIVGNEDTVSR@.L	11.18	3.67	3.05	0.33
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.TAGHYELPWVEK#.Y	10.65	1.91	5.56	0.18
Q9WUK4_RFC2_MOUSE	Rfc2	Replication factor C subu	K.VAEGVNSLLQM*AGLLAR@.L	5.85	2.61	2.24	0.45
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	K.EGLALPSTLAR@.R	58.23	27.61	2.11	0.47
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	R.ETANAIVSQQTPQR@.L	33.99	16.70	2.04	0.49
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	K.TVAQSQQLETSSQR@.D	66.13	21.10	3.13	0.32
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	R.VQQYPFTEDQEIPETDWEVYLR@.E	13.73	5.40	2.54	0.39
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	R.VVIQEM*LK#.T	48.34	30.28	1.60	0.63
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	K.VVLLTEVDK#LTK#.D	4.95	3.43	1.44	0.69
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	R.ETANAIVSQQTPQR@.L	15.17	4.79	3.17	0.32
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	K.K#IEISTIASNYHLEVNPSDAGNSDR@.V	10.86	5.18	2.10	0.48
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	K.TVAQSQQLETSSQR@.D	21.24	6.76	3.14	0.32
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	K.EGLALPSTLAR@.R	39.82	11.93	3.34	0.30
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	R.ETANAIVSQQTPQR.L	28.75	7.24	3.97	0.25
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	K.TVAQSQQLETSSQR@.D	35.40	7.28	4.86	0.21
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	R.VQQYPFTEDQEIPETDWEVYLR@.E	17.66	5.18	3.41	0.29
Q8R323_RFC3_MOUSE	Rfc3	Replication factor C subu	R.VVIQEM*LK#.T	30.69	9.11	3.37	0.30
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.AITFLQSATR.L	69.83	21.22	3.29	0.30
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	R.ELFGPELFR@.L	122.62	31.34	3.91	0.26
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	R.GTPATAGSSGETK#.K	6.98	2.52	2.77	0.36
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.IGNEEIAYLVK#.I	69.39	27.08	2.56	0.39
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.ISEGDLR@.K	103.58	42.36	2.45	0.41
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.IVILDEADSM*TSAAQAALR@.R	21.55	6.42	3.36	0.30
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.IVILDEADSM*TSAAQAALR@.R	29.47	9.31	3.17	0.32
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.IVILDEADSMTSAAQAALR@.R	11.09	4.11	2.70	0.37
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	R.K#AITFLQSATR@.L	26.03	9.84	2.65	0.38
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	R.K#SLEGADLPNLLFYGPPGTGK#.T	65.71	24.16	2.72	0.37
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.NFAQLTVSGSR@.S	63.36	22.78	2.78	0.36
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.SLEGADLPNLLFYGPPGTGK#.T	42.08	19.66	2.14	0.47
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.TSTILAAAR@.E	97.79	23.95	4.08	0.24
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	R.VLELNASDER@.G	169.36	61.48	2.75	0.36
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	R.ELFGPELFR@.L	14.99	3.98	3.76	0.27
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.SLEGADLPNLLFYGPPGTGK#.T	8.53	8.33	1.02	0.98
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	R.VLELNASDER@.G	13.14	3.67	3.58	0.28
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.AITFLQSATR@.L	8.87	2.94	3.02	0.33
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	R.ELFGPELFR@.L	11.93	3.74	3.19	0.31
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.IGNEEIAYLVK#.I	5.35	2.18	2.45	0.41
Q99J62_RFC4_MOUSE	Rfc4	Replication factor C subu	K.SLEGADLPNLLFYGPPGTGK#.T	12.80	2.65	4.83	0.21
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.ALVTLSSGDM*R@.R	28.88	7.63	3.78	0.26
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.DK#EFGSM*VLELNASDDR@.G	11.14	5.81	1.92	0.52
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.FGPLTPELM*VPR.L	53.83	16.25	3.31	0.30
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.FGPLTPELMVPR@.L	10.69	2.86	3.73	0.27
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.GPILSFASTR@.T	94.62	29.25	3.24	0.31
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.IQLSSLIAAFQVTR@.D	27.80	9.42	2.95	0.34
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.LEHVVQEENVDISEDGM*K#.A	45.89	13.69	3.35	0.30
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.LSVGTSEK#.I	37.63	15.28	2.46	0.41
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.LVILDEADAM*TQDAQNALR@.R	18.31	5.95	3.08	0.32
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.LVILDEADAM*TQDAQNALR@.R	8.62	4.67	1.85	0.54
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.M*ADIEYR@.L	46.22	16.65	2.78	0.36
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.VDFPSSVR.I	36.63	14.46	2.53	0.39
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.YR@PQTLADLISHQDILSTIQK#.F	27.38	4.88	5.61	0.18
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.ALVTLSSGDM*R@.R	10.50	3.29	3.19	0.31
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.FGPLTPELM*VPR@.L	27.29	8.10	3.37	0.30
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.GPILSFASTR@.T	39.24	11.57	3.39	0.29
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.LEHVVQEENVDISEDGM*K#.A	15.11	4.73	3.19	0.31
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.M*ADIEYR@.L	10.51	1.68	6.26	0.16
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.YR@PQTLADLISHQDILSTIQK#.F	9.37	3.26	2.88	0.35
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.ALNILQSTNM*AFGK#.V	21.41	5.95	3.60	0.28
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.ALVTLSSGDM*R@.R	22.22	3.14	7.07	0.14
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.DK#EFGSM*VLELNASDDR@.G	15.61	6.68	2.34	0.43
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.FGPLTPELM*VPR@.L	47.67	14.91	3.20	0.31
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.GPILSFASTR@.T	75.50	22.97	3.29	0.30
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.IQLSSLIAAFQVTR@.D	21.11	6.24	3.38	0.30
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	R.LPHLLLYGPPGTGK#.T	7.38	2.64	2.79	0.36
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.LVILDEADAM*TQDAQNALR@.R	11.34	3.30	3.44	0.29
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.M*ADIEYR@.L	18.55	5.37	3.46	0.29
Q9D0F6_RFC5_MOUSE	Rfc5	Replication factor C subu	K.YR@PQTLADLISHQDILSTIQK#.F	11.39	4.29	2.65	0.38
P48377_RFX1_MOUSE	Rfx1	MHC class II regulatory fa	R.ASPATVQWLLDNYETAEGVSLPR@.S	10.34	5.57	1.86	0.54
P48377_RFX1_MOUSE	Rfx1	MHC class II regulatory fa	R.ASPATVQWLLDNYETAEGVSLPR@.S	8.31	7.72	1.08	0.93
P48377_RFX1_MOUSE	Rfx1	MHC class II regulatory fa	R.SVVQATPQTK#.A	7.15	4.90	1.46	0.69
P48377_RFX1_MOUSE	Rfx1	MHC class II regulatory fa	K.TAGTPAATVQQLQVHSVQQSVPVTQER@.S	5.07	1.98	2.56	0.39
Q9JL61_RFX5_MOUSE	Rfx5	DNA-binding protein Rfx	K.GSESPEM*GPEVSPAPR@.D	8.62	2.53	3.41	0.29
Q9JL61_RFX5_MOUSE	Rfx5	DNA-binding protein Rfx	K.NVVESLEGGGPK#.K	7.37	4.78	1.54	0.65
Q9JL61_RFX5_MOUSE	Rfx5	DNA-binding protein Rfx	R.SFSSIVQVAR@.Y	8.00	1.95	4.10	0.24
Q9JL61_RFX5_MOUSE	Rfx5	DNA-binding protein Rfx	K.TGAR@PQGGADAGEPTTLLQR@.L	16.68	3.87	4.32	0.23
Q8VCG9_RFXAP_MOUSE	Rfxap	Regulatory factor X-assoc	K.SDQALGSGGPSAASTGNVK#.L	6.31	1.36	4.65	0.21
Q99PG4_RGS18_MOUSE	Rgs18	Regulator of G-protein si	K.EPQQIILK.A	3.47	11.00	0.32	3.17
Q8BHC7_RHBL4_MOUSE	Rhbdd1	Rhomboid-related prote	R.NYDVYTAGLSEEEQLER@.A	4.42	2.70	1.63	0.61
Q921J2_RHEB_MOUSE	Rheb	GTP-binding protein Rhe	K.ALAESWNAAFLESSAK#.E	23.60	11.27	2.09	0.48
Q921J2_RHEB_MOUSE	Rheb	GTP-binding protein Rhe	R.IILEAEK#IDGAASQGK#.S	35.14	15.57	2.26	0.44
Q921J2_RHEB_MOUSE	Rheb	GTP-binding protein Rhe	R.K#IAILGYR@.S	28.79	4.11	7.00	0.14
Q921J2_RHEB_MOUSE	Rheb	GTP-binding protein Rhe	K.SSLTIQFVEGQFVDSYDPTIENTFTK#.L	6.02	4.72	1.28	0.78
Q921J2_RHEB_MOUSE	Rheb	GTP-binding protein Rhe	K.VQIPIM*LVGNK#.K	7.23	3.81	1.90	0.53
Q9QUI0_RHOA_MOUSE	Rhoa	Transforming protein Rh	R.EVFEM*ATR@.A	8.72	5.84	1.49	0.67
Q9QUI0_RHOA_MOUSE	Rhoa	Transforming protein Rh	K.QVELALWDTAGQEDYDR@.L	7.28	3.42	2.13	0.47

P84096_RHOG_MOUSE	Rhog	Rho-related GTP-binding	K.EYIPTVFDNYSAQSAVDGR@.T	2.94	1.90	1.54	0.65
P84096_RHOG_MOUSE	Rhog	Rho-related GTP-binding	R.LK#EQGQAPITPQQGQALAK#.Q	9.62	3.89	2.47	0.40
Q6QI06_RICTR_MOUSE	Rictor	Rapamycin-insensitive c	R.LSDGFVAAEAK#.T	10.48	1.55	6.76	0.15
Q6QI06_RICTR_MOUSE	Rictor	Rapamycin-insensitive c	R.YLIQDSSILQK#.V	16.27	2.38	6.83	0.15
Q6QI06_RICTR_MOUSE	Rictor	Rapamycin-insensitive c	K.YVDLIEEQLNEALTTYR@.K	9.62	4.02	2.39	0.42
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.FASDLIEPVTLDTPLSK#.N	49.09	12.51	3.92	0.25
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.GEIHSAVVDFEALNVIIR@.L	7.80	3.38	2.31	0.43
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.LGTM*ANSIIR@.N	19.86	6.13	3.24	0.31
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.TIGDLSTLTASEIK#.T	25.70	5.50	4.67	0.21
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.FASDLIEPVTLDTPLSK#.N	5.03	2.00	2.51	0.40
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.SGSEVLTLLLK#.S	4.50	1.67	2.69	0.37
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.AQM*STEIDSAR@.V	15.39	4.66	3.30	0.30
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.FASDLIEPVTLDTPLSK#.N	19.18	7.20	2.66	0.38
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.GLEEIPIFDISEK#.A	28.19	8.35	3.38	0.30
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.LGTM*ANSIIR@.N	9.15	3.11	2.94	0.34
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.LTDESPIQENLTEK#.G	5.52	4.42	1.25	0.80
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.SQEDEISPVNK#.I	17.63	7.87	2.24	0.45
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.TIGDLSTLTASEIK#.T	17.35	4.46	3.89	0.26
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.VIAGSSPEGVETM*ELNVR@.N	11.36	4.25	2.67	0.37
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.VSDSSLSPEK#.F	9.80	1.25	7.82	0.13
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.ALWVISK#.Q	19.57	4.80	4.07	0.25
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.AQM*STEIDSAR@.V	13.08	2.97	4.41	0.23
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.DASDAVVSAIWK#.E	12.01	9.16	1.31	0.76
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.DGDPK#PAVENASLEDLTTEEK#.N	11.59	3.28	3.53	0.28
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.EIFATFTR@PLALLYENSK#.L	6.01	3.18	1.89	0.53
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.FASDLIEPVTLDTPLSK#.N	29.10	6.17	4.71	0.21
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.GATALEM*GM*PLLLQK#.Q	15.53	4.10	3.79	0.26
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.GEIHSAVVDFEALNVIIR@.L	10.31	1.54	6.68	0.15
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.GLEEIPIFDISEK#.A	35.40	7.15	4.95	0.20
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.IVLSLEPLEHPLISSPSFFSK#.Y	33.52	13.66	2.45	0.41
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.LGTM*ANSIIR@.N	11.23	1.56	7.19	0.14
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.LIEQAPVQM*GEESVR@.W	7.97	4.66	1.71	0.58
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.LTDESPIQENLTEK#.G	17.28	5.98	2.89	0.35
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.M*TGEEGK#EVIAEIEK#.N	25.73	8.29	3.10	0.32
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.NDAFVAADSEK#.S	15.37	3.93	3.91	0.26
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.R@ASQGLISAVENSESDSSEAK#EEVSR@.K	9.97	1.81	5.50	0.18
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.SDSENLANAGK#.K	5.85	1.31	4.48	0.22
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.SGSEVLTLLLK#.S	49.18	17.39	2.83	0.35
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.TDLQVPETAPETR@.E	6.69	4.08	1.64	0.61
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.TEQIVNEDSQAAALAPNPK#.T	14.11	1.88	7.50	0.13
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.TSGEPSVNAEIDQNR@.R	9.51	2.35	4.05	0.25
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	K.VIAGSSPEGVETM*ELNVR@.N	13.38	4.32	3.10	0.32
Q6PR54_RIF1_MOUSE	Rif1	Telomere-associated pro	R.VILQDSAGPADSLQAPPK#GEEK#.S	10.17	3.05	3.33	0.30
O35730_RING1_MOUSE	Ring1	E3 ubiquitin-protein liga	R.GVAGGGEGPEEPALPSLEGVSEK#.Q	7.51	4.44	1.69	0.59
O35730_RING1_MOUSE	Ring1	E3 ubiquitin-protein liga	R.LHNQQALSSSIEEGLR@.M	23.84	9.44	2.53	0.40
O35730_RING1_MOUSE	Ring1	E3 ubiquitin-protein liga	R.SLR@PDPNFDALISK#.I	29.41	38.45	0.76	1.31
O35730_RING1_MOUSE	Ring1	E3 ubiquitin-protein liga	R.SLR@PDPNFDALISK#.I	25.09	16.61	1.51	0.66
Q9QZL0_RIPK3_MOUSE	Ripk3	Receptor-interacting seri	K.GGFGVVFR@.A	15.25	6.45	2.36	0.42
Q9QZL0_RIPK3_MOUSE	Ripk3	Receptor-interacting seri	R.QAQDTSVGPATPAR@.T	16.09	3.90	4.12	0.24
Q9QZL0_RIPK3_MOUSE	Ripk3	Receptor-interacting seri	R.QAQDTSVGPATPAR@.T	7.19	3.32	2.17	0.46
Q9QZL0_RIPK3_MOUSE	Ripk3	Receptor-interacting seri	R.DLK#PSNILLDPELHAK#.L	15.40	3.85	4.00	0.25
Q9QZL0_RIPK3_MOUSE	Ripk3	Receptor-interacting seri	K.GGFGVVFR@.A	12.14	2.90	4.18	0.24
Q9QZL0_RIPK3_MOUSE	Ripk3	Receptor-interacting seri	R.QAQDTSVGPATPAR@.T	9.13	3.29	2.78	0.36
Q14B01_Q14B01_MOUSE	Rnf113a2	Protein Rnf113a2 OS=M	K.DTSM*GNASSGM*VR@.K	3.69	3.16	1.17	0.85
Q14B01_Q14B01_MOUSE	Rnf113a2	Protein Rnf113a2 OS=M	R.K#AEGGASSTPEDADGI.-	7.56	2.76	2.73	0.37
Q9ET26_RN114_MOUSE	Rnf114	E3 ubiquitin-protein liga	R.DGAAQSAK#PASETDPLSR@.F	14.80	10.91	1.36	0.74
Q9ET26_RN114_MOUSE	Rnf114	E3 ubiquitin-protein liga	K.YQNYIM*EGVK#.A	12.63	7.05	1.79	0.56
Q9CQE0_RN138_MOUSE	Rnf138	E3 ubiquitin-protein liga	R.ALDLENIM*R@.R	92.44	46.43	1.99	0.50
Q9CQJ4_RING2_MOUSE	Rnf2	E3 ubiquitin-protein liga	K.HNNQQALSHSIEEGLK#.I	28.22	9.06	3.12	0.32
Q9CQJ4_RING2_MOUSE	Rnf2	E3 ubiquitin-protein liga	R.TPQEAITDGLEIVVSPR@.S	38.52	11.12	3.46	0.29
Q9CQJ4_RING2_MOUSE	Rnf2	E3 ubiquitin-protein liga	K.TWELSLYELQR@.T	17.03	6.00	2.84	0.35
Q9CQJ4_RING2_MOUSE	Rnf2	E3 ubiquitin-protein liga	R.TPQEAITDGLEIVVSPR.S	4.19	3.11	1.35	0.74
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	R.AVEEQIEYLQK#.K	26.82	11.04	2.43	0.41
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	R.DK#VQLM*AAEK#.K	7.22	3.68	1.96	0.51
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	R.ER@GDGQEPAFSFLATLASSSSEEM*ESQLQER@.V	2.92	1.99	1.46	0.68
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	R.HLAEVLER@.V	30.35	8.94	3.39	0.29
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	R.IEFEQTLAANEQAGPINR@.E	10.27	4.04	2.54	0.39
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	K.LGGVSSTEELDIR@.T	21.55	9.44	2.28	0.44
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	K.LHDFQDEIVENSVTK#.E	10.48	4.05	2.58	0.39
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	K.LLK#EEK#EELADQVLTLK#.T	22.91	9.00	2.54	0.39
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	R.LQELTDLLQEK#.H	25.91	7.61	3.40	0.29
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	K.LR@QDFEEVTTQNEK#.L	31.14	12.65	2.46	0.41
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	K.LR@TEVIQLEDTLAQVR@.K	23.86	10.51	2.27	0.44
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	R.R@AVSQIVTVYDK#LQEK#.V	6.08	2.23	2.73	0.37
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	K.R@YDLDQGLGDLLTER@.K	10.08	2.93	3.44	0.29
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	K.TAVEDSGTTVETIK#.L	24.51	8.79	2.79	0.36
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	R.TEVIQLEDTLAQVR@.K	22.28	6.31	3.53	0.28
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	K.VYGAGSSLYGGTITINAR@.K	9.92	4.15	2.39	0.42
Q5DTM8_BRE1A_MOUSE	Rnf20	E3 ubiquitin-protein liga	R.YDLDQGLGDLLTER.K	8.65	3.05	2.84	0.35
Q8BFU3_RN214_MOUSE	Rnf214	RING finger protein 214	K.TADSEVNTDQDIEK#.N	5.32	3.42	1.55	0.64
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	R.ALQGSLGGVEK#.E	17.45	6.34	2.75	0.36
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	R.EGPSLGPPPAASTLSR@.A	16.58	4.39	3.78	0.26
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	R.GDSEAPGEVAR@.V	13.97	4.04	3.46	0.29
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	R.IEFEQNLAANEQAGPINR@.E	12.75	5.83	2.19	0.46
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	R.ISLEYSELQDK#.V	12.04	5.33	2.26	0.44
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	K.K#EELVSSEDDAQALTPVTQGLPSR@.G	15.04	4.43	3.40	0.29
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	R.K#VEVYADADEILQEEIK#EYK#.A	9.00	1.60	5.63	0.18
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	K.LLR@EEK#DELGEQVLGLK#.S	17.17	7.51	2.29	0.44
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	K.LQAELQGAVR@.T	18.96	5.73	3.31	0.30
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	R.QATDDATLLIVNR@.Y	7.72	4.23	1.82	0.55
Q3U319_BRE1B_MOUSE	Rnf40	E3 ubiquitin-protein liga	K.TTTTLIEPIR@.L	23.47	6.50	3.61	0.28
Q9DBU5_RNF6_MOUSE	Rnf6	E3 ubiquitin-protein liga	R.AK#EQLASQPGSDSAASDGDSESLR@.A	3.71	3.23	1.15	0.87
Q3UZ01_RBM40_MOUSE	Rnpc3	RNA-binding protein 40	K.IFPK#PNLNITEEITEDSDEIPSQFISR@.K	7.21	2.75	2.62	0.38
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	K.DHIM*EIFSTYGK#.I	67.37	26.55	2.54	0.39
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	K.DHIMEIFSTYGK#.I	26.18	11.33	2.31	0.43
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	K.GYAYVEFENPDEAEK#.A	410.30	194.90	2.11	0.48
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	K.MIDM*PVER@.M	28.86	12.88	2.24	0.45
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	K.M*IDMPVER.M	34.33	15.22	2.26	0.44
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	K.M*IDM*PVER@.M	272.49	117.97	2.31	0.43
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	R.NVTK#DHIM*EIFSTYGK#.I	156.69	55.11	2.84	0.35
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	R.NVTK#DHIMEIFSTYGK#.I	23.12	5.85	3.95	0.25
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	K.GYAYVEFENPDEAEK#.A	14.03	12.94	1.08	0.92
Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	K.M*IDM*PVER@.M	6.76	7.44	0.91	1.10

Q99M28_RNPS1_MOUSE	Rnps1	RNA-binding protein wit	K.GYAYVEFENPDEAEK#.A	8.34	3.71	2.25	0.45
P70336_ROCK2_MOUSE	Rock2	Rho-associated protein k	R.GAFGEVQLVR@.H	10.38	11.53	0.90	1.11
P70336_ROCK2_MOUSE	Rock2	Rho-associated protein k	K.M*QTQQVNTLK#.M	5.83	1.37	4.26	0.23
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	R.ATAFNEQVDK.F	11.74	13.77	0.85	1.17
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	R.ATAFNEQVDKFFPLIEVNK.V	6.00	44.65	0.13	7.44
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	K.EKNEQAFEEVFQNANFR.S	1.78	11.89	0.15	6.69
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	K.SENLGQGDKADYFSTVAAVVFLR.K	2.64	19.73	0.13	7.47
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	R.SLSVLSSSTVIVNPDIPEAYK.L	1.37	5.66	0.24	4.14
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	R.VKLETYNDESR.I	5.13	23.27	0.22	4.53
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	K.VVPIASLTPYQSK.W	7.06	42.11	0.17	5.96
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	R.ATAFNEQVDKFFPLIEVNK.V	25.57	27.61	0.93	1.08
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	K.FIVNTLK#.D	17.02	18.42	0.92	1.08
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	K.LFSLELVDESGEIR@.A	39.20	34.15	1.15	0.87
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	K.NEQAFEEVFQNANFR.S	5.21	6.87	0.76	1.32
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	K.SENLGQGDK#ADYFSTVAAVVFLR@.K	20.80	19.48	1.07	0.94
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	R.SLSVLSSSTVIVNPDIPEAYK#.L	5.79	8.15	0.71	1.41
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	R.VKLETYNDESR.I	4.86	6.18	0.79	1.27
Q8VEE4_RFA1_MOUSE	Rpa1	Replication protein A 70	K.VVPIASLTPYQSK#.W	28.95	28.19	1.03	0.97
Q62193_RFA2_MOUSE	Rpa2	Replication protein A 32	K.APTNIVYK#.I	41.64	60.50	0.69	1.45
Q62193_RFA2_MOUSE	Rpa2	Replication protein A 32	K.IDDM*TAPPM*DVR.Q	34.22	38.84	0.88	1.14
Q62193_RFA2_MOUSE	Rpa2	Replication protein A 32	R.IGDVEISQVTIVGIIR@.H	24.52	23.42	1.05	0.95
Q62193_RFA2_MOUSE	Rpa2	Replication protein A 32	K.IDDM*TAPPM*DVR.Q	2.47	8.93	0.28	3.61
Q9CQ71_RFA3_MOUSE	Rpa3	Replication protein A 14	K.EDTNRFDLELYNEAVK.I	43.58	61.32	0.71	1.41
Q9CQ71_RFA3_MOUSE	Rpa3	Replication protein A 14	K.EDTNRFDLELYNEAVK.I	2.72	2.83	0.96	1.04
Q9CQ71_RFA3_MOUSE	Rpa3	Replication protein A 14	K.M*FILSDGEGK#.N	30.10	41.49	0.73	1.38
Q9CQ71_RFA3_MOUSE	Rpa3	Replication protein A 14	K.NGTIELM*EPLDEEISGIVEVVGK.V	7.58	9.10	0.83	1.20
Q9D706_RPAP3_MOUSE	Rpap3	RNA polymerase II-associ	R.EK#PALIFEVLER@.L	24.71	9.95	2.48	0.40
Q9D706_RPAP3_MOUSE	Rpap3	RNA polymerase II-associ	K.GHWDDVFLDSTQR@.H	11.67	8.07	1.45	0.69
Q9D706_RPAP3_MOUSE	Rpap3	RNA polymerase II-associ	K.GM*DADPYNPVLPTNR@.A	4.96	11.15	0.45	2.25
Q9D706_RPAP3_MOUSE	Rpap3	RNA polymerase II-associ	K.IEAVSDTSAPQAQVGVK#.Q	22.42	8.55	2.62	0.38
Q9D706_RPAP3_MOUSE	Rpap3	RNA polymerase II-associ	K.NLDPDVFNQIIK#.I	18.92	14.17	1.34	0.75
Q9D706_RPAP3_MOUSE	Rpap3	RNA polymerase II-associ	K.VLELEPDNFEATNELR@.K	9.52	8.81	1.08	0.93
Q9JJ80_RPF2_MOUSE	Rpf2	Ribosome production fa	K.NLLIDFFR@.G	18.60	9.55	1.95	0.51
Q9JJ80_RPF2_MOUSE	Rpf2	Ribosome production fa	R.IELEEM*GPSLDLVM*R@.R	5.43	15.28	0.36	2.81
Q9JJ80_RPF2_MOUSE	Rpf2	Ribosome production fa	K.NISQDTFGTTFGR@.I	6.17	1.86	3.32	0.30
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.FNADEFEDM*VAEK#.R	25.32	6.61	3.83	0.26
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.DGFHIR@.V	62.43	24.05	2.60	0.39
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.FK#FPGR@.Q	78.88	31.89	2.47	0.40
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.FNADEFEDM*VAEK#.R	100.64	38.94	2.58	0.39
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.FNADEFEDMVAEK#.R	7.11	1.81	3.93	0.25
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.FNADEFEDM*VAEK#R@.L	178.09	47.03	3.79	0.26
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.FNADEFEDM*VAEKR.L	13.17	2.11	6.25	0.16
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	R.GAFGKPQGTVAR.V	199.57	49.26	4.05	0.25
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	R.IFDLGR.K	461.83	142.32	3.24	0.31
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	R.VHIGQVIM*SIR@.T	228.15	61.36	3.72	0.27
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	R.VHIGQVIM*SIR.T	52.07	14.04	3.71	0.27
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.DGFHIR@.V	32.80	6.55	5.01	0.20
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.FNADEFEDM*VAEK#.R	21.27	4.46	4.77	0.21
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	R.IFDLGR.K	104.32	23.80	4.38	0.23
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	R.VHIGQVIM*SIR@.T	50.92	9.78	5.21	0.19
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.DGFHIR@.V	63.67	8.74	7.28	0.14
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.EHVIEALR@.R	31.36	8.25	3.80	0.26
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.EHVIEALR@R@.A	16.02	3.18	5.04	0.20
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	K.FNADEFEDM*VAEK#.R	36.95	9.42	3.92	0.26
Q6ZWV3_RL10_MOUSE	Rpl10	60S ribosomal protein L1	R.IFDLGR.K	181.24	36.28	5.00	0.20
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.AGK#FPSLLTHNENM*VAK#.V	164.20	34.01	4.83	0.21
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	R.DTLYEAVR.E	337.23	77.69	4.34	0.23
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.FLETVELQISLK#.N	8.75	2.50	3.50	0.29
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	R.ILGPGLNK#.A	413.24	113.13	3.65	0.27
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.K#YDAFLASESLIK#.Q	357.35	73.34	4.87	0.21
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.YDAFLASESLIK#.Q	41.47	11.45	3.62	0.28
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	R.DTLYEAVR@.E	357.91	76.91	4.65	0.21
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.FLETVELQISLK#.N	12.50	4.71	2.66	0.38
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.FPSLLTHNENM*VAK#.V	21.56	4.74	4.55	0.22
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	R.ILGPGLNK#.A	1225.65	369.36	3.32	0.30
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.K#YDAFLASESLIK#.Q	551.37	94.14	5.86	0.17
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.K#YDAFLASESLIK#.Q	231.84	48.72	4.76	0.21
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.VSR@DTLYEAVR@.E	19.18	5.93	3.23	0.31
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.VSR@DTLYEAVR@.E	2.24	1.41	1.60	0.63
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.YDAFLASESLIK#.Q	98.71	22.05	4.48	0.22
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	R.DTLYEAVR@.E	166.35	48.39	3.44	0.29
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.FLETVELQISLK#.N	7.89	2.65	2.98	0.34
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	R.ILGPGLNK#.A	337.92	108.79	3.11	0.32
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.K#YDAFLASESLIK#.Q	146.15	37.88	3.86	0.26
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.YDAFLASESLIK#.Q	14.34	2.61	5.50	0.18
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.AVDIPHM*DIEALK#.K	37.80	11.29	3.35	0.30
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	R.DTLYEAVR.E	135.11	36.38	3.71	0.27
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	R.ILGPGLNK#.A	229.62	67.11	3.42	0.29
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.K#YDAFLASESLIK#.Q	147.53	42.60	3.46	0.29
P53026_RL10A_MOUSE	Rpl10a	60S ribosomal protein L1	K.YDAFLASESLIK#.Q	22.65	6.52	3.48	0.29
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.VLEQLTGQTPVFSK#.A	72.93	19.00	3.84	0.26
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.YDGIILPGK#.-	73.54	25.41	2.89	0.35
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.AEEILEK#.G	771.85	253.33	3.05	0.33
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	R.GAK#AEEILEK#.G	64.94	15.63	4.16	0.24
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	R.GAKAEEILEK.G	77.79	23.77	3.27	0.31
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	R.K#NNFSDTGNFGFGIQEHIDLGIK#.Y	8.84	2.88	3.07	0.33
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.NNFSDTGNFGFGIQEHIDLGIK#.Y	33.52	10.29	3.26	0.31
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.VLEQLTGQTPVFSK#.A	1525.86	516.78	2.95	0.34
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.VR@EYELR@.K	165.43	49.48	3.34	0.30
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	R.WFQQK.Y	558.54	91.62	6.10	0.16
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.YDGIILPGK#.-	792.01	293.08	2.70	0.37
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.AEEILEK#.G	49.89	15.40	3.24	0.31
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.VLEQLTGQTPVFSK#.A	43.61	11.51	3.79	0.26
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.YDGIILPGK#.-	67.97	17.30	3.93	0.25
Q9CXW4_RL11_MOUSE	Rpl11	60S ribosomal protein L1	K.VLEQLTGQTPVFSK#.A	48.97	11.88	4.12	0.24
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	K.HSGNITFDEIVNIAR@.Q	51.10	18.48	2.77	0.36
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	R.QAQIEVVPSASALIIK#.A	51.16	22.65	2.26	0.44
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	R.ELSGTIK#.E	617.08	189.54	3.26	0.31
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	K.HSGNITFDEIVNIAR@.Q	1037.39	266.33	3.90	0.26
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	K.HSGNITFDEIVNIAR.Q	262.05	77.52	3.38	0.30
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	K.IGPLGLSPK#.K	1913.37	566.04	3.38	0.30
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	K.K#VGDDIAK#.A	462.06	125.58	3.68	0.27
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	R.QAQIEVVPSASALIIK#.A	1444.37	444.55	3.25	0.31

P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	K.VGDDIAK#.A	82.25	26.77	3.07	0.33
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	K.HSGNITFDEIVNIAR@.Q	64.87	18.54	3.50	0.29
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	R.QAQIEVVPSASALIIK#.A	37.23	9.28	4.01	0.25
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	K.HSGNITFDEIVNIAR@.Q	21.34	8.34	2.56	0.39
P35979_RL12_MOUSE	Rpl12	60S ribosomal protein L1	R.QAQIEVVPSASALIIK#.A	24.67	6.33	3.90	0.26
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.AK#EAAEQDVEK#.K	133.20	26.14	5.10	0.20
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.AK#EAAEQDVEK#.K	314.33	66.19	4.75	0.21
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.EAAEQDVEK#.K	242.99	57.26	4.24	0.24
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.EAAEQDVEK#K#.K	6.15	2.07	2.97	0.34
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.GFSLEELR@.V	1093.92	216.99	5.04	0.20
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.KGDSSAEELK.L	305.82	67.24	4.55	0.22
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.K#GDSSAEELK#LATQLTGPVMPIR@.N	18.06	4.21	4.29	0.23
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.LATQLTGPVM*PIR@.N	922.78	179.23	5.15	0.19
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.LATQLTGPVMPIR@.N	127.06	29.57	4.30	0.23
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.STESLQANVQR@.L	1537.35	301.15	5.10	0.20
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.TIGISVDPR@.R	1266.86	238.43	5.31	0.19
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.VDTWFNQPAR@.K	479.63	96.77	4.96	0.20
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.VITEEEK#.N	246.78	54.96	4.49	0.22
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.AK#EAAEQDVEK#.K	24.28	6.35	3.83	0.26
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.EAAEQDVEK#.K	42.85	8.40	5.10	0.20
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.GFSLEELR@.V	315.87	67.48	4.68	0.21
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.K#GDSSAEELK#.L	40.73	12.72	3.20	0.31
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.LATQLTGPVM*PIR@.N	367.03	78.96	4.65	0.22
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.LILFPR@.K	335.66	68.56	4.90	0.20
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.STESLQANVQR@.L	275.94	55.61	4.96	0.20
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.TIGISVDPR@.R	190.94	199.72	0.96	1.05
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.VDTWFNQPAR@.K	152.60	34.43	4.43	0.23
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.VITEEEK#.N	44.71	12.97	3.45	0.29
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.VITEEEK#NFK#.A	64.79	14.17	4.57	0.22
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.AK#EAAEQDVEK#.K	10.51	1.25	8.39	0.12
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.EAAEQDVEK#.K	11.22	4.18	2.68	0.37
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.GFSLEELR@.V	68.50	16.86	4.06	0.25
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.K#GDSSAEELK#.L	14.97	9.28	1.61	0.62
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.LATQLTGPVMPIR@.N	7.86	7.66	1.03	0.98
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.STESLQANVQR@.L	68.55	18.99	3.61	0.28
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.TIGISVDPR@.R	60.06	17.78	3.38	0.30
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.VDTWFNQPAR@.K	37.78	10.16	3.72	0.27
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	R.GFSLEELR@.V	46.86	12.18	3.85	0.26
P47963_RL13_MOUSE	Rpl13	60S ribosomal protein L1	K.STESLQANVQR@.L	28.48	7.32	3.89	0.26
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.FAYLGR@.L	111.22	16.02	6.94	0.14
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	R.M*VVPAALK#.V	61.29	15.70	3.90	0.26
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.R@GQAALER@.L	27.72	5.75	4.82	0.21
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.VLDGIPPPYDK#.K	16.55	4.53	3.65	0.27
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	R.K#FAYLGR@.L	53.90	8.73	6.18	0.16
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	R.M*VVPAALK#.V	227.16	18.69	12.16	0.08
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	R.MVVPAALK#.V	12.83	3.96	3.24	0.31
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.VLDGIPPPYDK#.K	56.42	13.49	4.18	0.24
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.YLAFLR@.K	316.38	51.90	6.10	0.16
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.YQAVTATLEEK#.R	323.24	50.08	6.45	0.15
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.FAYLGR@.L	47.33	7.81	6.06	0.16
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.VLDGIPPPYDK#.K	9.62	2.65	3.63	0.28
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.YQAVTATLEEK#.R	81.81	13.54	6.04	0.17
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.FAYLGR@.L	69.69	11.37	6.13	0.16
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.VLDGIPPPYDK#.K	14.42	3.61	4.00	0.25
P19253_RL13A_MOUSE	Rpl13a	60S ribosomal protein L1	K.YQAVTATLEEK#.R	73.43	13.59	5.40	0.19
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.AAIAAAAAAAAAK#.A	786.98	143.57	5.48	0.18
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.LVAIVDVIDQNR.A	647.74	132.79	4.88	0.20
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.M*TDFDR@FK#.V	39.31	7.97	4.93	0.20
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	R.YVEVGR@.V	307.05	67.30	4.56	0.22
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.AAIAAAAAAAAAK#.A	1310.34	244.85	5.35	0.19
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.LVAIVDVIDQNR@.A	1618.26	351.37	4.61	0.22
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.M*TDFDR@.F	104.66	28.77	3.64	0.27
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.M*TDFDR@FK#.V	100.03	19.35	5.17	0.19
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	R.R@YVEVGR@.V	111.63	21.84	5.11	0.20
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	R.YVEVGR@.V	585.31	122.37	4.78	0.21
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.AAIAAAAAAAAAK#.A	137.42	26.75	5.14	0.19
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.LVAIVDVIDQNR@.A	148.81	23.27	6.39	0.16
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.AAIAAAAAAAAAK#.A	102.43	9.63	10.63	0.09
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.LVAIVDVIDQNR@.A	22.36	4.10	5.46	0.18
Q9CR57_RL14_MOUSE	Rpl14	60S ribosomal protein L1	K.LVAIVDVIDQNR.A	141.71	23.33	6.07	0.16
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.FFEVILIDPFHK#.A	203.76	27.94	7.29	0.14
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.NTLQLHR@.Y	113.86	23.00	4.95	0.20
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.QGYVIYR@.I	165.60	28.25	5.86	0.17
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.SLQSVAEER@.A	432.74	64.55	6.70	0.15
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.VLNSYWVGEDSTYK#.F	119.79	21.88	5.48	0.18
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.YIQELWR@.K	159.60	31.78	5.02	0.20
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.FFEVILIDPFHK#.A	47.46	8.61	5.51	0.18
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.SLQSVAEER@.A	388.31	78.93	4.92	0.20
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.VLNSYWVGEDSTYK#.F	83.16	14.84	5.60	0.18
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.YIQELWR@.K	123.35	23.57	5.23	0.19
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.FFEVILIDPFHK#.A	257.66	40.00	6.44	0.16
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.NTLQLHR@.Y	127.15	20.81	6.11	0.16
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.QGYVIYR@.I	145.75	20.99	6.94	0.14
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.R@NPDTQWITK#PVHK#.H	18.14	1.62	11.20	0.09
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.SLQSVAEER@.A	239.62	46.83	5.12	0.20
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.VLNSYWVGEDSTYK#.F	119.23	21.47	5.55	0.18
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.YIQELWR@.K	129.41	19.35	6.69	0.15
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.FFEVILIDPFHK#.A	25.09	8.24	3.04	0.33
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.GATYGKPVHHGVNQLK.F	73.87	11.44	6.46	0.15
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.NTLQLHR@.Y	109.45	25.06	4.37	0.23
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.SLQSVAEER@.A	241.28	47.03	5.13	0.19
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	R.VLNSYWVGEDSTYK#.F	98.97	19.34	5.12	0.20
Q9CZM2_RL15_MOUSE	Rpl15	60S ribosomal protein L1	K.YIQELWR@.K	107.96	17.91	6.03	0.17
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	K.NAESNAELK#.G	37.96	9.44	4.02	0.25
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	K.QWGWTQGR@.W	26.38	5.75	4.59	0.22
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	R.YSLDPENPTK#.S	51.00	13.93	3.66	0.27
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	R.ETAQAIK#.G	308.75	80.80	3.82	0.26
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	K.K#SAEFLLHM*LK#.N	248.75	57.01	4.36	0.23
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	K.K#SAEFLLHMLK#.N	56.18	14.39	3.90	0.26
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	K.NAESNAELK#.G	386.19	109.03	3.54	0.28
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	K.QWGWTQGR@.W	189.09	41.98	4.50	0.22
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	K.YLK#DVTLK#.K	74.88	16.85	4.44	0.23
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	K.YLK#DVTLK#K#.Q	157.44	29.38	5.36	0.19

Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	R.YSLDPENPTK#.S	444.01	136.02	3.26	0.31
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	R.YSLDPENPTK#.S	27.48	9.22	2.98	0.34
Q9CPR4_RL17_MOUSE	Rpl17	60S ribosomal protein L1	K.NAESNAELK#.G	13.91	5.07	2.75	0.36
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.GTVLLSGPR@.K	161.79	28.46	5.68	0.18
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.ILTFDQLALESPK#.G	240.17	44.80	5.36	0.19
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.SQDIYLR@.L	99.25	16.39	6.06	0.17
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.TAVVVGTVTDDVR@.I	265.10	47.28	5.61	0.18
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.TNR@PPLSLSR@.M	144.20	29.15	4.95	0.20
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.TNSTFNQVVLK#.R	81.39	116.41	0.70	1.43
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.GTVLLSGPR@.K	319.76	53.04	6.03	0.17
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.ILTFDQLALESPK#.G	380.01	53.46	7.11	0.14
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.R@TNSTFNQVVLK#.R	15.32	2.00	7.68	0.13
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.SQDIYLR@.L	338.57	47.02	7.20	0.14
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.TAVVVGTVTDDVR@.I	504.33	80.34	6.28	0.16
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.TNR@PPLSLSR@.M	1081.91	170.85	6.33	0.16
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.TNSTFNQVVLK#.R	256.26	39.21	6.54	0.15
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.ILTFDQLALESPK#.G	111.53	26.16	4.26	0.23
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.TAVVVGTVTDDVR@.I	108.76	16.54	6.58	0.15
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.TNSTFNQVVLK#.R	31.14	22.79	1.37	0.73
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.GTVLLSGPR@.K	59.28	13.06	4.54	0.22
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.ILTFDQLALESPK#.G	165.17	37.59	4.39	0.23
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.SQDIYLR@.L	56.20	10.01	5.62	0.18
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	K.TAVVVGTVTDDVR@.I	103.90	16.94	6.13	0.16
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.TNR@PPLSLSR@.M	96.07	14.41	6.67	0.15
P35980_RL18_MOUSE	Rpl18	60S ribosomal protein L1	R.TNSTFNQVVLK#.R	30.34	8.29	3.66	0.27
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	R.IFAPNHVVAK#.S	31.88	11.29	2.82	0.35
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	K.NFGIWLR@.Y	71.54	14.32	5.00	0.20
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	K.R@PNTFF.-	54.52	12.29	4.44	0.23
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	R.AHSIQIM*K#VEEIAAGK#.C	16.78	3.47	4.84	0.21
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	R.FWYFVSQLK#.K	27.53	11.32	2.43	0.41
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	R.FWYFVSQLK#K#.M	12.59	2.11	5.96	0.17
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	K.NFGIWLR@.Y	196.65	40.09	4.91	0.20
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	K.R@PNTFF.-	77.67	16.87	4.60	0.22
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	K.VEEIAAGK#.C	144.14	39.92	3.61	0.28
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	K.NFGIWLR@.Y	61.76	14.28	4.32	0.23
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	K.VEEIAAGK#.C	98.36	22.21	4.43	0.23
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	R.AHSIQIM*K#.V	65.27	18.10	3.61	0.28
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	K.NFGIWLR@.Y	119.59	23.52	5.08	0.20
P62717_RL18A_MOUSE	Rpl18a	60S ribosomal protein L1	K.VEEIAAGK#.C	174.28	38.44	4.53	0.22
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	R.HMYHSLYLK#.V	26.22	3.90	6.72	0.15
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	R.ILM*EHIHK#.L	34.61	5.10	6.79	0.15
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.K#VWLDPNETNEIANANSR@.Q	68.85	11.46	6.01	0.17
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	R.LASSVLR@.C	808.27	138.09	5.85	0.17
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.LLADQAEAR@.R	1361.08	229.22	5.94	0.17
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.TLSK#EEETK#K#.-	14.98	3.90	3.85	0.26
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.VWLDPNETNEIANANSR@.Q	240.12	38.45	6.25	0.16
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	R.HMYHSLYLK#.V	11.15	2.51	4.44	0.23
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	R.ILM*EHIHK#.L	29.60	4.51	6.56	0.15
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.K#LLADQAEAR@.R	35.99	5.16	6.97	0.14
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.K#VWLDPNETNEIANANSR@.Q	118.85	21.09	5.64	0.18
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	R.LASSVLR@.C	1190.53	214.52	5.55	0.18
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.LLADQAEAR@.R	1389.72	256.61	5.42	0.18
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.TLSK#EEETK#K#.-	19.75	5.23	3.78	0.26
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.VK#GNVFK#.N	128.86	28.64	4.50	0.22
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.VWLDPNETNEIANANSR@.Q	220.02	40.14	5.48	0.18
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.VWLDPNETNEIANANSR@.Q	56.95	14.77	3.86	0.26
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.LLADQAEAR@.R	88.89	14.53	6.12	0.16
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.VWLDPNETNEIANANSR@.Q	14.69	2.89	5.07	0.20
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.LLADQAEAR@.R	36.72	4.90	7.50	0.13
P84099_RL19_MOUSE	Rpl19	60S ribosomal protein L1	K.VWLDPNETNEIANANSR@.Q	5.02	2.13	2.35	0.42
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	K.GDIVDIK#.G	26.97	5.68	4.75	0.21
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	K.GTWVQLK#.R	51.19	11.46	4.47	0.22
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	K.HGVVPLATYM*R@.I	12.64	4.96	2.55	0.39
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	K.K#GDIVDIK#.G	175.23	52.41	3.34	0.30
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.TNGK#EPELLEPIPYEFM*A.-	15.97	4.86	3.29	0.30
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.TNGK#EPELLEPIPYEFM*A.-	9.82	2.40	4.09	0.24
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.VYNVTQHAVGIIVNK#.Q	142.34	39.91	3.57	0.28
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.DSFLK#R@.V	587.45	150.74	3.90	0.26
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	K.EK#GTWVQLK#.R	31.62	6.45	4.90	0.20
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	K.GDIVDIK#.G	97.65	26.83	3.64	0.27
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	K.GTWVQLK#.R	270.40	54.72	4.94	0.20
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	K.HGVVPLATYM*R@.I	114.77	27.49	4.17	0.24
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	K.HGVVPLATYMR@.I	34.76	8.35	4.16	0.24
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.K#HGVVPLATYM*R@.I	51.31	10.06	5.10	0.20
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.TNGK#EPELLEPIPYEFM*A.-	113.76	35.95	3.16	0.32
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.VYNVTQHAVGIIVNK#.Q	762.50	219.54	3.47	0.29
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.TNGK#EPELLEPIPYEFM*A.-	6.99	2.27	3.08	0.32
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.VYNVTQHAVGIIVNK#.Q	69.35	19.78	3.51	0.29
O09167_RL21_MOUSE	Rpl21	60S ribosomal protein L2	R.VYNVTQHAVGIIVNK#.Q	32.07	13.25	2.42	0.41
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	K.AGNLGGGVVTIER@.S	28.84	16.21	1.78	0.56
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	R.YFQINQDEEEEEDED.-	6.61	6.61	1.00	1.00
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	K.AGNLGGGVVTIER@.S	400.73	172.65	2.32	0.43
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	K.ESYELR.Y	121.78	59.93	2.03	0.49
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	K.ITVTSEVPFSK#.R	281.34	128.01	2.20	0.45
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	K.SK#ITVTSEVPFSK#.R	33.35	16.74	1.99	0.50
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	K.SKITVTSEVPFSK.R	13.65	8.15	1.67	0.60
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	R.VVANSK#ESYELR@.Y	6.76	2.35	2.88	0.35
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	K.AGNLGGGVVTIER@.S	9.75	6.16	1.58	0.63
P67984_RL22_MOUSE	Rpl22	60S ribosomal protein L2	K.AGNLGGGVVTIER@.S	6.57	2.91	2.26	0.44
Q9D7S7_RL22L_MOUSE	Rpl22l1	60S ribosomal protein L2	R.FHLDLTHPVEDGIFDSGNFEQFLR@.E	55.00	3.76	14.62	0.07
Q9D7S7_RL22L_MOUSE	Rpl22l1	60S ribosomal protein L2	K.TGNLGNVVHIER@.L	85.53	18.16	4.71	0.21
Q9D7S7_RL22L_MOUSE	Rpl22l1	60S ribosomal protein L2	R.VVASDK#ETYELR@.Y	11.03	1.49	7.42	0.13
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	K.GSAITGPVAK#.E	16.93	5.59	3.03	0.33
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.LPAAGVGDM*VM*ATVK#.K	15.65	6.92	2.26	0.44
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	K.NLYIISVK#.G	21.24	12.35	1.72	0.58
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	K.DGVFLYFEDNAGVIVNNK#GEM*K#.G	13.05	6.51	2.00	0.50
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	K.GSAITGPVAK#.E	208.97	110.28	1.89	0.53
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.LNRLPAAGVGDM*VM*ATVK.K	219.91	87.10	2.52	0.40
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.LNR@LPAAGVGDM*VMATVK#.K	7.59	3.25	2.34	0.43
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.LNR@LPAAGVGDMVMATVK#.K	7.28	3.22	2.26	0.44
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.LPAAGVGDM*VM*ATVK#.K	243.87	102.26	2.38	0.42
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.LPAAGVGDMVM*ATVK#.K	11.37	4.66	2.44	0.41
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.LPAAGVGDMVMATVK#.K	11.29	4.20	2.69	0.37

P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	K.NLYIISVK#.G	442.73	161.66	2.74	0.37
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.R@K#DGVFLYFEDNAGVIVNNK#.G	17.17	4.53	3.79	0.26
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.LPAAGVGDM*VM*ATVK#.K	11.91	6.77	1.76	0.57
P62830_RL23_MOUSE	Rpl23	60S ribosomal protein L2	R.LPAAGVGDM*VM*ATVK#.K	7.31	4.27	1.71	0.58
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.FPLTTESAM*K#.K	11.73	2.49	4.72	0.21
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.IEDNNTLVFIVDVK#.A	8.21	1.13	7.25	0.14
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.K#LYDIDVAK#.V	27.46	4.90	5.60	0.18
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	R.LAPDYDALDVANK#.I	38.21	24.21	1.58	0.63
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.EAPAPPK#AEAK#.A	235.96	45.45	5.19	0.19
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.FPLTTESAM*K#.K	237.43	51.52	4.61	0.22
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.FPLTTESAMK#.K	35.71	7.53	4.74	0.21
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.FPLTTESAM*K#K#.I	227.40	53.16	4.28	0.23
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.IEDNNTLVFIVDVK#.A	95.27	20.87	4.56	0.22
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.K#EAPAPPK#.A	30.89	9.64	3.20	0.31
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.K#EAPAPPK#AEAK#.A	342.07	57.07	5.99	0.17
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.K#IEDNNTLVFIVDVK#.A	291.36	45.23	6.44	0.16
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.K#LYDIDVAK#.V	498.86	96.03	5.20	0.19
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	R.LAPDYDALDVANK#.I	2195.93	413.27	5.31	0.19
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	R.LAPDYDALDVANK#IGII.-	8.46	2.81	3.01	0.33
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.LDHYAIIK#.F	70.55	15.21	4.64	0.22
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.LYDIDVAK#.V	836.39	167.08	5.01	0.20
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	R.NK#LDHYAIIK#.F	314.66	52.31	6.02	0.17
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	R.NK#LDHYAIIK#FPLTTESAMK#.K	9.78	3.55	2.75	0.36
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.VNTLIR@PDGEK#.K	681.73	127.33	5.35	0.19
P62751_RL23A_MOUSE	Rpl23a	60S ribosomal protein L2	K.VNTLIRPDGEKK.A	131.47	22.58	5.82	0.17
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	R.AITGASLADIM*AK#.R	71.65	16.88	4.25	0.24
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	R.AITGASLADIMAK#.R	8.61	2.03	4.23	0.24
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	R.QINWTVLYR@.R	58.15	12.63	4.60	0.22
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	K.VFQFLNAK#.C	42.89	9.22	4.65	0.21
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	R.AITGASLADIM*AK#.R	915.48	207.29	4.42	0.23
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	R.AITGASLADIMAK#.R	99.97	23.84	4.19	0.24
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	K.GQSEEIQK#.K	74.60	20.52	3.64	0.28
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	K.K#GQSEEIQK#.K	34.23	8.63	3.96	0.25
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	R.QINWTVLYR@.R	684.62	162.65	4.21	0.24
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	K.VFQFLNAK#.C	907.55	233.87	3.88	0.26
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	R.AITGASLADIM*AK#.R	41.44	24.56	1.69	0.59
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	R.QINWTVLYR@.R	16.71	4.57	3.66	0.27
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	K.VFQFLNAK#.C	25.58	5.35	4.78	0.21
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	R.AITGASLADIM*AK#.R	21.76	7.84	2.77	0.36
Q8BP67_RL24_MOUSE	Rpl24	60S ribosomal protein L2	K.VFQFLNAK#.C	15.30	3.58	4.27	0.23
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.DDEVQVVR@.G	36.96	9.92	3.72	0.27
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	R.HFNAPSHIR@.R	94.11	36.12	2.61	0.38
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.YK#EETIEK#.M	8.19	3.64	2.25	0.44
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.YVIYIER@.V	48.43	9.89	4.90	0.20
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.DDEVQVVR@.G	695.83	200.44	3.47	0.29
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.FNPFVTSDR@.S	581.89	169.71	3.43	0.29
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.GKYKEETIEK.M	19.01	6.81	2.79	0.36
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	R.HFNAPSHIR.R	50.57	11.15	4.54	0.22
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	R.HFNAPSHIR@.R	1089.17	269.58	4.04	0.25
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.IM*SSPLSK#.E	426.64	124.41	3.43	0.29
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	R.K#DDEVQVVR@.G	280.45	81.79	3.43	0.29
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	R.KDDEVQVVR.G	291.44	79.70	3.66	0.27
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	R.K#IMSSPLSK#.E	14.97	6.57	2.28	0.44
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	R.KIM*SSPLSK.E	649.45	169.06	3.84	0.26
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.K#YVIYIER@.V	139.89	40.40	3.46	0.29
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	R.LK#LDK#DR@.K	109.10	34.96	3.12	0.32
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	-.M*K#FNPFVTSDR@.S	298.32	72.08	4.14	0.24
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.VVQVYR@.K	1703.77	448.86	3.80	0.26
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.YK#EETIEK#.M	358.29	92.72	3.86	0.26
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.YK#EETIEK#M*QE.-	93.84	28.07	3.34	0.30
P61255_RL26_MOUSE	Rpl26	60S ribosomal protein L2	K.YVIYIER@.V	1368.79	402.85	3.40	0.29
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.VVLVLAGR@.Y	12.29	3.75	3.28	0.31
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	R.YSVDIPLDK#.T	16.13	5.27	3.06	0.33
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.DVFR@DPALK#.R	81.05	25.55	3.17	0.32
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.NIDDGTSDR@PYSHALVAGIDR@.Y	72.69	19.54	3.72	0.27
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.NIDDGTSDR@PYSHALVAGIDR@YPR@.K	29.82	8.47	3.52	0.28
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.NK#WFFQK#.L	63.40	13.65	4.64	0.22
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.TVVNK#DVFR@.D	21.12	5.97	3.54	0.28
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.TVVNK#DVFR@DPALK#.R	4.86	2.16	2.25	0.44
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.VK#FEER@.Y	231.02	48.50	4.76	0.21
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.VVLVLAGR@.Y	2719.79	734.53	3.70	0.27
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	K.VYNYNHLM*PTR.Y	108.03	26.62	4.06	0.25
P61358_RL27_MOUSE	Rpl27	60S ribosomal protein L2	R.YSVDIPLDK#.T	1527.18	451.51	3.38	0.30
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	K.LWTLVSEQTR@.V	7.95	3.32	2.40	0.42
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	K.TGVAPIIDVVR@.S	124.63	29.59	4.21	0.24
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	R.INFDK#YHPGYFGK#.V	61.01	16.85	3.62	0.28
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	K.LWTLVSEQTR@.V	146.92	45.19	3.25	0.31
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	K.NK#TGVAPIIDVVR@.S	100.23	23.21	4.32	0.23
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	K.NKTGVAPIIDVVR.S	15.75	4.66	3.38	0.30
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	K.TGVAPIIDVVR@.S	2078.33	580.81	3.58	0.28
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	K.LWTLVSEQTR@.V	9.05	2.14	4.24	0.24
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	K.TGVAPIIDVVR@.S	66.39	12.93	5.14	0.19
P14115_RL27A_MOUSE	Rpl27a	60S ribosomal protein L2	K.TGVAPIIDVVR@.S	40.03	10.11	3.96	0.25
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.GVVVVM*K#.R	107.21	22.98	4.67	0.21
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	R.K#TVGVEPAADGK#.G	19.01	5.70	3.33	0.30
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	R.NK#QTYSTEPNNLK#.A	29.27	4.60	6.37	0.16
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.QTYSTEPNNLK#.A	97.17	23.29	4.17	0.24
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.TVGVEPAADGK#.G	201.23	36.99	5.44	0.18
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	R.ATLSSIR.H	1051.82	186.54	5.64	0.18
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.GVVVVMK#.R	40.14	8.16	4.92	0.20
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.GVVVVM*K#.R	324.65	73.56	4.41	0.23
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	R.K#PATSYVR@.T	289.19	52.37	5.52	0.18
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	R.NKQTYSTEPNNLK.A	204.47	38.01	5.38	0.19
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.QTYSTEPNNLK#.A	286.23	63.24	4.53	0.22
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	R.RASAILR.S	293.57	66.37	4.42	0.23
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	R.SQK#PVVVK#.R	101.51	29.10	3.49	0.29
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.TVGVEPAADGK#.G	531.46	106.22	5.00	0.20
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	R.YNGLIHR@.K	33.09	10.16	3.26	0.31
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.YR@PDLR@.M	458.64	100.22	4.58	0.22
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.TVGVEPAADGK#.G	39.94	9.87	4.05	0.25
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.QTYSTEPNNLK#.A	17.46	3.91	4.46	0.22
P41105_RL28_MOUSE	Rpl28	60S ribosomal protein L2	K.TVGVEPAADGK#.G	41.65	7.43	5.60	0.18
P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	K.AQASAPAQAPK#.G	207.22	36.64	5.66	0.18

P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	K.GAQAPVK#AP.-	165.07	31.47	5.24	0.19
P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	R.LAFIAHPK#.L	50.14	8.87	5.65	0.18
P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	K.AQASAPAQAPK#.G	842.73	181.43	4.64	0.22
P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	K.GAQAPVK#AP.-	748.57	128.56	5.82	0.17
P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	R.LAFIAHPK#.L	371.68	46.76	7.95	0.13
P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	K.AQASAPAQAPK#.G	64.80	13.40	4.83	0.21
P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	R.LAFIAHPK#.L	16.00	5.19	3.08	0.32
P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	K.AQASAPAQAPK#.G	30.54	11.59	2.64	0.38
P47915_RL29_MOUSE	Rpl29	60S ribosomal protein L2	R.LAFIAHPK#.L	10.49	5.09	2.06	0.49
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.AFM*GPLK#K#.D	55.10	14.69	3.75	0.27
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.AGM*THIVR@.E	27.39	6.55	4.18	0.24
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.AHLM*EIQVNGGTVAEK#.L	41.86	13.60	3.08	0.32
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.DDASK#PVHLTAFLGYK#.A	183.96	50.19	3.67	0.27
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.ER@LEQQVPVNQVFGQDEM*IDVIGVTK#.G	212.25	44.61	4.76	0.21
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.ER@LEQQVPVNQVFGQDEMIDVIGVTK#.G	41.52	11.01	3.77	0.27
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.FIDTTSK#.F	330.95	71.51	4.63	0.22
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.HGSLGFLPR@.K	430.80	118.57	3.63	0.28
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.IGQGYLIK#.D	612.84	144.72	4.23	0.24
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.IIAHTQM*R@.L	55.05	13.60	4.05	0.25
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.K#AHLM*EIQVNGGTVAEK#.L	16.16	3.84	4.20	0.24
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.K#SLLVQTK#.R	148.98	41.00	3.63	0.28
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.LEQQVPVNQVFGQDEM*IDVIGVTK#.G	180.32	42.09	4.28	0.23
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.LEQQVPVNQVFGQDEMIDVIGVTK#.G	47.03	11.25	4.18	0.24
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.NNASTDYDLSDK#.S	269.88	78.15	3.45	0.29
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.SINPLGGFVHYGEVTNDFIM*LK#.G	282.75	66.36	4.26	0.23
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.SINPLGGFVHYGEVTNDFIMLK#.G	95.55	21.86	4.37	0.23
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.VAFSVAR@.A	494.80	116.81	4.24	0.24
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.AFM*GPLK#K#.D	28.17	6.73	4.19	0.24
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.AHLM*EIQVNGGTVAEK#.L	19.93	5.21	3.83	0.26
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.DDASK#PVHLTAFLGYK#.A	122.56	22.31	5.49	0.18
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.ER@LEQQVPVNQVFGQDEM*IDVIGVTK#.G	89.80	14.42	6.23	0.16
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.ER@LEQQVPVNQVFGQDEMIDVIGVTK#.G	16.38	2.36	6.95	0.14
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.FIDTTSK#.F	174.31	29.49	5.91	0.17
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.HGSLGFLPR@.K	194.67	34.79	5.60	0.18
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.IGQGYLIK#.D	232.15	53.91	4.31	0.23
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.K#AHLM*EIQVNGGTVAEK#.L	5.61	26.20	0.21	4.67
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.K#SLLVQTK#.R	44.10	10.90	4.04	0.25
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.LEQQVPVNQVFGQDEMIDVIGVTK#.G	15.12	4.83	3.13	0.32
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.NNASTDYDLSDK#.S	127.77	24.96	5.12	0.20
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.SINPLGGFVHYGEVTNDFIM*LK#.G	150.35	27.14	5.54	0.18
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.SINPLGGFVHYGEVTNDFIMLK#.G	47.67	8.74	5.46	0.18
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.VAFSVAR@.A	275.36	42.96	6.41	0.16
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.DDASK#PVHLTAFLGYK#.A	125.72	31.17	4.03	0.25
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.ER@LEQQVPVNQVFGQDEM*IDVIGVTK#.G	106.82	15.76	6.78	0.15
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.ER@LEQQVPVNQVFGQDEMIDVIGVTK#.G	18.66	3.30	5.65	0.18
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.FQTM*EEK#K#.A	6.17	2.36	2.61	0.38
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.HGSLGFLPR@.K	214.85	39.04	5.50	0.18
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.IGQGYLIK#.D	185.04	33.04	5.60	0.18
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.IIAHTQM*R@.L	32.32	7.97	4.05	0.25
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.K#FSAPR@.H	26.57	9.85	2.70	0.37
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.K#SLLVQTK#.R	47.28	7.01	6.74	0.15
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.LEQQVPVNQVFGQDEM*IDVIGVTK#.G	95.92	18.11	5.30	0.19
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.NNASTDYDLSDK#.S	126.04	25.21	5.00	0.20
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.SINPLGGFVHYGEVTNDFIM*LK#.G	193.96	36.16	5.36	0.19
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	K.SINPLGGFVHYGEVTNDFIMLK#.G	26.27	3.67	7.16	0.14
P27659_RL3_MOUSE	Rpl3	60S ribosomal protein L3	R.VAFSVAR@.A	188.39	27.78	6.78	0.15
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.K#SEIEYYAM*LAK#.T	13.75	6.16	2.23	0.45
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.KSEIEYYAM*LAK.T	27.15	8.68	3.13	0.32
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.LQLVM*K#.S	39.26	12.18	3.22	0.31
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.LQLVMK#.S	10.08	3.66	2.76	0.36
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	K.SEIEYYAM*LAK#.T	10.05	5.30	1.90	0.53
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.K#SEIEYYAM*LAK#.T	74.60	19.10	3.91	0.26
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.KSEIEYYAM*LAK.T	99.99	26.89	3.72	0.27
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.KSEIEYYAMLAK.T	28.15	6.98	4.03	0.25
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	K.K#SLESINSR@.L	273.37	70.72	3.87	0.26
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.LQLVM*K#.S	842.55	300.18	2.81	0.36
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.LQLVMK#.S	70.49	22.77	3.10	0.32
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	K.SEIEYYAM*LAK#.T	197.50	54.50	3.62	0.28
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	K.SEIEYYAMLAK#.T	38.67	11.38	3.40	0.29
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	K.SLESINSR@.L	784.59	210.29	3.73	0.27
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	R.K#SEIEYYAM*LAK#.T	14.47	4.35	3.33	0.30
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	K.SEIEYYAM*LAK#.T	6.40	1.89	3.39	0.30
P62889_RL30_MOUSE	Rpl30	60S ribosomal protein L3	K.SLESINSR@.L	24.62	7.09	3.47	0.29
P62900_RL31_MOUSE	Rpl31	60S ribosomal protein L3	K.EM*GTPDVR@.I	633.64	213.80	2.96	0.34
P62900_RL31_MOUSE	Rpl31	60S ribosomal protein L3	R.EYTINIHK#R@.I	39.59	22.99	1.72	0.58
P62900_RL31_MOUSE	Rpl31	60S ribosomal protein L3	R.K#R@NEDEDSPNK#.L	3.50	1.43	2.45	0.41
P62900_RL31_MOUSE	Rpl31	60S ribosomal protein L3	K.LYTLVTYVPVTTFK#.N	617.84	196.07	3.15	0.32
P62900_RL31_MOUSE	Rpl31	60S ribosomal protein L3	R.NEDEDSPNK#LYTLVTYVPVTTFK#.N	163.17	52.00	3.14	0.32
P62900_RL31_MOUSE	Rpl31	60S ribosomal protein L3	K.RNEDEDSPNKLYTLVTYVPVTTFK.N	16.30	4.99	3.26	0.31
P62900_RL31_MOUSE	Rpl31	60S ribosomal protein L3	R.SAINEVVTR@.E	1616.93	472.67	3.42	0.29
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	R.AAQLAIR@.V	1734.61	343.14	5.06	0.20
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	R.FK#GQILM*PNIGYGSNK#.K	78.37	20.12	3.89	0.26
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	R.FK#GQILMPNIGYGSNK#.K	10.59	2.86	3.70	0.27
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	R.FKGQILM*PNIGYGSNKK.T	39.73	10.73	3.70	0.27
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	K.FLVHNVK#.E	103.71	16.37	6.34	0.16
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	K.GQILM*PNIGYGSNK#.K	29.06	7.76	3.75	0.27
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	K.GQILMPNIGYGSNK#.K	6.02	1.66	3.62	0.28
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	K.GQILM*PNIGYGSNK#K#.T	6.27	1.99	3.15	0.32
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	K.HM*LPSGFR@.K	148.00	13.52	10.95	0.09
P62911_RL32_MOUSE	Rpl32	60S ribosomal protein L3	K.HM*LPSGFR@K#.F	143.31	26.37	5.44	0.18
Q9D1R9_RL34_MOUSE	Rpl34	60S ribosomal protein L3	R.IVYLYTK#.K	71.15	17.12	4.16	0.24
Q9D1R9_RL34_MOUSE	Rpl34	60S ribosomal protein L3	R.LSYNTASNK#.T	19.88	5.14	3.86	0.26
Q9D1R9_RL34_MOUSE	Rpl34	60S ribosomal protein L3	R.AFLIEEQK#.I	922.75	195.91	4.71	0.21
Q9D1R9_RL34_MOUSE	Rpl34	60S ribosomal protein L3	R.LSYNTASNK#.T	411.75	92.30	4.46	0.22
Q9D1R9_RL34_MOUSE	Rpl34	60S ribosomal protein L3	K.R@AFLIEEQK#.I	87.47	18.43	4.75	0.21
Q9D1R9_RL34_MOUSE	Rpl34	60S ribosomal protein L3	R.R@LSYNTASNK#.T	223.65	41.01	5.45	0.18
Q9D1R9_RL34_MOUSE	Rpl34	60S ribosomal protein L3	R.AFLIEEQK#.I	25.14	9.12	2.76	0.36
Q6ZWV7_RL35_MOUSE	Rpl35	60S ribosomal protein L3	R.VLTVINQTQK#.E	22.09	4.18	5.28	0.19
Q6ZWV7_RL35_MOUSE	Rpl35	60S ribosomal protein L3	K.K#K#EELLK#.Q	93.99	15.96	5.89	0.17
Q6ZWV7_RL35_MOUSE	Rpl35	60S ribosomal protein L3	K.QLDDLK#VELSQLR@.V	570.78	121.26	4.71	0.21
Q6ZWV7_RL35_MOUSE	Rpl35	60S ribosomal protein L3	R.VLTVINQTQK#.E	1100.92	216.72	5.08	0.20
Q6ZWV7_RL35_MOUSE	Rpl35	60S ribosomal protein L3	K.YK#PLDLR@PK#.K	708.57	85.19	8.32	0.12
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	R.DETEFYLGK#.R	27.11	4.74	5.72	0.17

O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	K.IEGVYAR@.D	40.38	40.91	0.99	1.01
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	K.NNTVTPGGK#PNK#.T	5.72	12.09	0.47	2.12
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	R.VM*LYPSR@I.-	20.68	5.23	3.95	0.25
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	K.AIFAGYK#.R	177.77	55.37	3.21	0.31
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	K.AIFAGYK#R@.G	76.33	23.04	3.31	0.30
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	R.DETEFYLGK#.R	123.92	44.19	2.80	0.36
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	R.DETEFYLGKR.C	100.22	24.00	4.17	0.24
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	K.IEGVYAR@.D	561.07	149.89	3.74	0.27
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	K.NNTVTPGGKPNK.T	95.82	33.84	2.83	0.35
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	R.VM*LYPSR@.I	350.93	117.37	2.99	0.33
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	R.VM*LYPSR@I.-	751.38	218.64	3.44	0.29
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	R.VMLYPSR@I.-	33.16	10.08	3.29	0.30
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	R.VM*LYPSR@I.-	17.55	4.55	3.86	0.26
O55142_RL35A_MOUSE	Rpl35a	60S ribosomal protein L3	K.NNTVTPGGK#PNK#.T	10.63	2.38	4.47	0.22
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.EELSNVLAAMR@.K	17.51	2.63	6.65	0.15
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.K#R@EELSNVLAAMR@.K	15.92	3.16	5.04	0.20
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.YPM*AVGLNK#.G	77.56	15.48	5.01	0.20
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.YPMAVGLNK#.G	16.03	2.86	5.60	0.18
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.EELSNVLAAM*R@.K	227.65	43.25	5.26	0.19
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.EELSNVLAAMR@.K	24.88	3.34	7.45	0.13
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.KREELSNVLAAM*R.K	307.18	68.45	4.49	0.22
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.YPM*AVGLNK#.G	232.01	45.69	5.08	0.20
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.YPM*AVGLNK#.G	18.91	3.24	5.84	0.17
Q6ZWZ4_Q6ZWZ4_MOUSE	Rpl36	60S ribosomal protein L3	R.YPM*AVGLNK#.G	12.02	3.91	3.07	0.33
P83882_RL36A_MOUSE	Rpl36a	60S ribosomal protein L3	K.HFELGGDK#.K	28.10	9.36	3.00	0.33
P83882_RL36A_MOUSE	Rpl36a	60S ribosomal protein L3	R.K#GQVIQF.-	32.49	7.13	4.56	0.22
P83882_RL36A_MOUSE	Rpl36a	60S ribosomal protein L3	K.DSLYAQGK#.R	187.17	41.80	4.48	0.22
P83882_RL36A_MOUSE	Rpl36a	60S ribosomal protein L3	K.GK#DSLYAQGK#.R	122.99	26.02	4.73	0.21
P83882_RL36A_MOUSE	Rpl36a	60S ribosomal protein L3	K.HFELGGDK#.K	87.68	18.58	4.72	0.21
P83882_RL36A_MOUSE	Rpl36a	60S ribosomal protein L3	R.K#GQVIQF.-	374.55	76.17	4.92	0.20
Q9D823_RL37_MOUSE	Rpl37	60S ribosomal protein L3	R.K#YNWSAK#.A	256.92	48.28	5.32	0.19
P61514_RL37A_MOUSE	Rpl37a	60S ribosomal protein L3	K.TVAGGAWTYNTTSAVTVK#.S	5.06	1.64	3.09	0.32
P61514_RL37A_MOUSE	Rpl37a	60S ribosomal protein L3	K.IEISQHAK#.Y	72.59	27.36	2.65	0.38
P61514_RL37A_MOUSE	Rpl37a	60S ribosomal protein L3	K.K#IEISQHAK#.Y	520.75	145.57	3.58	0.28
P61514_RL37A_MOUSE	Rpl37a	60S ribosomal protein L3	K.K#VGIVGK#.Y	352.13	100.27	3.51	0.28
P61514_RL37A_MOUSE	Rpl37a	60S ribosomal protein L3	K.TVAGGAWTYNTTSAVTVK#.S	303.50	80.43	3.77	0.27
P61514_RL37A_MOUSE	Rpl37a	60S ribosomal protein L3	R.YGASLRK.M	157.97	46.52	3.40	0.29
P61514_RL37A_MOUSE	Rpl37a	60S ribosomal protein L3	K.TVAGGAWTYNTTSAVTVK#.S	5.60	2.19	2.55	0.39
Q9JJI8_RL38_MOUSE	Rpl38	60S ribosomal protein L3	K.IEEIK#DFLLTAR@.R	22.19	12.11	1.83	0.55
Q9JJI8_RL38_MOUSE	Rpl38	60S ribosomal protein L3	R.K#IEEIK#DFLLTAR@.R	81.59	83.57	0.98	1.02
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.APIR@PDIVNFVHTNLR@.K	65.90	17.78	3.71	0.27
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.AWNDIK#K#.V	57.56	11.35	5.07	0.20
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.GTADK#K#PAVGK#.K	6.06	1.46	4.14	0.24
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.IEEVPELPLVVEDK#.V	140.04	25.89	5.41	0.18
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.IEEVPELPLVVEDK#VEGYK#K#.T	476.15	99.82	4.77	0.21
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.K#LEAAATALATK#.S	341.21	86.86	3.93	0.25
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.LDELYGTWR@.K	19.95	4.34	4.59	0.22
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.LEAAATALATK#.S	128.97	32.80	3.93	0.25
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.M*FAPTK#.T	242.07	49.54	4.89	0.20
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.M*M*NTDLSR@.I	209.36	41.04	5.10	0.20
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.MM*NTDLSR@.I	13.40	3.01	4.45	0.22
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.NIPGITLLNVSK#.L	833.50	186.36	4.47	0.22
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.NVTLPAVFK#.A	558.98	123.97	4.51	0.22
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.QPYAVSELAGHQTSAESWGTGR@.A	191.72	39.52	4.85	0.21
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.R@NTILR@.Q	56.49	13.64	4.14	0.24
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.TK#EAVQLLK#.K	84.31	21.62	3.90	0.26
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.APIRPDIVNFVHTNLR.K	51.15	11.27	4.54	0.22
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.EAVQLLK#K#.L	19.92	2.92	6.83	0.15
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.KLDELYGTWR.K	49.32	10.77	4.58	0.22
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.K#LEAAATALATK#.S	129.24	27.86	4.64	0.22
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.LDELYGTWR@.K	8.77	2.71	3.23	0.31
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.LEAAATALATK#.S	100.50	18.69	5.38	0.19
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.M*M*NTDLSR@.I	85.78	18.02	4.76	0.21
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.NIPGITLLNVSK#.L	362.65	77.91	4.65	0.21
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.NNR@QPYAVSELAGHQTSAESWGTGR@.A	9.74	1.75	5.56	0.18
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.NVTLPAVFK#.A	188.38	44.63	4.22	0.24
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.QPYAVSELAGHQTSAESWGTGR@.A	62.75	13.70	4.58	0.22
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.IEEVPELPLVVEDK#VEGYK#K#.T	102.77	19.23	5.34	0.19
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.K#LEAAATALATK#.S	42.20	9.66	4.37	0.23
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.LDELYGTWR@.K	10.35	2.72	3.81	0.26
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.LEAAATALATK#.S	54.32	8.23	6.60	0.15
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.M*M*NTDLSR@.I	45.93	10.17	4.51	0.22
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	R.NIPGITLLNVSK#.L	161.51	27.53	5.87	0.17
Q9D8E6_RL4_MOUSE	Rpl4	60S ribosomal protein L4	K.NVTLPAVFK#.A	87.91	16.07	5.47	0.18
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.EFNAEVHR@.K	72.21	24.42	2.96	0.34
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	R.ENPVYEK#.K	194.26	68.64	2.83	0.35
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	R.FPGYDSESK#.E	53.41	15.63	3.42	0.29
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.HIM*GQNVADYM*R@.Y	100.22	27.80	3.60	0.28
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.NNVTPDMM*EEM*YK#.K	12.10	4.02	3.01	0.33
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.R@FPGYDSESK#.E	166.06	49.49	3.36	0.30
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	R.YLM*EEDEDAYK#K#.Q	571.58	179.76	3.18	0.31
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.EFNAEVHR@.K	26.28	4.77	5.51	0.18
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.GAVDGGLSIPHSTK#.R	244.30	40.40	6.05	0.17
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.HIM*GQNVADYM*R@.Y	83.65	16.35	5.11	0.20
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.HIM*GQNVADYM*R.Y	42.86	6.04	7.09	0.14
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.RFPGYDSESK.E	54.79	12.08	4.54	0.22
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	R.YLM*EEDEDAYK#K#.Q	23.41	4.57	5.12	0.20
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.EFNAEVHR@.K	32.28	10.10	3.20	0.31
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.HIM*GQNVADYM*R@.Y	37.91	4.93	7.69	0.13
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.K#ASFLR@.A	37.38	16.00	2.34	0.43
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.QFSQYIK#.N	142.48	23.64	6.03	0.17
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.R@FPGYDSESK#.E	48.62	10.36	4.69	0.21
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	K.TDYYAR@.K	59.13	12.50	4.73	0.21
P47962_RL5_MOUSE	Rpl5	60S ribosomal protein L5	R.YLM*EEDEDAYK#K#.Q	165.38	33.49	4.94	0.20
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.AVDLQILPK#.I	1457.57	310.50	4.69	0.21
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.AVPQLQGYLR@.S	1065.63	201.87	5.28	0.19
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.EK#VLATVTK#.T	67.00	15.94	4.20	0.24
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.FVIATSTK#.V	920.80	190.11	4.84	0.21
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.HLTDAYFK#.K	739.11	150.78	4.90	0.20
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.HQEGEIFDTEK#.E	83.61	19.77	4.23	0.24
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.HQEGEIFDTEKEK.Y	394.44	75.72	5.21	0.19
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.HQEGEIFDTEK#EK#YEITEQR@.K	706.41	129.46	5.46	0.18
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.K#AGSDAAASR@PR@.A	9.07	2.84	3.20	0.31

P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.K#PFSQHVR@.R	35.68	8.40	4.25	0.24
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.QLDSGLLLVTGPLVINR@.V	357.02	66.97	5.33	0.19
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.SSITPGTVLIILTGR@.H	775.05	158.50	4.89	0.20
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.VDISDVK#.I	928.34	224.46	4.14	0.24
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.YEITEQR@.K	322.51	71.89	4.49	0.22
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.YYPTEDVPR@.K	598.81	133.52	4.48	0.22
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.AVDLQILPK#.I	221.52	58.24	3.80	0.26
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.HLTDAYFK#.K	155.53	43.74	3.56	0.28
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.HQEGEIFDTEK#.E	9.50	2.40	3.95	0.25
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.HQEGEIFDTEK#EK#YEITEQR@.K	101.58	28.15	3.61	0.28
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.QLDSGLLLVTGPLVINR@.V	46.67	11.83	3.94	0.25
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.SSITPGTVLIILTGR@.H	109.35	33.80	3.24	0.31
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.VDISDVK#.I	147.57	42.11	3.50	0.29
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.VLATVTK#.T	116.69	40.98	2.85	0.35
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.YEITEQR@.K	23.84	4.68	5.10	0.20
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.YYPTEDVPR@.K	105.67	31.32	3.37	0.30
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	K.HLTDAYFK#.K	18.10	3.37	5.38	0.19
P47911_RL6_MOUSE	Rpl6	60S ribosomal protein L6	R.SSITPGTVLIILTGR@.H	11.93	3.01	3.96	0.25
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.AGNFYVPAEPK#.L	342.55	45.58	7.51	0.13
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.ASINM*LR@.I	781.16	105.62	7.40	0.14
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.ASINMLR@.I	185.08	26.13	7.08	0.14
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.EANNFLWPFK#.L	342.82	48.21	7.11	0.14
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.FK#EANNFLWPFK#.L	353.42	46.38	7.62	0.13
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.GINGVSPK#.V	181.62	21.87	8.30	0.12
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.IALTDNSLIAR@.S	2148.24	301.46	7.13	0.14
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.IVEPYIAWGYPNLK#.S	644.52	107.08	6.02	0.17
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.K#AGNFYVPAEPK#.L	110.62	21.54	5.14	0.19
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.K#TTHFVEGGDAGNR@EDQINR@.L	27.68	4.14	6.69	0.15
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.K#VATVPGTLK#.K	81.24	9.01	9.02	0.11
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.K#VATVPGTLK#K#.K	214.67	45.16	4.75	0.21
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.K#VLQLLR@.L	571.56	58.22	9.82	0.10
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.K#VPAVPETLK#.K	465.08	60.80	7.65	0.13
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.LAFVIR@.I	963.45	128.57	7.49	0.13
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.NFAELK#.V	278.86	45.82	6.09	0.16
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.QIFNGTFVK#.L	263.57	38.05	6.93	0.14
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.R@IALTDNSLIAR@.S	64.09	10.71	5.98	0.17
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.SVNELIYK#.R	760.02	93.13	8.16	0.12
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.TTHFVEGGDAGNREDQINR.L	429.21	44.91	9.56	0.10
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.VATVPGTLK#.K	427.61	58.30	7.33	0.14
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.VATVPGTLK#K#.K	89.82	12.96	6.93	0.14
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.VPAVPETLK#.K	166.96	26.58	6.28	0.16
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.ASINM*LR@.I	18.79	7.47	2.52	0.40
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.EANNFLWPFK#.L	19.46	8.73	2.23	0.45
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.FK#EANNFLWPFK#.L	16.42	3.97	4.14	0.24
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.IALTDNSLIAR@.S	112.01	27.95	4.01	0.25
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.IVEPYIAWGYPNLK#.S	51.38	12.39	4.15	0.24
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.LAFVIR@.I	44.41	7.90	5.62	0.18
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.SVNELIYK#.R	35.89	7.22	4.97	0.20
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.EANNFLWPFK#.L	19.02	4.72	4.03	0.25
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.IALTDNSLIAR@.S	103.43	24.00	4.31	0.23
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	R.IVEPYIAWGYPNLK#.S	33.08	9.95	3.33	0.30
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.LAFVIR@.I	51.50	8.16	6.31	0.16
P14148_RL7_MOUSE	Rpl7	60S ribosomal protein L7	K.TTHFVEGGDAGNR@EDQINR@.L	36.93	11.19	3.30	0.30
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.AAGK#GDVPTK#.R	34.76	13.21	2.63	0.38
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.AGVNTVTTLVENK#.K	1545.44	371.80	4.16	0.24
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.AGVNTVTTLVENKK.A	931.97	253.11	3.68	0.27
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.HWGGNVLGPK#.S	758.55	181.46	4.18	0.24
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.K#VAPAPAVVK#.K	225.19	85.73	2.63	0.38
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.K#VVNPLFEK#.R	775.09	215.35	3.60	0.28
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.LK#VPPAINQFTQALDR@.Q	1209.56	270.77	4.47	0.22
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.NFGIGQDIQPK#.R	1156.50	286.29	4.04	0.25
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.QTATQLLK#.L	774.05	213.74	3.62	0.28
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.R@HWGGNVLGPK#.S	114.14	38.60	2.96	0.34
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.RPPVLR.A	854.27	214.54	3.98	0.25
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.VPPAINQFTQALDR@.Q	242.95	71.66	3.39	0.29
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.VVNPLFEK#.R	254.09	71.15	3.57	0.28
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.AGVNTVTTLVENK#.K	22.50	12.20	1.84	0.54
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.NFGIGQDIQPK#.R	17.37	5.69	3.05	0.33
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.AGVNTVTTLVENK#.K	121.13	19.40	6.24	0.16
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.AGVNTVTTLVENK#K#.A	82.42	16.71	4.93	0.20
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.HWGGNVLGPK#.S	55.91	16.21	3.45	0.29
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.K#VAPAPAVVK#.K	28.53	4.52	6.32	0.16
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.LK#VPPAINQFTQALDR@.Q	120.70	24.76	4.87	0.21
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.NFGIGQDIQPK#.R	110.34	26.96	4.09	0.24
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.VVNPLFEK#.R	34.01	9.72	3.50	0.29
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.AGVNTVTTLVENK#.K	109.58	17.49	6.26	0.16
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.HWGGNVLGPK#.S	73.13	15.38	4.75	0.21
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	R.LK#VPPAINQFTQALDR@.Q	133.74	27.89	4.80	0.21
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.NFGIGQDIQPK#.R	114.68	23.51	4.88	0.20
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.VPPAINQFTQALDR@.Q	16.58	2.89	5.74	0.17
P12970_RL7A_MOUSE	Rpl7a	60S ribosomal protein L7	K.VVNPLFEK#.R	44.15	10.90	4.05	0.25
Q9D8M4_RL7L_MOUSE	Rpl7l1	60S ribosomal protein L7	R.IEGVSLLVK#.S	13.66	5.63	2.43	0.41
Q9D8M4_RL7L_MOUSE	Rpl7l1	60S ribosomal protein L7	R.TVEPYVTWGFPNLK#.S	6.70	4.10	1.63	0.61
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.AVDFAER@.H	1176.02	256.80	4.58	0.22
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.AVVGVVAGGGR@.I	2424.23	545.79	4.44	0.23
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	K.DIIHDPGR@.G	404.32	98.48	4.11	0.24
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	K.GIVK#DIIHDPGR@.G	264.27	57.25	4.62	0.22
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.IDK#PILK#.A	481.96	116.07	4.15	0.24
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.K#GAGSVFR@.A	348.34	59.40	5.86	0.17
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.K#VGLIAAR@.R	535.57	103.90	5.15	0.19
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	K.K#VISSANR@.A	59.25	16.76	3.53	0.28
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	K.VGLIAAR@.R	651.08	125.50	5.19	0.19
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.VK#LPSGSK#K#.V	28.06	18.05	1.55	0.64
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.AVDFAER@.H	187.40	57.00	3.29	0.30
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.AVVGVVAGGGR@.I	345.57	114.15	3.03	0.33
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	K.DIIHDPGR@.G	31.64	15.93	1.99	0.50
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.IDK#PILK#.A	59.30	36.53	1.62	0.62
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.K#GAGSVFR@.A	49.19	18.66	2.64	0.38
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.K#VGLIAAR@.R	111.79	27.45	4.07	0.25
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	K.VGLIAAR@.R	50.58	9.44	5.36	0.19
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.AVDFAER@.H	53.23	14.22	3.74	0.27
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.AVVGVVAGGGR@.I	136.98	25.50	5.37	0.19
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	K.DIIHDPGR@.G	25.98	7.40	3.51	0.28

P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.AVDFAER@.H	34.64	8.44	4.11	0.24
P62918_RL8_MOUSE	Rpl8	60S ribosomal protein L8	R.AVVGVVAGGGR@.I	71.53	10.84	6.60	0.15
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.DELILEGNDIELVSNSAALIQQATTVK#.N	10.98	57.18	0.19	5.21
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.DFNHINVELSLLGK#.K	13.17	4.24	3.10	0.32
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.FLDGIYVSEK#.G	53.89	15.42	3.50	0.29
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.SVYAHFPINVVIQENGSLVEIR@.N	11.25	2.21	5.09	0.20
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.TILSNQTVDIPENVEITLK#.G	23.19	5.51	4.21	0.24
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.DELILEGNDIELVSNSAALIQQATTVK#.N	35.49	10.52	3.37	0.30
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.DFNHINVELSLLGK#.K	180.31	56.53	3.19	0.31
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.DFNHINVELSLLGK#K#.K	14.04	4.79	2.93	0.34
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.FLDGIYVSEK#.G	539.57	178.53	3.02	0.33
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.GVTLGFR@.Y	295.84	85.50	3.46	0.29
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.K#FLDGIYVSEK#.G	209.51	66.52	3.15	0.32
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.KFLDGIYVSEK.G	115.43	36.54	3.16	0.32
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	-.M*K#TILSNQTVDIPENVEITLK#.G	43.64	8.94	4.88	0.20
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.R@DFNHINVELSLLGK#.K	27.98	5.89	4.75	0.21
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.SVYAHFPINVVIQENGSLVEIR@.N	71.73	22.47	3.19	0.31
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.TILSNQTVDIPENVEITLK#.G	164.77	56.99	2.89	0.35
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.DELILEGNDIELVSNSAALIQQATTVK#.N	8.09	3.73	2.17	0.46
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.DFNHINVELSLLGK#.K	24.73	4.18	5.92	0.17
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.FLDGIYVSEK#.G	40.32	9.56	4.22	0.24
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.SVYAHFPINVVIQENGSLVEIR@.N	14.44	6.51	2.22	0.45
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.DFNHINVELSLLGK#.K	17.39	3.40	5.12	0.20
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.FLDGIYVSEK#.G	67.00	12.94	5.18	0.19
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.GVTLGFR@.Y	43.14	6.21	6.95	0.14
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	R.SVYAHFPINVVIQENGSLVEIR@.N	10.57	1.91	5.54	0.18
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.TILSNQTVDIPENVEITLK#.G	34.55	7.56	4.57	0.22
P51410_RL9_MOUSE	Rpl9	60S ribosomal protein L9	K.TILSNQTVDIPENVEITLK#.G	38.47	6.64	5.79	0.17
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AEAK#EESEESDEDM*GFGLFD.-	120.94	28.09	4.31	0.23
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AEAK#EESEESDEDMGFGLFD.-	15.20	2.71	5.61	0.18
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#.A	1029.88	326.02	3.16	0.32
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#AEAK#.E	67.78	25.70	2.64	0.38
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AVVLM*GK#.N	195.98	88.71	2.21	0.45
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AVVLMGK#.N	31.09	9.60	3.24	0.31
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.DMLLANK#VPAAAR@.A	8.07	2.81	2.87	0.35
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.EDLTEIR@.D	59.20	24.49	2.42	0.41
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.EDLTEIR@DM*LLANK#.V	101.19	32.09	3.15	0.32
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.EESEESDEDM*GFGLFD.-	37.40	37.40	1.00	1.00
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GHLENNPALEK#.L	611.32	206.42	2.96	0.34
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GNVGFVFTK#.E	449.44	164.63	2.73	0.37
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GNVGFVFTK#EDLTEIR@.D	170.80	48.84	3.50	0.29
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GNVGFVFTKEDLTEIRDM*LLANK.V	29.32	9.78	3.00	0.33
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GTIEILSDVQLIK#.T	915.28	263.56	3.47	0.29
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.IIQLLDDYPK#.C	1025.16	280.36	3.66	0.27
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.QM*QQIR@.M	88.63	30.50	2.91	0.34
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.TSFFQALGITTK#.I	898.50	282.06	3.19	0.31
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#.A	24.54	16.14	1.52	0.66
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GTIEILSDVQLIK#.T	35.01	13.83	2.53	0.40
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.TSFFQALGITTK#.I	50.22	19.40	2.59	0.39
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AEAK#EESEESDEDM*GFGLFD.-	22.30	4.90	4.55	0.22
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#.A	205.27	54.64	3.76	0.27
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GHLENNPALEK#.L	110.27	30.56	3.61	0.28
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GNVGFVFTK#.E	98.49	25.16	3.91	0.26
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GNVGFVFTK#EDLTEIR@.D	13.70	6.60	2.08	0.48
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GTIEILSDVQLIK#.T	171.89	38.10	4.51	0.22
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.IIQLLDDYPK#.C	237.55	56.89	4.18	0.24
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AEAK#EESEESDEDM*GFGLFD.-	21.11	3.58	5.90	0.17
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#.A	208.59	50.41	4.14	0.24
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.EDLTEIR@.D	43.87	10.36	4.24	0.24
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.EDLTEIR@DM*LLANK#.V	27.10	5.29	5.12	0.20
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.EESEESDEDM*GFGLFD.-	10.66	10.66	1.00	1.00
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GHLENNPALEK#.L	232.04	45.39	5.11	0.20
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GNVGFVFTK#.E	98.40	17.81	5.53	0.18
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GNVGFVFTK#EDLTEIR@.D	24.05	4.26	5.64	0.18
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	R.GTIEILSDVQLIK#.T	200.01	37.70	5.31	0.19
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.IIQLLDDYPK#.C	257.69	43.24	5.96	0.17
P14869_RLA0_MOUSE	Rplp0	60S acidic ribosomal pro	K.TSFFQALGITTK#.I	235.52	45.67	5.16	0.19
P47955_RLA1_MOUSE	Rplp1	60S acidic ribosomal pro	K.AAGVSVEPFWPGLFAK#.A	115.64	38.44	3.01	0.33
P47955_RLA1_MOUSE	Rplp1	60S acidic ribosomal pro	K.K#EESEESEDDM*GFGLFD.-	31.30	6.21	5.04	0.20
P47955_RLA1_MOUSE	Rplp1	60S acidic ribosomal pro	K.AAGVSVEPFWPGLFAK#.A	2608.42	677.09	3.85	0.26
P47955_RLA1_MOUSE	Rplp1	60S acidic ribosomal pro	K.K#EESEESEDDM*GFGLFD.-	611.02	135.07	4.52	0.22
P47955_RLA1_MOUSE	Rplp1	60S acidic ribosomal pro	K.K#EESEESEDDMGFGLFD.-	61.78	15.06	4.10	0.24
P47955_RLA1_MOUSE	Rplp1	60S acidic ribosomal pro	K.AAGVSVEPFWPGLFAK#.A	22.37	7.83	2.86	0.35
P47955_RLA1_MOUSE	Rplp1	60S acidic ribosomal pro	K.AAGVSVEPFWPGLFAK#.A	17.56	3.99	4.41	0.23
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.NIEDVIAQGVGK#.L	8.78	3.74	2.35	0.43
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.ILDSVGIEADDDR@.L	65.08	19.34	3.36	0.30
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.ILDSVGIEADDDR@LNK#.V	2494.64	701.33	3.56	0.28
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.ILDSVGIEADDDR@LNK#.V	178.63	47.43	3.77	0.27
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.K#EESEESDDDM*GFGLFD.-	480.07	109.23	4.40	0.23
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.K#EESEESDDDMGFGLFD.-	14.48	3.20	4.52	0.22
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.K#ILDSVGIEADDDR@LNK#.V	365.45	123.13	2.97	0.34
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK#.K	1017.18	310.56	3.28	0.31
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK#.K	38.66	12.50	3.09	0.32
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK#K#.D	145.28	42.63	3.41	0.29
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK#K#DEK#.K	625.94	164.83	3.80	0.26
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	-.M*R@YVASYLLAALGGNSSPSAK#.D	175.66	48.89	3.59	0.28
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	K.NIEDVIAQGVGK#.L	3227.08	834.28	3.87	0.26
P99027_RLA2_MOUSE	Rplp2	60S acidic ribosomal pro	R.YVASYLLAALGGNSSPSAK#.D	593.09	173.01	3.43	0.29
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	R.APDELHYTYLDTFGR@PVIVAYK#.K	18.07	9.88	1.83	0.55
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	R.ASSFVLALEPELESR.L	19.63	17.85	1.10	0.91
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	R.FPLFGGWK#.T	15.80	9.62	1.64	0.61
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	R.FVDHVFDEQVIDSLTVK#.I	25.27	16.85	1.50	0.67
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	R.FVDHVFDEQVIDSLTVK#.I	2.59	1.85	1.40	0.71
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	R.HFDETVNR@.Y	20.85	13.87	1.50	0.67
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	K.IDHILDAL.-	19.71	19.71	1.00	1.00
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	K.NLVEQHIQDIVVHYTFNK#.V	17.82	18.01	0.99	1.01
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	K.VTAEVVLVHPGGGSTSR@.A	17.70	12.08	1.46	0.68
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	R.ASSFVLALEPELESR@.L	13.33	7.49	1.78	0.56
Q91YQ5_RPN1_MOUSE	Rpn1	Dolichyl-diphosphooligc	K.VTAEVVLVHPGGGSTSR@.A	11.84	6.34	1.87	0.54
Q9DBG6_RPN2_MOUSE	Rpn2	Dolichyl-diphosphooligc	R.LGKEETVLATVQALQTASHLSQQADLR.N	30.42	15.47	1.97	0.51
Q9DBG6_RPN2_MOUSE	Rpn2	Dolichyl-diphosphooligc	R.LQVSNVLSQPLAQAAVK#.L	14.63	8.06	1.81	0.55
Q9DBG6_RPN2_MOUSE	Rpn2	Dolichyl-diphosphooligc	K.NFESLSEAFSVASAAAALSQNR.Y	16.82	14.50	1.16	0.86
Q9DBG6_RPN2_MOUSE	Rpn2	Dolichyl-diphosphooligc	R.NIVEEIEDLVAR@.L	46.04	31.66	1.45	0.69

Q9DBG6_RPN2_MOUSE	Rpn2	Dolichyl-diphosphooligc	K.TGQEVVFVAEPDNK#.N	11.32	10.23	1.11	0.90
Q9DBG6_RPN2_MOUSE	Rpn2	Dolichyl-diphosphooligc	R.YHVPVVVVPEGSTSDTQEQAILR@.L	21.24	14.11	1.51	0.66
Q9DBG6_RPN2_MOUSE	Rpn2	Dolichyl-diphosphooligc	R.YHVPVVVVPEGSTSDTQEQAILR@.L	5.01	4.14	1.21	0.83
Q99JH1_RP25L_MOUSE	Rpp25l	Ribonuclease P protein s	R.NLLGLALGR@.L	24.70	15.75	1.57	0.64
Q8VDS4_RPR1A_MOUSE	Rprd1a	Regulation of nuclear pre	K.DFAPVIVEAFK#.H	36.53	14.44	2.53	0.40
Q8VDS4_RPR1A_MOUSE	Rprd1a	Regulation of nuclear pre	R.IASLPVEVQEVSLLEK#.I	72.32	29.70	2.44	0.41
Q8VDS4_RPR1A_MOUSE	Rprd1a	Regulation of nuclear pre	R.IQSLPDLSR@.L	37.02	17.91	2.07	0.48
Q8VDS4_RPR1A_MOUSE	Rprd1a	Regulation of nuclear pre	R.K#LTFLYLANDVIQNSK#.R	26.12	16.25	1.61	0.62
Q8VDS4_RPR1A_MOUSE	Rprd1a	Regulation of nuclear pre	K.LTFLYLANDVIQNSK#.R	34.16	15.91	2.15	0.47
Q8VDS4_RPR1A_MOUSE	Rprd1a	Regulation of nuclear pre	R.M*LADFLR@.C	30.20	11.49	2.63	0.38
Q8VDS4_RPR1A_MOUSE	Rprd1a	Regulation of nuclear pre	R.SVYENDVLEQLK#.H	32.73	15.63	2.09	0.48
Q8VDS4_RPR1A_MOUSE	Rprd1a	Regulation of nuclear pre	R.VLSIWEER@.S	28.25	15.21	1.86	0.54
Q9CSU0_RPR1B_MOUSE	Rprd1b	Regulation of nuclear pre	K.ALQDLENAASGDATVR@.Q	39.91	14.66	2.72	0.37
Q9CSU0_RPR1B_MOUSE	Rprd1b	Regulation of nuclear pre	K.IASLPQEVQDVSLLEK#.I	34.10	11.98	2.85	0.35
Q9CSU0_RPR1B_MOUSE	Rprd1b	Regulation of nuclear pre	R.LAAELEDR@.R	28.48	19.53	1.46	0.69
Q9CSU0_RPR1B_MOUSE	Rprd1b	Regulation of nuclear pre	R.LLNIWQER@.S	36.67	11.87	3.09	0.32
Q9CSU0_RPR1B_MOUSE	Rprd1b	Regulation of nuclear pre	R.M*LVEYTQNQK#.E	33.69	13.36	2.52	0.40
Q9CSU0_RPR1B_MOUSE	Rprd1b	Regulation of nuclear pre	R.SVYGGEFIQQLK#.L	30.33	21.87	1.39	0.72
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.APQFQESVTSFR@.S	9.49	1.91	4.96	0.20
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.ASSSSASSAGALESSLDR@.K	15.94	5.83	2.74	0.37
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.ASVGQSPVLPSTTFK#.L	21.02	6.43	3.27	0.31
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.ESFADVLPEAAALVK#.D	17.75	8.52	2.08	0.48
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.GPTSTSVDSIDGTPVR@DER@.S	34.00	15.78	2.15	0.46
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.IISPGSSTPSSTR@.S	7.65	2.24	3.42	0.29
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.ISSILSSLTSVM*K#.N	27.11	7.85	3.45	0.29
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.ISSILSSLTSVMK#.N	50.53	9.25	5.46	0.18
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.LSDATEYQPILSSYNHR@.A	17.88	7.85	2.28	0.44
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.NGPSLTEALENAGIFYEAQYK#.E	12.26	3.19	3.84	0.26
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.NLLSSTQSFIPK#.S	29.15	9.29	3.14	0.32
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.NTGVSSASR@PSPGIPTSPSNLSSGLK#.T	17.13	4.16	4.11	0.24
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.SEDQIELK#.E	26.19	5.83	4.50	0.22
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.SQALIEELLM*YK#.R	30.61	5.37	5.70	0.18
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.TPAPATTPSHNPLANILSK#.V	20.03	10.08	1.99	0.50
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.VEITPESILSALSK#.T	49.20	16.16	3.05	0.33
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.APQFQESVTSFR@.S	13.46	5.30	2.54	0.39
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.ASVGQSPVLPSTTFK#.L	18.89	6.86	2.75	0.36
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.EAPTHLPSVDLSNPFTK#.E	25.33	7.05	3.60	0.28
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.ESFADVLPEAAALVK#.D	20.35	7.54	2.70	0.37
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.GPTSTSVDSIDGTPVR@DER@.S	29.03	16.40	1.77	0.56
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.IISPGSSTPSSTR@.S	8.87	3.96	2.24	0.45
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.ISSILSSLTSVM*K#.N	24.50	7.71	3.18	0.31
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.LSSPPGLFGAFNIR@.G	12.69	3.75	3.39	0.30
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.NGPSLTEALENAGIFYEAQYK#.E	12.40	4.73	2.62	0.38
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.NTGVSSASR@PSPGIPTSPSNLSSGLK#.T	13.40	2.81	4.77	0.21
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.NVYPEDM*IVALR@.E	14.45	2.53	5.71	0.18
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.SIFSSQSTLAAPAGHPPTSGVEK#.V	17.58	6.01	2.92	0.34
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	R.SQALIEELLM*YK#.R	20.21	6.55	3.08	0.32
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.TPAPATTPSHNPLANILSK#.V	8.95	7.28	1.23	0.81
Q6NXI6_RPRD2_MOUSE	Rprd2	Regulation of nuclear pre	K.VEITPESILSALSK#.T	46.75	10.32	4.53	0.22
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	R.IAIYELLFK#.E	23.90	8.20	2.91	0.34
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	K.AEAGAGSATEFQFR@.G	183.61	69.68	2.64	0.38
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	R.DYLHLPPEIVPATLR@.R	95.29	39.57	2.41	0.42
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	R.DYLHLPPEIVPATLR@R@.S	15.16	7.59	2.00	0.50
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	R.HFYWYLTNEGIQYLR@.D	23.90	11.29	2.12	0.47
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	K.HPELADK#.N	53.53	28.72	1.86	0.54
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	K.HPELADK#NVPNLHVM*K#.A	2.33	2.91	0.80	1.25
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	R.IAIYELLFK#.E	518.61	202.14	2.57	0.39
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	K.K#AEAGAGSATEFQFR@.G	181.60	63.28	2.87	0.35
P63325_RS10_MOUSE	Rps10	40S ribosomal protein S1	K.NVPNLHVM*K#.A	37.85	14.22	2.66	0.38
P62281_RS11_MOUSE	Rps11	40S ribosomal protein S1	R.DYLHYIR@.K	24.52	6.24	3.93	0.25
P62281_RS11_MOUSE	Rps11	40S ribosomal protein S1	K.EAIEGTYIDK#.K	5.99	2.55	2.35	0.43
P62281_RS11_MOUSE	Rps11	40S ribosomal protein S1	K.EAIEGTYIDK#K#.C	9.53	3.85	2.48	0.40
P62281_RS11_MOUSE	Rps11	40S ribosomal protein S1	R.DYLHYIR@.K	124.43	44.28	2.81	0.36
P62281_RS11_MOUSE	Rps11	40S ribosomal protein S1	K.EAIEGTYIDK#K#.C	105.32	33.06	3.19	0.31
P62281_RS11_MOUSE	Rps11	40S ribosomal protein S1	R.ILSGVVTK#.M	381.05	144.02	2.65	0.38
P62281_RS11_MOUSE	Rps11	40S ribosomal protein S1	K.EAIEGTYIDK#.K	9.59	2.49	3.85	0.26
P63323_RS12_MOUSE	Rps12	40S ribosomal protein S1	K.DVIEEYFK#.C	85.74	47.04	1.82	0.55
P63323_RS12_MOUSE	Rps12	40S ribosomal protein S1	K.ESQAKDVIEEYFK.C	6.16	4.10	1.50	0.67
P63323_RS12_MOUSE	Rps12	40S ribosomal protein S1	K.TALIHDGLAR@.G	20.50	13.78	1.49	0.67
P62301_RS13_MOUSE	Rps13	40S ribosomal protein S1	R.DSHGVAQVR@.F	110.44	36.70	3.01	0.33
P62301_RS13_MOUSE	Rps13	40S ribosomal protein S1	K.GLSQSALPYR@.R	421.27	151.87	2.77	0.36
P62301_RS13_MOUSE	Rps13	40S ribosomal protein S1	K.GLTPSQIGVILR@.D	232.72	92.31	2.52	0.40
P62301_RS13_MOUSE	Rps13	40S ribosomal protein S1	K.K#GLTPSQIGVILR@.D	160.77	68.02	2.36	0.42
P62301_RS13_MOUSE	Rps13	40S ribosomal protein S1	K.KGLTPSQIGVILR.D	39.37	12.75	3.09	0.32
P62301_RS13_MOUSE	Rps13	40S ribosomal protein S1	R.LILIESR.I	786.78	277.68	2.83	0.35
P62301_RS13_MOUSE	Rps13	40S ribosomal protein S1	K.R@VLPPNWK#.Y	11.23	5.42	2.07	0.48
P62301_RS13_MOUSE	Rps13	40S ribosomal protein S1	K.SK#GLAPDLPEDLYHLIK#.K	66.24	27.51	2.41	0.42
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	K.ADR@DESSPYAAM*LAAQDVAQR@.C	8.16	4.89	1.67	0.60
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	R.IEDVTPIPSDSTR@.R	21.77	7.93	2.74	0.36
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	K.ADR@DESSPYAAM*LAAQDVAQR@.C	101.97	35.44	2.88	0.35
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	K.ADR@DESSPYAAMLAAQDVAQR@.C	27.41	7.84	3.50	0.29
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	R.DESSPYAAM*LAAQDVAQR@.C	5.35	3.04	1.76	0.57
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	R.IEDVTPIPSDSTR.R	238.69	99.44	2.40	0.42
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	R.IEDVTPIPSDSTRR.K	415.84	152.94	2.72	0.37
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	K.IGRIEDVTPIPSDSTR.R	54.83	20.14	2.72	0.37
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	K.IGR@IEDVTPIPSDSTR@.R	2.56	2.10	1.22	0.82
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	K.IGR@IEDVTPIPSDSTR@R@.K	14.46	5.17	2.80	0.36
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	R.TK#TPGPGAQSALR@.A	305.64	108.35	2.82	0.35
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	K.TPGPGAQSALR@.A	582.10	233.64	2.49	0.40
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	K.VKADRDESSPYAAM*LAAQDVAQR.C	82.90	23.76	3.49	0.29
P62264_RS14_MOUSE	Rps14	40S ribosomal protein S1	K.TPGPGAQSALR@.A	18.64	6.94	2.68	0.37
P62843_RS15_MOUSE	Rps15	40S ribosomal protein S1	R.DMIILPEM*VGSM*VGVYNGK#.T	3.78	2.29	1.65	0.61
P62843_RS15_MOUSE	Rps15	40S ribosomal protein S1	K.EAPPM*EK#PEVVK#.T	42.57	12.17	3.50	0.29
P62843_RS15_MOUSE	Rps15	40S ribosomal protein S1	K.HGR@PGIGATHSSR@.F	5.40	2.57	2.10	0.48
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.FDVQLK#DLEK#.W	24.00	8.45	2.84	0.35
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.HGYIGEFEIIDDHR@.A	84.54	29.90	2.83	0.35
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.IVVNLTGR.L	125.65	52.95	2.37	0.42
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.M*NVLADALK#.S	71.67	31.25	2.29	0.44
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.QFGFIVLTTSAGIM*DHEEAR@.R	18.21	8.27	2.20	0.45
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.QFGFIVLTTSAGIMDHEEAR@.R	4.42	3.55	1.24	0.80
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.WQNNLLPSR@.Q	40.64	18.54	2.19	0.46
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.FDVQLK#DLEK#.W	46.61	16.32	2.86	0.35
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.HGYIGEFEIIDDHR@.A	78.40	24.10	3.25	0.31

P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.IVVNLTGR@.L	79.81	31.70	2.52	0.40
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.M*NVLADALK#.S	128.28	48.75	2.63	0.38
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.QFGFIVLTTSAGIMDHEEAR@.R	8.10	3.76	2.15	0.46
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.WQNNLLPSR@.Q	57.47	21.50	2.67	0.37
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.FDVQLK#.D	41.96	16.08	2.61	0.38
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.HGYIGEFEIIDDHR@.A	57.89	20.92	2.77	0.36
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.IVVNLTGR@.L	81.34	26.81	3.03	0.33
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.M*NVLADALK#.S	50.26	17.79	2.83	0.35
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.QFGFIVLTTSAGIM*DHEEAR@.R	25.52	6.54	3.90	0.26
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.WQNNLLPSR@.Q	24.33	16.25	1.50	0.67
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.FDVQLK#.D	64.31	11.53	5.58	0.18
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.HGYIGEFEIIDDHR@.A	55.64	15.61	3.56	0.28
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.IVVNLTGR@.L	83.16	24.09	3.45	0.29
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.M*NVLADALK#.S	54.77	16.60	3.30	0.30
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	R.QFGFIVLTTSAGIM*DHEEAR@.R	24.89	4.85	5.13	0.19
P62245_RS15A_MOUSE	Rps15a	40S ribosomal protein S1	K.WQNNLLPSR@.Q	26.22	53.40	0.49	2.04
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.ALVAYYQK#.Y	32.52	14.81	2.20	0.46
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.EIKDILIQYDR.T	25.31	8.89	2.85	0.35
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	R.FAGVDIR@.V	47.89	17.36	2.76	0.36
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.LLEPVLLLGK#.E	90.91	37.23	2.44	0.41
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	R.TLLVADPR@.R	32.87	11.95	2.75	0.36
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.ALVAYYQK#.Y	283.48	116.39	2.44	0.41
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.DILIQYDR@.T	74.84	25.98	2.88	0.35
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.EIKDILIQYDR.T	276.73	103.57	2.67	0.37
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	R.FAGVDIR@.V	479.00	168.32	2.85	0.35
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.GPLQSVQVFGR@.K	331.53	126.72	2.62	0.38
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.LLEPVLLLGK#.E	1057.99	444.77	2.38	0.42
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	R.TLLVADPR@.R	377.19	158.36	2.38	0.42
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	R.FAGVDIR@.V	28.25	7.91	3.57	0.28
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.LLEPVLLLGK#.E	86.72	23.87	3.63	0.28
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	R.TLLVADPR@.R	27.60	11.53	2.39	0.42
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.ALVAYYQK#.Y	15.80	4.24	3.73	0.27
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	R.FAGVDIR@.V	41.78	15.75	2.65	0.38
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.GGGHVAQIYAIR@.Q	20.84	3.16	6.60	0.15
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	K.LLEPVLLLGK#.E	144.10	30.86	4.67	0.21
P14131_RS16_MOUSE	Rps16	40S ribosomal protein S1	R.TLLVADPR@.R	37.70	13.19	2.86	0.35
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	K.LLDFGSLSNLQVTQPTVGM*NFK#.T	25.65	11.64	2.20	0.45
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	K.LLDFGSLSNLQVTQPTVGM*NFK#.T	2.92	1.89	1.55	0.65
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	R.DNYVPEVSALDQEIIEVDPDTK#.E	21.29	7.55	2.82	0.35
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	R.DNYVPEVSALDQEIIEVDPDTK#.E	8.18	3.54	2.31	0.43
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	K.LLDFGSLSNLQVTQPTVGM*NFK#.T	373.96	111.96	3.34	0.30
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	K.LLDFGSLSNLQVTQPTVGMNFK#.T	20.56	7.04	2.92	0.34
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	R.R@DNYVPEVSALDQEIIEVDPDTK#.E	10.65	1.90	5.61	0.18
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	R.RDNYVPEVSALDQEIIEVDPDTKEM*LK.L	23.38	6.86	3.41	0.29
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	K.LLDFGSLSNLQVTQPTVGM*NFK#.T	19.43	9.65	2.01	0.50
P63276_RS17_MOUSE	Rps17	40S ribosomal protein S1	K.LLDFGSLSNLQVTQPTVGM*NFK#.T	17.21	6.50	2.65	0.38
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	K.ADIDLTK#.R	41.40	14.85	2.79	0.36
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	K.ADIDLTK#R@.A	36.82	10.99	3.35	0.30
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	R.AGELTEDEVER@.V	497.17	162.77	3.05	0.33
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	R.HFWGLR@.V	106.40	29.62	3.59	0.28
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	K.IAFAITAIK#.G	321.99	112.26	2.87	0.35
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	K.IPDWFLNR@.Q	1046.04	327.58	3.19	0.31
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	R.K#ADIDLTK#.R	170.64	74.13	2.30	0.43
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	R.K#IAFAITAIK#.G	69.91	21.74	3.22	0.31
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	R.KIAFAITAIK.G	26.82	8.97	2.99	0.33
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	K.LREDLER.L	246.44	84.45	2.92	0.34
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	K.R@AGELTEDEVER@.V	77.35	24.64	3.14	0.32
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	K.RAGELTEDEVER.V	176.84	54.32	3.26	0.31
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	R.VITIM*QNPR@.Q	456.19	151.44	3.01	0.33
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	R.VITIMQNPR@.Q	38.81	14.42	2.69	0.37
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	R.VLNTNIDGR@.R	462.18	137.03	3.37	0.30
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	R.YAHVVLR@.K	65.97	19.05	3.46	0.29
P62270_RS18_MOUSE	Rps18	40S ribosomal protein S1	K.YSQVLANGLDNK#.L	101.96	28.62	3.56	0.28
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	R.ALAAFLK#.K	229.06	93.70	2.44	0.41
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	R.ALAAFLK#K#.S	71.26	23.04	3.09	0.32
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	K.DVNQQEFVR@.A	582.38	202.32	2.88	0.35
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	K.ELAPYDENWFYTR@.A	51.02	16.02	3.19	0.31
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	R.GGAGVGSM*TK#.I	23.87	9.53	2.51	0.40
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	K.HK#ELAPYDENWFYTR@.A	76.93	29.69	2.59	0.39
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	R.HLYLR@.G	188.26	57.74	3.26	0.31
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	R.IAGQVAAANK#.K	57.66	25.57	2.26	0.44
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	K.LK#VPEWVDTVK#.L	365.92	129.33	2.83	0.35
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	R.R@VLQALEGLK#.M	557.10	191.51	2.91	0.34
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	R.VLQALEGLK#.M	502.68	207.95	2.42	0.41
Q9CZX8_RS19_MOUSE	Rps19	40S ribosomal protein S1	K.VPEWVDTVK#.L	116.60	50.16	2.32	0.43
Q8C6B9_AROS_MOUSE	Rps19bp1	Active regulator of SIRT1	K.AEGTVFTEEDFQK#.F	7.33	3.95	1.86	0.54
Q8C6B9_AROS_MOUSE	Rps19bp1	Active regulator of SIRT1	R.GLELLAASEAPR@.A	23.29	11.25	2.07	0.48
Q8C6B9_AROS_MOUSE	Rps19bp1	Active regulator of SIRT1	K.SALAEYQK#.R	9.64	4.50	2.14	0.47
Q8C6B9_AROS_MOUSE	Rps19bp1	Active regulator of SIRT1	R.STVPESVTQQILQQNQGR@.K	20.31	12.58	1.61	0.62
Q8C6B9_AROS_MOUSE	Rps19bp1	Active regulator of SIRT1	R.STVPESVTQQILQQNQGR.K	8.77	6.87	1.28	0.78
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.ATFDAISK#.T	356.12	124.07	2.87	0.35
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.EVATAIR@.G	236.94	73.41	3.23	0.31
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	R.GTGIVSAPVPK#.K	433.96	180.03	2.41	0.41
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.LSIVPVR@.R	134.60	52.05	2.59	0.39
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.LSIVPVR@R@.G	89.98	35.32	2.55	0.39
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.SLEEIYLFSLPIK#.E	509.23	193.19	2.64	0.38
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.SPYQEFTDHLVK#.T	285.68	103.30	2.77	0.36
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.TYSYLTPDLWK#.E	242.58	95.44	2.54	0.39
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.ATFDAISK#.T	46.63	10.49	4.44	0.23
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	R.GTGIVSAPVPK#.K	55.67	14.52	3.83	0.26
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.LSIVPVR@.R	27.64	7.47	3.70	0.27
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.SLEEIYLFSLPIK#.E	74.59	21.21	3.52	0.28
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.SPYQEFTDHLVK#.T	53.90	15.22	3.54	0.28
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.TYSYLTPDLWK#.E	31.94	12.48	2.56	0.39
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.ATFDAISK#.T	74.34	16.55	4.49	0.22
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	R.GTGIVSAPVPK#.K	64.07	12.73	5.03	0.20
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.LSIVPVR@.R	23.85	6.32	3.78	0.26
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.SLEEIYLFSLPIK#.E	57.94	10.64	5.44	0.18
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.SPYQEFTDHLVK#.T	66.61	15.60	4.27	0.23
P25444_RS2_MOUSE	Rps2	40S ribosomal protein S2	K.TYSYLTPDLWK#.E	34.07	9.61	3.54	0.28
P60867_RS20_MOUSE	Rps20	40S ribosomal protein S2	K.DTGK#TPVEPEVAIHR@.I	78.37	35.49	2.21	0.45
P60867_RS20_MOUSE	Rps20	40S ribosomal protein S2	K.TPVEPEVAIHR@.I	63.64	27.12	2.35	0.43
Q9CQR2_RS21_MOUSE	Rps21	40S ribosomal protein S2	K.DHASIQM*NVAEVDR@.T	8.78	4.96	1.77	0.57

Q9CQR2_RS21_MOUSE	Rps21	40S ribosomal protein S2	R.M*GESDDSILR.L	52.77	35.73	1.48	0.68
P62267_RS23_MOUSE	Rps23	40S ribosomal protein S2	K.VANVSLLALYK#.G	81.84	30.05	2.72	0.37
P62267_RS23_MOUSE	Rps23	40S ribosomal protein S2	K.ANPFGGASHAK#.G	143.04	57.09	2.51	0.40
P62267_RS23_MOUSE	Rps23	40S ribosomal protein S2	K.GHAVGDIPGVR@.F	41.61	34.61	1.20	0.83
P62267_RS23_MOUSE	Rps23	40S ribosomal protein S2	R.K#GHAVGDIPGVR@.F	279.19	83.29	3.35	0.30
P62267_RS23_MOUSE	Rps23	40S ribosomal protein S2	K.VANVSLLALYK#.G	665.02	254.42	2.61	0.38
P62267_RS23_MOUSE	Rps23	40S ribosomal protein S2	R.K#GHAVGDIPGVR@.F	16.57	5.64	2.94	0.34
P62267_RS23_MOUSE	Rps23	40S ribosomal protein S2	K.VANVSLLALYK#.G	29.78	9.68	3.08	0.32
P62267_RS23_MOUSE	Rps23	40S ribosomal protein S2	K.VANVSLLALYK#.G	24.45	7.89	3.10	0.32
P62849_RS24_MOUSE	Rps24	40S ribosomal protein S2	R.HGLYEK#.K	82.12	25.89	3.17	0.32
P62849_RS24_MOUSE	Rps24	40S ribosomal protein S2	R.K#QM*VIDVLHPGK#.A	47.98	13.03	3.68	0.27
P62849_RS24_MOUSE	Rps24	40S ribosomal protein S2	R.K#QMVIDVLHPGK#.A	15.18	6.63	2.29	0.44
P62849_RS24_MOUSE	Rps24	40S ribosomal protein S2	K.TTGFGM*IYDSLDYAK#.K	305.27	79.55	3.84	0.26
P62849_RS24_MOUSE	Rps24	40S ribosomal protein S2	K.TTGFGMIYDSLDYAK#.K	65.35	23.19	2.82	0.35
P62849_RS24_MOUSE	Rps24	40S ribosomal protein S2	K.TTPDVIFVFGFR@.T	136.25	38.94	3.50	0.29
P62852_RS25_MOUSE	Rps25	40S ribosomal protein S2	R.DK#LNNLVLFDK#.A	16.34	6.54	2.50	0.40
P62852_RS25_MOUSE	Rps25	40S ribosomal protein S2	K.LITPAVVSER@.L	59.79	25.62	2.33	0.43
P62852_RS25_MOUSE	Rps25	40S ribosomal protein S2	R.AALQELLSK#.G	661.23	203.96	3.24	0.31
P62852_RS25_MOUSE	Rps25	40S ribosomal protein S2	R.AQVIYTR@.N	184.88	60.65	3.05	0.33
P62852_RS25_MOUSE	Rps25	40S ribosomal protein S2	R.DKLNNLVLFDK.A	97.28	30.04	3.24	0.31
P62852_RS25_MOUSE	Rps25	40S ribosomal protein S2	K.LITPAVVSER@.L	545.37	182.12	2.99	0.33
P62852_RS25_MOUSE	Rps25	40S ribosomal protein S2	K.LNNLVLFDK#.A	77.76	33.57	2.32	0.43
P62852_RS25_MOUSE	Rps25	40S ribosomal protein S2	K.VR@DK#LNNLVLFDK#.A	28.54	6.01	4.75	0.21
P62855_RS26_MOUSE	Rps26	40S ribosomal protein S2	R.NIVEAAAVR@.D	85.50	26.80	3.19	0.31
P62855_RS26_MOUSE	Rps26	40S ribosomal protein S2	R.DISEASVFDAYVLPK#.L	135.04	38.39	3.52	0.28
P62855_RS26_MOUSE	Rps26	40S ribosomal protein S2	R.NIVEAAAVR@.D	538.25	168.16	3.20	0.31
P62855_RS26_MOUSE	Rps26	40S ribosomal protein S2	R.NIVEAAAVR@.D	58.57	16.40	3.57	0.28
P62855_RS26_MOUSE	Rps26	40S ribosomal protein S2	R.NIVEAAAVR@.D	83.90	18.14	4.63	0.22
Q6ZWY3_RS27L_MOUSE	Rps27l	40S ribosomal protein S2	R.LVQSPNSYFM*DVK#.C	13.55	4.15	3.26	0.31
Q6ZWY3_RS27L_MOUSE	Rps27l	40S ribosomal protein S2	R.DLLHPSLEEEK#K#K#.H	19.55	9.25	2.11	0.47
Q6ZWY3_RS27L_MOUSE	Rps27l	40S ribosomal protein S2	R.LVQSPNSYFM*DVK#.C	109.07	42.12	2.59	0.39
Q6ZWY3_RS27L_MOUSE	Rps27l	40S ribosomal protein S2	R.LVQSPNSYFMDVK#.C	18.50	5.07	3.65	0.27
Q6ZWY3_RS27L_MOUSE	Rps27l	40S ribosomal protein S2	R.LVQSPNSYFM*DVK#.C	14.74	6.40	2.30	0.43
Q6ZWY3_RS27L_MOUSE	Rps27l	40S ribosomal protein S2	R.LVQSPNSYFM*DVK#.C	21.74	6.93	3.14	0.32
P62858_RS28_MOUSE	Rps28	40S ribosomal protein S2	R.EGDVLTLLESER@.E	302.09	130.07	2.32	0.43
P62858_RS28_MOUSE	Rps28	40S ribosomal protein S2	R.VEFMDDTSR@.S	8.00	1.27	6.29	0.16
P62858_RS28_MOUSE	Rps28	40S ribosomal protein S2	R.VEFM*DDTSR.S	78.03	27.25	2.86	0.35
P62858_RS28_MOUSE	Rps28	40S ribosomal protein S2	R.EGDVLTLLESER@.E	26.62	7.52	3.54	0.28
P62274_RS29_MOUSE	Rps29	40S ribosomal protein S2	K.DIGFIK#LD.-	342.05	125.79	2.72	0.37
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.AELNEFLTR@.E	440.08	160.73	2.74	0.37
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.DEILPTTPISEQK#.G	351.81	137.07	2.57	0.39
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.ELAEDGYSGVEVR@.V	667.23	250.61	2.66	0.38
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.ELTAVVQK#.R	346.62	120.72	2.87	0.35
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.FGFPEGSVELYAEK#.V	401.90	157.74	2.55	0.39
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.FIM*ESGAK#.G	266.70	104.43	2.55	0.39
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.FVADGIFK#.A	300.14	117.85	2.55	0.39
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.FVADGIFK#AELNEFLTR@.E	20.52	8.35	2.46	0.41
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.FVDGLM*IHSGDPVNYYVDTAVR@.H	177.32	65.25	2.72	0.37
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.GGK#PEPPAM*PQPVPTA.-	318.83	141.88	2.25	0.44
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.GGK#PEPPAMPQPVPTA.-	104.15	47.27	2.20	0.45
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.IM*LPWDPSGK#.I	111.72	40.47	2.76	0.36
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.IR@ELTAVVQK#.R	88.57	33.44	2.65	0.38
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.IRELTAVVQK.R	159.86	56.69	2.82	0.35
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.K#FVADGIFK#.A	217.35	86.34	2.52	0.40
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.KPLPDHVSIVEPK.D	142.09	56.33	2.52	0.40
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.QGVLGIK#.V	299.94	122.33	2.45	0.41
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.R@FGFPEGSVELYAEK#.V	41.00	13.31	3.08	0.32
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.TEIIILATR@.T	637.12	214.98	2.96	0.34
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.TQNVLGEK#.G	588.46	236.85	2.48	0.40
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.AELNEFLTR@.E	29.80	14.26	2.09	0.48
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.ELAEDGYSGVEVR.V	24.32	12.18	2.00	0.50
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.FGFPEGSVELYAEK#.V	20.76	9.53	2.18	0.46
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.GGK#PEPPAM*PQPVPTA.-	16.33	6.02	2.71	0.37
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.K#PLPDHVSIVEPK#.D	12.01	4.05	2.97	0.34
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.TEIIILATR@.T	19.90	7.67	2.59	0.39
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.AELNEFLTR@.E	27.80	9.64	2.89	0.35
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.DEILPTTPISEQK#.G	21.28	7.16	2.97	0.34
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.ELAEDGYSGVEVR@.V	35.95	13.20	2.72	0.37
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.FGFPEGSVELYAEK#.V	24.46	7.01	3.49	0.29
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.FVDGLM*IHSGDPVNYYVDTAVR@.H	16.52	8.14	2.03	0.49
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.GGK#PEPPAM*PQPVPTA.-	22.14	8.47	2.61	0.38
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	K.K#PLPDHVSIVEPK#.D	8.39	5.56	1.51	0.66
P62908_RS3_MOUSE	Rps3	40S ribosomal protein S3	R.TEIIILATR@.T	26.75	12.79	2.09	0.48
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	R.ADGYEPPVQESV.-	153.79	153.79	1.00	1.00
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.APAM*FNIR@.N	448.78	143.94	3.12	0.32
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.APAMFNIR@.N	29.77	14.61	2.04	0.49
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.DWYDVK#.A	127.73	45.33	2.82	0.35
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	R.EVQTNDLK#.E	260.85	99.32	2.63	0.38
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	R.EVQTNDLKEVVNK.L	60.22	24.76	2.43	0.41
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.IASDGLK#.G	332.29	113.74	2.92	0.34
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.K#VVDPFSK#.K	17.50	8.75	2.00	0.50
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.M*M*EIM*TR.E	128.62	39.95	3.22	0.31
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.TSYAQHQQVR@.Q	43.67	14.44	3.02	0.33
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.TTDGYLLR@.L	422.22	143.40	2.94	0.34
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.VER@ADGYEPPVQESV.-	8.77	2.23	3.94	0.25
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	R.VFEVSLADLQNDEVAFR@.K	187.90	67.56	2.78	0.36
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	R.VFEVSLADLQNDEVAFR@.K	110.19	56.46	1.95	0.51
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	R.VFEVSLADLQNDEVAFRK.F	369.26	120.23	3.07	0.33
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.VVDPFSK#.K	299.89	120.42	2.49	0.40
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	R.ADGYEPPVQESV.-	18.19	18.19	1.00	1.00
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.APAM*FNIR@.N	23.65	9.10	2.60	0.38
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	R.VFEVSLADLQNDEVAFR@K#.F	29.97	6.75	4.44	0.23
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.APAM*FNIR@.N	27.51	4.11	6.69	0.15
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	K.LM*ELHGEGGSSGK#.A	5.38	3.17	1.69	0.59
P97351_RS3A_MOUSE	Rps3a	40S ribosomal protein S3	R.VFEVSLADLQNDEVAFR@.K	40.21	4.46	9.01	0.11
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.DANGNSFATR@.L	41.65	15.16	2.75	0.36
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.GNK#PWISLPR@.G	152.85	50.47	3.03	0.33
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.HPGSFDVVHVK#.D	136.01	49.30	2.76	0.36
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.IGVITNR@.E	1310.98	415.05	3.16	0.32
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.LIYDTK#.G	466.79	159.73	2.92	0.34
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.LSNIFVIGK#.G	624.56	213.00	2.93	0.34
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.LTIAEER@.D	359.53	130.46	2.76	0.36
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.TDITYPAGFM*DVISIDK#.T	80.28	32.01	2.51	0.40

P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.TDITYPAGFMDVISIDK#.T	56.88	21.63	2.63	0.38
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.TIR@YPDPLIK#.V	108.72	29.17	3.73	0.27
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.VNDTIQIDLETGK#.I	123.19	50.39	2.44	0.41
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.VNDTIQIDLETGK#ITDFIK#.F	57.91	29.45	1.97	0.51
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.VR@TDITYPAGFM*DVISIDK#.T	19.97	13.70	1.46	0.69
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.VR@TDITYPAGFMDVISIDK#.T	13.30	4.86	2.73	0.37
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.YALTGDEVK#.K	229.86	74.30	3.09	0.32
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.YALTGDEVK#K#.I	214.41	61.65	3.48	0.29
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.YPDPLIK#.V	126.09	26.43	4.77	0.21
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.DANGNSFATR@.L	23.67	13.56	1.75	0.57
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.GNK#PWISLPR@.G	48.59	24.90	1.95	0.51
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.HPGSFDVVHVK#.D	23.90	11.65	2.05	0.49
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.IGVITNR@.E	199.77	93.19	2.14	0.47
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.LSNIFVIGK#.G	237.48	141.70	1.68	0.60
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.LTIAEER@.D	133.26	64.94	2.05	0.49
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.TDITYPAGFM*DVISIDK#.T	28.91	13.87	2.08	0.48
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.TIR@YPDPLIK#.V	49.66	31.10	1.60	0.63
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.VNDTIQIDLETGK#.I	55.05	34.98	1.57	0.64
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.VNDTIQIDLETGK#ITDFIK#.F	61.56	32.37	1.90	0.53
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.VR@TDITYPAGFM*DVISIDK#.T	10.52	11.88	0.89	1.13
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.YPDPLIK#.V	31.90	21.95	1.45	0.69
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.GNK#PWISLPR@.G	20.72	5.81	3.57	0.28
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.HPGSFDVVHVK#.D	30.11	11.44	2.63	0.38
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.IGVITNR@.E	71.15	18.62	3.82	0.26
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.LSNIFVIGK#.G	49.84	15.80	3.15	0.32
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.LTIAEER@.D	49.51	14.71	3.37	0.30
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.TDITYPAGFM*DVISIDK#.T	8.81	3.05	2.89	0.35
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.IGVITNR@.E	43.97	11.36	3.87	0.26
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.LSNIFVIGK#.G	45.92	10.75	4.27	0.23
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	R.TDITYPAGFM*DVISIDK#.T	8.78	2.00	4.40	0.23
P62702_RS4X_MOUSE	Rps4x	40S ribosomal protein S4	K.VNDTIQIDLETGK#.I	8.46	2.64	3.21	0.31
P97461_RS5_MOUSE	Rps5	40S ribosomal protein S5	K.GSSNSYAIK#.K	19.88	7.64	2.60	0.38
P97461_RS5_MOUSE	Rps5	40S ribosomal protein S5	R.QAVDVSPLR@.R	18.17	9.76	1.86	0.54
P97461_RS5_MOUSE	Rps5	40S ribosomal protein S5	K.WSTDDVQINDISLQDYIAVK#.E	6.30	2.64	2.39	0.42
P97461_RS5_MOUSE	Rps5	40S ribosomal protein S5	K.GSSNSYAIK#.K	133.39	50.13	2.66	0.38
P97461_RS5_MOUSE	Rps5	40S ribosomal protein S5	R.QAVDVSPLR@.R	31.58	13.31	2.37	0.42
P97461_RS5_MOUSE	Rps5	40S ribosomal protein S5	K.WSTDDVQINDISLQDYIAVK#.E	20.11	9.09	2.21	0.45
P97461_RS5_MOUSE	Rps5	40S ribosomal protein S5	K.WSTDDVQINDISLQDYIAVK#.E	29.50	16.32	1.81	0.55
P97461_RS5_MOUSE	Rps5	40S ribosomal protein S5	R.QAVDVSPLR@.R	25.50	4.51	5.65	0.18
P97461_RS5_MOUSE	Rps5	40S ribosomal protein S5	K.WSTDDVQINDISLQDYIAVK#.E	10.04	2.17	4.63	0.22
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	K.DIPGLTDTTVPR@.R	529.27	127.69	4.15	0.24
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	K.GEK#DIPGLTDTTVPR@.R	21.16	6.90	3.07	0.33
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	K.K#GEK#DIPGLTDTTVPR@.R	122.31	21.97	5.57	0.18
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	R.K#LFNLSK#.E	88.71	23.52	3.77	0.27
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	K.LIEVDDER@.K	1012.25	222.65	4.55	0.22
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	K.LIEVDDER@K#.L	114.85	20.94	5.48	0.18
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	R.M*ATEVAADALGEEWK#.G	220.41	50.04	4.40	0.23
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	R.MATEVAADALGEEWK#.G	36.75	12.21	3.01	0.33
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	R.M*ATEVAADALGEEWK#GYVVR@.I	98.77	18.44	5.36	0.19
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	K.NK#EEAAEYAK#.L	119.20	28.51	4.18	0.24
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	R.M*ATEVAADALGEEWK#.G	12.31	3.38	3.65	0.27
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	K.DIPGLTDTTVPR@.R	13.39	3.69	3.63	0.28
P62754_RS6_MOUSE	Rps6	40S ribosomal protein S6	R.M*ATEVAADALGEEWK#.G	7.51	3.57	2.11	0.47
P18653_KS6A1_MOUSE	Rps6ka1	Ribosomal protein S6 kin	R.DLK#PENILLDEEGHIK#.L	10.92	3.53	3.09	0.32
P18653_KS6A1_MOUSE	Rps6ka1	Ribosomal protein S6 kin	K.LGM*PQFLSTEAQSLLR@.A	5.76	1.90	3.03	0.33
Q9Z2B9_KS6A4_MOUSE	Rps6ka4	Ribosomal protein S6 kin	R.IGPVAQDLLQR@.L	10.97	4.54	2.42	0.41
Q9Z1M4_KS6B2_MOUSE	Rps6kb2	Ribosomal protein S6 kin	R.IGGGLGDAADVQR@.H	8.90	14.51	0.61	1.63
P62082_RS7_MOUSE	Rps7	40S ribosomal protein S7	R.TLTAVHDAILEDLVFPSEIVGK#.R	19.81	9.84	2.01	0.50
P62082_RS7_MOUSE	Rps7	40S ribosomal protein S7	K.AIIIFVPVPQLK#.S	80.39	55.13	1.46	0.69
P62082_RS7_MOUSE	Rps7	40S ribosomal protein S7	K.HVVFIAQR.R	61.30	37.11	1.65	0.61
P62082_RS7_MOUSE	Rps7	40S ribosomal protein S7	K.IVKPNGEKPDEFESGISQALLELEM*NSDLK.A	23.65	16.27	1.45	0.69
P62082_RS7_MOUSE	Rps7	40S ribosomal protein S7	K.LTGK#DVNFEFPEFQL.-	14.44	7.90	1.83	0.55
P62082_RS7_MOUSE	Rps7	40S ribosomal protein S7	R.TLTAVHDAILEDLVFPSEIVGK#.R	124.41	68.42	1.82	0.55
P62082_RS7_MOUSE	Rps7	40S ribosomal protein S7	R.TLTAVHDAILEDLVFPSEIVGK#R@.I	34.93	17.83	1.96	0.51
P62082_RS7_MOUSE	Rps7	40S ribosomal protein S7	K.VETFSGVYK#.K	26.16	16.91	1.55	0.65
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.ADGYVLEGK#.E	537.97	133.69	4.02	0.25
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.ELEFYLR@.K	287.92	76.72	3.75	0.27
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.IIDVVYNASNNELVR@.T	297.15	70.48	4.22	0.24
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.ISSLLEEQFQQGK#.L	558.12	186.59	2.99	0.33
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.KYELGRPAANTK.I	9.94	2.56	3.89	0.26
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.LTPEEEEILNK#.K	828.01	270.37	3.06	0.33
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.QWYESHYALPLGR@.K	144.20	40.32	3.58	0.28
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.YELGR@PAANTK#.I	50.15	11.41	4.40	0.23
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.ADGYVLEGK#.E	106.32	27.54	3.86	0.26
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.ADGYVLEGK#ELEFYLR@.K	13.82	3.50	3.95	0.25
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.ELEFYLR@.K	75.20	22.34	3.37	0.30
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.IIDVVYNASNNELVR@.T	198.15	54.05	3.67	0.27
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.ISSLLEEQFQQGK#.L	270.11	73.82	3.66	0.27
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.LTPEEEEILNK#.K	285.37	89.50	3.19	0.31
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.QWYESHYALPLGR@.K	99.49	24.80	4.01	0.25
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.ADGYVLEGK#.E	45.38	8.47	5.36	0.19
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.ELEFYLR@.K	48.57	10.92	4.45	0.22
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.IIDVVYNASNNELVR@.T	53.43	12.47	4.28	0.23
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.ISSLLEEQFQQGK#.L	70.53	17.34	4.07	0.25
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.ADGYVLEGK#.E	31.23	7.85	3.98	0.25
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.ELEFYLR@.K	35.34	7.42	4.76	0.21
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	R.IIDVVYNASNNELVR@.T	29.57	5.86	5.05	0.20
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.ISSLLEEQFQQGK#.L	56.48	14.59	3.87	0.26
P62242_RS8_MOUSE	Rps8	40S ribosomal protein S8	K.LTPEEEEILNK#.K	78.01	22.05	3.54	0.28
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	K.IEDFLER@.R	35.51	12.70	2.80	0.36
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	R.IGVLDEGK#.M	62.21	15.50	4.01	0.25
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	K.LDYILGLK#.I	39.21	31.55	1.24	0.80
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	R.LFEGNALLR@.R	49.30	21.69	2.27	0.44
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	K.LIGEYGLR@.N	66.64	20.67	3.22	0.31
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	K.M*K#LDYILGLK#.I	18.24	6.54	2.79	0.36
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	K.QVVNIPSFIVR@.L	29.89	9.20	3.25	0.31
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	R.R@LQTQVFK#.L	44.49	11.39	3.91	0.26
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	K.HIDFSLR@.S	116.87	35.47	3.29	0.30
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	K.IEDFLER@.R	194.82	45.76	4.26	0.23
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	R.IGVLDEGK#.M	168.85	54.04	3.12	0.32
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	K.K#GQGGAGAGDDEEED.-	13.99	5.84	2.40	0.42
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	R.K#QVVNIPSFIVR@.L	271.75	61.52	4.42	0.23
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S9	R.KQVVNIPSFIVR.L	25.89	5.93	4.37	0.23

Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.LDYILGLK#.I	100.35	31.83	3.15	0.32
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	R.LFEGNALLR@.R	491.21	116.88	4.20	0.24
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.LIGEYGLR@.N	407.06	105.34	3.86	0.26
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	R.LQTQVFK#.L	103.86	55.91	1.86	0.54
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.M*K#LDYILGLK#.I	95.77	29.37	3.26	0.31
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.QVVNIPSFIVR@.L	169.47	49.03	3.46	0.29
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	R.R@LFEGNALLR@.R	77.00	14.90	5.17	0.19
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	R.R@LQTQVFK#.L	219.79	49.81	4.41	0.23
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	R.SPYGGGR@PGR@.V	41.89	10.25	4.09	0.24
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.SRLDQELK.L	191.66	40.35	4.75	0.21
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.IEDFLER@.R	42.71	12.14	3.52	0.28
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	R.IGVLDEGK#.M	37.80	10.26	3.68	0.27
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.K#GQGGAGAGDDEEED.-	4.36	2.37	1.84	0.54
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.LDYILGLK#.I	44.77	34.98	1.28	0.78
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	R.LFEGNALLR@.R	53.76	11.63	4.62	0.22
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.M*K#LDYILGLK#.I	10.53	2.27	4.65	0.22
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.IEDFLER@.R	69.46	15.95	4.35	0.23
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	R.IGVLDEGK#.M	63.66	14.78	4.31	0.23
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.K#GQGGAGAGDDEEED.-	7.60	2.75	2.77	0.36
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.LDYILGLK#.I	37.17	18.04	2.06	0.49
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	R.LFEGNALLR@.R	89.83	18.93	4.75	0.21
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.LIGEYGLR@.N	118.38	24.90	4.76	0.21
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.M*K#LDYILGLK#.I	15.47	3.13	4.94	0.20
Q6ZWN5_RS9_MOUSE	Rps9	40S ribosomal protein S	K.QVVNIPSFIVR@.L	43.04	8.44	5.10	0.20
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.AIVAIENPADVSVISSR@.N	232.10	138.15	1.68	0.60
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.EHPWEVMPDLYFYR@DPEEIEK#EEQAAAEK#.A	17.17	7.36	2.33	0.43
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	K.FAAATGATPIAGR@.F	290.46	169.24	1.72	0.58
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	K.FLAAGTHLGGTNLDFQM*EQYIYK#.R	44.78	25.91	1.73	0.58
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.FTPGTFTNQIQAAFR@.E	61.21	32.09	1.91	0.52
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	K.GAHSVGLM*WWM*LAR@.E	11.51	4.95	2.33	0.43
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.K#SDGIYIINLK#.R	21.50	15.17	1.42	0.71
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.LLVVTDPR@.A	220.51	134.47	1.64	0.61
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	K.SDGIYIINLK#.R	52.06	34.19	1.52	0.66
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.AIVAIENPADVSVISSR@.N	11.16	7.62	1.46	0.68
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	K.FAAATGATPIAGR@.F	19.29	14.06	1.37	0.73
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	K.FLAAGTHLGGTNLDFQM*EQYIYK#.R	4.85	2.81	1.72	0.58
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.FTPGTFTNQIQAAFR@.E	9.05	4.92	1.84	0.54
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.LLVVTDPR@.A	22.47	10.91	2.06	0.49
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.AIVAIENPADVSVISSR.N	14.57	7.26	2.01	0.50
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	K.FAAATGATPIAGR@.F	17.09	6.61	2.58	0.39
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	K.FLAAGTHLGGTNLDFQM*EQYIYK#.R	5.44	1.19	4.58	0.22
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.FTPGTFTNQIQAAFR@.E	5.76	3.36	1.71	0.58
P14206_RSSA_MOUSE	Rpsa	40S ribosomal protein S	R.LLVVTDPR@.A	17.79	3.93	4.53	0.22
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	K.DTTFAQVLK#.D	7.84	1.80	4.36	0.23
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	R.ENALLELSK#.K	95.89	12.94	7.41	0.13
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	R.IMESGSELSK#.T	18.37	2.83	6.48	0.15
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	R.IM*ESGSELSK#.T	52.32	7.15	7.32	0.14
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	K.IYQWINELSSPETR@.E	57.78	9.96	5.80	0.17
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	R.LTSLGVIGALVK#.T	234.76	35.58	6.60	0.15
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	K.NLQEGQVTDPR@.G	99.35	27.46	3.62	0.28
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	K.TVATFILQK#.I	150.50	23.75	6.34	0.16
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	R.WLAQLVK#.N	23.37	5.00	4.67	0.21
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	R.IM*ESGSELSK#.T	8.24	6.26	1.32	0.76
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	K.IYQWINELSSPETR@.E	6.35	2.78	2.28	0.44
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	R.LTSLGVIGALVK#.T	24.61	15.86	1.55	0.64
Q9JKY0_RCD1_MOUSE	Rqcd1	Cell differentiation prote	K.NLQEGQVTDPR@.G	8.93	9.08	0.98	1.02
Q80X95_RRAGA_MOUSE	Rraga	Ras-related GTP-binding	K.M*DLVQEDQR@.D	7.65	1.58	4.83	0.21
P10833_RRAS_MOUSE	Rras	Ras-related protein R-Ras	K.LR@LNVDEAFEQLVR@.A	9.00	4.41	2.04	0.49
P10833_RRAS_MOUSE	Rras	Ras-related protein R-Ras	R.VK#DR@DDFPIVLVGNK#.A	9.76	5.37	1.82	0.55
P62071_RRAS2_MOUSE	Rras2	Ras-related protein R-Ras	R.LDILDTAGQEEFGAM*R@.E	9.66	3.70	2.61	0.38
P62071_RRAS2_MOUSE	Rras2	Ras-related protein R-Ras	R.QVTQEEGQQLAR@.Q	7.63	2.68	2.85	0.35
Q99PL5_RRBP1_MOUSE	Rrbp1	Ribosome-binding protei	K.ETSYEEALANQR@.K	3.79	3.75	1.01	0.99
Q99PL5_RRBP1_MOUSE	Rrbp1	Ribosome-binding protei	K.GEGVQNQAKK#GVEGAQNQGK#.K	8.40	2.05	4.09	0.24
Q99PL5_RRBP1_MOUSE	Rrbp1	Ribosome-binding protei	K.LLATEQEDAAVAK#.S	14.51	10.21	1.42	0.70
Q99PL5_RRBP1_MOUSE	Rrbp1	Ribosome-binding protei	R.SIEALLEAGQAQDTQASHAEANQQQTR@.L	4.90	2.86	1.72	0.58
Q99PL5_RRBP1_MOUSE	Rrbp1	Ribosome-binding protei	R.DALNQATSQVESK#.Q	7.33	2.51	2.92	0.34
P07742_RIR1_MOUSE	Rrm1	Ribonucleoside-diphosp	R.YPFESPEAQLLNK.Q	5.04	6.86	0.73	1.36
P07742_RIR1_MOUSE	Rrm1	Ribonucleoside-diphosp	R.YPFESPEAQLLNK#.Q	8.69	10.49	0.83	1.21
P56183_RRP1_MOUSE	Rrp1	Ribosomal RNA processi	R.ATGGFTPDELLK#.V	9.43	5.21	1.81	0.55
P56183_RRP1_MOUSE	Rrp1	Ribosomal RNA processi	K.EAGSEAESSSADPGPGR@.K	3.36	1.54	2.18	0.46
P56183_RRP1_MOUSE	Rrp1	Ribosomal RNA processi	R.ATGGFTPDELLK#.V	16.64	9.06	1.84	0.54
P56183_RRP1_MOUSE	Rrp1	Ribosomal RNA processi	K.EAGSEAESSSADPGPGR@.K	10.66	2.92	3.65	0.27
Q6P5B0_RRP12_MOUSE	Rrp12	RRP12-like protein OS=	R.VLATQPGPGR@.G	7.81	2.86	2.72	0.37
Q6P5B0_RRP12_MOUSE	Rrp12	RRP12-like protein OS=	R.ALSQAAVEEEEEEEEEEPVQSK#.G	10.77	4.12	2.61	0.38
Q6P5B0_RRP12_MOUSE	Rrp12	RRP12-like protein OS=	K.AM*DLAQAGSTVESK#.I	5.04	2.74	1.84	0.54
Q6P5B0_RRP12_MOUSE	Rrp12	RRP12-like protein OS=	R.FGSNQEDALQR@.Y	11.33	3.60	3.15	0.32
Q6P5B0_RRP12_MOUSE	Rrp12	RRP12-like protein OS=	K.SDLTVDAVK#.L	8.35	4.05	2.06	0.48
Q6P5B0_RRP12_MOUSE	Rrp12	RRP12-like protein OS=	R.SWLLPVIR@.D	18.44	7.41	2.49	0.40
Q6P5B0_RRP12_MOUSE	Rrp12	RRP12-like protein OS=	K.VLDPASSDFTR@.L	18.07	4.49	4.03	0.25
Q9CYX7_RRP15_MOUSE	Rrp15	RRP15-like protein OS=	R.GVVQLFNAVQK#.H	16.11	6.81	2.37	0.42
Q9CYX7_RRP15_MOUSE	Rrp15	RRP15-like protein OS=	R.GVVQLFNAVQK#.H	8.67	2.37	3.66	0.27
Q91YK2_RRP1B_MOUSE	Rrp1b	Ribosomal RNA processi	R.SHFQPDTQNLDAVAVPK#.V	12.96	1.97	6.59	0.15
Q91YK2_RRP1B_MOUSE	Rrp1b	Ribosomal RNA processi	K.VPDSESEPDTAQR@.Q	9.24	3.79	2.44	0.41
Q9D1C9_RRP7A_MOUSE	Rrp7a	Ribosomal RNA-processi	K.TVELQEK#PDLAESPTEPK#.S	42.50	29.01	1.47	0.68
Q9D1C9_RRP7A_MOUSE	Rrp7a	Ribosomal RNA-processi	K.WISDYEDSVLDPEALR.M	6.79	5.47	1.24	0.81
Q9DB85_RRP8_MOUSE	Rrp8	Ribosomal RNA-processi	R.TSTATIDPSK#PSPESM*SPNSSHTLSR@.K	9.20	3.87	2.37	0.42
Q9DB85_RRP8_MOUSE	Rrp8	Ribosomal RNA-processi	R.YLNEQLYSGPSSAAR@.R	13.22	5.75	2.30	0.43
Q91WM3_U3IP2_MOUSE	Rrp9	U3 small nucleolar RNA-i	R.AFEEDQVAGR.L	14.50	9.97	1.45	0.69
Q91WM3_U3IP2_MOUSE	Rrp9	U3 small nucleolar RNA-i	R.AK#PAPGPGAAPVAGK#.R	23.37	13.42	1.74	0.57
Q91WM3_U3IP2_MOUSE	Rrp9	U3 small nucleolar RNA-i	R.DAVSGLAFR@.K	13.17	10.74	1.23	0.82
Q91WM3_U3IP2_MOUSE	Rrp9	U3 small nucleolar RNA-i	K.EIQAPAPTDIR.V	11.49	10.82	1.06	0.94
Q91WM3_U3IP2_MOUSE	Rrp9	U3 small nucleolar RNA-i	R.K#TEEEEEEELEETAQEK#.K	10.47	6.93	1.51	0.66
Q91WM3_U3IP2_MOUSE	Rrp9	U3 small nucleolar RNA-i	K.LYLEQLR.Q	201.96	7.61	26.54	0.04
Q91WM3_U3IP2_MOUSE	Rrp9	U3 small nucleolar RNA-i	K.VWNAAENSYVETLFGHQDAVAALDALSR@.E	5.98	3.68	1.63	0.62
Q9CYH6_RRS1_MOUSE	Rrs1	Ribosome biogenesis reg	R.DNTQLLINQLWR@.L	21.11	8.79	2.40	0.42
Q9CYH6_RRS1_MOUSE	Rrs1	Ribosome biogenesis reg	K.ELELEFDLGNLLASDR@NPPTVLR@.Q	6.67	0.00	#DIV/0!	0.00
Q9CYH6_RRS1_MOUSE	Rrs1	Ribosome biogenesis reg	R.K#FQPLFGDFAAEK#.K	16.75	6.96	2.41	0.42
Q9CYH6_RRS1_MOUSE	Rrs1	Ribosome biogenesis reg	R.K#FQPLFGDFAAEK#K#.N	5.44	2.20	2.47	0.40
Q9CYH6_RRS1_MOUSE	Rrs1	Ribosome biogenesis reg	R.QAGPSPEAELR@.A	36.31	13.44	2.70	0.37
Q9CYH6_RRS1_MOUSE	Rrs1	Ribosome biogenesis reg	R.VEEAVVAR@.L	59.95	24.44	2.45	0.41
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	K.GIDSSVPDIESLSQK#.A	11.78	5.85	2.01	0.50
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	K.LDNAQTSGM*EDTSETK#.G	7.69	9.53	0.81	1.24
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	K.LEEQLQDLDVALK#.K	8.11	4.86	1.67	0.60

E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	R.NSTASENTEITSER@.K	13.22	6.80	1.94	0.51
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	R.R@ADGEDGVEGEPASLQTADK#K#.D	3.23	3.61	0.89	1.12
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	K.AQIDPVLLK#.N	19.24	10.44	1.84	0.54
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	R.DSQPSALPSEQESSK#.K	15.02	5.63	2.67	0.37
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	R.FDEFDEAIDEAIEDDIK#EADGGGVGR@.G	21.84	8.47	2.58	0.39
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	K.GIDSSVPDIESLSQK#.A	19.66	11.15	1.76	0.57
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	K.LDNAQTSGM*EDTSETK#.G	14.20	8.43	1.68	0.59
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	K.LSPIPEEVVR@.G	15.83	8.73	1.81	0.55
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	R.NR@NELAETLALLK#.A	13.00	7.88	1.65	0.61
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	R.NSTASENTEITSER.K	20.92	8.41	2.49	0.40
E9PWW9_E9PWW9_MOUSE	Rsf1	Protein Rsf1 OS=Mus mu	R.R@ADGEDGVEGEPASLQTADK#K#.D	6.96	3.77	1.85	0.54
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.ALLATETPEASAPGTSGK#.K	41.76	26.44	1.58	0.63
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.ATSLLTQSGLASSAPAK#.S	49.72	25.65	1.94	0.52
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.HGVNTISQIIPFK#.T	18.80	9.35	2.01	0.50
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.IGHTGM*ETEHIVDNILAVSEM*LSEK#.L	11.23	5.67	1.98	0.51
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.K#ATSLLTQSGLASSAPAK#.S	18.01	9.18	1.96	0.51
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.K#AVEVISNR@.S	28.74	14.42	1.99	0.50
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.K#K#VPVSVNLLAK#.N	62.75	31.91	1.97	0.51
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.K#PEASSFSTPR@.K	18.08	12.17	1.49	0.67
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.K#VPVSVNLLAK#.N	17.90	8.98	1.99	0.50
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.LLGSFEVFITDAR@.I	44.21	17.79	2.48	0.40
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	-.M*KGSASESPSASVAEATTTDVQVTPTALLQLDR.E	11.17	4.35	2.57	0.39
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.SVSLPIFSSFVTSQDENAVSLR@.S	26.91	13.50	1.99	0.50
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.VPVSVNLLAK.N	27.33	17.42	1.57	0.64
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.ALLATETPEASAPGTSGK#.K	37.76	18.52	2.04	0.49
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.ATSLLTQSGLASSAPAK#.S	34.71	17.00	2.04	0.49
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.HGVNTISQIIPFK#.T	18.87	8.46	2.23	0.45
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.K#ALLATETPEASAPGTSGK#.K	11.95	5.47	2.19	0.46
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.K#PEASSFSTPR@.K	13.97	5.48	2.55	0.39
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.K#VPVSVNLLAK#.N	13.24	7.64	1.73	0.58
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.LLGSFEVFITDAR@.I	50.86	17.86	2.85	0.35
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	-.M*K#GSASESPSASVAEATTTDVQVTPTALLQLDR@.E	9.09	3.51	2.59	0.39
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.SVSLPIFSSFVTSQDENAVSLR@.S	23.86	8.43	2.83	0.35
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.VPVSVNLLAK#.N	16.99	9.08	1.87	0.53
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.ALLATETPEASAPGTSGK#.K	24.52	11.09	2.21	0.45
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.ATSLLTQSGLASSAPAK#.S	21.96	6.69	3.28	0.30
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.AVEVISNR@.S	20.62	5.59	3.69	0.27
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.GSASESPSASVAEATTTDVQVTPTALLQLDR@.E	7.86	3.21	2.45	0.41
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.HGVNTISQIIPFK#.T	22.97	9.86	2.33	0.43
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.K#ALLATETPEASAPGTSGK#.K	5.78	2.88	2.01	0.50
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	R.K#PEASSFSTPR@.K	12.78	3.45	3.71	0.27
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.SVSLPIFSSFVTSQDENAVSLR@.S	45.77	17.33	2.64	0.38
Q8BVY0_RL1D1_MOUSE	Rsl1d1	Ribosomal L1 domain-co	K.SVSLPIFSSFVTSQDENAVSLR.S	16.59	3.19	5.20	0.19
Q99L28_RLP24_MOUSE	Rsl24d1	Probable ribosome bioge	K.ELTVDNSFEFEK#.R	26.71	14.34	1.86	0.54
Q9DBU6_RSRC1_MOUSE	Rsrc1	Serine/Arginine-related p	K.AVEPSEVQHVTAASGPASAAAEPPSTGK#.E	15.28	7.23	2.11	0.47
Q9DBU6_RSRC1_MOUSE	Rsrc1	Serine/Arginine-related p	K.EIEAIESDSFVQQTFR.S	7.36	4.90	1.50	0.67
Q9DBU6_RSRC1_MOUSE	Rsrc1	Serine/Arginine-related p	R.VK#EIEAIESDSFVQQTFR@.S	30.92	17.45	1.77	0.56
A2RTL5_RSRC2_MOUSE	Rsrc2	Arginine/serine-rich coil	R.GM*GLGFTSSM*R@.G	8.23	8.47	0.97	1.03
A2RTL5_RSRC2_MOUSE	Rsrc2	Arginine/serine-rich coil	R.NLDAQYEM*AR.S	36.70	36.85	1.00	1.00
A2RTL5_RSRC2_MOUSE	Rsrc2	Arginine/serine-rich coil	R.NTAM*DAQEALAR@.R	44.61	37.06	1.20	0.83
A2RTL5_RSRC2_MOUSE	Rsrc2	Arginine/serine-rich coil	K.SQSAEIWEK#.L	7.20	6.29	1.15	0.87
A2RTL5_RSRC2_MOUSE	Rsrc2	Arginine/serine-rich coil	R.GM*GLGFTSSM*R.G	12.35	13.63	0.91	1.10
A2RTL5_RSRC2_MOUSE	Rsrc2	Arginine/serine-rich coil	R.NLDAQYEM*AR.S	26.65	28.22	0.94	1.06
A2RTL5_RSRC2_MOUSE	Rsrc2	Arginine/serine-rich coil	R.NTAM*DAQEALAR.R	31.06	26.10	1.19	0.84
Q3UC65_RSRP1_MOUSE	Rsrp1	Arginine/serine-rich prot	K.ALGTANFDLPASLR@.A	11.33	8.45	1.34	0.75
Q01730_RSU1_MOUSE	Rsu1	Ras suppressor protein 1	R.ALYLSDNDFEILPPDIGK#.L	9.11	5.38	1.69	0.59
Q01730_RSU1_MOUSE	Rsu1	Ras suppressor protein 1	R.DNDLISLPK#.E	48.57	14.50	3.35	0.30
Q01730_RSU1_MOUSE	Rsu1	Ras suppressor protein 1	K.EIGELTQLK#.E	37.67	14.00	2.69	0.37
Q01730_RSU1_MOUSE	Rsu1	Ras suppressor protein 1	R.LNTLPR@.G	47.12	21.70	2.17	0.46
Q01730_RSU1_MOUSE	Rsu1	Ras suppressor protein 1	K.LQILSLR@.D	24.25	12.17	1.99	0.50
Q01730_RSU1_MOUSE	Rsu1	Ras suppressor protein 1	R.LTVLPPELGNLDLTGQK#.Q	17.86	10.07	1.77	0.56
Q9D7H3_RTCA_MOUSE	RtcA	RNA 3'-terminal phospha	R.AFVAGVLPLK#.V	20.29	12.65	1.60	0.62
Q9D7H3_RTCA_MOUSE	RtcA	RNA 3'-terminal phospha	R.DLYVSIQPVQEAR@.D	8.76	4.60	1.90	0.53
Q9D7H3_RTCA_MOUSE	RtcA	RNA 3'-terminal phospha	R.GVNADK#VGIEAAEM*LLANLR@.H	9.69	7.02	1.38	0.72
Q9D7H3_RTCA_MOUSE	RtcA	RNA 3'-terminal phospha	R.VEVDGGIM*EGGGQILR@.V	11.31	4.70	2.40	0.42
Q9D7H3_RTCA_MOUSE	RtcA	RNA 3'-terminal phospha	R.AFVAGVLPLK#.V	8.53	2.83	3.02	0.33
Q9D7H3_RTCA_MOUSE	RtcA	RNA 3'-terminal phospha	R.GVNADK#VGIEAAEM*LLANLR@.H	4.56	1.16	3.94	0.25
Q9D7H3_RTCA_MOUSE	RtcA	RNA 3'-terminal phospha	R.AFVAGVLPLK#.V	14.25	3.19	4.47	0.22
Q9D7H3_RTCA_MOUSE	RtcA	RNA 3'-terminal phospha	R.GVNADK#VGIEAAEM*LLANLR@.H	5.76	1.74	3.32	0.30
Q9D7H3_RTCA_MOUSE	RtcA	RNA 3'-terminal phospha	R.VEVDGGIM*EGGGQILR@.V	5.41	2.24	2.42	0.41
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	R.GGGVGGFLPAM*K#.Q	27.65	13.59	2.03	0.49
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	R.GLGHQVATDALVAM*EK#.A	27.68	17.45	1.59	0.63
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	K.GM*AAAGNYAWVNR@.S	16.30	7.70	2.12	0.47
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	K.K#GFVPNM*QVEGVFYVNDALEK#.L	4.43	1.60	2.76	0.36
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	K.LM*FEELR@.N	18.84	8.53	2.21	0.45
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	K.LVM*EEAPESYK#.N	49.42	26.28	1.88	0.53
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	R.NLDFQDVLDK#.L	15.80	9.32	1.70	0.59
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	R.NLDFQDVLDK#LADM*GIAIR@.V	17.24	8.83	1.95	0.51
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	R.NYNDELQFLDK#.I	11.46	6.14	1.87	0.54
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	K.QIGNVAALPGIVHR@.S	41.76	23.57	1.77	0.56
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	R.SSM*TFLTR@.Q	18.52	10.05	1.84	0.54
Q99LF4_RTCB_MOUSE	Rtcb	tRNA-splicing ligase RtcB	K.VEQHVVDGK#.E	9.86	3.90	2.53	0.40
A2AQ19_RTF1_MOUSE	Rtf1	RNA polymerase-associat	R.VAEITGVVETAK#.V	17.16	7.02	2.45	0.41
Q9ES97_RTN3_MOUSE	Rtn3	Reticulon-3 OS=Mus mus	K.TQIDHYVGIAR@.D	219.56	64.38	3.41	0.29
Q9ES97_RTN3_MOUSE	Rtn3	Reticulon-3 OS=Mus mus	K.YK#TQIDHYVGIAR@.D	21.89	6.20	3.53	0.28
Q9ES97_RTN3_MOUSE	Rtn3	Reticulon-3 OS=Mus mus	K.SEEGHPFK#.A	25.27	8.32	3.04	0.33
Q9ES97_RTN3_MOUSE	Rtn3	Reticulon-3 OS=Mus mus	K.TQIDHYVGIAR@.D	193.44	50.24	3.85	0.26
Q9ES97_RTN3_MOUSE	Rtn3	Reticulon-3 OS=Mus mus	K.YK#TQIDHYVGIAR@.D	91.86	20.47	4.49	0.22
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.AYLESEVAISEELVQK#.Y	136.20	38.33	3.55	0.28
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.AYLESEVAISEELVQK#.Y	104.37	33.32	3.13	0.32
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.GPLPAAPPTAPER@.Q	370.02	149.23	2.48	0.40
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.HQAQIDHYLGLANK#.S	343.56	113.02	3.04	0.33
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.KPAAGLSAAPVPPAAAPLLDFSSDSVPPAPR.G	135.54	60.09	2.26	0.44
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.LFLVDDLVDSLK#.F	68.72	30.63	2.24	0.45
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.R@LFLVDDLVDSLK#.F	13.49	2.72	4.96	0.20
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	K.SDEGHPFR@.A	57.17	18.75	3.05	0.33
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.SLTAVLSAELNK#.T	15.65	4.61	3.40	0.29
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.SPAASAPSLPPAAAVLPSK#.L	28.67	10.90	2.63	0.38
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	K.TSVVDLLYWR@.D	21.57	7.20	3.00	0.33
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	K.YSNSALGHVNSTIK#.E	52.44	19.54	2.68	0.37
Q8BH78_Q8BH78_MOUSE	Rtn4	RTN4 OS=Mus musculus (	R.GSGSVVVDLLYWR@.D	114.69	36.77	3.12	0.32
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	R.AYLESEVAISEELVQK#.Y	4.89	1.72	2.84	0.35
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus	K.EHGYLGNLSAVASTEGTIEETLNEASR@.E	9.54	3.22	2.97	0.34

Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus R.GPLPAAPPTAPER@.Q	13.31	7.57	1.76	0.57
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus R.HQAQIDHYLGLANK#.S	15.37	4.08	3.77	0.27
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus K.LSTEPSPEFSNYSEIAK#.F	10.07	4.37	2.30	0.43
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus R.ATNPFVNR@.E	15.47	4.53	3.41	0.29
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus K.LEPENPPPYEEAM*SVALK#.T	6.04	4.22	1.43	0.70
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus K.LSTEPSPEFSNYSEIAK#.F	16.44	5.61	2.93	0.34
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus K.M*K#ESETFSDSSPIEIIDEFPTFVSAK#.D	4.12	3.04	1.35	0.74
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus K.TSVVDLLYWR@.D	12.49	1.29	9.66	0.10
Q99P72_RTN4_MOUSE	Rtn4	Reticulon-4 OS=Mus mus K.VPLLLPNVSALESQIEM*GNIVK#PK#.V	23.36	4.69	4.99	0.20
Q9ER80_RTP4_MOUSE	Rtp4	Receptor-transporting pı K.IALTSNASLGEK#.V	8.33	3.51	2.37	0.42
Q9ER80_RTP4_MOUSE	Rtp4	Receptor-transporting pı K.TFQDFGNR@.T	8.59	3.11	2.76	0.36
Q9ER80_RTP4_MOUSE	Rtp4	Receptor-transporting pı K.IALTSNASLGEK#.V	9.67	5.32	1.82	0.55
Q9D394_RUFY3_MOUSE	Rufy3	Protein RUFY3 OS=Mus m K.NYVEELNR@.H	16.67	3.89	4.28	0.23
Q9D394_RUFY3_MOUSE	Rufy3	Protein RUFY3 OS=Mus m R.TAEGQALSEAR@.K	7.01	2.36	2.97	0.34
Q64131_RUNX3_MOUSE	Runx3	Runt-related transcriptic R.GSLSTTSHFSSQAQTPIQGSSDLNPFSDPR@.Q	8.01	6.88	1.16	0.86
Q64131_RUNX3_MOUSE	Runx3	Runt-related transcriptic K.M*GENSGALSAQATAGPGGR@.T	5.16	3.85	1.34	0.75
Q64131_RUNX3_MOUSE	Runx3	Runt-related transcriptic R.SFPTLQSLTESR@.F	3.37	3.82	0.88	1.13
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.ALESSIAPIVIFASNR@.G	198.34	79.89	2.48	0.40
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.AVLLAGPPGTGK#.T	316.31	126.90	2.49	0.40
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.DSIEK#EHVEEISELFYDAK#.S	95.26	38.86	2.45	0.41
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.GLGLDESGLAK#.Q	362.59	161.76	2.24	0.45
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.GTEDITSPHGIPLDLLDR@.V	205.72	93.57	2.20	0.45
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.GTEDITSPHGIPLDLLDR.V	10.28	6.00	1.71	0.58
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.ILADQQDK#.Y	40.81	14.11	2.89	0.35
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.ILADQQDKYM*K.-	42.17	19.64	2.15	0.47
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.K#TEVLM*ENFR@.R	139.89	56.43	2.48	0.40
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.KTEVLM*ENFR.R	28.64	17.08	1.68	0.60
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.LDPSIFESLQK#.E	355.50	167.94	2.12	0.47
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.QAASGLVGQENAR@.E	263.01	103.89	2.53	0.39
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.TALALAIAQELGSK#.V	245.55	111.76	2.20	0.46
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.TEVLM*ENFR.R	46.99	22.28	2.11	0.47
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.TISHVIIGLK#.T	249.62	122.23	2.04	0.49
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.TM*LYTPQEM*K#.Q	88.87	42.23	2.10	0.48
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.TMLYTPQEM*K#.Q	16.75	7.11	2.36	0.42
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.TM*LYTPQEMK#.Q	14.82	6.33	2.34	0.43
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.TMLYTPQEMK#.Q	19.46	5.60	3.48	0.29
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.VEAGDVIYIEANSGAVK#.R	87.88	36.26	2.42	0.41
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.YSVQLLTPANLLAK#.I	384.79	158.39	2.43	0.41
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.ALESSIAPIVIFASNR@.G	16.78	7.91	2.12	0.47
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.DSIEK#EHVEEISELFYDAK#.S	12.69	10.72	1.18	0.85
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.GLGLDESGLAK#.Q	37.22	15.67	2.38	0.42
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.GTEDITSPHGIPLDLLDR@.V	31.61	10.50	3.01	0.33
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.LDPSIFESLQK#.E	53.48	17.76	3.01	0.33
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.QAASGLVGQENAR@.E	21.41	7.80	2.74	0.36
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.TALALAIAQELGSK#.V	20.93	8.24	2.54	0.39
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.TISHVIIGLK#.T	30.55	7.36	4.15	0.24
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.VEAGDVIYIEANSGAVK#.R	10.93	23.46	0.47	2.15
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.YSVQLLTPANLLAK#.I	52.03	16.63	3.13	0.32
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.ALESSIAPIVIFASNR@.G	11.10	5.08	2.18	0.46
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.GLGLDESGLAK#.Q	22.22	7.46	2.98	0.34
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc R.GTEDITSPHGIPLDLLDR@.V	15.11	6.55	2.31	0.43
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.LDPSIFESLQK#.E	28.13	9.75	2.89	0.35
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.QAASGLVGQENAR@.E	15.95	3.65	4.36	0.23
P60122_RUVB1_MOUSE	Ruvbl1	RuvB-like 1 OS=Mus musc K.TALALAIAQELGSK#.V	31.28	7.43	4.21	0.24
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.AAGVVLEM*IR@.E	215.96	84.86	2.54	0.39
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.AAGVVLEMIR@.E	48.81	18.60	2.62	0.38
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.ALESDM*APVLIM*ATNR@.G	58.42	19.51	2.99	0.33
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.ALESDM*APVLIMATNR@.G	24.83	20.93	1.19	0.84
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.ALESDMAPVLIM*ATNR@.G	4.84	1.35	3.58	0.28
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.ALESDMAPVLIM*ATNR@.G	8.19	2.84	2.88	0.35
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.ALESDMAPVLIMATNR@.G	9.61	3.90	2.47	0.41
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.AVLIAGQPGTGK#.T	528.38	216.07	2.45	0.41
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.DK#VQAGDVITIDK#.A	99.31	43.09	2.30	0.43
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.DYDAM*GSQTK#.F	24.23	8.97	2.70	0.37
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.EYQDAFLFNELK#.G	18.23	8.97	2.03	0.49
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.EYQDAFLFNELK#GETM*DTS.-	71.21	27.51	2.59	0.39
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.EYQDAFLFNELK#GETMDTS.-	8.56	3.03	2.82	0.35
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.GLGLDDALEPR@.Q	356.22	160.84	2.21	0.45
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.GTSYQSPHGIPIDLLDR.L	9.50	4.82	1.97	0.51
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.IGLETSLR.Y	499.71	180.81	2.76	0.36
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.IKEETEIIEGEVVEIQIDRPATGTGSK.V	26.88	6.43	4.18	0.24
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.K#GTEVQVDDIK#R@.V	270.48	112.77	2.40	0.42
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.M*IESLTK#.D	144.85	65.28	2.22	0.45
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.MIESLTK#.D	33.12	11.99	2.76	0.36
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.QASQGM*VGQLAAR@.R	205.69	79.66	2.58	0.39
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.QASQGMVGQLAAR@.R	29.03	8.78	3.31	0.30
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.R@AAGVVLEM*IR@.E	135.82	57.06	2.38	0.42
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.R@AAGVVLEMIR@.E	21.18	8.46	2.50	0.40
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.R@K#EVVHTVSLHEIDVINSR@.T	15.25	2.88	5.30	0.19
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.TAIAM*GMAQALGPDTPFTAIAGSEIFSLEM*SK#.T	8.88	3.59	2.47	0.40
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.TEALTQAFR@.R	506.30	112.18	4.51	0.22
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.TQGFLALFSGDTGEIK#.S	281.27	100.40	2.80	0.36
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.TQGFLALFSGDTGEIK#SEVR@.E	112.35	43.76	2.57	0.39
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.TTEM*ETIYDLGTK#.M	241.59	96.44	2.51	0.40
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.TTEMETIYDLGTK#.M	19.68	25.99	0.76	1.32
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.VQAGDVITIDK#.A	78.50	34.75	2.26	0.44
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.VYSLFLDESR.S	256.13	95.14	2.69	0.37
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.AVLIAGQPGTGK#.T	35.99	15.47	2.33	0.43
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.DK#VQAGDVITIDK#.A	19.31	7.06	2.73	0.37
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.EYQDAFLFNELK#GETM*DTS.-	3.65	2.29	1.60	0.63
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.K#GTEVQVDDIK#R@.V	16.49	8.12	2.03	0.49
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.LLIVSTSPYSEK#.D	14.53	6.09	2.38	0.42
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.QASQGM*VGQLAAR@.R	10.58	5.73	1.85	0.54
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.TEALTQAFR@.R	70.85	9.03	7.85	0.13
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.TTEM*ETIYDLGTK#.M	24.56	6.72	3.65	0.27
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.VQAGDVITIDK#.A	9.32	4.87	1.92	0.52
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.AVLIAGQPGTGK#.T	21.84	7.23	3.02	0.33
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.IGLETSLR@.Y	15.44	4.46	3.46	0.29
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.LLIVSTSPYSEK#.D	9.05	4.62	1.96	0.51
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc R.QASQGM*VGQLAAR@.R	7.61	2.19	3.47	0.29
Q9WTM5_RUVB2_MOUSE	Ruvbl2	RuvB-like 2 OS=Mus musc K.TTEM*ETIYDLGTK#.M	16.03	6.35	2.53	0.40
Q9CQK7_RWDD1_MOUSE	Rwdd1	RWD domain-containing K.FTYSEKYPDETPLYEIFSQENLEDNDVSDILK.L	9.66	3.71	2.61	0.38
Q9CQK7_RWDD1_MOUSE	Rwdd1	RWD domain-containing K.LFHGTPVTIENFLSWK#.A	9.78	6.01	1.63	0.61

Q9CQK7_RWDD1_MOUSE	Rwdd1	RWD domain-containing	K.LNEIVDQIK#.T	33.40	19.60	1.70	0.59
Q9CQK7_RWDD1_MOUSE	Rwdd1	RWD domain-containing	K.YPDETPLYEIFSQENLEDNDVSDILK#.L	3.46	2.45	1.41	0.71
Q9CPR1_RWDD4_MOUSE	Rwdd4	RWD domain-containing	R.ELSPVSFQYR@.I	21.10	7.45	2.83	0.35
Q9CPR1_RWDD4_MOUSE	Rwdd4	RWD domain-containing	R.GWNWVDVVK#.H	8.23	4.45	1.85	0.54
P28700_RXRA_MOUSE	Rxra	Retinoic acid receptor R	R.AGWNELLIASFSHR@.S	15.61	6.56	2.38	0.42
P28700_RXRA_MOUSE	Rxra	Retinoic acid receptor R	K.ILEAELAVEPK#.T	11.40	2.91	3.91	0.26
P28700_RXRA_MOUSE	Rxra	Retinoic acid receptor R	R.IPHFSELPLDDQVILLR@.A	28.08	7.49	3.75	0.27
P28700_RXRA_MOUSE	Rxra	Retinoic acid receptor R	K.LIGDTPIDTFLM*EM*LEAPHQAT.-	9.28	9.28	1.00	1.00
P28700_RXRA_MOUSE	Rxra	Retinoic acid receptor R	K.QLFTLVEWAK#.R	16.46	5.36	3.07	0.33
P28700_RXRA_MOUSE	Rxra	Retinoic acid receptor R	R.AGWNELLIASFSHR@.S	7.65	1.76	4.34	0.23
P28700_RXRA_MOUSE	Rxra	Retinoic acid receptor R	R.IPHFSELPLDDQVILLR@.A	7.05	3.16	2.23	0.45
P28700_RXRA_MOUSE	Rxra	Retinoic acid receptor R	K.QLFTLVEWAK#.R	8.21	1.56	5.28	0.19
P28704_RXRB_MOUSE	Rxrb	Retinoic acid receptor R	R.AIILFNPDAK#.G	10.43	2.66	3.92	0.26
P28704_RXRB_MOUSE	Rxrb	Retinoic acid receptor R	K.GLSNPGEVEILR@.E	10.10	3.39	2.98	0.34
P28704_RXRB_MOUSE	Rxrb	Retinoic acid receptor R	R.ILEAELAVEQK#.S	9.20	3.81	2.41	0.41
P28704_RXRB_MOUSE	Rxrb	Retinoic acid receptor R	R.IPHFSSLPLDDQVILLR@.A	9.96	3.95	2.52	0.40
P28704_RXRB_MOUSE	Rxrb	Retinoic acid receptor R	K.GLSNPGEVEILR@.E	10.22	1.89	5.40	0.19
P50543_S10AB_MOUSE	S100a11	Protein S100-A11 OS=Mu	K.NQKDPGVLDR.M	25.79	35.65	0.72	1.38
P50543_S10AB_MOUSE	S100a11	Protein S100-A11 OS=Mu	K.TEFLSFM*NTELAAFTK#.N	11.88	30.85	0.39	2.60
Q9D708_Q9D708_MOUSE	S100a16	Protein S100a16 OS=Mu	K.AVVVLVENFYK#.Y	9.54	2.87	3.33	0.30
Q9EP69_SAC1_MOUSE	Sacm1l	Phosphatidylinositide p	R.TQLGLLM*DGFNSLLR@.Y	7.87	2.76	2.85	0.35
Q9EP69_SAC1_MOUSE	Sacm1l	Phosphatidylinositide p	K.VVTNQDGVFR@.S	6.77	1.94	3.49	0.29
Q9R1T2_SAE1_MOUSE	Sae1	SUMO-activating enzyme	R.AQNLNPM*VDVK#.V	8.41	4.48	1.88	0.53
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	R.APTAALSPEPQDSK#EDVK#K#.F	24.60	16.87	1.46	0.69
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	R.EPADAPGGGTGM*DREPVGLEEPVEQSSTAAQLPEATSQELVR.A	11.12	4.38	2.54	0.39
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	R.LQAQWER@.E	27.63	15.49	1.78	0.56
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	K.M*SSVEEDSDTK#R@.L	6.70	3.64	1.84	0.54
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	R.NFWVSGLSSTTR@.A	37.15	18.86	1.97	0.51
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	K.REPADAPGGGTGM*DREPVGLEEPVEQSSTAAQLPEATSQELVR.A	17.20	7.93	2.17	0.46
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	K.SEPVK#EEGSELEQPFAQATSSVGPDR@.K	16.25	9.50	1.71	0.58
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	K.SK#DADDQK#PGPSER@.S	17.48	13.57	1.29	0.78
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	R.NFWVSGLSSTTR@.A	13.44	5.76	2.34	0.43
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	K.REPADAPGGGTGM*DREPVGLEEPVEQSSTAAQLPEATSQELVR.A	7.21	4.00	1.80	0.55
D3YXK2_SAFB1_MOUSE	Safb	Scaffold attachment fact	K.SEPVK#EEGSELEQPFAQATSSVGPDR@.K	10.21	5.44	1.88	0.53
Q80YR5_SAFB2_MOUSE	Safb2	Scaffold attachment fact	K.AFK#EEGQEPEEVGISWGAVSK#.R	6.59	3.64	1.81	0.55
Q80YR5_SAFB2_MOUSE	Safb2	Scaffold attachment fact	R.ELADAPGGGGGTR@.H	24.09	9.40	2.56	0.39
Q80YR5_SAFB2_MOUSE	Safb2	Scaffold attachment fact	K.HAVDEEVFK#NTLEASVSDLK#.V	6.80	5.31	1.28	0.78
Q80YR5_SAFB2_MOUSE	Safb2	Scaffold attachment fact	R.LDAFQER@.R	35.72	19.86	1.80	0.56
Q80YR5_SAFB2_MOUSE	Safb2	Scaffold attachment fact	R.LEGGGM*ASQDQGGR@.V	7.73	4.38	1.77	0.57
Q80YR5_SAFB2_MOUSE	Safb2	Scaffold attachment fact	R.NLWVSGLSSSTR@.A	14.66	9.71	1.51	0.66
Q80YR5_SAFB2_MOUSE	Safb2	Scaffold attachment fact	K.NTLEASVSDLK#.V	15.54	5.88	2.64	0.38
Q80YR5_SAFB2_MOUSE	Safb2	Scaffold attachment fact	K.VTLADEEAPM*EPENEK#.I	11.59	6.01	1.93	0.52
Q80YR5_SAFB2_MOUSE	Safb2	Scaffold attachment fact	R.ELADAPGGGGGTR.H	8.94	7.01	1.28	0.78
D3YXK1_SAMD1_MOUSE	Samd1	Atherin OS=Mus musculu	K.VLQQGHFEDDDPDGLLG.-	5.33	5.33	1.00	1.00
G5E8A7_G5E8A7_MOUSE	Samd4b	Serine/threonine-protei	R.NALQELQQIIITPIK#.A	5.75	2.99	1.93	0.52
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	K.APDVELKAEDFIVDVINVDYGM*EDKNPIDR.V	16.81	10.85	1.55	0.65
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	R.DFTK#PQDGDIIAPLITPLK#.W	32.38	21.55	1.50	0.67
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	K.FAEQLIR@.V	44.20	23.16	1.91	0.52
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	K.IAGSFLPFLDEDR@.L	13.25	8.05	1.65	0.61
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	R.IIDTPQFQR@.L	52.32	24.40	2.14	0.47
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	R.INK#EQVSQLLPEK#.F	20.54	15.67	1.31	0.76
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	K.ISNLIDIM*ITDAFLK#.A	15.93	8.72	1.83	0.55
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	R.ISTAIDDM*EAFTK#.L	41.73	21.86	1.91	0.52
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	K.NYGLVPEEDITFIK#.E	38.20	26.43	1.45	0.69
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	K.ADPYVEITGTAGK#.K	22.23	4.77	4.66	0.21
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	R.DFTK#PQDGDIIAPLITPLK#.W	16.93	3.53	4.80	0.21
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	K.FAEQLIR@.V	29.67	6.67	4.45	0.22
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	K.IAGSFLPFLDEDR@LEDLGVSSLEER@.K	57.39	12.96	4.43	0.23
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	R.IIDTPQFQR@.L	27.12	5.57	4.87	0.21
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	R.ISTAIDDM*EAFTK#.L	20.70	10.50	1.97	0.51
Q60710_SAMH1_MOUSE	Samhd1	Deoxynucleoside triphos	K.YLGETQPK#.R	24.88	15.29	1.63	0.61
Q8BIH0_SP130_MOUSE	Sap130	Histone deacetylase com	R.INELIQGNM*QR@.C	9.93	3.61	2.75	0.36
Q8BIH0_SP130_MOUSE	Sap130	Histone deacetylase com	R.LTNLQEGIIPK#.K	21.34	5.44	3.92	0.25
Q8BIH0_SP130_MOUSE	Sap130	Histone deacetylase com	K.LVM*DQISEAR@.D	10.61	5.44	1.95	0.51
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	K.FQIGDYLDIAITPPNR.A	12.35	10.81	1.14	0.87
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	K.GTDDSM*TLQSQK.F	3.02	2.81	1.07	0.93
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	K.EIGSTM*SGR@.K	33.35	18.35	1.82	0.55
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	K.FQIGDYLDIAITPPNR@.A	198.86	110.72	1.80	0.56
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	R.GNVPSSELQIYTWM*DATLK#.E	31.79	14.35	2.22	0.45
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	R.GNVPSSELQIYTWM*DATLK#.E	31.31	12.41	2.52	0.40
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	R.GNVPSSELQIYTWMDATLK#.E	7.00	3.67	1.91	0.52
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	K.GTDDSM*TLQSQK#.F	41.69	20.65	2.02	0.50
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	K.GTHFNFAIVFM*DLK#.R	8.42	3.82	2.21	0.45
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	K.K#EPEK#PIDR@.E	7.70	7.59	1.01	0.99
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	K.KEPEKPIDREK.T	4.85	1.59	3.06	0.33
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	R.KGTDDSM*TLQSQK.F	46.82	28.42	1.65	0.61
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	R.K#GTDDSM*TLQSQK#.F	102.27	48.09	2.13	0.47
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	R.KGTDDSMTLQSQK.F	23.01	10.66	2.16	0.46
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	R.M*DEFSR@.G	104.66	28.77	3.64	0.27
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	R.VKEIGSTM*SGR.K	56.71	24.62	2.30	0.43
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	R.VTQEEIK#.K	157.36	88.08	1.79	0.56
O55128_SAP18_MOUSE	Sap18	Histone deacetylase com	K.FQIGDYLDIAITPPNR@.A	7.78	6.36	1.22	0.82
Q02614_S30BP_MOUSE	Sap30bp	SAP30-binding protein O	K.EGM*DM*NYIIQR@.K	10.13	4.43	2.29	0.44
Q02614_S30BP_MOUSE	Sap30bp	SAP30-binding protein O	K.K#GTTTNATATSTSTASTAVADAQK#.R	6.92	4.38	1.58	0.63
Q02614_S30BP_MOUSE	Sap30bp	SAP30-binding protein O	K.TTVISAVGTIVK#.K	15.96	6.34	2.52	0.40
Q99JZ4_Q99JZ4_MOUSE	Sar1a	GTP-binding protein SAR	R.EIFGLYGQTTGK#.G	14.86	6.87	2.16	0.46
Q99JZ4_Q99JZ4_MOUSE	Sar1a	GTP-binding protein SAR	K.LVFLGLDNAGK#.T	32.80	13.66	2.40	0.42
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.EAAGTTAAAGTGGTTEQPPR@.H	7.91	6.05	1.31	0.76
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.ADDLLPLGDQTQDGDFGSR@.L	56.34	22.25	2.53	0.39
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.ASSGDASSLSIEETNK#.L	83.21	27.66	3.01	0.33
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.DKGVLQDGEDVLVNVNM*VDKER.A	29.18	10.80	2.70	0.37
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.DK#GVLQDGEDVLVNVNMVDK#ER@.A	8.84	2.25	3.93	0.25
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.DLQGLTVEHAIDSFR.E	26.26	10.10	2.60	0.38
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.DLQGLTVEHAIDSFR@EGETVVLTLK#.D	21.48	6.89	3.12	0.32
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.EAAGTTAAAGTGGTTEQPPR@.H	90.20	31.96	2.82	0.35
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.EAGTK#EEPVAADVINPMALR@.Q	31.07	24.94	1.25	0.80
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.EEPVAADVINPM*ALR@.Q	8.81	3.95	2.23	0.45
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.EGETVVLTLK#.D	70.09	35.83	1.96	0.51
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.GWEEEEDPER@.K	7.98	3.28	2.43	0.41
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.IEYVDETGR@.K	69.04	21.86	3.16	0.32
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.IEYVDETGR@K#.L	22.82	14.56	1.57	0.64
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.K#LDEEALLK#K#.M	110.03	37.43	2.94	0.34
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.LASEYLSPEEM*VTFK#.K	21.81	12.39	1.76	0.57

Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.LEQGGMADGLR@.E	14.74	8.60	1.71	0.58
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.LEQGGM*ADGLR@.E	86.31	28.96	2.98	0.34
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.LGLK#PLEVNAVK#.K	113.29	55.38	2.05	0.49
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.LGLKPLEVNAVKK.E	81.48	21.62	3.77	0.27
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.LLEEM*DQEFGVSTLVEEEFEQR@.R	58.21	25.21	2.31	0.43
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.LLEEMDQEFGVSTLVEEEFEQR@.R	12.62	5.81	2.17	0.46
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.LLEEM*DQEFGVSTLVEEEFEQR@R@.Q	19.31	6.75	2.86	0.35
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.LQAQSLSSVGPR@.L	206.76	83.31	2.48	0.40
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.M*SSSDTPLGTVALLQEK#.Q	51.12	22.90	2.23	0.45
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.M*SSSDTPLGTVALLQEK#.Q	23.14	8.07	2.87	0.35
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.QHQDFSASSTTILDEEPIVNR@.G	51.11	19.15	2.67	0.37
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.QLQQLQQLR@.D	111.00	35.30	3.14	0.32
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.R@DDGYEAAASSK#.A	9.54	3.84	2.49	0.40
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.R@QDLYSAR@.D	84.99	31.97	2.66	0.38
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.SQAEPSER@.R	12.73	4.85	2.62	0.38
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.TLGEDDPWLDDTAAWIER@.S	24.18	9.24	2.62	0.38
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.TLGEDDPWLDDTAAWIER.S	31.54	12.16	2.59	0.39
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.TLGEIPTYGLAGNR@.E	8.69	22.54	0.39	2.59
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.TPYIVLSGSGK#.S	110.41	48.99	2.25	0.44
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.VPEVEEEALEDEEK#DPVAQPPPSDDTR@.V	2.59	2.01	1.29	0.77
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.ADDLLPLGDQTQDGDFGSR@.L	6.33	27.51	0.23	4.35
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.ASSGDASSLSIEETNK#.L	9.99	3.59	2.78	0.36
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.EAAGTTAAAGTGGTTEQPPR.H	8.79	4.06	2.16	0.46
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	R.LEQGGM*ADGLR@.E	12.75	6.03	2.12	0.47
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.LLEEM*DQEFGVSTLVEEEFEQR@.R	8.26	4.16	1.98	0.50
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.M*SSSDTPLGTVALLQEK#.Q	10.91	4.37	2.50	0.40
Q9Z315_SNUT1_MOUSE	Sart1	U4/U6.U5 tri-snRNP-assc	K.QHQDFSASSTTILDEEPIVNR@.G	5.80	2.70	2.15	0.47
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.SNQVTAPEYVFLISELAGEQR@.F	6.28	3.98	1.58	0.63
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.AGFLIGDGAGVGK#.G	10.90	29.60	0.37	2.72
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.SNQVTAPEYVFLISELAGEQR@.F	6.39	3.28	1.95	0.51
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	K.TGLAVLELQNK#.L	11.33	2.41	4.69	0.21
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.VVSNDDGSISYESR@.S	8.62	1.96	4.41	0.23
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.AGFLIGDGAGVGK#.G	6.42	16.07	0.40	2.50
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	K.IEEVLLSQSYVK#.M	8.73	2.51	3.47	0.29
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.LGIWGEGTPFR@.E	11.39	2.85	4.00	0.25
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.QGLIGVGLINVEDR@.S	8.04	1.96	4.11	0.24
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.SELDVPVEILNITEK#.Q	13.45	3.81	3.53	0.28
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	K.SIDPDSIQSALLASGLGSK#.R	7.93	1.93	4.11	0.24
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.SNQVTAPEYVFLISELAGEQR@.F	12.23	3.12	3.91	0.26
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	K.TGLAVLELQNK#.L	14.82	5.21	2.85	0.35
Q689Z5_SBNO1_MOUSE	Sbno1	Protein strawberry notcł	R.VVYASATGASEPR.N	12.99	4.53	2.86	0.35
Q5U4C3_SFR19_MOUSE	Scaf1	Splicing factor, arginine/	R.SGGSSTASGGPGSLK#.K	2.19	2.84	0.77	1.30
Q6PFF0_Q6PFF0_MOUSE	Scaf4	Protein Scaf4 OS=Mus mu	K.DLSIGNPIPTVVSGAR@.G	8.85	4.84	1.83	0.55
Q6PFF0_Q6PFF0_MOUSE	Scaf4	Protein Scaf4 OS=Mus mu	K.HVVQIVEK#.F	10.00	6.89	1.45	0.69
Q6PFF0_Q6PFF0_MOUSE	Scaf4	Protein Scaf4 OS=Mus mu	K.DLSIGNPIPTVVSGAR@.G	17.07	6.11	2.79	0.36
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	R.VLNLWQK#.N	11.45	3.15	3.63	0.28
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	K.VPGLYVIDSIVR@.Q	46.85	15.22	3.08	0.32
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	K.TFNSELYSLNDYK#PPISK#.A	6.74	2.60	2.59	0.39
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	R.VLNLWQK#.N	14.47	5.19	2.79	0.36
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	K.VPGLYVIDSIVR@.Q	53.73	13.77	3.90	0.26
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	K.ASEPVK#EPVQTAQSPAPVEK#.E	6.20	2.75	2.26	0.44
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	R.FSNNIISTFQNLYR@.C	14.03	4.13	3.40	0.29
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	K.VK#VDDLDGFAEGGM*IDQETVNAEWETVK#.A	4.64	1.69	2.75	0.36
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	R.VLNLWQK#.N	26.82	9.89	2.71	0.37
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	K.VPGLYVIDSIVR@.Q	64.35	23.68	2.72	0.37
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	K.ASEPVK#EPVQTAQSPAPVEK#.E	6.16	2.49	2.47	0.40
Q6DID3_SCAF8_MOUSE	Scaf8	Protein SCAF8 OS=Mus m	R.VLNLWQK#.N	20.36	1.38	14.74	0.07
Q8K021_SCAM1_MOUSE	Scamp1	Secretory carrier-associa	K.AQQEFATGVM*SNK#.T	15.44	6.71	2.30	0.43
Q8K021_SCAM1_MOUSE	Scamp1	Secretory carrier-associa	K.TVQTAAANAASTAATSAAQNAFK#.G	34.38	15.66	2.20	0.46
Q9ERN0_SCAM2_MOUSE	Scamp2	Secretory carrier-associa	R.TGASFQQAQEEFSQGIFSSR@.T	20.78	10.86	1.91	0.52
O35609_SCAM3_MOUSE	Scamp3	Secretory carrier-associa	K.AQQEFAAGVFSNPAVR@.T	35.46	13.45	2.64	0.38
O35609_SCAM3_MOUSE	Scamp3	Secretory carrier-associa	R.DTGNPFPDSGELDNPFQDPAVIQHR@PSQQYATLDVYNPFENR@.E	4.79	3.87	1.24	0.81
O35609_SCAM3_MOUSE	Scamp3	Secretory carrier-associa	R.ELQHVALGGAGTR@.Q	45.46	13.91	3.27	0.31
O35609_SCAM3_MOUSE	Scamp3	Secretory carrier-associa	R.NYGSYSTQASAAAATAELLK#.K	19.28	3.01	6.41	0.16
O35609_SCAM3_MOUSE	Scamp3	Secretory carrier-associa	R.TAAANAAAGAAENAFR@.A	50.12	16.41	3.06	0.33
Q61009_SCRB1_MOUSE	Scarb1	Scavenger receptor class	R.FGAPLFLSHPHFYNADPVLSEAVLGLNPNPK#.E	8.62	2.27	3.79	0.26
Q61009_SCRB1_MOUSE	Scarb1	Scavenger receptor class	R.VFEGIPTYR@.F	9.71	5.08	1.91	0.52
Q8BRF7_SCFD1_MOUSE	Scfd1	Sec1 family domain-cont	R.FGQDIISPLLSVK#.E	47.95	20.90	2.29	0.44
Q8BRF7_SCFD1_MOUSE	Scfd1	Sec1 family domain-cont	K.GSPFPEVAESVQQELESYR@.A	5.28	2.74	1.92	0.52
Q8BRF7_SCFD1_MOUSE	Scfd1	Sec1 family domain-cont	R.LIDLHTNVATAVLEHIK#.A	11.64	3.75	3.10	0.32
Q8BRF7_SCFD1_MOUSE	Scfd1	Sec1 family domain-cont	K.LTSAVSSLPELLEK#.K	27.75	23.44	1.18	0.84
Q8BRF7_SCFD1_MOUSE	Scfd1	Sec1 family domain-cont	R.NQLYESYYLNFISAISR@.S	6.28	1.52	4.14	0.24
Q8BRF7_SCFD1_MOUSE	Scfd1	Sec1 family domain-cont	R.SK#LEDIANAALAASAVTQVAK#.V	34.18	11.26	3.03	0.33
Q8BRF7_SCFD1_MOUSE	Scfd1	Sec1 family domain-cont	K.SLLDVISDPDAGTPEDK#.M	10.76	4.68	2.30	0.43
Q8BRF7_SCFD1_MOUSE	Scfd1	Sec1 family domain-cont	R.VM*NTGSQFVM*EGVK#.N	14.11	4.92	2.87	0.35
Q8BRF7_SCFD1_MOUSE	Scfd1	Sec1 family domain-cont	R.FGQDIISPLLSVK#.E	10.44	4.86	2.15	0.47
Q6QIY3_SCNAA_MOUSE	Scn10a	Sodium channel protein	K.GSLSVLR@TFR@.L	2.40	15.66	0.15	6.51
P32020_NLTP_MOUSE	Scp2	Non-specific lipid-transfe	K.LQNLQLQPGK.A	3.55	9.30	0.38	2.62
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	R.AGTLQVGDR@.V	5.94	1.78	3.34	0.30
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	R.ALAALPSAGSLQR@.G	16.18	5.05	3.20	0.31
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	K.ALEIADFSGNPLSR@.L	12.55	8.50	1.48	0.68
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	R.FQTEDDAQTGEK#.V	8.81	3.19	2.76	0.36
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	K.LEQLDLGGNDLEVLPDTLGALPNLR@.E	9.59	2.49	3.85	0.26
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	K.LGLSDNEIQR@.L	10.48	3.36	3.12	0.32
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	R.LLEVNQQSLLGLTHAEAVQLLR@.S	24.97	4.72	5.30	0.19
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	R.LPDGFTQLR@.S	11.20	5.77	1.94	0.52
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	R.LPLLQPETPVSLR@.Q	20.36	5.65	3.60	0.28
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	R.SLEELLLDANQLR@.E	11.25	4.36	2.58	0.39
Q80U72_SCRIB_MOUSE	Scrib	Protein scribble homolo;	R.VSVIQFEDTLEGEEDAEEAAAEK#R@.G	9.76	2.18	4.48	0.22
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	R.AEAGGLK#EQELSWGLHQIVK#.A	7.51	1.90	3.95	0.25
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	K.ATGSAVSIFVYDVK#PGAEEQTQVAK#.A	11.62	4.71	2.47	0.41
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	K.FFQELSK#.S	24.87	10.70	2.33	0.43
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	R.FVETNLFLEEIQIK#EPAEK#.Q	28.32	10.94	2.59	0.39
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	K.IGSYLSASTR@.H	13.61	5.12	2.66	0.38
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	R.LLQQM*EQFIQYLDEPTVNTQIFPHVTHGFLDTNPAIR@.E	4.40	2.52	1.75	0.57
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	K.LNEANLNVELM*K#.H	32.21	6.79	4.74	0.21
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	R.DFPFELSPEPPEGGPPGPWILHR@.G	6.68	1.91	3.51	0.29
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	K.LESVSEDPTQLAEVEK#.D	9.19	15.03	0.61	1.64
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	K.LESVSEDPTQLAEVEK#DVHAASSPGTGGAAASWAGWAVTGVSSLTSK#.L	7.59	1.57	4.85	0.21
Q9EQC5_NTKL_MOUSE	Scyl1	N-terminal kinase-like pr	K.LNEANLNVELM*K#.H	77.95	5.03	15.50	0.06
Q8CFE4_SCYL2_MOUSE	Scyl2	SCY1-like protein 2 OS=M	K.LILPELGPVFK#.Q	18.76	11.36	1.65	0.61
Q8CFE4_SCYL2_MOUSE	Scyl2	SCY1-like protein 2 OS=M	K.VTADVTSAVM*GNPVTR@.E	8.45	3.22	2.62	0.38
Q80UZ2_SDA1_MOUSE	Sdad1	Protein SDA1 homolog O	K.LPSNLPQLQNLIK#.R	6.26	3.04	2.06	0.49

Q80UZ2_SDA1_MOUSE	Sdad1	Protein SDA1 homolog O	K.LDSM*PM*EER@.K	5.19	2.23	2.32	0.43
O35988_SDC4_MOUSE	Sdc4	Syndecan-4 OS=Mus mus	R.ETEVIDPQDLLEGR@.Y	20.44	6.63	3.08	0.32
Q9DCT5_SDF2_MOUSE	Sdf2	Stromal cell-derived fact	R.YGSGSGQQSVTGVTSVDDSNSYWR@.I	5.40	2.18	2.48	0.40
Q9ESP1_SDF2L_MOUSE	Sdf2l1	Stromal cell-derived fact	K.AM*EGIFIK#PGADLSTGHDEL.-	13.54	11.62	1.16	0.86
Q61112_CAB45_MOUSE	Sdf4	45 kDa calcium-binding	K.YSEFFTGSK.L	8.85	13.56	0.65	1.53
Q63918_SDPR_MOUSE	Sdpr	Serum deprivation-respo	K.FQHPNTDM*LQEKPSSPSPM*PSSTPSPSLNLGSTEEAIR.D	2.34	1.60	1.46	0.69
Q63918_SDPR_MOUSE	Sdpr	Serum deprivation-respo	K.LVNM*LDAVR@.E	32.54	24.42	1.33	0.75
Q63918_SDPR_MOUSE	Sdpr	Serum deprivation-respo	K.VLIFQEESEIPASVFVK.E	25.52	20.88	1.22	0.82
Q63918_SDPR_MOUSE	Sdpr	Serum deprivation-respo	K.YQASTSNTVSK#.L	23.94	20.74	1.15	0.87
Q63918_SDPR_MOUSE	Sdpr	Serum deprivation-respo	K.GIQNDLTK#.L	37.00	22.15	1.67	0.60
Q63918_SDPR_MOUSE	Sdpr	Serum deprivation-respo	K.QVQPAVLHVDQTA.-	42.34	42.34	1.00	1.00
Q63918_SDPR_MOUSE	Sdpr	Serum deprivation-respo	R.R@GNNSAVGSNADLTIEEDEEEEPVALQQAQQVR@.Y	4.88	2.18	2.24	0.45
Q63918_SDPR_MOUSE	Sdpr	Serum deprivation-respo	K.VLIFQEESEIPASVFVK#EPVPSAAEGK#EELADENK#.S	15.96	2.61	6.12	0.16
Q63918_SDPR_MOUSE	Sdpr	Serum deprivation-respo	K.YQASTSNTVSK#.L	45.37	23.19	1.96	0.51
Q9R0P6_SC11A_MOUSE	Sec11a	Signal peptidase comple	R.GDLLFLTNR@.V	7.31	3.69	1.98	0.50
Q9R0P6_SC11A_MOUSE	Sec11a	Signal peptidase comple	R.VGEIVVFR.I	20.05	14.46	1.39	0.72
Q9D1M0_SEC13_MOUSE	Sec13	Protein SEC13 homolog	K.GQGSVSASITEGQQNEQ.-	14.67	14.67	1.00	1.00
Q9D1M0_SEC13_MOUSE	Sec13	Protein SEC13 homolog	R.NGGQILIADLR@.G	38.29	15.54	2.46	0.41
F7BPW6_F7BPW6_MOUSE	Sec16a	Protein Sec16a (Fragmen	R.APSLTSDSEGK#.K	7.13	1.66	4.30	0.23
F7BPW6_F7BPW6_MOUSE	Sec16a	Protein Sec16a (Fragmen	K.FATNEAIQR@.T	20.56	15.57	1.32	0.76
F7BPW6_F7BPW6_MOUSE	Sec16a	Protein Sec16a (Fragmen	K.SVLTQPGAYSPVLISQLTQM*ASQLR@.L	4.66	3.19	1.46	0.69
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	K.ANNLSSLSK#.K	12.55	45.82	0.27	3.65
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.GEALSALDSK#.A	17.12	4.86	3.52	0.28
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.IM*VANIEEVLQR@.G	10.80	4.37	2.47	0.40
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	K.K#LAFAYLEDLHSEFDEQHGK#.K	11.91	5.25	2.27	0.44
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.NLGSINTELQDVQR@.I	15.84	5.89	2.69	0.37
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.VADGLPLAASM*QEDEQSGR@.D	11.10	4.42	2.51	0.40
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.GEALSALDSK#.A	50.60	9.91	5.10	0.20
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.IM*VANIEEVLQR@.G	50.83	9.12	5.58	0.18
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	K.K#LAFAYLEDLHSEFDEQHGK#.K	31.12	13.69	2.27	0.44
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.NLGSINTELQDVQR@.I	43.29	9.27	4.67	0.21
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.R@NLGSINTELQDVQR@.I	25.10	2.79	8.99	0.11
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.VADGLPLAASM*QEDEQSGR@.D	21.17	5.60	3.78	0.26
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.VADGLPLAASMQEDEQSGR@.D	3.22	2.00	1.61	0.62
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.VADGLPLAASM*QEDEQSGR@DLQQYQSQAK#.Q	5.02	1.17	4.29	0.23
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.DLQQYQSQAK#.Q	9.30	8.29	1.12	0.89
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.NLGSINTELQDVQR@.I	9.92	4.90	2.02	0.49
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.GEALSALDSK#.A	10.90	6.41	1.70	0.59
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.NLGSINTELQDVQR@.I	9.97	7.09	1.41	0.71
O08547_SC22B_MOUSE	Sec22b	Vesicle-trafficking protei	R.VADGLPLAASM*QEDEQSGR@.D	7.34	5.56	1.32	0.76
Q01405_SC23A_MOUSE	Sec23a	Protein transport protei	R.HLLQAPVDDAQEILHSR@.F	13.77	12.72	1.08	0.92
Q01405_SC23A_MOUSE	Sec23a	Protein transport protei	R.M*VVPVAALFTPLK#.E	8.63	5.66	1.52	0.66
Q01405_SC23A_MOUSE	Sec23a	Protein transport protei	R.SPFLQVFNNSPDESSYYR@.H	5.58	2.67	2.09	0.48
Q01405_SC23A_MOUSE	Sec23a	Protein transport protei	R.M*VVPVAALFTPLK#.E	6.88	3.83	1.80	0.56
Q9D662_SC23B_MOUSE	Sec23b	Protein transport protei	R.AESEEGPDVLR@.W	11.69	2.68	4.36	0.23
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.TTFEDLIQR@.C	6.78	3.97	1.71	0.59
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.AQDGSSPLSLQDLIEK#.V	27.95	8.75	3.20	0.31
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.AVQLTQALDTNTVGALLAEK#.M	13.60	4.19	3.24	0.31
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.IALALNK#.V	16.92	5.96	2.84	0.35
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.IEASQTEFEK#.N	9.23	4.16	2.22	0.45
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	R.ISVYSIM*GGSIDGLR@.Q	24.91	6.70	3.72	0.27
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	R.K#AVQLTQALDTNTVGALLAEK#.M	14.53	6.44	2.26	0.44
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.LVTFESVAVPLQQGAEQQR@.R	35.87	10.74	3.34	0.30
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.LVTFESVAVPLQQGAEQQR.R	16.15	5.76	2.80	0.36
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	R.M*ADAIILAIAGGQELLAQTQK#.K	39.93	15.58	2.56	0.39
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	R.R@QPVFISQVVTEK#DFLNR@.S	16.04	5.74	2.80	0.36
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.TTFEDLIQR@.C	18.32	6.17	2.97	0.34
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.VVLSQASK#.L	18.51	7.54	2.45	0.41
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.YLELLGYR@.K	31.53	12.07	2.61	0.38
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.AQDGSSPLSLQDLIEK#.V	21.27	7.44	2.86	0.35
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.AQGK#PVSGQESSQSPYER@.Q	18.42	4.71	3.91	0.26
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.AVQLTQALDTNTVGALLAEK#.M	11.54	3.00	3.84	0.26
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	R.ISVYSIM*GGSIDGLR@.Q	13.92	3.16	4.41	0.23
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	R.K#AVQLTQALDTNTVGALLAEK#.M	9.86	2.81	3.51	0.28
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	K.LVTFESVAVPLQQGAEQQR@.R	18.92	5.43	3.48	0.29
Q3UPL0_SC31A_MOUSE	Sec31a	Protein transport protei	R.R@QPVFISQVVTEK#DFLNR@.S	8.07	1.79	4.50	0.22
P61620_S61A1_MOUSE	Sec61a1	Protein transport protei	K.AFSPTTVNTGR@.G	38.88	13.22	2.94	0.34
P61620_S61A1_MOUSE	Sec61a1	Protein transport protei	K.IIEVGDTPK#.D	20.11	9.04	2.22	0.45
P60060_SC61G_MOUSE	Sec61g	Protein transport protei	K.LIHIPINNIIVGG.-	12.79	12.79	1.00	1.00
Q8BU14_SEC62_MOUSE	Sec62	Translocation protein SE	K.K#GEDALFTTR@.E	8.60	2.40	3.59	0.28
Q8R2U0_SEH1_MOUSE	Seh1l	Nucleoporin SEH1 OS=M	K.VQIFEYNENTR@.K	10.87	6.18	1.76	0.57
Q3UQA7_SELH_MOUSE	Selh	Selenoprotein H OS=Mus	R.HAAALSQALQLEAPELPVQVNPSKPR.R	2.61	3.16	0.83	1.21
Q3UQA7_SELH_MOUSE	Selh	Selenoprotein H OS=Mus	K.LK#FPEPQEVVEELK#K#.Y	6.62	12.66	0.52	1.91
Q3UQA7_SELH_MOUSE	Selh	Selenoprotein H OS=Mus	R.VELWTGIK.K	13.81	20.90	0.66	1.51
Q8VHC3_SELM_MOUSE	Selm	Selenoprotein M OS=Mu	R.DEINALVQELGFYR@.K	6.44	7.94	0.81	1.23
P62342_SELT_MOUSE	Selt	Selenoprotein T OS=Mus	R.IEGENYLPQPIYR@.H	4.88	3.72	1.31	0.76
Q9EP97_SENP3_MOUSE	Senp3	Sentrin-specific protease	R.LGLLGALM*AEDGM*R@.G	5.01	2.32	2.16	0.46
Q9EP97_SENP3_MOUSE	Senp3	Sentrin-specific protease	R.LGLLGALM*AEDGM*R.G	13.33	6.43	2.07	0.48
Q9EP97_SENP3_MOUSE	Senp3	Sentrin-specific protease	K.SGGGFGPDPGSGTTVPTR@.R	12.04	5.13	2.35	0.43
Q9EP97_SENP3_MOUSE	Senp3	Sentrin-specific protease	K.SLVLQLIQSYQR@.M	8.21	2.42	3.40	0.29
Q9EP97_SENP3_MOUSE	Senp3	Sentrin-specific protease	R.TITYFDSQR@.T	13.31	4.84	2.75	0.36
Q8BUH8_SENP7_MOUSE	Senp7	Sentrin-specific protease	R.VILTDIR.Q	1.94	19.44	0.10	10.04
Q8C1B7_SEP11_MOUSE	Sept11	Septin-11 OS=Mus musc	K.AAAQLLQSQAQQSGAQQTK#.K	25.22	12.09	2.09	0.48
Q8C1B7_SEP11_MOUSE	Sept11	Septin-11 OS=Mus musc	K.ELEEEVSNFQK#.K	10.65	4.68	2.27	0.44
Q8C1B7_SEP11_MOUSE	Sept11	Septin-11 OS=Mus musc	R.NLSLSGHVGFDSLPDQLVNK#.S	13.90	3.55	3.91	0.26
Q8C1B7_SEP11_MOUSE	Sept11	Septin-11 OS=Mus musc	K.R@NEFLGELQK#.K	9.86	1.88	5.23	0.19
Q8C1B7_SEP11_MOUSE	Sept11	Septin-11 OS=Mus musc	K.STLM*DTLFNTK#.F	9.29	8.92	1.04	0.96
Q8C1B7_SEP11_MOUSE	Sept11	Septin-11 OS=Mus musc	R.SYELQESNVR@.L	23.42	5.54	4.22	0.24
Q8C1B7_SEP11_MOUSE	Sept11	Septin-11 OS=Mus musc	R.VNM*EDLR@.E	24.66	6.94	3.55	0.28
Q9ERR7_SEP15_MOUSE	Sept15	15 kDa selenoprotein OS	R.FPQVQAFVR.S	43.91	27.86	1.58	0.63
Q9ERR7_SEP15_MOUSE	Sept15	15 kDa selenoprotein OS	K.LLDDNGNIAEELSILK#.W	24.97	20.01	1.25	0.80
Q9ERR7_SEP15_MOUSE	Sept15	15 kDa selenoprotein OS	K.WNTDSVEEFLSEK#LER@.I	12.45	7.88	1.58	0.63
P42208_SEPT2_MOUSE	Sept2	Septin-2 OS=Mus muscul	K.QQPTQFINPETPGYVGFANLPNQVHR@.K	12.90	2.40	5.37	0.19
P42208_SEPT2_MOUSE	Sept2	Septin-2 OS=Mus muscul	K.STLINSLFLTDLYPER@.I	35.38	9.67	3.66	0.27
P42208_SEPT2_MOUSE	Sept2	Septin-2 OS=Mus muscul	K.TIISYIDEQFER@.Y	29.41	12.87	2.29	0.44
P42208_SEPT2_MOUSE	Sept2	Septin-2 OS=Mus muscul	R.TVQIEASTVEIEER@.G	19.41	7.39	2.63	0.38
P42208_SEPT2_MOUSE	Sept2	Septin-2 OS=Mus muscul	K.VNIVPVIAK#.A	10.40	4.06	2.56	0.39
O55131_SEPT7_MOUSE	Sept7	Septin-7 OS=Mus muscul	K.FEDYLNAESR@.V	12.59	2.67	4.71	0.21
O55131_SEPT7_MOUSE	Sept7	Septin-7 OS=Mus muscul	K.NLEGYVGFANLPNQVYR@.K	11.96	2.78	4.29	0.23
O55131_SEPT7_MOUSE	Sept7	Septin-7 OS=Mus muscul	K.SPLAQM*EEER@.R	2.99	3.38	0.89	1.13
O55131_SEPT7_MOUSE	Sept7	Septin-7 OS=Mus muscul	K.NLEGYVGFANLPNQVYR@.K	3.37	3.67	0.92	1.09
Q80UG5_SEPT9_MOUSE	Sept9	Septin-9 OS=Mus muscul	K.ADTLTLEER@.V	19.75	4.34	4.55	0.22
Q80UG5_SEPT9_MOUSE	Sept9	Septin-9 OS=Mus muscul	K.IPEGSAVPATDAAPK#.R	17.59	3.69	4.77	0.21

Q80UG5_SEPT9_MOUSE	Sept9	Septin-9 OS=Mus muscul	R.R@TEITIVK#PQESVLR@.R	13.54	1.42	9.55	0.10
Q80UG5_SEPT9_MOUSE	Sept9	Septin-9 OS=Mus muscul	K.VVNIVPVIAK#.A	20.62	5.08	4.06	0.25
Q9CY58_PAIRB_MOUSE	Serbp1	Plasminogen activator in	R.FDQLFDDESDPFEVLK#.A	26.76	12.77	2.10	0.48
Q9CY58_PAIRB_MOUSE	Serbp1	Plasminogen activator in	R.R@PDQQLQGDGK#.L	16.58	9.14	1.81	0.55
Q9CY58_PAIRB_MOUSE	Serbp1	Plasminogen activator in	K.SAAQAAAQTNSNAAGK#.Q	33.22	19.79	1.68	0.60
Q9CY58_PAIRB_MOUSE	Serbp1	Plasminogen activator in	K.SSASAPDVDDPEAFPALA.-	19.18	19.18	1.00	1.00
Q9CY58_PAIRB_MOUSE	Serbp1	Plasminogen activator in	K.SAAQAAAQTNSNAAGK#.Q	5.50	2.92	1.89	0.53
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.AVAISLPK#.G	876.64	476.71	1.84	0.54
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.AVLSAEK#.L	1137.64	519.76	2.19	0.46
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.DEEVHTGLGELLR@.S	14.97	5.95	2.52	0.40
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.DNQSGSLLFIGR@.L	1913.80	759.92	2.52	0.40
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.GDK#M*R@DEL.-	100.43	40.11	2.50	0.40
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.GVVEVTHDLQK#.H	946.05	439.44	2.15	0.46
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.HLAGLGLTEAIDK#.N	310.53	153.62	2.02	0.49
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.HLAGLGLTEAIDK#NK#.A	2193.22	762.24	2.88	0.35
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.HLAGLGLTEAIDK#NK#ADLSR@.M	18.76	2.49	7.54	0.13
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.K#AVAISLPK#.G	774.25	340.42	2.27	0.44
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.K#DLYLASVFHATAFEWDTEGNPFDQDIYGR@EELR@.S	7.81	5.37	1.46	0.69
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.K#PLEAAAPGTAEK#.L	234.64	60.92	3.85	0.26
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LFYADHPFIFLVR.D	256.28	100.37	2.55	0.39
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LFYADHPFIFLVR@.D	2155.72	900.61	2.39	0.42
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQM*VEM*PLAHK#.L	1102.54	508.07	2.17	0.46
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQM*VEM*PLAHK#.L	90.07	37.22	2.42	0.41
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQMVEM*PLAHK#.L	105.22	54.21	1.94	0.52
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQMVEM*PLAHK#.L	13.72	6.60	2.08	0.48
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQM*VEMPLAHK#.L	91.84	38.82	2.37	0.42
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQMVEMPLAHK#.L	58.53	23.49	2.49	0.40
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LR@DEEVHTGLGELLR@.S	1553.18	590.77	2.63	0.38
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LR@DEEVHTGLGELLR@.S	76.90	24.67	3.12	0.32
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LSSLIILM*PHHVEPLER.L	12.27	6.94	1.77	0.57
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LSSLIILMPHHVEPLER@.L	173.53	81.39	2.13	0.47
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LSSLIILMPHHVEPLER@.L	421.99	194.01	2.18	0.46
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.LYGPSSVSFADDFVR@.S	1913.34	838.97	2.28	0.44
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.LYGPSSVSFADDFVR@.S	14.81	9.00	1.65	0.61
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.R@SALQSINEWASQTTDGK#LPEVTK#.D	6.60	2.43	2.71	0.37
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SALQSINEWASQTTDGK#.L	100.29	42.17	2.38	0.42
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SALQSINEWASQTTDGKLPEVTK.D	1127.54	442.61	2.55	0.39
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.STGLAFSLYQAM*AK#.D	822.78	363.21	2.27	0.44
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.STGLAFSLYQAMAK#.D	100.87	47.68	2.12	0.47
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SYTVGVTM*M*HR@.T	201.38	85.87	2.35	0.43
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SYTVGVTM*MHR.T	33.11	16.11	2.06	0.49
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SYTVGVTMM*HR.T	28.39	11.40	2.49	0.40
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SYTVGVTMMHR.T	21.87	9.48	2.31	0.43
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TDGALLVNAM*FFKPHWDEK.F	161.22	65.85	2.45	0.41
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TDGALLVNAMFFK#PHWDEK#.F	143.77	54.77	2.63	0.38
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TGLYNYYDDEK#.E	89.95	47.16	1.91	0.52
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TGLYNYYDDEK#EK#.L	1171.55	561.22	2.09	0.48
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TGLYNYYDDEKEKLQM*VEM*PLAHK.L	168.14	62.40	2.69	0.37
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.AVAISLPK#.G	633.94	221.38	2.86	0.35
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.AVLSAEK#.L	57.42	31.10	1.85	0.54
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.DNQSGSLLFIGR@.L	1267.72	405.33	3.13	0.32
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.GDK#M*R@DEL.-	46.21	15.43	2.99	0.33
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.GVVEVTHDLQK#.H	243.77	63.76	3.82	0.26
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.HLAGLGLTEAIDK#.N	64.14	18.52	3.46	0.29
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.HLAGLGLTEAIDK#NK#.A	817.05	234.99	3.48	0.29
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.K#AVAISLPK#.G	302.81	91.30	3.32	0.30
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.K#PLEAAAPGTAEK#.L	3.92	1.25	3.14	0.32
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LFYADHPFIFLVR.D	114.94	39.62	2.90	0.34
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LFYADHPFIFLVR@.D	732.92	217.66	3.37	0.30
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQM*VEM*PLAHK#.L	35.25	10.85	3.25	0.31
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQM*VEM*PLAHK#.L	249.94	75.69	3.30	0.30
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LR@DEEVHTGLGELLR@.S	80.99	45.79	1.77	0.57
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LSSLIILMPHHVEPLER@.L	82.69	36.13	2.29	0.44
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.LYGPSSVSFADDFVR@.S	96.39	58.78	1.64	0.61
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.STGLAFSLYQAM*AK#.D	21.31	13.94	1.53	0.65
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SYTVGVTMMHR@.T	2.93	2.52	1.16	0.86
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SYTVGVTM*M*HR@.T	87.33	28.36	3.08	0.32
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TGLYNYYDDEK#.E	33.83	10.43	3.24	0.31
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TGLYNYYDDEK#EK#.L	335.61	98.20	3.42	0.29
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.AVAISLPK#.G	136.43	82.83	1.65	0.61
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.DNQSGSLLFIGR@.L	241.03	138.83	1.74	0.58
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.GVVEVTHDLQK#.H	140.60	91.50	1.54	0.65
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.HLAGLGLTEAIDK#.N	75.95	39.84	1.91	0.52
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.HLAGLGLTEAIDK#NK#.A	375.25	190.04	1.97	0.51
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.K#AVAISLPK#.G	85.17	50.62	1.68	0.59
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.K#PLEAAAPGTAEK#.L	16.73	5.92	2.82	0.35
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQM*VEM*PLAHK#.L	72.68	50.46	1.44	0.69
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LRDEEVHTGLGELLR.S	230.58	114.06	2.02	0.49
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LSSLIILM*PHHVEPLER@.L	110.19	61.47	1.79	0.56
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LSSLIILMPHHVEPLER@.L	53.52	27.96	1.91	0.52
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.LYGPSSVSFADDFVR@.S	358.97	198.61	1.81	0.55
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SALQSINEWASQTTDGK#.L	8.71	5.86	1.49	0.67
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SALQSINEWASQTTDGKLPEVTK.D	109.84	61.45	1.79	0.56
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.STGLAFSLYQAM*AK#.D	100.64	53.89	1.87	0.54
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.STGLAFSLYQAM*AK#.D	15.75	7.60	2.07	0.48
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.STGLAFSLYQAMAK#.D	10.27	7.74	1.33	0.75
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SYTVGVTM*M*HR.T	27.86	18.38	1.52	0.66
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TDGALLVNAMFFK#PHWDEK#.F	20.60	10.34	1.99	0.50
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TGLYNYYDDEK#.E	7.22	3.87	1.87	0.54
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.TGLYNYYDDEK#EK#.L	190.70	124.87	1.53	0.65
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.AVAISLPK#.G	80.74	40.54	1.99	0.50
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.DNQSGSLLFIGR.L	132.51	49.77	2.66	0.38
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.HLAGLGLTEAIDK#.N	51.71	24.15	2.14	0.47
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.HLAGLGLTEAIDK#NK#.A	193.12	62.74	3.08	0.32
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.K#AVAISLPK#.G	37.28	19.18	1.94	0.51
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.K#PLEAAAPGTAEK#.L	11.34	3.06	3.70	0.27
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LQM*VEM*PLAHK#.L	41.39	26.69	1.55	0.64
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LR@DEEVHTGLGELLR@.S	124.54	41.94	2.97	0.34
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	K.LSSLIILM*PHHVEPLER@.L	54.49	27.87	1.96	0.51
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.LYGPSSVSFADDFVR@.S	214.31	86.92	2.47	0.41
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SALQSINEWASQTTDGK#.L	8.96	3.06	2.93	0.34
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.SALQSINEWASQTTDGKLPEVTK.D	56.50	19.07	2.96	0.34
P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus musc	R.STGLAFSLYQAM*AK#.D	50.15	18.39	2.73	0.37

P19324_SERPH_MOUSE	Serpinh1	Serpin H1 OS=Mus muscu	R.SYTVGVTM*M*HR@.T	15.16	7.22	2.10	0.48
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	R.EAYHLPLPM*AAEPLPSSSVSGEEAR@.L	9.86	5.24	1.88	0.53
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	K.FK#LDEFYIGQIPLK#.E	9.39	6.57	1.43	0.70
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	K.SGGITGIEAFAFGSGLR@.G	4.63	1.50	3.09	0.32
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	R.VLATLVQEM*K#.S	11.66	5.55	2.10	0.48
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	R.EAYHLPLPM*AAEPLPSSSVSGEEAR@.L	28.86	4.84	5.96	0.17
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	K.FK#LDEFYIGQIPLK#.E	9.54	1.59	6.01	0.17
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	K.FQGSGAAAETTEAR@.R	14.21	3.34	4.25	0.24
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	R.K#TVSFSAAEEAPVPEPSTAAPLQAK#.S	2.50	3.79	0.66	1.52
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	K.LIVDPALDPALR@.R	22.94	6.55	3.50	0.29
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	K.LK#EPGM*LSLVDWAK#.S	8.96	2.84	3.15	0.32
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	R.LLSAIGTSAIM*DSDLLK#.L	11.08	2.50	4.42	0.23
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	R.LPHR@EEAEIAESK#.V	31.33	7.41	4.23	0.24
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	K.SGGITGIEAFAFGSGLR@.G	27.36	8.76	3.12	0.32
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	K.TVSFSAAEEAPVPEPSTAAPLQAK#.S	11.70	3.67	3.19	0.31
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	R.VLATLVQEM*K#.S	28.42	6.57	4.33	0.23
E9PYH6_E9PYH6_MOUSE	Setd1a	Protein Setd1a OS=Mus n	K.YTPVEDLQDPR@.C	6.44	2.11	3.05	0.33
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	K.LFEQEVAQR@.E	10.95	10.58	1.03	0.97
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	K.LPTSEPEADTETEPK#.D	3.63	2.34	1.55	0.65
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	K.TAEADTSSELAK#.K	4.73	4.28	1.11	0.90
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	R.HAYEEEYESK#.G	4.21	5.90	0.71	1.40
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	K.LFEQEVAQR@.E	8.81	5.90	1.49	0.67
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	R.LQSVVVVPK#.N	22.16	9.63	2.30	0.43
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	K.LVPSGSELTFDYQFQR.Y	7.94	7.72	1.03	0.97
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	K.TAEADTSSELAK#.K	5.32	3.83	1.39	0.72
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	K.TLEHLPIPTK#.N	11.28	7.71	1.46	0.68
E9Q5F9_SETD2_MOUSE	Setd2	Histone-lysine N-methylt	K.TSRPQELPVYSDDFEDLPNK.S	22.43	12.92	1.74	0.58
O88974_SETB1_MOUSE	Setdb1	Histone-lysine N-methylt	R.APAEPSYR@.A	8.08	5.86	1.38	0.73
O88974_SETB1_MOUSE	Setdb1	Histone-lysine N-methylt	R.GK#NPLLVPLLYDFR@.R	9.00	4.20	2.14	0.47
A2AKX3_SETX_MOUSE	Setx	Probable helicase senata	K.EPMKADTHR@VLMK.V	15.40	1.05	14.61	0.07
A2AKX3_SETX_MOUSE	Setx	Probable helicase senata	R.WAILTAR@.N	11.81	3.84	3.07	0.33
A2AKX3_SETX_MOUSE	Setx	Probable helicase senata	K.LLTSQDLQFQR@.L	6.15	2.68	2.30	0.44
Q64213_SF01_MOUSE	Sf1	Splicing factor 1 OS=Mus	R.AYIVQLQIEDLTR@.K	14.97	10.46	1.43	0.70
Q64213_SF01_MOUSE	Sf1	Splicing factor 1 OS=Mus	R.ILR@PWQSSETR@.S	22.63	8.36	2.71	0.37
Q64213_SF01_MOUSE	Sf1	Splicing factor 1 OS=Mus	R.AYIVQLQIEDLTR@.K	24.33	15.70	1.55	0.65
Q64213_SF01_MOUSE	Sf1	Splicing factor 1 OS=Mus	R.HTLITEMVALNPDFKPPADYKPPATR.V	13.00	6.22	2.09	0.48
Q64213_SF01_MOUSE	Sf1	Splicing factor 1 OS=Mus	K.TVIPGM*PTVIPPGLTR@.E	9.89	5.12	1.93	0.52
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.ASK#PLPPAPAPDEYLVSPITGEK#.I	52.32	25.76	2.03	0.49
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.EDPTPSK#PVVGIIYPPPEVR@.N	13.87	6.85	2.03	0.49
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	R.EK#QSDDEVYAPGLDIESSLK#.Q	24.24	9.05	2.68	0.37
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.FNFLNPNDPYHAYYR@.H	56.05	25.42	2.21	0.45
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.IGEEEIQK#PEEK#.V	61.71	29.66	2.08	0.48
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	R.IGLLDPR@.W	54.68	25.72	2.13	0.47
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.LNGQGLVFTLPLTDQVSVIK#.V	14.49	5.68	2.55	0.39
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.LQYEGIFIK#.D	41.02	18.80	2.18	0.46
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.LTAQFVAR@.N	52.32	22.93	2.28	0.44
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	R.QFLTQLM*QK#.E	26.54	10.30	2.58	0.39
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.QPIEEEASSK#.E	15.74	6.49	2.43	0.41
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.QSDDEVYAPGLDIESSLK#.Q	12.01	6.51	1.85	0.54
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	R.R@TDIFGVEETAIGK#.K	29.00	8.78	3.30	0.30
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	R.RTDIFGVEETAIGKK.I	54.40	23.11	2.35	0.42
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	R.TQQAAQANITLQEQIEAIHK#.A	67.75	21.17	3.20	0.31
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.VMQQQQQATQQQLPQK#.V	3.40	2.14	1.59	0.63
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.VM*QQQQQATQQQLPQK#.V	53.71	22.66	2.37	0.42
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.VQAQVIQETIVPK#.E	75.75	39.16	1.93	0.52
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.ASK#PLPPAPAPDEYLVSPITGEK#.I	9.67	5.88	1.64	0.61
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	R.IGLLDPR@.W	10.47	5.93	1.77	0.57
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.LTAQFVAR@.N	9.57	2.36	4.06	0.25
Q8K4Z5_SF3A1_MOUSE	Sf3a1	Splicing factor 3A subuni	K.VQAQVIQETIVPK#.E	17.20	6.72	2.56	0.39
Q62203_SF3A2_MOUSE	Sf3a2	Splicing factor 3A subuni	R.DTEM*GQQSLLFQIDYPEIAEGIM*PR@.H	15.10	5.20	2.90	0.34
Q62203_SF3A2_MOUSE	Sf3a2	Splicing factor 3A subuni	K.TGSGGVASSSESNR@.D	11.11	4.86	2.29	0.44
Q62203_SF3A2_MOUSE	Sf3a2	Splicing factor 3A subuni	R.WQYLLM*AAEPYETIAFK#.V	6.59	3.20	2.06	0.48
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	K.AR@ENPSEEAQNLVEFTDEEGYGR@.Y	8.65	2.67	3.24	0.31
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	R.ENPSEEAQNLVEFTDEEGYGR@.Y	7.78	2.58	3.02	0.33
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	K.SLESLDTSLFAK#.N	32.91	16.83	1.96	0.51
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	R.VK#PLQDQNELFGK#.I	22.17	10.37	2.14	0.47
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	K.AR@ENPSEEAQNLVEFTDEEGYGR@.Y	11.02	3.94	2.80	0.36
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	K.EELNAISGPNEFAEFYNR@.L	4.56	3.81	1.20	0.84
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	R.ENPSEEAQNLVEFTDEEGYGR@.Y	6.26	3.82	1.64	0.61
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	R.K#EELNAISGPNEFAEFYNR@.L	5.02	1.83	2.75	0.36
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	K.SALLALGLK#.C	32.54	12.07	2.70	0.37
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	K.SLESLDTSLFAK#.N	47.45	19.72	2.41	0.42
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	R.VKPLQDQNELFGK.I	48.31	20.12	2.40	0.42
Q9D554_SF3A3_MOUSE	Sf3a3	Splicing factor 3A subuni	R.YLEM*LLEYLQDYTDR@.V	12.35	4.54	2.72	0.37
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.AAGLATM*ISTM*RPDIDNM*DEYVR.N	27.56	15.82	1.74	0.57
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.AIGPHDVLATLLNNLK#.V	51.87	40.97	1.27	0.79
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.AIGYLIPLM*DAEYANYYTR@.E	7.93	5.95	1.33	0.75
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.EVM*LILIR@.E	35.27	32.13	1.10	0.91
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.GAEYVSAR@.E	58.08	30.28	1.92	0.52
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.GDTPGHATPGHGGATSSAR@.K	29.25	20.72	1.41	0.71
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.GGDSIGETPTPGASK#.R	25.07	17.45	1.44	0.70
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.GLAAFLK.A	13.85	14.46	0.96	1.04
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.GSETPGATPGSK#.I	12.49	9.05	1.38	0.72
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.IYNSIYIGSQDALIAHYPR@.I	32.12	30.28	1.06	0.94
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.K#AALDEAQGVGLDSTGYYDQEIYGGSDSR@.F	11.47	10.58	1.08	0.92
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.LLVDVDESTLSPEEQK.E	9.90	10.06	0.98	1.02
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.LLVDVDESTLSPEEQK#ER@.K	67.02	56.41	1.19	0.84
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.M*VM*ETIEK#.I	28.02	15.87	1.77	0.57
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.NR@PLSDEELDAM*FPEGYK#.V	33.81	24.49	1.38	0.72
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.SLSFLFEYIGEM*GK#.D	6.61	4.16	1.59	0.63
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.SLVEIIEHGLVDEQQK#.V	93.69	61.19	1.53	0.65
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.SR@WDETPASQM*GGSTPVLTPGK#.T	7.89	6.39	1.24	0.81
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.TEILPPFFK#.H	72.18	59.74	1.21	0.83
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.THEDIEAQIR@.E	30.81	18.23	1.69	0.59
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.TM*IISPER@.L	21.69	14.32	1.52	0.66
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.VGAAEIISR@.I	79.37	68.23	1.16	0.86
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.VPELNVQNGVLK#.S	10.64	9.40	1.13	0.88
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.WDQTADQTPGATPK#.K	7.63	7.34	1.04	0.96
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.AALDEAQGVGLDSTGYYDQEIYGGSDSR@.F	17.51	9.33	1.88	0.53
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.AIGPHDVLATLLNNLK#.V	65.60	47.82	1.37	0.73
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.AIGYLIPLM*DAEYANYYTR@.E	10.01	5.87	1.70	0.59
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.ATVNTFGYIAK#.A	61.21	23.66	2.59	0.39
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.EFQSPDEEM*K#K#.I	5.74	3.96	1.45	0.69

Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.EVM*LILIR@.E	46.04	22.04	2.09	0.48
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.FAGYVTSIAATELEDDDDDYSSSTSLLGQK#.K	46.87	18.86	2.48	0.40
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.GAEYVSAR@.E	32.26	13.56	2.38	0.42
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.GDTPGHATPGHGGATSSAR@.K	60.53	25.07	2.41	0.41
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.GGDSIGETPTPGASK#.R	47.11	23.48	2.01	0.50
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.GLAAFLK#.A	46.11	23.71	1.95	0.51
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.GSETPGATPGSK#.I	19.62	8.84	2.22	0.45
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.IM*GNLGAADIDHK#.L	16.36	7.88	2.08	0.48
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.IYNSIYIGSQDALIAHYPR@.I	38.81	15.92	2.44	0.41
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.KAALDEAQGVGLDSTGYYDQEIYGGSDSR.F	15.13	8.83	1.71	0.58
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.LLVDVDESTLSPEEQK#.E	24.82	15.79	1.57	0.64
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.LLVDVDESTLSPEEQK#ER@.K	56.23	30.47	1.85	0.54
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.M*VM*ETIEK#.I	34.24	17.30	1.98	0.51
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.NR@PLSDEELDAM*FPEGYK#.V	48.60	33.84	1.44	0.70
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.QLVDTTVELANK#.V	38.91	19.89	1.96	0.51
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.QQAADLISR.T	54.83	29.01	1.89	0.53
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.SLVEIIEHGLVDEQQK#.V	137.68	77.84	1.77	0.57
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.SR@WDETPASQM*GGSTPVLTPGK#.T	8.91	6.24	1.43	0.70
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.SVNDQPSGNLPFLKPDDIQYFDK.L	53.36	37.30	1.43	0.70
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.TDR@GGDSIGETPTPGASK#.R	14.75	5.32	2.77	0.36
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.TEILPPFFK#.H	100.73	56.58	1.78	0.56
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.THEDIEAQIR.E	29.27	11.61	2.52	0.40
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.TM*IISPER@.L	24.16	13.94	1.73	0.58
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.VGAAEIISR@.I	117.73	58.28	2.02	0.50
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.VLPPPAGYVPIR@.T	43.36	29.64	1.46	0.68
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.VPELNVQNGVLK#.S	30.96	19.50	1.59	0.63
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	K.VVNGAAASQPPSK#.R	9.77	3.68	2.65	0.38
Q99NB9_SF3B1_MOUSE	Sf3b1	Splicing factor 3B subuni	R.WDETPASQM*GGSTPVLTPGK#.T	5.96	5.19	1.15	0.87
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.EALQEK#EEQK#.T	13.66	10.83	1.26	0.79
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.ESRQEEM*NSQQEEEEM*ETDTR.S	8.63	4.83	1.79	0.56
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.FTVAELK#.Q	138.02	81.95	1.68	0.59
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.GIEK#PPFELPDFIK#.R	113.90	128.63	0.89	1.13
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.IDIDYQK.L	118.34	103.91	1.14	0.88
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.IEEAM*DGSETPQLFTVLPEKR.T	36.38	29.64	1.23	0.81
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.IFEAFK#.L	85.08	54.85	1.55	0.64
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.IPQALEK#.I	118.14	96.19	1.23	0.81
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.KGPAPELQGVEVALAPEELELDPM*AM*TQK.Y	37.95	38.10	1.00	1.00
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.KGPAPELQGVEVALAPEELELDPM*AMTQK.Y	4.23	5.17	0.82	1.22
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.KGPAPELQGVEVALAPEELELDPMAM*TQK.Y	5.49	4.19	1.31	0.76
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.KGPAPELQGVEVALAPEELELDPMAMTQK.Y	4.71	4.31	1.09	0.91
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.KPGDLSDELR.I	52.96	42.75	1.24	0.81
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.K#PGDLSDELR@.I	101.08	76.59	1.32	0.76
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.LAEIGAPIQGSR.E	91.42	77.94	1.17	0.85
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.LAQQQAALLM*QQEER@.A	16.74	11.28	1.48	0.67
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.LAQQQAALLMQQEER@.A	14.38	10.52	1.37	0.73
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.LLVHLK#.A	32.22	23.46	1.37	0.73
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.LTIHGDLYYEGK#.E	48.42	41.94	1.15	0.87
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.M*ESSAVPK.K	14.80	15.61	0.95	1.05
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.QAAVLM*EQER@.Q	37.49	27.94	1.34	0.75
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.QAAVLMEQER@.Q	19.76	12.57	1.57	0.64
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.RGIEKPPFELPDFIK.R	12.66	14.62	0.87	1.16
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.SSLGQSASETEEDTVSISK#.K	24.58	19.43	1.26	0.79
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.TGIQEM*R@.E	36.29	22.51	1.61	0.62
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.VGEPVALSEEER.L	83.88	72.50	1.16	0.86
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.VPPPWLIAMQR.Y	11.26	10.37	1.09	0.92
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.YGPPPSYPNLK#.I	41.09	38.66	1.06	0.94
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.GIEKPPFELPDFIK.R	16.49	13.48	1.22	0.82
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.IDIDYQK#.L	17.00	8.91	1.91	0.52
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.KGPAPELQGVEVALAPEELELDPM*AM*TQK.Y	5.50	4.49	1.22	0.82
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	K.LAQQQAALLM*QQEER@.A	5.64	5.42	1.04	0.96
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.SSLGQSASETEEDTVSISK.K	5.81	4.46	1.30	0.77
Q3UJB0_Q3UJB0_MOUSE	Sf3b2	Protein Sf3b2 OS=Mus m	R.VGEPVALSEEER.L	10.61	6.67	1.59	0.63
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.AEVIM*NYHVGETVLSLQK#.T	55.56	44.21	1.26	0.80
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.AGNGQWASVIR@.V	22.08	9.78	2.26	0.44
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.AVM*ISAIEK#.Q	40.34	28.03	1.44	0.69
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.DYIVVGSDSGR.I	64.14	38.34	1.67	0.60
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.ELAAEM*AAAFLNENLPESIFGAPK#.A	49.55	37.49	1.32	0.76
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.FLAVGLVDNTVR@.I	226.13	177.41	1.27	0.78
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.FSNTGEDWYVLVGVAK#.D	55.14	39.61	1.39	0.72
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.HGLEVSEM*AVSELPGNPNAVWTVR@.R	39.63	30.94	1.28	0.78
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.HIANYISGIQTIGHR@.V	84.38	56.64	1.49	0.67
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.IHQETFGK#.S	33.40	26.45	1.26	0.79
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.ILELLR@PDPNTGK#.V	36.25	36.75	0.99	1.01
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.ITLETDEDM*VTEIR@.L	68.31	46.69	1.46	0.68
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.IVILEYQPSK#.N	122.67	87.46	1.40	0.71
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.K#FVIHPESNNLIIIETDHNAYTEATK#.A	40.43	34.99	1.16	0.87
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.LGAVFNQVAFPLQYTPR@.K	122.70	82.66	1.48	0.67
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.LPPNTNDEVDEDPTGNK#.A	24.12	24.57	0.98	1.02
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.LPPNTNDEVDEDPTGNK#.A	9.14	7.55	1.21	0.83
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.LVYILNR@.D	152.17	106.04	1.43	0.70
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	-.M*FLYNLTLQR@.A	42.33	32.33	1.31	0.76
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	-.MFLYNLTLQR@.A	15.89	11.89	1.34	0.75
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.M*QGQEAVLAM*SSR@.S	37.84	27.49	1.38	0.73
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.NDLDDPER.G	17.95	14.38	1.25	0.80
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.NENQLIIFADDTYPR@.W	46.57	33.13	1.41	0.71
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.NFGDQPDIR@.C	49.21	37.79	1.30	0.77
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.QVVIALTGGELVYFEM*DPSGQLNEYTER@.K	8.35	5.06	1.65	0.61
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.R@NENQLIIFADDTYPR@.W	8.22	8.94	0.92	1.09
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.SM*FFFLAQTEQGDIFK#.I	15.09	10.19	1.48	0.68
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.SMFFFLAQTEQGDIFK#.I	10.21	8.80	1.16	0.86
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.SVAGGFVYTYK#.L	89.01	67.42	1.32	0.76
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.SWLSYSYQSR@.F	32.36	18.92	1.71	0.58
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.SYYFPVK#.N	78.64	58.72	1.34	0.75
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.TPVEEVPAAIAPFQGR.V	90.47	70.50	1.28	0.78
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.TVLDPVTGDLSDTR.T	145.95	111.18	1.31	0.76
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.VIVSDVQESFIWVR@.Y	101.71	66.46	1.53	0.65
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.WVTTASLLDYDTVAGADK#.F	21.57	12.38	1.74	0.57
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.AVM*ISAIEK#.Q	29.17	17.00	1.72	0.58
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.FLAVGLVDNTVR@.I	175.21	116.31	1.51	0.66
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.FSNTGEDWYVLVGVAK#.D	27.31	14.16	1.93	0.52
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	R.HGLEVSEM*AVSELPGNPNAVWTVR@.R	26.16	11.67	2.24	0.45
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.HIANYISGIQTIGHR@.V	29.22	21.84	1.34	0.75
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni	K.IHQETFGK#.S	20.32	22.78	0.89	1.12

Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni K.ITLETDEDM*VTEIR@.L	28.36	16.60	1.71	0.59
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.IVPGQFLAVDPK#.G	54.17	110.80	0.49	2.05
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.KQQM*AEEM*VEAAGEDERELAAEM*AAAFLNENLPESIFGAPK.A	4.84	3.45	1.40	0.71
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni K.LGAVFNQVAFPLQYTPR@.K	66.70	35.99	1.85	0.54
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.LPPNTNDEVDEDPTGNK#.A	17.21	11.02	1.56	0.64
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.LTISSPLEAHK#.A	77.02	38.23	2.01	0.50
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni K.LVYILNR@.D	62.78	41.27	1.52	0.66
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni -.M*FLYNLTLQR@.A	25.64	18.17	1.41	0.71
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.M*QGQEAVLAM*SSR@.S	16.55	13.72	1.21	0.83
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.M*QGQEAVLAMSSR@.S	11.93	1.24	9.58	0.10
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.NENQLIIFADDTYPR@.W	24.91	20.20	1.23	0.81
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni K.NFGDQPDIR@.C	33.70	23.43	1.44	0.70
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni K.SM*FFFLAQTEQGDIFK#.I	23.07	10.81	2.13	0.47
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.SVAGGFVYTYK#.L	40.83	26.97	1.51	0.66
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.SWLSYSYQSR.F	19.32	9.87	1.96	0.51
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.SYYFPVK#.N	41.86	29.67	1.41	0.71
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni K.TPVEEVPAAIAPFQGR@.V	50.80	48.73	1.04	0.96
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.TVLDPVTGDLSDTR@.T	86.47	54.65	1.58	0.63
Q921M3_SF3B3_MOUSE	Sf3b3	Splicing factor 3B subuni R.WVTTASLLDYDTVAGADK.F	8.92	6.87	1.30	0.77
Q8QZY9_SF3B4_MOUSE	Sf3b4	Splicing factor 3B subuni K.NLDVGANIFIGNLDPEIDEK#.L	11.53	12.71	0.91	1.10
Q8QZY9_SF3B4_MOUSE	Sf3b4	Splicing factor 3B subuni K.NLDVGANIFIGNLDPEIDEK.L	16.69	13.15	1.27	0.79
Q8QZY9_SF3B4_MOUSE	Sf3b4	Splicing factor 3B subuni R.NQDATVYVGGLDEK#.V	125.35	107.12	1.17	0.85
Q8QZY9_SF3B4_MOUSE	Sf3b4	Splicing factor 3B subuni R.VTGQHQGYGFVEFLSEEDADYAIK.I	78.51	52.35	1.50	0.67
Q923D4_SF3B5_MOUSE	Sf3b5	Splicing factor 3B subuni K.M*LQPSGPPADKPEEN.-	8.02	10.60	0.76	1.32
Q923D4_SF3B5_MOUSE	Sf3b5	Splicing factor 3B subuni K.MLQPSGPPADK#PEEN.-	12.59	5.10	2.47	0.40
Q923D4_SF3B5_MOUSE	Sf3b5	Splicing factor 3B subuni K.M*LQPSGPPADK#PEEN.-	78.55	65.31	1.20	0.83
Q923D4_SF3B5_MOUSE	Sf3b5	Splicing factor 3B subuni R.YTIHSQLEHLQSK#.Y	13.52	9.09	1.49	0.67
P59708_SF3B6_MOUSE	Sf3b6	Splicing factor 3B subuni R.GTAYVVYEDIFDAK#.N	58.02	32.84	1.77	0.57
P59708_SF3B6_MOUSE	Sf3b6	Splicing factor 3B subuni K.ITAEEM*YDIFGK#.Y	73.19	43.59	1.68	0.60
P59708_SF3B6_MOUSE	Sf3b6	Splicing factor 3B subuni K.ITAEEMYDIFGK#.Y	51.81	31.70	1.63	0.61
P59708_SF3B6_MOUSE	Sf3b6	Splicing factor 3B subuni R.VGNTPETR@.G	41.49	19.61	2.12	0.47
P59708_SF3B6_MOUSE	Sf3b6	Splicing factor 3B subuni R.YLVVLYYNANR@.A	19.66	12.17	1.62	0.62
Q8VIJ6_SFPQ_MOUSE	Sfpq	Splicing factor, proline- K.AELDDTPM*R@.G	31.16	23.63	1.32	0.76
Q8VIJ6_SFPQ_MOUSE	Sfpq	Splicing factor, proline- K.DK#LESEM*EDAYHEHQANLLR@.Q	26.36	19.91	1.32	0.76
Q8VIJ6_SFPQ_MOUSE	Sfpq	Splicing factor, proline- R.FAQHGTFEYEYSQR@.W	26.29	18.88	1.39	0.72
Q8VIJ6_SFPQ_MOUSE	Sfpq	Splicing factor, proline- R.FATHAAALSVR@.N	65.69	36.11	1.82	0.55
Q8VIJ6_SFPQ_MOUSE	Sfpq	Splicing factor, proline- R.FGQGGAGPVGGQGPR.G	44.11	29.32	1.50	0.66
Q8VIJ6_SFPQ_MOUSE	Sfpq	Splicing factor, proline- R.LFVGNLPADITEDEFK#.R	8.40	10.16	0.83	1.21
Q8VIJ6_SFPQ_MOUSE	Sfpq	Splicing factor, proline- K.YGEPGEVFINK#.G	44.69	28.18	1.59	0.63
Q3USH5_SFSWA_MOUSE	Sfswap	Splicing factor, suppress K.DGQISSAIVSSVQSK#.I	4.45	2.72	1.64	0.61
Q3USH5_SFSWA_MOUSE	Sfswap	Splicing factor, suppress R.NSQFDFLR@.F	8.02	5.08	1.58	0.63
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro K.FLALLAEEQDVNK#.M	26.81	8.28	3.24	0.31
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.LAAGASVLK#.R	15.70	4.49	3.50	0.29
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.LPQENFNNLR@.Y	19.77	8.53	2.32	0.43
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.NPTETAASAEDM*TR@.K	6.97	3.18	2.19	0.46
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro K.SLTSLDTALAELR@.D	21.51	5.07	4.24	0.24
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro K.VSSQQVSEELPPVTVPAPATTPAPTPAPASM*AVR@.E	3.81	1.91	2.00	0.50
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.DVLQPLSR@.L	12.81	4.16	3.08	0.32
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.ILAEFEM*TLER@.D	8.65	4.58	1.89	0.53
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.LSEEELPAILK#.H	29.07	7.60	3.82	0.26
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.TPETAEFLGEDLLQVEQR@.L	31.29	12.82	2.44	0.41
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.TPETAEFLGEDLLQVEQR@.L	13.24	4.67	2.83	0.35
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro K.FLALLAEEQDVNK#.M	69.43	16.15	4.30	0.23
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.ILAEFEM*TLER@.D	18.82	9.99	1.88	0.53
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.LPQENFNNLR@.Y	46.97	10.43	4.50	0.22
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.NPTETAASAEDM*TR@.K	39.16	9.01	4.35	0.23
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.R@LPASPVISNM*PAQVDQGVATEDR@.G	36.21	6.30	5.75	0.17
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.R@LPASPVISNMPAQVDQGVATEDR@.G	7.19	2.20	3.27	0.31
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.R@LVGTSLR@.A	68.90	12.28	5.61	0.18
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro K.SLTSLDTALAELR@.D	70.23	12.96	5.42	0.18
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.THLQDLGR@.D	30.49	6.92	4.41	0.23
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.TPETAEFLGEDLLQVEQR@.L	46.08	8.40	5.49	0.18
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro K.VSSQQVSEELPPVTVPAPATTPAPTPAPASM*AVR@.E	16.24	4.26	3.81	0.26
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.VYGVSLR@.T	45.92	12.18	3.77	0.27
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro K.FLALLAEEQDVNK#.M	12.07	6.96	1.73	0.58
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.LPQENFNNLR@.Y	7.53	2.54	2.96	0.34
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro K.SLTSLDTALAELR@.D	10.92	28.62	0.38	2.62
A2A5V4_A2A5V4_MOUSE	Sh3bp1	SH3 domain-binding pro R.TPETAEFLGEDLLQVEQR@.L	14.80	2.20	6.73	0.15
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.ALYDFEPENDGELGFR@.E	43.31	19.56	2.21	0.45
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.ASQLVSEK#.V	56.56	26.67	2.12	0.47
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.AVAEVLVR@.T	93.21	415.15	0.22	4.45
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.DSLDIEVK#.Q	35.24	19.27	1.83	0.55
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.ELGGESNFGDALLDAGESM*K#.R	9.08	4.88	1.86	0.54
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.IPDEELR@.Q	53.74	31.35	1.71	0.58
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.ITASSSFR@.S	116.56	47.24	2.47	0.41
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.LTM*LNTVSK#.I	33.28	19.20	1.73	0.58
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.LTMLNTVSK#.I	11.46	4.29	2.67	0.37
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus R.QAVQILEELADK#.L	35.10	15.98	2.20	0.46
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus R.QAVQILEELADK#LK#.R	84.66	38.78	2.18	0.46
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus R.TIEYLQPNPASR@.A	66.22	34.05	1.94	0.51
Q62419_SH3G1_MOUSE	Sh3gl1	Endophilin-A2 OS=Mus K.VGGAEGTKLDDDFKDM*EK.K	35.98	13.06	2.75	0.36
Q9JK48_SHLB1_MOUSE	Sh3glb1	Endophilin-B1 OS=Mus R.AVQFTEEK#.L	35.52	23.23	1.53	0.65
Q9JK48_SHLB1_MOUSE	Sh3glb1	Endophilin-B1 OS=Mus R.ELIQTSALNFLTPLR@.N	21.66	10.17	2.13	0.47
Q9JK48_SHLB1_MOUSE	Sh3glb1	Endophilin-B1 OS=Mus K.GK#VPITYLELLN.-	27.02	11.25	2.40	0.42
Q9JK48_SHLB1_MOUSE	Sh3glb1	Endophilin-B1 OS=Mus K.LAADAGTFLSR.A	22.38	11.82	1.89	0.53
Q9JK48_SHLB1_MOUSE	Sh3glb1	Endophilin-B1 OS=Mus K.QTEVLLQPNPNAR.I	7.21	4.80	1.50	0.67
Q91WA6_SHRPN_MOUSE	Sharpin	Sharpin OS=Mus muscul R.LSQAIAGGDEK#.A	4.38	1.49	2.93	0.34
P98083_SHC1_MOUSE	Shc1	SHC-transforming protei R.ELFDDPSYVNIQNLDK#.A	10.69	6.73	1.59	0.63
P98083_SHC1_MOUSE	Shc1	SHC-transforming protei R.ESTTTPGQYVLTGLQSGQPK#.H	4.60	2.08	2.21	0.45
P98083_SHC1_MOUSE	Shc1	SHC-transforming protei R.VPPPPQSM*SM*AEQLQGEPWFHGK#.L	3.50	2.93	1.19	0.84
P98083_SHC1_MOUSE	Shc1	SHC-transforming protei R.ESTTTPGQYVLTGLQSGQPK#.H	2.50	1.81	1.39	0.72
Q9CZN7_Q9CZN7_MOUSE	Shmt2	Protein Shmt2 OS=Mus R.EYSLQVLR@.N	6.88	8.16	0.84	1.19
Q9CZN7_Q9CZN7_MOUSE	Shmt2	Protein Shmt2 OS=Mus K.ISATSIFFESM*PYK.V	10.26	11.17	0.92	1.09
Q9CZN7_Q9CZN7_MOUSE	Shmt2	Protein Shmt2 OS=Mus R.LGAPALTSR.Q	26.91	22.55	1.19	0.84
Q9CZN7_Q9CZN7_MOUSE	Shmt2	Protein Shmt2 OS=Mus R.LIIAGTSAYAR@.L	36.85	32.20	1.14	0.87
Q9CZN7_Q9CZN7_MOUSE	Shmt2	Protein Shmt2 OS=Mus K.LNPQTGLIDYDQLALTAR@.L	10.47	9.73	1.08	0.93
Q9CZN7_Q9CZN7_MOUSE	Shmt2	Protein Shmt2 OS=Mus K.SFLLKDPETSQR.L	22.29	21.11	1.06	0.95
Q9CZN7_Q9CZN7_MOUSE	Shmt2	Protein Shmt2 OS=Mus R.SGLIFYR.K	14.61	20.74	0.70	1.42
Q9CZN7_Q9CZN7_MOUSE	Shmt2	Protein Shmt2 OS=Mus R.VLELVSITANK#.N	21.59	19.28	1.12	0.89
Q9CZN7_Q9CZN7_MOUSE	Shmt2	Protein Shmt2 OS=Mus K.YADVVTTTTHK.T	3.24	5.27	0.61	1.63
O88520_SHOC2_MOUSE	Shoc2	Leucine-rich repeat prot R.ELDLEENK#LESLPNEIAYLK#.D	5.61	8.00	0.70	1.43
O88520_SHOC2_MOUSE	Shoc2	Leucine-rich repeat prot R.ELDLEENK#LESLPNEIAYLK#.D	16.97	5.76	2.95	0.34
O88520_SHOC2_MOUSE	Shoc2	Leucine-rich repeat prot K.ELTQLTELYLYSNK#.L	8.06	2.67	3.02	0.33

O88520_SHOC2_MOUSE	Shoc2	Leucine-rich repeat prot	K.ESSAAQPGVAFSVDNTIK#.R	8.29	3.60	2.30	0.43
O88520_SHOC2_MOUSE	Shoc2	Leucine-rich repeat prot	K.LVLTNNQLSTLPR.G	18.65	5.64	3.31	0.30
O88520_SHOC2_MOUSE	Shoc2	Leucine-rich repeat prot	K.ESSAAQPGVAFSVDNTIK#.R	12.69	2.63	4.82	0.21
Q60520_SIN3A_MOUSE	Sin3a	Paired amphipathic heli	K.SLLNEIESIYDER@.Q	7.91	2.89	2.74	0.36
Q60520_SIN3A_MOUSE	Sin3a	Paired amphipathic heli	K.AADIIDGLR@.K	10.83	1.65	6.55	0.15
Q60520_SIN3A_MOUSE	Sin3a	Paired amphipathic heli	R.LK#VEDALSYLDQVK#.L	14.93	3.40	4.40	0.23
Q60520_SIN3A_MOUSE	Sin3a	Paired amphipathic heli	R.SAEAYENFLR@.C	12.34	28.63	0.43	2.32
Q60520_SIN3A_MOUSE	Sin3a	Paired amphipathic heli	R.SLLDGNIDSSQYEDSLR@.E	4.59	3.18	1.44	0.69
Q60520_SIN3A_MOUSE	Sin3a	Paired amphipathic heli	K.SLLNEIESIYDER@.Q	18.73	7.13	2.63	0.38
Q60520_SIN3A_MOUSE	Sin3a	Paired amphipathic heli	R.YM*SSDTTSPELR@.E	11.74	3.51	3.35	0.30
Q62141_SIN3B_MOUSE	Sin3b	Paired amphipathic heli	R.FGSDPATYNGFLEIM*K#.E	3.70	2.14	1.73	0.58
Q62141_SIN3B_MOUSE	Sin3b	Paired amphipathic heli	K.LPVHVEDALTYLDQVK#.I	7.95	3.33	2.39	0.42
Q62141_SIN3B_MOUSE	Sin3b	Paired amphipathic heli	R.YVEQYVGSEGASSSSTEGFLLK#PVFLQR@.N	5.17	2.41	2.14	0.47
Q62141_SIN3B_MOUSE	Sin3b	Paired amphipathic heli	R.GQEDLLSEFGQFLPEAK#.R	5.72	3.57	1.60	0.62
Q8VDQ8_SIR2_MOUSE	Sirt2	NAD-dependent protein	R.LLDELTLEGVTR.Y	6.53	5.89	1.11	0.90
Q62231_SIX1_MOUSE	Six1	Homeobox protein SIX1	R.ELAEATGLTTTQVSNWFK.N	9.02	7.24	1.25	0.80
Q62231_SIX1_MOUSE	Six1	Homeobox protein SIX1	R.ELAEATGLTTTQVSNWFK.N	2.81	3.96	0.71	1.41
Q61321_SIX4_MOUSE	Six4	Homeobox protein SIX4	R.FLWSLPQSDLLR@.G	7.18	2.27	3.16	0.32
Q6NZR5_Q6NZR5_MOUSE	Skiv2l	Protein Skiv2l OS=Mus m	R.DK#GPATPDVPHPDDLIGFK#.L	6.52	14.73	0.44	2.26
Q6NZR5_Q6NZR5_MOUSE	Skiv2l	Protein Skiv2l OS=Mus m	R.FLLSDQSLLLLPEYHQR@.V	17.43	7.77	2.24	0.45
Q6NZR5_Q6NZR5_MOUSE	Skiv2l	Protein Skiv2l OS=Mus m	R.TLGYVDEAGTVK#.L	7.43	2.36	3.15	0.32
Q6NZR5_Q6NZR5_MOUSE	Skiv2l	Protein Skiv2l OS=Mus m	K.TVVAEYAIALAQK#.H	8.65	4.25	2.03	0.49
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.AIGNTELENK#.F	53.28	16.52	3.23	0.31
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.DLDVEGTDEPIFGK#.K	32.72	13.34	2.45	0.41
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.ETIEILFSEGLIK#.A	24.00	7.96	3.01	0.33
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.EYPFILDAFQR@.E	61.78	22.59	2.73	0.37
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.GIVILM*VDEK#.M	24.26	12.05	2.01	0.50
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.GPSNVFK#.I	20.23	9.72	2.08	0.48
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.IEDSINEDLSLADLM*PR.V	16.47	5.81	2.84	0.35
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.IVIPNEENVVIYYK#.I	45.30	19.64	2.31	0.43
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.K#AQIALDIK#.S	19.13	7.55	2.53	0.39
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.M*TDVFEGSIIR@.C	18.60	8.10	2.30	0.44
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.TVLQM*DELK#.C	8.89	3.90	2.28	0.44
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.VEEINPEYM*LEK#.S	20.45	8.79	2.33	0.43
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.VIFTSPIK#.A	86.27	41.21	2.09	0.48
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.VK#NEGDDFGWGVVVNFSK#.K	10.72	6.94	1.54	0.65
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.WISSGEYIQM*SGR@.A	14.08	4.69	3.00	0.33
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.AIGNTELENK#.F	29.78	10.16	2.93	0.34
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.DLDVEGTDEPIFGK#.K	32.63	12.17	2.68	0.37
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.ETIEILFSEGLIK#.A	8.77	3.65	2.40	0.42
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.EYPFILDAFQR@.E	47.71	14.75	3.24	0.31
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.GIVILM*VDEK#.M	24.02	5.29	4.54	0.22
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.IEDSINEDLSLADLM*PR@.V	12.17	3.79	3.21	0.31
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.IVIPNEENVVIYYK#.I	31.53	14.21	2.22	0.45
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.LGFATSSDVIEM*K#.G	13.79	3.39	4.07	0.25
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	K.LPQVEHVLPLLK#.R	14.86	8.16	1.82	0.55
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.TVLQM*DELK#.C	12.70	3.60	3.53	0.28
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.VEEINPEYM*LEK#.S	10.95	5.99	1.83	0.55
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.VIFTSPIK#.A	66.58	20.36	3.27	0.31
Q9CZU3_SK2L2_MOUSE	Skiv2l2	Superkiller viralicidic act	R.WISSGEYIQM*SGR@.A	9.24	3.11	2.97	0.34
Q9WTX5_SKP1_MOUSE	Skp1	S-phase kinase-associate	K.NDFTEEEEAQVR@.K	7.95	3.88	2.05	0.49
Q9WTX5_SKP1_MOUSE	Skp1	S-phase kinase-associate	K.NDFTEEEEAQVR@.K	62.60	26.87	2.33	0.43
Q9WTX5_SKP1_MOUSE	Skp1	S-phase kinase-associate	K.R@TDDIPVWDQEFLK#.V	34.27	12.39	2.77	0.36
Q9WTX5_SKP1_MOUSE	Skp1	S-phase kinase-associate	R.TDDIPVWDQEFLK#.V	35.05	13.72	2.56	0.39
Q9WTX5_SKP1_MOUSE	Skp1	S-phase kinase-associate	K.TFNIK#NDFTEEEEAQVR@.K	13.15	10.93	1.20	0.83
Q9WTX5_SKP1_MOUSE	Skp1	S-phase kinase-associate	K.TM*LEDLGM*DDEGDDDPVPLPNVNAAILK#.K	19.57	6.96	2.81	0.36
Q9WTX5_SKP1_MOUSE	Skp1	S-phase kinase-associate	K.TM*LEDLGM*DDEGDDDPVPLPNVNAAILKK.V	7.94	2.56	3.10	0.32
Q8CI08_SLAI2_MOUSE	Slain2	SLAIN motif-containing	K.LNDVTDVQILAR@.M	6.78	2.18	3.10	0.32
Q8CI08_SLAI2_MOUSE	Slain2	SLAIN motif-containing	R.VGVSTPSSGAASPR@.G	12.81	7.08	1.81	0.55
P55012_S12A2_MOUSE	Slc12a2	Solute carrier family 12	R.EGAQYLM*QAAGLGR@.M	5.65	3.36	1.68	0.59
Q8R4T9_UT2_MOUSE	Slc14a2	Urea transporter 2 OS=M	K.ALSYITGEMK#.E	9.53	2.42	3.93	0.25
P53986_MOT1_MOUSE	Slc16a1	Monocarboxylate transp	K.AAQSPQQHSSGDPTEEESPV.-	23.45	23.45	1.00	1.00
P53986_MOT1_MOUSE	Slc16a1	Monocarboxylate transp	R.EGK#EDEASTDVDEK#PK#.E	13.95	7.90	1.77	0.57
P53986_MOT1_MOUSE	Slc16a1	Monocarboxylate transp	K.LSVFQTINK#.F	11.54	4.88	2.36	0.42
P53986_MOT1_MOUSE	Slc16a1	Monocarboxylate transp	K.SDANTDLIGGSPK#.G	17.89	7.76	2.31	0.43
O35874_SATT_MOUSE	Slc1a4	Neutral amino acid trans	K.ETVDSFLDLLR@.N	7.81	3.58	2.18	0.46
Q9ESU7_Q9ESU7_MOUSE	Slc1a5	Neutral amino acid trans	K.EVLDSFLDLVR@.N	17.10	1.45	11.77	0.08
Q9ESU7_Q9ESU7_MOUSE	Slc1a5	Neutral amino acid trans	K.M*PSSEPELIQVK#.N	6.30	2.46	2.56	0.39
Q8JZU2_TXTP_MOUSE	Slc25a1	Tricarboxylate transport	R.GLSSLLYGSIPK#.A	6.35	4.59	1.38	0.72
Q9CR62_M2OM_MOUSE	Slc25a11	Mitochondrial 2-oxoglut	R.AVVVNAAQLASYSQSK#.Q	6.43	1.81	3.55	0.28
Q8VEM8_MPCP_MOUSE	Slc25a3	Phosphate carrier protei	K.ALYSNILGEENTYLWR@.T	15.16	8.43	1.80	0.56
Q8VEM8_MPCP_MOUSE	Slc25a3	Phosphate carrier protei	K.FGFYEVFK#.A	11.06	10.62	1.04	0.96
Q8VEM8_MPCP_MOUSE	Slc25a3	Phosphate carrier protei	K.GSTASQVLQR@.L	42.32	21.28	1.99	0.50
Q8VEM8_MPCP_MOUSE	Slc25a3	Phosphate carrier protei	R.IQTQPGYANTLR@.E	42.33	21.13	2.00	0.50
Q8VEM8_MPCP_MOUSE	Slc25a3	Phosphate carrier protei	R.LPR@PPPPEM*PESLK#.K	12.82	15.25	0.84	1.19
Q8VEM8_MPCP_MOUSE	Slc25a3	Phosphate carrier protei	K.ALYSNILGEENTYLWR@.T	2.62	2.90	0.90	1.11
Q8VEM8_MPCP_MOUSE	Slc25a3	Phosphate carrier protei	K.FGFYEVFK#.A	8.45	6.19	1.37	0.73
Q8VEM8_MPCP_MOUSE	Slc25a3	Phosphate carrier protei	R.IQTQPGYANTLR@.E	7.61	5.00	1.52	0.66
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	K.DFLAGGIAAAVSK#.T	48.71	29.31	1.66	0.60
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	K.EQGFLSFWR@.G	37.25	16.99	2.19	0.46
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	K.GAWSNVLR.G	63.08	34.72	1.82	0.55
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	R.GM*GGAFVLVLYDEIK#.K	15.75	7.29	2.16	0.46
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	K.GM*LPDPK#.N	34.87	20.08	1.74	0.58
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	R.GNLANVIR.Y	83.60	50.93	1.64	0.61
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	R.M*M*MQSGRKGADIMYTGTLDCWR@.K	1.77	4.00	0.44	2.27
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	R.YFPTQALNFAFK#.D	120.17	77.62	1.55	0.65
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	K.EQGFLSFWR@.G	8.14	2.90	2.80	0.36
P48962_ADT1_MOUSE	Slc25a4	ADP/ATP translocase 1 O	R.YFPTQALNFAFK#.D	10.00	8.19	1.22	0.82
P51881_ADT2_MOUSE	Slc25a5	ADP/ATP translocase 2 O	R.AAYFGIYDTAK#.G	37.77	19.08	1.98	0.51
P51881_ADT2_MOUSE	Slc25a5	ADP/ATP translocase 2 O	K.DFLAGGVAAAISK#.T	58.88	31.07	1.90	0.53
P51881_ADT2_MOUSE	Slc25a5	ADP/ATP translocase 2 O	K.EQGVLSFWR@.G	44.52	20.38	2.18	0.46
Q9JIM1_S29A1_MOUSE	Slc29a1	Equilibrative nucleoside	K.ALADPTVALPAR@.S	19.42	8.00	2.43	0.41
P17809_GTR1_MOUSE	Slc2a1	Solute carrier family 2, fa	R.DLQEM*KEEGR.Q	4.36	2.57	1.70	0.59
P17809_GTR1_MOUSE	Slc2a1	Solute carrier family 2, fa	K.VTILELFR@.S	31.52	20.21	1.56	0.64
P17809_GTR1_MOUSE	Slc2a1	Solute carrier family 2, fa	K.VTILELFR@.S	17.69	7.38	2.40	0.42
Q61420_S35A1_MOUSE	Slc35a1	CMP-sialic acid transport	R.QDTTSIQQEATSK#.E	5.02	2.96	1.70	0.59
P97858_S35B1_MOUSE	Slc35b1	Solute carrier family 35	K.ILIQFFDTAR@.V	10.94	4.82	2.27	0.44
Q91ZN5_S35B2_MOUSE	Slc35b2	Adenosine 3'-phospho 5'	K.APDEVLLAPR@.T	26.82	8.01	3.35	0.30
Q91ZN5_S35B2_MOUSE	Slc35b2	Adenosine 3'-phospho 5'	K.FVSFPTQVLAK#.A	17.28	8.10	2.13	0.47
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	K.EALSSWLQDGVDGFQFR@.D	4.94	3.19	1.55	0.65
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	K.GQNEDPGSLLTQFR@.R	34.00	12.36	2.75	0.36
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	R.IGDLQAFVGR@.D	61.10	26.72	2.29	0.44
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	K.LLLSTDSAR@.Q	41.78	16.16	2.59	0.39

P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	K.M*K#EALSSWLQDGVDGFQFR@.D	11.36	4.40	2.58	0.39
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	K.QINPTLGSQEDFK#DLLQSAK#.K	47.07	12.54	3.75	0.27
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	K.SHLEYLSTLK#.V	20.74	8.20	2.53	0.40
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	K.VAEDETEAGVK#.F	27.16	13.27	2.05	0.49
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	R.YLVVLNFR@.D	16.67	7.84	2.13	0.47
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	R.IGDLQAFVGR@.D	41.61	39.41	1.06	0.95
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	K.M*K#EALSSWLQDGVDGFQFR@.D	9.90	5.67	1.74	0.57
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	K.VAEDETEAGVK#.F	18.18	25.91	0.70	1.43
P10852_4F2_MOUSE	Slc3a2	4F2 cell-surface antigen	R.YLVVLNFR.D	8.79	7.38	1.19	0.84
A2AMH5_A2AMH5_MOUSE	Slc44a1	Choline transporter-like	R.ELK#PM*ASGASSA.-	6.78	3.04	2.23	0.45
A2AMH5_A2AMH5_MOUSE	Slc44a1	Choline transporter-like	K.LPVPASAPIPFFHR@.C	7.82	3.80	2.06	0.49
A2AMH5_A2AMH5_MOUSE	Slc44a1	Choline transporter-like	R.NLPFTPILASVNR@.L	10.20	7.52	1.36	0.74
Q8BY89_CTL2_MOUSE	Slc44a2	Choline transporter-like	R.K#PDDM*PAFPLFSAFGR@.A	8.64	2.23	3.88	0.26
Q9Z127_LAT1_MOUSE	Slc7a5	Large neutral amino acid	K.DM*GQGDASNLQQK#.L	2.55	1.66	1.54	0.65
Q9Z127_LAT1_MOUSE	Slc7a5	Large neutral amino acid	R.AVATPAAAAAEEER@.Q	22.88	8.29	2.76	0.36
Q9Z127_LAT1_MOUSE	Slc7a5	Large neutral amino acid	K.DM*GQGDASNLQQK#.L	7.81	3.49	2.24	0.45
Q9Z127_LAT1_MOUSE	Slc7a5	Large neutral amino acid	R.LFFVGSR@.E	20.77	7.18	2.89	0.35
Q9Z127_LAT1_MOUSE	Slc7a5	Large neutral amino acid	R.R@GDGADPEGEGVTLQR@.N	4.70	1.40	3.37	0.30
Q9Z127_LAT1_MOUSE	Slc7a5	Large neutral amino acid	R.AVATPAAAAAEEER@.Q	15.46	12.84	1.20	0.83
Q9Z127_LAT1_MOUSE	Slc7a5	Large neutral amino acid	K.DM*GQGDASNLQQK.L	3.30	4.55	0.73	1.38
Q9Z127_LAT1_MOUSE	Slc7a5	Large neutral amino acid	R.LFFVGSR@.E	10.09	6.05	1.67	0.60
P70441_NHRF1_MOUSE	Slc9a3r1	Na(+)/H(+) exchange regu	R.LLVVDPETDER@.L	6.47	2.68	2.41	0.41
B1ARD6_B1ARD6_MOUSE	Slfn9	Protein Slfn9 OS=Mus mu	R.FQHIIIDEAQNFR@.T	12.75	8.48	1.50	0.67
B1ARD6_B1ARD6_MOUSE	Slfn9	Protein Slfn9 OS=Mus mu	K.GYSPQDIAVLFSTDR@.E	6.22	2.97	2.10	0.48
B1ARD6_B1ARD6_MOUSE	Slfn9	Protein Slfn9 OS=Mus mu	R.NADK#IAEFLQQELQK#.I	15.93	5.57	2.86	0.35
O54988_SLK_MOUSE	Slk	STE20-like serine/threon	R.SSEVGTDEALDDTQK#.A	6.84	1.27	5.38	0.19
Q3URD3_SLMAP_MOUSE	Slmap	Sarcolemmal membrane-	K.ELVEAQELAR@.T	6.91	3.60	1.92	0.52
Q3URD3_SLMAP_MOUSE	Slmap	Sarcolemmal membrane-	K.ENVLLSSELQR@.Q	6.47	7.01	0.92	1.08
Q3URD3_SLMAP_MOUSE	Slmap	Sarcolemmal membrane-	R.HVYLDEPIK#.I	7.78	3.23	2.41	0.42
Q3URD3_SLMAP_MOUSE	Slmap	Sarcolemmal membrane-	K.IEALQADNDFTNER@.L	7.21	2.07	3.49	0.29
Q8CH25_SLTM_MOUSE	Sltm	SAFB-like transcription	R.AR@FPDTASVQSSFER@.R	10.40	5.87	1.77	0.57
Q8CH25_SLTM_MOUSE	Sltm	SAFB-like transcription	R.FPDTASVQSSFER@.R	4.20	2.69	1.56	0.64
Q8CH25_SLTM_MOUSE	Sltm	SAFB-like transcription	K.NIWVSGLSSNTK#.A	9.78	9.42	1.04	0.96
Q8CH25_SLTM_MOUSE	Sltm	SAFB-like transcription	R.TELHGQLISVEK#.V	34.35	13.57	2.53	0.40
Q8CH25_SLTM_MOUSE	Sltm	SAFB-like transcription	K.TTQEFVEAEAIEDR@.E	5.38	3.63	1.48	0.67
Q8BHJ9_SLU7_MOUSE	Slu7	Pre-mRNA-splicing facto	K.EIM*QIDER@.K	10.50	7.44	1.41	0.71
Q8BHJ9_SLU7_MOUSE	Slu7	Pre-mRNA-splicing facto	K.YGGQEHLDAPPAELLLAQTEDYVEYSR@.H	4.78	1.93	2.48	0.40
P70340_SMAD1_MOUSE	Smad1	Mothers against decapen	R.VESPVLPPVLVPR@.H	24.79	15.74	1.57	0.64
Q62432_SMAD2_MOUSE	Smad2	Mothers against decapen	R.VETPVLPPVLVPR@.H	19.48	12.81	1.52	0.66
Q62432_SMAD2_MOUSE	Smad2	Mothers against decapen	R.VGETFHASQPSLTVDGFTDPSNSER@.F	5.60	4.62	1.21	0.83
Q62432_SMAD2_MOUSE	Smad2	Mothers against decapen	K.VLTQM*GSPSVR@.C	6.46	2.15	3.00	0.33
Q62432_SMAD2_MOUSE	Smad2	Mothers against decapen	R.VETPVLPPVLVPR@.H	18.10	5.43	3.33	0.30
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.DSEAGSSTPTTSTR@.S	4.77	1.76	2.71	0.37
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.GLDPVEILQER@.E	9.04	5.44	1.66	0.60
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.IQELENLPGSLAGDLR@.T	5.02	3.17	1.58	0.63
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.IVDAVIK#.Y	14.12	6.09	2.32	0.43
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.AGGLGLNLQSADTVIIFDSDWNPHQDLQAQDR@.A	8.68	2.77	3.13	0.32
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.AIEEGTLEEIEEEVR@.Q	36.35	10.87	3.35	0.30
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.AQIM*AYK#.M	54.26	13.05	4.16	0.24
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.ASGK#FELLDR@.I	58.01	12.69	4.57	0.22
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.DSEAGSSTPTTSTR@.S	57.91	16.10	3.60	0.28
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.DTALETALNAK#.A	95.26	25.23	3.78	0.26
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.ELPEYYELIR.K	105.42	31.68	3.33	0.30
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.EVDYSDSLTEK#.Q	59.82	21.37	2.80	0.36
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.FELLDR@.I	40.55	14.88	2.73	0.37
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.FNVLLTTYEYIIK#.D	40.26	10.64	3.78	0.26
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.GLDPVEILQER@.E	122.79	34.58	3.55	0.28
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.GLQSYYAVAHAVTER.V	16.79	3.97	4.22	0.24
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.GVLLTDGSEK#.D	24.52	14.37	1.71	0.59
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.HEEEFDLFM*R@.M	30.87	5.09	6.07	0.16
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.HIIENAK#QDVDDEYGVSQALAR@.G	22.33	9.85	2.27	0.44
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.HIIENAK#QDVDDEYGVSQALAR@.G	24.53	4.85	5.05	0.20
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.HQEYLNSILQHAK#.D	26.49	8.07	3.28	0.30
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.IGQQNEVR@.V	80.09	21.08	3.80	0.26
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.IPDPDSDDVSEVDAR@.H	19.46	6.04	3.22	0.31
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.IQELENLPGSLAGDLR@.T	88.49	28.56	3.10	0.32
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.ITPIQK#PR@.G	39.69	11.07	3.59	0.28
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.IVDAVIK#.Y	86.43	21.55	4.01	0.25
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.K#AENAEGQTPAIGPDGEPLDETSQM*SDLPVK#.V	10.75	3.41	3.16	0.32
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.KIPDPDSDDVSEVDAR.H	27.85	9.72	2.87	0.35
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.LM*EEDELPSWIIK#.D	5.70	3.04	1.87	0.53
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.LNVDQK#.V	21.10	5.48	3.85	0.26
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.QDVDDEYGVSQALAR@.G	27.45	7.97	3.44	0.29
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.QLSEVFIQLPSR@.K	44.16	12.05	3.66	0.27
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.R@DTALETALNAK#.A	6.17	3.25	1.90	0.53
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.TIQTIALITYLM*EHK#R@.L	15.44	4.13	3.74	0.27
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.TLM*NTIM*QLR@.K	34.61	13.56	2.55	0.39
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	R.VDLNEEETILIIR@.R	94.92	29.55	3.21	0.31
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.VIQAGM*FDQK#.S	82.20	21.58	3.81	0.26
Q3TKT4_SMCA4_MOUSE	Smarca4	Transcription activator B	K.YK#LNVDQK#.V	19.10	6.16	3.10	0.32
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.DFNQFIK.A	4.34	7.25	0.60	1.67
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.ANR@FEYLLK#.Q	54.68	28.63	1.91	0.52
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	K.ANYAVDAYFR@.E	17.39	10.44	1.67	0.60
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	K.DIDILNSAGK#.M	27.77	22.64	1.23	0.82
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	K.EIQEPDPTYEEK#.M	39.13	27.33	1.43	0.70
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.ENM*ELEEK#.E	9.31	8.18	1.14	0.88
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	K.ESEITDEDIDGILER@.G	59.29	34.61	1.71	0.58
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.FEDSPSYVK#.W	47.97	51.52	0.93	1.07
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.FEYLLK#.Q	20.00	15.82	1.26	0.79
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.FITDNTVEER@.I	109.09	76.43	1.43	0.70
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	K.FVFM*LSTR.A	16.10	10.47	1.54	0.65
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.HGATHVFASK#.E	49.95	36.84	1.36	0.74
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.ILM*K#DIDILNSAGK#.M	16.85	9.61	1.75	0.57
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	K.IM*AQIER@.G	48.25	34.74	1.39	0.72
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	K.IYVGLSK.M	72.36	46.47	1.56	0.64
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.K#ANYAVDAYFR@.E	28.92	17.64	1.64	0.61
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.LDGQTPHDERQDSINAYNEPNSTK.F	13.30	10.91	1.22	0.82
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.LDSIVIQQGR@.L	25.73	24.51	1.05	0.95
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.LFELLEK#.E	64.67	62.79	1.03	0.97
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.LFELLEK#EILYYR@.K	9.98	6.60	1.51	0.66
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	K.LGFDK#ENVYDELR@.Q	38.31	30.65	1.25	0.80
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	R.LLNILM*QLR@.K	73.33	55.79	1.31	0.76
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-	K.LLTQGFTNWNK#.R	20.26	11.26	1.80	0.56

Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.LR@DYQVR@.G	18.61	14.02	1.33	0.75
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.LR@LDSIVIQQGR@.L	63.35	37.89	1.67	0.60
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.LVDQNLNK#.I	80.45	68.51	1.17	0.85
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.NFTM*DTESSVYNFEGEDYR@EK#.Q	36.06	23.21	1.55	0.64
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.QDSINAYNEPNSTK#.F	17.47	11.06	1.58	0.63
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.QNLLSVGDYR@.H	40.41	23.87	1.69	0.59
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.QTELFAHFIQPAAQK#.T	41.61	25.55	1.63	0.61
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.R@TEQEEDEELLTESSK#.A	22.43	16.74	1.34	0.75
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.SPDLPNAAQAQKEEQLKIDEAEPLNDEELEEK.E	10.77	3.18	3.38	0.30
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.TEQEEDEELLTESSK#.A	30.07	25.83	1.16	0.86
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.TLQTISLLGYM*K#.H	35.50	22.86	1.55	0.64
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.TLQTISLLGYMK#.H	2.93	34.39	0.09	11.73
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.TPEEVIEYSAVFWER@.C	19.60	13.91	1.41	0.71
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.VLIFSQM*TR@.L	45.34	37.14	1.22	0.82
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.VLIFSQMTR@.L	17.48	8.08	2.16	0.46
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.YK#APFHQLR@.I	35.08	26.65	1.32	0.76
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.ANR@FEYLLK#.Q	70.13	36.43	1.93	0.52
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.ANYAVDAYFR.E	25.23	13.55	1.86	0.54
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.DDIENIAR@.E	25.66	19.03	1.35	0.74
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.DFNQFIK#.A	74.31	35.07	2.12	0.47
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.EIQEPDPTYEEK#.M	46.03	34.26	1.34	0.74
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.ENM*ELEEK#EK#.A	6.71	4.07	1.65	0.61
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.ESEITDEDIDGILER@.G	134.35	72.11	1.86	0.54
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.FEDSPSYVK#.W	70.69	49.42	1.43	0.70
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.FEYLLK#.Q	34.90	18.56	1.88	0.53
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.FITDNTVEER@.I	195.72	104.58	1.87	0.53
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.FVFM*LSTR@.A	24.86	16.73	1.49	0.67
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.IDEAEPLNDEELEEK#.E	24.11	13.39	1.80	0.56
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.ILM*KDIDILNSAGK.M	32.95	16.41	2.01	0.50
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.IM*AQIER.G	65.10	33.73	1.93	0.52
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.K#ANYAVDAYFR@.E	12.53	6.29	1.99	0.50
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.KANYAVDAYFR.E	34.68	14.65	2.37	0.42
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.LDGQTPHDER.Q	14.09	6.35	2.22	0.45
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.LDGQTPHDER@QDSINAYNEPNSTK#.F	26.52	12.87	2.06	0.49
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.LDSIVIQQGR@.L	62.60	36.90	1.70	0.59
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.LFELLEK#.E	156.73	90.75	1.73	0.58
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.LGFDK#ENVYDELR@.Q	54.05	31.65	1.71	0.59
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.LLNILM*QLR@.K	101.62	53.14	1.91	0.52
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.LLTQGFTNWNK#.R	34.94	19.39	1.80	0.55
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.LR@LDSIVIQQGR@.L	123.57	68.18	1.81	0.55
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.LVDQNLNK#.I	224.56	104.30	2.15	0.46
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.M*VVLDK#.L	46.98	33.54	1.40	0.71
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.QDSINAYNEPNSTK#.F	28.30	13.66	2.07	0.48
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.QNLLSVGDYR@.H	46.70	20.38	2.29	0.44
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.QPNVQDFQFFPPR@.L	11.58	7.80	1.49	0.67
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.R@TEQEEDEELLTESSK#.A	38.47	27.94	1.38	0.73
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.SPDLPNAAQAQK#.E	25.15	14.11	1.78	0.56
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.SPDLPNAAQAQK#EEQLK#.I	16.82	12.02	1.40	0.71
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.TEQEEDEELLTESSK#.A	51.38	38.54	1.33	0.75
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.TLQTISLLGYM*K#.H	82.46	39.20	2.10	0.48
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.TLQTISLLGYMK#.H	12.31	48.35	0.25	3.93
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.TPEEVIEYSAVFWER@.C	22.97	13.09	1.75	0.57
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	K.TPEEVIEYSAVFWER.C	17.62	15.10	1.17	0.86
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.VLIFSQM*TR@.L	75.10	34.84	2.16	0.46
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.VLIFSQMTR@.L	24.16	11.66	2.07	0.48
Q91ZW3_SMCA5_MOUSE	Smarca5	SWI/SNF-related matrix-a	R.YK#APFHQLR@.I	63.20	35.04	1.80	0.55
Q04692_SMRCD_MOUSE	Smarcad1	SWI/SNF-related matrix-a	K.LISQGTIEESM*LK#.I	8.49	3.20	2.66	0.38
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	K.ASEVEEILDGNDEK#.Y	17.47	5.24	3.33	0.30
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	K.AVSISTEPPTYLR@.E	201.79	57.13	3.53	0.28
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	K.DHGYTTLATSVTLLK#.A	26.38	6.36	4.15	0.24
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	K.FQLEDDGEFYM*IGSEVGNYLR@.M	6.64	3.98	1.67	0.60
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	R.LDM*EIDGQK#.L	26.45	9.95	2.66	0.38
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	K.LNIHVGNISLVDQFEWDM*SEK#.E	3.57	2.92	1.22	0.82
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	K.LNIHVGNISLVDQFEWDM*SEK#ENSPEK#.F	7.30	3.70	1.97	0.51
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	R.QQIESYPTDSILEDQSDQR@.V	24.48	9.90	2.47	0.40
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	R.QQIESYPTDSILEDQSDQR.V	8.00	4.84	1.65	0.61
Q9Z0H3_SNF5_MOUSE	Smarcb1	SWI/SNF-related matrix-a	K.TYAFSENPLPTVEIAIR@.N	60.68	34.77	1.75	0.57
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.AALEEFSR@.V	122.03	39.92	3.06	0.33
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.EKPIDLQNFGLR.T	122.43	36.26	3.38	0.30
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.FDLQNPSR@.M	25.97	14.65	1.77	0.56
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.FWESPDTVSQLDSVR@.V	39.88	19.38	2.06	0.49
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.GGTVADLDEQDEEAVTTGGK#.E	5.65	1.78	3.18	0.31
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.HFEELETIM*DR@.E	37.05	11.77	3.15	0.32
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.HFEELETIM*DR@.E	28.26	9.00	3.14	0.32
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.HLAAVEER@.K	324.80	98.13	3.31	0.30
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.HVTNPAFTK#.L	76.75	20.94	3.67	0.27
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.K#DSENTPVK#.G	9.08	3.09	2.94	0.34
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.K#GQASLYGK#.R	17.75	5.17	3.44	0.29
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.K#VEHEISEGNVATAAAAALASAATK#.A	84.96	25.56	3.32	0.30
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.K#YVHADAPTNK#.T	35.64	13.24	2.69	0.37
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.LR@HFEELETIM*DR@.E	7.78	2.32	3.36	0.30
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.M*ETDPDGQQPEK#.A	4.41	2.29	1.93	0.52
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.NFM*IDTYR@.L	143.89	44.37	3.24	0.31
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.NFMIDTYR@.L	32.94	7.09	4.65	0.22
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.NTEK#EQDSDVSEDVK#PEEK#.E	2.58	1.30	1.99	0.50
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.NVEM*FM*NIEK#.T	19.11	3.47	5.51	0.18
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.R@FDLQNPSR@.M	30.34	6.87	4.42	0.23
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.SK#TPEIYLAYR@.N	139.11	37.00	3.76	0.27
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.SLVALLVETQM*K#.K	142.90	45.33	3.15	0.32
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.SLVALLVETQMK#.K	50.51	20.47	2.47	0.41
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.SLVALLVETQM*K#K#.L	23.42	5.77	4.06	0.25
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.SPQVPAAQQM*LNFPEK#.N	35.85	13.05	2.75	0.36
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.TPEIYLAYR@.N	100.69	26.45	3.81	0.26
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.AENK#VENESDEGDK#IQDR@.E	10.51	4.02	2.61	0.38
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.DM*EDPTPVPNIEEVVLPK#.N	6.85	1.53	4.48	0.22
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.FDLQNPSR@.M	24.21	15.26	1.59	0.63
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.FWESPDTVSQLDSVR.V	29.12	8.17	3.56	0.28
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.GGTVADLDEQDEEAVTTGGK#.E	10.57	2.70	3.91	0.26
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.HFEELETIMDR.E	6.43	4.33	1.49	0.67
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.HLAAVEER@.K	147.64	32.49	4.54	0.22
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.HVTNPAFTK#.L	58.93	12.34	4.78	0.21
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.K#VEHEISEGNVATAAAAALASAATK#.A	11.67	4.13	2.82	0.35
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.LR@HFEELETIM*DR@.E	6.69	2.71	2.47	0.40

P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.M*ETDPDGQQPEK#.A	4.35	1.31	3.32	0.30
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.NFM*IDTYR@.L	96.85	23.33	4.15	0.24
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.NFMIDTYR@.L	17.33	4.75	3.65	0.27
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.NVEM*FM*NIEK#.T	10.92	3.40	3.22	0.31
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.R@ALPEFFNGK#.N	6.53	3.76	1.74	0.58
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.R@FDLQNPSR@.M	21.61	5.12	4.22	0.24
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.SK#TPEIYLAYR@.N	105.21	23.82	4.42	0.23
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.SLVALLVETQM*K#.K	121.71	33.93	3.59	0.28
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.SLVALLVETQMK#.K	25.97	12.92	2.01	0.50
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	R.SPQVPAAQQM*LNFPEK#.N	18.06	4.82	3.75	0.27
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.TPEIYLAYR@.N	65.74	18.56	3.54	0.28
P97496_SMRC1_MOUSE	Smarcc1	SWI/SNF complex subuni	K.VEHEISEGNVATAAAAALASAATK#.A	8.52	2.98	2.86	0.35
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.DIGEGNLSTAAAAALAAAAVK#.A	152.38	42.26	3.61	0.28
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.DIGEGNLSTAAAAALAAAAVK#.A	75.88	23.79	3.19	0.31
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.EEEQEDLTK#DM*DEPSPVPNVEEVTLPK#.T	4.84	2.33	2.07	0.48
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.HVSNAPLTK#.L	39.00	8.05	4.84	0.21
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.K#GPSTPYTK#.S	59.54	17.44	3.41	0.29
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.M*KEEVPTALVEAHVR.K	66.12	16.66	3.97	0.25
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.NPDLHEDNVTEQTHHIIIPSYAAWFDYNSVHAIER@.R	4.37	3.14	1.39	0.72
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.NVEM*FM*TIEK#.S	24.35	7.16	3.40	0.29
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.R@YDFQNPSR@.M	32.36	6.90	4.69	0.21
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.SALEEFSK#.M	93.51	27.52	3.40	0.29
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.YDFQNPSR@.M	25.18	8.36	3.01	0.33
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.YIQAEPPTNK#.S	50.90	14.33	3.55	0.28
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.YYEAADTVTQFDNVR@.L	53.35	10.32	5.17	0.19
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.ADPAFGLESSGIAGTASDEPER@.I	12.40	3.11	3.99	0.25
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.DIGEGNLSTAAAAALAAAAVK#.A	185.99	53.88	3.45	0.29
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.DM*DEPSPVPNVEEVTLPK#.T	14.14	8.28	1.71	0.59
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.EALEYQR@.Q	85.36	18.92	4.51	0.22
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.EEEQEDLTK#.D	10.11	3.24	3.12	0.32
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.EGGGAVEEEAK#EEISEVPK#.K	6.97	1.70	4.11	0.24
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.HVSNAPLTK#.L	80.57	17.98	4.48	0.22
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.K#GPSTPYTK#.S	79.77	21.43	3.72	0.27
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.K#YIQAEPPTNK#.S	6.19	1.31	4.71	0.21
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.NVEM*FM*TIEK#.S	51.73	9.23	5.60	0.18
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.RYDFQNPSR.M	38.32	6.73	5.69	0.18
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.SALEEFSK#.M	139.95	37.08	3.77	0.26
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.SPSPSPTPEAK#.K	16.05	5.11	3.14	0.32
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.WILDTDTFNEWM*NEEDYEVSDDK#SPVSR@.R	12.53	2.41	5.21	0.19
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	R.YDFQNPSR@.M	43.22	10.58	4.09	0.24
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.YIQAEPPTNK#.S	77.53	15.94	4.86	0.21
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.YYEAADTVTQFDNVR@.L	71.50	17.41	4.11	0.24
Q6PDG5_SMRC2_MOUSE	Smarcc2	SWI/SNF complex subuni	K.YYEAADTVTQFDNVR@.L	26.82	7.56	3.55	0.28
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.ELVPESQAYM*DLLAFER@.K	33.90	5.90	5.74	0.17
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.FSEIPQR@.L	34.31	12.31	2.79	0.36
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.FSSFFK#.S	19.92	6.73	2.96	0.34
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.IHETIETINQLK#.T	39.32	7.93	4.96	0.20
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.IR@ELVPESQAYM*DLLAFER@.K	30.59	5.98	5.11	0.20
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.IR@ELVPESQAYMDLLAFER@.K	8.08	2.48	3.26	0.31
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.LDIQEALK#.R	8.00	1.86	4.29	0.23
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.LLEDAALSK#.Y	45.75	16.37	2.79	0.36
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.R@LDIQEALK#.R	17.57	6.35	2.77	0.36
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.R@QELEQALGIR@.N	26.59	4.52	5.89	0.17
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.SDAEDGEGTVASWELR@.V	15.77	4.42	3.57	0.28
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.TATTQETDGFQVK#.R	40.66	12.48	3.26	0.31
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.TM*TDVVGNPEEER@.R	24.96	8.82	2.83	0.35
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.ELVPESQAYMDLLAFER@.K	5.95	3.26	1.83	0.55
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.FSEIPQR@.L	18.89	6.37	2.97	0.34
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.FSSFFK#.S	17.67	7.28	2.43	0.41
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.IHETIETINQLK#.T	26.65	6.31	4.22	0.24
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.IR@ELVPESQAYM*DLLAFER@.K	29.48	6.00	4.91	0.20
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.IR@ELVPESQAYMDLLAFER@.K	8.70	2.22	3.92	0.26
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.LDIQEALK#.R	12.43	2.78	4.48	0.22
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.LLEDAALSK#.Y	30.68	5.28	5.81	0.17
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.R@LDIQEALK#.R	10.41	2.77	3.76	0.27
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.R@QELEQALGIR@.N	26.68	8.33	3.20	0.31
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	K.SDAEDGEGTVASWELR@.V	11.89	3.18	3.74	0.27
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.ELVPESQAYM*DLLAFER@.K	5.85	1.61	3.64	0.27
Q61466_SMRD1_MOUSE	Smarcd1	SWI/SNF-related matrix-	R.IR@ELVPESQAYM*DLLAFER@.K	13.74	2.94	4.67	0.21
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	R.AAFYHQPWAQEAVGR@.H	23.19	5.89	3.94	0.25
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	K.ADGDNAGTAGTPGGTPAADK#.V	7.04	1.39	5.08	0.20
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	K.IHETIESINQLK#.T	41.74	18.30	2.28	0.44
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	R.IYISNTFSPSK#.A	15.61	5.35	2.92	0.34
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	R.M*PTTQETDGFQVK#.R	10.88	3.46	3.15	0.32
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	R.R@QELEQVLGIR@.L	42.56	17.76	2.40	0.42
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	K.ADGDNAGTAGTPGGTPAADK#.V	4.28	2.46	1.74	0.57
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	K.IHETIESINQLK#.T	50.92	14.62	3.48	0.29
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	R.IYISNTFSPSK#.A	19.38	7.81	2.48	0.40
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	R.M*PTTQETDGFQVK#.R	11.67	3.86	3.02	0.33
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	R.R@QELEQVLGIR@.L	42.00	11.35	3.70	0.27
Q99JR8_SMRD2_MOUSE	Smarcd2	SWI/SNF-related matrix-	K.SLVIELDK#ELYGPDNHLVEWHR@.M	10.91	2.45	4.46	0.22
Q6P9Z1_SMRD3_MOUSE	Smarcd3	SWI/SNF-related matrix-	R.AAPPPGQSQAQGQGQPVPTAPAR@.S	11.72	6.16	1.90	0.53
Q6P9Z1_SMRD3_MOUSE	Smarcd3	SWI/SNF-related matrix-	K.GYVQDLLR@.S	27.42	7.42	3.69	0.27
Q6P9Z1_SMRD3_MOUSE	Smarcd3	SWI/SNF-related matrix-	R.LYISNTFNPAK#PDAEDSDGSIASWELR@.V	8.98	2.82	3.18	0.31
Q6P9Z1_SMRD3_MOUSE	Smarcd3	SWI/SNF-related matrix-	R.R@QELEQSLVVR@.N	25.20	8.20	3.07	0.33
Q6P9Z1_SMRD3_MOUSE	Smarcd3	SWI/SNF-related matrix-	R.TPTTQETDGFQVK#.R	26.16	9.82	2.66	0.38
Q6P9Z1_SMRD3_MOUSE	Smarcd3	SWI/SNF-related matrix-	K.VM*TDVAGNPEEER@.R	17.27	5.13	3.37	0.30
Q6P9Z1_SMRD3_MOUSE	Smarcd3	SWI/SNF-related matrix-	R.AAPPPGQSQAQGQGQPVPTAPAR@.S	3.41	2.58	1.32	0.76
Q6P9Z1_SMRD3_MOUSE	Smarcd3	SWI/SNF-related matrix-	K.GYVQDLLR@.S	12.01	4.72	2.55	0.39
Q6P9Z1_SMRD3_MOUSE	Smarcd3	SWI/SNF-related matrix-	R.SAIVQALWQYVK#.T	8.09	2.55	3.17	0.32
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.AEAALEEESR@.Q	36.42	11.49	3.17	0.32
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.ASNPDLK#.L	26.21	10.36	2.53	0.40
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.AYHNSPAYLAYINAK#.S	10.20	12.11	0.84	1.19
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.DLTDEEKQEYLNEYEAEK.I	19.75	5.59	3.53	0.28
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.DLTDEEKQEYLNEYEAEKIEYNESM*K.A	32.45	8.32	3.90	0.26
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.DLTDEEKQEYLNEYEAEKIEYNESMK.A	20.83	5.53	3.77	0.27
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.FLESTDSFNNELK#.R	37.65	12.23	3.08	0.32
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.IAAEIAQAEEQAR@.K	142.71	306.60	0.47	2.15
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.K#LEAELLQIEER@.H	123.90	35.96	3.45	0.29
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.K#VWDQVK#.A	22.69	6.12	3.71	0.27
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.LGGNPGTNSR@.V	48.16	14.42	3.34	0.30
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.LISEILSESVVPDVR@.S	156.58	45.20	3.46	0.29
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.LWEIGK#.I	49.62	14.84	3.34	0.30

O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.R@PSYAPPPTPAPATQM*PSTPGFVGYNPYSHLAYNNYR@.L	15.29	4.05	3.77	0.26
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.SQSSM*APEEEQVANK#.A	18.97	6.95	2.73	0.37
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.SR@AEAALEEESR@.Q	64.13	18.64	3.44	0.29
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.FLESTDSFNNELK#.R	7.14	5.81	1.23	0.81
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.IAAEIAQAEEQAR@.K	59.76	80.90	0.74	1.35
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.K#LEAELLQIEER@.H	30.54	11.12	2.75	0.36
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.LISEILSESVVPDVR.S	29.15	10.94	2.67	0.38
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.LISEILSESVVPDVR@.S	22.23	8.98	2.47	0.40
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.R@PSYAPPPTPAPATQM*PSTPGFVGYNPYSHLAYNNYR@.L	4.62	1.84	2.51	0.40
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	R.SQSSM*APEEEQVANK#.A	3.14	2.35	1.34	0.75
O54941_SMCE1_MOUSE	Smarce1	SWI/SNF-related matrix-	K.SR@AEAALEEESR@.Q	11.18	2.28	4.90	0.20
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.AATLAQELEK#.F	72.71	35.31	2.06	0.49
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.AFVSM*VYSEEGAEDR@.T	22.51	11.81	1.91	0.52
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.AQVQLQLFK#.L	68.86	24.08	2.86	0.35
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.DK#FQETSDEFEAAR@.K	53.97	22.49	2.40	0.42
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.DLTLEENQVK#.K	30.14	15.04	2.00	0.50
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.ELNQVM*EQLGDAR@.I	7.76	6.65	1.17	0.86
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.EVTAIETK#.L	53.57	20.68	2.59	0.39
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.FQETSDEFEAAR@.K	7.75	5.97	1.30	0.77
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.FR@PM*DNLSGGEK#.T	7.55	4.50	1.68	0.60
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.GTM*DDISQEEGSSQGEESVSGSQR@.T	26.40	15.13	1.75	0.57
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.HLALNLQEK#.S	78.81	30.95	2.55	0.39
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.IDEINK#ELNQVM*EQLGDAR@.I	9.39	5.10	1.84	0.54
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.IEK#LEEYITTSK#.Q	50.94	21.97	2.32	0.43
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.IIDETM*AQLQDLK#.N	57.52	21.93	2.62	0.38
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.IIDETMAQLQDLK#.N	16.92	6.71	2.52	0.40
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.K#DENEIEK#.L	13.77	7.73	1.78	0.56
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.K#LEGELTEEVEM*AK#.R	17.29	7.24	2.39	0.42
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.LGIQLDFEK#.N	55.40	22.25	2.49	0.40
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.LNEQQSVLQR@.I	61.35	27.55	2.23	0.45
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.LVIDVIR.Y	84.15	35.46	2.37	0.42
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.LYHNEVEIEK#.L	12.57	4.30	2.93	0.34
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.NFLVFQGAVESIAM*K#.N	21.16	11.03	1.92	0.52
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.NFLVFQGAVESIAM*K#.N	13.02	6.67	1.95	0.51
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.NFLVFQGAVESIAMK#.N	8.68	7.27	1.19	0.84
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.NM*DAIIVDSEK#.T	36.34	19.62	1.85	0.54
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.R@LEFENQK#.T	31.68	13.18	2.40	0.42
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.SGELAQEYDK#R@.K	64.92	20.52	3.16	0.32
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.SK#LESELANFGPR@.I	56.44	24.64	2.29	0.44
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.SNLM*DAISFVLGEK#.T	39.18	18.50	2.12	0.47
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.TALFEEISR.S	85.36	34.25	2.49	0.40
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.TVALDGTLFQK#.S	70.00	30.84	2.27	0.44
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.VIVGGSSEYK#.I	61.15	24.51	2.50	0.40
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.VLTFDLTK#.Y	19.80	6.67	2.97	0.34
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.VLTFDLTK#YPDANPNPNEQ.-	16.56	5.45	3.04	0.33
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.VVQLHEYSEELEK#.L	57.39	25.96	2.21	0.45
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.YSQSDLEQTK#.T	59.74	23.52	2.54	0.39
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.AFVSM*VYSEEGAEDR@.T	10.52	4.49	2.34	0.43
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.AFVSMVYSEEGAEDR@.T	5.52	2.13	2.59	0.39
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.AQVQLQLFK#.L	22.33	7.28	3.07	0.33
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.DK#FQETSDEFEAAR@.K	22.84	6.46	3.53	0.28
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.DLTLEENQVK#.K	16.14	6.20	2.60	0.38
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.GTM*DDISQEEGSSQGEESVSGSQR@.T	14.17	5.83	2.43	0.41
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.HLALNLQEK#.S	37.55	18.55	2.02	0.49
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.IEK#LEEYITTSK#.Q	32.10	11.91	2.69	0.37
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.IIDETM*AQLQDLK#.N	25.63	9.33	2.75	0.36
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.IIDETMAQLQDLK#.N	7.25	3.39	2.14	0.47
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.K#DENEIEK#.L	8.19	3.30	2.48	0.40
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.K#LEGELTEEVEM*AK#.R	8.90	3.24	2.75	0.36
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.LGIQLDFEK#.N	24.84	8.41	2.95	0.34
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.LIEIENFK#.S	42.16	19.86	2.12	0.47
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.LNEQQSVLQR@.I	36.75	13.65	2.69	0.37
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.LVIDVIR@.Y	53.94	18.05	2.99	0.33
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.NFLVFQGAVESIAM*K#.N	12.46	4.01	3.11	0.32
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.NM*DAIIVDSEK#.T	21.08	8.42	2.50	0.40
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.SGVISGGASDLK#.A	44.01	10.02	4.39	0.23
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.SK#LESELANFGPR@.I	20.61	13.43	1.54	0.65
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.SNLM*DAISFVLGEK#.T	38.30	10.26	3.73	0.27
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.TALFEEISR.S	77.35	14.82	5.22	0.19
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.TVALDGTLFQK#.S	34.70	16.00	2.17	0.46
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	R.VIVGGSSEYK#.I	36.99	14.94	2.48	0.40
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.VLTFDLTK#YPDANPNPNEQ.-	4.69	2.18	2.16	0.46
Q9CU62_SMC1A_MOUSE	Smc1a	Structural maintenance	K.YSQSDLEQTK#.T	23.49	9.50	2.47	0.40
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.ALEEELAGLK#.N	68.93	43.03	1.60	0.62
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.AM*NVLTEAEER@.Y	25.69	13.87	1.85	0.54
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.AMNVLTEAEER@.Y	9.53	3.69	2.58	0.39
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.ASNLQDLVYK#.N	37.44	19.30	1.94	0.52
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.AYEGQIEK#.M	40.16	23.35	1.72	0.58
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.DNSTATALEVVAGER@.L	40.98	21.88	1.87	0.53
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.EGM*FNNANVLFK#.T	18.42	9.47	1.95	0.51
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.EHASNEQQLDAVNEAIK#.A	57.94	28.78	2.01	0.50
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.ELQNSM*AEDSK#.A	10.12	8.27	1.22	0.82
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.ENLTELSGGQR@.S	32.72	22.88	1.43	0.70
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.FVDGVSTVAR@.F	41.45	18.43	2.25	0.44
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.GLVASLINVK#.D	56.08	33.72	1.66	0.60
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.ILATIEDLDQK#.K	25.25	12.37	2.04	0.49
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.IVNLQEVLSENEK#.K	31.14	16.89	1.84	0.54
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.K#LNYEENK#EEK#.L	30.73	19.06	1.61	0.62
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.LYIAYQFLR@.A	24.95	13.69	1.82	0.55
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.LYNVVVDTEVTAK#.K	30.09	13.79	2.18	0.46
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.M*LSDYDWINAEK#.H	17.31	15.40	1.12	0.89
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.NQALNIAWQK#.V	23.41	16.96	1.38	0.72
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.QIITAQDNIIK#.D	15.32	7.89	1.94	0.51
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.QQEVEAITLELEELKR.E	42.11	21.94	1.92	0.52
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.SAGELK#EM*QDK#.I	6.20	4.07	1.52	0.66
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.SIILEGFK#.S	45.26	24.84	1.82	0.55
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.SSYLEYQK#.V	21.70	168.48	0.13	7.76
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.TILEEEITPTIQK#.L	59.88	32.07	1.87	0.54
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.VLNM*KPPEILSM*IEEAAGTR.M	16.83	7.96	2.11	0.47
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.YEALENK#.M	8.90	3.25	2.74	0.37
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.ALEEELAGLK#.N	51.76	16.88	3.07	0.33
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.AM*NVLTEAEER@.Y	14.81	5.44	2.72	0.37
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.DNSTATALEVVAGER@.L	28.15	8.61	3.27	0.31

Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.EGM*FNNANVLFK#.T	12.00	5.33	2.25	0.44
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.EHASNEQQLDAVNEAIK#.A	34.77	12.41	2.80	0.36
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.ELQNSM*AEDSK#.A	7.21	3.00	2.40	0.42
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.ELQNSMAEDSK#.A	5.72	2.07	2.77	0.36
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.ENLTELSGGQR@.S	24.47	4.93	4.96	0.20
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.FVDGVSTVAR.F	31.77	6.97	4.56	0.22
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.GLVASLINVK#.D	40.66	14.11	2.88	0.35
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.HNLQNNESQLK#.I	19.20	7.37	2.61	0.38
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.ILATIEDLDQK#.K	16.36	6.75	2.43	0.41
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.IVNLQEVLSENEK#.K	24.97	6.87	3.63	0.28
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.IVNLQEVLSENEK#K#.I	44.83	15.69	2.86	0.35
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.LYIAYQFLR@.A	14.75	5.26	2.81	0.36
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.LYNVVVDTEVTAK#.K	23.52	7.98	2.95	0.34
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.M*LSDYDWINAEK#.H	17.20	6.70	2.57	0.39
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.QQEVEAITLELEELK#R@.E	31.57	18.99	1.66	0.60
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.SAGELK#EM*QDK#.I	7.97	2.27	3.52	0.28
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.SIILEGFK#.S	45.71	15.29	2.99	0.33
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.SQAASILTK#.F	30.93	11.69	2.65	0.38
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.TIEESEETLK#.S	37.42	12.38	3.02	0.33
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	K.TILEEEITPTIQK#.L	48.80	15.35	3.18	0.31
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.TVTLGGDVFDPHGTLSGGAR@.S	63.02	18.29	3.45	0.29
Q8CG48_SMC2_MOUSE	Smc2	Structural maintenance	R.YTIIPLNK#.I	34.26	7.24	4.73	0.21
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.AILNGIDSINK#.V	15.85	8.72	1.82	0.55
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.AK#DLQDELAGNSEQR@.K	27.01	13.41	2.01	0.50
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.AK#LDELSAK#.R	27.54	10.87	2.53	0.39
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.ALDQFVNFSEQK#.E	35.84	17.52	2.05	0.49
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.ALEYTIYNQELNETR@.A	36.84	11.57	3.18	0.31
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.DFVEDDTTHG.-	39.62	39.62	1.00	1.00
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.DK#M*EDIER@.Q	11.83	4.22	2.80	0.36
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.DLEDTEANK#EK#.N	7.89	4.11	1.92	0.52
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.DLQDELAGNSEQR@.K	20.20	8.90	2.27	0.44
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.DSILSEM*K#.M	22.59	10.99	2.06	0.49
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.DSILSEMK#.M	10.85	3.95	2.75	0.36
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.DTAYPETNDAIPM*ISK#.L	15.58	7.61	2.05	0.49
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.EENAEQQALAAK#.R	44.99	22.15	2.03	0.49
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.ELGSLPQEAFEK#.Y	48.64	24.18	2.01	0.50
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.ESLK#AELGTDLLSQLSLEDQK#.R	7.81	5.38	1.45	0.69
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.GALTGGYYDTR@.K	51.72	24.97	2.07	0.48
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.GSGSQSSVPSVDQFTGVGIR@.V	48.85	22.03	2.22	0.45
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.HNVIVGR@.N	43.83	33.86	1.29	0.77
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.INNEIDQLM*NQM*QQIETQQR@.K	10.21	6.80	1.50	0.67
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.INNEIDQLMNQMQQIETQQR@.K	6.51	2.99	2.18	0.46
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.KAEEELGELEAK.L	22.22	13.42	1.66	0.60
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.K#EESISLM*K#.E	20.79	10.41	2.00	0.50
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.K#GDVEGSQSQDEGEGSGESER@.G	27.07	15.36	1.76	0.57
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.K#GDVEGSQSQDEGEGSGESER@.G	2.63	1.58	1.66	0.60
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.LAQATQER@.T	20.67	10.51	1.97	0.51
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.LFYHIVDSDEVSTK#.I	69.60	27.75	2.51	0.40
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.LHTLEEEK#EELAQYQK#.W	20.88	21.04	0.99	1.01
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.M*NLPGEVTFLPLNK#.L	29.44	16.87	1.75	0.57
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.MNLPGEVTFLPLNK#.L	7.00	3.03	2.31	0.43
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.NDVM*NLLESAGFSR@.S	23.36	10.59	2.21	0.45
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.NFSEVFQK#.L	44.90	24.02	1.87	0.54
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.NLEQYNK#LDQDLNEVK#.A	50.55	27.26	1.85	0.54
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.QVIIQGFR@.S	58.66	19.67	2.98	0.34
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.R@ALEYTIYNQELNETR@.A	12.63	13.78	0.92	1.09
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.R@LDQVEQELNELR@.E	4.03	2.20	1.83	0.55
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.SEDLDNSIDK#TEAGIK#.E	5.59	2.06	2.72	0.37
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.SIM*ELM*NVLELR@.K	18.48	8.26	2.24	0.45
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.SLDQAINDK#.K	60.18	26.72	2.25	0.44
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.SM*EVSTQLAR.A	26.86	13.32	2.02	0.50
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.SNPYYIVK#.Q	33.74	18.22	1.85	0.54
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.VDALNDEIR.Q	50.37	26.06	1.93	0.52
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.VETYLNENLR@.K	53.53	22.27	2.40	0.42
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.VSHIDVITAEM*AK#.D	15.40	8.78	1.75	0.57
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.ALDQFVNFSEQK#.E	13.51	5.68	2.38	0.42
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.ALEYTIYNQELNETR@.A	20.25	7.04	2.88	0.35
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.DFVEDDTTHG.-	16.60	16.60	1.00	1.00
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.DLQDELAGNSEQR@.K	6.60	2.74	2.41	0.42
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.DTAYPETNDAIPM*ISK#.L	8.09	3.83	2.11	0.47
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.ELGSLPQEAFEK#.Y	26.51	11.25	2.36	0.42
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.ESLK#AELGTDLLSQLSLEDQK#.R	8.89	3.92	2.27	0.44
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.ETEGGTVLTATTSELEAINK#.R	6.66	1.57	4.24	0.24
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.GSGSQSSVPSVDQFTGVGIR@.V	22.83	7.58	3.01	0.33
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.INNEIDQLM*NQM*QQIETQQR@.K	3.89	3.01	1.29	0.77
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.INQM*ATAPDSQR@.L	43.83	15.55	2.82	0.35
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.K#AEEELGELEAK#.L	18.00	5.22	3.45	0.29
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.K#GDVEGSQSQDEGEGSGESER@.G	17.56	4.48	3.92	0.26
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.LAQATQER@.T	16.65	6.41	2.60	0.39
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.M*NLPGEVTFLPLNK#.L	23.97	8.79	2.73	0.37
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.NDVM*NLLESAGFSR@.S	9.63	6.29	1.53	0.65
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.QVIIQGFR@.S	24.10	10.36	2.33	0.43
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.SIM*ELM*NVLELR@.K	13.88	12.61	1.10	0.91
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.SLDQAINDK#.K	24.84	10.23	2.43	0.41
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.SYR@DQTIVDPFSSK#.H	9.74	5.81	1.68	0.60
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.VDALNDEIR@.Q	19.49	4.59	4.24	0.24
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	R.VETYLNENLR.K	26.57	8.51	3.12	0.32
Q9CW03_SMC3_MOUSE	Smc3	Structural maintenance	K.VSHIDVITAEM*AK#.D	6.90	5.12	1.35	0.74
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.DSTSVYHISGK#.K	7.41	5.70	1.30	0.77
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.DTLVANNLDQATR@.V	29.93	12.61	2.37	0.42
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.FTQLDLEDVQVR@.E	32.47	18.51	1.75	0.57
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.HNTAVSQLSK#.A	36.19	14.63	2.47	0.40
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.IIDKEGDDYEVLPNSNFYVSR.T	19.94	7.34	2.72	0.37
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.IPGIYGR@.L	21.51	9.04	2.38	0.42
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.LGDLGAIDEK#.Y	17.81	8.50	2.09	0.48
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.LTQEEINLK#.S	28.21	11.38	2.48	0.40
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.NIAIEFLTLENEM*FK#.K	13.56	4.58	2.96	0.34
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.NIAIEFLTLENEM*FK#.K	18.83	6.39	2.94	0.34
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.QAFYFALR@.D	14.02	6.37	2.20	0.45
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.SK#M*EVAQSELDIYLSR@.H	11.02	5.38	2.05	0.49
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.SLVHDLFQK#.V	8.56	6.42	1.33	0.75
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.TAETSLPEIQK#.E	21.80	10.10	2.16	0.46
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.TVINETTTR@.N	26.06	22.07	1.18	0.85

Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.VLDAIIQEK#.K	28.71	14.29	2.01	0.50
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.VVTLQGQIIEQSGTM*SGGGSK#.V	13.48	6.37	2.12	0.47
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.DTLVANNLDQATR@.V	60.08	27.37	2.19	0.46
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.ELEANVLTTAPDR@.K	21.47	10.93	1.96	0.51
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.FTQLDLEDVQVR@.E	96.36	43.07	2.24	0.45
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.HNIGIATFIGLDK#.M	14.46	8.48	1.71	0.59
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.HNTAVSQLSK#.A	54.73	27.84	1.97	0.51
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.IAEITTQK#.E	59.73	29.70	2.01	0.50
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.IIDK#EGDDYEVLPNSNFYVSR@.T	41.17	21.09	1.95	0.51
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.IPGIYGR@.L	57.80	22.63	2.55	0.39
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.LGDLGAIDEK#.Y	42.94	15.39	2.79	0.36
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.LK#LEQIDGHISEHNSK#.I	28.35	7.69	3.69	0.27
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.LLEENVSVFK#.K	32.85	15.88	2.07	0.48
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.LM*ITHIVNQNFK#.S	27.72	14.64	1.89	0.53
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.LPQTQQELK#.E	78.94	37.41	2.11	0.47
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.LTQEEINLK#.S	64.68	26.85	2.41	0.42
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.M*GSSVIDEISVEEVNK#.M	17.60	6.42	2.74	0.36
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.NIAIEFLTLENEM*FK#.K	26.94	9.71	2.77	0.36
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.NIEDK#AEEVINNTK#.T	10.99	5.98	1.84	0.54
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.NNM*FEISDR@.L	7.55	3.25	2.32	0.43
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.QAFYFALR@.D	23.76	9.49	2.50	0.40
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.SK#M*EVAQSELDIYLSR@.H	21.64	12.65	1.71	0.58
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.SLVHDLFQK#.V	19.00	5.77	3.29	0.30
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.SLVHDLFQK#VEEAK#.S	36.27	13.00	2.79	0.36
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.SNVLSNEM*K#.A	34.80	17.42	2.00	0.50
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.TAETSLPEIQK#.E	46.92	18.03	2.60	0.38
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.TVINETTTR.N	73.55	33.91	2.17	0.46
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	K.VLDAIIQEK#.K	66.95	29.22	2.29	0.44
Q8CG47_SMC4_MOUSE	Smc4	Structural maintenance	R.VVTLQGQIIEQSGTM*SGGGSK#.V	50.53	26.63	1.90	0.53
Q924W5_SMC6_MOUSE	Smc6	Structural maintenance	R.EAFTADGDQVFAGR@.Y	5.82	2.78	2.10	0.48
Q924W5_SMC6_MOUSE	Smc6	Structural maintenance	R.GQTTLPFR@PVTQEEDDSAS.-	3.56	2.09	1.71	0.59
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	R.DSTEYFIIFEPR@.L	11.71	6.58	1.78	0.56
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	R.EIQDDM*QTLYINTASDSFEFK#.A	5.02	1.62	3.10	0.32
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	K.FSFGLLDSPFR@.V	36.87	15.21	2.42	0.41
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	K.GSAEITTLVLAENSPGR@.D	10.10	19.29	0.52	1.91
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	K.ITEQNELK#.K	13.32	10.87	1.23	0.82
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	K.ITLEANSQSVSVQGIR@.F	15.72	8.16	1.93	0.52
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	R.K#PADSAHITNDDER@.F	14.59	5.34	2.73	0.37
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	K.LTFM*DLELK#.L	10.00	5.98	1.67	0.60
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	K.LVPDSQPATPAVSNVR@.S	15.61	7.82	2.00	0.50
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	R.NLIFQM*YDEGER@EINITPSLAEK#.I	12.20	8.03	1.52	0.66
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	R.NR@K#PADSAHITNDDER@.F	5.79	1.32	4.39	0.23
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	K.STIEGPTIK#.L	17.37	7.67	2.26	0.44
Q6P5D8_SMHD1_MOUSE	Smchd1	Structural maintenance	R.VQLVSGPPTK#.L	21.06	8.80	2.39	0.42
P61406_EST1A_MOUSE	Smg6	Telomerase-binding prot	R.VADNQELQLSNLLSR@.D	4.88	1.91	2.56	0.39
Q8VE18_SMG8_MOUSE	Smg8	Protein SMG8 OS=Mus m	K.AVSVGEAGGAGDPGAAAGDSLR@.G	9.37	3.52	2.67	0.38
Q8VE18_SMG8_MOUSE	Smg8	Protein SMG8 OS=Mus m	K.LYEVAIDGK#EEDLGSPTGELTSK#.I	7.71	4.49	1.72	0.58
Q8VE18_SMG8_MOUSE	Smg8	Protein SMG8 OS=Mus m	K.VLEGFLDIDTK#.F	7.03	5.32	1.32	0.76
Q8VE18_SMG8_MOUSE	Smg8	Protein SMG8 OS=Mus m	K.AVSVGEAGGAGDPGAAAGDSLR@.G	3.63	1.14	3.19	0.31
Q9DB90_SMG9_MOUSE	Smg9	Protein SMG9 OS=Mus m	R.AGPGSSPLFSLLPGYR@.G	12.93	7.82	1.65	0.60
Q9DB90_SMG9_MOUSE	Smg9	Protein SMG9 OS=Mus m	K.EGQR@PTQPVYQIQNR@.G	12.82	4.46	2.88	0.35
Q9DB90_SMG9_MOUSE	Smg9	Protein SMG9 OS=Mus m	R.GM*GTAAPTAM*DPVVGQAK#.L	5.27	2.34	2.25	0.44
P97801_SMN_MOUSE	Smn1	Survival motor neuron p	R.GTGQSDDSDIWDDTALIK#.A	11.24	2.57	4.37	0.23
Q3UKJ7_SMU1_MOUSE	Smu1	WD40 repeat-containing	K.AAVKDVEEEKFPTQLSR.H	21.14	27.17	0.78	1.29
Q3UKJ7_SMU1_MOUSE	Smu1	WD40 repeat-containing	K.DSSQILSASFDQTIR.I	16.78	19.84	0.85	1.18
Q3UKJ7_SMU1_MOUSE	Smu1	WD40 repeat-containing	R.DTEM*LATGAQDGK.I	14.02	14.61	0.96	1.04
Q3UKJ7_SMU1_MOUSE	Smu1	WD40 repeat-containing	R.LM*ALLGQALK.W	13.38	15.88	0.84	1.19
Q3UKJ7_SMU1_MOUSE	Smu1	WD40 repeat-containing	K.SLGSTAGTDITVNSVILLPK.N	10.32	14.84	0.70	1.44
Q3UKJ7_SMU1_MOUSE	Smu1	WD40 repeat-containing	R.SNTVVIM*NM*QGQIVR.S	7.16	9.69	0.74	1.35
Q3UKJ7_SMU1_MOUSE	Smu1	WD40 repeat-containing	R.YIHLENLLAR@.S	25.13	23.13	1.09	0.92
Q6P5C5_SMUG1_MOUSE	Smug1	Single-strand selective m	R.SLAEGFLEEELR@.L	6.04	6.85	0.88	1.13
O09044_SNP23_MOUSE	Snap23	Synaptosomal-associate	R.ILGLAIESQDAGIK#.T	15.76	7.16	2.20	0.45
O09044_SNP23_MOUSE	Snap23	Synaptosomal-associate	K.NM*ALDM*GNEIDAQNQQIQK#.I	3.28	1.93	1.70	0.59
O09044_SNP23_MOUSE	Snap23	Synaptosomal-associate	R.ILGLAIESQDAGIK#.T	11.85	8.50	1.39	0.72
Q8R570_SNP47_MOUSE	Snap47	Synaptosomal-associate	R.FIGK#PDVAYQLISAK#.M	9.59	3.53	2.71	0.37
Q8R570_SNP47_MOUSE	Snap47	Synaptosomal-associate	K.IELLEDALVLR@.N	8.16	3.07	2.66	0.38
Q8R570_SNP47_MOUSE	Snap47	Synaptosomal-associate	K.DLQQQSEQLDSVLK#.G	3.64	1.82	2.00	0.50
Q9Z266_SNAPN_MOUSE	Snapin	SNARE-associated protei	R.VVLVNNILQNAQER@.L	16.19	6.50	2.49	0.40
Q9CZ28_SNF8_MOUSE	Snf8	Vacuolar-sorting protein	K.FAQDVSQDDLIR.A	9.77	6.48	1.51	0.66
Q8BIZ6_SNIP1_MOUSE	Snip1	Smad nuclear-interacting	K.EK#PSFELSGALLEDTNTFR@.G	23.26	17.69	1.32	0.76
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.ADEVLEILK#.T	21.57	12.26	1.76	0.57
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.ANSNLVLQADR@.S	49.37	19.61	2.52	0.40
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.DEPTGEVLSLVGK#.L	59.63	33.38	1.79	0.56
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.DIDAFWLQR@.Q	69.43	39.22	1.77	0.56
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.DTLGLFLR@.E	17.59	11.27	1.56	0.64
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.EEASDDDM*EGDEAVVR@.C	9.94	3.34	2.97	0.34
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.EEEK#LELQK#.L	21.42	11.31	1.89	0.53
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.EEEVTGPVIAPLFPQK#.R	21.06	17.62	1.20	0.84
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.EEGWWVVIGDAK#.S	31.33	16.29	1.92	0.52
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.EGSASTEVLR@.T	69.44	39.04	1.78	0.56
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.EIDLLLGQTDDTR@.Y	53.06	25.79	2.06	0.49
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.ESIEEPSAK#.I	61.04	25.58	2.39	0.42
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.ETLLNGVGYLHEGLSPM*ER@.R	6.22	7.81	0.80	1.26
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.FQIM*NEIVYEK#.I	19.55	13.77	1.42	0.70
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.FYDDAIVSQK#.K	81.72	36.32	2.25	0.44
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.GDPLLDQR@.R	17.13	12.67	1.35	0.74
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.GLFYFDNSFRPVPLEQTYVGITEK.K	58.32	32.86	1.77	0.56
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.GLIEIISNAAEYENIPIR@.H	214.70	99.36	2.16	0.46
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.GLIEIISNAAEYENIPIR.H	38.96	21.81	1.79	0.56
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.GNIIISTPEK#.W	39.27	19.90	1.97	0.51
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.GNIIISTPEK#WDILSR@.R	9.42	5.21	1.81	0.55
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.GTQVYSPEK#.G	36.72	20.10	1.83	0.55
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.GVESVFDIM*EM*EDEER.N	4.53	2.66	1.71	0.59
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.GVESVFDIM*EM*EDEERNALLQLTDSQIADVAR.F	3.10	2.81	1.10	0.91
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.GWAQLTDK#.T	18.19	14.63	1.24	0.80
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.GYEEVHVPALK#PK#PFGSEEQLLPVEK#.L	27.61	12.82	2.15	0.46
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.GYTLLSEGIDEM*VGIIYKPK.T	17.35	14.22	1.22	0.82
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.HINM*DGTINVDDFK#.I	55.11	26.72	2.06	0.48
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.HLILPEK#.Y	29.85	15.66	1.91	0.52
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.HLILPEK#YPPPTELLDLQPLPVSALR@.N	28.84	19.33	1.49	0.67
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.HLILPEK#YPPPTELLDLQPLPVSALR@.N	6.43	3.26	1.97	0.51
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.IVALSSSLSNAK#.D	78.53	44.00	1.78	0.56
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.K#ADEVLEILK#.T	72.12	33.22	2.17	0.46

Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.KADEVLEILK.T	26.67	15.85	1.68	0.59
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.K#PVIVFVPSR@.K	22.28	12.47	1.79	0.56
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.LELSVHLQPITR@.S	19.33	13.41	1.44	0.69
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.LIGLSATLPNYEDVATFLR@.V	44.20	24.26	1.82	0.55
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.LPDM*LNAEIVLGNVQNAK#.D	28.16	16.57	1.70	0.59
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.M*DTDLETM*DLDQGGEALAPR@.Q	36.41	25.45	1.43	0.70
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.M*EADPELSK#.F	46.53	30.00	1.55	0.64
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.MQLSAELQSDTEEILSK#.A	6.33	6.72	0.94	1.06
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.M*TQNPNYYNLQGISHR@.H	50.45	35.40	1.43	0.70
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.MTQNPNYYNLQGISHR@.H	8.27	4.01	2.07	0.48
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.NALLQLTDSQIADVAR@.F	29.87	15.62	1.91	0.52
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.NIEMTQEDVR@.L	6.42	3.20	2.01	0.50
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.NIEM*TQEDVR.L	140.60	85.99	1.64	0.61
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.QDAVDYLTWTFLYR@.R	10.83	6.95	1.56	0.64
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.SGGPVVVLVQLER@.E	48.28	11.18	4.32	0.23
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.SLQYEYK#.A	44.10	18.48	2.39	0.42
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.SLVQEM*VGSFGK.R	51.24	20.30	2.52	0.40
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.SNSLISIK#.R	70.05	28.28	2.48	0.40
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.SPTLYGISHDDLK#GDPLLDQR@.R	20.16	13.20	1.53	0.65
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.TGNFQVTELGR@.I	86.37	42.64	2.03	0.49
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.TIENK#QDAVDYLTWTFLYR@.R	10.64	5.90	1.80	0.55
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.TLVEDLFADK#.H	19.43	10.57	1.84	0.54
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.TR@R@DEPTGEVLSLVGK#.L	18.65	10.79	1.73	0.58
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.TYTQLVR@.L	82.83	45.66	1.81	0.55
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.VELTITPDFQWDEK#.V	33.42	17.51	1.91	0.52
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.VFSLSSEFK#.N	80.89	47.41	1.71	0.59
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.VVLLTGETSTDLK#.L	98.95	57.41	1.72	0.58
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.YAQAGFEGFK#.T	72.68	38.02	1.91	0.52
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	R.YPNIELSYEVVDK#DSIR@.S	23.84	31.44	0.76	1.32
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.YPPPTELLDLQPLPVSALR@.N	17.86	13.19	1.35	0.74
Q6P4T2_U520_MOUSE	Snrnp200	U5 small nuclear ribonuc	K.YPPPTELLDLQPLPVSALR.N	5.77	3.76	1.54	0.65
Q6PE01_SNR40_MOUSE	Snrnp40	U5 small nuclear ribonuc	R.FVYVWDTTSR@.R	93.80	63.77	1.47	0.68
Q6PE01_SNR40_MOUSE	Snrnp40	U5 small nuclear ribonuc	R.GHADSVTGLSLSSEGSYLLSNAMDNTVR@.V	8.44	5.07	1.66	0.60
Q6PE01_SNR40_MOUSE	Snrnp40	U5 small nuclear ribonuc	R.K#GPELPLVPVK#.R	30.37	27.35	1.11	0.90
Q6PE01_SNR40_MOUSE	Snrnp40	U5 small nuclear ribonuc	K.TVAVWDSETGER@.V	74.96	48.44	1.55	0.65
Q6PE01_SNR40_MOUSE	Snrnp40	U5 small nuclear ribonuc	R.FVYVWDTTSR@.R	8.19	5.77	1.42	0.70
Q62376_RU17_MOUSE	Snrnp70	U1 small nuclear ribonuc	R.DPIPYLPPLEK#.L	47.34	32.11	1.47	0.68
Q62376_RU17_MOUSE	Snrnp70	U1 small nuclear ribonuc	R.LGGGLGGTR@.R	41.55	24.62	1.69	0.59
Q62376_RU17_MOUSE	Snrnp70	U1 small nuclear ribonuc	R.RLGGGLGGTR.R	25.42	17.21	1.48	0.68
Q62376_RU17_MOUSE	Snrnp70	U1 small nuclear ribonuc	R.R@QQEVETELK#.M	13.78	8.84	1.56	0.64
Q62376_RU17_MOUSE	Snrnp70	U1 small nuclear ribonuc	R.VLVDVER.G	95.82	59.24	1.62	0.62
Q62376_RU17_MOUSE	Snrnp70	U1 small nuclear ribonuc	R.VNYDTTESK#.L	25.82	20.21	1.28	0.78
Q62189_SNRPA_MOUSE	Snrpa	U1 small nuclear ribonuc	R.ANHTIYINNLNEK#.I	19.18	14.38	1.33	0.75
Q62189_SNRPA_MOUSE	Snrpa	U1 small nuclear ribonuc	K.EVTSATNALR@.S	49.28	103.28	0.48	2.10
Q62189_SNRPA_MOUSE	Snrpa	U1 small nuclear ribonuc	R.HDIAFVEFDNEVQAGAAR@.D	15.08	6.95	2.17	0.46
Q62189_SNRPA_MOUSE	Snrpa	U1 small nuclear ribonuc	K.KAVQGGAAAPVVGAVQPVPGM*PPM*PQAPR.I	9.92	6.02	1.65	0.61
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.GGPSAGDVEAIK#.N	66.01	51.04	1.29	0.77
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.GLLQSGQIPGR@.E	71.43	50.56	1.41	0.71
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.IPVIENLGATLDQFDAIDFSDNEIRK.L	6.71	3.93	1.71	0.59
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.K#GGPSAGDVEAIK#.N	8.22	8.56	0.96	1.04
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	R.K#LDGFPLLR@.R	11.54	14.02	0.82	1.21
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.LDGFPLLR@.R	8.91	6.71	1.33	0.75
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.LTAELIEQAAQYTNAVR@.D	31.82	21.81	1.46	0.69
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.NAIANASTLAEVER@.L	80.36	53.47	1.50	0.67
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	R.SGPSDEGEEEIEDDTVTNGS.-	7.27	7.27	1.00	1.00
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.SLTYLSILR@.N	48.28	24.49	1.97	0.51
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.TFNPGAGLPTDK#.K	47.99	40.61	1.18	0.85
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.TLLVNNNR@.I	58.93	34.49	1.71	0.59
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.GLLQSGQIPGR@.E	9.88	5.36	1.84	0.54
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	R.KLDGFPLLR.R	10.58	6.82	1.55	0.64
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.LTAELIEQAAQYTNAVR@.D	9.17	3.49	2.62	0.38
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.NAIANASTLAEVER@.L	15.81	13.61	1.16	0.86
P57784_RU2A_MOUSE	Snrpa1	U2 small nuclear ribonuc	K.SLTYLSILR.N	10.89	8.69	1.25	0.80
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.GENLVSM*TVEGPPPK#.D	31.51	20.90	1.51	0.66
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.GENLVSM*TVEGPPPK#DTGIAR@.V	53.24	30.83	1.73	0.58
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.GENLVSMTVEGPPPK#DTGIAR@.V	17.48	50.39	0.35	2.88
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.GIPAGVPM*PQAPAGLAGPVR@.G	14.59	10.20	1.43	0.70
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	K.R@VLGLVLLR@.G	62.90	37.09	1.70	0.59
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.VLGLVLLR@.G	353.77	219.98	1.61	0.62
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.GENLVSM*TVEGPPPK#.D	15.47	11.95	1.29	0.77
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.GENLVSM*TVEGPPPK#DTGIAR@.V	40.01	28.90	1.38	0.72
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.GIPAGVPM*PQAPAGLAGPVR@.G	4.20	4.38	0.96	1.04
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.GIPAGVPMPQAPAGLAGPVR.G	7.63	6.14	1.24	0.80
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	K.M*LQHIDYR@.M	14.58	15.07	0.97	1.03
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	K.R@VLGLVLLR@.G	115.69	89.06	1.30	0.77
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.VLGLVLLR.G	195.06	124.39	1.57	0.64
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.GENLVSM*TVEGPPPK#.D	4.49	4.60	0.98	1.02
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	K.RVLGLVLLR.G	11.27	7.96	1.42	0.71
P27048_RSMB_MOUSE	Snrpb	Small nuclear ribonuclec	R.VLGLVLLR@.G	70.97	35.95	1.97	0.51
Q9CQI7_RU2B_MOUSE	Snrpb2	U2 small nuclear ribonuc	R.DALQGFK#.I	83.16	36.18	2.30	0.44
Q9CQI7_RU2B_MOUSE	Snrpb2	U2 small nuclear ribonuc	R.GQAFVIFK#.E	46.43	20.94	2.22	0.45
Q9CQI7_RU2B_MOUSE	Snrpb2	U2 small nuclear ribonuc	K.TDSDIISK#.M	31.36	18.88	1.66	0.60
Q9CQI7_RU2B_MOUSE	Snrpb2	U2 small nuclear ribonuc	K.TM*EQAAAAANK#.K	10.33	5.63	1.83	0.54
Q9CQI7_RU2B_MOUSE	Snrpb2	U2 small nuclear ribonuc	K.ELGSSTNALR.Q	23.42	16.09	1.46	0.69
Q9CQI7_RU2B_MOUSE	Snrpb2	U2 small nuclear ribonuc	K.TM*EQAAAAANK#.K	2.39	1.54	1.56	0.64
Q62241_RU1C_MOUSE	Snrpc	U1 small nuclear ribonuc	K.TTAAFQQGK#.I	15.14	18.02	0.84	1.19
P62315_SMD1_MOUSE	Snrpd1	Small nuclear ribonuclec	K.NR@EPVQLETLSIR@.G	19.64	6.15	3.19	0.31
P62315_SMD1_MOUSE	Snrpd1	Small nuclear ribonuclec	R.EPVQLETLSIR@.G	26.79	16.25	1.65	0.61
P62315_SMD1_MOUSE	Snrpd1	Small nuclear ribonuclec	K.LSHETVTIELK#.N	150.73	64.95	2.32	0.43
P62315_SMD1_MOUSE	Snrpd1	Small nuclear ribonuclec	K.NR@EPVQLETLSIR@.G	311.75	159.30	1.96	0.51
P62315_SMD1_MOUSE	Snrpd1	Small nuclear ribonuclec	K.NREPVQLETLSIR.G	45.46	29.32	1.55	0.65
P62315_SMD1_MOUSE	Snrpd1	Small nuclear ribonuclec	K.LSHETVTIELK#.N	31.83	12.24	2.60	0.38
P62315_SMD1_MOUSE	Snrpd1	Small nuclear ribonuclec	K.NGTQVHGTITGVDVSM*NTHLK#.A	3.91	2.49	1.57	0.64
P62315_SMD1_MOUSE	Snrpd1	Small nuclear ribonuclec	K.NR@EPVQLETLSIR@.G	41.03	27.90	1.47	0.68
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	R.EEEEFNTGPLSVLTQSVK#.N	29.59	21.50	1.38	0.73
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	R.GDSVIVVLR.N	195.15	129.77	1.50	0.66
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	K.M*FLR@GDSVIVVLR@.N	6.97	3.45	2.02	0.50
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	R.NPLIAGK#.-	194.91	113.31	1.72	0.58
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	K.REEEEFNTGPLSVLTQSVK.N	111.59	55.99	1.99	0.50
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	K.SEMTPEELQK#.R	22.31	10.75	2.08	0.48
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	K.SEM*TPEELQK#R@.E	10.02	6.33	1.58	0.63
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	K.SEM*TPEELQKREEEEFNTGPLSVLTQSVK.N	7.59	5.21	1.46	0.69
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	K.SEMTPEELQK#R@EEEEFNTGPLSVLTQSVK#.N	2.68	1.79	1.50	0.67

P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	K.SEMTPEELQKREEEEFNTGPLSVLTQSVK.N	19.33	13.20	1.46	0.68
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	R.EEEEFNTGPLSVLTQSVK#.N	6.64	3.98	1.67	0.60
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	R.GDSVIVVLR@.N	174.25	15.21	11.46	0.09
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	K.R@EEEEFNTGPLSVLTQSVK#.N	8.82	4.92	1.79	0.56
P62317_SMD2_MOUSE	Snrpd2	Small nuclear ribonuclec	K.SEM*TPEELQK#.R	14.86	5.80	2.56	0.39
P62320_SMD3_MOUSE	Snrpd3	Small nuclear ribonuclec	R.VAQLEQVYIR@.G	12.36	9.15	1.35	0.74
P62320_SMD3_MOUSE	Snrpd3	Small nuclear ribonuclec	R.VAQLEQVYIR@.G	270.10	166.40	1.62	0.62
P62320_SMD3_MOUSE	Snrpd3	Small nuclear ribonuclec	R.FLILPDM*LK#.N	69.29	26.58	2.61	0.38
P62320_SMD3_MOUSE	Snrpd3	Small nuclear ribonuclec	R.FLILPDMLK#.N	15.07	8.36	1.80	0.55
P62320_SMD3_MOUSE	Snrpd3	Small nuclear ribonuclec	R.VAQLEQVYIR@.G	48.10	21.44	2.24	0.45
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	K.GDNITLLQSVSN.-	11.10	11.10	1.00	1.00
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	K.VM*VQPINLIFR@.Y	26.22	19.75	1.33	0.75
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	R.IM*LK#GDNITLLQSVSN.-	17.68	7.65	2.31	0.43
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	R.IQVWLYEQVNM*R@.I	25.65	14.78	1.74	0.58
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	K.VM*VQPINLIFR@.Y	632.19	323.17	1.96	0.51
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	K.VMVQPINLIFR@.Y	32.71	17.65	1.85	0.54
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	K.GDNITLLQSVSN.-	16.63	16.63	1.00	1.00
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	K.VM*VQPINLIFR@.Y	61.58	31.65	1.95	0.51
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	K.VMVQPINLIFR.Y	12.40	9.12	1.36	0.74
P62305_RUXE_MOUSE	Snrpe	Small nuclear ribonuclec	K.VM*VQPINLIFR@.Y	14.11	7.55	1.87	0.54
P62307_RUXF_MOUSE	Snrpf	Small nuclear ribonuclec	R.GVEEEEEDGEM*R.E	5.95	4.45	1.34	0.75
P62307_RUXF_MOUSE	Snrpf	Small nuclear ribonuclec	R.GVEEEEEDGEM*R@E.-	69.26	36.51	1.90	0.53
P62307_RUXF_MOUSE	Snrpf	Small nuclear ribonuclec	R.GVEEEEEDGEMR@E.-	4.55	3.42	1.33	0.75
P62307_RUXF_MOUSE	Snrpf	Small nuclear ribonuclec	R.GVEEEEEDGEM*R@E.-	17.13	7.97	2.15	0.47
P62309_RUXG_MOUSE	Snrpg	Small nuclear ribonuclec	R.GNSIIM*LEALER.V	18.98	14.06	1.35	0.74
P62309_RUXG_MOUSE	Snrpg	Small nuclear ribonuclec	R.GNSIIM*LEALER@V.-	37.28	9.15	4.08	0.25
P62309_RUXG_MOUSE	Snrpg	Small nuclear ribonuclec	R.GNSIIMLEALER@V.-	5.11	3.20	1.60	0.63
Q61234_SNTA1_MOUSE	Snta1	Alpha-1-syntrophin OS=	K.GSVPYDAELSFALR@.T	9.00	5.00	1.80	0.56
Q61234_SNTA1_MOUSE	Snta1	Alpha-1-syntrophin OS=	K.M*PILISK#.I	12.04	4.60	2.62	0.38
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	K.AGLVELLLR@.E	26.80	11.90	2.25	0.44
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	R.SPSLGSDLTFATR@.T	20.66	26.73	0.77	1.29
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	K.AGLVELLLR@.E	10.85	5.72	1.90	0.53
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	K.AGLVELLLR@.E	43.34	14.36	3.02	0.33
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	K.IFPGLAADQSR@.A	17.41	6.53	2.66	0.38
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	R.LGDAILSVNGTDLR@.Q	10.16	3.40	2.99	0.33
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	R.SPSLGSDLTFATR@.T	17.89	6.11	2.93	0.34
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	K.AGLVELLLR@.E	44.40	13.54	3.28	0.30
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	R.GLGPPSPPAPPR@.G	25.71	6.45	3.98	0.25
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	K.IFPGLAADQSR@.A	19.69	7.46	2.64	0.38
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	K.K#PSLVSDLPWEGASPQSPSFSGSEDSGSPK#.H	8.09	2.42	3.35	0.30
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	R.LGDAILSVNGTDLR@.Q	6.59	2.45	2.69	0.37
Q61235_SNTB2_MOUSE	Sntb2	Beta-2-syntrophin OS=	R.NLSM*PDLENR@.L	10.85	4.19	2.59	0.39
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.LAEALYIADR@.K	7.63	10.95	0.70	1.43
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.LAPAQYIR@.Y	13.96	19.60	0.71	1.40
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	R.LLEDFGDGGAFPEIHVAQYPLDM*GR.K	10.40	16.04	0.65	1.54
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.M*SNALAIQVDPEGK#.I	8.42	12.06	0.70	1.43
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	R.SLQTSLVSSR.R	24.09	28.99	0.83	1.20
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	R.DISEVIALGVPNPR@.T	29.46	22.00	1.34	0.75
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	R.EGPVQFEEDPFGLDK.F	6.66	3.83	1.74	0.58
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.GM*DSGFAGGEDEIYNVYDQAWR@.G	9.88	6.40	1.54	0.65
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.IK#YDAIAR@.Q	20.63	12.37	1.67	0.60
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.LAEALYIADR@.K	26.29	17.05	1.54	0.65
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.LAEALYIADR@K#.A	28.00	17.59	1.59	0.63
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.LAPAQYIR@.Y	41.37	33.64	1.23	0.81
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	R.LLEDFGDGGAFPEIHVAQYPLDM*GR@.K	38.00	22.57	1.68	0.59
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.M*SNALAIQVDPEGK#.I	27.10	18.61	1.46	0.69
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	R.SLQTSLVSSR.R	88.17	51.96	1.70	0.59
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	R.TSNEVQYDQR@.L	31.18	18.46	1.69	0.59
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.VAAAM*PVR.A	58.89	34.24	1.72	0.58
Q9CSN1_SNW1_MOUSE	Snw1	SNW domain-containing	K.YTDLVPK#.E	23.15	20.98	1.10	0.91
Q9WV80_SNX1_MOUSE	Snx1	Sorting nexin-1 OS=Mus	R.AVGTQALSGAGLLK#.M	19.39	11.27	1.72	0.58
Q9WV80_SNX1_MOUSE	Snx1	Sorting nexin-1 OS=Mus	K.ELALNTALFAK#.S	6.76	4.46	1.52	0.66
Q9WV80_SNX1_MOUSE	Snx1	Sorting nexin-1 OS=Mus	K.SLAM*LGSSEDNTALSR@.A	10.47	5.19	2.02	0.50
Q9WV80_SNX1_MOUSE	Snx1	Sorting nexin-1 OS=Mus	K.YWEAFLPEAK#.A	5.99	6.74	0.89	1.13
Q9WV80_SNX1_MOUSE	Snx1	Sorting nexin-1 OS=Mus	R.ALSQLAEVEEK#.I	18.87	8.81	2.14	0.47
Q9WV80_SNX1_MOUSE	Snx1	Sorting nexin-1 OS=Mus	K.ELALNTALFAK#.S	8.78	4.40	2.00	0.50
Q9WV80_SNX1_MOUSE	Snx1	Sorting nexin-1 OS=Mus	K.SLAM*LGSSEDNTALSR@.A	9.90	4.17	2.37	0.42
Q9WV80_SNX1_MOUSE	Snx1	Sorting nexin-1 OS=Mus	K.YWEAFLPEAK#.A	10.39	2.97	3.49	0.29
O70493_SNX12_MOUSE	Snx12	Sorting nexin-12 OS=Mu	K.IVVPPLPGK#.A	30.56	16.74	1.83	0.55
O70493_SNX12_MOUSE	Snx12	Sorting nexin-12 OS=Mu	R.QGLEQFINK#.I	13.90	5.51	2.52	0.40
O70493_SNX12_MOUSE	Snx12	Sorting nexin-12 OS=Mu	R.TNLPIFK#.L	127.57	68.53	1.86	0.54
Q78ZM0_Q78ZM0_MOUSE	Snx3	Sorting nexin 3 OS=Mus	R.FTTYEIR@.V	115.35	49.04	2.35	0.43
Q78ZM0_Q78ZM0_MOUSE	Snx3	Sorting nexin 3 OS=Mus	R.K#QGLEQFINK#.V	53.91	50.36	1.07	0.93
Q78ZM0_Q78ZM0_MOUSE	Snx3	Sorting nexin 3 OS=Mus	R.LITK#PQNLNDAYGPPSNFLEIDVSNPQTVGVGR@.G	11.67	4.88	2.39	0.42
Q78ZM0_Q78ZM0_MOUSE	Snx3	Sorting nexin 3 OS=Mus	R.QLPFR@GDDGIFDDNFIEER@.K	15.47	6.23	2.48	0.40
Q78ZM0_Q78ZM0_MOUSE	Snx3	Sorting nexin 3 OS=Mus	K.VVVPPLPGK#.A	77.02	25.80	2.99	0.34
Q78ZM0_Q78ZM0_MOUSE	Snx3	Sorting nexin 3 OS=Mus	R.YSDFEWLR@.S	79.99	34.23	2.34	0.43
Q91YJ2_SNX4_MOUSE	Snx4	Sorting nexin-4 OS=Mus	K.ETVNETGFQLK#.A	8.04	6.06	1.33	0.75
Q91YJ2_SNX4_MOUSE	Snx4	Sorting nexin-4 OS=Mus	K.LFGQETPEQR@.E	16.53	7.51	2.20	0.45
Q91YJ2_SNX4_MOUSE	Snx4	Sorting nexin-4 OS=Mus	K.LSADNM*DPDFVER@.R	13.87	6.70	2.07	0.48
Q91YJ2_SNX4_MOUSE	Snx4	Sorting nexin-4 OS=Mus	R.VGLENFLLR@.V	44.84	20.83	2.15	0.46
Q91YJ2_SNX4_MOUSE	Snx4	Sorting nexin-4 OS=Mus	R.VGLENFLLR@.V	9.87	2.45	4.03	0.25
Q9D8U8_SNX5_MOUSE	Snx5	Sorting nexin-5 OS=Mus	K.ALIDYENSNK#.A	16.88	8.44	2.00	0.50
Q9D8U8_SNX5_MOUSE	Snx5	Sorting nexin-5 OS=Mus	K.TTLSTFQSPEFSVTR@.Q	20.30	9.53	2.13	0.47
Q6P8X1_SNX6_MOUSE	Snx6	Sorting nexin-6 OS=Mus	K.NLVELAELELK#.H	23.78	10.73	2.22	0.45
Q6P8X1_SNX6_MOUSE	Snx6	Sorting nexin-6 OS=Mus	R.SLVDYENANK#.A	12.39	7.52	1.65	0.61
F8WI30_F8WI30_MOUSE	Snx7	Sorting nexin-7 OS=Mus	R.GEFDSSEFEVR@.R	17.63	7.66	2.30	0.43
F8WI30_F8WI30_MOUSE	Snx7	Sorting nexin-7 OS=Mus	K.GK#LEEAHPTLIIPPLPEK#.F	4.61	2.73	1.69	0.59
F8WI30_F8WI30_MOUSE	Snx7	Sorting nexin-7 OS=Mus	R.IADHPTLTFNEDFK#.V	23.88	10.30	2.32	0.43
F8WI30_F8WI30_MOUSE	Snx7	Sorting nexin-7 OS=Mus	R.LASGSSELAVGESPR.G	14.65	8.02	1.83	0.55
F8WI30_F8WI30_MOUSE	Snx7	Sorting nexin-7 OS=Mus	K.NRPEEFM*EM*NNFIETFSQK.I	5.04	3.68	1.37	0.73
F8WI30_F8WI30_MOUSE	Snx7	Sorting nexin-7 OS=Mus	R.SAFTDTAEQNIR@.Y	27.89	14.60	1.91	0.52
F8WI30_F8WI30_MOUSE	Snx7	Sorting nexin-7 OS=Mus	R.YQDFLWLK#.G	7.73	5.36	1.44	0.69
Q8CFD4_SNX8_MOUSE	Snx8	Sorting nexin-8 OS=Mus	R.AIDNAADLLIFGK#.E	19.12	7.52	2.54	0.39
Q8CFD4_SNX8_MOUSE	Snx8	Sorting nexin-8 OS=Mus	R.IVEQENVIQTM*ELR@.N	6.33	3.38	1.88	0.53
Q8CFD4_SNX8_MOUSE	Snx8	Sorting nexin-8 OS=Mus	R.IVEQENVIQTM*ELR@.N	3.90	1.18	3.31	0.30
Q8CFD4_SNX8_MOUSE	Snx8	Sorting nexin-8 OS=Mus	R.AIDNAADLLIFGK#.E	15.43	8.57	1.80	0.56
E1U8D0_SOGA1_MOUSE	Soga1	Protein SOGA1 OS=Mus	R.GLQEQLSQER@.Q	9.35	2.20	4.25	0.24
E1U8D0_SOGA1_MOUSE	Soga1	Protein SOGA1 OS=Mus	R.LSVLQQELNAFTR@.K	13.10	4.84	2.71	0.37
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.EGNK#EPILVDFK#.T	10.77	9.28	1.16	0.86
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.GM*NLLGGDENLGPEVGM*QETLLHPGEEPR@.D	3.00	1.80	1.66	0.60
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.IEEVLSGVLDTELR@.Y	14.01	5.16	2.72	0.37
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.SPEPVVTM*SVEYQK#.S	5.89	2.41	2.45	0.41

Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.IEEVLSGVLDTELR@.Y	5.36	2.41	2.22	0.45
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SEGQLNGETNPPIEGNQAGDTAASAR@.S	2.90	2.55	1.13	0.88
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.AGIEGPLLASEVER@.D	91.90	35.59	2.58	0.39
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.AQLLEIAK#.A	40.80	16.16	2.52	0.40
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.ASESSSEEK#DDYEIFVK#.V	17.81	3.68	4.84	0.21
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.ESSEDTEVPLPNK#.E	11.97	5.66	2.12	0.47
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.GFEFVTASALISESK#.Y	50.58	15.30	3.31	0.30
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.GM*NLLGGDENLGPEVGM*QETLLHPGEEPR@.D	22.07	9.23	2.39	0.42
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.GMNLLGGDENLGPEVGM*QETLLHPGEEPR@.D	3.26	1.77	1.84	0.54
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.GM*NLLGGDENLGPEVGMQETLLHPGEEPR@.D	2.79	2.25	1.24	0.81
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.ILPISETK#.E	63.98	30.10	2.13	0.47
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.LPEQPVEAPSEIADSSM*TR@PQESLELPK#.T	6.39	3.42	1.87	0.53
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.LTDLDK#AQLLEIAK#.A	40.50	13.20	3.07	0.33
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.SAASPVVISIPER@.A	28.56	15.77	1.81	0.55
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.SDLYENEYDR@.N	15.45	7.35	2.10	0.48
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SLSSQLALELDTVGTSK#.G	23.11	7.68	3.01	0.33
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.TTLVELPIAK#.V	15.45	12.87	1.20	0.83
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.AAELSVVSTSVISEQSEQPM*PGM*LEPSMTK#.I	4.55	2.47	1.84	0.54
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.AGIEGPLLASEVER@.D	46.77	27.06	1.73	0.58
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.ASESSSEEK#DDYEIFVK#.V	9.22	6.50	1.42	0.71
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.EIQQELSSGR@.S	30.62	15.71	1.95	0.51
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.ESSEDTEVPLPNK#.E	9.34	5.86	1.59	0.63
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.ESSEDTEVPLPNK#EIVPESGYSASIDEINEADLVR@PLLPK#.D	9.63	6.17	1.56	0.64
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.FR@EIQQELSSGR@.S	67.42	25.39	2.66	0.38
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.IEEVLSGVLDTELR@.Y	60.12	28.78	2.09	0.48
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.ILDSFTAAPVPM*STAALK#.S	12.21	5.17	2.36	0.42
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.ILDSFTAAPVPMSTAALK#.S	7.25	4.29	1.69	0.59
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.LAQDPYR@.L	229.74	108.33	2.12	0.47
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.LGQDPYR@.L	77.65	48.16	1.61	0.62
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.LTDLDK#AQLLEIAK#.A	23.82	10.18	2.34	0.43
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.SAASPVVISIPER@.A	17.25	38.77	0.44	2.25
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.SDLYENEYDR@.N	6.25	4.36	1.43	0.70
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SEGQLNGETNPPIEGNQAGDTAASAR@.S	21.45	9.50	2.26	0.44
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.SLETM*PPETSK#.T	34.76	21.84	1.59	0.63
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SLPNEEIVQK#.I	25.88	15.73	1.65	0.61
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SLSSQLALELDTVGTSK#.G	15.30	10.62	1.44	0.69
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SM*M*SAYER@.S	83.09	37.83	2.20	0.46
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SM*M*SPM*AER.S	59.81	30.45	1.96	0.51
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SM*MSPM*AER@.S	7.10	3.33	2.13	0.47
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SM*M*SSYER@.S	14.38	6.46	2.23	0.45
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SM*M*SSYSAADR@.S	48.93	19.41	2.52	0.40
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	R.SM*M*SSYTDR.S	21.53	7.79	2.76	0.36
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.SPEPVVTM*SVEYQK#.S	50.33	25.22	2.00	0.50
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.SPEPVVTMSVEYQK#.S	9.94	6.98	1.42	0.70
Q9QX47_SON_MOUSE	Son	Protein SON OS=Mus mu	K.TTLVELPIAK#.V	175.10	87.37	2.00	0.50
O89090_SP1_MOUSE	Sp1	Transcription factor Sp1	R.VGGLQGSDSLNIQQNQTSGGSLQGSQQK#.E	12.50	6.72	1.86	0.54
Q58A65_JIP4_MOUSE	Spag9	C-Jun-amino-terminal ki	K.ER@PISLGIFPLPAGDGLLTPDTQK#.G	5.59	2.12	2.63	0.38
Q9QYY8_SPAST_MOUSE	Spast	Spastin OS=Mus musculu	K.FDDIAGQELAK#.Q	12.53	4.30	2.91	0.34
Q9QYY8_SPAST_MOUSE	Spast	Spastin OS=Mus musculu	R.M*TDGYSGSDLTALAK#.D	7.48	2.64	2.83	0.35
Q3UMC0_SPAT5_MOUSE	Spata5	Spermatogenesis-associa	K.AGEVLLDVTQSPR@.D	13.52	12.07	1.12	0.89
Q3UMC0_SPAT5_MOUSE	Spata5	Spermatogenesis-associa	R.EVAIDVPNVSWSDIGGLENIK#.L	2.75	2.15	1.28	0.78
Q3UMC0_SPAT5_MOUSE	Spata5	Spermatogenesis-associa	R.IIYVPLPDAATR@.R	16.94	9.93	1.71	0.59
Q3UMC0_SPAT5_MOUSE	Spata5	Spermatogenesis-associa	K.VGLSEM*AQK#.N	8.07	7.57	1.07	0.94
Q3UMC0_SPAT5_MOUSE	Spata5	Spermatogenesis-associa	R.VLAQLLTEM*DGIEQLK#.N	8.68	3.46	2.51	0.40
Q3UMC0_SPAT5_MOUSE	Spata5	Spermatogenesis-associa	R.VLVLGATNR@PQALDAALR@.R	21.77	8.64	2.52	0.40
Q8K1N4_SPAS2_MOUSE	Spats2	Spermatogenesis-associa	R.ELEDPEFAAAETLDR@.T	23.05	3.13	7.37	0.14
Q8K1N4_SPAS2_MOUSE	Spats2	Spermatogenesis-associa	R.M*SEEQLVELR@.A	21.86	7.45	2.94	0.34
Q8K1N4_SPAS2_MOUSE	Spats2	Spermatogenesis-associa	K.SAPIQEEQPASSEK#.G	22.37	9.91	2.26	0.44
Q8K1N4_SPAS2_MOUSE	Spats2	Spermatogenesis-associa	K.SK#PK#PASEASGSAPDSSK#.S	13.51	5.16	2.62	0.38
Q8K1N4_SPAS2_MOUSE	Spats2	Spermatogenesis-associa	R.ELEDPEFAAAETLDR@.T	17.95	5.07	3.54	0.28
Q8K1N4_SPAS2_MOUSE	Spats2	Spermatogenesis-associa	R.M*SEEQLVELR@.A	15.11	2.25	6.71	0.15
Q8K1N4_SPAS2_MOUSE	Spats2	Spermatogenesis-associa	K.SAPIQEEQPASSEK#.G	17.66	3.83	4.61	0.22
Q9D083_SPC24_MOUSE	Spc24	Kinetochore protein Spc	R.QLITELQELR@.E	8.66	3.53	2.45	0.41
Q9CYN2_SPCS2_MOUSE	Spcs2	Signal peptidase comple	K.FFDHSGTLVM*DAYEPEISR@.L	7.66	5.45	1.41	0.71
Q6ZWQ7_Q6ZWQ7_MOUSE	Spcs3	Signal peptidase comple	K.NNALNQVVLWDK#.I	5.86	8.13	0.72	1.39
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	R.AEQLSQENEK#.L	8.75	4.49	1.95	0.51
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.AIEASSTVGQTAENFEVQEM*LK#.V	13.44	11.48	1.17	0.85
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.ALLEADK#QK#.A	7.65	9.53	0.80	1.25
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.ELADLEEENR@.A	22.73	10.16	2.24	0.45
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	R.ELSVTISR@.E	13.47	7.29	1.85	0.54
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.HVSSLLAK#.M	26.04	14.17	1.84	0.54
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.LHNNQLISELEGSVIK#.L	20.15	8.03	2.51	0.40
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.LINLLQER@.V	39.28	18.32	2.14	0.47
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.M*EENQHSTAEELQATLQELSDQQQM*VQELTAENEK#.L	2.67	1.34	1.99	0.50
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	R.R@DPLAALAR@.E	15.27	7.74	1.97	0.51
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	R.SPLSGIPVR@.T	22.41	12.03	1.86	0.54
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	R.TAPAAAVSPM*QR@.H	7.15	2.69	2.66	0.38
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	R.TSPAPSDSATTVK#.S	26.72	15.07	1.77	0.56
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.TSTSGAISELTESR@.L	5.52	3.93	1.40	0.71
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.ELADLEEENR@.A	10.43	4.64	2.25	0.44
Q5SXY1_CYTSB_MOUSE	Specc1	Cytospin-B OS=Mus musc	K.LINLLQER@.V	18.45	7.23	2.55	0.39
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.LNALGFSLEQR@.L	8.08	6.30	1.28	0.78
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.AALAATLEEYK#.A	79.99	43.95	1.82	0.55
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.AALAATLEEYK#ATVASDQIEM*NR@.L	16.82	8.61	1.95	0.51
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.AALAATLEEYK#ATVASDQIEMNR@.L	12.45	6.96	1.79	0.56
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.AETLASSLQEDLAHTR.N	9.97	2.58	3.87	0.26
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.ATVASDQIEM*NR@.L	43.72	28.39	1.54	0.65
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.ATVASDQIEMNR@.L	19.13	11.15	1.72	0.58
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.DISASEGASPASLM*AM*GTTSPQLSLSSSPTASVTPSTR@.S	10.43	3.55	2.94	0.34
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.ETIIAHQPTDVESTLLQLQEQNTAIR@.E	11.63	9.08	1.28	0.78
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.FEREQLLGVQQHLSNTLK.M	28.42	17.40	1.63	0.61
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.HSISGPISTSK#PLTALSDK#R@.S	109.58	64.34	1.70	0.59
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.K#LPSVSQGANDVALAK#.R	27.32	9.17	2.98	0.34
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.LHDNLIISDLENTVK#.K	81.93	53.82	1.52	0.66
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.LK#AQLENEK#.Q	10.20	5.80	1.76	0.57
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.LNALGFSLEQR.L	64.78	38.59	1.68	0.60
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.M*AEQDNKEAQEM*IGALK.E	40.58	20.78	1.95	0.51
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.SEAQEEIGDLK#R@.R	7.33	2.39	3.07	0.33
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.SELEEK#DTER@.S	4.72	3.92	1.20	0.83
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.SFDSASQVPNAAAAAIPR@.T	49.03	28.36	1.73	0.58
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.SLLDEHHISYVIDEDVK#.S	62.77	42.29	1.48	0.67
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.SSTSSEPTPTVK#.T	69.31	40.74	1.70	0.59
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.STLDINEM*AR@.T	70.27	70.48	1.00	1.00

Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.TAAEGDIR@.M	39.78	17.94	2.22	0.45
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.TER@PDWQNVM*LYVTAIYK#.Y	10.81	5.57	1.94	0.51
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.TER@PDWQNVMLYVTAIYK#.Y	9.01	7.91	1.14	0.88
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.TK#DVEILHLR@.N	71.30	24.24	2.94	0.34
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.TPPAAAVSPM*QR@.H	32.42	22.71	1.43	0.70
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.TPPAAAVSPMQR@.H	8.23	6.08	1.35	0.74
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.VAELYSIHNSGDK#SDIQDLLESVR@.L	37.16	18.51	2.01	0.50
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.VAELYSIHNSGDKSDIQDLLESVR.L	113.63	52.34	2.17	0.46
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.VK#DLLTLAK#.T	22.41	11.83	1.89	0.53
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.VYNYM*NAVER@.D	35.20	18.60	1.89	0.53
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.YM*DLAENAR@.F	68.47	43.00	1.59	0.63
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.YMDLAENAR@.F	10.64	7.12	1.49	0.67
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.YM*ELEQR@.Y	69.91	39.14	1.79	0.56
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.AALAATLEEYK#.A	39.05	32.89	1.19	0.84
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.ATVASDQIEMNR@.L	6.76	2.05	3.30	0.30
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.ATVASDQIEM*NR@.L	11.75	4.32	2.72	0.37
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.ETIIAHQPTDVESTLLQLQEQNTAIR@.E	17.06	6.07	2.81	0.36
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.ETIIAHQPTDVESTLLQLQEQNTAIR@EELNQLK#.N	21.89	6.71	3.26	0.31
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.HSISGPISTSK#PLTALSDK#.R	7.59	3.63	2.09	0.48
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.HSISGPISTSK#PLTALSDK#R@.S	52.14	18.84	2.77	0.36
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.IIESEQK#.G	17.93	7.17	2.50	0.40
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.LHDNLIISDLENTVK#.K	63.00	29.45	2.14	0.47
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.M*AEQDNKEAQEM*IGALK.E	23.39	8.31	2.82	0.36
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.QIEDLNM*TLEK#.L	11.06	3.08	3.58	0.28
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.SDM*K#ETIFELEDEVEQHR@.A	13.04	4.96	2.63	0.38
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.SEAQEEIGDLK#.R	12.47	5.15	2.42	0.41
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.SFDSASQVPNAAAAAIPR@.T	23.48	10.22	2.30	0.44
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.SLLDEHHISYVIDEDVK#.S	42.79	20.36	2.10	0.48
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.SSTSSEPTPTVK#.T	31.05	15.56	2.00	0.50
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.TK#DVEILHLR@.N	29.14	7.50	3.88	0.26
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.TPPAAAVSPM*QR@.H	16.54	9.07	1.82	0.55
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.VAELYSIHNSGDKSDIQDLLESVR.L	60.46	23.97	2.52	0.40
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	K.VK#DLLTLAK#.T	14.28	5.08	2.81	0.36
Q2KN98_CYTSA_MOUSE	Specc1l	Cytospin-A OS=Mus musc	R.VYNYM*NAVER@.D	13.80	10.59	1.30	0.77
Q62504_MINT_MOUSE	Spen	Msx2-interacting proteir	R.GLDETVSIASR@.S	5.58	24.21	0.23	4.34
Q62504_MINT_MOUSE	Spen	Msx2-interacting proteir	K.ITSVISR@.M	44.97	11.95	3.76	0.27
Q62504_MINT_MOUSE	Spen	Msx2-interacting proteir	R.YGLVFFR@.Q	12.23	3.72	3.29	0.30
Q9JIA7_SPHK2_MOUSE	Sphk2	Sphingosine kinase 2 OS=	R.GVPLSGDQEITPELLPR@.K	6.00	1.99	3.02	0.33
Q9JIA7_SPHK2_MOUSE	Sphk2	Sphingosine kinase 2 OS=	R.LLILVNPFGGR@.G	7.42	1.52	4.87	0.21
Q61142_SPIN1_MOUSE	Spin1	Spindlin-1 OS=Mus musc	K.GTVLDQVPVNPSLYLIK#.Y	12.73	14.71	0.87	1.16
Q61142_SPIN1_MOUSE	Spin1	Spindlin-1 OS=Mus musc	R.VSALEVLPDR.V	78.23	50.03	1.56	0.64
Q61142_SPIN1_MOUSE	Spin1	Spindlin-1 OS=Mus musc	K.GTVLDQVPVNPSLYLIK.Y	4.94	8.52	0.58	1.73
Q9WTK8_SPO11_MOUSE	Spo11	Meiotic recombination p	R.GAGETPAGATR.V	1.68	26.25	0.06	15.59
Q3TFQ1_SPRY7_MOUSE	Spryd7	SPRY domain-containing	K.IQSTGIWGIGVATQK#.V	6.86	1.57	4.36	0.23
Q3TFQ1_SPRY7_MOUSE	Spryd7	SPRY domain-containing	K.VNLNQIPLGR@.D	5.41	3.78	1.43	0.70
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.EAFLNTEDK#GDSLDSVEALIK#.K	10.81	2.28	4.74	0.21
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.IAALQAFADQLIAVDHYAK#.G	17.35	12.37	1.40	0.71
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LAALADQWQFLVQK#.S	6.85	11.23	0.61	1.64
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LEESLEYQQFVANVEEEEAWINEK#.M	6.34	2.34	2.71	0.37
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.SSLSSAQADFNQLAELDR@.Q	6.85	27.21	0.25	3.97
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.ADVVESWIGEK#.E	38.31	17.93	2.14	0.47
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.AINVQEEK#.I	106.21	71.73	1.48	0.68
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.AK#LDENSAFLQFNWK#.A	10.60	6.37	1.66	0.60
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.ALINADELANDVAGAEALLDR@.H	239.32	100.62	2.38	0.42
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.ALINADELANDVAGAEALLDR.H	116.74	42.92	2.72	0.37
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.ASAFNSWFENAEEDLTDPVR@.C	8.02	5.23	1.53	0.65
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DADETK#EWIEEK#.N	30.52	8.96	3.41	0.29
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DAEELEK#WIQEK#.L	20.25	8.65	2.34	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DGHVSLQEYM*AFM*ISR@.E	10.31	3.98	2.59	0.39
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DLAALEDK#.V	25.28	8.20	3.08	0.32
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DLAALEDK#VK#.A	81.46	33.50	2.43	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DLAALGDK#.V	35.88	15.65	2.29	0.44
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DLAALGDK#VNSLGETAQR@.L	128.33	45.92	2.79	0.36
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.DLASVNNLLK.K	10.89	10.12	1.08	0.93
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DLASVQALLR@.K	135.12	53.47	2.53	0.40
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.DLIGVQNLLK#.K	38.10	16.36	2.33	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.DLNSQADSLM*TSSAFDTSQVK#.E	31.37	15.84	1.98	0.51
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DLSSVQTLLTK#.Q	168.72	81.14	2.08	0.48
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DLTGVQNLR@.K	100.51	40.94	2.45	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.DLTNVQNLQK#.K	30.24	16.35	1.85	0.54
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DLTSWVTEM*K#.A	47.93	20.56	2.33	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DLTSWVTEMK#.A	15.57	4.87	3.20	0.31
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DM*DDEESWIK#.E	17.00	10.30	1.65	0.61
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DTEQVDNWM*SK#.Q	23.22	8.94	2.60	0.38
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DVDEIEAWISEK#.L	96.62	46.28	2.09	0.48
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DVDETIGWIK#.E	52.74	32.65	1.62	0.62
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.DVEDEETWIR@.E	77.76	31.73	2.45	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.DVTGAEALLER@.H	76.59	33.73	2.27	0.44
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.EAALTNEEVGADLEQVEVLQK#.K	119.44	53.95	2.21	0.45
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.EAFLNTEDK#GDSLDSVEALIK#.K	238.90	94.12	2.54	0.39
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.EANELQQWITEK#.E	94.16	43.12	2.18	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.EANQQQQFNR@.N	53.74	23.38	2.30	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.EELITNWEQIR@.T	17.72	6.03	2.94	0.34
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.EELYQNLTR@.E	50.34	21.49	2.34	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.EKEPIVGSTDYGKDEDSAEALLK.K	18.24	14.19	1.29	0.78
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.EK#EQLM*ASDDFGR@.D	8.07	4.34	1.86	0.54
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.EK#LDILDQER@.T	13.61	7.63	1.78	0.56
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.ELPTAFDYVEFTR@.S	117.70	104.53	1.13	0.89
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.ENLLEEQGSIALR@.Q	98.32	46.98	2.09	0.48
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.EQLM*ASDDFGR@.D	24.53	9.82	2.50	0.40
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.EQLM*ASDDFGR@DLASVQALLR@.K	17.48	5.58	3.13	0.32
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.FNR@DVDETIGWIK#.E	41.12	20.37	2.02	0.50
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.GEIDAHEDSFK#.S	8.92	3.90	2.29	0.44
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.GK#DLIGVQNLLK#.K	94.04	28.80	3.26	0.31
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.GK#DLIGVQNLLK#K#.H	11.10	6.06	1.83	0.55
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.GLVSSDELAK#.D	55.34	23.53	2.35	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.GLVSSDELAKDVTGAEALLER.H	196.09	81.50	2.41	0.42
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.GLVSSDELAK#DVTGAEALLER@.H	10.07	4.12	2.44	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.GNAM*VEEGHFAAEDVK#.A	9.37	3.93	2.38	0.42
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.GR@ELPTAFDYVEFTR@.S	44.67	13.61	3.28	0.30
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.GVIDM*GNSLIER@.G	69.00	30.29	2.28	0.44
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.HALLEADVAAHQDR@.I	66.51	26.70	2.49	0.40
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.HQAFEAELHANADR@.I	135.69	64.60	2.10	0.48

P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.HQAFEAELSANQSR@.I	18.45	5.29	3.49	0.29
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.HQALQAEIAGHEPR@.I	67.57	31.14	2.17	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.HQLLEADISAHEDR@.L	37.50	19.32	1.94	0.52
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.IAALQAFADQLIAVDHYAK#.G	377.96	170.11	2.22	0.45
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.IDGITIQAR@.Q	61.93	30.84	2.01	0.50
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.IEDLGAAM*EEALILDNK#.Y	11.62	7.00	1.66	0.60
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.IEDLGAAMEEALILDNK#.Y	6.47	4.93	1.31	0.76
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.ITALDEFATK#.L	159.01	64.92	2.45	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#ASAFNSWFENAEEDLTDPVR@.C	11.25	3.80	2.96	0.34
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#FEEFQTDLAAHEER@.V	69.42	29.96	2.32	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#GDILTLLNSTNK#.D	23.01	8.34	2.76	0.36
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#GDILTLLNSTNK#DWWK#.V	29.94	17.81	1.68	0.59
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#HEAFETDFTVHK#.D	32.38	17.67	1.83	0.55
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#HEALM*SDLSAYGSSIQALR@.E	13.85	3.79	3.65	0.27
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#HQALQAEIAGHEPR@.I	16.54	6.37	2.60	0.39
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#IEDLGAAM*EEALILDNK#.Y	64.53	23.02	2.80	0.36
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#IEDLGAAMEEALILDNK#.Y	21.50	12.30	1.75	0.57
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.K#LDPAQSASR@.E	85.63	45.88	1.87	0.54
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.KLSDDNTIGQEEIQQR.L	26.52	11.45	2.32	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.K#VEDLFLTFAK#.K	83.11	45.51	1.83	0.55
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.KVEDLFLTFAK.K	73.65	29.78	2.47	0.40
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LAALADQWQFLVQK#.S	127.78	54.72	2.33	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LAQFVEHWK#.E	119.70	55.42	2.16	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LDENSAFLQFNWK#.A	35.05	15.75	2.22	0.45
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LDILDQER@.T	19.36	8.26	2.34	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LEAELAAHEPAIQGVLDTGK#.K	21.07	11.35	1.86	0.54
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LEAELAAHEPAIQGVLDTGK#K#.L	12.76	4.50	2.83	0.35
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LEESLEYQQFVANVEEEEAWINEK#.M	40.75	16.64	2.45	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LFGAAEVQR@.F	150.55	62.32	2.42	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LGDSHDLQR.F	45.16	19.40	2.33	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LGESQTLQQFSR.D	116.97	53.70	2.18	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LK#DLNSQADSLM*TSSAFDTSQVK#.E	58.66	24.26	2.42	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LK#DLNSQADSLMTSSAFDTSQVK#.E	7.65	4.20	1.82	0.55
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LLVSSEDYGR@.D	60.63	28.11	2.16	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LLVSSEDYGR@DLTGVQNLR@.K	14.46	11.52	1.26	0.80
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LM*VHTVATFNSIK#.E	48.07	15.74	3.05	0.33
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.LQQSHPLSASQIQVK#.R	102.53	43.45	2.36	0.42
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LSDDNTIGQEEIQQR@.L	98.36	45.69	2.15	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LSELNQK#.W	42.50	23.72	1.79	0.56
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.LSILSEER@.T	117.63	48.32	2.43	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.M*K#QVEELYQSLLELGEK#.R	93.67	4.95	18.91	0.05
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.M*NEVISLWK#.K	50.79	26.76	1.90	0.53
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.MNEVISLWK#.K	13.07	4.62	2.83	0.35
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.M*QHNLEQQIQAR@.N	67.55	24.30	2.78	0.36
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.M*QHNLEQQIQAR@.N	13.89	5.92	2.35	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.M*TLVASEDYGDTLAAIQGLLK#.K	106.20	48.38	2.20	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.NTTGVTEEALK#.E	47.41	21.62	2.19	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.QDEVNAAWQR.L	20.90	10.62	1.97	0.51
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.QEFAQHANAFHQWIQETR@.T	10.42	5.25	1.99	0.50
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.QFQDAGHFDAENIK#K#.K	88.16	40.83	2.16	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.QQNFNTGIK#.D	21.58	15.57	1.39	0.72
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.QQVAPM*DDETGK#ELVLALYDYQEK#.S	47.72	19.11	2.50	0.40
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.QVEELYQSLLELGEK#.R	4.92	2.94	1.67	0.60
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.R@AQLADSFHLQQFFR@.D	29.55	9.59	3.08	0.32
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.R@EELITNWEQIR@.T	86.97	36.28	2.40	0.42
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.R@LEAELAAHEPAIQGVLDTGK#.K	10.08	4.19	2.41	0.42
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.R@LEAELAAHEPAIQGVLDTGK#K#.L	47.45	20.29	2.34	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.R@QDLEDSLQAQQYFADANEAESWM*R@.E	27.51	13.18	2.09	0.48
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.R@QDLEDSLQAQQYFADANEAESWMR@.E	6.61	2.40	2.75	0.36
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.SADESGQALLAASHYASDEVR@.E	179.69	74.36	2.42	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.SADESGQALLAASHYASDEVR@.E	4.41	1.54	2.86	0.35
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.SK#LGESQTLQQFSR@.D	23.83	9.02	2.64	0.38
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.SLQQLAEER@.S	151.25	60.10	2.52	0.40
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.SQLLGSAHEVQR.F	43.70	16.46	2.66	0.38
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.SSEEIESAFR@.A	105.50	47.48	2.22	0.45
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.SSLSSAQADFNQLAELDR@.Q	117.75	53.81	2.19	0.46
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.TALLELWELR@.R	67.86	31.77	2.14	0.47
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.TATDEAYK#DPSNLQGK#.V	124.51	66.05	1.89	0.53
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.TK#QDEVNAAWQR@.L	37.75	15.39	2.45	0.41
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.VAEDLESEGLM*AEEVQAVQQQEVYGAM*PR@.D	40.52	17.38	2.33	0.43
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.VAEDLESEGLMAEEVQAVQQQEVYGAM*PR@.D	6.85	4.11	1.67	0.60
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.VASNPYTWFTM*EALEETWR@.N	21.03	9.89	2.13	0.47
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.VLETAEDIQER@.R	197.56	87.63	2.25	0.44
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.VNEVSQFAAK#.L	140.63	69.94	2.01	0.50
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	R.WTQLLANSATR@.K	38.30	21.35	1.79	0.56
P16546_SPTN1_MOUSE	Sptan1	Spectrin alpha chain, nor	K.YTEHSTVGLAQQWDQLDQLGM*R@.M	47.40	21.44	2.21	0.45
E9Q447_E9Q447_MOUSE	Sptan1	Spectrin alpha chain, nor	R.QGQIDNQYQSLLELGEK#.R	31.65	13.62	2.32	0.43
E9Q447_E9Q447_MOUSE	Sptan1	Spectrin alpha chain, nor	R.QGQIDNQYQSLLELGEKR.K	31.66	9.07	3.49	0.29
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.AFEDEM*SGR.S	53.48	26.87	1.99	0.50
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.AK#DEQSAVSM*LK#.K	22.18	11.22	1.98	0.51
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.AQTLPTSVVTITSESSPGK#.R	30.78	11.72	2.63	0.38
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.DASVAEAWLLGQEPYLSSR.E	34.09	14.63	2.33	0.43
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.DASVAEAWLLGQEPYLSSR@.E	85.40	44.47	1.92	0.52
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.DLDDFQSWLSR@.T	81.70	39.17	2.09	0.48
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.DLM*LWM*EDVIR@.Q	26.46	9.67	2.74	0.37
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.DLVAIEAK#.L	115.92	59.17	1.96	0.51
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.DQNTVETLQR@.M	77.02	33.27	2.31	0.43
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.DTGNIGQER@.V	49.49	22.97	2.15	0.46
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.DVEDEILWVGER@.M	66.54	32.65	2.04	0.49
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.DVSSVELLM*NNHQGIK#.A	17.95	7.35	2.44	0.41
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.EAASELLM*R@.L	48.60	19.13	2.54	0.39
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.EAEK#LESEHPDQAQAILSR@.L	58.62	24.25	2.42	0.41
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.EASLGEASK#.L	49.53	31.03	1.60	0.63
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.EIEELQSQAQALSQEGK#.S	45.37	21.80	2.08	0.48
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.EIGQSVDEVEK#.L	102.70	40.47	2.54	0.39
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.EIQGHQPR@.I	17.79	7.57	2.35	0.43
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.ENEVLEAWK#.S	76.63	32.10	2.39	0.42
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.EQWANLEQLSAIR@.K	74.88	31.36	2.39	0.42
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.ETWLSENQR@.L	35.98	16.06	2.24	0.45
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.EVDDLEQWIAER@.E	88.95	35.72	2.49	0.40
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.EVVAGSHELGQDYEHVTM*LQER@.F	31.44	13.45	2.34	0.43
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.FANSLVGVQQQLQAFNTYR.T	14.28	6.50	2.20	0.46
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.FESLEPEM*NNQASR@.V	65.55	30.69	2.14	0.47

Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.FESLEPEMNNQASR@.V	5.17	3.31	1.56	0.64
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.GDQVSQNGLPAEQGSPR@.M	4.62	2.65	1.74	0.57
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.GNLEVLLFTIQSK#.M	95.91	39.90	2.40	0.42
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.HKDVAEEITNYRPTIDTLHEQASALPQAHAESPDVK.G	26.44	7.22	3.66	0.27
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.HLLGVEDLLQK#.H	92.24	38.69	2.38	0.42
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.HQAFM*AELASNK#.E	7.00	2.66	2.63	0.38
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.HQILEQAVEDYAETVHQLSK#.T	136.25	62.36	2.18	0.46
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.HR@PDLIDFDK#.L	97.57	47.25	2.06	0.48
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.IDDIFER@.S	110.47	49.95	2.21	0.45
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.ILSSDDYGK#.D	31.79	12.23	2.60	0.38
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.INAVVETGR@.R	54.57	20.49	2.66	0.38
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.ITDLYTDLR@.D	82.33	39.45	2.09	0.48
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.IVSSNDVGHDEYSTQSLVK#.K	159.89	73.07	2.19	0.46
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.K#HEAIETDIAAYEER@.V	66.85	28.70	2.33	0.43
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.K#HYASEEIK#EK#.L	23.66	12.88	1.84	0.54
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.K#K#EIEELQSQAQALSQEGK#.S	25.99	14.29	1.82	0.55
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.K#QALQDTLALYK#.M	6.84	2.30	2.98	0.34
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.LAEISDVWEEM*K#.T	46.59	26.42	1.76	0.57
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.LAEISDVWEEMK#.T	20.89	9.92	2.11	0.47
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.LAGIEER@.C	82.73	38.36	2.16	0.46
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.LEM*NLGLQK#.I	38.56	19.56	1.97	0.51
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.LLDPEDISVDHPDEK.S	10.15	5.95	1.70	0.59
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.LLEVLSGER.L	132.92	53.28	2.49	0.40
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.LLTQHENIK#NEIDNYEEDYQK#.M	99.50	50.29	1.98	0.51
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.LLTQHENIKNEIDNYEEDYQK.M	27.30	10.15	2.69	0.37
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.LQAAYAGDK#.A	61.76	20.89	2.96	0.34
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.LSDGNEYLFQAK#.D	31.21	12.21	2.56	0.39
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.LTTLELLEVR@.R	146.58	65.64	2.23	0.45
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.LVSDGNINSDR.I	121.07	55.62	2.18	0.46
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.LVSQDNFGFDLPAVEAATK#.K	107.60	54.01	1.99	0.50
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.M*LTAQDM*SYDEAR@.N	26.69	11.47	2.33	0.43
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.M*WEVLESTTQTK#.A	15.30	10.04	1.52	0.66
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.NEIDNYEEDYQK#.M	13.55	6.00	2.26	0.44
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.QAEAFLNNQEYVLAHTEM*PTTLEGAEAAIK#.K	47.24	20.92	2.26	0.44
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.QAEAFLNNQEYVLAHTEMPTTLEGAEAAIK#.K	13.84	6.40	2.16	0.46
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.QALQDTLALYK#.M	73.77	31.14	2.37	0.42
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.QLQEDAAR@.L	49.40	19.26	2.56	0.39
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.QQM*LENQM*EVR@.K	18.34	9.32	1.97	0.51
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.SAATWDER@.F	35.40	14.95	2.37	0.42
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.SALPAQSAATLPAR@.T	103.49	41.57	2.49	0.40
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.SNAHYNLQNAFNLAEQHLGLTK#.L	13.68	4.44	3.08	0.32
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.SQNIITDSSSLNAEAIR@.Q	117.95	49.83	2.37	0.42
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.SQNIITDSSSLNAEAIR@.Q	48.65	19.60	2.48	0.40
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.TK#VIESTQDLGNDLAGVM*ALQR@.K	22.69	12.20	1.86	0.54
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.TLETPAAQM*EGFLNR@.K	29.60	11.39	2.60	0.38
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.TLETPAAQMEGFLNR.K	19.24	7.69	2.50	0.40
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.TQILAASYELHK#.F	24.48	11.42	2.14	0.47
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.TQTAIASEDM*PNTLTEAEK#.L	19.39	15.07	1.29	0.78
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.TQTAIASEDMPNTLTEAEK#.L	12.84	8.07	1.59	0.63
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.VAVVNQIAR@.Q	206.96	80.14	2.58	0.39
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.VDTVNNM*ADELINSGHSDAATIAEWK#.D	43.36	16.26	2.67	0.37
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.VIESTQDLGNDLAGVM*ALQR@.K	87.31	47.67	1.83	0.55
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.VIESTQDLGNDLAGVM*ALQR.K	30.43	13.93	2.18	0.46
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.VIESTQDLGNDLAGVMALQR@.K	15.76	7.49	2.10	0.48
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.VIESTQDLGNDLAGVMALQR.K	7.08	3.45	2.05	0.49
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.VLDNAIETEK#.M	80.49	46.75	1.72	0.58
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	K.VLLLSQDYGK#.H	111.98	52.26	2.14	0.47
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.VQAVVAVAR@.E	205.75	95.75	2.15	0.47
Q62261_SPTB2_MOUSE	Sptbn1	Spectrin beta chain, non	R.WDVDDWDNENSSAR@.L	9.54	6.37	1.50	0.67
Q9R112_SQRD_MOUSE	Sqrdl	Sulfide:quinone oxidore	K.EGNALFTFPNTPVK#.C	6.19	1.09	5.70	0.18
Q9R112_SQRD_MOUSE	Sqrdl	Sulfide:quinone oxidore	R.VGAENVAIVEPSER@.H	8.82	3.41	2.59	0.39
Q9R112_SQRD_MOUSE	Sqrdl	Sulfide:quinone oxidore	K.YADALQEIIR@.E	14.44	2.99	4.82	0.21
Q9R112_SQRD_MOUSE	Sqrdl	Sulfide:quinone oxidore	K.YADALQEIIR@.E	9.26	8.62	1.07	0.93
Q64337_SQSTM_MOUSE	Sqstm1	Sequestosome-1 OS=Mus	R.LTPTTPESSSTGTEDK#.S	10.62	3.31	3.21	0.31
Q64337_SQSTM_MOUSE	Sqstm1	Sequestosome-1 OS=Mus	K.NYDIGAALDTIQYSK#.H	10.82	5.93	1.82	0.55
Q64337_SQSTM_MOUSE	Sqstm1	Sequestosome-1 OS=Mus	K.NYDIGAALDTIQYSK#.H	13.23	4.17	3.18	0.31
Q497V5_SRBD1_MOUSE	Srbd1	S1 RNA-binding domain-	K.VLNVDIPR@.S	18.45	7.43	2.48	0.40
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	R.AEQEIAALVEQLTPIER@.Y	10.43	7.57	1.38	0.73
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	K.DLLPVAVDILPESEK#.T	4.12	3.00	1.37	0.73
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	R.SPGPSHPIFWTYTEAAR@.R	8.56	3.76	2.28	0.44
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	R.AEQEIAALVEQLTPIER@.Y	17.77	5.86	3.03	0.33
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	K.DLLPVAVDILPESEK#.T	16.70	7.02	2.38	0.42
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	R.FDLIGLEGR@.V	8.65	4.89	1.77	0.56
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	R.SPFYLDSLEEK#.R	12.39	8.92	1.39	0.72
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	R.SPGPSHPIFWTYTEAAR@.R	7.56	5.40	1.40	0.71
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	K.TPIPLLLR@.G	14.41	6.50	2.22	0.45
A0A087WQ44_A0A087WQ44_MOUSE	Srcap	Protein Srcap OS=Mus m	R.VLIFTQM*TR@.M	10.86	16.66	0.65	1.53
Q8BZX4_SREK1_MOUSE	Srek1	Splicing regulatory gluta	R.FAFVEFADQNSVPR@.A	20.57	8.83	2.33	0.43
Q8BZX4_SREK1_MOUSE	Srek1	Splicing regulatory gluta	R.TVYVGNLNSQTTTADQLLEFFK#.Q	23.90	8.69	2.75	0.36
Q8BZX4_SREK1_MOUSE	Srek1	Splicing regulatory gluta	R.EAQSFISAAIEPESGK#.S	10.87	3.35	3.24	0.31
Q8BZX4_SREK1_MOUSE	Srek1	Splicing regulatory gluta	R.FAFVEFADQNSVPR@.A	23.78	7.16	3.32	0.30
Q8BZX4_SREK1_MOUSE	Srek1	Splicing regulatory gluta	R.M*AGDETQPTR@.F	7.38	1.93	3.82	0.26
Q8BZX4_SREK1_MOUSE	Srek1	Splicing regulatory gluta	R.TVYVGNLNSQTTTADQLLEFFK#.Q	26.45	7.39	3.58	0.28
Q4V9W2_SR1IP_MOUSE	Srek1ip1	Protein SREK1IP1 OS=Mu	K.R@DIVLDVSSTSSEDSDEENEELNK#LQALQEK#.R	15.53	2.81	5.53	0.18
Q4V9W2_SR1IP_MOUSE	Srek1ip1	Protein SREK1IP1 OS=Mu	R.SYSSATEEDSAK#.Q	5.63	2.24	2.52	0.40
Q91Z67_SRGP2_MOUSE	Srgap2	SLIT-ROBO Rho GTPase-a	R.ANQQETEQFYFTK#.M	8.87	3.73	2.38	0.42
Q91Z67_SRGP2_MOUSE	Srgap2	SLIT-ROBO Rho GTPase-a	R.FVQVSEDSGR@.L	10.64	7.01	1.52	0.66
Q91Z67_SRGP2_MOUSE	Srgap2	SLIT-ROBO Rho GTPase-a	R.NEYLLALEATNASVFK#.Y	8.90	3.78	2.35	0.43
Q91Z67_SRGP2_MOUSE	Srgap2	SLIT-ROBO Rho GTPase-a	K.VLNELYSVM*K#.T	8.39	13.50	0.62	1.61
Q91Z67_SRGP2_MOUSE	Srgap2	SLIT-ROBO Rho GTPase-a	R.FVQVSEDSGR@.L	6.64	8.87	0.75	1.34
P16254_SRP14_MOUSE	Srp14	Signal recognition partic	K.FQM*AYSNLLR@.A	12.55	3.28	3.83	0.26
P16254_SRP14_MOUSE	Srp14	Signal recognition partic	K.FQMAYSNLLR@.A	4.05	4.14	0.98	1.02
P16254_SRP14_MOUSE	Srp14	Signal recognition partic	R.K#ISTVVSSK#.E	46.58	14.82	3.14	0.32
P16254_SRP14_MOUSE	Srp14	Signal recognition partic	R.K#SSVEGLEPAENK#.C	8.66	3.48	2.49	0.40
G5E8T3_G5E8T3_MOUSE	Srp19	Signal recognition partic	K.SGGADPSLQQGEGSK#.K	29.99	12.94	2.32	0.43
G5E8T3_G5E8T3_MOUSE	Srp19	Signal recognition partic	K.SVM*LYVAEM*IPK#.L	39.18	14.79	2.65	0.38
G5E8T3_G5E8T3_MOUSE	Srp19	Signal recognition partic	K.SVMLYVAEM*IPK#.L	2.60	3.12	0.83	1.20
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.AFK#DK#VDVASVIVTK#.L	16.03	5.29	3.03	0.33
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	R.AGAFDQLK#.Q	70.35	22.83	3.08	0.32
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.DK#VDVASVIVTK#.L	23.83	7.48	3.18	0.31
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	R.DM*YEQFQNIM*K#.M	37.22	7.90	4.71	0.21
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	R.DVQELLTQYTK#.F	44.75	128.21	0.35	2.87
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.FK#NENFEIIIVDTSGR@.H	85.64	26.82	3.19	0.31

P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.GGGALSAVAATK#.S	59.92	15.48	3.87	0.26
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.HGQFTLR@.D	92.79	34.69	2.67	0.37
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	R.IPFYGSYTEM*DPVIIASEGVEK#.F	42.73	10.23	4.18	0.24
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.LAYYYQR@.K	51.97	18.81	2.76	0.36
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.LDDNEALIEK#.L	26.46	12.32	2.15	0.47
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.LLGM*GDIEGLIDK#.V	5.17	4.20	1.23	0.81
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.LLGM*GDIEGLIDK#VNELK#.L	22.36	13.69	1.63	0.61
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.SAIDLEEM*ASGLNK#.R	25.68	11.28	2.28	0.44
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	R.SLSNATIINEEVLNAM*LK#.E	8.98	3.94	2.28	0.44
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	R.SLSNATIINEEVLNAMLK#.E	10.11	3.05	3.31	0.30
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.SPIIFIGTGEHIDDFEPFK#.T	129.57	41.41	3.13	0.32
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.VDVASVIVTK#.L	41.08	8.98	4.58	0.22
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	R.DVQELLTQYTK#.F	8.44	2.79	3.02	0.33
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.GGGALSAVAATK#.S	17.57	6.33	2.78	0.36
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	R.IPFYGSYTEM*DPVIIASEGVEK#.F	8.11	1.80	4.50	0.22
P14576_SRP54_MOUSE	Srp54	Signal recognition partic	K.SPIIFIGTGEHIDDFEPFK#.T	24.20	9.64	2.51	0.40
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.ANK#EFGDSLSLEILQIIK#.E	33.31	10.71	3.11	0.32
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.IFLLGLADNEAAIVQAESEETK#.E	12.95	5.19	2.49	0.40
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.IFLLGLADNEAAIVQAESEETK#ER@.L	92.28	20.70	4.46	0.22
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.LASAFTEEQAVLYNQR@.V	25.22	6.36	3.97	0.25
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.NSLK#DLPDVQELITQVR@.S	39.86	5.67	7.04	0.14
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.QAATM*SEVEWR@.G	18.80	3.95	4.77	0.21
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.QIPGGGSGGGGSGSGGGGGGSGGGR@.S	5.91	1.93	3.06	0.33
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.SGGTEGLLAEK#LEALITQTR@.A	16.93	6.73	2.51	0.40
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.SPR@PQDLIR@.L	43.25	6.37	6.79	0.15
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.VEEISPNIR@.Y	69.38	18.07	3.84	0.26
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.VSNLQYLHSYLTYIK#.L	33.26	6.08	5.47	0.18
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.VTEELLTDNR@.Y	33.90	8.75	3.87	0.26
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.WSEALVLYDR@.V	15.34	5.25	2.92	0.34
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.YLLLVLM*DAER@.A	14.62	4.99	2.93	0.34
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.ANK#EFGDSLSLEILQIIK#.E	18.96	6.36	2.98	0.34
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.IFLLGLADNEAAIVQAESEETK#.E	8.01	3.59	2.23	0.45
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.IFLLGLADNEAAIVQAESEETKER.L	53.33	16.36	3.26	0.31
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.LASAFTEEQAVLYNQR@.V	7.72	2.52	3.07	0.33
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.NSLK#DLPDVQELITQVR@.S	18.40	9.22	2.00	0.50
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.SGGTEGLLAEK#LEALITQTR@.A	19.48	8.97	2.17	0.46
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.YANEVSSHGGASK#.N	3.41	1.47	2.32	0.43
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.YLLLVLM*DAER@.A	6.58	1.42	4.63	0.22
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.ANK#EFGDSLSLEILQIIK#.E	12.45	5.75	2.16	0.46
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.DLPDVQELITQVR@.S	18.64	20.18	0.92	1.08
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.DYALDGESGK#.V	16.45	5.46	3.01	0.33
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.IFLLGLADNEAAIVQAESEETK#.E	16.79	4.60	3.65	0.27
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.IFLLGLADNEAAIVQAESEETK#ER@.L	72.93	19.23	3.79	0.26
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.LASAFTEEQAVLYNQR@.V	24.04	2.97	8.09	0.12
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.LEALITQTR@.A	9.63	4.63	2.08	0.48
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.NSLK#DLPDVQELITQVR@.S	34.76	10.83	3.21	0.31
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	K.QIPGGGSGGGGSGSGGGGGGSGGGR@.S	2.99	1.73	1.73	0.58
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.SGGTEGLLAEK#LEALITQTR@.A	32.29	13.99	2.31	0.43
Q8BMA6_SRP68_MOUSE	Srp68	Signal recognition partic	R.VEEISPNIR@.Y	17.63	6.28	2.81	0.36
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.AIELLQEFSDQHPENAAEIK#.L	32.72	19.66	1.66	0.60
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.EAVSDLEQLWK#.Q	11.87	5.11	2.32	0.43
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.ELYGQVLYR@.L	11.69	5.37	2.18	0.46
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.GTQGATAGASSELDASK#.A	14.49	8.51	1.70	0.59
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.LTNAEGVEFK#.L	22.88	9.52	2.40	0.42
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	R.TEEALQLYNQIIK#.L	17.82	9.53	1.87	0.54
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.VDVEALENSPGATYIR@.K	11.28	5.06	2.23	0.45
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.VLANNSLSFEK#.A	11.80	6.54	1.81	0.55
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.ELYGQVLYR@.L	6.72	2.35	2.86	0.35
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.VLANNSLSFEK#.A	5.27	3.05	1.73	0.58
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.DIHTLAQLISAYSLVDPEK#.A	97.61	29.70	3.29	0.30
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.DIHTLAQLISAYSLVDPEK#AK#.A	19.42	5.99	3.24	0.31
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.EAVSDLEQLWK#.Q	34.71	12.16	2.85	0.35
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.GTQGATAGASSELDASK#.A	59.46	17.08	3.48	0.29
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.LTNAEGVEFK#.L	48.16	12.46	3.86	0.26
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	R.NSQDDYDEER@.K	8.99	3.25	2.77	0.36
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	R.TEEALQLYNQIIK#.L	62.78	18.24	3.44	0.29
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.VLANNSLSFEK#.A	62.60	24.46	2.56	0.39
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	R.YGQNSDFTR@.A	39.49	11.47	3.44	0.29
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.AIELLQEFSDQHPENAAEIK#.L	29.32	4.81	6.10	0.16
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.DIHTLAQLISAYSLVDPEK#.A	15.02	2.65	5.66	0.18
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.DIHTLAQLISAYSLVDPEK#AK#.A	8.66	2.15	4.03	0.25
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.EAVSDLEQLWK#.Q	10.87	4.56	2.38	0.42
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.GTQGATAGASSELDASK#.A	18.70	3.05	6.12	0.16
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.LTNAEGVEFK#.L	12.71	6.47	1.96	0.51
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.TIESATQQTDK#.L	55.71	16.09	3.46	0.29
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	K.VLANNSLSFEK#.A	17.97	12.09	1.49	0.67
F8VQC1_F8VQC1_MOUSE	Srp72	Signal recognition partic	R.YGQNSDFTR@.A	13.86	2.43	5.70	0.18
O70551_SRPK1_MOUSE	Srpk1	SRSF protein kinase 1 OS	K.FSAGNFLINPLEPK.N	5.06	6.54	0.77	1.29
O70551_SRPK1_MOUSE	Srpk1	SRSF protein kinase 1 OS	K.FSAGNFLINPLEPK#.N	9.00	2.95	3.05	0.33
P47758_SRPRB_MOUSE	Srprb	Signal recognition partic	R.AVVFVVDSAAFQR@.E	12.48	9.15	1.36	0.73
P47758_SRPRB_MOUSE	Srprb	Signal recognition partic	R.DTQTSITDSSAIYK#.V	11.27	9.47	1.19	0.84
P47758_SRPRB_MOUSE	Srprb	Signal recognition partic	R.GDTGSADIQDLEK#.W	14.60	9.52	1.53	0.65
P47758_SRPRB_MOUSE	Srprb	Signal recognition partic	R.SAAPSTLDSSSTAPAQLGK#.K	17.50	12.17	1.44	0.70
P47758_SRPRB_MOUSE	Srprb	Signal recognition partic	R.VGDGAGGAFQPYLDSLR.Q	9.87	5.13	1.92	0.52
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.AASPSPQSVR@.R	41.05	10.89	3.77	0.27
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.APQTSSPPPVR@.R	65.56	17.81	3.68	0.27
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.AVTIATPATAAPAAVSAATTTSAQEEPAAAPEPR@.K	120.73	38.02	3.18	0.31
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.DSSVQEATSTSDILK#.A	41.35	14.13	2.93	0.34
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.EK#AVTIATPATAAPAAVSAATTTSAQEEPAAAPEPR@.K	5.10	2.37	2.15	0.46
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.K#ETESEAEDDNLDDLER@.H	185.70	45.53	4.08	0.25
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.K#PPAPPSPVQSQSPSTNWSPAVPAK#.K	18.95	5.36	3.54	0.28
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.K#PPAPPSPVQSQSPSTNWSPAVPAK#K#.A	18.67	9.37	1.99	0.50
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.K#VELSESEEDK#GSK#.M	53.39	20.71	2.58	0.39
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.M*AAADSVQQR@.R	89.44	26.71	3.35	0.30
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.MAAADSVQQR@.R	33.34	11.02	3.03	0.33
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.M*K#DSSVQEATSTSDILK#.A	98.73	27.20	3.63	0.28
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.QNQQSSSDSGSSSTSEDER@PK#.R	10.64	1.51	7.06	0.14
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.R@YSPPIQR@.R	50.47	11.85	4.26	0.23
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.SPELPEPSVR@.M	24.02	6.05	3.97	0.25
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.SSASLSGSSSSSSSSR@.S	3.77	1.60	2.36	0.42
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.TASPPPPPK#.R	7.15	2.41	2.97	0.34
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.VNLEVIK#PWITK#.R	197.79	61.53	3.21	0.31
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.APQTSSPPPVR@.R	12.18	5.15	2.36	0.42

Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.AVTIATPATAAPAAVSAATTTSAQEEPAAAPEPR@.K	19.29	6.29	3.07	0.33
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.K#ETESEAEDDNLDDLER@.H	30.66	6.64	4.61	0.22
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	R.K#VELSESEEDK#GSK#.M	60.94	14.28	4.27	0.23
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.M*AAADSVQQR@.R	16.51	7.39	2.23	0.45
Q52KI8_SRRM1_MOUSE	Srrm1	Serine/arginine repetitiv	K.VNLEVIK#PWITK#.R	37.02	10.32	3.59	0.28
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SVVQTTPVAGSQSLSSGTVAK#.S	32.42	6.64	4.88	0.20
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPM*SVLQQTGGSM*M*DGPGPR.I	3.11	6.72	0.46	2.16
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.VPLSAYDR@.V	47.55	8.77	5.42	0.18
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.AAFGISDSYVDGSSFDPQR@.R	15.54	5.78	2.69	0.37
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.EETPGQR@PVVTETHQLAELNEK#.K	12.17	3.82	3.18	0.31
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.EM*PGSNIESSPEVEER@PAVLSALDQSQSQPSK#.A	6.43	1.74	3.70	0.27
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.HASSSPESLK#PTPAPGSR@.R	25.70	5.59	4.60	0.22
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.HLEAALVK#.R	61.02	28.08	2.17	0.46
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.IHTTALTGQSPPLASGHQGEGDAPSVEPGATNIQQPSSPAPSTK#.Q	9.00	2.96	3.04	0.33
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.IPAASAAAM*NLASAR@.T	23.18	10.38	2.23	0.45
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.M*SQVPAPVPLM*SLR@.T	25.03	18.19	1.38	0.73
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.M*SQVPAPVPLMSLR@.T	6.96	6.39	1.09	0.92
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.RPNPDILDHER.K	38.74	17.45	2.22	0.45
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SAHGTAPVNIAGSR@.T	21.91	3.89	5.63	0.18
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SGSSQELDGK#PSASPQER@.S	55.00	21.49	2.56	0.39
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SHSGSSPEVDSK#.S	42.49	1.48	28.63	0.03
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SLSYSPVER@.R	36.48	3.83	9.52	0.11
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SM*LQTPPDQNLSGSK#.S	4.35	2.55	1.70	0.59
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SPGM*LEPLGSAR.T	34.34	17.39	1.98	0.51
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SSSASPELK#.D	47.06	17.01	2.77	0.36
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SSSELSPEVVEK#.V	30.07	9.30	3.23	0.31
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SSTGPELPAPTPLLVEQHVDSPR@PLAAIPSSQEPVNPSSEASPTR@.G	8.62	3.78	2.28	0.44
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.STSSASDHNGM*LSGPAPGISHAEGGEPPASTGAQQPSTLAALQPAK#.E	3.64	1.44	2.53	0.39
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SVVQTTPVAGSQSLSSGTVAK#.S	45.46	5.22	8.70	0.11
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TAVAPSAVNLADPR@.T	17.28	5.41	3.20	0.31
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPAAAAAM*NLASPR@.T	11.21	4.42	2.53	0.39
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPAASAVNLAGAR@.T	43.21	11.40	3.79	0.26
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPAGLAPTNLSSSR@.M	31.46	12.14	2.59	0.39
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPM*SVLQQTGGSM*M*DGPGPR.I	29.79	23.73	1.26	0.80
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPPVALSSSR@.M	42.14	16.56	2.54	0.39
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TSAIPASVNLADSR@.T	32.21	14.41	2.23	0.45
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.VGLFSSQK#.V	47.25	19.47	2.43	0.41
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.VSSPVLETVQQR@.T	52.49	19.29	2.72	0.37
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.AAFGISDSYVDGSSFDPQR@.R	53.66	17.63	3.04	0.33
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.AAFGISDSYVDGSSFDPQRR.A	144.82	38.37	3.77	0.26
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.DK#FSPTQDR@PESSTVLK#.V	125.82	41.19	3.05	0.33
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.EELNGSFLNQTEADPSVDM*K#.E	5.97	3.42	1.74	0.57
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.EETPGQR@PVVTETHQLAELNEK#.K	23.99	7.47	3.21	0.31
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.EM*PGSNIESSPEVEERPAVLSALDQSQSQPSK.A	41.20	11.57	3.56	0.28
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.EMPGSNIESSPEVEER@PAVLSALDQSQSQPSK#.A	30.44	8.91	3.42	0.29
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.ER@GPSPEGSSSSESSPEHAPK#.S	8.68	2.97	2.92	0.34
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.GHTQTWPDTSSPEVM*QTQVESPLLQSK#.S	45.76	12.59	3.63	0.28
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.GHTQTWPDTSSPEVMQTQVESPLLQSK#.S	17.23	8.26	2.09	0.48
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.HASSSPESLK#PTPAPGSR@.R	134.25	25.12	5.34	0.19
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.HLEAALVK#.R	234.52	60.65	3.87	0.26
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.HSLSGSSPGM*K#.D	38.34	9.04	4.24	0.24
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.HSLSGSSPGMK#.D	19.33	14.25	1.36	0.74
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.IALALTAISLGTAR@PPPSM*SAAGLAAR@.M	26.79	12.03	2.23	0.45
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.IPAASAAAM*NLASAR@.T	45.45	18.41	2.47	0.41
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.IPAASAAAMNLASAR@.T	14.88	2.39	6.23	0.16
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.LM*LLEK#DVNPGAK#.E	24.67	8.74	2.82	0.35
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.M*ELGTPLR@.H	59.21	12.93	4.58	0.22
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.MELGTPLR@.H	24.22	6.16	3.93	0.25
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.M*SQVPAPVPLM*SLR.T	74.87	29.66	2.52	0.40
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.M*SQVPAPVPLMSLR@.T	15.99	17.76	0.90	1.11
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.MSQVPAPVPLMSLR@.T	10.56	4.98	2.12	0.47
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.NSGPVSEVNTGFSPEVK#.E	111.80	35.83	3.12	0.32
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.NSGPVSEVNTGFSPEVK#EELNGSFLNQTEADPSVDM*KEQSR.S	7.67	3.89	1.97	0.51
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.R@PNPDILDHER@.K	126.00	35.03	3.60	0.28
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SASSSPEIR@.S	39.95	17.60	2.27	0.44
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SAVR@PSPSPER@.S	11.43	2.59	4.42	0.23
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SEISTDPK#.L	166.42	57.22	2.91	0.34
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SESDSSPDSK#PK#.T	2.12	1.66	1.28	0.78
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SFLVQSR@.L	124.77	40.06	3.11	0.32
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SGM*SPEQSK#.T	4.73	2.33	2.03	0.49
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SGSESSVEQK#.N	23.89	8.08	2.96	0.34
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SGSSPGLR@.D	171.46	71.39	2.40	0.42
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SGSSQELDGK#PSASPQER@.S	136.07	35.27	3.86	0.26
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SHSGSSPEVDSK#.S	9.94	2.74	3.63	0.28
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SLLPNSSQDELM*EVEK#.S	37.40	15.61	2.40	0.42
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SLLPNSSQDELMEVEK#.S	21.50	6.85	3.14	0.32
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SLLPNSSQDELMEVEK#SEQPLSQVLPSLSPEHK#.E	8.01	2.90	2.76	0.36
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SM*LQTPPDQNLSGSK#.S	59.95	18.42	3.25	0.31
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.SMLQTPPDQNLSGSK#.S	13.66	5.03	2.71	0.37
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SPGM*LEPLGSAR@.T	79.87	29.95	2.67	0.37
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SPSVSSPEPTEK#.S	27.55	6.54	4.21	0.24
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SSSASPELK#.D	63.34	14.97	4.23	0.24
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SSSELSPEVVEK#.V	126.71	32.29	3.92	0.25
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SSSPVTELTAR.S	74.85	16.66	4.49	0.22
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SSTGPELPAPTPLLVEQHVDSPRPLAAIPSSQEPVNPSSEASPTR.G	20.36	8.07	2.52	0.40
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.SSVPENHAQSR@.I	18.04	8.61	2.10	0.48
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TAPAANLASR.I	102.97	38.58	2.67	0.37
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TAVAPSAVNLADPR@.T	63.83	11.15	5.73	0.17
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.TK#PDSSIYPLVDSK#.S	201.83	59.25	3.41	0.29
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.TKPDSSIYPLVDSK.S	47.37	15.49	3.06	0.33
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPAAAAAM*NLASPR@.T	26.81	7.81	3.43	0.29
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPAALAALSLTGSGTPPTAANYPSSSR@.T	23.47	3.76	6.24	0.16
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPAASAVNLAGAR@.T	107.87	20.27	5.32	0.19
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPAGLAPTNLSSSR@.M	30.20	4.15	7.28	0.14
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPM*SVLQQTGGSM*MDGPGPR@.I	3.72	2.06	1.81	0.55
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPPVALSSSR@.M	55.68	16.95	3.28	0.30
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TPQAPTPANLVVGPR@.S	29.95	5.73	5.23	0.19
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	R.TSAIPASVNLADSR.T	78.56	22.20	3.54	0.28
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.VGLFSSQK#.V	189.64	76.24	2.49	0.40
Q8BTI8_SRRM2_MOUSE	Srrm2	Serine/arginine repetitiv	K.VSSPVLETVQQR@.T	187.75	52.05	3.61	0.28
Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	R.AGPALGEGER@.K	26.98	12.41	2.17	0.46
Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	R.DLDAPDDVDFF.-	14.22	14.22	1.00	1.00
Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	R.ESLSEEEAQK#.M	36.13	15.57	2.32	0.43

Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	K.FVTSNTQELGK#.D	26.20	10.81	2.42	0.41
Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	R.ILEQEEEEEQAGK#.T	46.41	21.06	2.20	0.45
Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	R.KDPEQEVEK.F	14.07	8.89	1.58	0.63
Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	R.LGSIAEIDLGVPPPIM*K#.S	8.16	5.47	1.49	0.67
Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	K.LLLYLR.I	26.30	12.59	2.09	0.48
Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	R.ESLSEEEAQK#.M	9.90	4.32	2.29	0.44
Q99MR6_SRRT_MOUSE	Srrt	Serrate RNA effector mol	R.ILEQEEEEEQAGK#.T	8.63	3.91	2.21	0.45
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.DAEDAVYGR@.D	374.11	149.59	2.50	0.40
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.DGTGVVEFVR@.K	727.23	291.02	2.50	0.40
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.DGYDYDGYR@.L	549.25	203.37	2.70	0.37
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	K.DIEDVFYK#.Y	251.63	100.72	2.50	0.40
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	K.EDM*TYAVR@.K	95.49	41.23	2.32	0.43
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.GGPPFAFVEFEDPR@.D	224.16	106.26	2.11	0.47
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.GGPPFAFVEFEDPR@DAEDAVYGR@.D	5.77	2.37	2.44	0.41
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.IYVGNLPPDIR@.T	247.14	116.84	2.12	0.47
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.K#EDMTYAVR@.K	106.22	46.38	2.29	0.44
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.K#EDM*TYAVR@.K	202.58	88.87	2.28	0.44
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.LR@VEFPR@.S	152.95	64.85	2.36	0.42
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.R@GGPPFAFVEFEDPR@.D	33.12	20.82	1.59	0.63
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.RGGPPFAFVEFEDPRDAEDAVYGR.D	71.33	27.27	2.62	0.38
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.SHEGETAYIR@.V	442.75	175.51	2.52	0.40
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.TK#DIEDVFYK#.Y	802.91	310.11	2.59	0.39
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.VVVSGLPPSGSWQDLK#.D	138.77	58.03	2.39	0.42
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.DGTGVVEFVR@.K	16.48	7.50	2.20	0.45
Q6PDM2_SRSF1_MOUSE	Srsf1	Serine/arginine-rich splic	R.SHEGETAYIR@.V	4.67	11.04	0.42	2.36
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.DAEDALHNLDR@.K	12.00	5.81	2.06	0.48
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.GFAYVQFEDVR.D	120.40	67.56	1.78	0.56
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.QIEIQFAQGDR@.K	71.02	32.79	2.17	0.46
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.SFDYNYR@.R	63.92	25.46	2.51	0.40
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.YGPIVDVYVPLDFYTR@.R	166.59	101.96	1.63	0.61
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.YLR@PPNTSLFVR@.N	161.13	87.29	1.85	0.54
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.GFAYVQFEDVR@.D	42.88	26.43	1.62	0.62
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.GFAYVQFEDVR@DAEDALHNLDR@K#.W	2.48	3.08	0.81	1.24
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.SFDYNYR.R	51.64	25.85	2.00	0.50
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.YDDYDR@.Y	17.38	10.20	1.70	0.59
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.YLRPPNTSLFVR.N	187.53	116.70	1.61	0.62
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.YLRPPNTSLFVR.N	16.60	8.94	1.86	0.54
Q9R0U0_SRS10_MOUSE	Srsf10	Serine/arginine-rich splic	R.YGPIVDVYVPLDFYTR@.R	12.64	8.75	1.45	0.69
Q3UIX4_Q3UIX4_MOUSE	Srsf11	Protein Srsf11 OS=Mus m	R.ALIVVPYAEGVIPDETK#.A	29.81	8.88	3.36	0.30
Q3UIX4_Q3UIX4_MOUSE	Srsf11	Protein Srsf11 OS=Mus m	R.TLFGFLGK#.I	83.60	13.38	6.25	0.16
Q3UIX4_Q3UIX4_MOUSE	Srsf11	Protein Srsf11 OS=Mus m	R.ALIVVPYAEGVIPDETK#.A	23.78	12.72	1.87	0.53
Q3UIX4_Q3UIX4_MOUSE	Srsf11	Protein Srsf11 OS=Mus m	K.FHDPDSAVVAQHLTNTVFVDR@.A	10.33	3.12	3.31	0.30
Q3UIX4_Q3UIX4_MOUSE	Srsf11	Protein Srsf11 OS=Mus m	R.LFPPDDSPLPVSSR.V	160.83	246.58	0.65	1.53
Q3UIX4_Q3UIX4_MOUSE	Srsf11	Protein Srsf11 OS=Mus m	R.TLFGFLGK#.I	48.98	15.70	3.12	0.32
Q62093_SRSF2_MOUSE	Srsf2	Serine/arginine-rich splic	R.DAEDAM*DAM*DGAVLDGR@.E	92.10	33.18	2.78	0.36
Q62093_SRSF2_MOUSE	Srsf2	Serine/arginine-rich splic	R.DAEDAMDAM*DGAVLDGR@.E	13.14	5.88	2.23	0.45
Q62093_SRSF2_MOUSE	Srsf2	Serine/arginine-rich splic	R.DAEDAM*DAMDGAVLDGR@.E	10.22	5.30	1.93	0.52
Q62093_SRSF2_MOUSE	Srsf2	Serine/arginine-rich splic	R.DAEDAMDAMDGAVLDGR@.E	9.05	2.39	3.79	0.26
Q62093_SRSF2_MOUSE	Srsf2	Serine/arginine-rich splic	K.SPPK#SPEEEGAVSS.-	6.87	4.74	1.45	0.69
Q62093_SRSF2_MOUSE	Srsf2	Serine/arginine-rich splic	K.VDNLTYR@.T	428.42	186.74	2.29	0.44
Q62093_SRSF2_MOUSE	Srsf2	Serine/arginine-rich splic	R.VGDVYIPR@.D	510.02	223.45	2.28	0.44
Q62093_SRSF2_MOUSE	Srsf2	Serine/arginine-rich splic	R.YGGGGYGR@.R	52.99	27.89	1.90	0.53
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	R.AFGYYGPLR@.S	57.75	30.41	1.90	0.53
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	R.NPPGFAFVEFEDPR@.D	211.70	111.58	1.90	0.53
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	R.AFGYYGPLR@.S	1509.58	701.38	2.15	0.46
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	R.DAADAVR@.E	135.20	65.22	2.07	0.48
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	R.GPPPSWGR.R	77.61	41.94	1.85	0.54
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	R.NPPGFAFVEFEDPR@.D	527.55	283.49	1.86	0.54
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	R.NRGPPPSWGR.R	113.71	12.65	8.99	0.11
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	R.VELSNGEK#R@.S	18.05	12.59	1.43	0.70
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	R.VR@VELSNGEK#.R	124.66	45.37	2.75	0.36
P84104_SRSF3_MOUSE	Srsf3	Serine/arginine-rich splic	K.VYVGNLGNNGNK#.T	54.94	28.19	1.95	0.51
Q8VE97_SRSF4_MOUSE	Srsf4	Serine/arginine-rich splic	R.LIVENLSSR@.C	2043.95	660.69	3.09	0.32
Q8VE97_SRSF4_MOUSE	Srsf4	Serine/arginine-rich splic	R.QAGEVTYADAHK#.G	122.34	42.03	2.91	0.34
Q8VE97_SRSF4_MOUSE	Srsf4	Serine/arginine-rich splic	R.VIVEHAR@.G	128.29	75.75	1.69	0.59
Q8VE97_SRSF4_MOUSE	Srsf4	Serine/arginine-rich splic	R.AEGESEAPNPEPR@.A	122.69	68.80	1.78	0.56
Q8VE97_SRSF4_MOUSE	Srsf4	Serine/arginine-rich splic	K.ILEVDLK#.N	91.35	49.58	1.84	0.54
Q8VE97_SRSF4_MOUSE	Srsf4	Serine/arginine-rich splic	R.LIVENLSSR@.C	328.23	165.88	1.98	0.51
Q8VE97_SRSF4_MOUSE	Srsf4	Serine/arginine-rich splic	K.NEGVIEFVSYSDMK#.R	6.73	4.75	1.42	0.71
Q8VE97_SRSF4_MOUSE	Srsf4	Serine/arginine-rich splic	K.NGYGFVEFDDLR@.D	26.67	12.38	2.15	0.46
O35326_SRSF5_MOUSE	Srsf5	Serine/arginine-rich splic	R.DADDAVYELDGK#.E	103.57	31.46	3.29	0.30
O35326_SRSF5_MOUSE	Srsf5	Serine/arginine-rich splic	R.GFGFVEFEDPR@.D	214.94	73.35	2.93	0.34
O35326_SRSF5_MOUSE	Srsf5	Serine/arginine-rich splic	K.LNEGVVEFASYGDLK#.N	328.04	105.33	3.11	0.32
O35326_SRSF5_MOUSE	Srsf5	Serine/arginine-rich splic	K.R@GFGFVEFEDPR@.D	49.29	16.20	3.04	0.33
O35326_SRSF5_MOUSE	Srsf5	Serine/arginine-rich splic	R.VSWQDLK#.D	310.57	131.04	2.37	0.42
O35326_SRSF5_MOUSE	Srsf5	Serine/arginine-rich splic	R.DADDAVYELDGK#.E	6.51	4.36	1.49	0.67
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.ALDK#LDGTEINGR@.N	161.13	48.87	3.30	0.30
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.DADDAVYELNSK#.E	243.29	83.21	2.92	0.34
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.DK#YGPPVR@.T	164.55	58.59	2.81	0.36
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.DR@DGYSYGSR@.S	26.31	8.11	3.24	0.31
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.FFSGYGR@.L	293.62	93.32	3.15	0.32
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.LLEIDLK#.N	620.80	189.78	3.27	0.31
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	K.NGYGFVEFEDSR@.D	48.23	13.15	3.67	0.27
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	K.NGYGFVEFEDSRDADDAVYELNSK.E	70.79	19.55	3.62	0.28
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.TNEGVIEFR@.S	741.32	232.92	3.18	0.31
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.DADDAVYELNSK#.E	28.37	10.90	2.60	0.38
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.DR@DGYSYGSR@.S	4.82	1.42	3.39	0.29
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.LLEIDLK#.N	103.65	48.29	2.15	0.47
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	K.NGYGFVEFEDSR@.D	7.12	3.49	2.04	0.49
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	K.NGYGFVEFEDSR@DADDAVYELNSK#.E	9.88	5.75	1.72	0.58
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.TNEGVIEFR.S	91.20	42.92	2.12	0.47
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.LLEIDLK#.N	11.20	3.28	3.42	0.29
Q3TWW8_SRSF6_MOUSE	Srsf6	Serine/arginine-rich splic	R.TNEGVIEFR@.S	9.93	3.02	3.29	0.30
Q8BL97_SRSF7_MOUSE	Srsf7	Serine/arginine-rich splic	R.AFSYYGPLR@.T	260.30	115.99	2.24	0.45
Q8BL97_SRSF7_MOUSE	Srsf7	Serine/arginine-rich splic	R.NPPGFAFVEFEDPR@DAEDAVR@.G	6.45	3.67	1.75	0.57
Q8BL97_SRSF7_MOUSE	Srsf7	Serine/arginine-rich splic	R.R@PFDPNDR@.C	142.17	68.18	2.09	0.48
Q8BL97_SRSF7_MOUSE	Srsf7	Serine/arginine-rich splic	R.SGSIIGSR.Y	112.81	39.45	2.86	0.35
Q8BL97_SRSF7_MOUSE	Srsf7	Serine/arginine-rich splic	R.VELSTGM*PR@.R	174.86	90.55	1.93	0.52
Q8BL97_SRSF7_MOUSE	Srsf7	Serine/arginine-rich splic	R.VELSTGMPR@.R	28.13	14.70	1.91	0.52
Q8BL97_SRSF7_MOUSE	Srsf7	Serine/arginine-rich splic	K.VYVGNLGTGAGK#.G	548.85	252.11	2.18	0.46
Q8BL97_SRSF7_MOUSE	Srsf7	Serine/arginine-rich splic	R.AFSYYGPLR@.T	9.88	3.95	2.50	0.40
Q8BL97_SRSF7_MOUSE	Srsf7	Serine/arginine-rich splic	K.VYVGNLGTGAGK#.G	11.73	7.08	1.66	0.60
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.DAEDAIYGR@.N	69.34	39.50	1.76	0.57

Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	K.DGM*GM*VEYLR@.K	37.72	22.89	1.65	0.61
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	K.DLEDLFYK#.Y	13.33	8.70	1.53	0.65
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.EK#DLEDLFYK#.Y	105.41	61.89	1.70	0.59
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.FEDPR@DAEDAIYGR@.N	84.78	55.28	1.53	0.65
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.HGLVPFAFVR@.F	90.23	56.03	1.61	0.62
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.IYVGNLPSDVR@.E	223.22	134.49	1.66	0.60
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.K#EDM*EYALR@.K	37.61	19.72	1.91	0.52
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.SHEGETSYIR.V	32.87	21.48	1.53	0.65
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.SHEGETSYIR@.V	66.60	37.70	1.77	0.57
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.VLVSGLPPSGSWQDLK#.D	18.86	13.84	1.36	0.73
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.DAEDAIYGR@.N	16.46	8.09	2.03	0.49
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	K.DGM*GM*VEYLR@.K	15.33	8.58	1.79	0.56
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.FEDPR@DAEDAIYGR@.N	66.24	44.05	1.50	0.66
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.HGLVPFAFVR@.F	85.02	56.64	1.50	0.67
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.IYVGNLPSDVR@.E	183.61	106.38	1.73	0.58
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.SHEGETSYIR.V	22.80	17.70	1.29	0.78
Q9D0B0_SRSF9_MOUSE	Srsf9	Serine/arginine-rich splic	R.VLVSGLPPSGSWQDLK#.D	15.55	12.21	1.27	0.79
Q62280_SSXT_MOUSE	Ss18	Protein SSXT OS=Mus mu	R.GK#GEITPAAIQK#.M	7.93	1.32	6.02	0.17
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.DTNLLILFK#.E	16.96	8.95	1.90	0.53
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.DTNLLILFK#EDYFAK#.K	10.29	4.86	2.12	0.47
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.FVEIPGQK#.Y	151.99	101.86	1.49	0.67
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.GNR@PGYAGAPK#.G	21.30	13.96	1.53	0.66
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.GSIFAVFDSIQSAK#.K	248.37	166.21	1.49	0.67
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.ITDDQQESLNK#.W	161.75	106.61	1.52	0.66
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.K#FVEIPGQK#.Y	44.19	35.90	1.23	0.81
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.LDEGWVPLETMIK#.F	38.68	28.32	1.37	0.73
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.LM*EVSADK#.T	27.57	17.64	1.56	0.64
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	R.LTTDFNVIVQALSK#.S	131.92	88.74	1.49	0.67
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.MTALEAK#.I	40.04	24.31	1.65	0.61
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	R.NANNGNLLLR@.N	38.00	19.28	1.97	0.51
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	R.SPSR@PLPEVTDEYK#NDVK#.N	56.58	34.26	1.65	0.61
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.YK#DTNLLILFK#.E	138.52	97.12	1.43	0.70
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.ITDDQQESLNK.W	3.00	4.10	0.73	1.37
P32067_LA_MOUSE	Ssb	Lupus La protein homolc	K.GSIFAVFDSIQSAK.K	6.55	6.44	1.02	0.98
Q8R2K3_Q8R2K3_MOUSE	Ssbp1	Single-stranded DNA bin	R.QATTIIADNIIFLSDQTK.E	8.01	12.49	0.64	1.56
Q8R2K3_Q8R2K3_MOUSE	Ssbp1	Single-stranded DNA bin	R.SGDSEVYQM*GDVSQK.T	11.73	17.56	0.67	1.50
Q9CY50_SSRA_MOUSE	Ssr1	Translocon-associated pr	K.FLVGFTNK#.G	56.25	43.53	1.29	0.77
Q9CY50_SSRA_MOUSE	Ssr1	Translocon-associated pr	K.GEDFPANNIVK#.F	24.24	24.13	1.00	1.00
Q9CY50_SSRA_MOUSE	Ssr1	Translocon-associated pr	K.GTEDFIVESLDASFR.Y	29.57	24.47	1.21	0.83
Q9CY50_SSRA_MOUSE	Ssr1	Translocon-associated pr	K.GTEDFIVESLDASFR@.Y	17.61	9.79	1.80	0.56
Q9DCF9_SSRG_MOUSE	Ssr3	Translocon-associated pr	K.QQSEEDLLLQDFSR@.N	27.44	24.62	1.11	0.90
Q62186_SSRD_MOUSE	Ssr4	Translocon-associated pr	R.NNEDVSIIPPLFTVSVDHR@.G	15.39	8.34	1.84	0.54
Q08943_SSRP1_MOUSE	Ssrp1	FACT complex subunit SS	K.ASSGLLYPLER.G	14.45	25.49	0.57	1.76
Q08943_SSRP1_MOUSE	Ssrp1	FACT complex subunit SS	R.FDEISFVNFAR@.G	13.63	19.94	0.68	1.46
Q08943_SSRP1_MOUSE	Ssrp1	FACT complex subunit SS	R.FYVPPTQEDGVDPVEAFAQNVLSK#.A	8.87	10.72	0.83	1.21
Q08943_SSRP1_MOUSE	Ssrp1	FACT complex subunit SS	K.IPYTTVLR.L	12.60	12.85	0.98	1.02
Q08943_SSRP1_MOUSE	Ssrp1	FACT complex subunit SS	K.VDNIQAGELTEGIWR.R	6.14	8.91	0.69	1.45
P56873_SSA27_MOUSE	Sssca1	Sjoegren syndrome/scler	K.AAQAPPLPAAPPNTDAVASTQTALLQK#.L	6.85	3.92	1.75	0.57
P56873_SSA27_MOUSE	Sssca1	Sjoegren syndrome/scler	K.AAQAPPLPAAPPNTDAVASTQTALLQK#.L	25.93	12.81	2.02	0.49
Q924W7_ST5_MOUSE	St5	Suppression of tumorige	K.TFLPGAGNEVLELR@.R	12.00	5.51	2.18	0.46
Q8BZ71_STAC3_MOUSE	Stac3	SH3 and cysteine-rich do	K.GDEAGGYVK#VYTGR@.K	59.12	2.45	24.09	0.04
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	K.DGIEFAFK#.Y	10.33	5.40	1.92	0.52
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	K.FLTEQM*M*ER@.R	14.92	4.45	3.35	0.30
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.FNHSVEDLLQEGEEADDDDIYNVLSTLK#R@.L	11.85	1.88	6.30	0.16
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	K.ITDGSPSK#EDLLVLR@.K	21.22	10.45	2.03	0.49
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.IVSM*TLDK#EYDVAVEAIR@.L	23.69	7.89	3.00	0.33
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.LELLLQK#.R	54.62	20.87	2.62	0.38
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	K.M*YSDAFLNDSYLK#.Y	11.46	3.67	3.13	0.32
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.NM*QNAEIIR@.K	9.75	3.49	2.80	0.36
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.NSLVTGGEDDR@M*SVNSGSSSSK#.T	10.18	3.64	2.80	0.36
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.SQLIDEFVDR@.F	18.89	11.26	1.68	0.60
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.HDPQAEEALAK.R	12.21	11.28	1.08	0.92
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.IVSM*TLDK#EYDVAVEAIR@.L	18.13	5.41	3.35	0.30
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.LELLLQK#.R	40.50	12.63	3.21	0.31
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	K.M*YSDAFLNDSYLK#.Y	10.79	3.76	2.87	0.35
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	R.SQLIDEFVDR@.F	16.78	8.18	2.05	0.49
Q9D3E6_STAG1_MOUSE	Stag1	Cohesin subunit SA-1 OS	K.YYNDYGDIIK#.E	14.12	4.64	3.05	0.33
O35638_STAG2_MOUSE	Stag2	Cohesin subunit SA-2 OS	R.ERTELKPDFFDPASIM*DESVLGVSM*F.-	4.62	1.75	2.64	0.38
O35638_STAG2_MOUSE	Stag2	Cohesin subunit SA-2 OS	R.IVSM*TLDK#EYDVAVQAIK#.L	17.21	5.10	3.38	0.30
O35638_STAG2_MOUSE	Stag2	Cohesin subunit SA-2 OS	R.LLEDFLQEGEEPDEDDAYQVLSTLK#R@.I	9.98	2.84	3.51	0.29
O35638_STAG2_MOUSE	Stag2	Cohesin subunit SA-2 OS	R.IVSM*TLDK#EYDVAVQAIK#.L	21.63	6.02	3.59	0.28
O35638_STAG2_MOUSE	Stag2	Cohesin subunit SA-2 OS	R.LLEDFLQEGEEPDEDDAYQVLSTLK#.R	15.84	5.67	2.79	0.36
O35638_STAG2_MOUSE	Stag2	Cohesin subunit SA-2 OS	R.R@DPEEDGLM*K#.R	7.86	4.41	1.78	0.56
O88811_STAM2_MOUSE	Stam2	Signal transducing adapt	K.SM*K#EEGVTFPSAGSQTVAAAAK#.N	5.75	5.35	1.08	0.93
O88811_STAM2_MOUSE	Stam2	Signal transducing adapt	K.VLEALDLYNK#.L	10.42	3.09	3.38	0.30
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.ELSAVTFPDIIR@.N	10.87	12.55	0.87	1.16
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.FTYEPDPITK#.N	11.56	7.91	1.46	0.68
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.M*FLM*LDNK.R	6.32	7.67	0.82	1.21
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.TELISVSEVHPSR@.L	11.76	8.85	1.33	0.75
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.VM*AAENIPENPLK.Y	11.48	10.38	1.11	0.90
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.ELSAVTFPDIIR.N	8.52	9.69	0.88	1.14
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.FHDLLSQLDDQYSR@.F	5.58	5.92	0.94	1.06
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.FLEQVHQLYDDSFPM*EIR.Q	7.01	10.57	0.66	1.51
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.FNQAQEGNIQNTVM*LDK.Q	3.18	4.47	0.71	1.40
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.QYLAQWLEK.Q	4.22	2.63	1.61	0.62
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.TLEELQDEYDFK.C	3.08	8.61	0.36	2.79
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.VM*AAENIPENPLK#.Y	3.44	4.04	0.85	1.17
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.ALLK#DQQPGTFLLR@.F	22.79	12.49	1.82	0.55
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.DQQPGTFLLR@.F	17.54	40.32	0.43	2.30
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.EGAITFTWVER.S	22.41	13.53	1.66	0.60
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.ELSAVTFPDIIR@.N	52.03	33.56	1.55	0.64
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.FHDLLSQLDDQYSR@.F	15.65	10.58	1.48	0.68
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.FNQAQEGNIQNTVM*LDK#.Q	7.85	5.19	1.51	0.66
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.FTYEPDPITK#.N	33.84	19.33	1.75	0.57
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.GLNADQLSM*LGEK#.L	18.07	12.42	1.45	0.69
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.K#LEELEQK#.F	26.96	14.74	1.83	0.55
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.LLGPNAGPDGLIPWTR@.F	101.71	66.46	1.53	0.65
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.LQELNYNLK#.V	29.74	15.72	1.89	0.53
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.QDWEHAAYDVSFATIR@.F	10.85	2.71	4.00	0.25
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.SDQK#QEQLLLHK#.M	13.89	7.96	1.75	0.57
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.TLEELQDEYDFK#.C	16.14	7.93	2.03	0.49
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.VM*AAENIPENPLK#.Y	20.13	13.99	1.44	0.69
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.DQQPGTFLLR@.F	27.61	67.00	0.41	2.43

Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.EGAITFTWVER@.S	29.56	18.67	1.58	0.63
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.ELSAVTFPDIIR@.N	65.21	37.81	1.72	0.58
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.FHDLLSQLDDQYSR@.F	27.76	11.58	2.40	0.42
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.FLEQVHQLYDDSFPM*EIR@.Q	18.73	8.99	2.08	0.48
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.FNQAQEGNIQNTVM*LDK#.Q	11.24	4.73	2.37	0.42
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.FTYEPDPITK#.N	38.11	17.66	2.16	0.46
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	R.IVGPEFDSM*M*STV.-	15.14	15.14	1.00	1.00
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.K#LEELEQK#.F	53.80	29.83	1.80	0.55
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.LLGPNAGPDGLIPWTR@.F	47.15	26.89	1.75	0.57
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.SDQK#QEQLLLHK#.M	15.78	13.69	1.15	0.87
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.TGVQFTVK#.S	19.21	11.79	1.63	0.61
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.TLEELQDEYDFK#.C	17.21	10.90	1.58	0.63
Q8C3V4_Q8C3V4_MOUSE	Stat1	Signal transducer and act	K.VM*AAENIPENPLK#.Y	34.07	23.11	1.47	0.68
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	R.AQEVQPPPAPEAVVESQQLEIENR@.I	8.30	3.29	2.52	0.40
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	K.EVLQSLPLTEIIR@.H	29.12	14.73	1.98	0.51
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	R.GLDSEQLGM*LR@.T	18.59	8.62	2.16	0.46
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	R.LTTLVDLLLPK#.L	30.12	15.01	2.01	0.50
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	K.M*LSGTFLLR@.F	19.06	6.92	2.75	0.36
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	K.MLSGTFLLR@.F	12.32	21.03	0.59	1.71
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	R.QVDELQQPLELK#.Q	7.63	3.50	2.18	0.46
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	R.AQEVQPPPAPEAVVESQQLEIENR@.I	9.86	6.89	1.43	0.70
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	K.EVLQSLPLTEIIR@.H	36.71	16.18	2.27	0.44
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	R.GLDSEQLGM*LR@.T	16.99	11.54	1.47	0.68
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	R.LTTLVDLLLPK#.L	35.14	16.02	2.19	0.46
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	R.QVDELQQPLELK#.Q	8.90	4.35	2.04	0.49
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	K.TSSSDPHQSQQAQLVQATANK#.V	5.55	3.28	1.69	0.59
Q9QXJ2_Q9QXJ2_MOUSE	Stat2	Signal transducer and act	R.YKGDM*FGQGVDLQNAQVM*ELLQR.L	11.46	15.71	0.73	1.37
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.EGGVTFTWVEK#.D	13.14	4.81	2.73	0.37
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.K#LEELQQK#.V	24.08	47.44	0.51	1.97
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.TQIQSVEPYTK#.Q	12.54	3.30	3.80	0.26
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.VM*NM*EESNNGSLSAEFK#.H	3.60	2.00	1.80	0.55
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.VVENLQDDFDFNYK#.T	10.88	3.62	3.01	0.33
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	R.YLEQLHQLYSDSFPM*ELR@.Q	12.00	7.12	1.69	0.59
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	R.LLQTAATAAQQGGQANHPTAAVVTEK#.Q	12.31	12.53	0.98	1.02
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.VVENLQDDFDFNYK#.T	7.40	4.51	1.64	0.61
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	R.YLEQLHQLYSDSFPM*ELR@.Q	8.40	7.23	1.16	0.86
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.EGGVTFTWVEK#.D	12.80	6.52	1.96	0.51
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	R.GLSIEQLTTLAEK#.L	41.86	13.64	3.07	0.33
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	R.LLQTAATAAQQGGQANHPTAAVVTEK#.Q	41.36	11.10	3.73	0.27
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.R@GLSIEQLTTLAEK#.L	10.46	22.74	0.46	2.17
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.SQGDM*QDLNGNNQSVTR@.Q	2.39	2.36	1.01	0.99
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.TQIQSVEPYTK#.Q	30.59	28.38	1.08	0.93
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.VVENLQDDFDFNYK#.T	12.39	2.29	5.42	0.18
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	R.YLEQLHQLYSDSFPM*ELR@.Q	14.51	5.87	2.47	0.40
P42227_STAT3_MOUSE	Stat3	Signal transducer and act	K.TQIQSVEPYTK#.Q	10.09	4.44	2.27	0.44
P42230_STA5A_MOUSE	Stat5a	Signal transducer and act	R.IQAQFAQLGQLNPQER@.M	5.60	1.79	3.14	0.32
P42230_STA5A_MOUSE	Stat5a	Signal transducer and act	R.LGDLNYLIYVFPDR@PK#DEVFAK#.Y	8.11	2.78	2.92	0.34
P42230_STA5A_MOUSE	Stat5a	Signal transducer and act	K.LQQTQEYFIIQYQESLR@.I	5.64	2.34	2.41	0.41
P42230_STA5A_MOUSE	Stat5a	Signal transducer and act	R.FSDSEIGGITIAWK#.F	4.99	3.64	1.37	0.73
P52633_STAT6_MOUSE	Stat6	Signal transducer and tra	R.GQDGSSQIENIQPFSAK#.D	7.47	2.42	3.08	0.32
P52633_STAT6_MOUSE	Stat6	Signal transducer and tra	R.TLVTSSFLVEK#.Q	13.45	4.88	2.76	0.36
Q9DBE7_Q9DBE7_MOUSE	Stau1	Double-stranded RNA-bi	R.EAEEENLNK#SEISQVFEIALK#.R	10.84	18.20	0.60	1.68
Q9DBE7_Q9DBE7_MOUSE	Stau1	Double-stranded RNA-bi	R.ELLYGGTSPTAETILK#.S	26.23	13.97	1.88	0.53
Q9DBE7_Q9DBE7_MOUSE	Stau1	Double-stranded RNA-bi	R.LAQIQQAK#.K	33.89	23.35	1.45	0.69
Q9DBE7_Q9DBE7_MOUSE	Stau1	Double-stranded RNA-bi	K.LLSELDQQSTEM*PR.T	17.97	12.68	1.42	0.71
Q9DBE7_Q9DBE7_MOUSE	Stau1	Double-stranded RNA-bi	K.LQTAPDYGQGM*NPISR@.L	12.78	9.58	1.33	0.75
Q9DBE7_Q9DBE7_MOUSE	Stau1	Double-stranded RNA-bi	R.NAAENMLEILGFK.V	18.04	18.33	0.98	1.02
Q9DBE7_Q9DBE7_MOUSE	Stau1	Double-stranded RNA-bi	R.TLQSEPLPER.L	34.08	29.97	1.14	0.88
Q9DBE7_Q9DBE7_MOUSE	Stau1	Double-stranded RNA-bi	R.VSVGEFVGEGEGK#.S	24.52	18.56	1.32	0.76
Q9DBE7_Q9DBE7_MOUSE	Stau1	Double-stranded RNA-bi	K.LLSELDQQSTEM*PR@.T	7.28	4.43	1.64	0.61
Q8CJ67_STAU2_MOUSE	Stau2	Double-stranded RNA-bi	K.AGPDYGQGM*NPISR@.L	3.83	7.15	0.54	1.87
Q60864_STIP1_MOUSE	Stip1	Stress-induced-phospho	R.LAYINPDLALEEK#.N	9.81	5.98	1.64	0.61
Q99KH8_STK24_MOUSE	Stk24	Serine/threonine-protei	K.LADFGVAGQLTDTQIK#R@.N	45.59	7.28	6.26	0.16
Q99KH8_STK24_MOUSE	Stk24	Serine/threonine-protei	K.NLENGTLQLSDLER@.N	4.92	1.58	3.10	0.32
Q99KH8_STK24_MOUSE	Stk24	Serine/threonine-protei	R.NTFVGTPFWM*APEVIK#.Q	5.63	2.64	2.13	0.47
Q99KH8_STK24_MOUSE	Stk24	Serine/threonine-protei	K.VLFLIPK#.N	23.22	8.96	2.59	0.39
Q9Z2W1_STK25_MOUSE	Stk25	Serine/threonine-protei	K.AANVLLSEQGDVK#.L	12.05	3.80	3.17	0.32
Q9JI10_STK3_MOUSE	Stk3	Serine/threonine-protei	K.LADFGVAGQLTDTM*AK#.R	5.70	2.56	2.23	0.45
Q9JI10_STK3_MOUSE	Stk3	Serine/threonine-protei	K.LADFGVAGQLTDTM*AK#.R	14.04	3.23	4.34	0.23
Q9JI10_STK3_MOUSE	Stk3	Serine/threonine-protei	K.LGEGSYGSVFK#.A	14.33	6.08	2.36	0.42
Q9JI10_STK3_MOUSE	Stk3	Serine/threonine-protei	R.VPQDGDFDFLK#.N	60.93	3.87	15.74	0.06
Q9JI10_STK3_MOUSE	Stk3	Serine/threonine-protei	K.LADFGVAGQLTDTM*AK#.R	5.22	3.39	1.54	0.65
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.DIK#PDNLLLDSK#.G	16.11	16.10	1.00	1.00
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.DIKPDNLLLDSK.G	5.07	4.75	1.07	0.94
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.ERPAAISIEIK.S	15.13	16.61	0.91	1.10
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.IGAPGVEEIKNNLFFEGVDWEHIR.E	3.90	3.13	1.25	0.80
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.LGLEDFESLK#.V	30.02	32.72	0.92	1.09
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	K.SIDDTSNFDEFPESDILK#PTVTTSSHPETDYK#.N	10.77	11.50	0.94	1.07
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.DIK#PDNLLLDSK#.G	14.43	13.02	1.11	0.90
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.DILVEADSLWVVK#.M	5.47	5.81	0.94	1.06
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.ER@PAAISIEIK#.S	16.62	12.05	1.38	0.73
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.IGAPGVEEIK#NNLFFEGVDWEHIR@.E	2.98	4.43	0.67	1.49
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.DIK#PDNLLLDSK#.G	19.33	14.99	1.29	0.78
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.DILVEADSLWVVK#.M	8.44	6.17	1.37	0.73
Q91VJ4_STK38_MOUSE	Stk38	Serine/threonine-protei	R.ER@PAAISIEIK#.S	12.21	13.72	0.89	1.12
P54116_STOM_MOUSE	Stom	Erythrocyte band 7 integ	K.VIAAEGEM*NASR.A	8.74	4.85	1.80	0.56
P54116_STOM_MOUSE	Stom	Erythrocyte band 7 integ	R.VQNATLAVANITNADSATR@.L	5.59	2.04	2.74	0.37
P54116_STOM_MOUSE	Stom	Erythrocyte band 7 integ	R.YLQTLTTIAAEK#.N	5.27	3.16	1.67	0.60
O70491_STRA6_MOUSE	Stra6	Stimulated by retinoic ac	R.K#AALTSAK#.A	15.38	1.47	10.46	0.10
Q9Z1Z2_STRAP_MOUSE	Strap	Serine-threonine kinase r	R.FSPDGELYASGSEDGTLR@.L	17.46	7.88	2.22	0.45
Q9Z1Z2_STRAP_MOUSE	Strap	Serine-threonine kinase r	K.GAVWGATLNK#.D	12.44	3.75	3.32	0.30
Q9Z1Z2_STRAP_MOUSE	Strap	Serine-threonine kinase r	K.IGFPETAEEELEEIASENSDSIYSSTPEVK#.A	8.76	4.27	2.05	0.49
Q9Z1Z2_STRAP_MOUSE	Strap	Serine-threonine kinase r	R.LWQTVVGK#.T	21.54	8.14	2.65	0.38
Q9Z1Z2_STRAP_MOUSE	Strap	Serine-threonine kinase r	K.TVDFTQDSNYLLTGGQDK#.L	17.85	6.62	2.70	0.37
Q9Z1Z2_STRAP_MOUSE	Strap	Serine-threonine kinase r	K.YDYNSGEELESYK#.G	19.49	5.78	3.37	0.30
Q8C079_STRP1_MOUSE	Strip1	Striatin-interacting prot	R.LLDGLEVTAR@.E	8.94	3.05	2.93	0.34
Q8C079_STRP1_MOUSE	Strip1	Striatin-interacting prot	R.TLLGLPPLPEDSIK#.V	8.47	3.04	2.79	0.36
O55106_STRN_MOUSE	Strn	Striatin OS=Mus muscul	K.EALK#EFDFLVTSEEGDNESR@.S	12.55	3.90	3.22	0.31
O55106_STRN_MOUSE	Strn	Striatin OS=Mus muscul	K.STSLDVEPIYTFR@.A	8.88	12.21	0.73	1.37
O55106_STRN_MOUSE	Strn	Striatin OS=Mus muscul	K.SVIDTSTIVR@.K	10.91	4.03	2.71	0.37
Q9ERG2_STRN3_MOUSE	Strn3	Striatin-3 OS=Mus muscu	R.IAFLQGER@.K	9.31	5.55	1.68	0.60
P58404_STRN4_MOUSE	Strn4	Striatin-4 OS=Mus muscu	K.ALIASAGADALAK#.V	13.25	7.25	1.83	0.55
P58404_STRN4_MOUSE	Strn4	Striatin-4 OS=Mus muscu	K.LQGILADLR@.D	9.32	4.93	1.89	0.53

P46978_STT3A_MOUSE	Stt3a	Dolichyl-diphosphooligc	R.IIFDDFR@.E	9.33	7.36	1.27	0.79
Q9WUD1_CHIP_MOUSE	Stub1	STIP1 homology and U bc	R.WNSIEERR@.I	4.68	2.34	2.00	0.50
Q9ER00_STX12_MOUSE	Stx12	Syntaxin-12 OS=Mus mus	K.ELGSLPLPLSASEQR@.Q	31.27	17.09	1.83	0.55
Q9ER00_STX12_MOUSE	Stx12	Syntaxin-12 OS=Mus mus	R.ISQATAQIK#.N	51.01	26.73	1.91	0.52
Q9ER00_STX12_MOUSE	Stx12	Syntaxin-12 OS=Mus mus	R.LM*NDFSSALNNFQVVQR@.K	14.99	5.62	2.67	0.38
Q9ER00_STX12_MOUSE	Stx12	Syntaxin-12 OS=Mus mus	R.LMNDFSSALNNFQVVQR@.K	2.55	1.72	1.48	0.68
Q9ER00_STX12_MOUSE	Stx12	Syntaxin-12 OS=Mus mus	K.NLM*SQLGTK#.Q	11.29	8.82	1.28	0.78
P70452_STX4_MOUSE	Stx4	Syntaxin-4 OS=Mus musc	K.AIEPQK#EEADENYNSVNTR@.M	7.33	3.48	2.11	0.47
P70452_STX4_MOUSE	Stx4	Syntaxin-4 OS=Mus musc	R.LGSPDDEFFQK#.V	20.07	3.47	5.79	0.17
P70452_STX4_MOUSE	Stx4	Syntaxin-4 OS=Mus musc	K.NILSSADYVER@.G	8.21	3.45	2.38	0.42
Q8K1E0_STX5_MOUSE	Stx5	Syntaxin-5 OS=Mus musc	R.APVSALPLAPNNLGGGPIILGAESR@.A	16.14	7.16	2.25	0.44
Q8K1E0_STX5_MOUSE	Stx5	Syntaxin-5 OS=Mus musc	K.LASM*SNDFK#.S	18.09	4.34	4.17	0.24
Q8K1E0_STX5_MOUSE	Stx5	Syntaxin-5 OS=Mus musc	K.QIAQLQDFVR@.A	15.59	3.98	3.91	0.26
Q9JKK1_STX6_MOUSE	Stx6	Syntaxin-6 OS=Mus musc	R.IGGELEEQAVM*LDDFSHELESTQSR@.L	2.32	2.62	0.89	1.13
O70439_STX7_MOUSE	Stx7	Syntaxin-7 OS=Mus musc	K.EFGSLPTTPSEQR@.Q	16.03	8.85	1.81	0.55
O70439_STX7_MOUSE	Stx7	Syntaxin-7 OS=Mus musc	R.LVAEFTTSLTNFQK#.A	9.24	4.80	1.92	0.52
O70439_STX7_MOUSE	Stx7	Syntaxin-7 OS=Mus musc	R.TLNQLGTPQDSPELR@.Q	10.02	8.39	1.19	0.84
P11031_TCP4_MOUSE	Sub1	Activated RNA polymeras	R.DDNM*FQIGK.M	2.76	20.05	0.14	7.26
P11031_TCP4_MOUSE	Sub1	Activated RNA polymeras	K.GISLNM*EQWSQLK.E	1.88	17.90	0.11	9.52
Q9Z2I9_SUCB1_MOUSE	Sucla2	Succinyl-CoA ligase [ADP-	K.INFDSNSAYR@.Q	14.58	5.99	2.44	0.41
Q9Z2I9_SUCB1_MOUSE	Sucla2	Succinyl-CoA ligase [ADP-	K.LYNLFLK#.Y	18.71	6.85	2.73	0.37
Q9Z2I8_SUCB2_MOUSE	Suclg2	Succinyl-CoA ligase [GDP	R.LEGTNVQEAQNILK#.S	7.90	1.99	3.97	0.25
Q8BR65_SDS3_MOUSE	Suds3	Sin3 histone deacetylase	R.QLQQLQEGTLQEYQK#.R	8.80	2.52	3.49	0.29
Q8BR65_SDS3_MOUSE	Suds3	Sin3 histone deacetylase	K.SQAIYLESK#.D	12.63	6.09	2.08	0.48
Q9CX34_SUGT1_MOUSE	Sugt1	Suppressor of G2 allele o	K.LEGQGDEPTPK#.Q	4.11	5.45	0.75	1.32
P61957_SUMO2_MOUSE	Sumo2	Small ubiquitin-related n	K.VAGQDGSVVQFK#.I	10.20	3.65	2.80	0.36
Q920B9_SP16H_MOUSE	Supt16h	FACT complex subunit SF	K.APGEQTVPALNLQNAFR.I	1.98	5.65	0.35	2.85
Q920B9_SP16H_MOUSE	Supt16h	FACT complex subunit SF	R.HTDVQFYTEVGEITTDLGK.H	2.88	2.84	1.01	0.99
Q920B9_SP16H_MOUSE	Supt16h	FACT complex subunit SF	R.NEGNIFPNPEATFVK.E	6.89	13.68	0.50	1.99
Q920B9_SP16H_MOUSE	Supt16h	FACT complex subunit SF	K.VEALTKEELEFEVPFR.D	5.81	12.19	0.48	2.10
Q920B9_SP16H_MOUSE	Supt16h	FACT complex subunit SF	R.NEGNIFPNPEATFVK#.E	7.97	8.91	0.89	1.12
Q920B9_SP16H_MOUSE	Supt16h	FACT complex subunit SF	K.NLGFGM*GIEFR.E	5.03	9.95	0.51	1.98
Q7TT00_SP20H_MOUSE	Supt20h	Transcription factor SPT2	R.LLDFLQK#.R	13.72	5.84	2.35	0.43
O55201_SPT5H_MOUSE	Supt5h	Transcription elongation	R.DVTNLTVGGFTPM*SPR@.I	7.06	5.05	1.40	0.72
O55201_SPT5H_MOUSE	Supt5h	Transcription elongation	R.GIYK#DDIAQVDYVEPSQNTISLK#.M	7.57	4.92	1.54	0.65
O55201_SPT5H_MOUSE	Supt5h	Transcription elongation	R.SLGGDVASDGDFLIFEGNR.Y	6.08	4.51	1.35	0.74
O55201_SPT5H_MOUSE	Supt5h	Transcription elongation	R.SSEAEEAEVEEDQR@.S	7.61	4.63	1.64	0.61
O55201_SPT5H_MOUSE	Supt5h	Transcription elongation	K.VR@DTYLDTQIVGQTGVIR@.S	7.89	4.73	1.67	0.60
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.AAEDDELEEEADWIYR@.N	14.17	6.53	2.17	0.46
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.ALDTTDM*ER@.L	25.46	11.52	2.21	0.45
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.ALQQFLYVQM*AK#.E	22.87	7.59	3.02	0.33
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.ETPETFYIGK#.L	29.15	11.99	2.43	0.41
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.FGLTPEQFGENLR@.D	25.82	9.91	2.61	0.38
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.FLLGYQPR@.G	42.20	13.54	3.12	0.32
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.FVEEEDDDEEEEEENLDDQDER@.G	10.18	2.57	3.96	0.25
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.GVEGYGNDQTYFEEIK#.Q	22.31	8.33	2.68	0.37
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.HETEQFPAEPLELAK#.D	26.68	11.38	2.34	0.43
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.IDTASLGDSTDSYIEVLDGSR@.V	29.17	11.27	2.59	0.39
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.IDTASLGDSTDSYIEVLDGSR@.V	13.01	4.29	3.03	0.33
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.IEYVTVTPEGFR@.Y	43.01	16.20	2.66	0.38
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.IK#EDGDEEGEGEEAEDEEQR@.G	4.71	1.32	3.57	0.28
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.IKEDGDEEGEGEEAEDEEQRGPELK.Q	47.67	19.98	2.39	0.42
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.K#FGLTPEQFGENLR@.D	10.63	1.64	6.47	0.15
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.K#LEELLIK#.T	35.63	14.74	2.42	0.41
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.K#M*AVDALEYDESAEDANPAGALEEILENPER@.L	19.88	10.08	1.97	0.51
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.LEDDDFDLIEENLGVK#.V	5.41	3.05	1.77	0.56
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.LK#DLDLDAFAEELER@.Q	74.29	23.89	3.11	0.32
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.M*AEQWLQEK#.E	8.82	55.46	0.16	6.29
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.M*AVDALEYDESAEDANPAGALEEILENPER@.L	14.27	5.61	2.54	0.39
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	K.M*QAYQYEQISADPDK#PLADGIR@.A	28.14	12.99	2.17	0.46
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.NQHFEVPFIAFYR@.K	34.71	15.17	2.29	0.44
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.QAVSLAR@.R	26.79	14.58	1.84	0.54
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.R@PQGESYDQAIR@.N	24.67	9.15	2.70	0.37
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.SIFEM*YEPSELESSHLTDQDNEIR@.A	14.28	5.52	2.59	0.39
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.SIFEMYEPSELESSHLTDQDNEIR@.A	3.18	2.84	1.12	0.89
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.SPNTEEIFNM*LTK#.E	29.55	12.63	2.34	0.43
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.TPASINATPANINLADLTR@.A	25.53	11.32	2.25	0.44
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.VAPYR@PDQQVEEDDDFM*DENQGK#.G	35.69	14.62	2.44	0.41
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.VLGIAFSSAR@.D	36.28	10.52	3.45	0.29
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.VNEVGVDVNR@.A	67.56	30.27	2.23	0.45
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.YM*VALQIAR@.E	9.64	3.50	2.75	0.36
Q62383_SPT6H_MOUSE	Supt6h	Transcription elongation	R.YVQPM*ASFAR@.D	23.87	9.69	2.46	0.41
Q9CZV5_ST65G_MOUSE	Supt7l	STAGA complex 65 subur	R.HSDPESDFYR@.G	9.11	2.76	3.30	0.30
Q9CZV5_ST65G_MOUSE	Supt7l	STAGA complex 65 subur	R.SLIATAQTQSQQQTEGVK#.A	6.69	2.92	2.30	0.44
Q64310_SURF4_MOUSE	Surf4	Surfeit locus protein 4 O	K.SM*FAGVPTM*R@.E	5.09	2.49	2.04	0.49
Q64310_SURF4_MOUSE	Surf4	Surfeit locus protein 4 O	R.M*WFQWSEQR@.D	13.31	84.42	0.16	6.34
Q64310_SURF4_MOUSE	Surf4	Surfeit locus protein 4 O	K.SM*FAGVPTM*R@.E	52.51	20.42	2.57	0.39
P70279_SURF6_MOUSE	Surf6	Surfeit locus protein 6 O	K.DTYLQDLAK#.K	9.73	3.44	2.83	0.35
P70279_SURF6_MOUSE	Surf6	Surfeit locus protein 6 O	K.ELQESGLIFNK#VEVTEEEPASK#.A	8.98	2.45	3.66	0.27
P70279_SURF6_MOUSE	Surf6	Surfeit locus protein 6 O	R.ESVFALDFLR@.Q	57.70	16.50	3.50	0.29
P70279_SURF6_MOUSE	Surf6	Surfeit locus protein 6 O	K.GLSSLGSPK#.D	26.80	7.50	3.57	0.28
P70279_SURF6_MOUSE	Surf6	Surfeit locus protein 6 O	K.GNLTPLTGR@.N	23.84	8.49	2.81	0.36
P70279_SURF6_MOUSE	Surf6	Surfeit locus protein 6 O	R.LLQEALK#.R	27.99	9.83	2.85	0.35
Q80U70_SUZ12_MOUSE	Suz12	Polycomb protein Suz12	K.ETLTTELQTR.K	8.41	6.14	1.37	0.73
Q80U70_SUZ12_MOUSE	Suz12	Polycomb protein Suz12	K.HGGGGGGGSGPSAGSGGGGFGGSAAAVAAAASGGK.S	3.17	2.83	1.12	0.90
Q80U70_SUZ12_MOUSE	Suz12	Polycomb protein Suz12	K.ASM*SEFLESEDGEVEQQR@.T	3.76	1.66	2.26	0.44
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	K.EFGETTSEQTEVAAR@.K	7.09	3.85	1.84	0.54
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	R.GAFEEEEEPSYPILGR@.V	4.87	2.42	2.01	0.50
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	K.NALTVAAEDSGVQTR@.G	6.49	2.53	2.57	0.39
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	K.VAGIQETVLTVTGK#.S	5.76	4.62	1.25	0.80
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	R.DDLLQEYTEQR@.L	10.53	4.72	2.23	0.45
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	K.EFGETTSEQTEVAAR.K	15.97	7.31	2.18	0.46
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	R.ESAEPGEPDSSTLSLAEK#.L	10.49	4.46	2.35	0.43
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	R.GAANDSTQFTVAGR.M	10.69	6.58	1.62	0.62
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	R.GAFEEEEEPSYPILGR@.V	8.44	4.59	1.84	0.54
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	K.GTSALM*TVELDEER@.G	10.30	4.27	2.41	0.41
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	K.M*SSNSNFSEVTLAGLASR@.E	5.64	2.52	2.24	0.45
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	K.NALTVAAEDSGVQTR@.G	14.29	7.14	2.00	0.50
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	K.VAGIQETVLTVTGK#.S	25.27	12.49	2.02	0.49
Q8K4L3_SVIL_MOUSE	Svil	Supervillin OS=Mus musc	R.YQTQPVTLGEVEQVQSGK#.L	6.89	4.61	1.50	0.67
Q6A028_SWP70_MOUSE	Swap70	Switch-associated protei	K.AIWHAFTALDLDR@.S	8.97	3.24	2.77	0.36
Q6A028_SWP70_MOUSE	Swap70	Switch-associated protei	K.LLAEQEELER@.Q	18.51	7.41	2.50	0.40
Q6A028_SWP70_MOUSE	Swap70	Switch-associated protei	K.LQEALEDER.Q	19.24	6.79	2.84	0.35

Q6A028_SWP70_MOUSE	Swap70	Switch-associated protei	R.QQM*EEQVAQK#.S	6.10	3.58	1.70	0.59
Q6A028_SWP70_MOUSE	Swap70	Switch-associated protei	K.SPLLITEDDAFK#.V	11.44	4.98	2.30	0.44
A0A0A0MQ99_A0A0A0MQ99_MOUSE	Swi5	DNA repair protein SWI5	R.SPQR@PFPM*IDENNDVSEEALSSDIK#.K	2.72	3.64	0.75	1.34
Q62209_SYCP1_MOUSE	Sycp1	Synaptonemal complex p	K.TISQLTEVK#.E	8.17	6.76	1.21	0.83
Q9D198_SYF2_MOUSE	Syf2	Pre-mRNA-splicing factor	R.K#LNHQEVVEEDK#R@.L	4.18	3.94	1.06	0.94
Q9D198_SYF2_MOUSE	Syf2	Pre-mRNA-splicing factor	K.LLEISAEDAER@.W	23.86	11.56	2.06	0.48
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	K.FVEGLIVTLSPR@.M	9.26	2.76	3.35	0.30
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.R@QEHDISLDR@.I	23.52	7.05	3.34	0.30
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.VVDLLNQAALITNDSK#.I	19.11	3.16	6.05	0.17
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.VVDLLNQAALITNDSK#.I	14.17	4.54	3.12	0.32
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	K.AEVLSFILEDVR@.A	8.05	1.46	5.53	0.18
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.AYLGM*STLGDLIFK#.R	14.55	4.44	3.28	0.30
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	K.FVEGLIVTLSPR@.M	9.96	4.06	2.45	0.41
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	K.ILASLVTQFDSGFK#.A	5.68	1.26	4.50	0.22
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.LSDVLK#PLTDAQVEAM*K#.L	22.29	5.50	4.06	0.25
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.TVIQSLTM*YPR@.L	9.29	2.50	3.71	0.27
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.VVDLLNQAALITNDSK#.I	12.95	3.58	3.62	0.28
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	K.AAVEQLLK#.F	31.59	5.74	5.51	0.18
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	K.AEVLSFILEDVR@.A	17.59	3.58	4.91	0.20
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.AYLGM*STLGDLIFK#.R	36.68	9.24	3.97	0.25
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	K.FVEGLIVTLSPR@.M	19.75	6.49	3.04	0.33
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	K.ILASLVTQFDSGFK#.A	12.44	4.12	3.02	0.33
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.LGGFVM*NILAR@.L	19.36	5.79	3.34	0.30
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.LM*ATQM*TAAGLGPGVEQTK#.Q	8.16	2.75	2.97	0.34
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.LSDVLK#PLTDAQVEAM*K#.L	51.55	16.37	3.15	0.32
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.R@QEHDISLDR@.I	33.27	9.84	3.38	0.30
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.SPQNLSHAVEEALK#.T	27.07	14.49	1.87	0.54
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.SQALLFIK#.R	16.45	8.61	1.91	0.52
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.TVIQSLTM*YPR@.L	21.92	8.89	2.47	0.41
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	R.VVDLLNQAALITNDSK#.I	39.56	12.11	3.27	0.31
Q80X82_SYMPK_MOUSE	Sympk	Symplekin OS=Mus musc	K.VVLEAPLITESALEVIR@.K	31.21	10.16	3.07	0.33
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	R.LFVGSIPK.S	4.39	6.90	0.64	1.57
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	R.NLANTVTEEILEK.S	3.20	24.85	0.13	7.77
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	R.TGYTLDVTTGQR.K	6.98	7.69	0.91	1.10
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	K.AGPIWDLR.L	14.14	16.62	0.85	1.18
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	R.AIEALK#EFNEDGALAVLQQFK#.D	27.56	23.39	1.18	0.85
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	R.KYGGPPPDSVYSGQQPSVGTEIFVGK.I	2.57	3.32	0.77	1.30
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	R.LFVGSIPK.S	23.37	28.87	0.81	1.24
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	R.LM*M*DPLTGLNR@.G	8.42	7.48	1.13	0.89
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	R.NLANTVTEEILEK#.S	35.65	29.52	1.21	0.83
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	R.TGYTLDVTTGQR.K	22.23	20.18	1.10	0.91
Q7TMK9_HNRPQ_MOUSE	Syncrip	Heterogeneous nuclear ri	K.VAEKLDEIYVAGLVAHSDLDER.A	12.17	10.44	1.17	0.86
Q6ZWQ0_SYNE2_MOUSE	Syne2	Nesprin-2 OS=Mus muscu	K.LLEPEDVDVVNPDEK#.S	6.91	4.48	1.54	0.65
Q6ZWQ0_SYNE2_MOUSE	Syne2	Nesprin-2 OS=Mus muscu	R.ADVLNDAYDSANR@YDELVAGALR@.I	6.81	2.55	2.67	0.37
Q6ZWQ0_SYNE2_MOUSE	Syne2	Nesprin-2 OS=Mus muscu	K.ASQQQLQDTESALSAHLQELTNAYK#.D	5.47	2.70	2.03	0.49
Q6ZWQ0_SYNE2_MOUSE	Syne2	Nesprin-2 OS=Mus muscu	R.EAIILETLQEDLPEISK#.T	9.37	4.83	1.94	0.52
Q6ZWQ0_SYNE2_MOUSE	Syne2	Nesprin-2 OS=Mus muscu	K.LLENVTQEQNELLK#.V	4.34	3.84	1.13	0.89
Q6ZWQ0_SYNE2_MOUSE	Syne2	Nesprin-2 OS=Mus muscu	K.LLEPEDVDVVNPDEK#.S	8.95	5.10	1.75	0.57
Q6ZWQ0_SYNE2_MOUSE	Syne2	Nesprin-2 OS=Mus muscu	R.VADIQSLLQSNEK#PLELQVM*ESSVLSK#.M	2.00	1.96	1.02	0.98
Q6ZWQ0_SYNE2_MOUSE	Syne2	Nesprin-2 OS=Mus muscu	R.VFEQISTSFPNLAPEGHPER@.A	8.01	9.97	0.80	1.24
O55100_SNG1_MOUSE	Syngr1	Synaptogyrin-1 OS=Mus r	K.AGGAFDPYTLVR@.Q	14.95	3.11	4.81	0.21
O55101_SNG2_MOUSE	Syngr2	Synaptogyrin-2 OS=Mus r	R.FLSQPQVVTR@.L	35.77	14.08	2.54	0.39
O55101_SNG2_MOUSE	Syngr2	Synaptogyrin-2 OS=Mus r	R.FLSQPQVVTR@.L	29.51	12.80	2.30	0.43
Q8R191_SNG3_MOUSE	Syngr3	Synaptogyrin-3 OS=Mus r	R.AGAAFDPVSFAR@.R	34.85	15.57	2.24	0.45
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	R.DHGEVGM*EEEPFALGAEASNFQQEPIAR@.D	7.37	4.72	1.56	0.64
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	R.GAAFSPIPR.S	18.41	9.91	1.86	0.54
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	R.GVAGHIM*EGYSEEASLLR@.H	6.32	4.04	1.57	0.64
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	R.LVDLEEEGTSQSR@.A	12.00	6.85	1.75	0.57
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	R.R@PLGNFTPPPTYAETLSTAPVASR@.V	22.65	11.76	1.93	0.52
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	R.SPTDSDVSLDSEDSGLK#.S	4.73	4.98	0.95	1.05
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	R.SSILLIDK#.V	22.00	9.24	2.38	0.42
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	R.TARPFGIQSPGTSQIEQSPM*M*GR.R	11.73	7.64	1.54	0.65
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	K.VASEEEEVPLVVYLK#.E	20.60	8.62	2.39	0.42
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	K.VTPNPDLLDLVQTADEK#.R	28.09	20.53	1.37	0.73
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	R.LVDLEEEGTSQSR@.A	7.06	3.18	2.22	0.45
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	K.VASEEEEVPLVVYLK#.E	5.97	3.24	1.84	0.54
E9Q3E2_E9Q3E2_MOUSE	Synpo	Synaptopodin OS=Mus m	K.VTPNPDLLDLVQTADEK#.R	7.79	5.47	1.42	0.70
Q5SV85_SYNRG_MOUSE	Synrg	Synergin gamma OS=Mus	R.ELEQTTDSK#PLGESFAEFR@.S	9.90	2.07	4.78	0.21
Q5SV85_SYNRG_MOUSE	Synrg	Synergin gamma OS=Mus	K.SVSTR@PQPAGSAAASAALASTK#.T	11.66	2.60	4.49	0.22
Q5SV85_SYNRG_MOUSE	Synrg	Synergin gamma OS=Mus	K.ILETTM*TPTGIDTAK#.L	5.65	3.27	1.73	0.58
Q5SV85_SYNRG_MOUSE	Synrg	Synergin gamma OS=Mus	K.SVSTR@PQPAGSAAASAALASTK#.T	13.53	4.99	2.71	0.37
Q99LM9_TADA1_MOUSE	Tada1	Transcriptional adapter 1	K.YAFGSNVTPQPYLK#.N	11.32	4.64	2.44	0.41
Q8CHV6_TAD2A_MOUSE	Tada2a	Transcriptional adapter 2	K.HFINNPLFASTLLNLK#.Q	7.09	3.42	2.08	0.48
D3Z4Z0_D3Z4Z0_MOUSE	Tada2b	MCG49644 OS=Mus mus	R.DYNLVPAFLGK#.D	19.50	6.96	2.80	0.36
Q8R0L9_TADA3_MOUSE	Tada3	Transcriptional adapter 3	K.ESGADGASTSPR@.N	4.67	5.46	0.86	1.17
Q8R0L9_TADA3_MOUSE	Tada3	Transcriptional adapter 3	K.GLIGPLTELDTK#.D	17.41	8.03	2.17	0.46
Q8R0L9_TADA3_MOUSE	Tada3	Transcriptional adapter 3	R.IK#EELIAQGLLESEDR@PAEDSEDEVLAELR@.K	32.41	7.48	4.33	0.23
Q8R0L9_TADA3_MOUSE	Tada3	Transcriptional adapter 3	K.IQEYEFTDDPIDVPR@.I	23.15	9.14	2.53	0.39
Q8R0L9_TADA3_MOUSE	Tada3	Transcriptional adapter 3	R.WAQEDLLEEQK#.D	8.47	2.66	3.19	0.31
Q8R0L9_TADA3_MOUSE	Tada3	Transcriptional adapter 3	R.YTAVLAR@.S	39.10	12.39	3.16	0.32
Q80UV9_TAF1_MOUSE	Taf1	Transcription initiation f	R.GLEDSNISYGSYEEPDPK#.S	6.20	1.97	3.15	0.32
Q80UV9_TAF1_MOUSE	Taf1	Transcription initiation f	R.IFDLQNK#.V	15.97	5.28	3.03	0.33
Q80UV9_TAF1_MOUSE	Taf1	Transcription initiation f	K.M*PESDFLIIR@.T	21.22	4.83	4.39	0.23
Q80UV9_TAF1_MOUSE	Taf1	Transcription initiation f	K.QLIESADEVR@.R	9.18	5.35	1.71	0.58
Q80UV9_TAF1_MOUSE	Taf1	Transcription initiation f	K.SFFAPEEENEEDFQM*K#.I	6.21	2.69	2.31	0.43
Q80UV9_TAF1_MOUSE	Taf1	Transcription initiation f	R.SR@EDAVDYSDINEVAEDESR@.R	10.68	3.41	3.14	0.32
Q80UV9_TAF1_MOUSE	Taf1	Transcription initiation f	R.TGM*DSNWWVLK#.S	6.62	1.95	3.40	0.29
Q80UV9_TAF1_MOUSE	Taf1	Transcription initiation f	R.WEVIDVVR@.T	15.14	6.24	2.42	0.41
Q80UV9_TAF1_MOUSE	Taf1	Transcription initiation f	K.YSFGALSQPGPHSVQPLLK#.H	19.22	9.35	2.06	0.49
Q8K0H5_TAF10_MOUSE	Taf10	Transcription initiation f	K.ASPAGTAGGPVAGVATAGTGPVAAR.A	19.96	6.90	2.89	0.35
Q8K0H5_TAF10_MOUSE	Taf10	Transcription initiation f	K.K#PHYFT.-	4.89	1.72	2.84	0.35
P61216_TAF13_MOUSE	Taf13	Transcription initiation f	R.VQVEDIVFLIR@.K	12.16	3.78	3.22	0.31
Q5HZG4_TAF3_MOUSE	Taf3	Transcription initiation f	K.IK#VEPVIPAPSPVIPR@.L	8.83	2.34	3.77	0.27
Q5HZG4_TAF3_MOUSE	Taf3	Transcription initiation f	K.TIDDSIDAVIAR@.A	8.44	3.81	2.21	0.45
E9QAP7_E9QAP7_MOUSE	Taf4a	Protein Taf4a OS=Mus mu	K.ALSTVSAQAAAAQK#.N	14.05	2.82	4.98	0.20
E9QAP7_E9QAP7_MOUSE	Taf4a	Protein Taf4a OS=Mus mu	R.DANLTALAAIGPR@.K	12.33	2.21	5.57	0.18
E9QAP7_E9QAP7_MOUSE	Taf4a	Protein Taf4a OS=Mus mu	K.DLVQNLLDGK#IEAEDFTSR@.L	12.46	4.37	2.85	0.35
E9QAP7_E9QAP7_MOUSE	Taf4a	Protein Taf4a OS=Mus mu	R.IM*LTTPQQIQLNQLQPVPVVK#PTVLPGTK#.A	4.53	2.13	2.12	0.47
E9QAP7_E9QAP7_MOUSE	Taf4a	Protein Taf4a OS=Mus mu	R.SPGVQPQLVLGGSAQPASLGTATAVQTGTPQR@.T	4.23	3.28	1.29	0.77
Q8C092_TAF5_MOUSE	Taf5	Transcription initiation f	K.AFEDLETDDFTTATGHINLPENSQELLLGTYM*TK#.S	2.78	1.43	1.94	0.52
Q8C092_TAF5_MOUSE	Taf5	Transcription initiation f	R.DGEILASGSM*DNTVR@.L	9.50	3.17	2.99	0.33
Q8C092_TAF5_MOUSE	Taf5	Transcription initiation f	R.FLATGATDGR@.V	21.48	4.44	4.84	0.21
Q8C092_TAF5_MOUSE	Taf5	Transcription initiation f	K.ILYGHSGPVYGASFSPDR@.N	8.42	3.21	2.62	0.38

Q8C092_TAF5_MOUSE	Taf5	Transcription initiation f	R.LLEEAVAGSGAPGELDGAGAEAASALLSR@.V	21.27	4.47	4.76	0.21
Q8C092_TAF5_MOUSE	Taf5	Transcription initiation f	R.LLEEAVAGSGAPGELDGAGAEAASALLSR@.V	9.93	1.83	5.41	0.18
Q91WQ5_TAF5L_MOUSE	Taf5l	TAF5-like RNA polymeras	K.LWDLASGTLFK#.E	8.05	3.77	2.14	0.47
Q91WQ5_TAF5L_MOUSE	Taf5l	TAF5-like RNA polymeras	R.SFLTDSDSQYSR@.E	7.52	2.22	3.39	0.29
Q91WQ5_TAF5L_MOUSE	Taf5l	TAF5-like RNA polymeras	K.YLASAGEDQR@.L	7.22	3.70	1.95	0.51
Q91WQ5_TAF5L_MOUSE	Taf5l	TAF5-like RNA polymeras	R.SFLTDSDSQYSR@.E	6.86	2.25	3.04	0.33
Q91WQ5_TAF5L_MOUSE	Taf5l	TAF5-like RNA polymeras	K.YLASAGEDQR@.L	7.18	3.95	1.82	0.55
Q62311_TAF6_MOUSE	Taf6	Transcription initiation f	R.AQAALQAQQVNR@.T	7.38	1.98	3.72	0.27
Q62311_TAF6_MOUSE	Taf6	Transcription initiation f	R.SVLDGPVLSNIDR@.I	6.73	3.39	1.99	0.50
Q62311_TAF6_MOUSE	Taf6	Transcription initiation f	R.AQAALQAQQVNR@.T	8.55	2.89	2.96	0.34
Q62311_TAF6_MOUSE	Taf6	Transcription initiation f	R.SVLDGPVLSNIDR@.I	9.55	2.66	3.59	0.28
Q8R2K4_TAF6L_MOUSE	Taf6l	TAF6-like RNA polymeras	R.LFQTAFPAPYGPSPASR@.Y	5.32	2.69	1.98	0.51
Q8R2K4_TAF6L_MOUSE	Taf6l	TAF6-like RNA polymeras	R.LFQTAFPAPYGPSPASR@.Y	6.95	2.37	2.93	0.34
Q8R2K4_TAF6L_MOUSE	Taf6l	TAF6-like RNA polymeras	K.VALQDLQTNSK#.I	7.87	1.93	4.08	0.24
Q9R1C0_TAF7_MOUSE	Taf7	Transcription initiation f	R.EK#EQLSSLQEELESLLEK#.-	22.70	4.95	4.59	0.22
Q9R1C0_TAF7_MOUSE	Taf7	Transcription initiation f	R.FQAVLDELK#.Q	6.35	1.22	5.19	0.19
Q9R1C0_TAF7_MOUSE	Taf7	Transcription initiation f	R.LLSTDAEAVSTR@.W	28.65	8.16	3.51	0.28
Q9EQH4_TAF8_MOUSE	Taf8	Transcription initiation f	R.M*VITAPPVTNQPVTPK#.A	6.52	2.59	2.52	0.40
Q9EQH4_TAF8_MOUSE	Taf8	Transcription initiation f	R.TLQVVVSSLLTEAGFESAEK#.A	16.03	4.30	3.73	0.27
Q8VI33_TAF9_MOUSE	Taf9	Transcription initiation f	R.ADQSFTSPPPR@.D	18.29	6.88	2.66	0.38
Q8VI33_TAF9_MOUSE	Taf9	Transcription initiation f	K.ATVDADDVR@.L	21.46	7.98	2.69	0.37
Q8VI33_TAF9_MOUSE	Taf9	Transcription initiation f	R.DFLLDIAR@.Q	30.76	10.57	2.91	0.34
Q8VI33_TAF9_MOUSE	Taf9	Transcription initiation f	R.FTVQM*PASQSPAVK#.A	13.39	3.97	3.38	0.30
Q8VI33_TAF9_MOUSE	Taf9	Transcription initiation f	R.LSVGSVSSR@PSTPTLGTPTPQTM*SVSTK#.V	9.38	4.59	2.05	0.49
Q8VI33_TAF9_MOUSE	Taf9	Transcription initiation f	R.VINQM*LEFAFR@.Y	7.64	2.42	3.16	0.32
Q8VI33_TAF9_MOUSE	Taf9	Transcription initiation f	R.VINQMLEFAFR@.Y	11.16	2.69	4.15	0.24
Q8VI33_TAF9_MOUSE	Taf9	Transcription initiation f	R.LSVGSVSSR@PSTPTLGTPTPQTM*SVSTK#.V	5.57	2.54	2.19	0.46
Q8VI33_TAF9_MOUSE	Taf9	Transcription initiation f	R.YVTTILDDAK#.I	5.68	1.27	4.46	0.22
P70347_TANK_MOUSE	Tank	TRAF family member-ass	R.IR@EQQEQLSFQQNLIDR@.L	4.95	2.21	2.24	0.45
Q5F2E8_TAOK1_MOUSE	Taok1	Serine/threonine-protei	K.AGNILLTEPGQVK#.L	9.92	1.17	8.49	0.12
P21958_TAP1_MOUSE	Tap1	Antigen peptide transpo	R.K#PLLLILDDATSALDAGNQLR@.V	14.15	12.36	1.14	0.87
P21958_TAP1_MOUSE	Tap1	Antigen peptide transpo	R.SFANEEGEAQK#.F	6.37	4.23	1.50	0.67
P21958_TAP1_MOUSE	Tap1	Antigen peptide transpo	K.STQVALEALSAM*PTVR.S	3.12	2.30	1.36	0.74
P21958_TAP1_MOUSE	Tap1	Antigen peptide transpo	K.GLVEFQDVSFAYPNQPK#.V	6.68	2.76	2.42	0.41
P21958_TAP1_MOUSE	Tap1	Antigen peptide transpo	R.K#PLLLILDDATSALDAGNQLR@.V	17.63	13.88	1.27	0.79
Q9R233_TPSN_MOUSE	Tapbp	Tapasin OS=Mus muscul	K.ATAASLTIPR@.N	13.28	6.53	2.03	0.49
Q9R233_TPSN_MOUSE	Tapbp	Tapasin OS=Mus muscul	R.FAYAPSALEGSPSLDAGPPPFGLEWR@.R	7.04	5.91	1.19	0.84
Q9R233_TPSN_MOUSE	Tapbp	Tapasin OS=Mus muscul	K.ATAASLTIPR.N	16.98	15.90	1.07	0.94
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.AFAFVTFADDK#.V	116.33	129.67	0.90	1.11
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.DYFSTFGEVLM*VQVK#.K	54.37	56.77	0.96	1.04
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.DYFSTFGEVLM*VQVK#.K	18.27	17.77	1.03	0.97
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.DYFSTFGEVLMVQVK.K	33.69	32.66	1.03	0.97
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.FGGNPGGFGNQGGFGNSR@.G	640.20	685.92	0.93	1.07
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.FTEYETQVK#.V	680.07	677.17	1.00	1.00
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.HMIDGR.W	22.51	23.91	0.94	1.06
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.K#M*DETDASSAVK#.V	281.11	299.43	0.94	1.07
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.LVEGILHAPDAGWGNLVYVVNYPK#.D	496.52	442.26	1.12	0.89
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.M*DETDASSAVK#.V	56.46	55.36	1.02	0.98
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.MDETDASSAVK.V	58.14	66.86	0.87	1.15
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.TSDLIVLGLPWK#.T	998.47	1058.62	0.94	1.06
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.TTEQDLK#DYFSTFGEVLM*VQVK#.K	227.50	219.21	1.04	0.96
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.TTEQDLKDYFSTFGEVLM*VQVK.K	3.70	4.73	0.78	1.28
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.TTEQDLKDYFSTFGEVLMVQVK.K	149.16	158.60	0.94	1.06
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.FGGNPGGFGNQGGFGNSR@.G	13.40	19.60	0.68	1.46
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.LVEGILHAPDAGWGNLVYVVNYPK.D	1.58	3.00	0.53	1.90
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.TSDLIVLGLPWK.T	5.32	8.91	0.60	1.67
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.AFAFVTFADDK.V	10.32	10.42	0.99	1.01
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.FGGNPGGFGNQGGFGNSR.G	30.62	29.35	1.04	0.96
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.FTEYETQVK.V	34.34	34.59	0.99	1.01
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.KM*DETDASSAVK.V	10.12	15.54	0.65	1.54
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.LVEGILHAPDAGWGNLVYVVNYPK#.D	32.96	35.14	0.94	1.07
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.QSPDEPLR@.S	22.64	34.29	0.66	1.51
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.TSDLIVLGLPWK#.T	46.08	49.21	0.94	1.07
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.TTEQDLKDYFSTFGEVLM*VQVK.K	7.63	17.13	0.45	2.24
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.FGGNPGGFGNQGGFGNSR@.G	16.25	17.14	0.95	1.05
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.FTEYETQVK.V	16.99	18.59	0.91	1.09
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	R.KM*DETDASSAVK.V	8.30	6.91	1.20	0.83
Q921F2_TADBP_MOUSE	Tardbp	TAR DNA-binding protei	K.TSDLIVLGLPWK#.T	29.26	28.41	1.03	0.97
Q60949_TBCD1_MOUSE	Tbc1d1	TBC1 domain family me	K.AILQQILLLR@.M	11.30	4.10	2.76	0.36
Q60949_TBCD1_MOUSE	Tbc1d1	TBC1 domain family me	R.GLQDHSASVDLDSSTSSTLSNTSK#.E	5.48	1.75	3.13	0.32
Q60949_TBCD1_MOUSE	Tbc1d1	TBC1 domain family me	R.SLTESLESILSR@.G	7.63	3.26	2.34	0.43
P58802_TB10A_MOUSE	Tbc1d10a	TBC1 domain family me	K.IM*QEAFLVQEVIELPVTER@.Q	12.39	4.60	2.69	0.37
Q9CXF4_TBC15_MOUSE	Tbc1d15	TBC1 domain family me	R.EFSFLDILR@.L	10.82	2.01	5.38	0.19
Q9CXF4_TBC15_MOUSE	Tbc1d15	TBC1 domain family me	K.INQQEEPGFEVITR@.I	6.24	2.49	2.50	0.40
Q9CXF4_TBC15_MOUSE	Tbc1d15	TBC1 domain family me	K.VTNYIFDSLR@.G	12.14	3.79	3.20	0.31
Q9CXF4_TBC15_MOUSE	Tbc1d15	TBC1 domain family me	K.VTNYIFDSLR@.G	11.43	4.41	2.59	0.39
Q8BYJ6_TBCD4_MOUSE	Tbc1d4	TBC1 domain family me	K.EILIAWDKK.L	6.18	4.61	1.34	0.75
Q80XQ2_TBCD5_MOUSE	Tbc1d5	TBC1 domain family me	R.GAFSGQAQPLLTLR@.S	7.77	2.93	2.66	0.38
Q80XQ2_TBCD5_MOUSE	Tbc1d5	TBC1 domain family me	K.TISSSPSIESLPGGR@.E	8.71	4.40	1.98	0.50
Q5SVR0_TBC9B_MOUSE	Tbc1d9b	TBC1 domain family me	R.VVGALVDQGIFEELTR@.D	6.49	2.85	2.28	0.44
Q5SVR0_TBC9B_MOUSE	Tbc1d9b	TBC1 domain family me	K.ADSSSVLPSPLSISTK#.S	5.76	2.07	2.78	0.36
Q5SVR0_TBC9B_MOUSE	Tbc1d9b	TBC1 domain family me	R.ANPFFVLQR@.R	9.27	4.12	2.25	0.44
Q9WUN2_TBK1_MOUSE	Tbk1	Serine/threonine-protei	R.LSSSQGTIESSLQDISSR@.L	7.26	1.37	5.29	0.19
Q9WUN2_TBK1_MOUSE	Tbk1	Serine/threonine-protei	R.FGSLTM*DGGLR@.N	11.42	3.81	3.00	0.33
Q9WUN2_TBK1_MOUSE	Tbk1	Serine/threonine-protei	R.LSSSQGTIESSLQDISSR@.L	13.09	2.90	4.51	0.22
Q9WUN2_TBK1_MOUSE	Tbk1	Serine/threonine-protei	K.VNLEAAELGEISDIHTK#.L	18.49	4.89	3.78	0.26
Q9QXE7_TBL1X_MOUSE	Tbl1x	F-box-like/WD repeat-co	K.HQEPVYSVAFSPDGK#.Y	7.44	3.81	1.95	0.51
Q9QXE7_TBL1X_MOUSE	Tbl1x	F-box-like/WD repeat-co	K.LAQQQANAAAAAAAAAATATSTAATTPAAAAQQNPPK#.N	7.05	4.87	1.45	0.69
Q8BHJ5_TBL1R_MOUSE	Tbl1xr1	F-box-like/WD repeat-co	K.GPIFALK#.W	26.22	13.82	1.90	0.53
Q8BHJ5_TBL1R_MOUSE	Tbl1xr1	F-box-like/WD repeat-co	K.LAQQHAAAAAAAAAATNQQGSAK#.N	8.75	2.34	3.74	0.27
Q8BHJ5_TBL1R_MOUSE	Tbl1xr1	F-box-like/WD repeat-co	K.GPIFALK#.W	14.43	2.25	6.40	0.16
Q8C4J7_TBL3_MOUSE	Tbl3	Transducin beta-like pro	K.VNILDVASGALLR@.S	9.42	4.64	2.03	0.49
Q8C4J7_TBL3_MOUSE	Tbl3	Transducin beta-like pro	K.SSGLHFLTAGDQGILR@.V	10.90	5.23	2.08	0.48
Q8C4J7_TBL3_MOUSE	Tbl3	Transducin beta-like pro	K.STAADSGPVLLQAQTTR@.R	5.05	2.36	2.14	0.47
Q8C4J7_TBL3_MOUSE	Tbl3	Transducin beta-like pro	R.TVPVFESVEASVLLPEQPAPALGVK#.S	10.20	6.59	1.55	0.65
Q8C4J7_TBL3_MOUSE	Tbl3	Transducin beta-like pro	K.VNILDVASGALLR@.S	16.00	7.97	2.01	0.50
P29037_TBP_MOUSE	Tbp	TATA-box-binding protei	R.AEIYEAFENIYPILK#.G	9.57	4.72	2.03	0.49
P29037_TBP_MOUSE	Tbp	TATA-box-binding protei	R.AEIYEAFENIYPILK#.G	8.29	3.93	2.11	0.47
O70306_TBX15_MOUSE	Tbx15	T-box transcription facto	K.TFNFPETVFTTVTAYQNQQITR@.L	6.86	4.59	1.50	0.67
O70306_TBX15_MOUSE	Tbx15	T-box transcription facto	K.TFNFPETVFTTVTAYQNQQITR@.L	13.58	6.69	2.03	0.49
P83940_ELOC_MOUSE	Tceb1	Transcription elongation	K.AM*LSGPGQFAENETNEVNFR@.E	14.51	4.80	3.02	0.33
P62869_ELOB_MOUSE	Tceb2	Transcription elongation	R.ADDTFEALR@.I	44.77	16.56	2.70	0.37
P62869_ELOB_MOUSE	Tceb2	Transcription elongation	R.IVEGILK#.R	75.01	23.38	3.21	0.31

P62869_ELOB_MOUSE	Tceb2	Transcription elongation	K.TTIFTDAK#.E	18.52	5.48	3.38	0.30
Q8CGF7_TCRG1_MOUSE	Tcerg1	Transcription elongation	R.VFFYNPTTR@.L	11.42	6.90	1.65	0.60
Q9EPQ8_TCF20_MOUSE	Tcf20	Transcription factor 20 C	R.LYGLQEALEIAR.E	5.51	12.70	0.43	2.31
Q9EPQ8_TCF20_MOUSE	Tcf20	Transcription factor 20 C	R.GNASPGAAAHDSISDYGPQDSR@.S	13.25	4.20	3.16	0.32
Q9EPQ8_TCF20_MOUSE	Tcf20	Transcription factor 20 C	R.LNPSLSQSVILPGGLVSM*ETK#.L	5.65	1.65	3.44	0.29
Q9EPQ8_TCF20_MOUSE	Tcf20	Transcription factor 20 C	R.LYGLQEALEIAR@.E	10.12	5.44	1.86	0.54
Q9EPQ8_TCF20_MOUSE	Tcf20	Transcription factor 20 C	K.QAVPIVEPQEPEIK#.L	7.17	4.50	1.59	0.63
Q9EPQ8_TCF20_MOUSE	Tcf20	Transcription factor 20 C	R.SASANSAEAGGDTVTLDDILSLK#.S	3.43	2.84	1.21	0.83
Q9EPQ8_TCF20_MOUSE	Tcf20	Transcription factor 20 C	K.SQSGQIK#EEDFEQSK#.S	13.45	5.99	2.25	0.45
Q9EPQ8_TCF20_MOUSE	Tcf20	Transcription factor 20 C	R.NVSGYPQYPSGQEK#.G	3.71	1.37	2.72	0.37
Q9JHF5_Q9JHF5_MOUSE	Tcirg1	A3 subunit of vacuolar-a	R.DLNESVSAFQR@.R	8.99	2.71	3.31	0.30
O08784_TCOF_MOUSE	Tcof1	Treacle protein OS=Mus r	K.VLTELLEQER.L	9.87	16.12	0.61	1.63
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.AFHNEAQVNPER@.K	43.98	22.88	1.92	0.52
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.EQLAIAEFAR@.S	111.37	54.20	2.05	0.49
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.FATEAAITILR@.I	64.73	32.24	2.01	0.50
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.ILATGANVILTTGGIDDM*YLK#.Y	15.34	7.19	2.13	0.47
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.LGVQVVITDPEKLDQIR.Q	66.64	39.11	1.70	0.59
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.M*LVDDIGDVTITNDGATILK#.L	20.31	10.26	1.98	0.51
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.M*LVDDIGDVTITNDGATILK#.L	15.35	8.04	1.91	0.52
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.NADELVK#.Q	56.13	29.83	1.88	0.53
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.SLLVIPNTLAVNAAQDSTDLVAK#.L	36.02	18.30	1.97	0.51
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.SQNVM*AAASIANIVK#.S	35.56	18.05	1.97	0.51
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.SSFGPVGLDK#.M	60.18	29.84	2.02	0.50
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.TSASIILR@.G	106.75	53.04	2.01	0.50
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.YFVEAGAM*AVR@.R	50.60	33.11	1.53	0.65
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.YINENLIINTDELGR@.D	17.57	6.12	2.87	0.35
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.YPVNSVNILK#.A	79.31	39.60	2.00	0.50
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.AFHNEAQVNPER@.K	52.70	18.16	2.90	0.34
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.EQLAIAEFAR@.S	130.98	49.05	2.67	0.37
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.FATEAAITILR@.I	146.71	54.08	2.71	0.37
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.ILATGANVILTTGGIDDM*YLK#.Y	44.12	23.05	1.91	0.52
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.LGVQVVITDPEK#LDQIR@.Q	108.64	49.55	2.19	0.46
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.LLEVEHPAAK#.V	133.83	69.65	1.92	0.52
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.M*LVDDIGDVTITNDGATILK#.L	28.44	8.15	3.49	0.29
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.NADELVK#.Q	41.57	19.99	2.08	0.48
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.QAGVFEPTIVK#.V	89.00	39.99	2.23	0.45
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.SLLVIPNTLAVNAAQDSTDLVAK#.L	147.96	52.17	2.84	0.35
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.SQNVM*AAASIANIVK#.S	79.81	35.47	2.25	0.44
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.SQNVMAAASIANIVK#.S	8.42	4.55	1.85	0.54
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.SSFGPVGLDK#.M	90.77	47.37	1.92	0.52
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.TSASIILR@.G	97.62	41.64	2.34	0.43
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.YFVEAGAM*AVR@.R	59.45	24.65	2.41	0.41
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.YFVEAGAMAVR@.R	14.24	5.40	2.64	0.38
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.YINENLIINTDELGR@.D	18.62	9.45	1.97	0.51
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.YPVNSVNILK#.A	112.98	43.85	2.58	0.39
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.EQLAIAEFAR@.S	73.19	11.17	6.55	0.15
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.FATEAAITILR@.I	54.00	11.99	4.50	0.22
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.ILATGANVILTTGGIDDM*YLK#.Y	29.59	11.01	2.69	0.37
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.LGVQVVITDPEK#LDQIR@.Q	38.64	8.01	4.82	0.21
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.LLEVEHPAAK#.V	13.23	2.76	4.79	0.21
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.M*LVDDIGDVTITNDGATILK#.L	25.71	5.39	4.77	0.21
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.QAGVFEPTIVK#.V	45.61	8.67	5.26	0.19
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.SLLVIPNTLAVNAAQDSTDLVAK#.L	82.44	14.95	5.51	0.18
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.SQNVM*AAASIANIVK#.S	47.52	6.44	7.38	0.14
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.SSFGPVGLDK#.M	54.56	8.69	6.28	0.16
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.TSASIILR@.G	59.04	10.97	5.38	0.19
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	K.YFVEAGAM*AVR@.R	37.32	7.83	4.77	0.21
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.YINENLIINTDELGR@.D	21.95	3.70	5.93	0.17
P11983_TCPA_MOUSE	Tcp1	T-complex protein 1 subu	R.YPVNSVNILK#.A	56.61	9.78	5.79	0.17
Q8K1H1_TDRD7_MOUSE	Tdrd7	Tudor domain-containin	K.LAGLEVLNDDPDLVK#.A	7.40	3.60	2.05	0.49
P30051_TEAD1_MOUSE	Tead1	Transcriptional enhancer	K.GPQNAFFLVK.F	6.15	16.99	0.36	2.76
Q3UH45_Q3UH45_MOUSE	Tecpr2	Protein Tecpr2 OS=Mus r	R.GSSVASSVASEQR@.S	3.42	3.05	1.12	0.89
Q9CY27_TECR_MOUSE	Tecr	Very-long-chain enoyl-Co	K.LPVGTTATLYFR@.D	9.57	7.07	1.35	0.74
Q9D7K2_TEN1L_MOUSE	Ten1	CST complex subunit TEN	R.M*EGGAFVVR@.A	11.65	3.47	3.35	0.30
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.DQAIALLK#.D	15.21	4.27	3.56	0.28
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.IPSK#DPLEETPEAPVPTNM*STAADLLR@.Q	3.10	1.87	1.66	0.60
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	K.VSAQGITLTDNQR@.K	38.29	10.64	3.60	0.28
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.AGSVSPGSPPYLQPR@.K	5.26	2.58	2.04	0.49
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.GPLDGSPYAQVQR@.V	3.78	77.96	0.05	20.61
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.SPVPTTLPGLR@.H	9.28	2.98	3.11	0.32
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	K.VSAQGITLTDNQR@.K	20.39	4.66	4.38	0.23
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.AGSVSPGSPPYLQPR@.K	8.51	2.74	3.11	0.32
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.DQAIALLK#.D	9.25	6.23	1.48	0.67
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.GPLDGSPYAQVQR@.V	14.84	42.07	0.35	2.84
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.IPSK#DPLEETPEAPVPTNM*STAADLLR@.Q	5.79	2.25	2.58	0.39
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	K.ISAGADQALATLTM*R@.K	7.05	3.67	1.92	0.52
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	K.LALPTAALYGLR@.L	24.06	10.15	2.37	0.42
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.NDPSVSVDYNTTEPAVR@.W	6.52	3.38	1.93	0.52
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	R.SPVPTTLPGLR@.H	20.54	10.91	1.88	0.53
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	K.VSAQGITLTDNQR@.K	16.32	5.19	3.14	0.32
Q8CGB6_TENC1_MOUSE	Tenc1	Tensin-like C1 domain-co	K.YLLFNLSEK#.R	7.80	3.04	2.56	0.39
P47226_TES_MOUSE	Tes	Testin OS=Mus musculus	R.NVM*ILTNPVAAK#.K	20.01	14.82	1.35	0.74
P47226_TES_MOUSE	Tes	Testin OS=Mus musculus	K.QPVAGSEGAQYR@.K	9.37	4.88	1.92	0.52
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	K.FLQALADGSSR@.L	11.00	3.57	3.08	0.32
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	K.VLDILLEHYPALITGR@.S	8.82	5.41	1.63	0.61
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	K.FLQALADGSSR@.L	13.40	6.51	2.06	0.49
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	R.IYDPQEGAVVVLPAESQQR@.L	8.53	4.54	1.88	0.53
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	R.LIQM*QPNR@.D	14.73	5.15	2.86	0.35
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	K.VLDILLEHYPALITGR@.S	16.42	6.87	2.39	0.42
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	K.FLQALADGSSR@.L	14.17	6.59	2.15	0.46
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	R.IYDPQEGAVVVLPAESQQR@.L	15.24	8.50	1.79	0.56
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	K.LENATATNFK#.T	8.25	4.35	1.90	0.53
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	R.SQSFDIM*QSAISK#.H	5.70	2.98	1.91	0.52
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	K.VLDILLEHYPALITGR@.S	11.60	5.94	1.95	0.51
Q3URQ0_TEX10_MOUSE	Tex10	Testis-expressed sequenc	R.WLAGLPLQLSYLGSR@.N	11.43	5.23	2.19	0.46
P40630_TFAM_MOUSE	Tfam	Transcription factor A, m	R.FSTEQLPK.F	1.80	20.64	0.09	11.45
P40630_TFAM_MOUSE	Tfam	Transcription factor A, m	R.SAYNIYVSESFQEAK.D	1.45	6.25	0.23	4.30
P40630_TFAM_MOUSE	Tfam	Transcription factor A, m	K.SWEEQM*AEVGR.S	1.98	5.43	0.37	2.74
P40630_TFAM_MOUSE	Tfam	Transcription factor A, m	K.VYEADFK.A	2.69	21.38	0.13	7.94
Q9ERA0_TFCP2_MOUSE	Tfcp2	Alpha-globin transcriptio	K.IAQLFSISPHQISQIYK#.Q	9.85	4.37	2.26	0.44
Q9ERA0_TFCP2_MOUSE	Tfcp2	Alpha-globin transcriptio	R.ILDIDIPM*SVGVIDPR.A	10.88	5.76	1.89	0.53
Q9ERA0_TFCP2_MOUSE	Tfcp2	Alpha-globin transcriptio	R.LFTNFSGADLLK#.L	20.91	12.03	1.74	0.58
Q08639_TFDP1_MOUSE	Tfdp1	Transcription factor Dp-1	K.QSQLQELILQQIAFK#.N	7.43	5.54	1.34	0.75

Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.ADLAVAIVYPLVK#.D	19.30	7.28	2.65	0.38
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	K.AEEHNIVFM*PVIGK#.R	10.61	3.69	2.87	0.35
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.AVSSNVGAYM*QPGAR@.E	9.40	5.47	1.72	0.58
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.DGEGHLDDDDDDER@ENFEITDWDLQNEFNPNR@.Q	3.01	2.65	1.13	0.88
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.DYSAPVNFISAGLK#.K	10.64	6.49	1.64	0.61
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	K.EVLTPGSWEAFM*LR@.N	9.36	4.99	1.88	0.53
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.GVVFVQGEK#.T	20.40	5.42	3.76	0.27
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.IFETLQDK#YYEEYR@.L	13.89	5.96	2.33	0.43
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	K.LILQPWK#.E	14.33	5.34	2.68	0.37
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.NVVAQWQPR@.N	11.39	3.05	3.73	0.27
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	K.SLLENDQLLSHSSQDLSSDAFHR@.L	6.41	3.53	1.82	0.55
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	K.TAEVLAHEER@.V	24.03	3.54	6.79	0.15
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.TEQEIIQSDR.Q	19.17	7.18	2.67	0.37
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.TTQSLQDFPVADSEEEAEEEFQK#ELSQWR@.K	3.63	1.79	2.03	0.49
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.ADLAVAIVYPLVK#.D	12.88	6.67	1.93	0.52
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	K.AEEHNIVFM*PVIGK#.R	19.94	6.24	3.20	0.31
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.AVSSNVGAYM*QPGAR@.E	6.49	4.07	1.59	0.63
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.DYSAPVNFISAGLK#.K	6.87	4.82	1.42	0.70
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	K.SLLENDQLLSHSSQDLSSDAFHR@.L	6.85	3.13	2.19	0.46
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	K.TAEVLAHEER@.V	5.69	3.99	1.43	0.70
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.TEQEIIQSDR@.Q	16.28	7.23	2.25	0.44
Q9ERA6_TFP11_MOUSE	Tfip11	Tuftelin-interacting prot	R.TTQSLQDFPVADSEEEAEEEFQK#ELSQWR@.K	3.40	1.66	2.04	0.49
Q3U1J1_TFPT_MOUSE	Tfpt	TCF3 fusion partner hom	R.TTATLDPTSPAPGEGPSGR@.K	11.68	5.73	2.04	0.49
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	R.AGEITFAEK#.V	7.63	4.18	1.83	0.55
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	R.DALGAGVAAK#.S	15.33	4.49	3.42	0.29
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	K.GYEEPDR@YVVVGAQR@.D	8.83	5.49	1.61	0.62
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	R.ILNIFGVIK#.G	20.51	5.77	3.56	0.28
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	K.LAADEEENADNNM*K#.A	11.43	4.32	2.65	0.38
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	K.LAETEETDK#SETM*ETEDVPTSSR@.L	11.34	4.91	2.31	0.43
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	K.LAQVFSDM*ISK#.D	8.60	5.15	1.67	0.60
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	K.LNSIEFADTIK#.Q	17.40	8.58	2.03	0.49
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	K.LTHDVELNLDYEM*YNSK#.L	3.93	2.43	1.61	0.62
Q62351_TFR1_MOUSE	Tfrc	Transferrin receptor prot	R.TAAEVAGQLIIK#.L	12.31	3.54	3.48	0.29
Q62219_TGFI1_MOUSE	Tgfb1i1	Transforming growth fac	R.DFLQLFAPR@.C	11.62	6.27	1.86	0.54
Q8CHW1_THAP1_MOUSE	Thap1	THAP domain-containing	R.ILQLEQQVEK#.L	6.55	3.09	2.12	0.47
Q9JJD0_THA11_MOUSE	Thap11	THAP domain-containing	R.VPTIFPLR@.G	25.34	9.97	2.54	0.39
Q9JJD0_THA11_MOUSE	Thap11	THAP domain-containing	R.VPTIFPLR@.G	33.63	8.54	3.94	0.25
P35441_TSP1_MOUSE	Thbs1	Thrombospondin-1 OS=	R.FVFGTTPEDILR.N	1.18	5.63	0.21	4.78
Q8R3N6_THOC1_MOUSE	Thoc1	THO complex subunit 1	K.ILIGNEELTR@.L	7.91	2.55	3.10	0.32
Q8R3N6_THOC1_MOUSE	Thoc1	THO complex subunit 1	K.YSEEVLAVFK#.S	5.81	4.61	1.26	0.79
Q8R3N6_THOC1_MOUSE	Thoc1	THO complex subunit 1	K.ILIGNEELTR@.L	8.06	5.78	1.39	0.72
Q8R3N6_THOC1_MOUSE	Thoc1	THO complex subunit 1	K.SVYQLLSENPPDGER@.F	6.05	6.44	0.94	1.06
B1AZI6_THOC2_MOUSE	Thoc2	THO complex subunit 2	K.LGLLEALLK#.V	10.95	7.05	1.55	0.64
B1AZI6_THOC2_MOUSE	Thoc2	THO complex subunit 2	R.LDPETLESLGLIK#.Q	17.89	8.32	2.15	0.46
B1AZI6_THOC2_MOUSE	Thoc2	THO complex subunit 2	K.LGLLEALLK#.V	27.35	11.96	2.29	0.44
B1AZI6_THOC2_MOUSE	Thoc2	THO complex subunit 2	K.SFDLLILK#.E	9.46	5.77	1.64	0.61
B1AZI6_THOC2_MOUSE	Thoc2	THO complex subunit 2	K.VLNLGQALER@.R	19.29	7.39	2.61	0.38
Q8VE80_THOC3_MOUSE	Thoc3	THO complex subunit 3	R.YVLGM*QELFR@.G	7.56	3.30	2.29	0.44
Q5U4D9_THOC6_MOUSE	Thoc6	THO complex subunit 6	R.SPEVLSGGEDGAVR@.L	10.69	4.82	2.22	0.45
Q5U4D9_THOC6_MOUSE	Thoc6	THO complex subunit 6	R.SSTPTTVFPIR@.A	9.81	7.68	1.28	0.78
Q5U4D9_THOC6_MOUSE	Thoc6	THO complex subunit 6	R.TSLEVPEINALLLVPK#.E	24.90	9.92	2.51	0.40
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.ASVSDLSPR@.E	6.29	1.16	5.44	0.18
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.DSR@PSQAAGDNQGDEAK#EQTFSGGTSQDIK#.G	13.75	9.37	1.47	0.68
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.GSESSK#PWPDATTYGAGSASR@.A	11.26	4.03	2.79	0.36
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.M*DSFDEDLAR@PSGLLAQER@.K	27.34	20.99	1.30	0.77
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.SPLQSVVVR@.R	30.75	15.04	2.04	0.49
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.SPPATGSAYGSSQK#EESAASGGAAYSK#.R	6.01	2.18	2.76	0.36
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.SPSELFAQHIVTIVHHVK#.E	4.67	4.44	1.05	0.95
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.SSFSITR.E	36.49	37.97	0.96	1.04
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.YK#DDPVDLR@.L	37.52	35.03	1.07	0.93
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.AEEM*EDEPFTER@.S	30.84	13.58	2.27	0.44
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.AEEYPEEAEER@.E	25.78	5.02	5.14	0.19
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.ASVSDLSPR@.E	121.22	37.25	3.25	0.31
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.DSR@PSQAAGDNQGDEAK#.E	50.32	18.07	2.78	0.36
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.DSRPSQAAGDNQGDEAK.E	9.72	3.96	2.45	0.41
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.DSRPSQAAGDNQGDEAKEQTFSGGTSQDIK.G	205.12	61.50	3.34	0.30
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.EAQVNVR@.M	250.12	91.79	2.72	0.37
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.EESAASGGAAYSK#.R	48.26	22.75	2.12	0.47
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.EK#GGFSDADVK#.M	24.03	5.55	4.33	0.23
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.EQTFSGGTSQDIK#.G	130.19	52.32	2.49	0.40
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.FSGEEGEIEDDESGTENR@EEK#.D	8.86	2.31	3.83	0.26
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.GGFSDADVK#.M	243.02	109.74	2.21	0.45
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.GR@K#EPEFDDEPK#.F	149.79	67.95	2.20	0.45
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.K#AEEM*EDEPFTER@.S	52.45	25.51	2.06	0.49
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.KAEEM*EDEPFTER.S	189.07	84.55	2.24	0.45
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.K#EPEFDDEPK#.F	16.51	17.58	0.94	1.07
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.M*DSFDEDLAR@PSGLLAQER@.K	223.55	81.60	2.74	0.37
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.MDSFDEDLAR@PSGLLAQER@.K	40.21	18.73	2.15	0.47
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.M*K#SDPFAPK#.T	52.51	20.84	2.52	0.40
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.SGK#WESLHTGK#.E	35.11	14.54	2.41	0.41
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.SIFQHIQSAQSQR@.S	311.70	110.65	2.82	0.35
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.SIFQHIQSAQSQR.S	52.61	17.66	2.98	0.34
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.SPLQSVVVR@.R	575.68	200.42	2.87	0.35
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.SPPATGSAYGSSQK#EESAASGGAAYSK#.R	79.42	24.99	3.18	0.31
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.SREEEWDPEYTPK.S	28.07	8.45	3.32	0.30
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.SSFSITR@.E	500.27	212.22	2.36	0.42
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.TDSEK#PFR@.G	93.82	41.32	2.27	0.44
F6YSQ2_F6YSQ2_MOUSE	Thrap3	Thyroid hormone recept	K.R@PSGLLAQER@.K	8.54	12.27	0.70	1.44
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.ASVSDLSPR@.E	35.12	9.18	3.83	0.26
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.DSR@PSQAAGDNQGDEAK#.E	12.01	4.86	2.47	0.40
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.DSRPSQAAGDNQGDEAKEQTFSGGTSQDIK.G	33.20	10.95	3.03	0.33
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.EQTFSGGTSQDIK#.G	29.90	10.45	2.86	0.35
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.GGFSDADVK#.M	54.61	16.54	3.30	0.30
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.GSESSK#PWPDATTYGAGSASR@.A	12.67	6.86	1.85	0.54
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.K#AEEM*EDEPFTER@.S	37.89	11.80	3.21	0.31
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	R.M*DSFDEDLARPSGLLAQER.K	45.23	14.10	3.21	0.31
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.SPLQSVVVR@.R	97.70	35.53	2.75	0.36
Q569Z6_TR150_MOUSE	Thrap3	Thyroid hormone recept	K.SPPATGSAYGSSQK#EESAASGGAAYSK#.R	8.90	3.88	2.29	0.44
P70318_TIAR_MOUSE	Tial1	Nucleolysin TIAR OS=Mu	R.FEDVVNQSSPK#.N	57.92	38.50	1.50	0.66
P70318_TIAR_MOUSE	Tial1	Nucleolysin TIAR OS=Mu	R.QTFSPFGQIM*EIR@.V	34.00	15.55	2.19	0.46
P70318_TIAR_MOUSE	Tial1	Nucleolysin TIAR OS=Mu	R.QTFSPFGQIMEIR.V	15.53	11.27	1.38	0.73
P70318_TIAR_MOUSE	Tial1	Nucleolysin TIAR OS=Mu	K.TLYVGNLSR.D	48.29	24.93	1.94	0.52
Q9R1X4_TIM_MOUSE	Timeless	Protein timeless homolo	R.AATFR@PGLVSETLSIR@.T	7.24	4.21	1.72	0.58

Q9R1X4_TIM_MOUSE	Timeless	Protein timeless homolo	K.LLALGLVSER@.R	9.16	2.74	3.35	0.30
Q9R1X4_TIM_MOUSE	Timeless	Protein timeless homolo	K.EFNFLEYLK#.R	10.02	3.61	2.78	0.36
Q9R1X4_TIM_MOUSE	Timeless	Protein timeless homolo	K.LLALGLVSER@.R	17.36	6.06	2.87	0.35
Q9R1X4_TIM_MOUSE	Timeless	Protein timeless homolo	K.QILSTPLPR@.Q	11.12	6.19	1.80	0.56
Q9R1X4_TIM_MOUSE	Timeless	Protein timeless homolo	R.QQLGAAQILQSDLLPILTQHR@.Q	12.60	8.52	1.48	0.68
P62075_TIM13_MOUSE	Timm13	Mitochondrial import in	K.VQIAVANAQELLQR.M	5.70	4.32	1.32	0.76
O35857_TIM44_MOUSE	Timm44	Mitochondrial import in	R.ILDISNVDLAM*GK#.M	8.12	3.30	2.46	0.41
O35857_TIM44_MOUSE	Timm44	Mitochondrial import in	K.LGELTGTVK#.E	9.91	4.24	2.34	0.43
O35857_TIM44_MOUSE	Timm44	Mitochondrial import in	K.TEM*SEVLTEILR@.V	11.59	4.40	2.64	0.38
Q99JR5_TINAL_MOUSE	Tinagl1	Tubulointerstitial nephri	R.EQNEASPTPR.C	7.69	11.33	0.68	1.47
Q99JR5_TINAL_MOUSE	Tinagl1	Tubulointerstitial nephri	K.ITGWGEETLPDGR@.T	15.95	22.92	0.70	1.44
Q99JR5_TINAL_MOUSE	Tinagl1	Tubulointerstitial nephri	R.LDGAWWFLR.R	13.36	20.31	0.66	1.52
Q99JR5_TINAL_MOUSE	Tinagl1	Tubulointerstitial nephri	R.LGTIRPSSTVM*NM*NEIYTVLGQGEVLPTAFEASEK.W	2.19	1.80	1.21	0.82
Q9DCD5_TJAP1_MOUSE	Tjap1	Tight junction-associatec	R.LEQEESLTDAER@.M	18.17	6.47	2.81	0.36
Q9DCD5_TJAP1_MOUSE	Tjap1	Tight junction-associatec	R.SGQEVASPSPSPSSSLSPGAVVPTSVIAR@.V	7.97	4.44	1.80	0.56
Q9DCD5_TJAP1_MOUSE	Tjap1	Tight junction-associatec	R.LEQEESLTDAER@.M	14.96	3.66	4.09	0.24
Q9DCD5_TJAP1_MOUSE	Tjap1	Tight junction-associatec	K.LLQQENEELR@.K	17.23	2.33	7.39	0.14
Q9DCD5_TJAP1_MOUSE	Tjap1	Tight junction-associatec	R.LQNSYTASQR@.T	8.83	1.40	6.29	0.16
Q9DCD5_TJAP1_MOUSE	Tjap1	Tight junction-associatec	R.QAISLSLVEDGSER@.A	7.88	1.96	4.02	0.25
Q9DCD5_TJAP1_MOUSE	Tjap1	Tight junction-associatec	K.TLDWEIVELTNK#.L	6.26	2.20	2.84	0.35
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.GGPAEGQLQENDR@.V	17.87	10.20	1.75	0.57
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.SVASSQPAK#PTK#.V	4.09	2.90	1.41	0.71
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.YQM*NNISTM*PK#.A	8.45	5.63	1.50	0.67
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.AEQLASVQYTLPK#.T	13.98	9.84	1.42	0.70
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.DNPHFQSGETSIVISDVLK#.G	10.79	4.33	2.49	0.40
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.EAGFLR@PVTIFGPIADVAR@.E	51.85	36.49	1.42	0.70
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.EAIQQQQNQLVWVSEGK#.A	6.30	2.03	3.10	0.32
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.EGLEEGDQILR@.V	20.09	12.30	1.63	0.61
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.EISQDSLAAR@.D	14.44	6.42	2.25	0.44
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.FEEPAPLSYDSR@.T	13.75	8.41	1.63	0.61
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.GEEVTILAQK#.K	10.19	8.18	1.25	0.80
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.GGPAEGQLQENDR@.V	9.68	5.01	1.93	0.52
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.HEEQPAPAYEVHNR@.Y	12.79	9.65	1.33	0.75
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.IVESDVGDSFYIR@.T	22.53	11.05	2.04	0.49
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.LAGGNDVGIFVAGVLEDSPAAK#.E	7.35	3.84	1.91	0.52
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.LGSWLAIR@.I	14.96	7.08	2.11	0.47
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.VNNVDFTNIIR@.E	10.18	7.45	1.37	0.73
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.YEVSSYTDQFSR@.N	13.99	9.84	1.42	0.70
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.AEQLASVQYTLPK#.T	86.63	36.96	2.34	0.43
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.AVEEVTVEK#.N	34.06	13.92	2.45	0.41
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.DGNIQEGDVVLK#.I	102.45	41.09	2.49	0.40
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.DLEQPSYR@.Y	91.83	42.91	2.14	0.47
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.DNPHFQSGETSIVISDVLK#.G	105.22	37.09	2.84	0.35
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.EAGFLR@PVTIFGPIADVAR@.E	273.11	99.28	2.75	0.36
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.EAGFLR@PVTIFGPIADVAR@.E	10.40	4.20	2.47	0.40
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.EAIQQQQNQLVWVSEGK#.A	24.99	11.16	2.24	0.45
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.EDLSAQPVQTK#.F	38.87	23.99	1.62	0.62
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.EDPPQTFYPQK#.S	17.00	5.00	3.40	0.29
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.EEAVLFLLDLPK#.G	76.78	39.17	1.96	0.51
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.EEPDIYQIAK#.S	54.09	24.90	2.17	0.46
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.EGLEEGDQILR@.V	122.53	51.30	2.39	0.42
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.EISQDSLAAR@.D	123.35	42.80	2.88	0.35
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.FEEPAPLSYDSR@.T	75.25	35.00	2.15	0.47
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.GEEVTILAQK#.K	52.30	19.03	2.75	0.36
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.GGPAEGQLQENDR@.V	70.96	24.95	2.84	0.35
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.GK#PETDAVDR@.S	35.24	10.44	3.38	0.30
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.INGTVTENM*SLTDAK#.T	19.57	8.97	2.18	0.46
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.IVESDVGDSFYIR@.T	127.37	57.94	2.20	0.45
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.KEPYSEEM*M*R.Q	26.91	4.66	5.77	0.17
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.K#GDSVGLR@.L	69.89	22.51	3.10	0.32
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.LAGGNDVGIFVAGVLEDSPAAK#.E	174.33	85.85	2.03	0.49
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.LGSWLAIR@.I	76.59	34.87	2.20	0.46
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.LSYLSAPGSEYSM*YSTDSR@.H	10.15	5.20	1.95	0.51
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.NR@AEQLASVQYTLPK#.T	22.62	8.69	2.60	0.38
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.QIIDQDK#HALLDVTPNAVDR@.L	15.64	9.28	1.68	0.59
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.SNHYDPEEDEEYYR@.K	14.48	7.13	2.03	0.49
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.SVASSQPAKPTK.V	39.36	18.46	2.13	0.47
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.SYEQVPPPGFTSK#.T	18.19	7.70	2.36	0.42
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.THFEYEK#ESPYGLSFNK#.G	13.25	3.86	3.44	0.29
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.VAM*VNGVSM*DNVEHAFAVQQLR@.K	10.16	4.91	2.07	0.48
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.VNNVDFTNIIR@.E	78.65	31.92	2.46	0.41
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.VVDTLYNGK#.L	30.70	10.41	2.95	0.34
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.YEQLPR@.T	43.66	22.81	1.91	0.52
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.YEVSSYTDQFSR@.N	92.84	41.40	2.24	0.45
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	K.YQM*NNISTM*PK#.A	32.35	11.97	2.70	0.37
P39447_ZO1_MOUSE	Tjp1	Tight junction protein ZC	R.YR@PEAQPYSSTGPK#.S	13.15	6.95	1.89	0.53
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.AEQM*ASVQNAQR@.E	36.66	16.28	2.25	0.44
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.ANEEYGLR.L	25.52	10.49	2.43	0.41
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.DGNLHEGDIILK#.I	107.63	39.01	2.76	0.36
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.DNPHFENGETSIVISDVLPGGPADGLLQENDR@.V	6.67	2.47	2.70	0.37
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.DSIQQQQNEAVWVSEGK#.M	8.11	4.59	1.77	0.57
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.EDAVLYLLEIPK#.G	39.18	19.16	2.05	0.49
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.EDAVLYLLEIPK#GETVTILAQSR@.A	50.85	30.28	1.68	0.60
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.GDSFFIR@.S	60.87	24.59	2.48	0.40
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.GETVTILAQSR@.A	26.34	10.37	2.54	0.39
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.GFEVIEEFDGR@.S	37.00	18.12	2.04	0.49
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.GFGIAVSGGR@.D	36.39	13.93	2.61	0.38
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.GLDQEDYGR@.S	60.64	24.17	2.51	0.40
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.GLVR@EDAVLYLLEIPK#.G	16.04	5.87	2.73	0.37
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.GLVR@EDAVLYLLEIPK#GETVTILAQSR@.A	30.27	8.57	3.53	0.28
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.HPDIYAVPIK#.A	27.99	13.54	2.07	0.48
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.IAAIVVK#.R	82.15	31.06	2.64	0.38
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.INGTVTENM*SLTDAR@.K	13.92	8.69	1.60	0.62
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.K#LFDQANK#.L	29.84	13.01	2.29	0.44
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.LAGGNDVGIFVAGIQEGTSAEQEGLQEGDQILK#.V	37.93	11.12	3.41	0.29
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.LATELPDLFQTAK#.T	142.88	50.36	2.84	0.35
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.LGSQIFIK#.E	116.42	43.63	2.67	0.37
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.LQLVVLR@.D	56.48	20.00	2.82	0.35
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.M*GATPTPFK#.S	62.09	28.86	2.15	0.46
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.M*QELQEAQNAR@.I	69.69	23.36	2.98	0.34
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.R@GYYSQPSR@.Y	12.78	4.38	2.92	0.34
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.RPVVLFGPIADIAM*ER.L	122.77	43.25	2.84	0.35
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.R@PVVLFGPIADIAMER@.L	37.73	14.58	2.59	0.39

Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.R@QQYSDQDYHSSTEK#.L	28.55	9.28	3.08	0.33
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.SNLPATAGSEIPGGSTK#.G	74.11	31.33	2.37	0.42
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.SQNR@EDSFDYSK#.S	32.56	16.21	2.01	0.50
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.SR@EDLAAAVSVSTK#.F	30.40	9.46	3.21	0.31
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.STGDITAAGVTEASR@.E	33.87	11.95	2.84	0.35
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.VFLRPSPEDEAIYGPNTK.M	104.44	42.05	2.48	0.40
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.VNTQDFR@.G	89.69	29.67	3.02	0.33
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.VVDTLYDGK#.L	89.05	34.54	2.58	0.39
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.YQEEGPVPQPR@.T	55.39	26.45	2.09	0.48
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.AEQM*ASVQNAQR@.E	14.36	4.57	3.14	0.32
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.DGNLHEGDIILK#.I	45.57	12.51	3.64	0.27
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.DSIQQQQNEAVWVSEGK#.M	8.08	2.02	4.01	0.25
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.EDAVLYLLEIPK#.G	18.31	6.36	2.88	0.35
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.GETVTILAQSR@.A	10.83	3.34	3.24	0.31
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.GFGIAVSGGR@.D	16.37	4.88	3.35	0.30
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.GLDQEDYGR@.S	25.69	10.92	2.35	0.43
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.K#LFDQANK#.L	16.85	4.26	3.96	0.25
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.LAGGNDVGIFVAGIQEGTSAEQEGLQEGDQILK#.V	18.28	3.44	5.31	0.19
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.LATELPDLFQTAK#.T	55.24	21.41	2.58	0.39
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.LGSQIFIK#.E	30.58	9.07	3.37	0.30
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.LQLVVLR@.D	24.36	8.91	2.74	0.37
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.R@PVVLFGPIADIAM*ER@.L	35.29	15.70	2.25	0.44
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.R@QQYSDQDYHSSTEK#.L	8.36	1.58	5.31	0.19
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.SNLPATAGSEIPGGSTK#.G	38.36	17.00	2.26	0.44
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	K.STGDITAAGVTEASR@.E	16.32	6.40	2.55	0.39
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.VFLR@PSPEDEAIYGPNTK#.M	37.88	16.86	2.25	0.44
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.VVDTLYDGK#.L	60.57	28.26	2.14	0.47
Q9Z0U1_ZO2_MOUSE	Tjp2	Tight junction protein ZC	R.YQEEGPVPQPR@.T	19.34	9.14	2.12	0.47
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.VLVQNAAGSQEK#.L	3.74	3.84	0.97	1.03
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AIAVTVQEM*VTK#.S	5.39	2.99	1.80	0.55
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.LLGEIAQGNENYAGIAAR@.D	5.47	2.19	2.50	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.TLAESALQLLYTAK#.E	10.04	4.07	2.47	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.VGAIPANALDDGQWSQGLISAAR@.M	5.29	0.96	5.52	0.18
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.VLVQNAAGSQEK#.L	10.47	4.74	2.21	0.45
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AAAFEDQENETVVVK#.E	214.73	98.15	2.19	0.46
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.AAM*EPIVISAK#.T	248.08	106.27	2.33	0.43
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.AAMEPIVISAK#.T	18.82	11.75	1.60	0.62
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.ADAEGESDLENSR@.K	36.43	15.18	2.40	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.ADAEGESDLENSR@K#.L	28.34	10.32	2.75	0.36
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.AEASQLGHK#.V	26.15	14.59	1.79	0.56
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AGFLDLK#.D	73.06	28.98	2.52	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AGFLDLKDFLPK.E	166.40	67.37	2.47	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AHATGAGPAGR@.Y	16.02	6.76	2.37	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AIAVTVQEM*VTK#.S	260.13	109.81	2.37	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AIAVTVQEMVTK#.S	42.32	17.25	2.45	0.41
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.ALAVNPR@.D	188.05	72.88	2.58	0.39
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.ALDGDFTEENR@.A	100.60	37.70	2.67	0.37
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.ALDYYM*LR@.N	108.17	37.55	2.88	0.35
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.ALEATTEHIR.Q	51.71	24.62	2.10	0.48
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.ALGDLISATK#.A	279.58	123.12	2.27	0.44
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.ALSTDPASPNLK#.S	211.11	115.52	1.83	0.55
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.AQVVSNLK#.G	262.34	95.37	2.75	0.36
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.ASGHPGDPESQQR@.L	11.09	6.65	1.67	0.60
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AVAEQIPLLVQGVR@.G	223.04	97.04	2.30	0.44
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AVASAAAALVLK#.A	164.31	84.91	1.94	0.52
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AVEDEATK#.G	48.27	20.38	2.37	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.AVTQALNR@.C	225.96	91.09	2.48	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.DHFGLEGDEESTM*LEDSVSPK#.K	23.94	12.44	1.92	0.52
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.DLDQASLAAVSQQLAPR@.E	110.30	46.06	2.39	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.DLDQASLAAVSQQLAPR.E	85.01	33.35	2.55	0.39
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.DPVQLNLLYVQAR@.D	46.40	19.36	2.40	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.EADESLNFEEQILEAAK#.S	192.68	85.96	2.24	0.45
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.EGAETFADHR@.E	22.71	12.24	1.85	0.54
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.EGISQEALHTQM*LTAVQEISHLIEPLASAAR@.A	139.09	54.76	2.54	0.39
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.EGISQEALHTQM*LTAVQEISHLIEPLASAAR@.A	20.66	9.69	2.13	0.47
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.ERIPEALAGPPNDFGLFLSDDDPK.K	32.40	12.46	2.60	0.38
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.EVANSTANLVK#.T	284.24	120.03	2.37	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.EVIQEWSLTNIK.R	29.10	13.83	2.10	0.48
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.FFYSDQNVDSR@.D	21.30	9.93	2.15	0.47
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.FFYSDQNVDSR@DPVQLNLLYVQAR@.D	28.65	8.06	3.55	0.28
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.FGQDFSTFLEAGVEM*AGQAPSQEDR@.A	85.95	37.60	2.29	0.44
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.FGQDFSTFLEAGVEMAGQAPSQEDR@.A	40.27	15.95	2.52	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.FLPSELRDEH.-	29.65	10.78	2.75	0.36
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.GAAAHPDSEEQQQR@.L	77.77	36.58	2.13	0.47
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.GAAAHPDSEEQQQR@.L	14.40	8.94	1.61	0.62
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.GLAGAVSELLR@.S	1284.18	401.46	3.20	0.31
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.GTPQDLAR@.A	197.38	87.68	2.25	0.44
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.IGITNHDEYSLVR@.E	286.64	115.27	2.49	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.IGITNHDEYSLVR.E	16.97	10.45	1.62	0.62
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.ILAQATSDLVNAIK#.A	384.76	179.46	2.14	0.47
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.ILAQATSDLVNAIK#ADAEGESDLENSR@.K	24.18	8.25	2.93	0.34
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.ILAQATSDLVNAIK#ADAEGESDLENSR@.K	4.12	1.29	3.20	0.31
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.IPEALAGPPNDFGLFLSDDDPK#.K	27.20	15.88	1.71	0.58
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.IPEALAGPPNDFGLFLSDDDPK#K#.G	69.80	31.41	2.22	0.45
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.ISIGNVVK#.T	173.44	70.90	2.45	0.41
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.K#GIWLEAGK#.A	25.90	11.59	2.24	0.45
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.K#LEQLK#PR@.A	28.52	15.91	1.79	0.56
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.KSTVLQQQYNR.V	20.53	10.26	2.00	0.50
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.K#STVLQQQYNR@.V	94.97	41.66	2.28	0.44
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.LAQAAQSSVATITR@.L	219.04	87.21	2.51	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.LASQAK#PAAVAAENEEIGAHIK#.H	185.46	72.02	2.58	0.39
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.LASQAKPAAVAAENEEIGAHIK.H	32.86	11.06	2.97	0.34
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.LGAASLGAEDPETQVVLINAVK#.D	209.96	83.75	2.51	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.LHTDDELNWLDHGR@.T	42.02	17.00	2.47	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.LK#PLPGETM*EK#.C	108.51	53.69	2.02	0.49
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.LLAALLEDEGGNGR@PLLQAAK#.G	204.90	71.19	2.88	0.35
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.LLGEIAQGNENYAGIAAR@.D	228.17	94.88	2.40	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.LLSDSLPPSTGTFQEAQSR@.L	25.00	11.18	2.24	0.45
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.LNEAAAGLNQAATELVQASR@.G	227.67	83.95	2.71	0.37
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.LNEAAAGLNQAATELVQASR.G	130.21	58.49	2.23	0.45
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.MATNAAAQNAIK#.K	19.52	7.93	2.46	0.41
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	R.M*ATNAAAQNAIK#.K	135.19	50.23	2.69	0.37
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu:	K.M*VGGIAQIIAAQEEM*LR@.K	55.94	23.90	2.34	0.43

P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.MVGGIAQIIAAQEEM*LR@.K	6.83	1.53	4.48	0.22
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.M*VGGIAQIIAAQEEMLR@.K	14.28	3.82	3.74	0.27
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.NGNLPEFGDAIATASK#.A	38.56	14.77	2.61	0.38
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.NLGTALAELR@.T	258.98	109.42	2.37	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.QAAASATQTIAAAQHAASAPK#.A	308.42	130.26	2.37	0.42
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	R.QEDVIATANLSR@.R	123.68	48.45	2.55	0.39
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.R@VAGSVTELIQAAEAM*K#.G	32.28	11.00	2.93	0.34
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	R.SAQPASAEPR.Q	120.58	43.52	2.77	0.36
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR@.G	84.84	43.73	1.94	0.52
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	R.SGASGPENFQVGSM*PPAQQQITSGQMHR@.G	10.70	4.39	2.44	0.41
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.SIAAATSALVK#.A	211.43	102.46	2.06	0.48
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.SNTSPEELGPLANQLTSDYGR@.L	101.67	48.80	2.08	0.48
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.SNTSPEELGPLANQLTSDYGR.L	89.39	45.44	1.97	0.51
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.SQLAAAAR@.A	145.27	71.04	2.04	0.49
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.STVLQQQYNR@.V	43.32	17.44	2.48	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TIM*VDDSK#.T	89.60	36.49	2.46	0.41
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TK#EVIQEWSLTNIK#.R	134.43	13.21	10.18	0.10
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TLAESALQLLYTAK#.E	618.11	267.12	2.31	0.43
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	R.TLR@EQGVEEHETLLLR@.R	26.67	6.01	4.44	0.23
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TLSHPQQM*ALLDQTK#.T	142.91	67.02	2.13	0.47
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TLSHPQQMALLDQTK#.T	31.13	13.29	2.34	0.43
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TM*LESAGGLIQTAR@.A	109.94	97.52	1.13	0.89
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TM*LESAGGLIQTAR@.A	45.70	14.22	3.21	0.31
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TMLESAGGLIQTAR@.A	28.03	12.22	2.29	0.44
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TSTPEDFIR@.M	233.76	95.94	2.44	0.41
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.TYGVSFFLVK#.E	149.57	48.71	3.07	0.33
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	R.VAGSVTELIQAAEAM*K#.G	122.54	50.34	2.43	0.41
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	R.VAGSVTELIQAAEAMK#.G	23.43	10.81	2.17	0.46
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VGAIPANALDDGQWSQGLISAAR@.M	226.70	98.01	2.31	0.43
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VGAIPANALDDGQWSQGLISAAR.M	49.83	21.63	2.30	0.43
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VGDDPAVWQLK#.N	117.12	56.55	2.07	0.48
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VLGEAM*TGISQNAK#.N	174.05	68.97	2.52	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VLGEAMTGISQNAK#.N	21.84	9.55	2.29	0.44
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VLVEDTK#.V	245.56	84.80	2.90	0.35
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VLVQNAAGSQEK#.L	437.57	192.05	2.28	0.44
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VM*VTNVTSLLK#.T	150.72	62.53	2.41	0.41
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VMVTNVTSLLK#.T	66.94	22.36	2.99	0.33
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VSHVLAALQAGNR@.G	158.43	62.89	2.52	0.40
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VSQM*AQYFEPLTLAAVGAASK#.T	210.36	93.43	2.25	0.44
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	K.VSQMAQYFEPLTLAAVGAASK#.T	15.49	7.68	2.02	0.50
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	R.YDQATDTILTVTENIFSSM*GDAGEM*VR@.Q	216.94	79.76	2.72	0.37
P26039_TLN1_MOUSE	Tln1	Talin-1 OS=Mus musculu	R.YDQATDTILTVTENIFSSM*GDAGEMVR@.Q	11.75	4.51	2.61	0.38
Q71LX4_TLN2_MOUSE	Tln2	Talin-2 OS=Mus musculu	R.DVM*EGSAM*LIQEAK#.Q	4.74	1.36	3.49	0.29
Q71LX4_TLN2_MOUSE	Tln2	Talin-2 OS=Mus musculu	R.EQGVDENETLLLR@.R	5.69	3.00	1.90	0.53
Q71LX4_TLN2_MOUSE	Tln2	Talin-2 OS=Mus musculu	K.GAAANPENEDQQQR@.L	4.80	2.72	1.77	0.57
Q71LX4_TLN2_MOUSE	Tln2	Talin-2 OS=Mus musculu	K.LGAASLGSNDPETQVVLINAIK#.D	6.33	2.60	2.43	0.41
Q71LX4_TLN2_MOUSE	Tln2	Talin-2 OS=Mus musculu	K.LLAALM*DDDVGSGEDLLR@.A	10.29	4.07	2.53	0.40
Q71LX4_TLN2_MOUSE	Tln2	Talin-2 OS=Mus musculu	K.NLATSLAELR@.T	13.79	6.61	2.09	0.48
Q71LX4_TLN2_MOUSE	Tln2	Talin-2 OS=Mus musculu	K.NVAQVAEDTVLQNR@.V	6.54	2.02	3.25	0.31
Q71LX4_TLN2_MOUSE	Tln2	Talin-2 OS=Mus musculu	R.VATNAAAQNAIK#.K	8.08	1.63	4.96	0.20
Q71LX4_TLN2_MOUSE	Tln2	Talin-2 OS=Mus musculu	R.VLAQATSDLVNAM*R@.S	7.87	2.57	3.06	0.33
Q9DBU0_TM9S1_MOUSE	Tm9sf1	Transmembrane 9 superf	K.SLSLGEVLDGDR@.M	8.34	3.84	2.17	0.46
Q9ET30_TM9S3_MOUSE	Tm9sf3	Transmembrane 9 superf	R.DAFVYAIK#.N	22.99	8.79	2.62	0.38
Q9ET30_TM9S3_MOUSE	Tm9sf3	Transmembrane 9 superf	K.SISHYHETLGEALQGVELEFSGLDIK#.F	42.88	9.64	4.45	0.22
Q8BH24_TM9S4_MOUSE	Tm9sf4	Transmembrane 9 superf	R.FEVIPQSIR@.L	11.91	3.34	3.57	0.28
Q8BH24_TM9S4_MOUSE	Tm9sf4	Transmembrane 9 superf	R.LGFTDVNK#.I	13.69	4.93	2.78	0.36
Q9D2C7_BI1_MOUSE	Tmbim6	Bax inhibitor 1 OS=Mus	K.INFDALLK#.F	15.23	8.15	1.87	0.54
Q9D2C7_BI1_MOUSE	Tmbim6	Bax inhibitor 1 OS=Mus	R.K#INFDALLK#.F	10.92	3.94	2.77	0.36
Q3V009_TMED1_MOUSE	Tmed1	Transmembrane emp24	R.NLQEDNLER@.V	12.55	5.58	2.25	0.44
Q3V009_TMED1_MOUSE	Tmed1	Transmembrane emp24	R.SIQM*LTLLR@.A	7.71	2.62	2.94	0.34
Q9D1D4_TMEDA_MOUSE	Tmed10	Transmembrane emp24	K.DLLVTGAYEITDQSGGAGGLR@.T	19.07	4.93	3.87	0.26
Q9D1D4_TMEDA_MOUSE	Tmed10	Transmembrane emp24	K.DLLVTGAYEITDQSGGAGGLR.T	13.99	3.28	4.27	0.23
Q9D1D4_TMEDA_MOUSE	Tmed10	Transmembrane emp24	R.EEIHKDLLVTGAYEITDQSGGAGGLR.T	8.49	2.38	3.57	0.28
Q9D1D4_TMEDA_MOUSE	Tmed10	Transmembrane emp24	R.IPDQLVILDM*K#.H	102.91	28.75	3.58	0.28
Q9D1D4_TMEDA_MOUSE	Tmed10	Transmembrane emp24	K.LKPLEVELR.R	319.13	98.15	3.25	0.31
Q9D1D4_TMEDA_MOUSE	Tmed10	Transmembrane emp24	K.NYEEIAK#.V	63.25	19.20	3.29	0.30
Q9D1D4_TMEDA_MOUSE	Tmed10	Transmembrane emp24	R.R@LEDLSESIVNDFAYM*K#.K	109.27	31.79	3.44	0.29
Q9D1D4_TMEDA_MOUSE	Tmed10	Transmembrane emp24	R.R@LEDLSESIVNDFAYMK#.K	5.32	2.50	2.13	0.47
Q9D1D4_TMEDA_MOUSE	Tmed10	Transmembrane emp24	R.RLEDLSESIVNDFAYM*KK.R	29.80	9.33	3.19	0.31
Q9R0Q3_TMED2_MOUSE	Tmed2	Transmembrane emp24	K.HEQEYM*EVR@.E	18.79	11.35	1.66	0.60
Q9R0Q3_TMED2_MOUSE	Tmed2	Transmembrane emp24	K.IVM*FTIDIGEAPK#.G	63.62	21.73	2.93	0.34
Q9R0Q3_TMED2_MOUSE	Tmed2	Transmembrane emp24	K.IVMFTIDIGEAPK#.G	17.78	8.22	2.16	0.46
Q8R1V4_TMED4_MOUSE	Tmed4	Transmembrane emp24	R.QLLDQVEQIQK#.E	12.56	2.74	4.58	0.22
Q9CXE7_TMED5_MOUSE	Tmed5	Transmembrane emp24	K.LEDILESINSIK#.S	6.47	2.37	2.73	0.37
D3YZZ5_D3YZZ5_MOUSE	Tmed7	Protein Tmed7 OS=Mus	K.QYDSFTFTASR@.N	14.12	2.58	5.48	0.18
D3YZZ5_D3YZZ5_MOUSE	Tmed7	Protein Tmed7 OS=Mus	K.TVYFDFQVGEDPPLFPSENR@.V	5.82	2.25	2.59	0.39
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	K.FSLFAGGM*LR@.V	7.74	3.09	2.51	0.40
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	R.QLVEQVEQIQK#.E	35.04	13.86	2.53	0.40
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	K.DK#LSELQLR@.V	26.11	9.82	2.66	0.38
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	K.FSLFAGGM*LR@.V	25.20	9.83	2.56	0.39
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	K.FSLFAGGMLR@.V	5.07	2.79	1.82	0.55
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	R.QLVEQVEQIQK#.E	43.70	16.13	2.71	0.37
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	R.QLVEQVEQIQK#EQNYQR@.W	6.15	1.69	3.63	0.28
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	K.FSLFAGGM*LR@.V	11.92	4.39	2.72	0.37
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	K.LSELQLR@.V	13.51	4.42	3.06	0.33
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	R.QLVEQVEQIQK#.E	23.62	9.23	2.56	0.39
Q99KF1_TMED9_MOUSE	Tmed9	Transmembrane emp24	R.QLVEQVEQIQK#.E	23.16	10.87	2.13	0.47
Q3UBX0_TM109_MOUSE	Tmem109	Transmembrane protein	K.ETSADILTQIGR@.S	52.40	27.24	1.92	0.52
Q9CQN6_TM14C_MOUSE	Tmem14c	Transmembrane protein	K.FM*PAGLIAGASLLM*VAK#.V	8.74	3.62	2.41	0.41
Q9CQN6_TM14C_MOUSE	Tmem14c	Transmembrane protein	K.FM*PAGLIAGASLLM*VAK#.V	6.90	3.30	2.09	0.48
P52875_TM165_MOUSE	Tmem165	Transmembrane protein	K.M*SPDEGQEELEEVQAELK#.K	16.70	9.50	1.76	0.57
P52875_TM165_MOUSE	Tmem165	Transmembrane protein	R.NQEPPAPAQQLQPQPAAVQGLEPAR@.A	21.97	11.43	1.92	0.52
P52875_TM165_MOUSE	Tmem165	Transmembrane protein	R.SQLTTIVLAAR@.E	20.26	12.18	1.66	0.60
Q9DCS1_T176A_MOUSE	Tmem176a	Transmembrane protein	R.IPASASTQSQGSSR@.V	2.59	2.76	0.94	1.07
Q91XE8_TM205_MOUSE	Tmem205	Transmembrane protein	R.GLGTEVPGNFQGPDPYR@.Q	3.16	1.78	1.77	0.56
Q9DAM7_TM263_MOUSE	Tmem263	Transmembrane protein	R.VTGGIFSVTK#.G	8.76	5.61	1.56	0.64
Q9CR67_TMM33_MOUSE	Tmem33	Transmembrane protein	R.ALLANALTSALR@.L	38.05	19.25	1.98	0.51
Q9CR67_TMM33_MOUSE	Tmem33	Transmembrane protein	K.GSNSLPLLR@.S	17.37	8.56	2.03	0.49
Q9CR67_TMM33_MOUSE	Tmem33	Transmembrane protein	K.LDTAM*WLSR@.L	7.30	5.76	1.27	0.79
Q9CR67_TMM33_MOUSE	Tmem33	Transmembrane protein	K.LSTNQQNILK#.F	17.97	11.42	1.57	0.64
Q9DBS1_TMM43_MOUSE	Tmem43	Transmembrane protein	R.FFLSAGLIDK#.I	10.36	4.93	2.10	0.48
Q9DBS1_TMM43_MOUSE	Tmem43	Transmembrane protein	R.RGDFFYHSENPKYPEVGDVR.V	13.47	9.50	1.42	0.71
Q9DBS1_TMM43_MOUSE	Tmem43	Transmembrane protein	K.TATSLAEGLSLVVSPDSIHSVAPENEGR@.L	16.83	13.32	1.26	0.79

Q9DBS1_TMM43_MOUSE	Tmem43	Transmembrane protein	K.VTSEPQPGFLER@.L	18.84	14.74	1.28	0.78
B9EKI3_TMF1_MOUSE	Tmf1	TATA element modulator	R.HEISELQQR@.L	7.47	4.91	1.52	0.66
B9EKI3_TMF1_MOUSE	Tmf1	TATA element modulator	R.LQVDM*DELEEK#.S	5.69	2.75	2.07	0.48
B9EKI3_TMF1_MOUSE	Tmf1	TATA element modulator	R.TVVDESENFFSAFLSPSDAHTIQK#.S	5.82	6.12	0.95	1.05
B9EKI3_TMF1_MOUSE	Tmf1	TATA element modulator	K.IQM*SSVESQNTLLR@.Q	4.79	2.57	1.86	0.54
B9EKI3_TMF1_MOUSE	Tmf1	TATA element modulator	R.LQVDM*DELEEK#.S	3.75	2.62	1.43	0.70
B9EKI3_TMF1_MOUSE	Tmf1	TATA element modulator	K.SSLQESSSPGQSR@.V	5.04	3.04	1.66	0.60
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.DLGDYK#DLDEDELLGK#.L	174.50	152.12	1.15	0.87
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.DLGDYK#DLDEDELLGK#.L	15.57	29.37	0.53	1.89
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	R.DNETLM*ELK#.I	55.12	51.51	1.07	0.93
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.HFSLAATR.S	328.30	233.97	1.40	0.71
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.LSESELK#.Q	144.71	102.82	1.41	0.71
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	R.LVEVNLNNIK#.N	264.89	237.23	1.12	0.90
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.M*LEENTNILK#.F	132.04	106.04	1.25	0.80
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.NNDLVR@.K	173.25	126.68	1.37	0.73
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.QLETVLDDLDPENALLPAGFR@.Q	63.60	52.46	1.21	0.82
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	R.QQLGTSVELEM*AK#.M	72.30	50.89	1.42	0.70
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.SATGPFDR@.E	121.81	88.39	1.38	0.73
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	R.SNDPVAVAFADM*LK#.V	80.26	66.88	1.20	0.83
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	R.SNDPVAVAFADM*LK.V	17.26	16.20	1.07	0.94
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	R.SNDPVAVAFADMLK.V	40.67	33.46	1.22	0.82
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.DLGDYKDLDEDELLGK.L	163.78	130.72	1.25	0.80
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.DLGDYK#DLDEDELLGK#.L	17.07	18.21	0.94	1.07
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.DLGDYK#DLDEDELLGK#LSESELK#.Q	23.46	18.88	1.24	0.80
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.DR@DDYVPYTGEK#.K	14.15	8.68	1.63	0.61
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.ILPVFDEPPNPTNVEESLK#R@.I	7.38	6.43	1.15	0.87
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	R.LLSYLEK#.Q	122.23	85.54	1.43	0.70
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.LSESELK#.Q	118.45	76.00	1.56	0.64
Q9JHJ0_TMOD3_MOUSE	Tmod3	Tropomodulin-3 OS=Mu	K.QLETVLDDLDPENALLPAGFR.Q	48.71	25.87	1.88	0.53
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.AEEPGVSDQSVFSSER@.E	7.03	6.69	1.05	0.95
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.AQPLR@AEEPGVSDQSVFSSER@.E	18.57	16.97	1.09	0.91
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.LEDKDDLDVTELSNEELLDQLVR.Y	23.16	12.64	1.83	0.55
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.LSQSSYQDSESLSPPR@.K	9.04	5.72	1.58	0.63
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	K.LTVAPFK#.G	14.02	9.44	1.49	0.67
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.LVSAAASPSLIR.E	47.52	22.09	2.15	0.46
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.SQVISPPLAQAIR@.D	19.16	13.48	1.42	0.70
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.SSTPLPTVSSSAENTR@.Q	11.74	8.02	1.46	0.68
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	K.SVVSHSLTTLGVEVSKPPPQHDKIEASEPSFPLHESILK.V	2.76	3.71	0.74	1.34
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.SYEAAASALQIAAHTAFVAK#.S	20.83	12.06	1.73	0.58
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	K.VDDEILGFISEATPR@.A	17.59	18.67	0.94	1.06
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	K.VDDEILGFISEATPR.A	18.19	13.82	1.32	0.76
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	K.VVEEEWQQIDR@.Q	19.07	13.14	1.45	0.69
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.YPVSSIEAAR@.I	55.19	30.57	1.81	0.55
Q61029_LAP2B_MOUSE	Tmpo	Lamina-associated polyp	K.ASSNESLVANR@.L	15.19	11.38	1.33	0.75
Q61029_LAP2B_MOUSE	Tmpo	Lamina-associated polyp	K.GAAGR@PLELSDFR@.M	24.70	20.41	1.21	0.83
Q61029_LAP2B_MOUSE	Tmpo	Lamina-associated polyp	K.HASSILPITEFSDITR.R	9.88	10.00	0.99	1.01
Q61029_LAP2B_MOUSE	Tmpo	Lamina-associated polyp	R.IDGAVISESTPIAETIK#.A	18.78	18.16	1.03	0.97
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.AEEPGVSDQSVFSSER@.E	7.48	4.61	1.62	0.62
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.AQPLRAEEPGVSDQSVFSSER.E	24.63	13.90	1.77	0.56
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.EVLQESER@.S	21.88	10.61	2.06	0.49
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	K.GPPDFSSDEER@EPTPVLGSGASVGR@.G	8.97	9.83	0.91	1.10
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.LEDK#DDLDVTELSNEELLDQLVR@.Y	35.23	10.39	3.39	0.30
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.LSQSSYQDSESLSPPR@.K	8.65	5.24	1.65	0.61
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.LVSAAASPSLIR@.E	46.34	21.07	2.20	0.45
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.SLFIPSESSYDR.C	16.39	8.31	1.97	0.51
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.SQVISPPLAQAIR@.D	22.30	9.50	2.35	0.43
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.SSTPLPTVSSSAENTR@.Q	19.03	9.57	1.99	0.50
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.SYEAAASALQIAAHTAFVAK#.S	2.98	1.63	1.83	0.55
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	K.VDDEILGFISEATPR@.A	25.34	11.47	2.21	0.45
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	K.VVEEEWQQIDR@.Q	32.98	15.98	2.06	0.48
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.YGVNPGPIVGTTR@.K	28.06	14.21	1.98	0.51
Q61033_LAP2A_MOUSE	Tmpo	Lamina-associated polyp	R.YPVSSIEAAR@.I	39.11	15.91	2.46	0.41
Q8VBT0_TMX1_MOUSE	Tmx1	Thioredoxin-related tran	K.VDVTEQTGLSGR@.F	15.21	6.98	2.18	0.46
Q8VBT0_TMX1_MOUSE	Tmx1	Thioredoxin-related tran	K.VDVTEQTGLSGR@.F	5.38	1.55	3.48	0.29
Q8VBT0_TMX1_MOUSE	Tmx1	Thioredoxin-related tran	K.VDVTEQTGLSGR@.F	13.15	3.33	3.95	0.25
Q9WUU8_TNIP1_MOUSE	Tnip1	TNFAIP3-interacting prot	K.IFEEDFQR@.E	7.21	1.57	4.58	0.22
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.AGAVDWTDQLGLR@.N	33.90	4.71	7.20	0.14
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.APAIRPGGTLGLSETADSDTR.L	43.05	10.14	4.25	0.24
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.APLPSSR@PQPDGEASQVEEVDGTWSLTGAAR@.Q	10.86	1.97	5.50	0.18
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.ASVSTNQDTDENDQELGM*K#.N	7.02	3.03	2.31	0.43
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.ATAQQNQEFGK#.S	12.04	2.42	4.97	0.20
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.AVGR@PAQLGAQGLEADAQQWEFGK#.R	7.50	2.89	2.60	0.38
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.AVGR@PAQLGAQGLEADAQQWEFGK#R@.E	16.92	3.85	4.39	0.23
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.DEGSWQDGDSSQEITR@.L	11.93	2.78	4.30	0.23
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.DSLGSFSTR@.D	22.16	4.82	4.60	0.22
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.DVGHLEEGASGGLLSPSTPHSR@.D	14.28	4.82	2.96	0.34
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.ELGVGQVDWGDDLGLR@.N	26.77	6.42	4.17	0.24
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.ENYEDQEPLVGHESPITLAAR@.E	8.71	7.27	1.20	0.83
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.ESGVGEPDWSGAEAGEFLK#.S	18.89	7.09	2.66	0.38
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.GYSSQDAEEQDR@EFEK#R@.D	15.73	4.29	3.67	0.27
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.HSLGQEVIGIGGSQDESEVPVR@.E	35.63	8.48	4.20	0.24
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.LFQDSTEPR@.A	21.22	4.12	5.15	0.19
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.LGTGESEEPR@.S	9.81	1.14	8.59	0.12
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.M*QAESQSPTNVDLEDK#ER@.E	24.45	4.19	5.83	0.17
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SAEEGEVTESK#.S	14.09	3.86	3.65	0.27
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.SAWFQDYSSGGGGSR@.V	14.34	3.58	4.00	0.25
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SPALLPSTVEGPPGAPLLQAK#.E	4.54	5.27	0.86	1.16
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SPPSGSQSLLEGIM*TASSSK#.G	5.72	2.25	2.54	0.39
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SPPSGSQSLLEGIMTASSSK#.G	4.58	0.00	#DIV/0!	0.00
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SPVGDTGLGK#.R	26.46	8.65	3.06	0.33
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.SSGSEGSSPNWLQALK#.L	11.15	2.45	4.54	0.22
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.SSGSLSPGLETEDPLEAR@.E	28.08	8.66	3.24	0.31
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.VGPDLELDPK#.S	30.21	7.09	4.26	0.23
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.VLLEEEGLAAGAGQGEPQEPSR@.A	25.31	5.84	4.33	0.23
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.VNLFPGLSPSALK#.A	40.18	10.44	3.85	0.26
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.WLDDLLASPPPNSGSAR@.R	9.47	3.83	2.47	0.40
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.AGAVDWTDQLGLR@.N	53.25	14.49	3.67	0.27
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.APAIR@PGGTLGLSETADSDTR@.L	76.47	15.56	4.91	0.20
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.APLPSSR@PQPDGEASQVEEVDGTWSLTGAAR@.Q	13.40	4.30	3.12	0.32
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.ASVSTNQDTDENDQELGM*K#.N	19.07	6.67	2.86	0.35
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.ATAQQNQEFGK#.S	55.71	16.09	3.46	0.29
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.AVGR@PAQLGAQGLEADAQQWEFGK#.R	11.27	3.22	3.50	0.29
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.DASLQDWEFGK#.R	9.44	3.56	2.65	0.38

P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.DEGSWQDGDSSQEITR@.L	14.93	5.29	2.82	0.35
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.DLPGQAEVGR@.H	55.75	18.85	2.96	0.34
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.DSLGSFSTR@.D	36.02	10.60	3.40	0.29
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.DVGHLEEGASGGLLSPSTPHSR@.D	44.43	16.21	2.74	0.36
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.DVGHLEEGASGGLLSPSTPHSR@.D	18.03	6.03	2.99	0.33
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.ELGVGQVDWGDDLGLR@.N	54.91	37.91	1.45	0.69
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.ENYEDQEPLVGHESPITLAAR@.E	59.37	20.66	2.87	0.35
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.ESGVGEPDWSGAEAGEFLK#.S	25.49	8.30	3.07	0.33
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.FSEGVLQPPSQDQEK#.L	10.14	8.11	1.25	0.80
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.GEGVSQVGPGTPPAPESPR@.K	8.85	5.48	1.61	0.62
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.GVGQADWTPDLGLR@.N	39.79	36.42	1.09	0.92
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.K#EILASPDR@.L	19.85	7.17	2.77	0.36
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.K#PISGVQGNDPGISLPQR@.D	19.64	8.53	2.30	0.43
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.LANISVPASESPR@.L	49.20	23.15	2.13	0.47
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.LFQDSTEPR@.A	33.98	11.65	2.92	0.34
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.M*QAESQSPTNVDLEDK#ER@.E	35.42	11.19	3.17	0.32
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.MQAESQSPTNVDLEDK#ER@.E	6.00	4.23	1.42	0.71
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.NLTSSPAM*NGDLAK#.L	3.79	3.46	1.10	0.91
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SAEEGEVTESK#.S	20.28	6.95	2.92	0.34
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.SAWFQDYSSGGGGSR@.V	22.23	7.51	2.96	0.34
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SLSSGFSPEEAQQQDEEFEK#.K	14.41	3.49	4.13	0.24
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SPALLPSTVEGPPGAPLLQAK#.E	37.86	19.48	1.94	0.51
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SPPSGSQSLLEGIM*TASSSK#.G	14.27	3.99	3.58	0.28
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SPPSGSQSLLEGIM*TASSSK#.G	9.96	4.45	2.24	0.45
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.SPVGDTGLGK#.R	36.36	14.53	2.50	0.40
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.SSGSLSPGLETEDPLEAR@.E	46.67	16.71	2.79	0.36
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.TWVTSSADPVSEHGGSTSAVR@.L	20.79	8.82	2.36	0.42
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.VGPDLELDPK#.S	57.99	18.69	3.10	0.32
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.VLLEEEGLAAGAGQGEPQEPSR@.A	38.24	12.59	3.04	0.33
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	K.VNLFPGLSPSALK#.A	77.74	22.29	3.49	0.29
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.VPSSDEEVVEEPQSR@.R	10.88	3.39	3.21	0.31
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.VSGAGLSPSR.K	52.19	13.48	3.87	0.26
P58871_TB182_MOUSE	Tnks1bp1	182 kDa tankyrase-1-bin	R.WLDDLLASPPPNSGSAR@.R	15.61	5.69	2.74	0.36
Q8BFY9_TNPO1_MOUSE	Tnpo1	Transportin-1 OS=Mus m	K.TLLENTAITIGR@.L	6.32	13.18	0.48	2.08
Q8BFY9_TNPO1_MOUSE	Tnpo1	Transportin-1 OS=Mus m	R.ALVM*LLEVR@.M	6.92	3.78	1.83	0.55
Q8BKI2_TNR6B_MOUSE	Tnrc6b	Trinucleotide repeat-con	K.DLGTTDSGPYFEK#.G	8.95	5.97	1.50	0.67
Q8BKI2_TNR6B_MOUSE	Tnrc6b	Trinucleotide repeat-con	K.GIQNIDPESDPYVTPGSVLGGTTTSPIVDTDHQLLR@.D	4.99	1.83	2.73	0.37
Q8BKI2_TNR6B_MOUSE	Tnrc6b	Trinucleotide repeat-con	R.QQQEQQLAR@.M	13.25	3.38	3.92	0.26
Q5SSZ5_TENS3_MOUSE	Tns3	Tensin-3 OS=Mus muscul	K.AGDLSNELVR@.H	20.87	5.40	3.87	0.26
Q5SSZ5_TENS3_MOUSE	Tns3	Tensin-3 OS=Mus muscul	K.ALSM*TLVQEPPPVSTVVHFK#.V	12.34	2.47	4.99	0.20
Q5SSZ5_TENS3_MOUSE	Tns3	Tensin-3 OS=Mus muscul	K.LLIPER@DPLEEIAENSPQTAANSAAELLK#.Q	11.28	4.99	2.26	0.44
Q5SSZ5_TENS3_MOUSE	Tns3	Tensin-3 OS=Mus muscul	K.LLIPER@DPLEEIAENSPQTAANSAAELLK#.Q	6.86	1.48	4.62	0.22
Q9QZ06_TOLIP_MOUSE	Tollip	Toll-interacting protein	R.GNK#DAAINSLLQM*GEES.-	3.95	2.45	1.61	0.62
Q9QZ06_TOLIP_MOUSE	Tollip	Toll-interacting protein	R.IAWTHITIPESLK#.Q	16.35	8.43	1.94	0.52
Q9QZ06_TOLIP_MOUSE	Tollip	Toll-interacting protein	R.ITPTQQQQIQLDAQAAQQLQYGGTVGTVGR@.L	5.23	2.42	2.16	0.46
Q9QZ06_TOLIP_MOUSE	Tollip	Toll-interacting protein	R.LSITVVQAK#.L	28.10	10.09	2.79	0.36
O88746_TOM1_MOUSE	Tom1	Target of Myb protein 1	R.AGLQSLETSGHLEDDFDM*FALTR@.G	7.39	4.66	1.59	0.63
O88746_TOM1_MOUSE	Tom1	Target of Myb protein 1	R.FHVLVANQDFVENVLVR@.T	6.32	6.86	0.92	1.09
O88746_TOM1_MOUSE	Tom1	Target of Myb protein 1	R.GDLSQHATPLPTPAVLPGDSPITPTPEQIGK#.L	5.96	3.85	1.55	0.65
O88746_TOM1_MOUSE	Tom1	Target of Myb protein 1	R.ILELIPR@.I	13.45	8.99	1.50	0.67
O88746_TOM1_MOUSE	Tom1	Target of Myb protein 1	R.TVFNSETPSR@.Q	18.23	8.22	2.22	0.45
O88746_TOM1_MOUSE	Tom1	Target of Myb protein 1	K.YEAPQTTDGLAGALDAR@.Q	8.90	3.69	2.41	0.41
Q5SRX1_TM1L2_MOUSE	Tom1l2	TOM1-like protein 2 OS=	R.VSNEEVTEELLHVNDDLNNVFLR@.Y	11.83	2.56	4.62	0.22
Q9CPQ3_TOM22_MOUSE	Tomm22	Mitochondrial import re	K.AEAEK#AEEELEEDDDDELDETLSER@.L	22.11	5.29	4.18	0.24
Q9CPQ3_TOM22_MOUSE	Tomm22	Mitochondrial import re	K.LQM*EQQQQLQQR@.Q	5.82	4.53	1.29	0.78
Q9CPQ3_TOM22_MOUSE	Tomm22	Mitochondrial import re	R.LWGLTEM*FPER@.V	18.28	7.84	2.33	0.43
Q9CPQ3_TOM22_MOUSE	Tomm22	Mitochondrial import re	R.QILLGPNTGLSGGM*PGALPPLPGK#M*.-	5.00	1.67	2.99	0.33
Q9QYA2_TOM40_MOUSE	Tomm40	Mitochondrial import re	K.FVNWQVDGEYR@.G	7.50	1.30	5.78	0.17
Q04750_TOP1_MOUSE	Top1	DNA topoisomerase 1 OS	K.AEEVATFFAK.M	8.68	23.81	0.36	2.74
Q04750_TOP1_MOUSE	Top1	DNA topoisomerase 1 OS	K.ELTAPDENVPAK#.I	6.43	21.42	0.30	3.33
Q04750_TOP1_MOUSE	Top1	DNA topoisomerase 1 OS	K.GPVFAPPYEPLPESVK.F	5.63	21.81	0.26	3.87
Q04750_TOP1_MOUSE	Top1	DNA topoisomerase 1 OS	R.TYNASITLQQQLK.E	5.20	8.74	0.59	1.68
Q04750_TOP1_MOUSE	Top1	DNA topoisomerase 1 OS	K.GPVFAPPYEPLPESVK.F	1.89	10.29	0.18	5.45
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.IFDEILVNAADNK#.Q	14.04	3.78	3.71	0.27
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.ELILFSNSDNER@.S	8.03	5.31	1.51	0.66
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.FLEEFITPIVK#.V	14.19	10.73	1.32	0.76
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.IFDEILVNAADNK#.Q	10.42	7.84	1.33	0.75
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.TPSLITDYR@.E	11.27	6.46	1.75	0.57
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.AKGEEQDFPVDLEDTIAPR.A	21.26	34.71	0.61	1.63
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.DK#VDETGNSLK#.V	30.74	21.68	1.42	0.71
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.DK#YGVFPLR@.G	18.02	12.94	1.39	0.72
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.ELILFSNSDNER@.S	76.21	50.10	1.52	0.66
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.FLEEFITPIVK#.V	141.19	80.06	1.76	0.57
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.FLYDDNQR@.V	25.02	15.27	1.64	0.61
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.FTVDLDSDEDFSGLDEKDEDEDFLPLDATPPK.A	2.19	2.50	0.87	1.14
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.FTVETASR.E	48.59	28.61	1.70	0.59
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.GEEQDFPVDLEDTIAPR@.A	5.59	3.84	1.46	0.69
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.GFQQISFVNSIATSK#.G	31.11	13.52	2.30	0.43
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.HVDYVADQIVSK#.L	20.67	11.51	1.80	0.56
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.IFDEILVNAADNK#.Q	24.65	15.60	1.58	0.63
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.IK#SENVEGTPAEDGAEPGSLR@.Q	50.09	26.26	1.91	0.52
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.IM*IM*TDQDQDGSHIK#.G	33.81	19.34	1.75	0.57
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.IPNFDVR@.E	31.20	22.89	1.36	0.73
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.IVGLQYK#.K	74.29	31.47	2.36	0.42
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.LDDANDAGSR@.N	17.22	14.72	1.17	0.85
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.LLDGEEPLPM*LPSYK#.N	20.34	17.52	1.16	0.86
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.M*QSLDKDIVALM*VR.R	24.28	16.12	1.51	0.66
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.NHM*WIFVNALIENPTFDSQTK#.E	9.38	3.70	2.53	0.39
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.NK#QEIAFYSLPEFEEWK#.S	26.71	14.13	1.89	0.53
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.QIM*ENAEINNIIK#.I	28.64	17.58	1.63	0.61
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.R@AYDIAGSTK#.D	22.01	51.12	0.43	2.32
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.SENVEGTPAEDGAEPGSLR@.Q	27.18	16.19	1.68	0.60
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.SYVDLYLK#.D	35.79	18.45	1.94	0.52
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.TLAVSGLGVVGR@.D	101.79	58.31	1.75	0.57
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.TPSLITDYR@.E	68.18	38.44	1.77	0.56
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.VIHEQVNPR@.W	52.13	36.39	1.43	0.70
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.YGVFPLR.G	25.65	19.89	1.29	0.78
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	R.YIFTM*LSPLAR@.L	11.92	11.21	1.06	0.94
Q01320_TOP2A_MOUSE	Top2a	DNA topoisomerase 2-al	K.YSGPEDDAAISLAFSK#.K	36.57	19.24	1.90	0.53
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.ASGSENEGDYNPGR@.K	2.91	1.74	1.68	0.60
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.ASPITNDGEDEFVPSDGLDKDEYAFSSGK.S	9.58	3.49	2.74	0.36
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.DK#LDETGVALK#.V	16.47	6.01	2.74	0.36
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.DLIQM*LVQR@.G	19.17	12.42	1.54	0.65

Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.EWLVGM*LGAESTK#.L	6.16	2.43	2.54	0.39
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.FDSNEEDTASVFAPSFGLK#.Q	2.23	1.55	1.44	0.70
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.HGFLEEFITPIVK#.A	23.97	18.14	1.32	0.76
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	R.HVDYVVDQVVSK#.L	10.75	6.16	1.75	0.57
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.KTSFDQDSDVDIFPSDFTSEPPALPR.T	10.68	4.25	2.51	0.40
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.LAQAEAAGLHK#.V	12.66	5.17	2.45	0.41
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	R.LHGLPEQFLYGTATK#.H	17.47	27.60	0.63	1.58
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	R.LLFPAVDDNLLK#.F	88.10	55.82	1.58	0.63
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.LQLEETM*PSPYGR@.R	7.90	3.05	2.59	0.39
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	R.NTVEITELPVR@.T	26.49	18.45	1.44	0.70
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.SLAVSGLGVIGR@.D	39.01	22.46	1.74	0.58
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.SQDFGNLFSFPSYSQK#.S	12.42	5.68	2.19	0.46
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.SSLAGSDGALTWVNNATK#.K	5.81	3.27	1.78	0.56
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	R.YAGPEDDAAITLAFSK#.K	17.53	12.67	1.38	0.72
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	R.YIFTM*LSSLAR.L	11.99	6.77	1.77	0.56
Q64511_TOP2B_MOUSE	Top2b	DNA topoisomerase 2-be	K.YTFDFSEEEDDDAAAADDSNDLEELK#VK#.A	4.71	2.40	1.96	0.51
Q6ZQF0_TOPB1_MOUSE	Topbp1	DNA topoisomerase 2-bi	R.FNQLNEDVTHVIVGDYDDDVR@.Q	16.70	3.63	4.59	0.22
Q6ZQF0_TOPB1_MOUSE	Topbp1	DNA topoisomerase 2-bi	K.GYILPEESYIHTNYQPAGIAVSDQPGNQTAVLDK#.S	3.35	1.63	2.05	0.49
Q6ZQF0_TOPB1_MOUSE	Topbp1	DNA topoisomerase 2-bi	K.LFK#PSFDVTDALAALETPNAASQK#.R	10.09	4.74	2.13	0.47
Q6ZQF0_TOPB1_MOUSE	Topbp1	DNA topoisomerase 2-bi	R.NDQEPFLVK#.F	11.66	3.09	3.77	0.27
Q6ZQF0_TOPB1_MOUSE	Topbp1	DNA topoisomerase 2-bi	R.DLNVSVTHLIAGEVGSK#.K	12.13	3.03	4.00	0.25
Q6ZQF0_TOPB1_MOUSE	Topbp1	DNA topoisomerase 2-bi	R.NDQEPFLVK#.F	12.20	5.81	2.10	0.48
Q9ER81_IFG15_MOUSE	Tor1aip2	Torsin-1A-interacting pr	R.VAGFNPALQLILSR@.T	8.95	5.98	1.50	0.67
Q9ER38_TOR3A_MOUSE	Tor3a	Torsin-3A OS=Mus muscu	R.DAFLGQDLPYTEETLDEIAK#.M	4.75	2.40	1.98	0.51
Q8BU11_TOX4_MOUSE	Tox4	TOX high mobility group	K.DPNEPQK#PVSAYALFFR@.D	20.60	4.03	5.11	0.20
Q8BU11_TOX4_MOUSE	Tox4	TOX high mobility group	R.DVFLAWVASR@.N	23.62	7.79	3.03	0.33
Q8BU11_TOX4_MOUSE	Tox4	TOX high mobility group	R.GLQVGQTSTATIQPSQQAQIVTR@.S	30.30	9.68	3.13	0.32
Q8BU11_TOX4_MOUSE	Tox4	TOX high mobility group	K.GQNPNATFGEVSK#.I	50.45	14.21	3.55	0.28
Q8BU11_TOX4_MOUSE	Tox4	TOX high mobility group	R.INLQQQPPPLQSK#.I	23.64	7.61	3.11	0.32
Q8BU11_TOX4_MOUSE	Tox4	TOX high mobility group	K.IVASM*WDSLGEEQK#.Q	15.11	5.38	2.81	0.36
Q8BU11_TOX4_MOUSE	Tox4	TOX high mobility group	K.IVASMWDSLGEEQK#.Q	9.65	3.17	3.04	0.33
Q8BU11_TOX4_MOUSE	Tox4	TOX high mobility group	K.GQNPNATFGEVSK#.I	8.63	3.28	2.63	0.38
Q8BU11_TOX4_MOUSE	Tox4	TOX high mobility group	R.INLQQQPPPLQSK#.I	9.28	1.55	6.00	0.17
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.DSFEVR@.V	155.90	85.04	1.83	0.55
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.ELNEALELK#.D	108.91	58.84	1.85	0.54
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.ELNEALELK#DAHATEESGDSR@.A	66.97	36.47	1.84	0.54
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.HSVVVPYEPPEAGSEYTTIHYK#.Y	40.70	24.54	1.66	0.60
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.K#K#PLDGEYFTLK#.I	156.40	78.81	1.98	0.50
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.KPLDGEYFTLK.I	105.74	61.88	1.71	0.59
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.R@PILTIITLEDSSGNLLGR@.D	348.90	154.35	2.26	0.44
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.R@TEEENFR@.K	46.48	21.97	2.12	0.47
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.SQHM*TEVVR@.R	20.15	14.27	1.41	0.71
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.TEEENFR.K	52.38	27.20	1.93	0.52
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.TYQGNYGFHLGFLQSGTAK#.S	5.30	3.52	1.50	0.67
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.VEGNLYPEYLEDR@.Q	210.77	114.89	1.83	0.55
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.VSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQK.T	35.78	20.09	1.78	0.56
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.DSFEVR.V	135.82	56.32	2.41	0.41
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.ELNEALELK#.D	167.10	70.51	2.37	0.42
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.ELNEALELK#DAHATEESGDSR@.A	47.18	22.77	2.07	0.48
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.HSVVVPYEPPEAGSEYTTIHYK#.Y	52.45	27.47	1.91	0.52
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.KKPLDGEYFTLK.I	229.39	99.66	2.30	0.43
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.K#PLDGEYFTLK#.I	121.63	58.86	2.07	0.48
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.RPILTIITLEDSSGNLLGR.D	536.36	212.80	2.52	0.40
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.R@TEEENFR@.K	67.37	29.64	2.27	0.44
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.SQHM*TEVVR@.R	24.25	9.60	2.53	0.40
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.TYQGNYGFHLGFLQSGTAK#.S	3.51	1.92	1.83	0.55
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.VEGNLYPEYLEDR.Q	317.11	129.36	2.45	0.41
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.VSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQK#.T	35.88	22.16	1.62	0.62
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.DAHATEESGDSR@.A	3.09	2.54	1.22	0.82
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.DSFEVR@.V	374.50	155.32	2.41	0.41
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.ELNEALELK#.D	306.07	138.82	2.20	0.45
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.ELNEALELK#DAHATEESGDSR@.A	73.53	28.37	2.59	0.39
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.FEMFR.E	25.33	12.07	2.10	0.48
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.HSVVVPYEPPEAGSEYTTIHYK.Y	108.00	47.48	2.27	0.44
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.K#K#PLDGEYFTLK#.I	317.41	146.26	2.17	0.46
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.KPLDGEYFTLK.I	210.30	97.01	2.17	0.46
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.R@PILTIITLEDSSGNLLGR@.D	710.36	296.28	2.40	0.42
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.R@PILTIITLEDSSGNLLGR@.D	24.59	8.90	2.76	0.36
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.R@TEEENFR@.K	120.46	53.35	2.26	0.44
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	K.SQHM*TEVVR.R	48.55	21.26	2.28	0.44
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.TEEENFR.K	147.68	58.80	2.51	0.40
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.VEGNLYPEYLEDR@.Q	561.87	241.48	2.33	0.43
P02340_P53_MOUSE	Tp53	Cellular tumor antigen p	R.VSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQK#.T	60.97	28.59	2.13	0.47
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.ASGTEAADFALPSSR@.G	12.63	2.93	4.30	0.23
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.LR@EQYGLGPYEAVTPLTK#.A	7.47	3.31	2.26	0.44
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.M*AVILSLEQGNR@.L	9.03	50.46	0.18	5.59
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.VITDVYYVDGTEVER@.K	12.07	4.00	3.01	0.33
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.AADISLDNLVEGK#.R	27.73	6.89	4.02	0.25
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.ANLLHFPSAQEEDK#ER@PDVTPK#.L	24.87	5.05	4.93	0.20
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.ASDPVESSHLGTSGSISQVIER@.L	10.52	1.91	5.51	0.18
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.ASGTEAADFALPSSR@.G	39.97	9.29	4.30	0.23
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.ASQEPFSPAEDVM*ETDLLEGLAANQDRPSK.M	15.24	4.97	3.07	0.33
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.DEPVR@PDQETQQPQVQEK#.E	48.61	8.20	5.93	0.17
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.EAQSEAPPSAPDR@.A	12.80	3.91	3.27	0.31
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.ELLEEGPQVQPSSEPEVSSTQEDLFDQSSK#.T	4.79	1.92	2.50	0.40
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.ENPFQNLK#.V	25.88	3.66	7.08	0.14
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.EQYGLGPYEAVTPLTK#.A	8.22	2.73	3.01	0.33
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.ESGELYYSIEK#.E	37.06	7.66	4.84	0.21
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.ESPVTVDAEVADDK#.Q	5.68	2.33	2.44	0.41
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.ETVVSGPLGVEDISPSM*SPDDK#.S	6.48	1.76	3.67	0.27
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.ETVVSGPLGVEDISPSM*SPDDK#SFTR@.I	9.69	1.91	5.07	0.20
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.GIHVVEEQNLPLVR@.S	23.26	6.03	3.86	0.26
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.ILDWQPR@.E	17.12	5.17	3.31	0.30
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.K#LPTSEEER@.S	10.22	2.99	3.42	0.29
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.LLDGPTGSSEEEEEFLEIPPFNK#.Q	14.67	4.38	3.35	0.30
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.LM*LSTSEYSQSSK#.M	11.39	2.63	4.33	0.23
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.LR@EQYGLGPYEAVTPLTK#.A	27.81	7.66	3.63	0.28
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.M*AVILSLEQGNR@.L	23.01	5.68	4.05	0.25
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	K.QDATVQTER@.G	16.38	1.54	10.66	0.09
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.QSEQPVK#PVGPVM*DDAAPEDSASPVSQQR@.A	9.20	2.96	3.10	0.32
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.SEALSSVLDQEEAM*DTK#.E	11.87	2.20	5.39	0.19
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.SEDR@PSSPQVSVAAVETK#.E	5.61	2.88	1.94	0.51
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.SNISSPVTPTAASSSSTTPTR@.K	14.51	2.30	6.30	0.16

P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.TEEDR@ENTQIDDTEPLSPVSNSK#.L	9.75	1.89	5.15	0.19
P70399_TP53B_MOUSE	Tp53bp1	Tumor suppressor p53-bi	R.VITDVYYVDGTEVER@.K	47.25	10.10	4.68	0.21
Q62393_TPD52_MOUSE	Tpd52	Tumor protein D52 OS=	R.ELTKVEEEIQTLSQVLAAK.E	11.23	8.33	1.35	0.74
Q9CYZ2_TPD54_MOUSE	Tpd52l2	Tumor protein D54 OS=	K.GVLSDFM*TDVPVDPGVVHR@.T	15.62	5.20	3.00	0.33
Q9CYZ2_TPD54_MOUSE	Tpd52l2	Tumor protein D54 OS=	R.TPVVEGLTEGEEEELR@AELAK#.V	13.60	6.24	2.18	0.46
Q9CYZ2_TPD54_MOUSE	Tpd52l2	Tumor protein D54 OS=	K.TSAALSTM*GSAISR@.K	35.16	11.66	3.02	0.33
Q9CYZ2_TPD54_MOUSE	Tpd52l2	Tumor protein D54 OS=	K.TSAALSTM*GSAISR.K	4.00	4.30	0.93	1.08
P17751_TPIS_MOUSE	Tpi1	Triosephosphate isomera	K.VVLAYEPVWAIGTGK#.T	13.33	20.61	0.65	1.55
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.AEFAER@.S	133.17	74.57	1.79	0.56
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	K.ATDAEADVASLNR@.R	49.31	27.00	1.83	0.55
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	K.GTEDELDKYSEALKDAQEK.L	14.60	11.53	1.27	0.79
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	K.HIAEDADR@.K	44.68	21.87	2.04	0.49
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.IQLVEEELDR@.A	239.48	144.88	1.65	0.60
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	K.KATDAEADVASLNR.R	28.42	20.22	1.41	0.71
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.KLVIIESDLER.A	70.14	25.76	2.72	0.37
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.K#LVIIESDLER@AEER@.A	136.99	81.92	1.67	0.60
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.K#YEEVAR@.K	94.61	67.60	1.40	0.71
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.LATALQK#.L	337.54	240.23	1.41	0.71
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	K.LEEAEK#AADESER@.G	133.26	91.27	1.46	0.68
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	K.LVIIESDLER@.A	83.88	48.51	1.73	0.58
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.R@IQLVEEELDR@.A	25.59	16.21	1.58	0.63
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.RIQLVEEELDRAQER.L	114.23	59.27	1.93	0.52
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	K.SIDDLEDELYAQK#.L	16.11	6.89	2.34	0.43
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.SK#QLEDELVSLQK#.K	82.78	38.91	2.13	0.47
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.SK#QLEDELVSLQK#K#.L	17.65	9.08	1.94	0.51
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	K.SLEAQAEK#.Y	50.76	29.86	1.70	0.59
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	K.YSQK#EDK#YEEEIK#.V	226.85	124.78	1.82	0.55
G5E8R1_G5E8R1_MOUSE	Tpm1	Tropomyosin 1, alpha, is	K.EENLSM*HQM*LDQTLLELNNM*.-	4.42	4.42	1.00	1.00
G5E8R1_G5E8R1_MOUSE	Tpm1	Tropomyosin 1, alpha, is	R.ETAEADVASLNR@.R	58.71	43.24	1.36	0.74
G5E8R1_G5E8R1_MOUSE	Tpm1	Tropomyosin 1, alpha, is	K.SIDDLEEK#.V	203.66	132.84	1.53	0.65
G5E8R1_G5E8R1_MOUSE	Tpm1	Tropomyosin 1, alpha, is	R.SLQEQADAAEER@.A	171.43	107.91	1.59	0.63
E9Q450_E9Q450_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.AELSEGQVR@.Q	56.61	44.68	1.27	0.79
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.IQLVEEELDR@.A	17.27	13.82	1.25	0.80
P58771_TPM1_MOUSE	Tpm1	Tropomyosin alpha-1 cha	R.LATALQK#.L	34.52	15.68	2.20	0.45
A2AIM4_A2AIM4_MOUSE	Tpm2	Tropomyosin beta chain	R.K#LVILEGELER@.S	24.92	15.04	1.66	0.60
A2AIM4_A2AIM4_MOUSE	Tpm2	Tropomyosin beta chain	K.QLEEEQQALQK#.K	13.16	9.97	1.32	0.76
A2AIM4_A2AIM4_MOUSE	Tpm2	Tropomyosin beta chain	K.SLIASEEEYSTK#.E	3.93	5.22	0.75	1.33
E9Q7Q3_E9Q7Q3_MOUSE	Tpm3	Tropomyosin alpha-3 cha	R.AREQAEAEVASLNR.R	31.82	16.21	1.96	0.51
E9Q7Q3_E9Q7Q3_MOUSE	Tpm3	Tropomyosin alpha-3 cha	R.AREQAEAEVASLNRR.I	45.49	16.96	2.68	0.37
E9Q7Q3_E9Q7Q3_MOUSE	Tpm3	Tropomyosin alpha-3 cha	K.TIDDLEDELYAQK#.L	6.13	3.03	2.02	0.49
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.AELAESR@.C	44.94	29.30	1.53	0.65
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.ALKDEEKM*ELQEIQLK.E	39.43	29.55	1.33	0.75
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.ALK#DEEK#MELQEIQLK#.E	18.87	13.47	1.40	0.71
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	K.IQVLQQQADDAEER@.A	89.39	70.87	1.26	0.79
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	K.IQVLQQQADDAEER@AER@.L	35.14	19.09	1.84	0.54
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.K#IQVLQQQADDAEER@.A	136.87	98.34	1.39	0.72
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.K#IQVLQQQADDAEER@AER@.L	35.88	22.90	1.57	0.64
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.K#LVIIEGDLER@.T	125.60	96.30	1.30	0.77
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.K#LVIIEGDLER@TEER@.A	59.06	28.80	2.05	0.49
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	K.LVIIEGDLER@.T	58.02	36.16	1.60	0.62
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.M*LDQTLLDLNEM*.-	108.91	108.91	1.00	1.00
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.MLDQTLLDLNEM*.-	9.15	9.15	1.00	1.00
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	R.MLDQTLLDLNEM.-	6.69	6.69	1.00	1.00
D3Z2H9_D3Z2H9_MOUSE	Tpm3-rs7	Uncharacterized protein	K.TIDDLEDK#LK#.C	30.87	28.43	1.09	0.92
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	K.AEGDAAALNR@.R	11.46	10.40	1.10	0.91
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	K.HITDEADR@.K	12.19	10.03	1.22	0.82
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	K.HITDEADR@K#YEEVAR@.K	27.62	22.20	1.24	0.80
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	K.IQALQQQADDAEDR@.A	26.07	13.94	1.87	0.53
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	K.IQALQQQADDAEDR@AQGLQR@.E	23.74	16.66	1.43	0.70
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	R.IQLLEEELDR@.A	24.10	19.47	1.24	0.81
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	R.K#IQALQQQADDAEDR@.A	28.46	18.96	1.50	0.67
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	R.KIQALQQQADDAEDRAQGLQR.E	10.73	5.65	1.90	0.53
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	R.K#LVILEGELK#.R	18.97	13.87	1.37	0.73
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	R.K#LVILEGELK#R@.A	21.21	21.96	0.97	1.04
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	K.LVILEGELK#.R	16.39	11.76	1.39	0.72
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	K.TIDDLEEK#.L	49.37	39.48	1.25	0.80
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	K.YSEK#EDK#YEEEIK#.L	5.01	4.41	1.14	0.88
Q6IRU2_TPM4_MOUSE	Tpm4	Tropomyosin alpha-4 cha	K.YSEK#EDK#YEEEIK#.L	61.54	46.58	1.32	0.76
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.ELQELQDSLNVER@.E	6.14	11.95	0.51	1.95
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.K#LELDILPLQEANAELSEK#.S	7.64	2.47	3.10	0.32
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.ASTALSNEQQAR@.R	65.17	21.91	2.97	0.34
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.DAVQAPLNVSLNEEGK#.S	18.70	7.61	2.46	0.41
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.EITSLQER.N	36.75	12.76	2.88	0.35
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.ELQELQDSLNVER@.E	41.24	11.48	3.59	0.28
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.FEVAQVESLR@.Y	50.32	15.69	3.21	0.31
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.FHNELNAHIK#.L	17.12	6.39	2.68	0.37
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.FK#VESEQQYFEIEK#.R	13.52	6.65	2.03	0.49
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.FK#VESEQQYFEIEK#R@.L	7.16	4.93	1.45	0.69
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.GIASTSDPPTANIK#PTPVVSTPSK#.V	20.92	9.74	2.15	0.47
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.GNHVIR@DEEVSSADISSSSEVISQHLVSYR@.N	16.94	4.66	3.64	0.28
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.HVEDLLTK#.L	25.13	9.78	2.57	0.39
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.IAELQHK#.L	14.33	11.75	1.22	0.82
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.K#LELDILPLQEANAELSEK#.S	97.48	36.23	2.69	0.37
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.K#LENEVEQR@.H	26.96	14.27	1.89	0.53
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.LAVAEVR@.A	70.94	15.27	4.64	0.22
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.LENSLAELEQLR@.E	54.16	17.39	3.12	0.32
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.LEQNLQQM*QAK#.V	13.31	4.91	2.71	0.37
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.LLHDQIEK#.L	21.82	4.59	4.75	0.21
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.LQEQVTDLR@.S	65.07	19.34	3.36	0.30
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.LQNEQLEK#.L	19.03	6.72	2.83	0.35
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.LSQEVEYLTEDVK#.R	5.59	1.49	3.76	0.27
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.LTELYNAYVETQDQLLLEK#.Q	16.16	6.74	2.40	0.42
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.NIEELQQQNQR@.L	34.94	8.85	3.95	0.25
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.NLGIQSQFTR@.A	38.60	14.46	2.67	0.37
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.NQQLINQQK#.D	10.37	6.12	1.70	0.59
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.NQQLINQQK#DPDTEEYR@K#.L	10.38	3.33	3.12	0.32
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.QEQIINTM*TQDLR@.G	13.62	3.97	3.43	0.29
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.QHLNNM*EAQLASQSTQR@.T	7.55	4.27	1.77	0.57
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.R@SSTSQTVSTPAPEPVIDSTEAIEAK#.A	8.77	5.23	1.68	0.60
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.SLEGQVENLQK#.T	38.75	12.59	3.08	0.32
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.SLQEQTVQLQSELSR.L	23.31	6.95	3.36	0.30
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.SNASLTNNQNLIQSLR@.E	11.56	5.09	2.27	0.44
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.SQEQILEILR@.F	44.68	13.25	3.37	0.30

F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.TDELLALGR@.E	30.65	14.10	2.17	0.46
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.TETM*NVVM*ETNK#.M	19.16	6.91	2.77	0.36
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	K.TLSTVQNEVQEALQR@.A	39.87	11.35	3.51	0.28
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.VLK#DEVSK#.S	23.17	7.26	3.19	0.31
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.VLLM*ELEEAR@.G	29.78	11.40	2.61	0.38
F6ZDS4_TPR_MOUSE	Tpr	Nucleoprotein TPR OS=	R.VLLMELEEAR@.G	9.74	3.67	2.65	0.38
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.ANGM*ELDGR@.R	36.26	21.45	1.69	0.59
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.GFAFVYFER@.I	229.51	122.46	1.87	0.53
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.GYDRYEDYDYR.R	250.30	137.54	1.82	0.55
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.GYDR@YEDYDYR@.R	40.26	16.44	2.45	0.41
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.IDDSKEAM*ER.A	31.30	25.45	1.23	0.81
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.IR@VDYSITK#.R	119.24	73.51	1.62	0.62
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.IR@VDYSITK#R@.A	26.37	13.10	2.01	0.50
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.YEDYDYR@.R	45.02	31.42	1.43	0.70
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.YGPLSGVNVVYDQR.T	338.87	183.53	1.85	0.54
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.GFAFVYFER.I	12.18	10.66	1.14	0.88
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.IDDSK#EAM*ER@.A	3.72	8.49	0.44	2.28
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.IRVDYSITK.R	11.27	11.25	1.00	1.00
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.YGPLSGVNVVYDQR@.T	14.13	10.33	1.37	0.73
Q6PFR5_TRA2A_MOUSE	Tra2a	Transformer-2 protein h	R.YGPLSGVNVVYDQR.T	7.21	4.80	1.50	0.67
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	R.DLR@EVFSK#.Y	69.57	36.41	1.91	0.52
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	R.GFAFVYFENVDDAK#.E	656.38	336.96	1.95	0.51
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	R.GFAFVYFENVDDAK#EAK#.E	19.82	10.97	1.81	0.55
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	R.GYDDR@DYYSR@.S	160.64	77.12	2.08	0.48
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	R.IR@VDFSITK#.R	56.40	29.69	1.90	0.53
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	R.VDFSITK#.R	294.03	179.19	1.64	0.61
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	K.YGPIADVSIVYDQQSR@.R	524.99	293.70	1.79	0.56
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	K.YGPIADVSIVYDQQSR@.R	102.52	59.21	1.73	0.58
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	R.GFAFVYFENVDDAK.E	13.90	11.72	1.19	0.84
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	R.IR@VDFSITK#.R	11.63	11.78	0.99	1.01
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	R.VDFSITK#.R	13.36	7.48	1.79	0.56
P62996_TRA2B_MOUSE	Tra2b	Transformer-2 protein h	K.YGPIADVSIVYDQQSR@.R	22.21	16.85	1.32	0.76
Q9CQN1_TRAP1_MOUSE	Trap1	Heat shock protein 75 k	K.AFLEALQNQAETSSK#.I	16.91	6.87	2.46	0.41
Q9CQN1_TRAP1_MOUSE	Trap1	Heat shock protein 75 k	R.AQLLQPTLEINPR@.H	13.20	4.85	2.72	0.37
Q9CQN1_TRAP1_MOUSE	Trap1	Heat shock protein 75 k	R.ELISNASDALEK#.L	15.49	21.55	0.72	1.39
Q9CQN1_TRAP1_MOUSE	Trap1	Heat shock protein 75 k	R.YESSALPAGQLTSLPDYASR@.M	9.12	3.83	2.38	0.42
Q9CQN1_TRAP1_MOUSE	Trap1	Heat shock protein 75 k	K.AFLEALQNQAETSSK#.I	13.69	7.85	1.74	0.57
Q9CQN1_TRAP1_MOUSE	Trap1	Heat shock protein 75 k	R.AQLLQPTLEINPR@.H	9.58	2.08	4.60	0.22
Q9CQN1_TRAP1_MOUSE	Trap1	Heat shock protein 75 k	R.YESSALPAGQLTSLPDYASR@.M	4.65	1.79	2.60	0.39
Q9CQP2_TPPC2_MOUSE	Trappc2	Trafficking protein partic	K.FAM*NPFYEPNSPIR@.S	2.90	2.27	1.28	0.78
O55013_TPPC3_MOUSE	Trappc3	Trafficking protein partic	K.FVQDTLK#GDGVTEIR@.M	7.23	3.62	2.00	0.50
Q9ES56_TPPC4_MOUSE	Trappc4	Trafficking protein partic	K.AGGLIYQWDSYSPR@.A	5.40	1.80	3.01	0.33
Q9CQA1_TPPC5_MOUSE	Trappc5	Trafficking protein partic	K.VLGALLFVK#.G	5.19	4.32	1.20	0.83
Q91XB0_TREX1_MOUSE	Trex1	Three-prime repair exon	R.QRFDDNLAILLR.A	3.81	5.63	0.68	1.48
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	K.EQLQVVLQR@.L	18.36	8.83	2.08	0.48
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	K.FR@APDLQGM*LQVLQEVTEAQR@.Y	8.25	4.58	1.80	0.55
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	K.LAESENEHAQQSK#.L	6.38	2.80	2.28	0.44
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	R.LK#EFK#PSPEEEQK#.V	27.87	20.42	1.36	0.73
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	K.TALIEEVAQEYKEQLQVVLQR.L	59.38	35.33	1.68	0.59
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	R.TYWENQIQK#.D	21.48	13.00	1.65	0.61
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	R.YEDLQAR@.N	55.35	22.23	2.49	0.40
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	K.TALIEEVAQEYK#EQLQVVLQR@.L	19.45	5.33	3.65	0.27
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	K.TALIEEVAQEYK#.E	6.77	3.33	2.03	0.49
E9Q987_E9Q987_MOUSE	Trim12c	Protein Trim12c OS=Mus	R.YEDLQAR@.N	14.33	6.23	2.30	0.43
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.DHTR@VPIEEAAK#.V	60.16	43.74	1.38	0.73
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	K.EAELAEK#NQALQELISELER@.R	24.67	17.96	1.37	0.73
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.FSNYPM*VLGAQR@.F	43.58	38.76	1.12	0.89
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.FSNYPMVLGAQR@.F	20.06	17.65	1.14	0.88
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.GSELELLQEVR@.I	163.32	134.84	1.21	0.83
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.HIANM*VENLK#.Q	75.25	67.77	1.11	0.90
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.HIANMVENLK#.Q	12.85	11.18	1.15	0.87
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.IHAEFALQNSLLAQEEQR@.Q	80.27	65.06	1.23	0.81
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	K.IHVALEK#.L	74.94	49.47	1.51	0.66
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.IRGSELELLQEVR.I	52.48	36.73	1.43	0.70
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	K.M*EM*DLTM*QR.T	46.51	39.62	1.17	0.85
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	K.MEM*DLTM*QR.T	8.66	5.69	1.52	0.66
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.M*GDTHQNVSDNEER.F	11.47	8.07	1.42	0.70
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	K.M*YWEVDVTQK#.E	46.23	41.85	1.10	0.91
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	K.MYWEVDVTQK#.E	8.89	7.76	1.15	0.87
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	K.NQALQELISELER@.R	220.48	187.57	1.18	0.85
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.NTANSWLIISK#.D	86.04	54.13	1.59	0.63
Q3U7K7_Q3U7K7_MOUSE	Trim21	E3 ubiquitin-protein liga	R.VPIEEAAK.V	95.87	101.21	0.95	1.06
Q61510_TRI25_MOUSE	Trim25	E3 ubiquitin/ISG15 ligas	K.FDTIYQVLVK#.K	6.38	3.71	1.72	0.58
Q61510_TRI25_MOUSE	Trim25	E3 ubiquitin/ISG15 ligas	K.IDLDHDLIM*GIYQGAADLK#.S	11.01	5.30	2.08	0.48
Q61510_TRI25_MOUSE	Trim25	E3 ubiquitin/ISG15 ligas	K.IDLDHDLIM*GIYQGAADLK#SELK#.H	4.98	1.62	3.07	0.33
Q61510_TRI25_MOUSE	Trim25	E3 ubiquitin/ISG15 ligas	K.ASAAQPDSVGVK#.A	22.67	23.91	0.95	1.05
Q61510_TRI25_MOUSE	Trim25	E3 ubiquitin/ISG15 ligas	K.FDTIYQVLVK#.K	12.77	4.88	2.61	0.38
Q61510_TRI25_MOUSE	Trim25	E3 ubiquitin/ISG15 ligas	K.IDLDHDLIM*GIYQGAADLK#.S	13.80	4.58	3.01	0.33
Q61510_TRI25_MOUSE	Trim25	E3 ubiquitin/ISG15 ligas	K.SR@TELLEYFVK#.V	18.67	6.32	2.95	0.34
Q61510_TRI25_MOUSE	Trim25	E3 ubiquitin/ISG15 ligas	K.VLENFLTK#.S	21.69	7.98	2.72	0.37
Q61510_TRI25_MOUSE	Trim25	E3 ubiquitin/ISG15 ligas	K.ASAAQPDSVGVK#.A	8.35	4.28	1.95	0.51
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.DIVENYFM*R.D	25.23	20.76	1.22	0.82
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	R.FASWALESDNNTALLLSK.K	16.62	11.48	1.45	0.69
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.IVAER@PGTNSTGPGPM*APPR@.A	29.61	13.35	2.22	0.45
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.K#LIYFQLHR@.A	10.65	8.97	1.19	0.84
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	R.LDLDLTSDSQPPVFK#.V	46.65	36.23	1.29	0.78
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.LSPPYSSPQEFAQDVGR@.M	29.47	12.66	2.33	0.43
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.M*AILQIM*K#.E	20.50	17.77	1.15	0.87
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	R.M*NDAFGDTK#.F	11.20	5.36	2.09	0.48
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.QGSGSSQPM*EVQEGYGFGSDDPYSSAEPHVSGM*K#.R	8.04	3.00	2.68	0.37
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.QGSGSSQPM*EVQEGYGFGSDDPYSSAEPHVSGM*KR.S	6.27	4.89	1.28	0.78
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	R.SGEGEVSGLLR@.K	53.25	27.51	1.94	0.52
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.VFPGSTTEDYNLIVIER.G	6.54	4.04	1.62	0.62
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	R.VLVNDAQK#.V	74.44	65.91	1.13	0.89
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.LSPPYSSPQEFAQDVGR@.M	4.29	4.71	0.91	1.10
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.LTEDKADVQSIIGLQR.F	937.35	9.81	95.53	0.01
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	R.M*NDAFGDTK#.F	4.01	3.42	1.17	0.85
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.ADVQSIIGLQR@.F	65.27	47.45	1.38	0.73
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.DHQYQFLEDAVR@.N	15.16	9.18	1.65	0.61
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.DIVENYFM*R@.D	105.46	70.35	1.50	0.67
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.DIVENYFMR.D	24.74	14.87	1.66	0.60
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	R.FASWALESDNNTALLLSK#.K	86.13	46.57	1.85	0.54
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedi	K.FSAVLVEPPPLNLPSAGLSSQELSGPGDGP.-	106.07	106.07	1.00	1.00

Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.GAAAAAAGQAGTVPPGAPGAPPLPGM*AIVK.E	4.66	2.24	2.08	0.48
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.IVAERPGTNSTGPGPM*APPR.A	143.93	114.81	1.25	0.80
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.IVAER@PGTNSTGPGPMAPPR@.A	28.18	26.76	1.05	0.95
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.K#LIYFQLHR@.A	39.17	31.08	1.26	0.79
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.K#LLASLVK#.R	114.25	83.81	1.36	0.73
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.LDLDLTSDSQPPVFK#.V	277.63	191.43	1.45	0.69
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.LSPPYSSPQEFAQDVGR@.M	93.23	67.23	1.39	0.72
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.LTEDK#ADVQSIIGLQR@.F	16.02	10.09	1.59	0.63
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.LTEDKADVQSIIGLQR.F	234.28	142.27	1.65	0.61
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.M*AILQIM*K#.E	99.92	63.22	1.58	0.63
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.MAILQIM*K#.E	23.58	18.15	1.30	0.77
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.MAILQIMK#.E	18.38	11.11	1.65	0.60
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.MNDAFGDTK#.F	11.04	8.92	1.24	0.81
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.M*NDAFGDTK#.F	77.94	47.97	1.62	0.62
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.QGSGSSQPM*EVQEGYGFGSDDPYSSAEPHVSGM*K#.R	6.87	3.38	2.03	0.49
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.QGSGSSQPM*EVQEGYGFGSDDPYSSAEPHVSGMK#.R	4.91	3.25	1.51	0.66
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.QGSGSSQPMEVQEGYGFGSDDPYSSAEPHVSGM*K#R@.S	4.36	4.11	1.06	0.94
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.SGEGEVSGLLR@.K	337.81	202.40	1.67	0.60
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.VFPGSTTEDYNLIVIER.G	84.75	55.10	1.54	0.65
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.VFPGSTTEDYNLIVIER@.G	28.60	18.96	1.51	0.66
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.VLVNDAQK#.V	204.71	140.55	1.46	0.69
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.VTEGQQER@.L	17.29	11.36	1.52	0.66
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.DHQYQFLEDAVR@.N	24.46	8.82	2.77	0.36
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.DIVENYFM*R@.D	50.74	18.53	2.74	0.37
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.EEDGSLSLDGADSTGVVAK#.L	10.01	6.35	1.58	0.63
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.FASWALESDNNTALLLSK#.K	42.15	16.95	2.49	0.40
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.FQWDLNAWTK#.S	20.22	7.83	2.58	0.39
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.IVAER@PGTNSTGPGPM*APPR@.A	39.70	26.86	1.48	0.68
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.K#LLASLVK#.R	37.57	15.84	2.37	0.42
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.LDLDLTSDSQPPVFK#.V	100.59	37.32	2.70	0.37
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.LSPPYSSPQEFAQDVGR@.M	47.09	18.22	2.58	0.39
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.LTEDK#ADVQSIIGLQR@.F	92.90	30.72	3.02	0.33
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.M*AILQIM*K#.E	46.57	15.25	3.05	0.33
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.SGEGEVSGLLR.K	90.63	29.74	3.05	0.33
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	K.VFPGSTTEDYNLIVIER.G	31.80	14.38	2.21	0.45
Q62318_TIF1B_MOUSE	Trim28	Transcription intermedia	R.VLVNDAQK#.V	110.82	46.98	2.36	0.42
Q9R1R2_TRIM3_MOUSE	Trim3	Tripartite motif-containi	K.GEFTNLQGVSAASSGR@.I	7.68	3.00	2.56	0.39
Q9R1R2_TRIM3_MOUSE	Trim3	Tripartite motif-containi	R.LGSAPEVLLVR@.K	24.18	7.90	3.06	0.33
Q9R1R2_TRIM3_MOUSE	Trim3	Tripartite motif-containi	R.QALVGQPASLTVTTK#.D	8.08	4.80	1.68	0.59
Q9R1R2_TRIM3_MOUSE	Trim3	Tripartite motif-containi	R.SVLNLGALLTTSATAHETVATGEGLR@.Q	15.72	5.92	2.65	0.38
Q9R1R2_TRIM3_MOUSE	Trim3	Tripartite motif-containi	K.VLQTQLDTLR@.Q	21.37	7.50	2.85	0.35
P15533_TR30A_MOUSE	Trim30a	Tripartite motif-containi	K.LEESENELEDQTELVR@.D	5.96	6.39	0.93	1.07
Q8CH72_TRI32_MOUSE	Trim32	E3 ubiquitin-protein liga	R.ELTLQDVELLK#.V	11.69	4.38	2.67	0.37
Q8CH72_TRI32_MOUSE	Trim32	E3 ubiquitin-protein liga	R.ITSLTQLTDNLTVLK#.I	9.35	3.72	2.51	0.40
Q99PP7_TRI33_MOUSE	Trim33	E3 ubiquitin-protein liga	K.LLQQQNDITGLSR@.Q	6.04	2.92	2.07	0.48
Q99PP7_TRI33_MOUSE	Trim33	E3 ubiquitin-protein liga	K.LLQQQNDITGLSR@.Q	20.21	8.60	2.35	0.43
Q99PP7_TRI33_MOUSE	Trim33	E3 ubiquitin-protein liga	K.VAIFTLINEINK#K#.G	5.22	1.89	2.77	0.36
Q99PP7_TRI33_MOUSE	Trim33	E3 ubiquitin-protein liga	K.LLQQQNDITGLSR@.Q	12.24	3.19	3.83	0.26
Q99PP6_TR34A_MOUSE	Trim34a	Tripartite motif-containi	R.FSLENLQANK#.H	6.20	3.45	1.80	0.56
Q8C006_TRI35_MOUSE	Trim35	Tripartite motif-containi	K.QLAEQTEALAR@.E	8.45	2.07	4.08	0.25
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.EQAASVGTQVEEAAER@.I	10.68	3.75	2.85	0.35
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.K#PGLEELLAGVDSNLVELEATR@.V	8.42	3.44	2.45	0.41
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.VVDLVGYR@.A	8.93	4.54	1.97	0.51
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.ALVEAAEEATR@.E	39.04	15.82	2.47	0.41
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	K.EGK#DQNPQEDDGVFIER@.G	17.99	7.35	2.45	0.41
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.EIVPVPAEGVAAFK#.T	16.49	7.59	2.17	0.46
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.EQAASVGTQVEEAAER@.I	13.63	7.74	1.76	0.57
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.K#PGLEELLAGVDSNLVELEATR@.V	17.97	7.24	2.48	0.40
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.SR@K#PGLEELLAGVDSNLVELEATR@.V	5.82	5.85	0.99	1.01
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.VAEK#EALALLR@.E	17.05	5.86	2.91	0.34
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	R.VVDLVGYR@.A	25.59	9.75	2.62	0.38
Q80VI1_TRI56_MOUSE	Trim56	E3 ubiquitin-protein liga	K.VVILDPK#.G	18.37	6.06	3.03	0.33
Q0KL02_TRIO_MOUSE	Trio	Triple functional domain	K.DNFDAFYSEVAELGR@.G	3.67	1.83	2.01	0.50
Q0KL02_TRIO_MOUSE	Trio	Triple functional domain	K.LQR@PLTPGSSDSLTASANYSK#.A	2.95	4.79	0.62	1.62
Q0KL02_TRIO_MOUSE	Trio	Triple functional domain	K.NILNELFQR@.E	13.66	6.38	2.14	0.47
Q0KL02_TRIO_MOUSE	Trio	Triple functional domain	R.VQDLLEFLHEK#.Q	12.36	4.55	2.71	0.37
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.LDEANAALDSASR@.L	5.89	3.43	1.72	0.58
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.SELTQSQTQGSSR@.N	3.34	1.44	2.31	0.43
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.VSAFHEDDM*DFGDVISSQQEINR@.L	7.47	1.94	3.85	0.26
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	K.AGELNQLLNAVK#.S	23.30	12.51	1.86	0.54
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	K.DLEIQALHAR@.I	25.23	708.09	0.04	28.07
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.IEELENLLQQGGSGVTVTDHSK#.V	16.32	4.09	3.99	0.25
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.ILILEM*DISK#.L	20.36	6.90	2.95	0.34
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.LDEANAALDSASR@.L	23.84	8.00	2.98	0.34
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.LFLEK#DEEIK#NLQK#.T	17.95	8.44	2.13	0.47
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.LIQLNQEK#DFEIAELK#K#.S	23.61	5.45	4.33	0.23
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.LK#LELSEAQQSALR@.Q	9.62	3.02	3.18	0.31
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.LQQALTDAENEIM*R@.L	14.45	5.19	2.78	0.36
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	K.LQVDYTGLIQSYEQNETK#.L	11.29	5.00	2.26	0.44
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.LSDSVAASSEVER@.K	13.68	4.68	2.93	0.34
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	K.LTHSEQALSDLQLTK#.Q	19.95	11.96	1.67	0.60
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.NVK#DDLLK#.E	8.02	4.74	1.69	0.59
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.QDSQTENSDIFQETK#.V	5.62	2.69	2.09	0.48
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	K.QM*ETSTLQNEVQR@.L	5.31	1.98	2.69	0.37
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.SELTQSQTQGSSR@.N	17.69	6.70	2.64	0.38
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	K.SLLSQEK#EELQISLSK#.L	15.16	7.88	1.92	0.52
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.SLNQDISLAEDNQK#.L	15.24	6.88	2.22	0.45
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.TENEELLEAYEEVR@.N	12.28	5.34	2.30	0.44
E9Q512_E9Q512_MOUSE	Trip11	Protein Trip11 OS=Mus n	R.VSAFHEDDM*DFGDVISSQQEINR@.L	22.13	7.37	3.00	0.33
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	K.IDPLALVQAIER.Y	7.34	8.14	0.90	1.11
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.IIEAAHQVGEDEISLSTLGR@.V	6.56	4.81	1.36	0.73
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	K.LPDIFSVYFR@.R	6.82	4.45	1.53	0.65
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.LVDNFQHEENLLQQVASK#.D	9.12	8.37	1.09	0.92
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.SSAVVVDAIPVFLEK#.L	11.71	6.43	1.82	0.55
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.HLDQEQQLK#.S	8.45	5.20	1.62	0.62
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	K.IDPLALVQAIER@.Y	45.57	18.74	2.43	0.41
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.IIEAAHQVGEDEISLSTLGR@.V	19.36	48.64	0.40	2.51
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.LLDTNPEINQSDSQDSR@.V	5.29	3.65	1.45	0.69
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	K.LPDIFSVYFR@.R	10.93	5.95	1.84	0.54
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	K.LPDYSSIDIM*R@.D	9.59	3.74	2.56	0.39
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.LSAQSNSNNIEPAR@.T	8.66	3.09	2.80	0.36
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.LVDLPLGLPFYK#.W	23.56	13.65	1.73	0.58
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.LVDNFQHEENLLQQVASK#.D	18.46	8.64	2.14	0.47

G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.QETSLTSHDLFDIDPVVAR@.S	13.17	8.51	1.55	0.65
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	R.SSAVVVDAIPVFLEK#.L	16.90	6.82	2.48	0.40
G5E870_TRIPC_MOUSE	Trip12	E3 ubiquitin-protein liga	K.TLFGVLYEVYSSSAGPAVR@.H	14.31	6.70	2.14	0.47
Q3UA06_PCH2_MOUSE	Trip13	Pachytene checkpoint pr	K.LSLLLSEISR@.K	12.52	9.36	1.34	0.75
Q3UA06_PCH2_MOUSE	Trip13	Pachytene checkpoint pr	R.NVQSVSIVDTELK#.A	8.03	4.95	1.62	0.62
Q9QXN3_TRIP4_MOUSE	Trip4	Activating signal cointegı	K.TPLDLAK#.A	48.02	6.51	7.37	0.14
Q9Z1Y4_TRIP6_MOUSE	Trip6	Thyroid receptor-interac	R.GIIR@PGSLDAEIDSLTSM*LADLDGGR@.S	24.34	11.97	2.03	0.49
A2RSY6_TRM1L_MOUSE	Trmt1l	TRMT1-like protein OS=M	R.NLGIVSVTSTDISSLYAK#.A	6.10	2.06	2.96	0.34
A2RSY6_TRM1L_MOUSE	Trmt1l	TRMT1-like protein OS=M	K.TTDDTTIDIYSAQGK#.R	6.30	4.35	1.45	0.69
A2RSY6_TRM1L_MOUSE	Trmt1l	TRMT1-like protein OS=M	K.VTINDLNENSVTLIQK#.N	5.34	2.48	2.15	0.46
A2RSY6_TRM1L_MOUSE	Trmt1l	TRMT1-like protein OS=M	K.DGNM*VEENPYR@.Q	3.84	1.48	2.60	0.39
A2RSY6_TRM1L_MOUSE	Trmt1l	TRMT1-like protein OS=M	R.NLGIVSVTSTDISSLYAK#.A	10.14	3.43	2.96	0.34
A2RSY6_TRM1L_MOUSE	Trmt1l	TRMT1-like protein OS=M	K.TTDDTTIDIYSAQGK#.R	5.21	2.04	2.55	0.39
A2RSY6_TRM1L_MOUSE	Trmt1l	TRMT1-like protein OS=M	K.VTINDLNENSVTLIQK#.N	6.05	2.24	2.71	0.37
A2RSY6_TRM1L_MOUSE	Trmt1l	TRMT1-like protein OS=M	K.VVVDSEEK#EEGDALEDDGTLGDIQVTR@.M	7.12	2.11	3.37	0.30
Q8BNV1_TRM2A_MOUSE	Trmt2a	tRNA (uracil-5-)-methyltr	K.AFQEFIR@.S	11.23	4.22	2.66	0.38
Q925H1_TRPS1_MOUSE	Trps1	Zinc finger transcription	R.LNPEALQAEQLNK#.Q	13.34	11.22	1.19	0.84
Q925H1_TRPS1_MOUSE	Trps1	Zinc finger transcription	K.SASLTQQYPASGESK#.T	6.90	8.84	0.78	1.28
Q925H1_TRPS1_MOUSE	Trps1	Zinc finger transcription	K.VYSLLNPDSK#.M	8.31	7.69	1.08	0.93
Q925H1_TRPS1_MOUSE	Trps1	Zinc finger transcription	R.LNPEALQAEQLNK#.Q	6.43	3.55	1.81	0.55
E9PWT1_E9PWT1_MOUSE	Trrap	Transformation/transcriı	R.FLTFLQDGEVQFLQEK#PAQQLR@.K	2.97	2.08	1.43	0.70
Q9EP53_TSC1_MOUSE	Tsc1	Hamartin OS=Mus muscu	R.VLELEILDLYGR@.L	7.34	1.46	5.02	0.20
Q9EP53_TSC1_MOUSE	Tsc1	Hamartin OS=Mus muscu	R.VLELESLLAK#.K	13.28	3.58	3.71	0.27
Q9EP53_TSC1_MOUSE	Tsc1	Hamartin OS=Mus muscu	R.VLELESLLAK#.K	6.53	3.89	1.68	0.60
Q61187_TS101_MOUSE	Tsg101	Tumor susceptibility gen	R.ASLISAVSDK#.L	18.05	6.96	2.59	0.39
Q61187_TS101_MOUSE	Tsg101	Tumor susceptibility gen	R.DGTISEDTIR@.A	49.26	17.67	2.79	0.36
Q61187_TS101_MOUSE	Tsg101	Tumor susceptibility gen	K.DLK#PVLDSYVFNDGSSR@.E	32.33	9.09	3.56	0.28
Q61187_TS101_MOUSE	Tsg101	Tumor susceptibility gen	R.ELVNLTGTIPVR@.Y	46.70	17.72	2.64	0.38
Q61187_TS101_MOUSE	Tsg101	Tumor susceptibility gen	R.GVIDLDVFLK#.H	28.20	10.32	2.73	0.37
Q61187_TS101_MOUSE	Tsg101	Tumor susceptibility gen	R.LDQEVAEVDK#NIELLK#.K	71.98	25.15	2.86	0.35
Q61187_TS101_MOUSE	Tsg101	Tumor susceptibility gen	R.QTVNVIAM*YK#.D	7.59	2.76	2.76	0.36
Q8BJU2_TSN9_MOUSE	Tspan9	Tetraspanin-9 OS=Mus m	K.EGLLLYNTENNVGLK#.N	8.24	2.29	3.59	0.28
Q8K0G5_TSSC1_MOUSE	Tssc1	Protein TSSC1 OS=Mus m	R.ALTPQTAETDAIR@.F	16.55	4.91	3.37	0.30
Q8K0G5_TSSC1_MOUSE	Tssc1	Protein TSSC1 OS=Mus m	K.NVLLHQAGEIWHISASPADK#.G	6.98	1.69	4.13	0.24
Q9JHE7_TSSC4_MOUSE	Tssc4	Protein TSSC4 OS=Mus m	K.YSLEDVSEASEQSNR@.D	6.42	3.93	1.63	0.61
Q91Z38_TTC1_MOUSE	Ttc1	Tetratricopeptide repeat	K.ASDDSSSELDEEYLIELEK#.N	4.78	2.16	2.21	0.45
Q80XJ3_TTC28_MOUSE	Ttc28	Tetratricopeptide repeat	R.ELLLTAADLLDLR@.L	4.18	1.40	2.98	0.34
O88196_TTC3_MOUSE	Ttc3	E3 ubiquitin-protein liga	R.LNSFGLDAIGPFFTR@.Y	5.81	2.30	2.53	0.40
Q9D6K7_TTC33_MOUSE	Ttc33	Tetratricopeptide repeat	R.AQLGLGEIVLAIR@.S	17.37	6.16	2.82	0.35
Q9D6K7_TTC33_MOUSE	Ttc33	Tetratricopeptide repeat	R.SQQLK#DEGAQLAENK#R@.Y	10.07	2.11	4.78	0.21
F8VPK0_F8VPK0_MOUSE	Ttc37	Protein Ttc37 OS=Mus m	K.ALLYTAVNQLAM*GSSTAEDK#SNTALK#.T	7.35	1.98	3.72	0.27
F8VPK0_F8VPK0_MOUSE	Ttc37	Protein Ttc37 OS=Mus m	K.ASELNPDSTYSVFK#.V	12.70	1.86	6.81	0.15
F8VPK0_F8VPK0_MOUSE	Ttc37	Protein Ttc37 OS=Mus m	K.VAAIQQILGR@.Y	16.26	3.55	4.58	0.22
F8VPK0_F8VPK0_MOUSE	Ttc37	Protein Ttc37 OS=Mus m	K.VALVDFLDGK#.A	24.37	8.48	2.87	0.35
F8VPK0_F8VPK0_MOUSE	Ttc37	Protein Ttc37 OS=Mus m	K.WSFSQVVTGLIDTGK#.T	8.91	1.33	6.69	0.15
Q5NC05_TTF2_MOUSE	Ttf2	Transcription terminatio	K.K#DVVIHR.F	2.81	9.13	0.31	3.25
Q5NC05_TTF2_MOUSE	Ttf2	Transcription terminatio	K.K#DVVIHR.F	19.08	18.67	1.02	0.98
Q5NC05_TTF2_MOUSE	Ttf2	Transcription terminatio	K.VSSLLAELEAIQK#.G	14.67	2.54	5.77	0.17
P38585_TTL_MOUSE	Ttl	Tubulin--tyrosine ligase (	K.EDGEGNVWIAK#.S	6.82	2.69	2.54	0.39
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AFVHWYVGEGM*EEGEFSEAR@.E	224.08	154.11	1.45	0.69
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AFVHWYVGEGM*EEGEFSEAR.E	5.15	3.44	1.50	0.67
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AFVHWYVGEGMEEGEFSEAR@.E	35.99	23.84	1.51	0.66
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AFVHWYVGEGM*EEGEFSEAREDM*AALEK.D	22.68	17.85	1.27	0.79
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AVFVDLEPTVIDEVR@.T	1105.07	817.24	1.35	0.74
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.DVNAAIATIK#.T	1284.48	830.55	1.55	0.65
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.DYEEVGVDSVEGEGEEEGEEY.-	36.53	36.53	1.00	1.00
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.EDAANNYAR@.G	106.25	80.64	1.32	0.76
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.EDMAALEK#.D	27.67	21.59	1.28	0.78
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.EDM*AALEK#DYEEVGVDSVEGEGEEEGEEY.-	70.07	38.66	1.81	0.55
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.EIIDLVLDR@.I	640.94	497.44	1.29	0.78
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.FDGALNVDLTEFQTNLVPYPR@.I	333.98	229.81	1.45	0.69
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.FDGALNVDLTEFQTNLVPYPR.I	106.77	82.20	1.30	0.77
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.FDLM*YAK#.R	260.15	194.30	1.34	0.75
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.FDLMYAK#.R	34.50	28.46	1.21	0.82
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.IHFPLATYAPVISAEK#.A	621.21	522.97	1.19	0.84
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LDHK#FDLM*YAK#.R	237.59	126.30	1.88	0.53
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LDHK#FDLMYAK#.R	39.16	45.00	0.87	1.15
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LIGQIVSSITASLR@.F	134.21	106.50	1.26	0.79
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LSVDYGK#.K	428.57	381.00	1.12	0.89
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LSVDYGK#K#.S	256.98	203.67	1.26	0.79
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.NLDIERPTYTNLNR.L	1119.34	814.79	1.37	0.73
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.QLFHPEQLITGK#.E	72.95	55.05	1.33	0.75
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.R@AFVHWYVGEGM*EEGEFSEAR@.E	22.40	16.35	1.37	0.73
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.RAFVHWYVGEGM*EEGEFSEAR.E	8.08	5.06	1.60	0.63
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.R@NLDIER@PTYTNLNR@.L	56.95	38.53	1.48	0.68
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.TIGGGDDSFNTFFSETGAGK#.H	71.70	42.91	1.67	0.60
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.VGINYQPPTVVPGGDLAK#.V	533.66	447.74	1.19	0.84
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AFVHWYVGEGM*EEGEFSEAR@.E	58.95	26.30	2.24	0.45
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AVFVDLEPTVIDEVR@.T	297.62	188.98	1.57	0.63
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.DVNAAIATIK#.T	68.77	27.25	2.52	0.40
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.EDAANNYAR@.G	6.68	3.82	1.75	0.57
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.EDM*AALEK#DYEEVGVDSVEGEGEEEGEEY.-	7.62	1.73	4.41	0.23
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.EIIDLVLDR@.I	158.72	51.50	3.08	0.32
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.GHYTIGK#EIIDLVLDR@.I	3.37	1.75	1.93	0.52
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.IHFPLATYAPVISAEK#.A	30.13	14.47	2.08	0.48
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.TIGGGDDSFNTFFSETGAGK#.H	47.82	29.89	1.60	0.63
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.VGINYQPPTVVPGGDLAK#.V	175.09	94.47	1.85	0.54
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AFVHWYVGEGM*EEGEFSEAR@.E	116.01	45.19	2.57	0.39
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AFVHWYVGEGMEEGEFSEAR@.E	18.06	9.55	1.89	0.53
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AVFVDLEPTVIDEVR@.T	654.45	263.71	2.48	0.40
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.DVNAAIATIK#.T	549.07	248.83	2.21	0.45
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.DYEEVGVDSVEGEGEEEGEEY.-	9.97	9.97	1.00	1.00
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.EDAANNYAR@.G	49.71	19.21	2.59	0.39
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.EDM*AALEK#DYEEVGVDSVEGEGEEEGEEY.-	22.07	8.93	2.47	0.40
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.EIIDLVLDR@.I	628.57	215.36	2.92	0.34
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.FDGALNVDLTEFQTNLVPYPR@.I	158.06	60.29	2.62	0.38
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.FDGALNVDLTEFQTNLVPYPR.I	58.76	25.74	2.28	0.44
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.FDLM*YAK#.R	99.80	40.47	2.47	0.41
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.IHFPLATYAPVISAEK#.A	332.62	134.56	2.47	0.40
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LIGQIVSSITASLR@.F	41.24	21.05	1.96	0.51
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LSVDYGK#.K	167.77	62.19	2.70	0.37
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LSVDYGK#K#.S	136.11	45.73	2.98	0.34
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.TIGGGDDSFNTFFSETGAGK#.H	410.01	148.39	2.76	0.36

P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.VGINYQPPTVVPGGDLAK#.V	316.06	136.35	2.32	0.43
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AFVHWYVGEGM*EEGEFSEAR@.E	181.47	61.56	2.95	0.34
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AFVHWYVGEGMEEGEFSEAR@.E	14.90	3.38	4.41	0.23
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.AVFVDLEPTVIDEVR@.T	1675.17	493.23	3.40	0.29
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.DVNAAIATIK#.T	910.42	294.91	3.09	0.32
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.EDAANNYAR@.G	112.46	30.56	3.68	0.27
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.EDM*AALEK#DYEEVGVDSVEGEGEEEGEEY.-	43.56	14.18	3.07	0.33
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.EIIDLVLDR@.I	1284.18	401.46	3.20	0.31
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.FDGALNVDLTEFQTNLVPYPR.I	91.75	28.30	3.24	0.31
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.FDLM*YAK#.R	148.42	47.62	3.12	0.32
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.GHYTIGK#.E	220.45	64.31	3.43	0.29
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.IHFPLATYAPVISAEK#.A	682.14	228.42	2.99	0.33
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LIGQIVSSITASLR@.F	60.50	17.26	3.50	0.29
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LIGQIVSSITASLR@.F	102.27	30.57	3.35	0.30
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LSVDYGK#.K	483.39	153.70	3.15	0.32
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.LSVDYGK#K#.S	227.61	66.85	3.40	0.29
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.NLDIER@PTYTNLNR@.L	64.34	20.31	3.17	0.32
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.QLFHPEQLITGK#EDAANNYAR@.G	78.22	24.65	3.17	0.32
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.QLFHPEQLITGKEDAANNYAR.G	311.90	85.42	3.65	0.27
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	R.R@NLDIER@PTYTNLNR@.L	30.81	12.24	2.52	0.40
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.TIGGGDDSFNTFFSETGAGK#.H	707.64	209.87	3.37	0.30
P68369_TBA1A_MOUSE	Tuba1a	Tubulin alpha-1A chain C	K.VGINYQPPTVVPGGDLAK#.V	744.85	236.92	3.14	0.32
P68373_TBA1C_MOUSE	Tuba1c	Tubulin alpha-1C chain C	K.DYEEVGADSAEGDDEGEEY.-	5.79	5.79	1.00	1.00
P68373_TBA1C_MOUSE	Tuba1c	Tubulin alpha-1C chain C	R.EDM*AALEK#DYEEVGADSAEGDDEGEEY.-	9.38	4.60	2.04	0.49
P68373_TBA1C_MOUSE	Tuba1c	Tubulin alpha-1C chain C	R.LISQIVSSITASLR@.F	182.43	123.22	1.48	0.68
P68373_TBA1C_MOUSE	Tuba1c	Tubulin alpha-1C chain C	R.LISQIVSSITASLR@.F	99.20	35.52	2.79	0.36
P68373_TBA1C_MOUSE	Tuba1c	Tubulin alpha-1C chain C	K.DYEEVGADSAEGDDEGEEY.-	4.35	4.35	1.00	1.00
P68373_TBA1C_MOUSE	Tuba1c	Tubulin alpha-1C chain C	R.LISQIVSSITASLR@.F	244.31	71.98	3.39	0.29
P68368_TBA4A_MOUSE	Tuba4a	Tubulin alpha-4A chain C	R.AVFVDLEPTVIDEIR@.N	15.63	15.53	1.01	0.99
P68368_TBA4A_MOUSE	Tuba4a	Tubulin alpha-4A chain C	K.DVNAAIAAIK.T	16.47	17.15	0.96	1.04
P68368_TBA4A_MOUSE	Tuba4a	Tubulin alpha-4A chain C	K.EIIDPVLDR@.I	13.69	16.05	0.85	1.17
P68368_TBA4A_MOUSE	Tuba4a	Tubulin alpha-4A chain C	R.AVFVDLEPTVIDEIR@.N	12.95	2.93	4.43	0.23
Q3UX10_TBAL3_MOUSE	Tubal3	Tubulin alpha chain-like	R.SFGGGTGSGFTSLLM*ER@.L	7.23	2.11	3.42	0.29
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.AILVDLEPGTM*DSVR@.S	896.77	645.56	1.39	0.72
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.AILVDLEPGTMDSVR@.S	98.85	70.37	1.40	0.71
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.ALTVPELTQQM*FDSK#.N	61.42	55.32	1.11	0.90
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.ALTVPELTQQMFDSK.N	15.12	15.74	0.96	1.04
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.EVDEQM*LNVQNK#.N	337.40	255.88	1.32	0.76
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.EVDEQMLNVQNK#.N	78.88	56.73	1.39	0.72
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.FPGQLNADLR.K	180.97	131.80	1.37	0.73
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.FPGQLNADLRK.L	14.97	9.52	1.57	0.64
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.FPGQLNADLR@K#.L	111.37	94.52	1.18	0.85
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.GHYTEGAELVDSVLDVVR@.K	884.04	630.50	1.40	0.71
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.GHYTEGAELVDSVLDVVR.K	52.10	36.18	1.44	0.69
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.GHYTEGAELVDSVLDVVR@K#.E	235.51	151.69	1.55	0.64
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.IM*NTFSVM*PSPK#.V	73.01	55.44	1.32	0.76
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.IMNTFSVM*PSPK#.V	9.10	12.24	0.74	1.35
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.IM*NTFSVMPSPK.V	5.71	6.77	0.84	1.18
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.IMNTFSVMPSPK.V	6.00	7.40	0.81	1.23
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.INVYYNEAAGNK#.Y	53.30	46.01	1.16	0.86
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.ISEQFTAM*FR@.R	908.22	664.76	1.37	0.73
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.ISEQFTAMFR@.R	80.96	45.50	1.78	0.56
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.LAVNM*VPFPR@.L	275.51	212.28	1.30	0.77
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.LAVNMVPFPR.L	153.41	105.68	1.45	0.69
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.LHFFM*PGFAPLTSR@.G	332.44	261.86	1.27	0.79
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.LHFFM*PGFAPLTSR.G	40.57	30.64	1.32	0.76
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.LHFFMPGFAPLTSR@.G	100.00	72.11	1.39	0.72
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.M*SATFIGNSTAIQELFK#R@.I	14.91	6.22	2.40	0.42
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.M*SM*KEVDEQM*LNVQNK.N	153.04	126.69	1.21	0.83
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.M*SM*KEVDEQMLNVQNK.N	33.51	21.25	1.58	0.63
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.NSSYFVEWIPNNVK#.T	454.95	296.43	1.53	0.65
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.R@ISEQFTAM*FR@.R	22.41	15.59	1.44	0.70
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.SGPFGQIFR@PDNFVFGQSGAGNNWAK#.G	234.85	170.57	1.38	0.73
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.YLTVAAIFR@.G	71.51	71.64	1.00	1.00
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.AILVDLEPGTM*DSVR@.S	468.18	192.11	2.44	0.41
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.AILVDLEPGTMDSVR@.S	35.83	14.88	2.41	0.42
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.EVDEQM*LNVQNK#.N	18.77	8.08	2.32	0.43
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.FWEVISDEHGIDPTGSYHGDSDLQLER@.I	8.01	4.94	1.62	0.62
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.GHYTEGAELVDSVLDVVR@.K	272.98	97.56	2.80	0.36
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.GHYTEGAELVDSVLDVVR.K	27.87	9.43	2.95	0.34
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.GHYTEGAELVDSVLDVVR@K#.E	382.63	98.75	3.87	0.26
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.INVYYNEAAGNK#.Y	22.44	11.22	2.00	0.50
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.IR@EEYPDR@.I	7.21	7.43	0.97	1.03
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.ISEQFTAM*FR@.R	90.86	40.38	2.25	0.44
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.LAVNM*VPFPR@.L	30.82	12.33	2.50	0.40
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.LHFFM*PGFAPLTSR@.G	18.28	7.04	2.60	0.38
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.NSSYFVEWIPNNVK#.T	65.77	31.00	2.12	0.47
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	85.70	30.85	2.78	0.36
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.YLTVAAIFR@.G	12.55	7.24	1.73	0.58
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.AILVDLEPGTM*DSVR.S	547.30	294.72	1.86	0.54
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.AILVDLEPGTMDSVR@.S	48.86	25.96	1.88	0.53
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.ALTVPELTQQM*FDSK#.N	28.99	16.89	1.72	0.58
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.EVDEQM*LNVQNK#.N	147.73	78.57	1.88	0.53
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.EVDEQMLNVQNK#.N	32.54	15.71	2.07	0.48
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.FPGQLNADLR@.K	93.16	49.17	1.89	0.53
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.FWEVISDEHGIDPTGSYHGDSDLQLER@.I	5.94	3.60	1.65	0.61
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.GHYTEGAELVDSVLDVVR@.K	582.55	269.68	2.16	0.46
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.GHYTEGAELVDSVLDVVR@K#.E	130.25	55.61	2.34	0.43
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.IM*NTFSVM*PSPK#.V	77.96	16.41	4.75	0.21
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.INVYYNEAAGNK#.Y	38.18	18.96	2.01	0.50
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.ISEQFTAM*FR@.R	428.86	202.48	2.12	0.47
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.ISEQFTAMFR@.R	46.45	21.86	2.12	0.47
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.KLAVNM*VPFPR.L	38.42	29.52	1.30	0.77
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.LAVNM*VPFPR.L	260.66	129.53	2.01	0.50
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.LAVNMVPFPR@.L	66.75	33.86	1.97	0.51
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.LHFFM*PGFAPLTSR@.G	329.11	149.62	2.20	0.45
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.LHFFM*PGFAPLTSR.G	30.31	17.69	1.71	0.58
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.LHFFMPGFAPLTSR@.G	78.42	33.22	2.36	0.42
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.M*SATFIGNSTAIQELFK#R@.I	12.65	4.80	2.64	0.38
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.M*SM*KEVDEQM*LNVQNK.N	88.28	38.68	2.28	0.44
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	K.NSSYFVEWIPNNVK#.T	296.49	141.62	2.09	0.48
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.SGPFGQIFR@PDNFVFGQSGAGNNWAK#.G	153.96	71.92	2.14	0.47
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain O	R.YLTVAAIFR@.G	55.41	33.54	1.65	0.61

Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.AILVDLEPGTM*DSVR@.S	999.46	372.58	2.68	0.37
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.AILVDLEPGTMDSVR@.S	77.33	29.46	2.62	0.38
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.ALTVPELTQQM*FDSK#.N	54.02	23.08	2.34	0.43
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.EVDEQM*LNVQNK#.N	327.46	108.37	3.02	0.33
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.EVDEQMLNVQNK#.N	44.92	18.72	2.40	0.42
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.FPGQLNADLR@.K	139.92	68.96	2.03	0.49
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.FPGQLNADLR@K#.L	110.15	36.24	3.04	0.33
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.FWEVISDEHGIDPTGSYHGDSDLQLER@.I	100.52	40.30	2.49	0.40
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.GHYTEGAELVDSVLDVVR@.K	949.30	317.62	2.99	0.33
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.GHYTEGAELVDSVLDVVR.K	44.32	12.43	3.56	0.28
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.GHYTEGAELVDSVLDVVR@K#.E	286.11	79.56	3.60	0.28
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.IM*NTFSVM*PSPK#.V	45.83	19.67	2.33	0.43
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.IMNTFSVM*PSPK#.V	6.20	2.53	2.45	0.41
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.INVYYNEAAGNK#.Y	36.18	18.26	1.98	0.50
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.ISEQFTAM*FR@.R	731.55	220.28	3.32	0.30
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.ISEQFTAMFR@.R	31.10	8.43	3.69	0.27
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.LAVNM*VPFPR@.L	293.20	103.96	2.82	0.35
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.LAVNMVPFPR@.L	136.14	47.01	2.90	0.35
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.LHFFM*PGFAPLTSR@.G	408.10	150.43	2.71	0.37
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.LHFFM*PGFAPLTSR.G	29.14	13.84	2.11	0.47
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.LHFFMPGFAPLTSR@.G	79.06	26.31	3.01	0.33
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.M*SATFIGNSTAIQELFK#.R	183.02	64.61	2.83	0.35
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.M*SATFIGNSTAIQELFK#R@.I	42.41	11.25	3.77	0.27
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.MSATFIGNSTAIQELFK#R@.I	16.36	3.05	5.37	0.19
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.M*SM*KEVDEQM*LNVQNK.N	161.21	49.69	3.24	0.31
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.NSSYFVEWIPNNVK#.T	403.69	131.29	3.07	0.33
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	K.R@ISEQFTAM*FR@.R	39.20	9.56	4.10	0.24
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.SGPFGQIFR@PDNFVFGQSGAGNNWAK#.G	217.05	59.68	3.64	0.27
Q7TMM9_TBB2A_MOUSE	Tubb2a	Tubulin beta-2A chain OS	R.YLTVAAIFR.G	88.80	37.65	2.36	0.42
Q9CWF2_TBB2B_MOUSE	Tubb2b	Tubulin beta-2B chain OS	R.INVYYNEATGNK#.Y	25.47	15.25	1.67	0.60
Q9CWF2_TBB2B_MOUSE	Tubb2b	Tubulin beta-2B chain OS	R.INVYYNEATGNK#.Y	33.53	20.85	1.61	0.62
Q9CWF2_TBB2B_MOUSE	Tubb2b	Tubulin beta-2B chain OS	R.INVYYNEATGNK#.Y	51.65	25.44	2.03	0.49
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.ALTVPELTQQM*FDAK#.N	71.49	43.77	1.63	0.61
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.ALTVPELTQQMFDAK#.N	21.91	18.23	1.20	0.83
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	K.FWEVISDEHGIDPSGNYVGDSDLQLER.I	2.59	5.17	0.50	2.00
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.IM*NTFSVVPSPK#.V	503.83	366.95	1.37	0.73
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.IMNTFSVVPSPK#.V	117.29	80.64	1.45	0.69
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.LHFFM*PGFAPLTAR@.G	39.03	39.60	0.99	1.01
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.LHFFMPGFAPLTAR@.G	13.46	9.36	1.44	0.70
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	K.M*SSTFIGNSTAIQELFK#.R	16.73	12.60	1.33	0.75
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.YLTVATVFR@.G	50.62	44.81	1.13	0.89
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.ALTVPELTQQM*FDAK#.N	4.67	3.13	1.49	0.67
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.IM*NTFSVVPSPK#.V	27.59	14.00	1.97	0.51
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.ALTVPELTQQM*FDAK#.N	43.86	16.46	2.66	0.38
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.ALTVPELTQQMFDAK#.N	15.37	6.01	2.56	0.39
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.IM*NTFSVVPSPK#.V	263.01	137.47	1.91	0.52
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.IMNTFSVVPSPK#.V	52.16	24.05	2.17	0.46
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.LHFFM*PGFAPLTAR@.G	15.36	8.26	1.86	0.54
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	K.M*SSTFIGNSTAIQELFK#.R	9.01	4.00	2.25	0.44
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.YLTVATVFR@.G	16.74	8.78	1.91	0.52
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.ALTVPELTQQM*FDAK#.N	80.10	21.46	3.73	0.27
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.ALTVPELTQQMFDAK#.N	23.68	8.84	2.68	0.37
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.IM*NTFSVVPSPK#.V	434.31	152.15	2.85	0.35
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.IMNTFSVVPSPK#.V	76.00	30.31	2.51	0.40
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.LHFFM*PGFAPLTAR@.G	27.74	9.85	2.82	0.36
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	K.M*SSTFIGNSTAIQELFK#.R	22.88	6.59	3.47	0.29
Q9ERD7_TBB3_MOUSE	Tubb3	Tubulin beta-3 chain OS=	R.YLTVATVFR@.G	32.28	12.61	2.56	0.39
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.AVLVDLEPGTM*DSVR@.S	103.01	54.54	1.89	0.53
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.INVYYNEATGGK#.Y	248.14	121.65	2.04	0.49
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.YLTVAAVFR@.G	392.93	249.80	1.57	0.64
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.AVLVDLEPGTM*DSVR@.S	154.86	43.97	3.52	0.28
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.YLTVAAVFR@.G	55.51	28.75	1.93	0.52
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.AVLVDLEPGTM*DSVR@.S	115.64	39.02	2.96	0.34
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.INVYYNEATGGK#.Y	93.67	32.29	2.90	0.34
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.YLTVAAVFR@.G	306.73	133.66	2.29	0.44
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.AVLVDLEPGTM*DSVR@.S	212.80	52.95	4.02	0.25
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.INVYYNEATGGK#.Y	201.85	43.50	4.64	0.22
P68372_TBB4B_MOUSE	Tubb4b	Tubulin beta-4B chain OS	R.YLTVAAVFR@.G	430.26	114.12	3.77	0.27
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	R.ALTVPELTQQVFDAK#.N	485.25	374.73	1.29	0.77
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.FWEVISDEHGIDPTGTYHGDSDLQLDR@.I	46.11	33.52	1.38	0.73
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	R.ISVYYNEATGGK#.Y	681.11	489.06	1.39	0.72
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.M*AVTFIGNSTAIQELFK#.R	247.41	161.32	1.53	0.65
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.MAVTFIGNSTAIQELFK#.R	60.20	45.69	1.32	0.76
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.M*AVTFIGNSTAIQELFKR.I	59.33	35.20	1.69	0.59
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	R.ALTVPELTQQVFDAK#.N	46.98	18.02	2.61	0.38
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.FWEVISDEHGIDPTGTYHGDSDLQLDR@.I	12.35	7.61	1.62	0.62
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	R.ISVYYNEATGGK#.Y	370.02	121.92	3.04	0.33
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.M*AVTFIGNSTAIQELFK#.R	41.02	14.17	2.89	0.35
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	R.ALTVPELTQQVFDAK#.N	371.41	193.48	1.92	0.52
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.FWEVISDEHGIDPTGTYHGDSDLQLDR@.I	31.91	20.18	1.58	0.63
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	R.ISVYYNEATGGK#.Y	279.08	152.45	1.83	0.55
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.M*AVTFIGNSTAIQELFK#.R	173.49	83.34	2.08	0.48
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.MAVTFIGNSTAIQELFK#.R	19.30	7.69	2.51	0.40
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	R.ALTVPELTQQVFDAK#.N	161.21	56.05	2.88	0.35
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	R.ALTVPELTQQVFDAK#.N	437.11	161.03	2.71	0.37
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	R.ISVYYNEATGGK#.Y	550.34	189.18	2.91	0.34
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.M*AVTFIGNSTAIQELFK#.R	229.41	75.04	3.06	0.33
P99024_TBB5_MOUSE	Tubb5	Tubulin beta-5 chain OS=	K.MAVTFIGNSTAIQELFK#.R	65.09	21.19	3.07	0.33
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.AALVDLEPGTM*DSVR@.S	56.22	42.59	1.32	0.76
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	K.EVDEQM*LAIQNK#.N	9.75	7.66	1.27	0.79
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	K.FWEVISDEHGIDQAGGYVGDSALQLER@.I	28.86	19.29	1.50	0.67
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.GPM*SM*KEVDEQM*LAIQNK.N	10.88	11.30	0.96	1.04
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.ISEQFSAM*FR@.R	35.88	29.59	1.21	0.82
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.ISVYYNESSSK#.K	46.68	31.35	1.49	0.67
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	K.LTTPTYGDLNHLVSATMSGVTTSLR@.F	9.58	6.26	1.53	0.65
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.SGPFGQLFR@PDNFIFGQTGAGNNWAK#.G	17.36	19.27	0.90	1.11
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.AALVDLEPGTM*DSVR@.S	31.62	14.47	2.19	0.46
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	K.FWEVISDEHGIDQAGGYVGDSALQLER@.I	4.69	2.48	1.89	0.53
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.ISVYYNESSSK#.K	17.07	6.60	2.59	0.39
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.AALVDLEPGTM*DSVR@.S	22.03	10.73	2.05	0.49
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	K.EVDEQM*LAIQNK#.N	5.19	6.40	0.81	1.23
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	K.FWEVISDEHGIDQAGGYVGDSALQLER@.I	13.00	6.74	1.93	0.52
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.ISEQFSAM*FR@.R	16.52	6.08	2.72	0.37

Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.SGPFGQLFRPDNFIFGQTGAGNNWAK.G	5.59	4.99	1.12	0.89
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.AALVDLEPGTM*DSVR@.S	44.36	14.49	3.06	0.33
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	K.EVDEQM*LAIQNK#.N	15.06	4.18	3.60	0.28
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	K.FWEVISDEHGIDQAGGYVGDSALQLER@.I	20.79	5.95	3.50	0.29
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.ISEQFSAM*FR@.R	26.45	5.72	4.63	0.22
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.ISVYYNESSSK#.K	20.32	7.86	2.58	0.39
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	K.LTTPTYGDLNHLVSATM*SGVTTSLR@.F	9.36	3.69	2.54	0.39
Q922F4_TBB6_MOUSE	Tubb6	Tubulin beta-6 chain OS=	R.SGPFGQLFRPDNFIFGQTGAGNNWAK.G	6.55	4.53	1.45	0.69
P83887_TBG1_MOUSE	Tubg1	Tubulin gamma-1 chain (	R.AVLLDLEPR@.V	29.19	27.52	1.06	0.94
P83887_TBG1_MOUSE	Tubg1	Tubulin gamma-1 chain (	K.KLVQTYSVFPNQDEM*SDVVVQPYNSLLTLK.R	6.53	4.59	1.42	0.70
P83887_TBG1_MOUSE	Tubg1	Tubulin gamma-1 chain (	K.LYNPENIYLSEHGGGAGNNWASGFSQGEK#.I	9.62	3.59	2.68	0.37
P83887_TBG1_MOUSE	Tubg1	Tubulin gamma-1 chain (	R.VIHSILNSSYAK#.L	22.72	15.91	1.43	0.70
P83887_TBG1_MOUSE	Tubg1	Tubulin gamma-1 chain (	R.AVLLDLEPR@.V	21.00	3.99	5.26	0.19
P83887_TBG1_MOUSE	Tubg1	Tubulin gamma-1 chain (	K.IHEDIFDIIDR@.E	6.02	2.98	2.02	0.50
P83887_TBG1_MOUSE	Tubg1	Tubulin gamma-1 chain (	R.LHFLM*TGYTPLTTDQSVASVR@.K	36.97	6.09	6.07	0.16
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	K.AASAPYFEILEK#.W	9.10	3.64	2.50	0.40
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	R.IHHDVNELLSLLR@.I	13.57	1.87	7.27	0.14
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	R.ILPVAASYSTVTR@.F	16.94	2.71	6.25	0.16
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	R.NLDPLVYLLSK#.L	13.96	4.68	2.98	0.34
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	K.VLLDFLM*EEK#.E	14.42	5.20	2.77	0.36
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	R.YTVLPQQIPSFLQK#.V	11.96	4.69	2.55	0.39
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	R.ILPVAASYSTVTR@.F	13.26	4.51	2.94	0.34
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	R.LTLDQGSVQGPPTETER@.I	13.03	3.83	3.41	0.29
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	R.NLDPLVYLLSK#.L	21.24	7.48	2.84	0.35
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	K.VLLDFLM*EEK#.E	17.93	3.68	4.87	0.21
Q921G8_GCP2_MOUSE	Tubgcp2	Gamma-tubulin comple	R.YTVLPQQIPSFLQK#.V	13.52	4.87	2.77	0.36
P58854_GCP3_MOUSE	Tubgcp3	Gamma-tubulin comple	R.DILYVFQGIDGK#.N	8.12	2.43	3.34	0.30
P58854_GCP3_MOUSE	Tubgcp3	Gamma-tubulin comple	R.DILYVFQGIDGK#.N	15.57	4.89	3.19	0.31
P58854_GCP3_MOUSE	Tubgcp3	Gamma-tubulin comple	R.YLLLGQGDFIR@.H	9.07	4.98	1.82	0.55
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	K.ADAVQDSEM*VELVELEIR@.E	4.28	1.90	2.26	0.44
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	K.ADAVQDSEMVELVELEIR@.E	4.75	1.91	2.49	0.40
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	R.AEAGDNLGALVR@.G	72.27	42.60	1.70	0.59
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	R.EHLLLAK#.Q	22.64	7.05	3.21	0.31
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	K.ELAM*PGEDLK#.L	34.74	13.68	2.54	0.39
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	R.ELLTEFGYK#.G	4.81	3.93	1.22	0.82
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	R.GTVVTGTLER@.G	78.06	34.12	2.29	0.44
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	K.K#YEEIDNAPEER@.A	9.11	4.23	2.15	0.46
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	K.LLDAVDTYIPVPTR.D	68.48	23.79	2.88	0.35
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	K.VEAQVYILSK#.E	12.12	3.45	3.51	0.28
Q8BFR5_EFTU_MOUSE	Tufm	Elongation factor Tu, mit	K.YEEIDNAPEER@.A	32.16	14.90	2.16	0.46
Q91YR1_TWF1_MOUSE	Twf1	Twinfilin-1 OS=Mus musc	K.INEVQTDVSVDTK#.H	5.84	2.53	2.31	0.43
Q78WZ7_RPA43_MOUSE	Twistnb	DNA-directed RNA polym	R.EQLDAELLR@.Y	8.60	7.55	1.14	0.88
Q78WZ7_RPA43_MOUSE	Twistnb	DNA-directed RNA polym	R.HQEDQDPIFQASDSSGYQSDHNK#K#.K	2.74	2.91	0.94	1.06
Q6PAM1_TXLNA_MOUSE	Txlna	Alpha-taxilin OS=Mus mu	R.VQDLTAGGITDIGSER@.R	4.17	3.10	1.34	0.74
P10639_THIO_MOUSE	Txn	Thioredoxin OS=Mus mus	K.EAFQEALAAAGDK#.L	14.03	16.60	0.85	1.18
Q9CQU0_TXD12_MOUSE	Txndc12	Thioredoxin domain-con	R.DEDFSPDGGYIPR.I	4.77	6.36	0.75	1.33
Q9CQU0_TXD12_MOUSE	Txndc12	Thioredoxin domain-con	K.YFYVSAEQVVQGM*K.E	3.08	3.87	0.80	1.26
Q91W90_TXND5_MOUSE	Txndc5	Thioredoxin domain-con	R.GYPTLLLFR.G	14.16	18.64	0.76	1.32
Q91W90_TXND5_MOUSE	Txndc5	Thioredoxin domain-con	R.GYPTLLWFR@.D	10.63	14.70	0.72	1.38
Q91W90_TXND5_MOUSE	Txndc5	Thioredoxin domain-con	K.SFEDTIAQGITFVK.F	17.63	18.62	0.95	1.06
Q9CQ79_TXND9_MOUSE	Txndc9	Thioredoxin domain-con	K.VIPTLALLR@.D	18.53	13.11	1.41	0.71
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	K.AVIDLNNR@.W	563.68	290.13	1.94	0.51
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	R.NPQNSSQSADGLR@.C	196.72	124.01	1.59	0.63
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	R.WFNGQPIHAELSPVTDFR@.E	90.52	56.34	1.61	0.62
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	K.AVIDLNNR@.W	168.07	73.80	2.28	0.44
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	R.NPQNSSQSADGLR@.C	15.59	10.19	1.53	0.65
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	R.WFNGQPIHAELSPVTDFR@.E	28.32	14.18	2.00	0.50
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	R.NPQNSSQSADGLR@.C	10.92	6.32	1.73	0.58
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	R.WFNGQPIHAELSPVTDFR@.E	8.86	6.51	1.36	0.73
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	K.AVIDLNNR@.W	19.88	6.72	2.96	0.34
Q9D883_U2AF1_MOUSE	U2af1	Splicing factor U2AF 35 k	R.NPQNSSQSADGLR@.C	13.62	5.95	2.29	0.44
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	K.AM*QAAGQIPATALLPTM*TPDGLAVTPTPVPVVGSQMTR@.Q	8.08	2.37	3.41	0.29
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	K.ELLTSFGPLK#.A	46.39	36.60	1.27	0.79
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	K.LFIGGLPNYLNDDQVK#.E	55.72	44.93	1.24	0.81
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.LGGLTQAPGNPVLAVQINQDK#.N	6.91	5.86	1.18	0.85
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	K.NFAFLEFR@.S	48.01	29.36	1.64	0.61
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.RLYVGNIPFGITEEAM*M*DFFNAQM*R.L	5.69	3.83	1.49	0.67
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.R@PHDYQPLPGM*SENPSVYVPGVVSTVVPDSAHK#.L	24.78	19.10	1.30	0.77
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.SVDETTQAM*AFDGIIFQGQSLK#.I	70.58	33.75	2.09	0.48
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.SVDETTQAM*AFDGIIFQGQSLK#.I	12.57	6.11	2.06	0.49
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.SVDETTQAMAFDGIIFQGQSLK#.I	32.30	17.32	1.87	0.54
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.SVDETTQAMAFDGIIFQGQSLK#.I	8.20	4.05	2.02	0.49
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	K.ELLTSFGPLK#.A	43.19	30.24	1.43	0.70
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.LGGLTQAPGNPVLAVQINQDK#.N	6.62	3.22	2.06	0.49
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.LGGLTQAPGNPVLAVQINQDK#.N	28.20	16.97	1.66	0.60
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.LGGLTQAPGNPVLAVQINQDKNFAFLEFR.S	15.79	7.61	2.07	0.48
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	K.NFAFLEFR@.S	42.87	23.06	1.86	0.54
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.RLYVGNIPFGITEEAM*M*DFFNAQM*R.L	4.73	4.35	1.09	0.92
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.SVDETTQAM*AFDGIIFQGQSLK#.I	44.26	22.01	2.01	0.50
P26369_U2AF2_MOUSE	U2af2	Splicing factor U2AF 65 k	R.SVDETTQAMAFDGIIFQGQSLK#.I	15.09	6.34	2.38	0.42
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.AAAEIYEEFLAAFEGSDGNK#.V	55.76	11.66	4.78	0.21
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.AWEDWAIYPEPFLIK#.L	35.56	11.98	2.97	0.34
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.DK#LEEILR@.G	141.40	248.83	0.57	1.76
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.EDEK#AAAEIYEEFLAAFEGSDGNK#.V	10.05	2.18	4.62	0.22
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.EGPM*FEAM*IM*NR.E	16.14	6.69	2.41	0.41
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.FQDELESGK#.R	63.26	22.79	2.78	0.36
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.GGVVNAAK#DEHETDEK#R@.G	27.60	8.55	3.23	0.31
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.K#PGQSFQEQVEHYR@.D	60.43	19.80	3.05	0.33
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.K#SNLELFK#EELK#.Q	51.35	12.86	3.99	0.25
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.LK#NPNAPM*LPPPK#.N	41.69	23.98	1.74	0.58
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.LYLVSDVLYNSSAK#.V	121.48	39.72	3.06	0.33
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.LYLVSDVLYNSSAK#.V	11.74	3.66	3.21	0.31
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.LYSILQGDSPTK#.W	121.18	35.29	3.43	0.29
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.M*IEFVVR@.E	36.68	9.27	3.96	0.25
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.MIEFVVR@.E	46.23	12.57	3.68	0.27
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.NLLALIHR@.M	151.36	52.22	2.90	0.34
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.SLDDDLDGVPLDATEDSK#.K	26.69	8.17	3.27	0.31
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.SLDDDLDGVPLDATEDSK#K#.N	37.13	11.49	3.23	0.31
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.SNLELFK#EELK#.Q	47.63	14.84	3.21	0.31
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	R.SSDVHSSGSSDAHM*DASGPSDSDM*PSR@.T	43.91	8.29	5.30	0.19
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.VANASYYR@.K	86.72	21.70	4.00	0.25
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.VAPSKWEAVDESELEAQAVTTSK.W	56.27	14.21	3.96	0.25
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SU	K.AAAEIYEEFLAAFEGSDGNK#.V	26.52	8.15	3.26	0.31

Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	R.AWEDWAIYPEPFLIK#.L	20.91	7.48	2.79	0.36
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	R.DK#LEEILR@.G	53.48	294.91	0.18	5.51
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	R.EINNPM*FR@.F	27.53	8.60	3.20	0.31
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	K.FQDELESGK#.R	40.81	12.40	3.29	0.30
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	K.K#PGQSFQEQVEHYR@.D	15.30	5.13	2.98	0.34
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	R.LK#NPNAPM*LPPPK#.N	21.45	7.11	3.01	0.33
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	R.LYLVSDVLYNSSAK#.V	69.57	21.05	3.30	0.30
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	K.LYSILQGDSPTK#.W	50.18	15.28	3.28	0.30
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	R.M*IEFVVR@.E	17.40	5.72	3.04	0.33
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	R.MIEFVVR@.E	14.55	6.40	2.27	0.44
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	R.NLLALIHR@.M	57.09	15.49	3.69	0.27
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	K.SLDDDLDGVPLDATEDSK#.K	10.60	4.36	2.43	0.41
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	K.SLDDDLDGVPLDATEDSK#K#.N	13.89	5.26	2.64	0.38
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	K.SNLELFK#.E	10.50	2.15	4.88	0.20
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	K.SNLELFK#EELK#.Q	45.01	16.19	2.78	0.36
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	R.TIQGHLQSENFK#.Q	16.95	6.08	2.79	0.36
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	K.VANASYYR@.K	23.05	7.74	2.98	0.34
Q6NV83_SR140_MOUSE	U2surp	U2 snRNP-associated SUF	K.WEAVDESELEAQAVTTSK#.W	5.70	3.00	1.90	0.53
Q8CGB3_UACA_MOUSE	Uaca	Uveal autoantigen with c	R.NLENVQNQM*K#.A	8.08	6.46	1.25	0.80
Q02053_UBA1_MOUSE	Uba1	Ubiquitin-like modifier-a	R.IYDDDFFQNLDGVANALDNIDAR@.M	8.49	4.54	1.87	0.53
Q02053_UBA1_MOUSE	Uba1	Ubiquitin-like modifier-a	R.LAGTQPLEVLEAVQR@.S	12.61	5.24	2.40	0.42
Q02053_UBA1_MOUSE	Uba1	Ubiquitin-like modifier-a	K.SLPASLVEPDFVM*TDFAK#.Y	7.98	4.04	1.97	0.51
Q02053_UBA1_MOUSE	Uba1	Ubiquitin-like modifier-a	R.YDGQVAVFGSDFQEK#.L	5.24	4.39	1.19	0.84
Q02053_UBA1_MOUSE	Uba1	Ubiquitin-like modifier-a	R.LAGTQPLEVLEAVQR@.S	11.05	5.14	2.15	0.47
Q02053_UBA1_MOUSE	Uba1	Ubiquitin-like modifier-a	R.LDQPM*TEIVSR@.V	7.10	3.04	2.34	0.43
Q9Z1F9_SAE2_MOUSE	Uba2	SUMO-activating enzyme	K.VTVLTLQDK#.I	8.70	4.27	2.04	0.49
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.EGIPPDQQR.L	51.43	9.97	5.16	0.19
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	-.M*QIFVK#.T	61.71	135.42	0.46	2.19
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	-.MQIFVK#.T	75.73	185.33	0.41	2.45
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.TITLEVEPSDTIENVK.A	173.41	350.77	0.49	2.02
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	R.TLSDYNIQK.E	145.17	343.18	0.42	2.36
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.AKIQDKEGIPPDQQR.L	3.23	17.81	0.18	5.51
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.EGIPPDQQR.L	25.26	158.56	0.16	6.28
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.ESTLHLVLR.L	94.26	561.49	0.17	5.96
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.IQDK#EGIPPDQQR@.L	11.83	71.58	0.17	6.05
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.IQDKEGIPPDQQR.L	62.65	459.29	0.14	7.33
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	-.M*QIFVK.T	209.83	1110.21	0.19	5.29
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	-.MQIFVK.T	107.23	580.20	0.18	5.41
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	-.MQIFVKTLTGKTITLEVEPSDTIENVK.A	2.02	11.28	0.18	5.58
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.QLEDGR.T	27.68	151.45	0.18	5.47
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.TITLEVEPSDTIENVK.A	473.75	2187.43	0.22	4.62
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.TITLEVEPSDTIENVKAK.I	13.38	79.69	0.17	5.96
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	R.TLSDYNIQK.E	270.57	1809.98	0.15	6.69
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.TLTGKTITLEVEPSDTIENVK.A	1.60	12.81	0.13	8.00
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	-.M*QIFVK#.T	93.13	45.89	2.03	0.49
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	-.MQIFVK#.T	40.95	22.15	1.85	0.54
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.TITLEVEPSDTIENVK#.A	198.67	96.48	2.06	0.49
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	R.TLSDYNIQK#.E	101.58	53.48	1.90	0.53
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.ESTLHLVLR.L	54.35	22.97	2.37	0.42
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	-.M*QIFVK#.T	94.98	59.49	1.60	0.63
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	-.MQIFVK#.T	37.87	11.70	3.24	0.31
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	K.TITLEVEPSDTIENVK#.A	250.05	120.59	2.07	0.48
P62984_RL40_MOUSE	Uba52	Ubiquitin-60S ribosomal	R.TLSDYNIQK#.E	122.73	44.79	2.74	0.36
Q91VX2_UBAP2_MOUSE	Ubap2	Ubiquitin-associated pro	R.ATALVTSGK#.A	18.76	9.38	2.00	0.50
Q91VX2_UBAP2_MOUSE	Ubap2	Ubiquitin-associated pro	R.DGNLANNPYSGDVTK#.F	26.53	13.02	2.04	0.49
Q91VX2_UBAP2_MOUSE	Ubap2	Ubiquitin-associated pro	K.GVSVSSGTGLPDM*TGSVYNK#.T	9.31	5.42	1.72	0.58
Q91VX2_UBAP2_MOUSE	Ubap2	Ubiquitin-associated pro	R.LPM*DYYGIPFAAPTALASR.D	22.81	8.95	2.55	0.39
Q91VX2_UBAP2_MOUSE	Ubap2	Ubiquitin-associated pro	K.NSVEEWTTEDWTEDLSETK#.V	3.75	1.95	1.93	0.52
Q91VX2_UBAP2_MOUSE	Ubap2	Ubiquitin-associated pro	K.QVVQATAEQM*R@.L	8.22	4.02	2.04	0.49
Q91VX2_UBAP2_MOUSE	Ubap2	Ubiquitin-associated pro	K.SQASK#PTYGSAPYWTN.-	3.67	6.15	0.60	1.68
Q91VX2_UBAP2_MOUSE	Ubap2	Ubiquitin-associated pro	K.SQPEPSPVLSQLSQR@.Q	22.79	14.13	1.61	0.62
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.DGSLASNPYSGDLTK#.F	22.27	17.43	1.28	0.78
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.FPLDYYSIPFPTPTTPLTGR.D	13.91	8.54	1.63	0.61
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.GFGDVGEAK#.G	39.96	9.52	4.20	0.24
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.GGSTTGSQFLEQFK#.T	37.72	14.87	2.54	0.39
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.IDLAVLLGK#.T	82.52	27.93	2.95	0.34
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.IFTASNVSSVPLPAENVTITAGQR@.I	39.24	12.71	3.09	0.32
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.LDFIGVEGSNYPR@.K	35.08	12.17	2.88	0.35
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.TATEEWGTEDWNEDLSETK#.I	11.43	3.83	2.99	0.33
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.TPSSM*ENDSSNLDPSQAPSLAQPLVFSNSK#.Q	11.11	3.40	3.27	0.31
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.DGSLASNPYSGDLTK.F	3.26	4.50	0.72	1.38
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.GGSTTGSQFLEQFK#.T	4.79	2.94	1.63	0.61
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.IDLAVLLGK#.T	11.29	4.92	2.29	0.44
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.IFTASNVSSVPLPAENVTITAGQR@.I	8.54	3.08	2.78	0.36
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.AINVLLEGNPDTHSWEMVGK#.K	13.48	3.20	4.22	0.24
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.DGSLASNPYSGDLTK#.F	106.37	36.34	2.93	0.34
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.FPLDYYSIPFPTPTTPLTGR@.D	40.47	15.18	2.67	0.38
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.GFGDVGEAK#.G	105.80	36.25	2.92	0.34
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.GGSTTGSQFLEQFK#.T	151.02	45.93	3.29	0.30
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.IDLAVLLGK#.T	215.02	59.50	3.61	0.28
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.IFTASNVSSVPLPAENVTITAGQR@.I	88.01	28.41	3.10	0.32
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.LAQMISDHNDADFEEK#.V	18.12	3.66	4.95	0.20
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.LDFIGVEGSNYPR@.K	91.92	26.30	3.50	0.29
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.QR@PQATAEQIR@.L	101.53	14.45	7.02	0.14
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.QR@PQATAEQIR@.L	30.52	5.60	5.45	0.18
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.R@YPSSISSSPQK#.D	59.31	15.26	3.89	0.26
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.TAQALAQLAAQHSQSGSTTTSSWDM*GSTTQSPSLVQYDLK#.S	25.27	6.19	4.08	0.25
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.TATEEWGTEDWNEDLSETK#.I	24.88	8.73	2.85	0.35
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.TPSSM*ENDSSNLDPSQAPSLAQPLVFSNSK#.Q	25.09	9.88	2.54	0.39
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.TPSSMENDSSNLDPSQAPSLAQPLVFSNSK#.Q	6.58	1.91	3.45	0.29
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.TQQSFEK#.Q	13.91	6.25	2.23	0.45
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.DGSLASNPYSGDLTK#.F	22.97	6.87	3.34	0.30
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.FPLDYYSIPFPTPTTPLTGR@.D	7.57	2.76	2.75	0.36
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.GGSTTGSQFLEQFK#.T	30.87	8.53	3.62	0.28
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.IDLAVLLGK#.T	57.32	16.01	3.58	0.28
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.IFTASNVSSVPLPAENVTITAGQR@.I	33.22	7.48	4.44	0.23
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.STSAPQM*SPGSSDNQSSSPQPAQQK#.L	7.28	2.71	2.68	0.37
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	R.TATEEWGTEDWNEDLSETK#.I	6.80	1.92	3.55	0.28
Q80X50_UBP2L_MOUSE	Ubap2l	Ubiquitin-associated pro	K.TPSSM*ENDSSNLDPSQAPSLAQPLVFSNSK#.Q	6.71	2.06	3.25	0.31
Q6ZWY6_U2D2B_MOUSE	Ube2d2b	Ubiquitin-conjugating er	R.SQWSPALTISK#.V	14.41	7.51	1.92	0.52
P60605_UB2G2_MOUSE	Ube2g2	Ubiquitin-conjugating er	K.ILLSVVSM*LAEPNDESGANVDASK#.M	6.65	4.96	1.34	0.75
P62257_UBE2H_MOUSE	Ube2h	Ubiquitin-conjugating er	K.HEVTILGGLNEFVVK#.F	37.11	18.09	2.05	0.49
P62257_UBE2H_MOUSE	Ube2h	Ubiquitin-conjugating er	R.VDLPDK#YPFK#.S	24.61	11.54	2.13	0.47

P61087_UBE2K_MOUSE	Ube2k	Ubiquitin-conjugating er	R.GEIAGPPDTPYEGGR@.Y	7.49	46.48	0.16	6.20
P61087_UBE2K_MOUSE	Ube2k	Ubiquitin-conjugating er	K.IPETYPFNPPK#.V	9.71	5.88	1.65	0.61
P61087_UBE2K_MOUSE	Ube2k	Ubiquitin-conjugating er	R.NAVIVALSSK#.S	16.58	16.40	1.01	0.99
P61087_UBE2K_MOUSE	Ube2k	Ubiquitin-conjugating er	K.VDLVDENFTELR@.G	11.96	3.31	3.61	0.28
P61087_UBE2K_MOUSE	Ube2k	Ubiquitin-conjugating er	K.VDLVDENFTELR@GEIAGPPDTPYEGGR@.Y	5.57	3.15	1.77	0.57
P61089_UBE2N_MOUSE	Ube2n	Ubiquitin-conjugating er	K.LELFLPEEYPM*AAPK#.V	31.09	16.84	1.85	0.54
P61089_UBE2N_MOUSE	Ube2n	Ubiquitin-conjugating er	R.LLAEPVPGIK#.A	67.08	30.66	2.19	0.46
P61089_UBE2N_MOUSE	Ube2n	Ubiquitin-conjugating er	K.TNEAQAIETAR@.A	80.71	27.53	2.93	0.34
P61089_UBE2N_MOUSE	Ube2n	Ubiquitin-conjugating er	R.YFHVVIAGPQDSPFEGGTFK#.L	11.63	6.16	1.89	0.53
Q921J4_UBE2S_MOUSE	Ube2s	Ubiquitin-conjugating er	K.EVTTLTADPPDGIK#.V	16.10	7.17	2.25	0.45
Q921J4_UBE2S_MOUSE	Ube2s	Ubiquitin-conjugating er	R.LLLENYEEYAAR@.A	27.60	9.76	2.83	0.35
Q921J4_UBE2S_MOUSE	Ube2s	Ubiquitin-conjugating er	R.LLLENYEEYAAR.A	7.65	4.97	1.54	0.65
Q9CZY3_UB2V1_MOUSE	Ube2v1	Ubiquitin-conjugating er	R.WTGM*IIGPPR@.T	6.80	3.00	2.26	0.44
P21126_UBL4A_MOUSE	Ubl4a	Ubiquitin-like protein 4A	K.LNLVVK#PLEK#.V	10.02	6.54	1.53	0.65
P21126_UBL4A_MOUSE	Ubl4a	Ubiquitin-like protein 4A	R.LTLDDIER@.L	14.57	8.51	1.71	0.58
P21126_UBL4A_MOUSE	Ubl4a	Ubiquitin-like protein 4A	R.LVDSPATPIWQLISK#.V	14.72	6.02	2.45	0.41
Q9EPV8_UBL5_MOUSE	Ubl5	Ubiquitin-like protein 5 (	K.LIAAQTGTR@.W	9.60	8.56	1.12	0.89
Q80WC1_UBN2_MOUSE	Ubn2	Ubinuclein-2 OS=Mus mu	K.VSLEPLPAR@.L	9.75	3.20	3.05	0.33
Q80WC1_UBN2_MOUSE	Ubn2	Ubinuclein-2 OS=Mus mu	K.VVPTLPEGLPVLLEK#.R	17.67	5.27	3.35	0.30
Q80WC1_UBN2_MOUSE	Ubn2	Ubinuclein-2 OS=Mus mu	K.VVPTLPEGLPVLLEK#.R	6.37	1.81	3.53	0.28
Q811S7_UBIP1_MOUSE	Ubp1	Upstream-binding protei	R.LLDLDIPM*SVGIIDTR.T	6.88	8.93	0.77	1.30
Q811S7_UBIP1_MOUSE	Ubp1	Upstream-binding protei	R.LLDLDIPM*SVGIIDTR@.T	16.32	8.90	1.83	0.55
Q80TP3_UBR5_MOUSE	Ubr5	E3 ubiquitin-protein liga	R.GDFLNYALSLM*R@.S	9.37	5.85	1.60	0.63
Q80TP3_UBR5_MOUSE	Ubr5	E3 ubiquitin-protein liga	K.LEHTAQTYSELQGER@.I	5.82	2.86	2.03	0.49
Q80TP3_UBR5_MOUSE	Ubr5	E3 ubiquitin-protein liga	R.LLTATNLVTLPNSR@.G	10.94	3.42	3.20	0.31
Q80TP3_UBR5_MOUSE	Ubr5	E3 ubiquitin-protein liga	K.LTYQDAVNLQNYVEEK#.L	5.77	4.74	1.22	0.82
Q80TP3_UBR5_MOUSE	Ubr5	E3 ubiquitin-protein liga	K.NSLEDLTAEDFR@.L	11.85	5.40	2.19	0.46
Q80TP3_UBR5_MOUSE	Ubr5	E3 ubiquitin-protein liga	R.REEAIAVTM*R@.F	11.85	2.83	4.18	0.24
Q80TP3_UBR5_MOUSE	Ubr5	E3 ubiquitin-protein liga	R.SVAIFTAGQESPIVLR@.D	15.91	5.04	3.16	0.32
Q80TP3_UBR5_MOUSE	Ubr5	E3 ubiquitin-protein liga	K.VATWVDETLSSVASK#.L	8.79	3.91	2.25	0.44
Q80TP3_UBR5_MOUSE	Ubr5	E3 ubiquitin-protein liga	R.VFM*EDVGAEPGSILTELGGFEVK#.E	12.32	3.33	3.70	0.27
P25976_UBF1_MOUSE	Ubtf	Nucleolar transcription f	R.FLESLPEEEQQR.V	4.56	13.27	0.34	2.91
Q99PL6_UBXN6_MOUSE	Ubxn6	UBX domain-containing	K.K#VTLPVPDQEGQEEFYVLGEDAR@.A	3.63	1.90	1.91	0.52
Q99PL6_UBXN6_MOUSE	Ubxn6	UBX domain-containing	K.SVLR@PELLAAIEQLS.-	18.31	5.49	3.34	0.30
Q6P5G6_UBXN7_MOUSE	Ubxn7	UBX domain-containing	R.FELLTNFPR@.R	9.96	5.56	1.79	0.56
Q6P5G6_UBXN7_MOUSE	Ubxn7	UBX domain-containing	K.GLIQQFTAITGASESVGK#.H	7.55	4.73	1.60	0.63
Q9WUP7_UCHL5_MOUSE	Uchl5	Ubiquitin carboxyl-termi	R.GAQVEEIWSLEPESFEK#.L	4.78	3.29	1.45	0.69
Q9WUP7_UCHL5_MOUSE	Uchl5	Ubiquitin carboxyl-termi	R.LYELDGLR@.E	14.08	35.64	0.40	2.53
Q9WUP7_UCHL5_MOUSE	Uchl5	Ubiquitin carboxyl-termi	K.WQPGEEPAGSVVQDSR@.L	5.04	2.82	1.79	0.56
P70362_UFD1_MOUSE	Ufd1l	Ubiquitin fusion degrada	K.AVLENALR@.N	28.74	10.53	2.73	0.37
P70362_UFD1_MOUSE	Ufd1l	Ubiquitin fusion degrada	R.FIAFSGEGQSLR@.K	41.46	12.45	3.33	0.30
P70362_UFD1_MOUSE	Ufd1l	Ubiquitin fusion degrada	K.IIM*PPSALDQLSR@.L	12.34	6.28	1.96	0.51
P70362_UFD1_MOUSE	Ufd1l	Ubiquitin fusion degrada	R.LNITYPM*LFK#.L	5.27	3.47	1.52	0.66
P61961_UFM1_MOUSE	Ufm1	Ubiquitin-fold modifier 1	K.FAAEEFK#VPAATSAIITNDGIGINPAQTAGNVFLK#.H	10.12	4.86	2.08	0.48
P61961_UFM1_MOUSE	Ufm1	Ubiquitin-fold modifier 1	K.VLSVPESTPFTAVLK#.F	31.39	7.19	4.37	0.23
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.AEEVKQDKDDIINIFSVASGHLYER.F	31.49	10.67	2.95	0.34
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.AIWAALQTQASSSAK#.N	12.00	9.74	1.23	0.81
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.ANPGAWILR@.L	17.63	11.93	1.48	0.68
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.AYNYVAQEVDGYHAFQTLTQIYNK#.V	29.89	14.59	2.05	0.49
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.EGETYYDVVAVVDPVTR@.E	11.29	8.63	1.31	0.76
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.EYLDLTASNNFYVDDFAR@.F	4.75	3.58	1.33	0.75
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.FLFVDADQIVR.T	13.72	11.37	1.21	0.83
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.GQYQGLSQDPNSLSNLDQDLPNNM*IHQVPIK#.S	6.69	3.51	1.91	0.52
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.IEYQFFEDK#.H	16.85	15.22	1.11	0.90
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.ILETTTFFQR@.A	38.98	25.88	1.51	0.66
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.INYVFR@.H	25.84	16.88	1.53	0.65
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.ISM*INNPSQEISDSSTPIFR.A	7.04	6.66	1.06	0.95
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.IVPEWQDYDQEIK.Q	18.59	16.45	1.13	0.89
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.K#YPYVEVNSILGIDSAYDQNR@K#.E	9.43	4.81	1.96	0.51
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.LGIEGLSLHNILK#.L	43.77	32.05	1.37	0.73
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.LNIQPSETDYAVDIR.S	90.82	25.25	3.60	0.28
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.LR@ELYPALEGQLK#.E	11.40	10.01	1.14	0.88
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.M*AKEETAEALAAGVDIAEFSVGGM*DVSLFK.E	6.16	4.03	1.53	0.65
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.QDK#DDIINIFSVASGHLYER@.F	3.96	3.68	1.08	0.93
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.SPAISWVNNLEVDSR@.Y	12.85	8.95	1.44	0.70
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.TAAIANSM*NYLTK#.K	14.64	11.85	1.24	0.81
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.TGETVK#VEHVVSVLEK#.K	19.15	15.35	1.25	0.80
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.VDALLSAQPK.G	12.97	14.50	0.89	1.12
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.VEEDVASDLVM*K#.V	19.49	14.64	1.33	0.75
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.VWQLQDLSFQTAAR@.I	13.44	14.21	0.95	1.06
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.YPSSNPESPVVILYSEIGHEEFSNIHHQLISK#.S	12.09	9.43	1.28	0.78
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.YVLEPEISFTADSSFAK.G	15.65	13.10	1.19	0.84
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.AEEVK#QDK#DDIINIFSVASGHLYER@.F	66.01	19.28	3.42	0.29
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.AEVEENQK#.Y	17.54	9.67	1.81	0.55
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.AIWAALQTQASSSAK#.N	61.23	38.91	1.57	0.64
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.ANPGAWILR@.L	62.76	44.16	1.42	0.70
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.AVYLGELSHDQDVVEYIM*NQPNVVPR@.I	48.43	29.53	1.64	0.61
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.AYNYVAQEVDGYHAFQTLTQIYNK#.V	126.36	71.04	1.78	0.56
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.DISQNFPTK#.A	43.18	33.62	1.28	0.78
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.EETAEALAAGVDIAEFSVGGM*DVSLFK#.E	54.55	30.81	1.77	0.56
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.EGETYYDVVAVVDPVTR@.E	74.13	46.30	1.60	0.62
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.ELYPALEGQLK#.E	89.56	71.88	1.25	0.80
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.EPVYLSGYGVELAIK#.S	20.94	13.95	1.50	0.67
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.EYLDLTASNNFYVDDFAR@.F	39.65	24.87	1.59	0.63
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.FLFVDADQIVR.T	72.85	54.63	1.33	0.75
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.FLSPLQQNLLK#.F	75.46	49.68	1.52	0.66
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.FSALDSR@.G	105.15	75.71	1.39	0.72
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.GQYQGLSQDPNSLSNLDQDLPNNM*IHQVPIK#.S	32.92	15.68	2.10	0.48
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.GQYQGLSQDPNSLSNLDQDLPNNM*IHQVPIK#.S	47.74	25.95	1.84	0.54
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK#.S	6.48	3.11	2.08	0.48
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.GYYEQTGVGPLPVVLFNGM*PFEK#.E	23.27	15.34	1.52	0.66
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.HLVESTNEM*APLK#.V	26.95	23.28	1.16	0.86
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.HLVESTNEM*APLK#VWQLQDLSFQTAAR@.I	7.76	4.43	1.75	0.57
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.HYISNPSK#EPVYLSGYGVELAIK#.S	13.35	15.86	0.84	1.19
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.IEYQFFEDK#.H	62.80	53.67	1.17	0.85
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.IGFIFVVNDSEDVDGM*QDAGVAVLR@.A	21.64	16.93	1.28	0.78
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.ILAASGALSLVVM*K#.D	13.63	8.84	1.54	0.65
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.ILETTTFFQR@.A	188.13	122.16	1.54	0.65
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.IM*M*LSVLK#.N	26.52	17.14	1.55	0.65
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.INYVFR@.H	135.81	83.37	1.63	0.61
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.ISM*INNPSQEISDSSTPIFR@.A	49.27	39.60	1.24	0.80
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.ISM*INNPSQEISDSSTPIFR.A	27.75	22.19	1.25	0.80
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.ISMINNPSQEISDSSTPIFR@.A	7.78	4.36	1.79	0.56

Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.IVPEWQDYDQEIK#.Q	109.06	72.56	1.50	0.67
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.IYSHDGTDSPPDANDVVVILNNFK#.S	99.96	65.41	1.53	0.65
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.K#ADM*ANEDLLSDGTNENESGFWDSFK#.W	25.65	14.14	1.81	0.55
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.K#YNFQYELVQYK#.W	29.30	20.40	1.44	0.70
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.K#YPYVEVNSILGIDSAYDQNR@.K	15.28	11.87	1.29	0.78
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.K#YPYVEVNSILGIDSAYDQNR@K#.E	13.55	12.57	1.08	0.93
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.LGIEGLSLHNILK#.L	243.06	168.73	1.44	0.69
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.LNIQPSETDYAVDIR@.S	180.19	125.54	1.44	0.70
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.LR@ELYPALEGQLK#.E	56.26	45.68	1.23	0.81
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.LSDM*PLK#.S	57.82	41.48	1.39	0.72
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.M*AKEETAEALAAGVDIAEFSVGGM*DVSLFK.E	33.83	20.18	1.68	0.60
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.NYLSPTFK#.E	90.06	59.54	1.51	0.66
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.QDK#DDIINIFSVASGHLYER@.F	23.56	21.73	1.08	0.92
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.QLLYDAIK#.H	91.42	65.25	1.40	0.71
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.QLQTLFQEEK#.E	45.37	29.49	1.54	0.65
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.SGYWASHLAGR.K	12.34	7.82	1.58	0.63
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.SPAISWVNNLEVDSR@.Y	63.44	41.78	1.52	0.66
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.TAAIANSM*NYLTK#.K	68.30	43.54	1.57	0.64
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.TAVSAQLR@.A	189.90	111.32	1.71	0.59
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.TGETVK#VEHVVSVLEK#.K	82.86	69.23	1.20	0.84
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.VDALLSAQPK#.G	74.07	62.21	1.19	0.84
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.VEEDVASDLVM*K#.V	61.23	42.54	1.44	0.69
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.VEHVVSVLEK#.K	67.90	45.78	1.48	0.67
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.VWQLQDLSFQTAAR@.I	68.32	49.88	1.37	0.73
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.YNFQYELVQYK#.W	31.37	18.06	1.74	0.58
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	K.YPYVEVNSILGIDSAYDQNR@K#.E	10.29	6.32	1.63	0.61
Q6P5E4_UGGG1_MOUSE	Uggt1	UDP-glucose:glycoprotei	R.YVLEPEISFTADSSFAK#.G	97.06	62.44	1.55	0.64
E9Q4X2_E9Q4X2_MOUSE	Uggt2	Protein Uggt2 OS=Mus m	R.IVPEWVTYDTEIR@.T	7.28	2.33	3.12	0.32
E9Q4X2_E9Q4X2_MOUSE	Uggt2	Protein Uggt2 OS=Mus m	K.SEDIYEITGHEGAEPETNVGNVIVVLNTFK#.S	4.96	1.71	2.90	0.34
Q8VDF2_UHRF1_MOUSE	Uhrf1	E3 ubiquitin-protein liga	K.SGFLVWR@.Y	13.95	13.17	1.06	0.94
Q8VDF2_UHRF1_MOUSE	Uhrf1	E3 ubiquitin-protein liga	R.TDSSEVVQAGEK.L	3.94	6.44	0.61	1.63
Q8VDF2_UHRF1_MOUSE	Uhrf1	E3 ubiquitin-protein liga	R.LNDTIQLLVR@.Q	18.93	14.49	1.31	0.77
Q8VDF2_UHRF1_MOUSE	Uhrf1	E3 ubiquitin-protein liga	R.QSLALPLSTK#.E	18.50	14.17	1.31	0.77
Q8VDF2_UHRF1_MOUSE	Uhrf1	E3 ubiquitin-protein liga	R.R@PLIASPSQPPPALR@.N	13.05	8.60	1.52	0.66
Q8VDF2_UHRF1_MOUSE	Uhrf1	E3 ubiquitin-protein liga	R.TDSSEVVQAGEK#.L	33.88	22.65	1.50	0.67
B2KF50_B2KF50_MOUSE	Uhrf1bp1	Protein Uhrf1bp1 OS=Mu	K.SLSGSTEGPAAAVR@.E	4.50	1.13	3.98	0.25
B2KF50_B2KF50_MOUSE	Uhrf1bp1	Protein Uhrf1bp1 OS=Mu	K.SDASSDQGAVSPEK#.V	2.31	1.62	1.42	0.70
Q7TMI3_UHRF2_MOUSE	Uhrf2	E3 ubiquitin-protein liga	K.ASDSTDAVEAFQLTPQQQR@.L	3.05	2.02	1.51	0.66
Q7TMI3_UHRF2_MOUSE	Uhrf2	E3 ubiquitin-protein liga	R.GFWYDAEITTLK#.T	6.52	4.48	1.45	0.69
Q7TMI3_UHRF2_MOUSE	Uhrf2	E3 ubiquitin-protein liga	R.IGAPSADQTLTNM*NR@.A	5.29	1.93	2.74	0.37
Q5U5Q9_UIMC1_MOUSE	Uimc1	BRCA1-A complex subuni	K.LLLEEEPTTSR@.G	16.02	9.04	1.77	0.56
P13439_UMPS_MOUSE	Umps	Uridine 5'-monophospha	K.FGSFVLK#.S	12.64	4.47	2.83	0.35
P13439_UMPS_MOUSE	Umps	Uridine 5'-monophospha	R.LLSQVADILFQTAK#.N	9.64	4.30	2.24	0.45
P13439_UMPS_MOUSE	Umps	Uridine 5'-monophospha	K.SGLSSPVYIDLR@.G	12.52	6.91	1.81	0.55
P13439_UMPS_MOUSE	Umps	Uridine 5'-monophospha	R.LLSQVADILFQTAK#.N	12.64	1.96	6.45	0.15
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.AGAK#PDQIGIITPYEGQR@.S	85.27	33.13	2.57	0.39
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.AGLSQSLFER@.L	100.38	40.43	2.48	0.40
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.ALVEGPLNNLR@.E	105.57	52.51	2.01	0.50
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.ANEHQGIGFLNDPR@.R	62.81	25.38	2.47	0.40
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.DETGELSSADEK#R@.Y	10.32	3.16	3.26	0.31
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.DINWDSSQWQPLIQDR@.C	9.71	3.71	2.61	0.38
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.EAIIPGSVYDR@.S	149.57	57.72	2.59	0.39
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.ESQTQDNITVR@.W	24.24	11.38	2.13	0.47
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.FM*TTAM*YDAR@.E	40.94	13.79	2.97	0.34
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.IAFFTLPK#.T	128.77	63.65	2.02	0.49
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.IPSEQEQLR@.A	75.22	36.75	2.05	0.49
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.KGFDFQWPQPDKPM*FFYVTQGQEEIASSGTSYLNR.T	3.38	2.77	1.22	0.82
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.K#LVNTVNPGAR@.F	30.23	15.35	1.97	0.51
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.LK#ESQTQDNITVR@.W	52.62	21.34	2.47	0.41
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.LLGHEVEDVVIK#.C	88.31	32.63	2.71	0.37
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.LNVALTR@.A	57.52	31.13	1.85	0.54
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.LYQEVEIASVDAFQGR.E	40.73	16.15	2.52	0.40
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.LYQEVEIASVDAFQGR@.E	19.77	10.09	1.96	0.51
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.NM*DSM*PELQK#.L	64.91	29.69	2.19	0.46
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.NVFLLGFIPAK#.A	95.27	42.69	2.23	0.45
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.QITAQQINKLEELWK.E	25.24	11.95	2.11	0.47
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.R@FTAQGLPDLNHSQVYAVK#.T	15.58	5.66	2.75	0.36
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.SQIDVALSQDSTYQGER@.A	19.57	9.53	2.05	0.49
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.TSQLLAELNFEEDEEDTYYTK#.D	9.76	3.48	2.80	0.36
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.TVLQR@PLSLIQGPPGTGK#.T	76.06	37.18	2.05	0.49
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.TVTSATIVYHLAR@.Q	11.63	5.67	2.05	0.49
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.VPDNYGDEIAIELR@.S	45.09	18.84	2.39	0.42
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.YEDAYQYQNIFGPLVK#.L	29.95	14.85	2.02	0.50
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.YGVIIVGNPK#.A	76.32	40.65	1.88	0.53
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.AGLSQSLFER@.L	28.08	11.34	2.48	0.40
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.ALVEGPLNNLR@.E	27.64	12.76	2.17	0.46
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.EAIIPGSVYDR@.S	215.30	61.42	3.51	0.29
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.FM*TTAM*YDAR@.E	8.90	3.57	2.49	0.40
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.IAFFTLPK#.T	44.30	17.90	2.47	0.40
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.IPSEQEQLR@.A	23.40	8.27	2.83	0.35
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.K#LVNTVNPGAR@.F	7.43	4.00	1.85	0.54
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.LK#ESQTQDNITVR@.W	18.81	8.35	2.25	0.44
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.LLGHEVEDVVIK#.C	26.06	8.10	3.22	0.31
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.LNVALTR@.A	18.15	7.47	2.43	0.41
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.LYQEVEIASVDAFQGR@.E	9.89	5.25	1.88	0.53
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.NM*DSM*PELQK#.L	13.44	6.89	1.95	0.51
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	R.NVFLLGFIPAK#.A	33.90	12.30	2.76	0.36
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.R@FTAQGLPDLNHSQVYAVK#.T	8.26	2.78	2.97	0.34
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.SQIDVALSQDSTYQGER@.A	6.20	2.53	2.46	0.41
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.TVLQR@PLSLIQGPPGTGK#.T	25.43	11.15	2.28	0.44
Q9EPU0_RENT1_MOUSE	Upf1	Regulator of nonsense tra	K.VPDNYGDEIAIELR@.S	73.04	8.42	8.68	0.12
A2AT37_A2AT37_MOUSE	Upf2	Protein Upf2 OS=Mus mu	K.AFVPAILFK#.D	16.47	5.98	2.76	0.36
A2AT37_A2AT37_MOUSE	Upf2	Protein Upf2 OS=Mus mu	R.ALFIVPR@.Q	13.99	4.44	3.15	0.32
A2AT37_A2AT37_MOUSE	Upf2	Protein Upf2 OS=Mus mu	K.YIAEAVASIVEAK#.L	9.95	1.40	7.10	0.14
Q3ULJ3_Q3ULJ3_MOUSE	Upf3a	MCG3697, isoform CRA_	R.LVASQPETAGER@.L	5.80	16.69	0.35	2.88
Q3ULL6_Q3ULL6_MOUSE	Upf3b	Protein Upf3b OS=Mus m	R.TTPLLSFLK#.N	16.35	8.83	1.85	0.54
Q3ULL6_Q3ULL6_MOUSE	Upf3b	Protein Upf3b OS=Mus m	K.FLESYATDNEK#.M	6.37	3.01	2.11	0.47
Q3ULL6_Q3ULL6_MOUSE	Upf3b	Protein Upf3b OS=Mus m	K.NQEDILLFR@.D	13.70	4.88	2.81	0.36
Q9CQY6_UQCC2_MOUSE	Uqcc2	Ubiquinol-cytochrome-c	K.LILSTDTLEEFQEM*NK#.S	7.14	3.63	1.97	0.51
Q9DB77_QCR2_MOUSE	Uqcrc2	Cytochrome b-c1 comple	K.AVAQGNLSSADVQAAK#.N	12.64	10.15	1.24	0.80
Q9DB77_QCR2_MOUSE	Uqcrc2	Cytochrome b-c1 comple	K.SM*AASGNLGHTPFLDEL.-	6.20	6.20	1.00	1.00
Q571H0_NPA1P_MOUSE	Urb1	Nucleolar pre-ribosomal-	R.EVTLALLALPEAHLLTQQGTQSLGK#.E	5.53	3.49	1.58	0.63
Q61069_USF1_MOUSE	Usf1	Upstream stimulatory fac	R.LSEELQGLDQLQLDNDVLR.Q	2.08	3.25	0.64	1.56

Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.ASQK#PQPNFPSPEYM*IFDHEFTK#.L	4.90	2.11	2.32	0.43
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.DQYNLLK#.V	34.43	11.92	2.89	0.35
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.EIIR@NDGVLLLQALTR@.S	36.45	15.68	2.33	0.43
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.ELEGVITK#.A	49.98	17.57	2.84	0.35
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.EQDDLLVLLADQDQK#.I	13.16	4.42	2.97	0.34
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.EQDLQLEELK#.Q	28.71	10.77	2.67	0.38
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.IVAFENAFER@.L	103.22	35.02	2.95	0.34
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.LM*DLLADSR@.E	80.99	62.81	1.29	0.78
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.LR@EEIEELK#SQQALLQGQLAEK#.D	7.14	2.35	3.04	0.33
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.LSALLQETK#.E	81.50	30.17	2.70	0.37
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.NDGVLLLQALTR@.S	70.43	27.73	2.54	0.39
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.QLGPPVQQIILVSPM*GVSR@.L	20.34	6.10	3.33	0.30
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.QLGPPVQQIILVSPM*GVSR.L	10.10	2.86	3.53	0.28
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.SQQALLQGQLAEK#DSLIENLK#.S	37.67	11.69	3.22	0.31
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.SVPVEGESEHVSAAK#.T	24.80	9.17	2.70	0.37
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.TLEQHDNIVTHYK#.N	49.69	19.63	2.53	0.39
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.TNNSNQNFFK#.E	25.23	7.42	3.40	0.29
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.EIIR@NDGVLLLQALTR@.S	25.26	7.46	3.39	0.30
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.EQDLQLEELK#QQVSTLK#.C	31.18	10.33	3.02	0.33
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.IVAFENAFER.L	58.64	17.73	3.31	0.30
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.LK#DLGHPVEEEDESGDQEDDDDEIDDGDK#DQDI.-	7.62	3.05	2.50	0.40
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.LM*DLLADSR@.E	32.54	21.61	1.51	0.66
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.LSALLQETK#.E	37.56	13.43	2.80	0.36
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.NDGVLLLQALTR@.S	34.82	12.33	2.82	0.35
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.QLGPPVQQIILVSPM*GVSR@.L	14.01	5.80	2.42	0.41
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	R.QSEDLGSQFTEIFIK#.Q	22.33	10.26	2.18	0.46
Q9Z1Z0_USO1_MOUSE	Uso1	General vesicular transpc	K.TNNSNQNFFK#.E	12.18	4.52	2.70	0.37
P52479_UBP10_MOUSE	Usp10	Ubiquitin carboxyl-termi	K.EGLVPVSEDPVAIK#.I	17.87	6.44	2.78	0.36
P52479_UBP10_MOUSE	Usp10	Ubiquitin carboxyl-termi	K.IAELLETVTLIHKPVSLQPR.G	23.68	14.50	1.63	0.61
P52479_UBP10_MOUSE	Usp10	Ubiquitin carboxyl-termi	K.NIDYPVDLEISR@.E	10.87	3.47	3.14	0.32
P52479_UBP10_MOUSE	Usp10	Ubiquitin carboxyl-termi	R.QADFVQTPITGIFGGHIR@.S	14.84	7.42	2.00	0.50
P52479_UBP10_MOUSE	Usp10	Ubiquitin carboxyl-termi	R.DIR@PGAAFEPTYIYR@.L	17.65	6.35	2.78	0.36
P52479_UBP10_MOUSE	Usp10	Ubiquitin carboxyl-termi	K.EGLVPVSEDPVAIK#.I	17.96	5.20	3.46	0.29
P52479_UBP10_MOUSE	Usp10	Ubiquitin carboxyl-termi	K.NIDYPVDLEISR@.E	14.58	2.89	5.04	0.20
P52479_UBP10_MOUSE	Usp10	Ubiquitin carboxyl-termi	R.QADFVQTPITGIFGGHIR@.S	14.33	1090.02	0.01	76.08
P52479_UBP10_MOUSE	Usp10	Ubiquitin carboxyl-termi	R.TVQDALESLVAR.E	35.75	8.62	4.15	0.24
B1AY13_UBP24_MOUSE	Usp24	Ubiquitin carboxyl-termi	R.LDLVGSSQPIK#.E	20.55	18.73	1.10	0.91
Q91W36_UBP3_MOUSE	Usp3	Ubiquitin carboxyl-termi	R.K#FDPFLDLSLDIPSQFR@.S	17.23	7.90	2.18	0.46
Q91W36_UBP3_MOUSE	Usp3	Ubiquitin carboxyl-termi	K.LLENSSLNSK#.L	18.72	6.46	2.90	0.35
Q3TIX9_SNUT2_MOUSE	Usp39	U4/U6.U5 tri-snRNP-assc	K.NPTIVNFPITNVDLR@.E	7.31	1.76	4.16	0.24
Q3V0C5_UBP48_MOUSE	Usp48	Ubiquitin carboxyl-termi	K.ALGLDTGQQQDAQEFSK#.L	5.08	2.14	2.37	0.42
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	R.AVDWIFSHIDDLDAEAAM*DISEGR@.S	5.14	1.61	3.19	0.31
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	R.DGLGGLPDIVR@.D	17.48	7.12	2.45	0.41
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	R.DR@VTSAVEALLSADSASR@.K	7.40	3.25	2.28	0.44
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	K.EEDTSAGTGDPPR@.K	6.58	3.46	1.90	0.53
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	K.EVQDGIAPR@.M	15.27	6.56	2.33	0.43
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	R.FASFPDYLVIQIK#.K	13.96	4.40	3.17	0.32
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	K.IFQNAPTDPTQDFSTQVAK#.L	8.19	2.80	2.92	0.34
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	R.IGEWELIQESGVPLKPLFGPGYTGIR.N	15.30	7.70	1.99	0.50
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	K.IVILPDYLEIAR@.D	23.89	13.67	1.75	0.57
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	R.QAEEEK#VPLPELVR@.A	12.15	4.84	2.51	0.40
P56399_UBP5_MOUSE	Usp5	Ubiquitin carboxyl-termi	R.SSENPNEVFR@.F	10.41	6.41	1.62	0.62
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	R.AGFIQDTSLILYEEVK#PNLTER@.I	12.65	7.74	1.63	0.61
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	R.LLEIVSYK#.I	35.36	16.28	2.17	0.46
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	K.LSEVLQAVTDHDIPQQLVER@.L	19.57	8.95	2.19	0.46
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	R.VLLDNVENK#.M	10.70	7.30	1.47	0.68
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	R.AGFIQDTSLILYEEVK#PNLTER@.I	21.97	5.90	3.72	0.27
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	K.ALDELM*DGDIIVFQK#DDPENDNSELPTAK#.E	3.71	2.47	1.50	0.67
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	R.FM*YDPQTDQNIK#.I	3.42	2.16	1.58	0.63
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	K.INDR@FEFPEQLPLDEFLQK#.T	17.75	7.11	2.50	0.40
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	R.LLEIVSYK#.I	11.72	4.80	2.44	0.41
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	R.LNTDPM*LLQFFK#.S	6.46	4.82	1.34	0.75
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	K.LSEVLQAVTDHDIPQQLVER@.L	12.09	5.90	2.05	0.49
Q6A4J8_UBP7_MOUSE	Usp7	Ubiquitin carboxyl-termi	R.VLLDNVENK#.M	13.13	4.50	2.92	0.34
Q9CZJ1_UTP11_MOUSE	Utp11l	Probable U3 small nuclec	R.FDVATHLQTAPELVDR@.V	19.50	8.91	2.19	0.46
Q640M1_UT14A_MOUSE	Utp14a	U3 small nucleolar RNA-a	R.ALQSYYEAR@.A	9.99	4.34	2.30	0.43
Q640M1_UT14A_MOUSE	Utp14a	U3 small nucleolar RNA-a	K.DSTSQEVLSELR@.A	4.71	3.79	1.24	0.80
Q640M1_UT14A_MOUSE	Utp14a	U3 small nucleolar RNA-a	K.LALSDLLGPLK#PSSSLAAVK#.K	10.17	5.01	2.03	0.49
Q640M1_UT14A_MOUSE	Utp14a	U3 small nucleolar RNA-a	K.LLEAIGSLSGK#.N	15.30	8.63	1.77	0.56
Q640M1_UT14A_MOUSE	Utp14a	U3 small nucleolar RNA-a	R.TPLEQEVFNLLHK#.N	21.16	8.48	2.49	0.40
Q8C7V3_UTP15_MOUSE	Utp15	U3 small nucleolar RNA-a	K.FIVLQELVEK.E	15.68	16.02	0.98	1.02
Q8C7V3_UTP15_MOUSE	Utp15	U3 small nucleolar RNA-a	K.FIVLQELVEK#EIDYQR@.E	12.40	8.11	1.53	0.65
Q8C7V3_UTP15_MOUSE	Utp15	U3 small nucleolar RNA-a	K.VDFSPQLPYNYAVTASSR@.I	6.08	3.33	1.83	0.55
Q8C7V3_UTP15_MOUSE	Utp15	U3 small nucleolar RNA-a	R.VLNFLIR@.N	21.70	13.11	1.66	0.60
Q8C7V3_UTP15_MOUSE	Utp15	U3 small nucleolar RNA-a	K.FIVLQELVEK#EIDYQR@.E	10.60	5.46	1.94	0.52
Q8C7V3_UTP15_MOUSE	Utp15	U3 small nucleolar RNA-a	R.VLNFLIR@.N	10.43	3.62	2.88	0.35
Q9JI13_SAS10_MOUSE	Utp3	Something about silenci	K.LTEVK#DELEPLLQLVEK#.G	22.59	12.34	1.83	0.55
Q9JI13_SAS10_MOUSE	Utp3	Something about silenci	K.LTEVK#DELEPLLQLVEK#.G	12.13	10.89	1.11	0.90
Q9JI13_SAS10_MOUSE	Utp3	Something about silenci	K.QAAAVALTDEPDFDGAALK#.Y	4.64	5.48	0.85	1.18
Q9JI13_SAS10_MOUSE	Utp3	Something about silenci	K.LTEVK#DELEPLLQLVEK#.G	10.49	4.96	2.12	0.47
Q8VCY6_UTP6_MOUSE	Utp6	U3 small nucleolar RNA-a	R.ELEIESQPGEEQPVSK#.Q	4.97	2.83	1.76	0.57
Q8VCY6_UTP6_MOUSE	Utp6	U3 small nucleolar RNA-a	K.M*LQGQSAELFVAK#.H	4.29	2.33	1.84	0.54
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.LLDLLEGLTGTSLPK#.E	12.29	5.41	2.27	0.44
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.LLASLEELIK#.W	13.56	5.26	2.58	0.39
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.LLEEYSGDDTR@.N	6.81	3.21	2.12	0.47
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.VFLADQPIEAPEEPR.R	9.54	4.61	2.07	0.48
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.AAQASLNALNDPIAVEQALQEK#.K	21.24	11.37	1.87	0.54
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.AAQASLNALNDPIAVEQALQEK#.K	2.33	2.44	0.95	1.05
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.AEAVHEALESLESVLR@.H	27.99	14.85	1.88	0.53
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.ALDETLENQK#.H	16.43	12.74	1.29	0.78
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.ALEEYQQQLENELK#.S	8.09	2.70	3.00	0.33
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.DFGPSSQHFLSTSVQLPWQR@.S	10.98	5.27	2.08	0.48
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.DFSFQEDSLK#.S	14.16	5.10	2.78	0.36
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.DLHLLEEITPR@.L	40.27	12.85	3.13	0.32
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.EGLSTEEVNDVLER@.V	39.48	12.41	3.18	0.31
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.ELGQTLIDGGILDDIISEK#.L	24.72	11.12	2.22	0.45
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.ENALQDSVLAR@.Q	23.27	8.06	2.89	0.35
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.EQAIILVNAR@.G	31.37	15.41	2.04	0.49
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.ESLGELDK#QLTTYLTDR@.I	7.69	3.60	2.14	0.47
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.EVETSLQR@.C	22.12	8.70	2.54	0.39
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.GGSQM*DM*LQR.K	11.00	4.61	2.39	0.42
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.GTPISESPR@.Q	37.71	14.90	2.53	0.40
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.HLDPNNDEK#M*DEEQAQIEEVLQR@.G	12.18	4.87	2.50	0.40

E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.IDAFQLPQEAQK#.I	17.97	8.80	2.04	0.49
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.IIADLEEEQR@.N	25.27	8.17	3.09	0.32
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.IQLQEDINAYFK#.Q	8.23	2.22	3.71	0.27
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.K#TIPVSSGITSSALPADYLVEINK#.I	6.99	2.07	3.38	0.30
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.LEDSSNQVTQAVAK#.L	35.35	11.65	3.03	0.33
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.LK#GESQQVLGYK#.R	33.98	8.02	4.24	0.24
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.LLASLEELIK#.W	38.73	16.69	2.32	0.43
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.LLDLLEGLTGTSLPK#.E	83.39	30.08	2.77	0.36
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.LLDPEDVAVHLPDK#K#.S	25.70	9.08	2.83	0.35
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.LLEEYSGDDTR@.N	13.74	5.77	2.38	0.42
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.LLQVSVDDR@.L	21.17	9.17	2.31	0.43
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.LLSELDDASLQVENVR@.E	27.62	10.06	2.75	0.36
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.LR@DFEADSEVIEK#.W	24.04	6.88	3.50	0.29
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.LR@PSEASFLK#.E	22.00	14.55	1.51	0.66
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.LVDYQSQLEK#.F	38.07	13.21	2.88	0.35
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.MESLPLGDDLPSLQK#.L	3.48	1.62	2.15	0.47
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.NVEETTEYLK#.T	11.37	3.94	2.88	0.35
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.QLGEVAAFGGSNIEPSVR@.S	10.60	7.94	1.34	0.75
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.QLQQLSSWLALTEER@.I	8.02	3.05	2.63	0.38
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.QQM*LDIQAEIDAHNDIFK#.S	5.93	6.13	0.97	1.03
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.QTLDQLSEIGQDVGQLLSNPK#.A	27.39	10.58	2.59	0.39
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.SLQNDLEAEQVK#.V	24.26	10.56	2.30	0.44
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.SM*DEQLTSLK#.V	25.26	10.47	2.41	0.41
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.STEALPER@AEAVHEALESLESVLR@.H	25.17	7.15	3.52	0.28
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.STSEGVIGDLDTEISWAK#.S	22.82	8.24	2.77	0.36
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.TIPVSSGITSSALPADYLVEINK#.I	28.54	9.39	3.04	0.33
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.TLAFR@EEIAPINLK#.V	20.64	9.00	2.29	0.44
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.TM*NDLSSQLSPLDLHPSLK#.M	23.99	8.31	2.89	0.35
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.VFLADQPIEAPEEPR.R	25.88	11.75	2.20	0.45
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.VLYNDLGAQVTEGK#.Q	28.10	9.80	2.87	0.35
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.WLQEAETTANVLADASQR@.E	9.19	3.71	2.48	0.40
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	R.WSTLVAEVEALQPR@.L	9.93	4.22	2.35	0.43
E9Q6R7_E9Q6R7_MOUSE	Utrn	Protein Utrn OS=Mus mu	K.YGDLEARPDDGQNEFSDIIK.S	24.19	10.50	2.30	0.43
Q91XL3_UXS1_MOUSE	Uxs1	UDP-glucuronic acid dec	R.VVSNFILQALQGEPLTVYGSGSQTR@.A	3.07	4.29	0.72	1.40
Q9WTZ0_UXT_MOUSE	Uxt	Protein UXT OS=Mus mus	R.YETFISDVLQR@.D	10.76	3.75	2.87	0.35
Q80WQ2_VAC14_MOUSE	Vac14	Protein VAC14 homolog	K.LVTPEDDEPDEPK#.S	8.35	3.97	2.10	0.48
Q80WQ2_VAC14_MOUSE	Vac14	Protein VAC14 homolog	R.GAVLPHFNVLFDGLSK#.L	7.92	4.64	1.71	0.59
Q80WQ2_VAC14_MOUSE	Vac14	Protein VAC14 homolog	K.LAADPDPNVK#.S	54.43	16.02	3.40	0.29
P63044_VAMP2_MOUSE	Vamp2	Vesicle-associated memb	R.ADALQAGASQFETSAAK#.L	29.78	15.80	1.88	0.53
P63044_VAMP2_MOUSE	Vamp2	Vesicle-associated memb	R.LQQTQAQVDEVVDIM*R@.V	11.99	4.01	2.99	0.33
P63044_VAMP2_MOUSE	Vamp2	Vesicle-associated memb	K.LSELDDR@.A	28.61	19.10	1.50	0.67
P63044_VAMP2_MOUSE	Vamp2	Vesicle-associated memb	K.LSELDDR@ADALQAGASQFETSAAK#.L	78.48	32.74	2.40	0.42
P63024_VAMP3_MOUSE	Vamp3	Vesicle-associated memb	R.LQQTQNQVDEVVDIM*R@.V	25.48	15.36	1.66	0.60
P63024_VAMP3_MOUSE	Vamp3	Vesicle-associated memb	R.R@LQQTQNQVDEVVDIM*R@.V	15.32	6.86	2.23	0.45
O70480_VAMP4_MOUSE	Vamp4	Vesicle-associated memb	K.HVQNQVDEVIDVM*QENITK#.V	2.67	1.67	1.60	0.63
O70480_VAMP4_MOUSE	Vamp4	Vesicle-associated memb	K.SESLSDNATAFSNR.S	4.36	2.61	1.67	0.60
P70280_VAMP7_MOUSE	Vamp7	Vesicle-associated memb	R.AFSFLNEVK#.K	20.59	8.79	2.34	0.43
P70280_VAMP7_MOUSE	Vamp7	Vesicle-associated memb	R.LELLIDK#TENLVDSSVTFK#.T	19.03	7.74	2.46	0.41
O70404_VAMP8_MOUSE	Vamp8	Vesicle-associated memb	K.NIM*TQNVER@.I	49.35	17.05	2.89	0.35
O70404_VAMP8_MOUSE	Vamp8	Vesicle-associated memb	R.NK#TEDLEATSEHFK#.T	34.89	14.11	2.47	0.40
O70404_VAMP8_MOUSE	Vamp8	Vesicle-associated memb	R.NLQSEVEGVK#.N	45.70	15.22	3.00	0.33
Q9WV55_VAPA_MOUSE	Vapa	Vesicle-associated memb	K.GPFTDVVTTNLK#.L	22.35	13.49	1.66	0.60
Q9WV55_VAPA_MOUSE	Vapa	Vesicle-associated memb	K.HEQILVLDPPSDLK#.F	21.23	13.60	1.56	0.64
Q9Z1Q9_SYVC_MOUSE	Vars	Valine--tRNA ligase OS=M	R.EAFLEEVWK#.W	9.79	4.31	2.27	0.44
Q9Z1Q9_SYVC_MOUSE	Vars	Valine--tRNA ligase OS=M	R.GPGQDPQAALGALGK#.A	17.17	9.69	1.77	0.56
Q9Z1Q9_SYVC_MOUSE	Vars	Valine--tRNA ligase OS=M	R.SLPIVFDDFVDM*EFGTGAVK#.I	5.57	3.24	1.72	0.58
Q9Z1Q9_SYVC_MOUSE	Vars	Valine--tRNA ligase OS=M	R.SLPIVFDDFVDM*EFGTGAVK#.I	11.28	4.93	2.29	0.44
Q9Z1Q9_SYVC_MOUSE	Vars	Valine--tRNA ligase OS=M	K.VPLEVQEADEAK#.L	16.20	6.99	2.32	0.43
Q9Z1Q9_SYVC_MOUSE	Vars	Valine--tRNA ligase OS=M	K.VPLEVQEADEAK#LQQTEAELR@.K	11.80	5.15	2.29	0.44
Q8C1W1_VASH1_MOUSE	Vash1	Vasohibin-1 OS=Mus mus	R.FPISFK#.T	17.70	3.46	5.11	0.20
Q62465_VAT1_MOUSE	Vat1	Synaptic vesicle membra	K.GVDIVM*DPLGGSDTAK#.G	9.21	5.12	1.80	0.56
Q62465_VAT1_MOUSE	Vat1	Synaptic vesicle membra	R.TVENVTVFGTASASK#.H	7.68	3.14	2.45	0.41
Q62465_VAT1_MOUSE	Vat1	Synaptic vesicle membra	K.VLLVPGPEK#ET.-	6.17	4.23	1.46	0.69
Q62465_VAT1_MOUSE	Vat1	Synaptic vesicle membra	K.VVTYGM*ANLLTGPK#.R	10.67	3.38	3.16	0.32
Q62465_VAT1_MOUSE	Vat1	Synaptic vesicle membra	K.GVDIVM*DPLGGSDTAK#.G	4.36	2.84	1.54	0.65
Q62465_VAT1_MOUSE	Vat1	Synaptic vesicle membra	K.GVDIVM*DPLGGSDTAK#.G	7.25	3.02	2.40	0.42
P29533_VCAM1_MOUSE	Vcam1	Vascular cell adhesion pr	K.ILETTFIPTIEDTGK#.S	15.13	3.69	4.10	0.24
P29533_VCAM1_MOUSE	Vcam1	Vascular cell adhesion pr	K.SLEVTFTPVIEDIGK#.A	9.38	4.17	2.25	0.44
P29533_VCAM1_MOUSE	Vcam1	Vascular cell adhesion pr	K.SVDGSYTIR@.Q	5.43	2.16	2.52	0.40
P29533_VCAM1_MOUSE	Vcam1	Vascular cell adhesion pr	R.TQVEVYSFPEDPVIK#.M	5.17	2.40	2.15	0.46
P29533_VCAM1_MOUSE	Vcam1	Vascular cell adhesion pr	K.ILETTFIPTIEDTGK#.S	8.96	5.02	1.78	0.56
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.AANFENHSGR@.L	6.11	3.38	1.81	0.55
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.AGEVINQPM*M*M*AAR.Q	31.22	10.91	2.86	0.35
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.ALASIDSK#.L	64.05	23.91	2.68	0.37
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.ALASQLQDSLK#.D	111.94	40.70	2.75	0.36
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.AQQVSQGLDVLTAK#.V	85.39	37.31	2.29	0.44
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.AVAGNISDPGLQK#.S	88.36	33.95	2.60	0.38
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.DPNASPGDAGEQAIR@.Q	14.12	7.33	1.93	0.52
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.DYLIDGSR@.G	45.07	18.05	2.50	0.40
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.EAFQPQEPDFPPPPPDLEQLR@.L	6.86	6.28	1.09	0.92
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.ELLPVLISAM*K#.I	84.38	42.53	1.98	0.50
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.ELTPQVISAAR@.I	42.64	18.38	2.32	0.43
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.GILSGTSDLLLTFDEAEVR@.K	37.39	12.74	2.94	0.34
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.GILSGTSDLLLTFDEAEVRK.I	50.36	18.17	2.77	0.36
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.GNDIIAAAK#.R	52.56	21.30	2.47	0.41
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.GQGASPVAM*QK#.A	40.26	9.54	4.22	0.24
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.GVGQAAIR@.G	70.10	28.45	2.46	0.41
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.GWLRDPNASPGDAGEQAIR.Q	60.30	26.53	2.27	0.44
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.IPTISTQLK#.I	68.08	34.25	1.99	0.50
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.K#IDAAQNWLADPNGGPEGEEQIR@.G	13.79	5.92	2.33	0.43
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.LLAVAATAPPDAPNR@EEVFDER@.A	85.37	31.63	2.70	0.37
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.LVQAAQM*LQSDPYSVPAR.D	16.25	7.50	2.17	0.46
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.M*LGQM*TDQVADLR@.A	31.69	11.89	2.66	0.38
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.M*SAEINEIIR@.V	31.46	17.98	1.75	0.57
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.M*TGLVDEAIDTK#.S	18.90	10.79	1.75	0.57
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.NQGIEEALK#.N	65.93	36.46	1.81	0.55
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.NQWIDNVEK#.M	37.24	12.82	2.91	0.34
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.QVATALQNLQTK#.T	56.38	22.36	2.52	0.40
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.SFLDSGYR@.I	42.35	15.40	2.75	0.36
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.SLGEIAALTSK#.L	49.84	19.29	2.58	0.39
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.STVEGIQASVK#.T	48.86	24.54	1.99	0.50
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.TNISDEESEQATEM*LVHNAQNLM*QSVK#.E	13.66	5.27	2.59	0.39
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.TNISDEESEQATEM*LVHNAQNLMQSVK#.E	5.51	2.94	1.87	0.53

Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.TNISDEESEQATEMLVHNAQNLMQSVK#.E	4.29	1.86	2.30	0.43
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.VAM*ANIQPQM*LVAGATSIAR@.R	18.41	6.81	2.70	0.37
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.VAMANIQPQM*LVAGATSIAR@.R	8.53	3.61	2.36	0.42
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.VLQLTSWDEDAWASK#.D	29.47	11.68	2.52	0.40
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.VM*LVNSM*NTVK#.E	24.45	12.78	1.91	0.52
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.WIDNPTVDDR@.G	46.80	21.61	2.17	0.46
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.AQQVSQGLDVLTAK#.V	25.69	7.80	3.29	0.30
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.AVAGNISDPGLQK#.S	12.09	6.41	1.89	0.53
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.ELLPVLISAM*K#.I	19.89	8.84	2.25	0.44
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	R.GILSGTSDLLLTFDEAEVR@.K	6.08	30.38	0.20	5.00
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.QVATALQNLQTK#.T	10.34	4.37	2.37	0.42
Q64727_VINC_MOUSE	Vcl	Vinculin OS=Mus muscul	K.STVEGIQASVK#.T	11.94	4.83	2.47	0.40
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.AVANETGAFFFLINGPEIM*SK.L	13.52	10.78	1.25	0.80
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.AVANETGAFFFLINGPEIM*SK#.L	7.17	8.30	0.86	1.16
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	K.DVDLEFLAK#.M	29.81	24.08	1.24	0.81
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.ELQELVQYPVEHPDK#.F	19.14	14.85	1.29	0.78
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	K.EM*VELPLR@.H	12.41	13.61	0.91	1.10
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.EVDIGIPDATGR.L	35.98	22.21	1.62	0.62
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.GGNIGDGGGAADR.V	9.99	10.47	0.95	1.05
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.IVSQLLTLM*DGLK#.Q	19.48	14.46	1.35	0.74
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.IVSQLLTLMDGLK#.Q	12.96	8.08	1.60	0.62
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.K#GDIFLVR@.G	40.30	35.33	1.14	0.88
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	K.LAGESESNLR@.K	35.96	21.99	1.64	0.61
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.LDQLIYIPLPDEK#.S	46.55	37.89	1.23	0.81
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.LIVDEAINEDNSVVSLSQPK#.M	27.88	21.93	1.27	0.79
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	K.M*DELQLFR@.G	18.82	15.86	1.19	0.84
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	R.WALSQSNPSALR@.E	19.34	17.47	1.11	0.90
Q01853_TERA_MOUSE	Vcp	Transitional endoplasmi	K.LAGESESNLR.K	4.23	5.03	0.84	1.19
Q8CDG3_VCIP1_MOUSE	Vcpip1	Deubiquitinating proteir	R.SSGDYSATFLPGLIPAEK#.C	5.13	2.94	1.74	0.57
Q8CDG3_VCIP1_MOUSE	Vcpip1	Deubiquitinating proteir	R.TGVIGVQPEEVTAAAK#.K	5.52	3.13	1.77	0.57
Q8CDG3_VCIP1_MOUSE	Vcpip1	Deubiquitinating proteir	R.VGDVQGQELESQLPTK#.I	10.35	5.43	1.91	0.52
Q8CDG3_VCIP1_MOUSE	Vcpip1	Deubiquitinating proteir	R.DGPSSAPATPTK#.A	6.49	2.51	2.58	0.39
Q8CDG3_VCIP1_MOUSE	Vcpip1	Deubiquitinating proteir	R.SSGDYSATFLPGLIPAEK#.C	7.64	3.40	2.25	0.45
Q8CDG3_VCIP1_MOUSE	Vcpip1	Deubiquitinating proteir	R.VGDVQGQELESQLPTK#.I	8.65	3.63	2.38	0.42
Q60932_VDAC1_MOUSE	Vdac1	Voltage-dependent anior	K.GYGFGLIK#.L	67.30	19.68	3.42	0.29
Q60932_VDAC1_MOUSE	Vdac1	Voltage-dependent anior	K.LGLGLEFQA.-	15.58	15.58	1.00	1.00
Q60932_VDAC1_MOUSE	Vdac1	Voltage-dependent anior	K.SENGLEFTSSGSANTETTK#.V	12.61	2.66	4.74	0.21
Q60932_VDAC1_MOUSE	Vdac1	Voltage-dependent anior	K.TDEFQLHTNVNDGTEFGGSIYQK#.V	40.60	8.90	4.56	0.22
Q60932_VDAC1_MOUSE	Vdac1	Voltage-dependent anior	K.TKSENGLEFTSSGSANTETTK.V	38.02	8.07	4.71	0.21
Q60932_VDAC1_MOUSE	Vdac1	Voltage-dependent anior	K.VNNSSLIGLGYTQTLK#PGIK#.L	61.14	16.11	3.80	0.26
Q60932_VDAC1_MOUSE	Vdac1	Voltage-dependent anior	R.VTQSNFAVGYK#.T	146.35	32.74	4.47	0.22
Q60932_VDAC1_MOUSE	Vdac1	Voltage-dependent anior	K.WNTDNTLGTEITVEDQLAR@.G	21.21	6.84	3.10	0.32
Q60932_VDAC1_MOUSE	Vdac1	Voltage-dependent anior	R.WTEYGLTFTEK#.W	67.94	19.39	3.50	0.29
Q60930_VDAC2_MOUSE	Vdac2	Voltage-dependent anior	K.GFGFGLVK#.L	41.50	13.92	2.98	0.34
Q60930_VDAC2_MOUSE	Vdac2	Voltage-dependent anior	K.LTFDTTFSPNTGK#.K	24.96	9.45	2.64	0.38
Q60930_VDAC2_MOUSE	Vdac2	Voltage-dependent anior	K.LTLSALVDGK#.S	55.48	16.10	3.45	0.29
Q60930_VDAC2_MOUSE	Vdac2	Voltage-dependent anior	R.SNFAVGYR@.T	49.43	13.21	3.74	0.27
Q60930_VDAC2_MOUSE	Vdac2	Voltage-dependent anior	K.VNNSSLIGVGYTQTLRPGVK.L	58.04	10.49	5.53	0.18
Q60930_VDAC2_MOUSE	Vdac2	Voltage-dependent anior	K.YQLDPTASISAK#.V	65.72	21.54	3.05	0.33
Q60931_VDAC3_MOUSE	Vdac3	Voltage-dependent anior	R.IETSINLAWTAGSNNTR@.F	3.43	4.04	0.85	1.18
Q60931_VDAC3_MOUSE	Vdac3	Voltage-dependent anior	K.LSQNNFALGYK#.A	36.07	12.18	2.96	0.34
Q60931_VDAC3_MOUSE	Vdac3	Voltage-dependent anior	K.LTLDTIFVPNTGK#.K	16.31	8.91	1.83	0.55
Q60931_VDAC3_MOUSE	Vdac3	Voltage-dependent anior	K.LTLDTIFVPNTGKK.S	34.29	10.77	3.18	0.31
Q60931_VDAC3_MOUSE	Vdac3	Voltage-dependent anior	K.VNNASLIGLGYTQTLR@PGVK#.L	21.61	5.72	3.78	0.26
Q60931_VDAC3_MOUSE	Vdac3	Voltage-dependent anior	K.WNTDNTLGTEISWENK#.L	12.77	2.91	4.39	0.23
Q60931_VDAC3_MOUSE	Vdac3	Voltage-dependent anior	K.LTLDTIFVPNTGK#.K	8.97	3.97	2.26	0.44
Q60931_VDAC3_MOUSE	Vdac3	Voltage-dependent anior	K.VNNASLIGLGYTQTLR@PGVK#.L	8.60	2.40	3.58	0.28
Q5SXC4_Q5SXC4_MOUSE	Vezf1	Protein Vezf1 OS=Mus mu	R.LWEEAVK#.A	17.65	8.42	2.09	0.48
Q91YD6_VILL_MOUSE	Vill	Villin-like protein OS=Mu	R.SLATPIFVVK#.Q	10.39	3.17	3.28	0.30
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.DNLAEDIM*R@.L	22.30	21.94	1.02	0.98
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.EEAESTLQSFR@.Q	85.87	80.95	1.06	0.94
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.EKLQEEM*LQREEAESTLQSFR.Q	6.74	6.34	1.06	0.94
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.EM*EENFALEAANYQDTIGR@.L	29.20	33.08	0.88	1.13
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.EMEENFALEAANYQDTIGR.L	6.25	5.43	1.15	0.87
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.EMEENFALEAANYQDTIGR@.L	11.81	11.38	1.04	0.96
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.ETNLESLPLVDTHSK#.R	5.25	7.70	0.68	1.47
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.EYQDLLNVK#.M	96.21	95.36	1.01	0.99
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.FADLSEAANR@.N	156.74	176.68	0.89	1.13
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.FANYIDK#.V	123.49	144.03	0.86	1.17
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.ILLAELEQLK#.G	204.85	214.29	0.96	1.05
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.ISLPLPTFSSLNLR@.E	166.95	226.19	0.74	1.35
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.K#VESLQEEIAFLK#.K	61.66	66.58	0.93	1.08
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.K#VESLQEEIAFLK#K#.L	111.45	111.53	1.00	1.00
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.LGDLYEEEM*R.E	45.15	49.70	0.91	1.10
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.LGDLYEEEMR@.E	22.36	26.49	0.84	1.18
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.LHDEEIQELQAQIQEQHVQIDVDVSK#PDLTAALR@.D	4.84	3.48	1.39	0.72
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.LHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR.D	2.98	5.39	0.55	1.81
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.LLQDSVDFSLADAINTEFK#.N	102.75	85.22	1.21	0.83
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.LLQDSVDFSLADAINTEFK.N	56.92	58.10	0.98	1.02
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.LQEEM*LQR.E	35.84	41.64	0.86	1.16
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.LQEEM*LQR@EEAESTLQSFR@.Q	26.11	26.80	0.97	1.03
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.LQEEMLQREEAESTLQSFR.Q	9.35	7.89	1.18	0.84
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.M*ALDIEIATYR.K	31.94	30.62	1.04	0.96
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.NLQEAEEWYK#.S	54.73	62.66	0.87	1.14
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.QDVDNASLAR@.L	138.36	153.64	0.90	1.11
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.QM*REM*EENFALEAANYQDTIGR.L	18.80	11.90	1.58	0.63
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.QQYESVAAK#.N	63.73	76.42	0.83	1.20
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.RQVDQLTNDK.A	12.17	13.98	0.87	1.15
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.SLYSSSPGGAYVTR.S	140.21	169.29	0.83	1.21
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.SYVTTSTR.T	112.84	142.96	0.79	1.27
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.TNEKVELQELNDR.F	157.83	152.77	1.03	0.97
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.VELQELNDR@.F	32.63	30.75	1.06	0.94
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.VEVER@DNLAEDIMR@.L	40.15	29.72	1.35	0.74
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.SLYSSSPGGAYVTR.S	5.84	2.56	2.28	0.44
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.DNLAEDIM*R@.L	4.96	6.44	0.77	1.30
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.EEAESTLQSFR.Q	22.15	27.94	0.79	1.26
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.EM*EENFALEAANYQDTIGR.L	8.91	7.36	1.21	0.83
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.EYQDLLNVK.M	40.29	43.24	0.93	1.07
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.FADLSEAANR.N	79.10	91.01	0.87	1.15
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.ILLAELEQLK.G	47.52	60.64	0.78	1.28
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.ISLPLPTFSSLNLR@.E	61.58	89.17	0.69	1.45
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.K#LHDEEIQELQAQIQEQHVQIDVDVSK#PDLTAALR@.D	2.77	4.00	0.69	1.44
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.KLHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR.D	7.02	12.75	0.55	1.82

P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.KVESLQEEIAFLK.K	49.14	47.98	1.02	0.98
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.KVESLQEEIAFLKK.L	32.83	32.69	1.00	1.00
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.LGDLYEEEM*R.E	13.50	13.99	0.96	1.04
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.LGDLYEEEMR.E	7.99	11.37	0.70	1.42
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.LHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR.D	8.16	9.35	0.87	1.15
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.LLQDSVDFSLADAINTEFK.N	16.30	19.42	0.84	1.19
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.LQEEM*LQR@EEAESTLQSFR@.Q	6.53	9.22	0.71	1.41
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.M*ALDIEIATYR@.K	12.72	16.86	0.75	1.33
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.NLQEAEEWYK#.S	23.28	30.17	0.77	1.30
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.QDVDNASLAR@.L	47.66	52.22	0.91	1.10
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.QQYESVAAK.N	26.35	38.81	0.68	1.47
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.SLYSSSPGGAYVTR.S	48.86	62.02	0.79	1.27
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.TNEKVELQELNDR.F	36.71	52.97	0.69	1.44
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.VEVERDNLAEDIM*R.L	24.55	31.03	0.79	1.26
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.FADLSEAANR.N	8.28	9.31	0.89	1.12
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	K.ILLAELEQLK.G	7.96	10.99	0.72	1.38
P20152_VIME_MOUSE	Vim	Vimentin OS=Mus muscu	R.LLQDSVDFSLADAINTEFK.N	3.90	5.72	0.68	1.47
Q6TEK5_VKORL_MOUSE	Vkorc1l1	Vitamin K epoxide reduc	R.GFGLLGSIFGK#.D	18.36	8.30	2.21	0.45
Q6TEK5_VKORL_MOUSE	Vkorc1l1	Vitamin K epoxide reduc	R.LVYLNEAWK#.R	5.93	4.54	1.31	0.76
Q78T54_VMA21_MOUSE	Vma21	Vacuolar ATPase assembl	K.AALNALQPPEFR@.N	5.25	5.77	0.91	1.10
Q91W86_VPS11_MOUSE	Vps11	Vacuolar protein sorting	K.AFLEHM*SEVQPDSPQGIYDTLLELR@.L	2.74	11.55	0.24	4.22
Q91W86_VPS11_MOUSE	Vps11	Vacuolar protein sorting	K.AFLEHM*SEVQPDSPQGIYDTLLELR@.L	4.80	141.93	0.03	29.56
B1ART1_B1ART1_MOUSE	Vps13d	Protein Vps13d OS=Mus	R.ALQITDFCQR@KSER@.S	5.14	2.46	2.09	0.48
Q920Q4_VPS16_MOUSE	Vps16	Vacuolar protein sorting	K.HQELDTLK#DLYNQDDNHQELGSFHIR@.A	7.73	1.60	4.84	0.21
Q920Q4_VPS16_MOUSE	Vps16	Vacuolar protein sorting	K.LAALADLEDWEELEK#.F	15.17	5.27	2.88	0.35
Q920Q4_VPS16_MOUSE	Vps16	Vacuolar protein sorting	K.LGDTPGVSYSDIAAR.A	17.04	5.69	2.99	0.33
Q920Q4_VPS16_MOUSE	Vps16	Vacuolar protein sorting	R.R@LM*VVGNAPESIQFVLDEDSYLVPELDGVR@.I	3.49	2.77	1.26	0.80
Q920Q4_VPS16_MOUSE	Vps16	Vacuolar protein sorting	R.STHEFLHEVPVASEEIFK#.I	10.19	2.32	4.39	0.23
Q920Q4_VPS16_MOUSE	Vps16	Vacuolar protein sorting	R.VAALQTAADAFYK#.A	15.54	3.26	4.77	0.21
Q920Q4_VPS16_MOUSE	Vps16	Vacuolar protein sorting	K.LAALADLEDWEELEK#.F	23.65	10.36	2.28	0.44
Q920Q4_VPS16_MOUSE	Vps16	Vacuolar protein sorting	K.LGDTPGVSYSDIAAR@.A	9.01	4.41	2.04	0.49
Q920Q4_VPS16_MOUSE	Vps16	Vacuolar protein sorting	R.VAALQTAADAFYK#.A	7.90	3.17	2.49	0.40
Q8R307_VPS18_MOUSE	Vps18	Vacuolar protein sorting	R.EM*EEATASAQR@.I	3.96	1.38	2.86	0.35
Q9CQ80_VPS25_MOUSE	Vps25	Vacuolar protein-sorting	R.K#LPVESIQIVLEELR@.K	8.72	3.29	2.65	0.38
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	K.EITGIGPSTTTETETIAK#.Y	28.16	15.89	1.77	0.56
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	K.ELALPGELTQSR@.S	43.85	26.55	1.65	0.61
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	K.EYDLIVHQLATYPDVNNSIK#.M	17.30	4.65	3.72	0.27
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	R.FESPDSQASAEQPEM*.-	20.50	20.50	1.00	1.00
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	K.HYLFYDGESVSGK#.V	7.04	2.97	2.37	0.42
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	K.IQHM*ELQLIK#.K	11.59	5.83	1.99	0.50
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	K.IYFLLVR@.I	23.76	9.90	2.40	0.42
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	R.LFLAGYDPTPTM*R@.D	39.21	17.39	2.25	0.44
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	K.QQEIILWR@.K	14.68	6.98	2.10	0.48
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	R.SYDFEFM*QVEKPYESYIGANVR.L	10.39	4.31	2.41	0.41
P40336_VP26A_MOUSE	Vps26a	Vacuolar protein sorting	K.YEIM*DGAPVK#GESIPIR@.L	15.23	8.89	1.71	0.58
Q8C0E2_VP26B_MOUSE	Vps26b	Vacuolar protein sorting	R.LFLAGYELTPTM*R@.D	10.95	4.86	2.25	0.44
Q8C0E2_VP26B_MOUSE	Vps26b	Vacuolar protein sorting	K.YFLFYDGETVSGK#.V	13.26	7.51	1.77	0.57
Q9D1C8_VPS28_MOUSE	Vps28	Vacuolar protein sorting	R.AM*DEIQPDLR.E	49.43	20.33	2.43	0.41
Q9D1C8_VPS28_MOUSE	Vps28	Vacuolar protein sorting	R.QM*LFDLESAYNAFNR@.F	16.68	8.53	1.95	0.51
Q9D1C8_VPS28_MOUSE	Vps28	Vacuolar protein sorting	K.YDNM*AELFAVVK#.T	23.47	8.69	2.70	0.37
Q9D2N9_VP33A_MOUSE	Vps33a	Vacuolar protein sorting	R.FLSQLEDGGTEYVIATTK#.L	6.65	1.83	3.64	0.27
Q9D2N9_VP33A_MOUSE	Vps33a	Vacuolar protein sorting	R.VNLNVLR@.E	7.37	3.06	2.41	0.42
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	R.ILVGTNLVR@.L	25.34	11.02	2.30	0.43
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.IPVDTYNNILTVLK#.L	22.26	7.97	2.79	0.36
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.IR@EDLPNLESSEETEQINK#.H	10.56	4.98	2.12	0.47
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.LFDIFSQQVATVIQSR@.Q	12.32	8.10	1.52	0.66
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	R.LSQLEGVNVER@.Y	16.18	9.93	1.63	0.61
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.NIIIALIDR@.L	13.74	7.22	1.90	0.53
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.VLETTVEIFNK#.L	8.76	6.06	1.45	0.69
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	R.ESPESEGPIYEGLIL.-	10.07	10.07	1.00	1.00
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	R.ILVGTNLVR.L	29.01	10.16	2.86	0.35
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.IPVDTYNNILTVLK#.L	22.97	10.08	2.28	0.44
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.IR@EDLPNLESSEETEQINK#.H	10.56	6.25	1.69	0.59
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.LFDIFSQQVATVIQSR@.Q	18.24	7.26	2.51	0.40
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.LNLEHIATSSAVSK#.E	14.74	6.67	2.21	0.45
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	R.LSQLEGVNVER@.Y	20.97	7.58	2.77	0.36
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	K.NIIIALIDR@.L	14.62	9.98	1.46	0.68
Q9EQH3_VPS35_MOUSE	Vps35	Vacuolar protein sorting	R.SDDPDQQYLILNTAR@.K	10.97	6.72	1.63	0.61
Q8CHS8_VP37A_MOUSE	Vps37a	Vacuolar protein sorting	K.SASSSAAGSPAGLTSLQQQK#.Q	4.30	1.80	2.39	0.42
Q8R0J7_VP37B_MOUSE	Vps37b	Vacuolar protein sorting	K.FLDGELPLDSFIDVYQSK#.R	4.44	3.71	1.20	0.84
Q8R0J7_VP37B_MOUSE	Vps37b	Vacuolar protein sorting	R.GM*EEAQTVQLNK#.E	7.11	5.18	1.37	0.73
Q8R5L3_VPS39_MOUSE	Vps39	Vam6/Vps39-like protei	K.IFTEDLPEVESLPR@.D	6.91	3.78	1.83	0.55
Q5KU39_VPS41_MOUSE	Vps41	Vacuolar protein sorting	K.AISPYLPR@.G	11.48	3.01	3.81	0.26
Q5KU39_VPS41_MOUSE	Vps41	Vacuolar protein sorting	K.ILVADSLSLLK#.K	9.63	3.16	3.05	0.33
Q5KU39_VPS41_MOUSE	Vps41	Vacuolar protein sorting	R.NFVEETVYLLSR@.M	14.01	4.39	3.19	0.31
P97390_VPS45_MOUSE	Vps45	Vacuolar protein sorting	K.AFVENYPQFK#.K	9.88	4.12	2.40	0.42
P97390_VPS45_MOUSE	Vps45	Vacuolar protein sorting	R.LK#ENLYPYLGPSTLR@.D	10.89	4.19	2.60	0.38
P97390_VPS45_MOUSE	Vps45	Vacuolar protein sorting	K.SFLEEVLASGLHSR@.S	13.41	4.46	3.01	0.33
Q8VEJ9_VPS4A_MOUSE	Vps4a	Vacuolar protein sorting	K.GILLFGPPGTGK#.T	14.19	9.75	1.46	0.69
Q8VEJ9_VPS4A_MOUSE	Vps4a	Vacuolar protein sorting	R.IYIPLPEEAAR@.A	12.89	5.27	2.45	0.41
P46467_VPS4B_MOUSE	Vps4b	Vacuolar protein sorting	R.LHLGSTQNSLTEADFQELGR@.K	18.11	13.87	1.31	0.77
Q3UVL4_VPS51_MOUSE	Vps51	Vacuolar protein sorting	K.GGATPPALLLLLSR@.L	9.08	2.75	3.30	0.30
Q3UVL4_VPS51_MOUSE	Vps51	Vacuolar protein sorting	R.GR@LEEELSSLEAELGPSPPAPDVLEFTDR@.G	3.43	3.39	1.01	0.99
Q3UVL4_VPS51_MOUSE	Vps51	Vacuolar protein sorting	R.LAQEQGGSDNSLLVR@.A	8.62	2.07	4.17	0.24
Q3UVL4_VPS51_MOUSE	Vps51	Vacuolar protein sorting	R.IDVFSPVEFNK#.V	12.70	1.91	6.67	0.15
Q3UVL4_VPS51_MOUSE	Vps51	Vacuolar protein sorting	K.LAAFAQELGGR@.Y	11.48	5.74	2.00	0.50
Q3UVL4_VPS51_MOUSE	Vps51	Vacuolar protein sorting	R.LAQEQGGSDNSLLVR@.A	9.85	3.34	2.95	0.34
Q3UVL4_VPS51_MOUSE	Vps51	Vacuolar protein sorting	R.LR@APGALLAAAGLSESATEIVER@.V	9.84	2.80	3.51	0.28
Q8C754_VPS52_MOUSE	Vps52	Vacuolar protein sorting	R.AADDSK#EVESFQQLLNAR@.T	8.29	1.01	8.20	0.12
Q8C754_VPS52_MOUSE	Vps52	Vacuolar protein sorting	K.QVELELQQIEQK#.S	7.27	3.05	2.38	0.42
Q8C754_VPS52_MOUSE	Vps52	Vacuolar protein sorting	R.VLSQPQLR@.A	7.15	3.33	2.14	0.47
Q8C754_VPS52_MOUSE	Vps52	Vacuolar protein sorting	R.TLQEQSGAM*NIR@.L	8.70	5.53	1.57	0.64
Q8CCB4_VPS53_MOUSE	Vps53	Vacuolar protein sorting	K.LLLFAIQR@.T	10.27	3.65	2.82	0.36
Q8CCB4_VPS53_MOUSE	Vps53	Vacuolar protein sorting	K.TSSSSGGLTISSLLK#.E	8.23	4.84	1.70	0.59
Q8CCB4_VPS53_MOUSE	Vps53	Vacuolar protein sorting	K.AAQTELGQQILADFEEAFPSQGTK#.R	20.98	5.48	3.83	0.26
Q8CCB4_VPS53_MOUSE	Vps53	Vacuolar protein sorting	K.M*VLLDLPSIGSQVVR@.K	7.63	1.87	4.08	0.25
Q8CCB4_VPS53_MOUSE	Vps53	Vacuolar protein sorting	K.TSSSSGGLTISSLLK#.E	14.85	3.95	3.76	0.27
Q8CCB4_VPS53_MOUSE	Vps53	Vacuolar protein sorting	R.TTNFEGFLAK#.R	12.74	1.96	6.51	0.15
Q62481_VPS72_MOUSE	Vps72	Vacuolar protein sorting	K.ITEELNLR@.S	86.89	35.99	2.41	0.41
Q62481_VPS72_MOUSE	Vps72	Vacuolar protein sorting	R.SLETYER@.L	28.12	10.71	2.63	0.38
Q62481_VPS72_MOUSE	Vps72	Vacuolar protein sorting	K.YITAHGLPPTASALGPGPPPPEPLPGSGPR.A	8.26	3.98	2.07	0.48
O89116_VTI1A_MOUSE	Vti1a	Vesicle transport throug	R.IAYSDEVR@NELLGDAGNSSENQR@.A	7.09	3.02	2.35	0.43
Q8R3P6_VWA9_MOUSE	Vwa9	von Willebrand factor A	K.EGDEVGAGITDDNEDENSANQIAGK#.I	13.26	3.55	3.74	0.27

Q8R3P6_VWA9_MOUSE	Vwa9	von Willebrand factor A	K.LIDLAYTPFHAVLK#.C	42.40	11.79	3.60	0.28
Q8R3P6_VWA9_MOUSE	Vwa9	von Willebrand factor A	R.SESNR@FPLPFPFPSK#.L	22.01	11.54	1.91	0.52
Q8R3P6_VWA9_MOUSE	Vwa9	von Willebrand factor A	R.HLVLPIALNK#.E	15.31	6.08	2.52	0.40
Q8R3P6_VWA9_MOUSE	Vwa9	von Willebrand factor A	K.LIDLAYTPFHAVLK#.C	22.48	6.94	3.24	0.31
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	R.ASLDLM*IR@.L	9.53	4.50	2.12	0.47
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	R.LLELEQDASSAK#.L	17.36	6.84	2.54	0.39
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	R.SM*DEFTASTPADLGEAGR@.L	9.90	3.01	3.29	0.30
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	R.ASLDLM*IR@.L	12.86	4.69	2.74	0.36
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	R.EYLPEGDFSIM*TEM*LK#.K	5.19	1.97	2.64	0.38
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	K.GSSYSESSEAAQLEEVTSVFEANSK#.C	5.52	3.41	1.62	0.62
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	R.LLELEQDASSAK#.L	26.52	7.93	3.35	0.30
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	K.SGEWQETSGEIQWVSTEK#.T	3.01	1.47	2.04	0.49
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	R.SM*DEFTASTPADLGEAGR@.L	11.83	3.47	3.41	0.29
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	K.TVTIPTQPYQEIVTALK#.C	28.01	7.91	3.54	0.28
Q65Z40_WAPL_MOUSE	Wapal	Wings apart-like protein	R.VLESVTVHNPENQSYLIAYK#.D	19.36	6.80	2.85	0.35
Q8VDD8_WASH1_MOUSE	Wash1	WAS protein family hom	R.ATLLESIR@.Q	22.97	6.57	3.50	0.29
Q8VDD8_WASH1_MOUSE	Wash1	WAS protein family hom	R.ATSQGGDLM*SDLFNK#.L	6.28	2.87	2.19	0.46
Q8VDD8_WASH1_MOUSE	Wash1	WAS protein family hom	K.GPSTGTSEGPGGAFSR@.M	7.21	3.67	1.96	0.51
Q8VDD8_WASH1_MOUSE	Wash1	WAS protein family hom	K.THTM*LGTEEEK#LFDAPLSISK#.R	6.87	2.45	2.80	0.36
Q8VDD8_WASH1_MOUSE	Wash1	WAS protein family hom	K.YPAPEHLQEYGSIFTGALDPGLQR@.R	18.20	6.67	2.73	0.37
Q8VDD8_WASH1_MOUSE	Wash1	WAS protein family hom	K.YVFLDPLAGAVTK#.T	21.72	9.22	2.36	0.42
Q923D5_WBP11_MOUSE	Wbp11	WW domain-binding pr	K.ADDASAATIEK.K	6.29	7.37	0.85	1.17
Q61048_WBP4_MOUSE	Wbp4	WW domain-binding pr	K.TVSSLGVAADGVAPVFK#.K	6.16	3.72	1.65	0.60
P59328_WDHD1_MOUSE	Wdhd1	WD repeat and HMG-box	R.LFTIGGVQK#.E	11.14	4.56	2.44	0.41
P59328_WDHD1_MOUSE	Wdhd1	WD repeat and HMG-box	K.SGAVFSSSQGWVNPFK#.V	4.29	3.32	1.29	0.77
P59328_WDHD1_MOUSE	Wdhd1	WD repeat and HMG-box	R.VEK#DYNDLFDGDDTSSAGDFLNDNAVEIPSFSK#.G	4.13	2.50	1.65	0.61
P59328_WDHD1_MOUSE	Wdhd1	WD repeat and HMG-box	K.VVDVM*DNSQQQTFR@.G	7.31	2.06	3.56	0.28
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.AELSQNISAR@.E	21.46	7.75	2.77	0.36
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	R.DLLLAIHPPNYIVLWNADTGTK#.L	5.32	2.03	2.62	0.38
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	R.DLLNELGSTK#EELTES.-	17.15	8.80	1.95	0.51
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.K#LLLDPDFSLLQR@.C	3.05	3.01	1.01	0.99
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.LIAM*YNDGAEVWDTK#.E	6.78	2.86	2.37	0.42
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.LLLDPDFSLLQR@.C	45.01	13.35	3.37	0.30
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.LPDLSLDNM*IGQSAIAGEEHPK#.G	11.03	6.43	1.72	0.58
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	R.NELQLVDLPTGR@.S	25.73	11.21	2.30	0.44
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.QYLAVVFK#.D	15.43	5.16	2.99	0.33
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	R.TLTGALNAHNK#.A	5.89	2.39	2.46	0.41
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	R.YLQTYGEWNR@.A	9.02	2.84	3.17	0.32
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.AELSQNISAR@.E	14.43	4.85	2.97	0.34
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	R.DLLNELGSTK#EELTES.-	11.54	5.15	2.24	0.45
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.LIAM*YNDGAEVWDTK#.E	6.08	2.06	2.95	0.34
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.LLLDPDFSLLQR@.C	30.94	15.65	1.98	0.51
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	K.LPDLSLDNM*IGQSAIAGEEHPK#.G	10.06	3.70	2.72	0.37
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	R.NELQLVDLPTGR@.S	19.14	13.65	1.40	0.71
Q8K1X1_WDR11_MOUSE	Wdr11	WD repeat-containing pr	R.YSLDISHIDYPENEEIK#.T	7.97	3.71	2.15	0.47
Q9JJA4_WDR12_MOUSE	Wdr12	Ribosome biogenesis pro	K.HM*ELENISSEEVVELEYVEK#.Y	6.43	2.57	2.50	0.40
Q9JJA4_WDR12_MOUSE	Wdr12	Ribosome biogenesis pro	K.LYSYSYSPTTSHVGA.-	19.02	19.02	1.00	1.00
Q9JJA4_WDR12_MOUSE	Wdr12	Ribosome biogenesis pro	K.WSPTHEQQLISGSLDNIVK#.L	9.46	3.53	2.68	0.37
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	R.DLFDFSTR@.I	42.19	16.42	2.57	0.39
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	K.NM*LGSQM*LPAR@.V	21.12	38.50	0.55	1.82
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	R.VATASLDQTVK#.L	102.27	39.16	2.61	0.38
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	R.VFDLEDEVR@.S	107.88	34.55	3.12	0.32
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	K.HLLGAEHGDEAQGGGLR@.L	12.82	4.04	3.18	0.31
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	R.LEQLQAVLSSYLEK#.N	8.16	3.45	2.36	0.42
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	R.VATASLDQTVK#.L	23.37	10.14	2.30	0.43
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	R.VFDLEDEVR.S	32.76	21.07	1.55	0.64
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	R.GLALLNGEYLLAAQQGK#.N	5.98	2.40	2.49	0.40
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	R.VATASLDQTVK#.L	15.94	6.28	2.54	0.39
Q4VBE8_WDR18_MOUSE	Wdr18	WD repeat-containing pr	R.VFDLEDEVR.S	18.56	16.03	1.16	0.86
Q8C6G8_WDR26_MOUSE	Wdr26	WD repeat-containing pr	R.LALLNVATQGVHLWDLQDR@.V	5.31	4.19	1.27	0.79
Q8C6G8_WDR26_MOUSE	Wdr26	WD repeat-containing pr	K.YLEYLEDGK#VLEALQVLR@.C	6.53	4.87	1.34	0.75
Q8C6G8_WDR26_MOUSE	Wdr26	WD repeat-containing pr	R.GYNFEDLTDR@.N	8.40	3.53	2.38	0.42
Q8C6G8_WDR26_MOUSE	Wdr26	WD repeat-containing pr	R.LALLNVATQGVHLWDLQDR@.V	19.31	9.84	1.96	0.51
Q8C6G8_WDR26_MOUSE	Wdr26	WD repeat-containing pr	K.YLEYLEDGK#VLEALQVLR@.C	9.87	4.46	2.21	0.45
Q8K4P0_WDR33_MOUSE	Wdr33	pre-mRNA 3' end process	R.EASFSPTDNK#.F	16.56	7.15	2.32	0.43
Q8K4P0_WDR33_MOUSE	Wdr33	pre-mRNA 3' end process	R.NLK#EELQVFR@.G	37.33	10.63	3.51	0.28
Q8K4P0_WDR33_MOUSE	Wdr33	pre-mRNA 3' end process	K.R@PDFAQQQAM*QQLTFDGK#.R	13.83	3.51	3.94	0.25
Q8K4P0_WDR33_MOUSE	Wdr33	pre-mRNA 3' end process	R.EASFSPTDNK#.F	16.49	3.26	5.06	0.20
Q8K4P0_WDR33_MOUSE	Wdr33	pre-mRNA 3' end process	R.GM*QGPPGPR@.E	10.02	9.58	1.05	0.96
Q8K4P0_WDR33_MOUSE	Wdr33	pre-mRNA 3' end process	R.GR@DNFPGPDDFGPEEGFDASDEAAR@.G	6.23	1.45	4.29	0.23
Q8K4P0_WDR33_MOUSE	Wdr33	pre-mRNA 3' end process	K.R@PDFAQQQAM*QQLTFDGK#.R	7.27	1.26	5.76	0.17
Q3TAQ9_Q3TAQ9_MOUSE	Wdr36	Protein Wdr36 OS=Mus r	R.FAVPEPSSDPQQSK.V	5.43	6.53	0.83	1.20
Q3TAQ9_Q3TAQ9_MOUSE	Wdr36	Protein Wdr36 OS=Mus r	R.LPPITQFAAEEAR.Q	17.94	7.99	2.25	0.45
Q3TAQ9_Q3TAQ9_MOUSE	Wdr36	Protein Wdr36 OS=Mus r	R.NLSPDDGGSVEVM*R@.S	6.27	3.49	1.80	0.56
Q3TAQ9_Q3TAQ9_MOUSE	Wdr36	Protein Wdr36 OS=Mus r	R.TLPSEPALLEELVK#.L	12.57	6.72	1.87	0.53
Q8CBE3_WDR37_MOUSE	Wdr37	WD repeat-containing pr	R.LAGEGQAIDGAELSK#.G	8.17	3.89	2.10	0.48
Q8CBE3_WDR37_MOUSE	Wdr37	WD repeat-containing pr	R.STLLELFGQIER@.E	12.08	5.75	2.10	0.48
Q8CBE3_WDR37_MOUSE	Wdr37	WD repeat-containing pr	R.STLLELFGQIER@.E	8.64	3.06	2.83	0.35
Q8CBE3_WDR37_MOUSE	Wdr37	WD repeat-containing pr	R.LAGEGQAIDGAELSK#.G	10.60	4.08	2.60	0.38
Q6ZQL4_WDR43_MOUSE	Wdr43	WD repeat-containing pr	K.LGSTEATIEER@.L	9.04	8.00	1.13	0.88
Q6ZQL4_WDR43_MOUSE	Wdr43	WD repeat-containing pr	R.FTTIR@PNESQPSDGITGLYFLSGAVHDR@.L	3.09	1.44	2.14	0.47
Q6ZQL4_WDR43_MOUSE	Wdr43	WD repeat-containing pr	K.LGSTEATIEER@.L	20.03	10.71	1.87	0.53
Q6ZQL4_WDR43_MOUSE	Wdr43	WD repeat-containing pr	K.LILLVTQVTASEK#.S	10.56	5.92	1.78	0.56
Q6ZQL4_WDR43_MOUSE	Wdr43	WD repeat-containing pr	R.LLNVWQVR@.S	13.46	6.66	2.02	0.49
Q91VM3_WIPI4_MOUSE	Wdr45	WD repeat domain phos	R.IYVYSFPDSPR@.K	12.86	6.64	1.94	0.52
P61965_WDR5_MOUSE	Wdr5	WD repeat-containing pr	K.FSPNGEWLASSSADK#.L	8.55	3.27	2.61	0.38
P61965_WDR5_MOUSE	Wdr5	WD repeat-containing pr	K.FTLAGHTK#.A	34.50	116.56	0.30	3.38
P61965_WDR5_MOUSE	Wdr5	WD repeat-containing pr	K.IWGAYDGK#FEK#.T	40.27	14.99	2.69	0.37
P61965_WDR5_MOUSE	Wdr5	WD repeat-containing pr	K.LGISDVAWSSDSNLLVSASDDK#.T	7.17	2.96	2.42	0.41
P61965_WDR5_MOUSE	Wdr5	WD repeat-containing pr	K.LGISDVAWSSDSNLLVSASDDK#TLK#.I	12.69	3.26	3.89	0.26
P61965_WDR5_MOUSE	Wdr5	WD repeat-containing pr	K.TLIDDDNPPVSFVK#.F	23.45	11.23	2.09	0.48
P61965_WDR5_MOUSE	Wdr5	WD repeat-containing pr	K.WIVSGSEDNLVYIWNLQTK#.E	15.05	5.89	2.55	0.39
P61965_WDR5_MOUSE	Wdr5	WD repeat-containing pr	K.WIVSGSEDNLVYIWNLQTK#.E	10.34	4.01	2.58	0.39
P61965_WDR5_MOUSE	Wdr5	WD repeat-containing pr	K.YILAATLDNTLK#.L	141.49	19.14	7.39	0.14
Q99ME2_WDR6_MOUSE	Wdr6	WD repeat-containing pr	R.GYPGLGVSSLSFK#.S	7.18	3.89	1.85	0.54
Q99ME2_WDR6_MOUSE	Wdr6	WD repeat-containing pr	R.VLAVTDVGSLYLYDLEVK#.S	3.21	1.32	2.43	0.41
Q99ME2_WDR6_MOUSE	Wdr6	WD repeat-containing pr	R.VLAVTDVGSLYLYDLEVK#.S	7.05	2.11	3.34	0.30
Q9ERF3_WDR61_MOUSE	Wdr61	WD repeat-containing pr	K.ENIETVVTGSLDDLVK#.V	29.38	8.27	3.55	0.28
Q9ERF3_WDR61_MOUSE	Wdr61	WD repeat-containing pr	K.SIDAGPVDAWTLAFSPDSQYLATGTHM*GK#.V	12.11	3.42	3.54	0.28
Q9ERF3_WDR61_MOUSE	Wdr61	WD repeat-containing pr	R.SLTFSPDSQLLVTASDDGYIK#.I	12.43	4.21	2.95	0.34
Q9ERF3_WDR61_MOUSE	Wdr61	WD repeat-containing pr	R.SLTFSPDSQLLVTASDDGYIK#.I	12.45	5.40	2.30	0.43
Q3U821_Q3U821_MOUSE	Wdr75	Protein Wdr75 OS=Mus r	R.NLDASAVIQGLVK#.D	8.23	4.35	1.89	0.53
A6PWY4_WDR76_MOUSE	Wdr76	WD repeat-containing pr	K.SIASAYFSPVTGNR.V	5.44	6.91	0.79	1.27

A6PWY4_WDR76_MOUSE	Wdr76	WD repeat-containing pr	R.VFDSSSISSQLPLLSTIR@.H	4.03	20.89	0.19	5.19
Q99J09_MEP50_MOUSE	Wdr77	Methylosome protein 50	R.ILLWDTR@.C	10.02	11.85	0.85	1.18
Q99J09_MEP50_MOUSE	Wdr77	Methylosome protein 50	K.IWDLAQQVSLNSYR@.A	7.11	4.68	1.52	0.66
Q99J09_MEP50_MOUSE	Wdr77	Methylosome protein 50	R.SDGSLLLGVSSLSGR@.C	17.51	17.94	0.98	1.02
Q5ND34_WDR81_MOUSE	Wdr81	WD repeat-containing pr	R.DR@PGTGEDDLEQATEALDSISLPGK#.A	6.03	3.16	1.91	0.52
Q5ND34_WDR81_MOUSE	Wdr81	WD repeat-containing pr	R.LAGSPALAPEPPLIPR@.L	10.38	3.34	3.11	0.32
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	K.IHVWNGESGIK#.V	24.26	9.58	2.53	0.39
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	K.LILISTNGSFIR@.L	21.87	7.04	3.10	0.32
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	K.R@VVALSM*SPVDDTFISGSLDK#.T	6.83	7.15	0.96	1.05
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	R.VVALSM*SPVDDTFISGSLDK#.T	40.20	12.70	3.17	0.32
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	R.VVALSMSPVDDTFISGSLDK#.T	9.87	4.21	2.34	0.43
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	K.YGVDLIR@.Y	50.58	20.47	2.47	0.40
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	R.YTHAANTVVYSSNK#.I	16.63	9.47	1.76	0.57
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	K.VAVLDGK#.H	21.47	8.76	2.45	0.41
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	R.VVALSM*SPVDDTFISGSLDK#.T	4.95	2.32	2.13	0.47
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	R.VVALSM*SPVDDTFISGSLDK#.T	7.42	1.95	3.81	0.26
Q8BFQ4_WDR82_MOUSE	Wdr82	WD repeat-containing pr	K.YGVDLIR@.Y	9.09	1.86	4.89	0.20
Q7TMQ7_WDR91_MOUSE	Wdr91	WD repeat-containing pr	K.IVDQLQQLM*QVYDLAALR@.D	5.65	4.19	1.35	0.74
Q8BVE8_NSD2_MOUSE	Whsc1	Histone-lysine N-methylt	R.ASATASSALGFNK#.S	24.76	13.28	1.86	0.54
Q8BVE8_NSD2_MOUSE	Whsc1	Histone-lysine N-methylt	K.NALQEAEAR@.F	20.09	11.06	1.82	0.55
Q8BVE8_NSD2_MOUSE	Whsc1	Histone-lysine N-methylt	K.R@ADDPAEDVDVEDAPR@.K	12.81	5.98	2.14	0.47
Q8BVE8_NSD2_MOUSE	Whsc1	Histone-lysine N-methylt	R.SIK#YDSLLEQGLVEAALVSK#.I	11.90	5.09	2.34	0.43
Q8BVE8_NSD2_MOUSE	Whsc1	Histone-lysine N-methylt	K.SLVAFEGEEQFEK#.L	7.39	2.93	2.52	0.40
Q8BVE8_NSD2_MOUSE	Whsc1	Histone-lysine N-methylt	K.NALQEAEAR@.F	16.18	4.15	3.90	0.26
Q8BVE8_NSD2_MOUSE	Whsc1	Histone-lysine N-methylt	K.SLVAFEGEEQFEK#.L	5.76	1.00	5.73	0.17
Q8BVE8_NSD2_MOUSE	Whsc1	Histone-lysine N-methylt	K.VQIYTADISEIPK.C	8.50	11.19	0.76	1.32
Q6P2L6_NSD3_MOUSE	Whsc1l1	Histone-lysine N-methylt	R.SEK#PAQSASSPEATSGSAGPVEK#.K	4.62	6.16	0.75	1.33
Q6P2L6_NSD3_MOUSE	Whsc1l1	Histone-lysine N-methylt	R.VEQYTFIYIDK#QPEEASSQAK#.K	3.47	4.54	0.76	1.31
Q6P2L6_NSD3_MOUSE	Whsc1l1	Histone-lysine N-methylt	K.EAIPVQPILSSVPTTETSTGVK#.F	8.27	4.25	1.95	0.51
Q6P2L6_NSD3_MOUSE	Whsc1l1	Histone-lysine N-methylt	K.IEQVFALQNATGDGK#.F	6.58	2.96	2.22	0.45
Q6P2L6_NSD3_MOUSE	Whsc1l1	Histone-lysine N-methylt	R.SEK#PAQSASSPEATSGSAGPVEK#.K	8.18	4.02	2.03	0.49
Q6P2L6_NSD3_MOUSE	Whsc1l1	Histone-lysine N-methylt	R.VEQYTFIYIDK#QPEEASSQAK#.K	9.26	4.27	2.17	0.46
Q6P2L6_NSD3_MOUSE	Whsc1l1	Histone-lysine N-methylt	K.VQVQVADLSEIPR@.C	5.66	4.11	1.38	0.73
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	R.SAGGEPGLEAGR@.A	18.04	8.50	2.12	0.47
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	K.VLSTGGPGSSLEAR@.S	12.54	3.86	3.25	0.31
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	R.AADSGER@PLATSPPGTVK#.S	25.15	9.49	2.65	0.38
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	R.EDM*APLNLSAR@.A	15.70	5.11	3.07	0.33
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	R.ELSLSPITGSKPSAASYLGPVATK.R	26.69	40.06	0.67	1.50
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	K.GLPDAPLGLTPSLTK#.K	27.83	13.26	2.10	0.48
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	R.SAGGEPGLEAGR@.A	25.00	10.72	2.33	0.43
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	K.SLPVSGTLEQVASR@.L	11.80	4.62	2.55	0.39
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	R.SPSDLHISPLTK#.K	58.40	21.52	2.71	0.37
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	K.TYIQTELPFK#.A	28.12	11.95	2.35	0.43
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	K.VLSTGGPGSSLEAR@.S	43.26	21.29	2.03	0.49
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	R.HLGVSDPDAK#.G	7.40	5.45	1.36	0.74
F6ZBR8_F6ZBR8_MOUSE	Wiz	Protein Wiz (Fragment) C	R.SAGGEPGLEAGR@.A	6.59	17.92	0.37	2.72
P83741_WNK1_MOUSE	Wnk1	Serine/threonine-protein	K.LGATVADSGVGR@.T	10.95	2.54	4.31	0.23
P83741_WNK1_MOUSE	Wnk1	Serine/threonine-protein	R.SQQQDDIEELETK#.A	7.35	2.29	3.21	0.31
O70283_WNT2B_MOUSE	Wnt2b	Protein Wnt-2b OS=Mus	R.TGDYLR@R@.R	62.81	18.81	3.34	0.30
Q91XU0_WRIP1_MOUSE	Wrnip1	ATPase WRNIP1 OS=Mus	K.AVDTLAYLSDGDAR@.T	10.40	22.16	0.47	2.13
Q91XU0_WRIP1_MOUSE	Wrnip1	ATPase WRNIP1 OS=Mus	R.AVGQETLLR@.S	19.68	6.25	3.15	0.32
Q91XU0_WRIP1_MOUSE	Wrnip1	ATPase WRNIP1 OS=Mus	R.M*LEGGEDPLYVAR.R	9.15	7.28	1.26	0.79
Q91XU0_WRIP1_MOUSE	Wrnip1	ATPase WRNIP1 OS=Mus	R.VLITENDVK#.E	18.36	6.80	2.70	0.37
Q91XU0_WRIP1_MOUSE	Wrnip1	ATPase WRNIP1 OS=Mus	K.AVDTLAYLSDGDAR@.T	12.89	21.23	0.61	1.65
Q91XU0_WRIP1_MOUSE	Wrnip1	ATPase WRNIP1 OS=Mus	R.ESYDAPPTPSGAR@.L	5.36	1.91	2.80	0.36
Q91XU0_WRIP1_MOUSE	Wrnip1	ATPase WRNIP1 OS=Mus	R.M*LEGGEDPLYVAR@.R	10.77	7.77	1.39	0.72
Q91XU0_WRIP1_MOUSE	Wrnip1	ATPase WRNIP1 OS=Mus	K.SIEVYSAYNNVK#.A	9.84	4.08	2.42	0.41
Q91XU0_WRIP1_MOUSE	Wrnip1	ATPase WRNIP1 OS=Mus	R.VLITENDVK#.E	18.81	4.71	4.00	0.25
Q9ER69_FL2D_MOUSE	Wtap	Pre-mRNA-splicing regula	R.M*LIQENQELGR@.Q	14.64	7.22	2.03	0.49
Q9ER69_FL2D_MOUSE	Wtap	Pre-mRNA-splicing regula	R.QQLAQYQQQQSQASAPSTSR@.T	9.04	2.34	3.86	0.26
Q9ER69_FL2D_MOUSE	Wtap	Pre-mRNA-splicing regula	K.QVQQPSVAQLR@.S	29.23	12.57	2.32	0.43
Q9ER69_FL2D_MOUSE	Wtap	Pre-mRNA-splicing regula	K.QYEAYVQALEGK#.Y	7.13	3.17	2.25	0.44
Q9ER69_FL2D_MOUSE	Wtap	Pre-mRNA-splicing regula	R.STM*VDPAINLFFLK#.M	22.41	11.72	1.91	0.52
Q9ER69_FL2D_MOUSE	Wtap	Pre-mRNA-splicing regula	R.TTSSEPVDQAEVTSK#.D	21.38	7.99	2.68	0.37
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.EEEDDVDLELR@.L	5.48	3.74	1.47	0.68
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.EIINTYTEAVQTVDPFK#.A	11.40	6.61	1.73	0.58
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.HENYDEALK#.L	14.35	8.77	1.64	0.61
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.LATVVNDER@.F	17.37	11.83	1.47	0.68
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	K.LSPESAEEYIEYLK#.S	11.56	7.92	1.46	0.68
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	K.M*ETASELGR@EEEDDVDLELR@.L	9.96	5.12	1.95	0.51
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.SER@PDLVFEEEDLPYEEEIM*R@.N	12.48	4.66	2.68	0.37
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.SHPLPETAVR@.G	19.94	44.45	0.45	2.23
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.AEYFDGSEPVQNR@.V	5.29	3.52	1.50	0.67
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.AVEPAQQYDM*FNIYIK#.R	5.97	4.13	1.45	0.69
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.DFTQVFDSYAQFEESM*IAAK#.M	8.70	3.60	2.42	0.41
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.EEEDDVDLELR@.L	5.76	4.30	1.34	0.75
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.EIINTYTEAVQTVDPFK#.A	16.17	8.42	1.92	0.52
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.HENYDEALK#.L	22.42	8.90	2.52	0.40
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.LATVVNDER@.F	28.88	14.22	2.03	0.49
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.LEQQSVPAAVFGSLK#ED.-	4.04	3.51	1.15	0.87
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	K.LSPESAEEYIEYLK#.S	31.64	9.80	3.23	0.31
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	R.SER@PDLVFEEEDLPYEEEIM*R@.N	30.31	14.59	2.08	0.48
Q9DCD2_SYF1_MOUSE	Xab2	Pre-mRNA-splicing factor	K.SSDR@LDEAAQR@.L	8.81	2.78	3.17	0.32
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.YYGLQILENVIK#.T	7.71	2.29	3.36	0.30
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.AVGHPFVIQLGR@.I	12.87	9.69	1.33	0.75
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.EFAGEDTSDLFLEER@.E	8.89	5.20	1.71	0.59
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.LLSEEVFDFSSGQITQVK#.A	8.00	3.94	2.03	0.49
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	R.M*AK#PEEVLVVENDQGEVVR@.E	12.30	6.08	2.02	0.49
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	R.VDTILEFSQNM*NTK#.Y	7.89	4.78	1.65	0.61
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.YYGLQILENVIK#.T	19.14	8.80	2.17	0.46
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.AIIASNIM*YIVGQYPR@.F	10.42	3.05	3.42	0.29
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.AVGHPFVIQLGR@.I	40.89	14.64	2.79	0.36
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.DTDSINLYK#.N	10.77	3.93	2.74	0.36
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.EFAGEDTSDLFLEER@.E	20.53	10.93	1.88	0.53
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	R.EPEVLSTM*AIIVNK#.L	8.25	4.82	1.71	0.58
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	R.ETLVYLTHLDYVDTEIIM*TK#.K	22.28	6.36	3.50	0.29
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.FLNVPM*FR@.N	8.98	4.51	1.99	0.50
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.LISGWVSR@.S	27.42	7.96	3.45	0.29
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.LLSEEVFDFSSGQITQVK#.A	52.41	21.71	2.41	0.41
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	R.M*AK#PEEVLVVENDQGEVVR@.E	34.15	12.65	2.70	0.37
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	R.M*AQEVLTHLK#.E	15.55	6.80	2.29	0.44
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	R.QLLDFSQK#.L	13.22	8.54	1.55	0.65
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.QM*LPLNTNIR@.L	9.15	7.03	1.30	0.77

Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.YM*LLPNQVWDSIIQQATK#.N	5.70	2.15	2.65	0.38
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.YVVGLIIK#.T	17.15	7.70	2.23	0.45
Q6P5F9_XPO1_MOUSE	Xpo1	Exportin-1 OS=Mus musc	K.YYGLQILENVIK#.T	47.26	19.52	2.42	0.41
Q924C1_XPO5_MOUSE	Xpo5	Exportin-5 OS=Mus musc	K.AVTVM*M*DPSSTQR@.Y	5.68	2.83	2.01	0.50
Q924C1_XPO5_MOUSE	Xpo5	Exportin-5 OS=Mus musc	R.LLDNLLALVR@.T	9.03	3.16	2.86	0.35
Q9EPK7_XPO7_MOUSE	Xpo7	Exportin-7 OS=Mus musc	R.TNNPLPLEQR@.I	12.36	5.96	2.07	0.48
Q60596_XRCC1_MOUSE	Xrcc1	DNA repair protein XRCC	R.TPAAAPASTPAQR@.A	8.71	8.13	1.07	0.93
P27641_XRCC5_MOUSE	Xrcc5	X-ray repair cross-comple	K.AFR@EEAIQFSEEQR@.F	13.78	7.02	1.96	0.51
P27641_XRCC5_MOUSE	Xrcc5	X-ray repair cross-comple	R.FNSFLEALR@.E	19.39	10.65	1.82	0.55
P27641_XRCC5_MOUSE	Xrcc5	X-ray repair cross-comple	R.HLM*LPDFDLLEDIGNK#.I	21.39	17.82	1.20	0.83
P27641_XRCC5_MOUSE	Xrcc5	X-ray repair cross-comple	R.SNPQVGVAFPYIK#.D	5.71	5.57	1.03	0.97
P27641_XRCC5_MOUSE	Xrcc5	X-ray repair cross-comple	K.TLFPLTEVIK#.K	32.71	25.47	1.28	0.78
P27641_XRCC5_MOUSE	Xrcc5	X-ray repair cross-comple	K.VGSVNPVENFR@.F	29.87	11.79	2.53	0.39
P27641_XRCC5_MOUSE	Xrcc5	X-ray repair cross-comple	R.HLM*LPDFDLLEDIGNK#.I	5.20	4.88	1.06	0.94
P27641_XRCC5_MOUSE	Xrcc5	X-ray repair cross-comple	K.TLFPLTEVIK#.K	15.05	6.69	2.25	0.44
P23475_XRCC6_MOUSE	Xrcc6	X-ray repair cross-comple	R.DSLIFLVDASR@.A	16.75	12.21	1.37	0.73
P23475_XRCC6_MOUSE	Xrcc6	X-ray repair cross-comple	K.IISSDR@DLLAVVFYGTEK#.D	25.73	20.68	1.24	0.80
P23475_XRCC6_MOUSE	Xrcc6	X-ray repair cross-comple	K.K#PGGFDVSVFYR@.D	17.11	8.84	1.94	0.52
P23475_XRCC6_MOUSE	Xrcc6	X-ray repair cross-comple	K.VELSEEELK#.A	20.88	14.60	1.43	0.70
P23475_XRCC6_MOUSE	Xrcc6	X-ray repair cross-comple	R.VLELDQFK#.G	18.09	9.49	1.91	0.52
P23475_XRCC6_MOUSE	Xrcc6	X-ray repair cross-comple	K.VTANQEQIDK#.M	13.78	9.33	1.48	0.68
P97789_XRN1_MOUSE	Xrn1	5'-3' exoribonuclease 1 O	R.APELFSYIAK#.N	18.83	2.58	7.31	0.14
P97789_XRN1_MOUSE	Xrn1	5'-3' exoribonuclease 1 O	K.FYIEEPPGTQK#.V	13.42	3.67	3.66	0.27
P97789_XRN1_MOUSE	Xrn1	5'-3' exoribonuclease 1 O	K.QILPFVYQTIVK#.D	8.40	1.96	4.29	0.23
Q9DBR1_XRN2_MOUSE	Xrn2	5'-3' exoribonuclease 2 O	R.DLTQNTAVSINFK#DPQFAEDYVFK#.A	9.01	1.51	5.96	0.17
Q9DBR1_XRN2_MOUSE	Xrn2	5'-3' exoribonuclease 2 O	R.ELTM*ASLPFPFDVER@.S	8.03	4.32	1.86	0.54
Q9DBR1_XRN2_MOUSE	Xrn2	5'-3' exoribonuclease 2 O	R.NSLGGDVLFVGK#.L	17.21	4.14	4.16	0.24
Q9DBR1_XRN2_MOUSE	Xrn2	5'-3' exoribonuclease 2 O	K.YAWQGVALLPFVDER@.R	11.70	4.51	2.59	0.39
P46938_YAP1_MOUSE	Yap1	Transcriptional coactivat	R.DESTDSGLSM*SSYSIPR.T	3.73	2.96	1.26	0.79
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	K.AADPPAENSSAPEAEQGGAE.-	147.92	147.92	1.00	1.00
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.EDGNEEDK#ENQGDETQGQQPPQR@.R	156.53	130.85	1.20	0.84
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.EDGNEEDKENQGDETQGQQPPQRR.Y	272.57	178.23	1.53	0.65
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.EDGNEEDK#ENQGDETQGQQPPQR@R@.Y	41.26	25.07	1.65	0.61
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	K.EDVFVHQTAIK.K	19.42	16.47	1.18	0.85
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	K.GAEAANVTGPGGVPVQGSK#.Y	308.07	332.25	0.93	1.08
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.NDTKEDVFVHQTAIK.K	221.22	191.34	1.16	0.86
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.NDTK#EDVFVHQTAIK#K#.N	192.58	161.32	1.19	0.84
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	K.NEGSESAPEGQAQQR.R	15.68	13.87	1.13	0.88
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.NYQQNYQNSESGEK.N	11.23	9.56	1.18	0.85
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.RPQYSNPPVQGEVM*EGADNQGAGEQGRPVR.Q	361.87	286.44	1.26	0.79
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.R@PQYSNPPVQGEVMEGADNQGAGEQGR@PVR@.Q	57.34	57.96	0.99	1.01
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.SVGDGETVEFDVVEGEK#.G	314.52	348.45	0.90	1.11
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.SVGDGETVEFDVVEGEK#GAEAANVTGPGGVPVQGSK#.Y	47.11	46.25	1.02	0.98
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	K.GAEAANVTGPGGVPVQGSK.Y	7.54	14.18	0.53	1.88
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.SVGDGETVEFDVVEGEK.G	5.25	12.88	0.41	2.45
P62960_YBOX1_MOUSE	Ybx1	Nuclease-sensitive eleme	R.SVGDGETVEFDVVEGEK#.G	10.53	5.40	1.95	0.51
Q9JKB3_YBOX3_MOUSE	Ybx3	Y-box-binding protein 3 (	K.AGEAPTENPAPATEQSSAE.-	15.97	15.97	1.00	1.00
Q9JKB3_YBOX3_MOUSE	Ybx3	Y-box-binding protein 3 (	K.GAEAANVTGPDGVPVEGSR.Y	63.19	90.12	0.70	1.43
Q9JKB3_YBOX3_MOUSE	Ybx3	Y-box-binding protein 3 (	R.NYAGEEEEEGSGSSEGFEPPAADGQFSGAR.N	4.11	3.13	1.31	0.76
Q9JKB3_YBOX3_MOUSE	Ybx3	Y-box-binding protein 3 (	R.SVGDGETVEFDVVEGEKGAEAANVTGPDGVPVEGSR.Y	4.54	6.51	0.70	1.44
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.ATEQLVSDILR@.Q	7.64	5.43	1.41	0.71
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.VDHLETIQQLLTAVVK#.K	10.73	5.02	2.14	0.47
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.ATEQLVSDILR@.Q	9.47	1.37	6.92	0.14
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	R.FYLPPTPGSGFVGDITQK#.I	3.53	1.82	1.94	0.52
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.IGITLQPVALHR@.N	11.17	5.42	2.06	0.48
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.IVSGSPISTPSPSPLPR@.T	13.41	4.95	2.71	0.37
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.LLLIPQGAILR@.A	49.46	9.40	5.26	0.19
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.LPVASQASQGTGSPIPK#.I	7.11	2.96	2.40	0.42
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	R.NADLTGDETSR@.L	17.64	4.33	4.08	0.25
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.NK#EHEIDVIDQR@.L	14.19	14.30	0.99	1.01
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.QVISAGEGTTQSPK#.I	14.63	3.90	3.75	0.27
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.TTLFTQAATAGQASLLK#.L	9.04	1.86	4.86	0.21
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	R.TYTGLQTLGAETVVDVELHR@.H	8.60	3.33	2.58	0.39
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.VDHLETIQQLLTAVVK#.K	14.35	5.25	2.73	0.37
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.AIVSGGGGTIVAQPVQTLTK#.T	8.73	1.73	5.04	0.20
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.IGITLQPVALHR@.N	11.49	2.11	5.44	0.18
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.LLLIPQGAILR@.A	20.50	6.19	3.31	0.30
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.LPTTVLPISVPNQAAPSSAPVAIAK#.V	14.72	4.36	3.37	0.30
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.LPVASQASQGTGSPIPK#.I	5.35	1.53	3.48	0.29
Q3TUF7_YETS2_MOUSE	Yeats2	YEATS domain-containin	K.VDHLETIQQLLTAVVK#.K	16.37	2.53	6.46	0.15
Q9CR11_YETS4_MOUSE	Yeats4	YEATS domain-containin	K.GVTIVK#PIVYGNVAR@.Y	10.41	9.78	1.06	0.94
Q9CR11_YETS4_MOUSE	Yeats4	YEATS domain-containin	K.HETEFAELEVK#.T	6.35	3.10	2.05	0.49
Q9CR11_YETS4_MOUSE	Yeats4	YEATS domain-containin	R.K#LEEDDQTK#DI.-	9.18	9.47	0.97	1.03
Q9CR11_YETS4_MOUSE	Yeats4	YEATS domain-containin	R.K#LEEDDQTK#DI.-	5.76	4.60	1.25	0.80
Q9CR11_YETS4_MOUSE	Yeats4	YEATS domain-containin	K.TSFEIAELK#.E	7.66	4.77	1.61	0.62
Q91XB7_YIF1A_MOUSE	Yif1a	Protein YIF1A OS=Mus m	R.TAASGPDSM*GGPAPR@.Q	9.47	4.46	2.13	0.47
Q91XB7_YIF1A_MOUSE	Yif1a	Protein YIF1A OS=Mus m	K.YFFAVDTAYVAK#.K	15.72	7.06	2.23	0.45
Q9CX30_YIF1B_MOUSE	Yif1b	Protein YIF1B OS=Mus m	K.ILAQAAAEGVPVR@.G	52.51	23.76	2.21	0.45
Q9CX30_YIF1B_MOUSE	Yif1b	Protein YIF1B OS=Mus m	K.YYFAVDTVYVGK#.K	7.03	9.35	0.75	1.33
Q9CX30_YIF1B_MOUSE	Yif1b	Protein YIF1B OS=Mus m	K.ILAQAAAEGVPVR@.G	3.03	10.64	0.29	3.51
Q8C407_YIPF4_MOUSE	Yipf4	Protein YIPF4 OS=Mus m	K.LNLGVSGDFIK#.E	42.66	12.52	3.41	0.29
Q9CQW1_YKT6_MOUSE	Ykt6	Synaptobrevin homolog	K.AAYDVSSFSFFQR@.S	13.92	3.77	3.69	0.27
Q9CQW1_YKT6_MOUSE	Ykt6	Synaptobrevin homolog	R.SDSLAGVVIADSEYPSR@.V	16.52	6.12	2.70	0.37
Q9CQW1_YKT6_MOUSE	Ykt6	Synaptobrevin homolog	R.SSVQEFM*TFTSQLIVER@.S	3.67	2.75	1.34	0.75
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	R.ITLR@PDPLPER@.S	19.84	8.08	2.46	0.41
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.TAIQQEPLESGAK#.N	48.08	16.55	2.91	0.34
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.VFSSEQGLGESSALSQSIIAAK#.D	20.01	8.84	2.26	0.44
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	R.VGFQYQGIM*QR@.H	16.39	6.73	2.44	0.41
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.VNSFQTVK#.S	21.62	10.68	2.02	0.49
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.AAQSNENLSDSQQEPTK#.S	18.27	5.56	3.29	0.30
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.ATQTYLQEK#.V	28.17	13.17	2.14	0.47
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	R.DK#EVEFGGPAPR@.V	44.08	8.19	5.38	0.19
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	R.DYQDDTLDSYSR@.E	7.55	3.44	2.20	0.46
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	R.GHEEFPVDGR@.N	10.36	1.68	6.15	0.16
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	R.GPASQFYITPNTSLSPR@.Q	10.77	2.48	4.34	0.23
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	R.HFDQFWSAAK#.T	15.13	3.81	3.97	0.25
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	R.ITLR@PDPLPER@.S	39.79	11.89	3.35	0.30
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.K#DAEEEESELGYIPK#.S	20.32	3.58	5.67	0.18
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	R.M*EDYLQLPDDYETR@.A	16.47	2.85	5.78	0.17
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.SGGLLADPPK#.G	19.19	5.29	3.63	0.28
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.SGGLLADPPK#GSFLEGPR@.G	11.82	3.69	3.20	0.31
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.SQAEPLSGNK#EPLADTSNNQQK#.N	35.56	9.70	3.67	0.27
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing pr	K.TAIQQEPLESGAK#.N	49.70	14.76	3.37	0.30

D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing prc	K.VEQIPYGER@.I	19.72	5.10	3.87	0.26
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing prc	K.VFSSEQGLGESSALSQSIIAAK#.D	55.09	10.18	5.41	0.18
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing prc	R.VLSLDDYFIAEVEK#.E	4.05	2.82	1.44	0.70
D3YWX2_D3YWX2_MOUSE	Ylpm1	YLP motif-containing prc	K.VNSFQTVK#.S	30.04	9.44	3.18	0.31
P62700_YPEL5_MOUSE	Ypel5	Protein yippee-like 5 OS=	K.VVNLQYSEVQDR@.V	15.89	7.90	2.01	0.50
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	R.DQK#EEGNDYDTR@.S	1.82	1.39	1.31	0.76
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	R.GISPIVFDR@.S	31.26	11.02	2.84	0.35
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	K.K#LNLAFR@.S	21.67	8.83	2.46	0.41
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	K.M*LGGVFK#.I	37.47	13.41	2.79	0.36
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	R.SEASDSGSESVSFTDGSVR@.S	21.27	4.08	5.22	0.19
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	R.SGSSASESYAGSEK#.K	8.42	3.29	2.56	0.39
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	R.VDDFLR@.R	21.32	8.72	2.44	0.41
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	K.YVLQDAR@.F	49.86	27.65	1.80	0.55
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	R.GISPIVFDR@.S	11.59	4.87	2.38	0.42
E9Q5K9_YTDC1_MOUSE	Ythdc1	YTH domain-containing p	R.SEASDSGSESVSFTDGSVR@.S	6.61	3.85	1.72	0.58
P59326_YTHD1_MOUSE	Ythdf1	YTH domain-containing f	K.APGM*NSLEQGM*VGLK.I	4.81	6.46	0.74	1.34
P59326_YTHD1_MOUSE	Ythdf1	YTH domain-containing f	K.APGM*NSLEQGM*VGLK#.I	4.07	2.01	2.02	0.49
P59326_YTHD1_MOUSE	Ythdf1	YTH domain-containing f	R.DTQEVPLEK#.A	66.78	39.02	1.71	0.58
P59326_YTHD1_MOUSE	Ythdf1	YTH domain-containing f	K.HTTSIFDDFSHYEK#.R	26.09	12.83	2.03	0.49
Q91YT7_YTHD2_MOUSE	Ythdf2	YTH domain-containing f	K.LGSTEVASSVPK.V	17.31	22.44	0.77	1.30
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	R.AITDGQAGFGNDTLSK#.V	21.87	23.22	0.94	1.06
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	K.IGGDLTAAVTK.T	21.08	36.66	0.57	1.74
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	K.VPGISSIEQGM*TGLK#.I	16.05	21.61	0.74	1.35
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	R.AITDGQAGFGNDTLSK.V	12.38	16.90	0.73	1.37
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	K.IGGDLTAAVTK.T	6.71	10.71	0.63	1.60
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	K.VPGISSIEQGM*TGLK.I	6.62	8.55	0.77	1.29
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	K.AINNYNPK#.D	12.85	10.74	1.20	0.84
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	R.AITDGQAGFGNDTLSK#.V	30.92	17.24	1.79	0.56
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	K.GNVGIGGSAVPPPPIK#.H	14.60	10.49	1.39	0.72
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	K.HTTSIFDDFAHYEK#.R	24.94	9.02	2.77	0.36
Q8BYK6_YTHD3_MOUSE	Ythdf3	YTH domain-containing f	K.VPGISSIEQGM*TGLK#.I	20.76	16.43	1.26	0.79
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.AVTEQGHELSNEER@.N	14.35	6.35	2.26	0.44
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.DSTLIM*QLLR@.D	117.95	57.89	2.04	0.49
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.DSTLIMQLLR@.D	59.48	21.53	2.76	0.36
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.EM*QPTHPIR@.L	16.31	8.42	1.94	0.52
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.K#EM*QPTHPIR@.L	29.57	14.06	2.10	0.48
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.LAEQAER@.Y	172.84	84.16	2.05	0.49
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	R.NLLSVAYK#.N	261.64	109.05	2.40	0.42
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.QTTVSNSQQAYQEAFEISK#.K	4.73	1.85	2.56	0.39
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.TAFDEAIAELDTLNEESYK#.D	9.52	5.48	1.74	0.58
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.TAFDEAIAELDTLNEESYK#.D	4.80	2.17	2.21	0.45
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	R.YDDM*AAAM*K#.A	39.52	16.78	2.36	0.42
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.YLILNATQAESK#.V	9.99	3.89	2.57	0.39
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	R.YLSEVASGENK#.Q	42.88	18.29	2.34	0.43
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.DSTLIM*QLLR@.D	18.48	8.44	2.19	0.46
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	R.NLLSVAYK#.N	114.23	51.15	2.23	0.45
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	R.YLSEVASGENK#.Q	8.49	13.06	0.65	1.54
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	K.LAEQAER@.Y	14.21	7.64	1.86	0.54
Q9CQV8_1433B_MOUSE	Ywhab	14-3-3 protein beta/alph	R.NLLSVAYK#.N	25.16	11.41	2.20	0.45
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	K.AASDIAM*TELPPTHPIR@.L	34.56	17.74	1.95	0.51
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	K.AASDIAMTELPPTHPIR@.L	10.12	451.93	0.02	44.66
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	K.EAAENSLVAYK#.A	216.87	88.83	2.44	0.41
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	K.EALQDVEDENQ.-	33.84	33.84	1.00	1.00
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	K.HLIPAANTGESK#.V	37.87	19.39	1.95	0.51
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	R.IISSIEQK#.E	127.93	45.43	2.82	0.36
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	R.IISSIEQK#EENK#.G	7.51	3.50	2.14	0.47
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	R.QM*VETELK#.L	33.37	18.41	1.81	0.55
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	K.VAGM*DVELTVEER@.N	123.13	40.30	3.06	0.33
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	K.VAGMDVELTVEER@.N	8.16	3.53	2.31	0.43
P62259_1433E_MOUSE	Ywhae	14-3-3 protein epsilon O	K.VAGM*DVELTVEER.N	2.97	5.85	0.51	1.97
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	R.ATVVESSEK#.A	45.69	19.75	2.31	0.43
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	R.DNLTLWTSDQQDDDGGEGNN.-	11.79	11.79	1.00	1.00
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	K.NVTELNEPLSNEER@.N	159.17	69.61	2.29	0.44
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	K.R@ATVVESSEK#.A	14.64	4.84	3.02	0.33
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	K.TAFDDAIAELDTLNEDSYK#.D	27.82	14.59	1.91	0.52
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	R.YLAEVATGEK#.R	99.96	33.14	3.02	0.33
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	R.YLAEVATGEK#R@.A	28.77	9.96	2.89	0.35
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	K.NVTELNEPLSNEER@.N	8.97	6.21	1.45	0.69
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	R.YLAEVATGEK#.R	18.21	4.94	3.69	0.27
P61982_1433G_MOUSE	Ywhag	14-3-3 protein gamma O	K.NVTELNEPLSNEER@.N	7.73	3.25	2.38	0.42
P68510_1433F_MOUSE	Ywhah	14-3-3 protein eta OS=M	K.M*K#GDYYR@.Y	18.56	8.74	2.12	0.47
P68510_1433F_MOUSE	Ywhah	14-3-3 protein eta OS=M	K.NSVVEASEAAYK#.E	41.41	32.07	1.29	0.77
P68510_1433F_MOUSE	Ywhah	14-3-3 protein eta OS=M	K.AVTELNEPLSNEDR@.N	21.24	9.98	2.13	0.47
P68510_1433F_MOUSE	Ywhah	14-3-3 protein eta OS=M	K.AVTELNEPLSNEDR@NLLSVAYK#.N	14.07	9.53	1.48	0.68
P68510_1433F_MOUSE	Ywhah	14-3-3 protein eta OS=M	K.NSVVEASEAAYK#.E	13.03	8.52	1.53	0.65
P68254_1433T_MOUSE	Ywhaq	14-3-3 protein theta OS=	K.AVTEQGAELSNEER@.N	37.82	19.82	1.91	0.52
P68254_1433T_MOUSE	Ywhaq	14-3-3 protein theta OS=	K.AVTEQGAELSNEER@.N	16.05	14.95	1.07	0.93
P68254_1433T_MOUSE	Ywhaq	14-3-3 protein theta OS=	K.AVTEQGAELSNEER@.N	6.80	3.04	2.24	0.45
P68254_1433T_MOUSE	Ywhaq	14-3-3 protein theta OS=	K.AVTEQGAELSNEER@.N	9.59	3.78	2.54	0.39
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	R.DNLTLWTSDTQGDEAEAGEGGEN.-	3.90	3.90	1.00	1.00
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.FLIPNASQPESK#.V	136.38	57.29	2.38	0.42
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.GIVDQSQQAYQEAFEISK#.K	100.41	42.66	2.35	0.42
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.SVTEQGAELSNEER@.N	254.42	93.73	2.71	0.37
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.TAFDEAIAELDTLSEESYK#.D	68.76	29.33	2.34	0.43
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	R.VVSSIEQK#.T	166.55	68.35	2.44	0.41
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	R.YLAEVAAGDDK#K#.G	242.12	82.38	2.94	0.34
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.FLIPNASQPESK#.V	32.72	19.30	1.70	0.59
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.GIVDQSQQAYQEAFEISK#.K	9.12	3.86	2.37	0.42
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.SVTEQGAELSNEER.N	41.80	54.62	0.77	1.31
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	R.VVSSIEQK#.T	52.63	47.29	1.11	0.90
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.GIVDQSQQAYQEAFEISK#.K	9.08	5.15	1.76	0.57
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.SVTEQGAELSNEER.N	15.15	10.33	1.47	0.68
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	R.VVSSIEQK#.T	13.48	10.12	1.33	0.75
P63101_1433Z_MOUSE	Ywhaz	14-3-3 protein zeta/delta	K.SVTEQGAELSNEER@.N	13.22	6.44	2.05	0.49
Q00899_TYY1_MOUSE	Yy1	Transcriptional repressor	K.SYLGGGAGAAGGGGADPGNK#.K	9.53	2.63	3.62	0.28
Q00899_TYY1_MOUSE	Yy1	Transcriptional repressor	K.DIDHETVVEEQIIGENSPPDYSEYM*TGK#.K	3.63	1.94	1.87	0.53
Q00899_TYY1_MOUSE	Yy1	Transcriptional repressor	R.FSLDFNLR@.T	19.15	9.69	1.98	0.51
Q8K0L9_ZBT20_MOUSE	Zbtb20	Zinc finger and BTB doma	K.LLLGYSDIEIPSVVSVQSVQK#.L	7.43	3.93	1.89	0.53
G3X9A3_G3X9A3_MOUSE	Zbtb21	Protein Zbtb21 OS=Mus r	R.VTVGGDAAAAAVAAAAAAAATR@.D	4.91	10.76	0.46	2.19
Q8BN78_KAISO_MOUSE	Zbtb33	Transcriptional regulator	K.FIAELGVPLSQVK#.S	10.10	3.22	3.13	0.32
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.QGEGSSGVSSVLQQPQPNPGPEK#ENVR@.T	2.74	2.91	0.94	1.06
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.TLEEILLER@.A	7.57	6.24	1.21	0.83
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.AEEPSGADDSPSGTK#.S	2.66	1.31	2.04	0.49

Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.DSSVLSSAQAASEPLLPEGSGPSSSQTATK#PR@.R	5.70	2.01	2.84	0.35
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.GEVETSGIGDSILNVK#.C	18.34	6.33	2.90	0.35
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.K#VESPETNIDK#.A	7.98	2.18	3.66	0.27
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.K#VESPETNIDK#APK#.K	27.21	18.01	1.51	0.66
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.LK#AEEPSGADDSPSGTK#.S	31.13	11.58	2.69	0.37
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.LSVQSNPSPQLR.S	52.35	20.07	2.61	0.38
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.M*EANETSDETISDPTK#.L	14.74	5.86	2.51	0.40
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.QGEGSSGVSSVLQQPQPNPGPEK#ENVR@.T	13.65	5.48	2.49	0.40
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.TFSEVLAEK#.K	21.94	8.26	2.66	0.38
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.TLEEILLER@.A	63.93	28.45	2.25	0.45
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.TSQLTVQQSK#.L	19.83	10.32	1.92	0.52
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.TVLPTVPESQEEEVK#.T	17.87	10.30	1.74	0.58
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	R.VAGK#PVLTAVSGVTR@.H	52.26	16.55	3.16	0.32
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	R.YVDGLFLPPSK#.T	15.62	8.75	1.79	0.56
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.LSVQSNPSPQLR@.S	5.92	2.31	2.56	0.39
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.TLEEILLER@.A	10.10	4.70	2.15	0.46
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.TSQLTVQQSK#.L	3.86	6.68	0.58	1.73
Q6NZF1_ZC11A_MOUSE	Zc3h11a	Zinc finger CCCH domain	K.TVLPTVPESQEEEVK#.T	4.44	5.00	0.89	1.12
E9Q784_E9Q784_MOUSE	Zc3h13	Protein Zc3h13 OS=Mus	K.DADSLFEHELGALNM*AALLR@.K	14.81	2.81	5.28	0.19
E9Q784_E9Q784_MOUSE	Zc3h13	Protein Zc3h13 OS=Mus	K.FTPGAVLLR@.V	15.48	4.20	3.69	0.27
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.AISEAQESVTK#.T	31.42	13.59	2.31	0.43
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	R.FSHDGEEEEEDEDYGTR@.I	17.51	7.30	2.40	0.42
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.LSEEIVVTPNQDSGM*K#.T	8.70	2.61	3.33	0.30
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.M*SIEDENFR@.K	6.94	2.08	3.34	0.30
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.QLDVQSSQVSEAGR@.L	13.21	3.51	3.76	0.27
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.AISEAQESVTK#.T	88.07	33.82	2.60	0.38
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	R.FSHDGEEEEEDEDYGTR@.I	24.44	9.00	2.71	0.37
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	R.GLLHPQQLHLLSR@.Q	25.36	7.50	3.38	0.30
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	R.HSYDDGASTR@.L	10.71	2.73	3.92	0.25
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.LSEEIVVTPNQDSGM*K#.T	20.73	7.48	2.77	0.36
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.M*SIEDENFR@.K	12.01	3.12	3.85	0.26
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.QLDVQSSQVSEAGR@.L	26.77	9.60	2.79	0.36
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	R.SVTTEPSSLK#.S	39.88	20.66	1.93	0.52
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	R.TSQEELLAEM*VQGQNR@.A	13.68	5.09	2.69	0.37
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.TTNYSAVPQK#.Q	28.15	15.75	1.79	0.56
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	R.VLSGHLM*QTR@.D	5.80	3.24	1.79	0.56
Q8BJ05_ZC3HE_MOUSE	Zc3h14	Zinc finger CCCH domain	K.AISEAQESVTK#.T	7.89	3.12	2.53	0.40
Q3TIV5_ZC3HF_MOUSE	Zc3h15	Zinc finger CCCH domain	R.DVEETGITVASVER@.F	18.14	9.05	2.00	0.50
Q3TIV5_ZC3HF_MOUSE	Zc3h15	Zinc finger CCCH domain	K.ELQELNELFKPVVAAQK.I	10.54	6.77	1.56	0.64
Q3TIV5_ZC3HF_MOUSE	Zc3h15	Zinc finger CCCH domain	R.EVFEFR@PELVNDDDEEADDTR@.Y	14.55	5.33	2.73	0.37
Q3TIV5_ZC3HF_MOUSE	Zc3h15	Zinc finger CCCH domain	R.DVEETGITVASVER@.F	22.05	9.76	2.26	0.44
Q3TIV5_ZC3HF_MOUSE	Zc3h15	Zinc finger CCCH domain	K.ELQELNELFK#PVVAAQK#.I	24.94	12.45	2.00	0.50
Q3TIV5_ZC3HF_MOUSE	Zc3h15	Zinc finger CCCH domain	R.EVFEFR@PELVNDDDEEADDTR@.Y	20.43	8.95	2.28	0.44
Q3TIV5_ZC3HF_MOUSE	Zc3h15	Zinc finger CCCH domain	K.ITLESFLAWK#.K	9.51	5.75	1.65	0.61
Q3TIV5_ZC3HF_MOUSE	Zc3h15	Zinc finger CCCH domain	R.SALGPNVTK#.I	16.10	9.03	1.78	0.56
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.AGAEEEEEK#GEGAPGEEGK#PDVQSVGEQEPTEAAK#.E	25.92	8.79	2.95	0.34
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.ASDLEEEENATR@.V	105.43	23.28	4.53	0.22
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.ASQQAAAPQPAVPGQPQQGSFVAHK#.E	126.84	57.66	2.20	0.45
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.AVEDAIAR@.K	104.34	23.81	4.38	0.23
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.DPSAQPPK#.S	30.02	17.45	1.72	0.58
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.DTTLEPYADPYYDYEIER@.F	57.12	25.26	2.26	0.44
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.ELDEHELDYDEEVPEEPAPAAQEEEAEK#.A	17.99	6.90	2.61	0.38
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.ESGSEQDLDGAGER@.A	62.33	12.14	5.13	0.19
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.ESTSVGPQVK#.R	89.14	46.26	1.93	0.52
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.GGQYENFR@.V	1628.45	14.02	116.19	0.01
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.GNYSLITK#.A	59.39	27.45	2.16	0.46
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.KPAPPPAPPQATK.T	30.30	15.58	1.95	0.51
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.LGVSVSPSR@.A	27.30	15.62	1.75	0.57
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.TKGEPAPPPGK.A	34.63	18.95	1.83	0.55
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.TLSGSGSGSGSSYSGSSSR@.S	10.91	2.62	4.17	0.24
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.VQSQEETR@SDEEDR@ASEPK#.S	24.35	6.44	3.78	0.26
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.VQYTEAEPYHNYR@.E	110.88	48.89	2.27	0.44
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.VQYTEAEPYHNYR.E	18.98	7.99	2.38	0.42
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.AGAEEEEEK#GEGAPGEEGK#PDVQSVGEQEPTEAAK#.E	30.88	12.39	2.49	0.40
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.APAAPADR@.K	71.41	19.48	3.66	0.27
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.ASDLEEEENATR@.V	55.25	12.95	4.27	0.23
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.ASQQAAAPQPAVPGQPQQGSFVAHK#.E	70.26	31.86	2.21	0.45
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.AVEDAIAR@.K	62.29	21.45	2.90	0.34
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.DTTLEPYADPYYDYEIER@.F	32.43	12.21	2.66	0.38
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.ELDEHELDYDEEVPEEPAPAAQEEEAEK#.A	23.94	9.46	2.53	0.39
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.ESTSVGPQVK#.R	86.00	28.54	3.01	0.33
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.GGQYENFR@.V	52.05	21.06	2.47	0.40
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.GNYSLITK#.A	19.36	12.24	1.58	0.63
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	K.K#PAPPPAPPQATK#.T	18.40	10.76	1.71	0.59
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.TK#GEPAPPPGK#.A	17.68	7.81	2.26	0.44
Q0P678_ZCH18_MOUSE	Zc3h18	Zinc finger CCCH domain	R.TLSGSGSGSGSSYSGSSSR@.S	6.65	1.52	4.36	0.23
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.GR@EDGELEEGELEDDGAEEVQDPPGGQER@.S	7.46	4.04	1.85	0.54
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.HAETSGGSGPGDSGPSDPR@.L	17.06	6.71	2.54	0.39
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	K.IPSLFEIVVR@PTGQLAEK#.L	16.48	10.73	1.54	0.65
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	K.TAEPASDTSAQPK#.G	9.41	3.13	3.01	0.33
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.VLAAGGLGQGSSSGQSSVLSGISLYDPR@.T	9.88	4.59	2.15	0.46
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	K.AEGSLHSSPAGPSSSK#.G	94.66	30.73	3.08	0.32
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.GR@EDGELEEGELEDDGAEEVQDPPGGQER@.S	11.94	3.84	3.11	0.32
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.HAETSGGSGPGDSGPSDPR@.L	52.65	17.52	3.00	0.33
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.K#SALEQPETGK#.A	7.26	2.34	3.10	0.32
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.LQK#PADPVAASR@.A	67.81	15.71	4.32	0.23
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	K.QDVPPVPAALQSLPALDPR@.L	7.28	3.18	2.29	0.44
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.QQTSSR@PQASVGEPSSSGLGDPR@.L	33.38	7.96	4.19	0.24
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.QRPGSTDPSTSGSNLPDFELLSR.I	37.65	7.02	5.37	0.19
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	K.TAEPASDTSAQPK#.G	45.66	14.61	3.12	0.32
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	K.TGTGSPFAGNSPAR@.E	10.11	2.72	3.72	0.27
E9Q8K8_E9Q8K8_MOUSE	Zc3h4	Zinc finger CCCH domain	R.VLAAGGLGQGSSSGQSSVLSGISLYDPR@.T	47.25	12.91	3.66	0.27
D6RI42_D6RI42_MOUSE	Zc3h7a	Protein Zc3h7a OS=Mus	K.SEEILIPTEIIEK#.L	6.24	2.34	2.67	0.37
F8VPP8_F8VPP8_MOUSE	Zc3h7b	Protein Zc3h7b OS=Mus	R.DLLFDPLGGVK#.R	21.26	8.93	2.38	0.42
F8VPP8_F8VPP8_MOUSE	Zc3h7b	Protein Zc3h7b OS=Mus	R.DLLFDPLGGVK#.R	29.67	6.88	4.31	0.23
F8VPP8_F8VPP8_MOUSE	Zc3h7b	Protein Zc3h7b OS=Mus	K.GLQFIQSTLPLK#QEEYEAFLLK#.L	16.93	5.07	3.34	0.30
F8VPP8_F8VPP8_MOUSE	Zc3h7b	Protein Zc3h7b OS=Mus	R.LGALDSFGSAR@.G	25.23	4.87	5.18	0.19
F8VPP8_F8VPP8_MOUSE	Zc3h7b	Protein Zc3h7b OS=Mus	K.LVQNLFAEGNDLFR@.E	19.88	4.75	4.19	0.24
F8VPP8_F8VPP8_MOUSE	Zc3h7b	Protein Zc3h7b OS=Mus	K.VFTSDSDASGWAYR@.F	8.61	2.20	3.91	0.26
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.ASQEFLEDGDPDGLFSR@.N	22.40	13.46	1.66	0.60
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.FVLLETGDQAGITR@.S	27.66	13.70	2.02	0.50
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.TSAAGFPLVAAQR@.N	26.55	23.48	1.13	0.88
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	K.YSHDVLSEQNFQVLK#.N	36.42	16.61	2.19	0.46

Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.FVLLETGDQAGITR.S	22.62	12.69	1.78	0.56
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.ASQEFLEDGDPDGLFSR@.N	8.47	5.44	1.56	0.64
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	K.EAVYSGVQSLR@.S	16.57	7.17	2.31	0.43
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.FVLLETGDQAGITR@.S	17.98	10.72	1.68	0.60
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.TSAAGFPLVAAQR@.N	29.42	11.11	2.65	0.38
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	K.YSHDVLSEQNFQVLK#.N	16.39	11.17	1.47	0.68
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.ASQEFLEDGDPDGLFSR@.N	10.27	4.00	2.57	0.39
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	K.EAVYSGVQSLR@.S	11.14	5.21	2.14	0.47
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.FVLLETGDQAGITR@.S	14.23	6.16	2.31	0.43
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	K.SSTHASVSPASEPSR@.M	17.51	6.72	2.60	0.38
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	R.TSAAGFPLVAAQR@.N	19.05	6.78	2.81	0.36
Q3UPF5_ZCCHV_MOUSE	Zc3hav1	Zinc finger CCCH-type an	K.YSHDVLSEQNFQVLK#.N	17.98	6.12	2.94	0.34
Q80YV2_NIPA_MOUSE	Zc3hc1	Nuclear-interacting part	R.ELIDEGIVPEEGGTEPK#.D	5.97	2.87	2.08	0.48
Q80YV2_NIPA_MOUSE	Zc3hc1	Nuclear-interacting part	R.SNQPAETDSM*SLSEK#.S	9.72	6.47	1.50	0.66
Q80YV2_NIPA_MOUSE	Zc3hc1	Nuclear-interacting part	R.SNQPAETDSM*SLSEK#.S	10.85	3.12	3.48	0.29
Q80YV2_NIPA_MOUSE	Zc3hc1	Nuclear-interacting part	R.ELIDEGIVPEEGGTEPK#.D	6.74	7.63	0.88	1.13
Q80YV2_NIPA_MOUSE	Zc3hc1	Nuclear-interacting part	R.SNQPAETDSM*SLSEK#.S	8.11	2.22	3.65	0.27
Q80YV2_NIPA_MOUSE	Zc3hc1	Nuclear-interacting part	R.SQDATVSPGSEQSEK#.S	6.64	1.51	4.39	0.23
Q80YV2_NIPA_MOUSE	Zc3hc1	Nuclear-interacting part	R.VETFSSLK#.W	10.19	4.22	2.41	0.41
Q9CX48_ZCH10_MOUSE	Zcchc10	Zinc finger CCHC domain	R.LLLQSIGETNIEK#.K	11.21	3.23	3.47	0.29
Q9ESX4_NO40_MOUSE	Zcchc17	Nucleolar protein of 40 k	K.DLDPNNVVIEQEER@.R	6.44	2.95	2.19	0.46
B2RVL6_ZCH24_MOUSE	Zcchc24	Zinc finger CCHC domain	R.GEALSSSVYR@.N	14.40	11.38	1.27	0.79
B2RVL6_ZCH24_MOUSE	Zcchc24	Zinc finger CCHC domain	K.GEGLTPYQGK#.K	9.36	6.43	1.46	0.69
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	R.FK#PGVISEELQDALGVTDK#.S	12.09	7.26	1.67	0.60
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.YQQVFSHIVPLEGQEM*QVK#.A	9.86	5.71	1.73	0.58
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.DVFASYLNSNIQSPSM*R@.S	11.03	2.16	5.11	0.20
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.EAELENSGLALYDGNDDADGETETGEIQNK#.N	7.28	3.50	2.08	0.48
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	R.FK#PGVISEELQDALGVTDK#.S	59.39	28.83	2.06	0.49
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	R.FK#PGVISEELQDALGVTDK#.S	4.41	1.93	2.29	0.44
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.IDGPLLQILFM*NNAISK#.Q	7.68	6.59	1.17	0.86
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.LGQPLLNENPQLTEGWEIPK#.Y	3.66	2.37	1.54	0.65
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.LVNYPGFNISTPR@.G	50.43	20.39	2.47	0.40
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.QYHQEIEEFVSNLVK#.R	27.36	11.49	2.38	0.42
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.R@FEEQQK#NDVEK#.T	42.00	17.58	2.39	0.42
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	R.YHAEEVEER@.F	7.06	2.34	3.02	0.33
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.YQQVFSHIVPLEGQEM*QVK#.A	42.17	16.33	2.58	0.39
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	R.FK#PGVISEELQDALGVTDK#.S	33.36	7.13	4.68	0.21
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.LVNYPGFNISTPR@.G	23.87	5.30	4.50	0.22
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.QYHQEIEEFVSNLVK#.R	10.45	1.88	5.55	0.18
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.R@FEEQQK#NDVEK#.T	18.82	5.17	3.64	0.27
Q9CYA6_ZCHC8_MOUSE	Zcchc8	Zinc finger CCHC domain	K.YQQVFSHIVPLEGQEM*QVK#.A	17.71	8.51	2.08	0.48
Q8R1J3_ZCHC9_MOUSE	Zcchc9	Zinc finger CCHC domain	R.ANVDPALGEFPFAK#.C	11.64	8.33	1.40	0.72
Q8R1J3_ZCHC9_MOUSE	Zcchc9	Zinc finger CCHC domain	K.GM*SADYEDVLDVPK#.L	6.27	4.35	1.44	0.69
Q8R1J3_ZCHC9_MOUSE	Zcchc9	Zinc finger CCHC domain	R.ANVDPALGEFPFAK.C	4.47	7.28	0.61	1.63
P23607_ZFA_MOUSE	Zfa	Zinc finger autosomal pr	K.IADPFVLSR@.H	16.38	7.43	2.21	0.45
Q61329_ZFHX3_MOUSE	Zfhx3	Zinc finger homeobox pr	K.ASASPGENDSGTGGEEPQR.D	5.48	1.50	3.66	0.27
Q61329_ZFHX3_MOUSE	Zfhx3	Zinc finger homeobox pr	K.GLPEEDEDLGQIFTIR@.R	5.81	5.20	1.12	0.89
Q61329_ZFHX3_MOUSE	Zfhx3	Zinc finger homeobox pr	R.LSSGLVSPAPSFYSK#.E	8.05	6.41	1.26	0.80
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.AFLPFGK#.I	30.89	11.44	2.70	0.37
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.DQSLSSNSILLVSELPEDGFTEEDIR@K#.A	25.94	5.03	5.16	0.19
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.DYQSEADLPIR@.S	18.37	7.38	2.49	0.40
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.LDSFSQVGPGSETVTQK#.D	5.48	2.68	2.05	0.49
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	R.LPTPSM*M*NDYYAASPR@.I	8.10	3.15	2.57	0.39
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.NK#DSNK#PVTVPANSEIK#.A	10.67	1.60	6.67	0.15
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	R.QQYPDWNPEILPSR@.R	5.20	3.33	1.56	0.64
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.QSSVTQVTEQSPK#.V	17.24	9.16	1.88	0.53
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.SENLEDDTLPEGK#.Q	19.22	9.96	1.93	0.52
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.SK#LDSFSQVGPGSETVTQK#.D	4.98	2.35	2.12	0.47
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.SM*TSDVPGDLDFLVPK#.A	15.28	5.70	2.68	0.37
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	R.SPFGIVK#.A	40.85	18.18	2.25	0.44
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.SSVLTVSNVYSSK#.S	9.79	2.42	4.04	0.25
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.TM*ETVSSSSSAK#.S	12.16	3.94	3.09	0.32
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.YIETM*PLVIK#.G	24.07	7.91	3.04	0.33
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.DQSLSSNSILLVSELPEDGFTEEDIR@K#.A	38.93	8.66	4.50	0.22
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.DYQSEADLPIR@.S	22.36	7.66	2.92	0.34
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.GVDQTSK#PDETGK#.S	5.92	1.57	3.78	0.26
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.LDSFSQVGPGSETVTQK#.D	6.69	3.14	2.13	0.47
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	R.LPTPSM*M*NDYYAASPR@.I	10.06	4.58	2.20	0.46
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	R.LVTVDEIGEVEESADITFATLNAK#.R	22.76	24.62	0.92	1.08
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	R.QM*DFPGESSSQSFFPVESGTK#.M	3.80	1.99	1.91	0.52
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	R.QQYPDWNPEILPSR@.R	8.29	2.80	2.96	0.34
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.QSSVTQVTEQSPK#.V	29.02	10.20	2.85	0.35
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.SAEESPSGTLEATEK#.E	6.94	1.59	4.36	0.23
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.SENLEDDTLPEGK#.Q	39.87	12.18	3.27	0.31
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.SM*TSDVPGDLDFLVPK#.A	20.30	6.64	3.05	0.33
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	R.SPFGIVK#.A	47.28	16.32	2.90	0.35
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.SSVLTVSNVYSSK#.S	18.80	5.43	3.46	0.29
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.TM*ETVSSSSSAK#.S	15.59	4.30	3.63	0.28
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.VILQLESPESALSMYNFLK#.Q	3.43	1.61	2.13	0.47
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.YGYTEDPLEVR@.I	30.58	8.99	3.40	0.29
E9QML5_E9QML5_MOUSE	Zfml	Zinc finger protein 638 O	K.YIETM*PLVIK#.G	46.19	13.57	3.40	0.29
Q6IQX8_Q6IQX8_MOUSE	Zfp219	Protein Zfp219 OS=Mus r	R.SLGSLTSLHPNPGEGSGQPAPAAGTQAR@.S	3.84	1.90	2.02	0.49
Q499D5_Q499D5_MOUSE	Zfp235	Protein Zfp235 OS=Mus r	K.CEVCGKGFTQR.S	1.91	73.21	0.03	38.36
E9Q1A5_E9Q1A5_MOUSE	Zfp384	Protein Zfp384 OS=Mus r	K.VASTLTEEGGGGGGGGGTVAPPK#PPR@.G	9.27	4.88	1.90	0.53
Q9CZP3_Q9CZP3_MOUSE	Zfp655	Protein Zfp655 OS=Mus r	R.EQDLQVFDLESK#.N	7.41	3.39	2.18	0.46
Q9CZP3_Q9CZP3_MOUSE	Zfp655	Protein Zfp655 OS=Mus r	R.FLQDTDM*EQGFSGGFPISK#PDGISER@.E	3.69	3.18	1.16	0.86
O88532_ZFR_MOUSE	Zfr	Zinc finger RNA-binding p	R.STAPAVAYDSK#.Q	6.11	13.42	0.46	2.20
O88532_ZFR_MOUSE	Zfr	Zinc finger RNA-binding p	K.AGYSQGATQYTQAQQAR@.Q	7.02	2.00	3.51	0.28
O88532_ZFR_MOUSE	Zfr	Zinc finger RNA-binding p	K.AISSASSPQSPGDALR@.R	17.21	6.00	2.87	0.35
O88532_ZFR_MOUSE	Zfr	Zinc finger RNA-binding p	K.GLSTTGNSSLNSTSNTK#.V	18.17	4.46	4.08	0.25
O88532_ZFR_MOUSE	Zfr	Zinc finger RNA-binding p	K.HATIYPTEEELQAVQK#.I	16.45	7.58	2.17	0.46
O88532_ZFR_MOUSE	Zfr	Zinc finger RNA-binding p	K.QAAAAAAAAAATAAWTGTTFTK#.K	9.01	3.56	2.53	0.40
O88532_ZFR_MOUSE	Zfr	Zinc finger RNA-binding p	K.QDAGSEPVTPASLAALQSDVQPVGHDYVEEVR@NDEGK#.V	11.98	3.58	3.35	0.30
O88532_ZFR_MOUSE	Zfr	Zinc finger RNA-binding p	K.VLGM*DPLPQM*NQR@.F	9.49	4.51	2.10	0.48
Q8VDM1_ZGPAT_MOUSE	Zgpat	Zinc finger CCCH-type wi	K.LLSTVDQESPAQEDAEYLAFQK#.A	6.05	2.21	2.74	0.37
Q8VDM1_ZGPAT_MOUSE	Zgpat	Zinc finger CCCH-type wi	K.LLSTVDQESPAQEDAEYLAFQK#.A	8.98	3.94	2.28	0.44
Q8VDM1_ZGPAT_MOUSE	Zgpat	Zinc finger CCCH-type wi	R.NVFDFLNEK#.L	8.50	8.59	0.99	1.01
Q9CPW7_ZMAT2_MOUSE	Zmat2	Zinc finger matrin-type p	R.RAEEDLTFEEDDEM*AAVM*GFSGFGSTK.K	7.06	5.82	1.21	0.82
Q9CPW7_ZMAT2_MOUSE	Zmat2	Zinc finger matrin-type p	R.STLDQVK#.K	21.27	19.22	1.11	0.90
Q6P1E1_ZMIZ1_MOUSE	Zmiz1	Zinc finger MIZ domain-c	R.SDLELQFK#.C	5.98	19.13	0.31	3.20
Q80W54_FACE1_MOUSE	Zmpste24	CAAX prenyl protease 1 h	R.IVLFDTLLEEYSVPNKDNQEESGM*EAR.N	5.67	6.91	0.82	1.22
Q80W54_FACE1_MOUSE	Zmpste24	CAAX prenyl protease 1 h	R.VPAELEQIM*DSDTFEK#.S	5.45	4.95	1.10	0.91
Q8BS54_Q8BS54_MOUSE	Zmym6	Protein Zmym6 OS=Mus	R.LSAEM*IETTNDSGR@.T	4.79	1.91	2.50	0.40

Q3UH28_Q3UH28_MOUSE	Zmynd8	Protein Zmynd8 OS=Mus	K.AM*TM*LTIEQLSYLLK#.F	4.67	1.66	2.82	0.35
Q3UH28_Q3UH28_MOUSE	Zmynd8	Protein Zmynd8 OS=Mus	R.ETPSSM*LLGSNQSSVSK#.R	7.10	2.94	2.42	0.41
Q3UH28_Q3UH28_MOUSE	Zmynd8	Protein Zmynd8 OS=Mus	K.FGVFNYSPFR@.T	5.32	1.57	3.39	0.29
Q3UH28_Q3UH28_MOUSE	Zmynd8	Protein Zmynd8 OS=Mus	R.VVWNASTVQQK#.E	35.72	13.58	2.63	0.38
Q3UH28_Q3UH28_MOUSE	Zmynd8	Protein Zmynd8 OS=Mus	K.AM*TM*LTIEQLSYLLK#.F	7.04	2.65	2.66	0.38
Q3UH28_Q3UH28_MOUSE	Zmynd8	Protein Zmynd8 OS=Mus	K.FGVFNYSPFR@.T	10.09	2.46	4.11	0.24
Q3UH28_Q3UH28_MOUSE	Zmynd8	Protein Zmynd8 OS=Mus	K.NTTGSTIAEIR@.R	16.75	3.74	4.48	0.22
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	K.ILTINEDGSLGLK#.T	10.97	6.20	1.77	0.56
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	R.AM*VVM*GGVSGQSAVSGELQESVLQDR@.S	5.07	3.28	1.54	0.65
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	K.ANM*LQEYSK#.F	7.05	3.56	1.98	0.51
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	K.GGLLTSEEDSGFSTSPK#.D	14.09	8.53	1.65	0.61
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	R.LPQGLQYALNVPISVK#.Q	14.96	6.84	2.19	0.46
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	K.QALLDSEGSADIDQVDNLQEGPSK#PVHSSTNYDDAM*QFLK#.K	2.35	2.24	1.05	0.96
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	K.QEITFTDVSEQLM*R@.D	6.87	2.94	2.34	0.43
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	R.SLK#QPLEQSQTISPLSSYEDSK#.V	9.25	6.10	1.52	0.66
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	R.SLPHQEILAADEVLQESEM*R@.Q	12.40	4.75	2.61	0.38
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	R.TSQNDAYLNSPSLNFVTDNQTLPNPPAFSSIDK#.Q	3.34	2.54	1.31	0.76
Q61624_ZN148_MOUSE	Znf148	Zinc finger protein 148 O	K.YAFELVDK#.Q	23.69	12.90	1.84	0.54
Q9ERU3_ZNF22_MOUSE	Znf22	Zinc finger protein 22 OS	R.NVDEK#PYK#.C	7.90	2.85	2.77	0.36
Q9ERU3_ZNF22_MOUSE	Znf22	Zinc finger protein 22 OS	K.SFFQSSNLIQHR@.R	5.23	1.94	2.69	0.37
Q91VN1_ZNF24_MOUSE	Znf24	Zinc finger protein 24 OS	K.QEM*ASAGESHEGPGTLNIGVPQLFK#.Y	5.51	2.96	1.86	0.54
Q99LI5_ZN281_MOUSE	Znf281	Zinc finger protein 281 O	K.SYLNFVSPLPDVVGQK#.S	10.53	4.25	2.48	0.40
Q99PP2_ZN318_MOUSE	Znf318	Zinc finger protein 318 (	K.VAQILGIDIFDK#.S	7.62	2.20	3.47	0.29
O88291_ZN326_MOUSE	Znf326	DBIRD complex subunit	R.ESVLTATSILNNPIVK#.A	13.76	6.42	2.14	0.47
O88291_ZN326_MOUSE	Znf326	DBIRD complex subunit	R.ESVLTATSILNNPIVK#.A	107.96	39.66	2.72	0.37
O88291_ZN326_MOUSE	Znf326	DBIRD complex subunit	R.FGPYESYDSR@.S	41.65	16.42	2.54	0.39
O88291_ZN326_MOUSE	Znf326	DBIRD complex subunit	K.GENPFEIQDHPQDQQIEGDEEDEEK#.I	36.59	14.00	2.61	0.38
O88291_ZN326_MOUSE	Znf326	DBIRD complex subunit	R.NQGGSSWEAPYSR@.S	19.58	7.90	2.48	0.40
O88291_ZN326_MOUSE	Znf326	DBIRD complex subunit	R.SGYGFNEPEQTR@.F	55.52	21.54	2.58	0.39
O88291_ZN326_MOUSE	Znf326	DBIRD complex subunit	R.SM*DSYLNQSYGM*DNHSGGGGGSR@.F	21.84	10.56	2.07	0.48
O88291_ZN326_MOUSE	Znf326	DBIRD complex subunit	R.ESVLTATSILNNPIVK#.A	17.20	5.20	3.31	0.30
Q922H9_ZN330_MOUSE	Znf330	Zinc finger protein 330 O	R.TYASGYAHYEEQES.-	10.71	10.71	1.00	1.00
Q9R0B7_ZN346_MOUSE	Znf346	Zinc finger protein 346 O	R.LADPAVSDLPAGK#.G	10.84	5.74	1.89	0.53
Q9R0B7_ZN346_MOUSE	Znf346	Zinc finger protein 346 O	K.TLVTLGSQTPVQTQPTPK#.D	8.72	5.88	1.48	0.67
Q8VD12_Z385A_MOUSE	Znf385a	Zinc finger protein 385A	R.GAAELAGTLTFSK#.E	41.66	16.72	2.49	0.40
Q8VD12_Z385A_MOUSE	Znf385a	Zinc finger protein 385A	R.LGPPTPGEPEAPAQDR.T	21.20	11.64	1.82	0.55
Q8VD12_Z385A_MOUSE	Znf385a	Zinc finger protein 385A	K.QPGSPSPPSVPESGQGVTK#.G	5.57	3.38	1.65	0.61
Q8VD12_Z385A_MOUSE	Znf385a	Zinc finger protein 385A	R.TAHGPILFSPY.-	24.05	24.05	1.00	1.00
Q69Z99_ZN512_MOUSE	Znf512	Zinc finger protein 512 O	K.VLQDLVPDDR@.K	11.58	7.44	1.56	0.64
Q69Z99_ZN512_MOUSE	Znf512	Zinc finger protein 512 O	K.AGK#EQGGNEELVGPDPEPVPAQPQK#.A	4.73	2.06	2.29	0.44
Q69Z99_ZN512_MOUSE	Znf512	Zinc finger protein 512 O	K.EQGGNEELVGPDPEPVPAQPQK#.A	4.65	5.42	0.86	1.17
Q69Z99_ZN512_MOUSE	Znf512	Zinc finger protein 512 O	K.IAVYHLQELASAELTK#.E	17.46	11.00	1.59	0.63
Q69Z99_ZN512_MOUSE	Znf512	Zinc finger protein 512 O	R.LGAVTATPGPTSLK#.Q	17.90	11.20	1.60	0.63
Q69Z99_ZN512_MOUSE	Znf512	Zinc finger protein 512 O	K.VLQDLVPDDR@.K	13.62	13.78	0.99	1.01
Q8BHZ4_ZN592_MOUSE	Znf592	Zinc finger protein 592 O	K.AAPLIVEVFNK#.V	7.75	3.52	2.20	0.45
Q8BHZ4_ZN592_MOUSE	Znf592	Zinc finger protein 592 O	K.AAPLIVEVFNK#.V	13.15	3.03	4.35	0.23
Q8BHZ4_ZN592_MOUSE	Znf592	Zinc finger protein 592 O	R.APAEPPATNVAAR@.G	6.08	2.58	2.36	0.42
Q9DB42_ZN593_MOUSE	Znf593	Zinc finger protein 593 O	R.AAGM*GSYVQPQR.L	8.59	8.59	1.00	1.00
Q80YR4_ZN598_MOUSE	Znf598	Zinc finger protein 598 O	K.TPGLAPTPQAYLVPENFR@.E	4.42	1.34	3.30	0.30
Q80YR4_ZN598_MOUSE	Znf598	Zinc finger protein 598 O	R.ASVAAQQQEETQR@.V	3.13	2.64	1.19	0.84
Q9D2D7_ZN687_MOUSE	Znf687	Zinc finger protein 687 O	K.LSPVTPTPEGPK#.V	10.44	4.73	2.21	0.45
Q9D2D7_ZN687_MOUSE	Znf687	Zinc finger protein 687 O	K.SATGPGTAGGSVISR@.T	19.14	6.20	3.09	0.32
Q9D2D7_ZN687_MOUSE	Znf687	Zinc finger protein 687 O	R.SSGSAEQSLVGLR@.V	22.19	8.57	2.59	0.39
Q9D2D7_ZN687_MOUSE	Znf687	Zinc finger protein 687 O	K.SVLGLVPQTLPK#.A	21.23	10.74	1.98	0.51
Q9D2D7_ZN687_MOUSE	Znf687	Zinc finger protein 687 O	R.TQSSLVEAFNK#.I	15.24	10.07	1.51	0.66
Q9D2D7_ZN687_MOUSE	Znf687	Zinc finger protein 687 O	R.VPSEPDPPAPLAEGAFLAETSFLK#.L	8.80	4.13	2.13	0.47
Q9D2D7_ZN687_MOUSE	Znf687	Zinc finger protein 687 O	K.VVSVQLGDGTR@.L	16.96	6.57	2.58	0.39
Q9D2D7_ZN687_MOUSE	Znf687	Zinc finger protein 687 O	K.SVLGLVPQTLPK#.A	18.17	8.12	2.24	0.45
Q9D2D7_ZN687_MOUSE	Znf687	Zinc finger protein 687 O	R.TQSSLVEAFNK#.I	11.59	11.42	1.02	0.99
Q6NZQ6_ZN740_MOUSE	Znf740	Zinc finger protein 740 O	R.AGSPDVLR@.C	35.48	15.64	2.27	0.44
Q8R0T2_ZN768_MOUSE	Znf768	Zinc finger protein 768 O	K.AFADSSYLLR@.H	7.24	1.35	5.38	0.19
Q8BJ90_ZN771_MOUSE	Znf771	Zinc finger protein 771 O	R.FSAASNLR@.Q	19.51	4.35	4.48	0.22
Q8BIF9_ZN787_MOUSE	Znf787	Zinc finger protein 787 O	R.LHPELSGPGVAAK#.V	29.72	10.05	2.96	0.34
Q8R1N0_ZN830_MOUSE	Znf830	Zinc finger protein 830 O	K.GATQGPSTGTVPQATK#.R	11.31	9.38	1.21	0.83
Q8R151_ZNFX1_MOUSE	Znfx1	NFX1-type zinc finger-co	K.DLGLVENSIR@.F	18.23	9.65	1.89	0.53
Q8R151_ZNFX1_MOUSE	Znfx1	NFX1-type zinc finger-co	R.FYDHLANLEGSLEK#.V	14.25	6.24	2.28	0.44
Q8R151_ZNFX1_MOUSE	Znfx1	NFX1-type zinc finger-co	K.GVSSNLFFVEHNFPEQEIQEGK#.S	7.62	4.37	1.74	0.57
Q8R151_ZNFX1_MOUSE	Znfx1	NFX1-type zinc finger-co	K.IQGSAGEISTSQEQLK#.A	4.20	2.88	1.46	0.69
Q8R151_ZNFX1_MOUSE	Znfx1	NFX1-type zinc finger-co	K.IVQALLTNK#.S	10.52	5.12	2.05	0.49
Q8R151_ZNFX1_MOUSE	Znfx1	NFX1-type zinc finger-co	R.LTYLVNLLM*R@.C	9.19	3.57	2.57	0.39
Q8R151_ZNFX1_MOUSE	Znfx1	NFX1-type zinc finger-co	K.VNIPFVR@.L	13.48	7.96	1.69	0.59
Q8R331_ZNHI1_MOUSE	Znhit1	Zinc finger HIT domain-c	R.QLEALENDNFQDDPHAGLPQLGK#.R	5.88	2.18	2.70	0.37
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	R.EESDGEYDEFGR@.K	35.85	15.31	2.34	0.43
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	R.ENVEYIER@EESDGEYDEFGR@.K	16.89	6.60	2.56	0.39
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	K.ESEGEEEDEDEDLSK#.Y	7.54	3.86	1.95	0.51
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	K.EVEDKESEGEEEDEDEDLSK.Y	124.37	46.31	2.69	0.37
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	R.TGYGGGFNER.E	75.94	23.66	3.21	0.31
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	K.YK#LDEDEDEDDADLSK#.Y	35.34	18.46	1.91	0.52
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	K.YK#LDEDEDEDDADLSK#YNLDASEEEDSNK#.K	6.59	1.97	3.35	0.30
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	K.YNLDASEEEDSNK#.K	9.50	3.74	2.54	0.39
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	R.ENVEYIER@.E	20.04	11.49	1.74	0.57
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	R.ENVEYIEREESDGEYDEFGR.K	2.60	2.38	1.09	0.91
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	K.ESEGEEEDEDEDLSK.Y	1.57	3.16	0.50	2.02
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	K.EVEDKESEGEEEDEDEDLSK.Y	6.78	8.58	0.79	1.27
Q9R020_ZRAB2_MOUSE	Zranb2	Zinc finger Ran-binding d	K.EVEDKESEGEEEDEDEDLSK.Y	11.62	6.06	1.92	0.52
Q5RJ54_ZSC26_MOUSE	Zscan26	Zinc finger and SCAN do	K.AFSLTSDLIR@.H	11.28	4.63	2.44	0.41
Q3UHH1_ZSWM8_MOUSE	Zswim8	Zinc finger SWIM domai	R.DGLVIPLVELSAK#.Q	12.07	4.35	2.77	0.36
Q3UHH1_ZSWM8_MOUSE	Zswim8	Zinc finger SWIM domai	K.LAYQESEVAALLK#.K	7.98	2.21	3.61	0.28
O54692_ZW10_MOUSE	Zw10	Centromere/kinetochor	R.DSVVLTLLK#.Q	13.27	7.95	1.67	0.60
O54692_ZW10_MOUSE	Zw10	Centromere/kinetochor	K.LQEYEEIIQSTEEFEK#.F	4.97	3.99	1.25	0.80
O54692_ZW10_MOUSE	Zw10	Centromere/kinetochor	R.LVLEVLQK#.Q	15.29	4.94	3.10	0.32
Q8R060_ZWILC_MOUSE	Zwilch	Protein zwilch homolog	K.R@HHVSAVTAR@.G	12.94	2.49	5.19	0.19
Q8R060_ZWILC_MOUSE	Zwilch	Protein zwilch homolog	R.AAEEFYAR@.L	8.87	1.34	6.60	0.15
Q8R060_ZWILC_MOUSE	Zwilch	Protein zwilch homolog	K.FLLVLADGIR@.T	18.05	6.24	2.89	0.35
Q9CQU5_ZWINT_MOUSE	Zwint	ZW10 interactor OS=Mu	K.EVLAEAAAILEPVGLQEEAELPAK#.I	4.93	3.76	1.31	0.76
Q62523_ZYX_MOUSE	Zyx	Zyxin OS=Mus musculus	R.GPLSQAPTPAPK#.F	12.94	7.58	1.71	0.59
Q62523_ZYX_MOUSE	Zyx	Zyxin OS=Mus musculus	K.EVEELEQLTQQLM*QDM*EHPQR@.Q	7.65	3.05	2.51	0.40
Q62523_ZYX_MOUSE	Zyx	Zyxin OS=Mus musculus	K.FSPGAPSGPGPQPNQK#.M	16.92	6.28	2.69	0.37
Q62523_ZYX_MOUSE	Zyx	Zyxin OS=Mus musculus	R.GPLSQAPTPAPK#.F	42.87	49.68	0.86	1.16
Q62523_ZYX_MOUSE	Zyx	Zyxin OS=Mus musculus	K.QHPQPPPAQNQNQVR@.S	12.87	4.98	2.59	0.39
Q62523_ZYX_MOUSE	Zyx	Zyxin OS=Mus musculus	K.VNPFR@PGDSEPPVAAGAQR@.A	32.13	8.30	3.87	0.26
Q6KAQ7_ZZZ3_MOUSE	Zzz3	ZZ-type zinc finger-conta	R.LLQTIAVLEAQR@.S	23.87	3.31	7.21	0.14
Q6KAQ7_ZZZ3_MOUSE	Zzz3	ZZ-type zinc finger-conta	R.SIAHPEEISSHSQVR@.S	7.88	1.39	5.66	0.18

Q6KAQ7_ZZZ3_MOUSE	Zzz3	ZZ-type zinc finger-contai	R.SQAVQDLESLGK#.H	25.49	6.84	3.72	0.27
Q6KAQ7_ZZZ3_MOUSE	Zzz3	ZZ-type zinc finger-contai	R.TPNLYIYSR@.K	14.47	4.40	3.29	0.30
Q6KAQ7_ZZZ3_MOUSE	Zzz3	ZZ-type zinc finger-contai	R.VVQLPEIM*WDQYTNSLGNFER@.E	4.10	3.88	1.06	0.95
Q8BZR9_CQ085_MOUSE		Uncharacterized protein	R.ASGAEEDDSELQR.A	5.51	3.22	1.71	0.58
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.AGVM*ALANLLQIQR@.H	30.65	13.81	2.22	0.45
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	R.HDDYLVM*LK#.A	28.18	19.02	1.48	0.67
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.HILGFDTGDAVLNEAAQILR@.L	76.59	28.37	2.70	0.37
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.INEAIVAVQAIIADPK#.T	23.95	11.97	2.00	0.50
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	R.LEYGDNAEK#.Y	28.62	15.08	1.90	0.53
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.NAEPLINLDVNNPDFK#.A	41.19	18.08	2.28	0.44
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	R.NFIVWLEDQK#.I	33.82	9.59	3.53	0.28
IGKC_MOUSE		Ig kappa chain C region O	K.DSTYSMSSTLTLTK.D	2.97	19.71	0.15	6.64
IGKC_MOUSE		Ig kappa chain C region O	R.QNGVLNSWTDQDSK.D	3.84	45.40	0.08	11.83
IGKC_MOUSE		Ig kappa chain C region O	K.WKIDGSER.Q	2.61	77.65	0.03	29.79
Q9CXL3_CG050_MOUSE		Uncharacterized protein	R.EAGIAATQTAK#.V	41.44	33.88	1.22	0.82
Q9CXL3_CG050_MOUSE		Uncharacterized protein	R.TSEAGPDKETASTLVQEASPELSPEER.R	22.41	18.16	1.23	0.81
Q9CXL3_CG050_MOUSE		Uncharacterized protein	K.VQTLPAK#PSAATLALEYLQGWAQK#.Q	25.37	19.71	1.29	0.78
KV2A7_MOUSE		Ig kappa chain V-II region	R.FSGSGSGTDFTLK.I	4.40	1673.63	0.00	379.95
KV2A7_MOUSE		Ig kappa chain V-II region	R.FSGVPDR.F	1.31	3700.41	0.00	2815.42
Q8VDP2_CX056_MOUSE		UPF0428 protein CXorf5	K.FSSVTVSTIDEEEEEIEAR@.E	5.57	3.96	1.41	0.71
Q8VDP2_CX056_MOUSE		UPF0428 protein CXorf5	R.LQELAELEAK#.K	13.84	7.19	1.92	0.52
Q8VDP2_CX056_MOUSE		UPF0428 protein CXorf5	K.NAPVTFIVDGAVVK#.F	24.32	16.98	1.43	0.70
Q05AH6_CK084_MOUSE		Uncharacterized protein	R.GLR@PLELPVTPVIEQGNK#.K	10.93	3.39	3.23	0.31
Q8BGA7_CG026_MOUSE		Uncharacterized protein	R.LGLILFDHM*VPLVEEINR@.L	11.76	2.65	4.43	0.23
Q9CYI0_NJMU_MOUSE		Protein Njmu-R1 OS=Mu	R.SGGINAETPSGDDFSLSLVDTNLPSEVEPELR@.S	3.81	2.13	1.79	0.56
Q9CYI0_NJMU_MOUSE		Protein Njmu-R1 OS=Mu	K.SVVAVLEEFMR@.E	6.55	2.17	3.01	0.33
Q80X32_CE024_MOUSE		UPF0461 protein C5orf2	R.AADQFDLYSSQQNK.Y	0.00	3.75	0.00	#DIV/0!
Q80X32_CE024_MOUSE		UPF0461 protein C5orf2	R.NIEIKDELK.K	2.36	8.33	0.28	3.53
Q9D937_CK098_MOUSE		Uncharacterized protein	K.AAM*EVEAPSK#.S	17.41	4.21	4.14	0.24
Q9D937_CK098_MOUSE		Uncharacterized protein	K.APQDVAM*EDLEDK#S.-	16.40	4.61	3.56	0.28
Q9D937_CK098_MOUSE		Uncharacterized protein	K.IK#APQDVAM*EDLEDK#S.-	15.76	5.02	3.14	0.32
Q9D937_CK098_MOUSE		Uncharacterized protein	R.QVVGAVIDEGLTTK#.H	56.02	13.57	4.13	0.24
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.AGVM*ALANLLQIQR.H	47.13	19.56	2.41	0.41
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.AGVM*ALANLLQIQR@.H	12.89	3.77	3.42	0.29
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.EGLPVALEK#.H	82.48	38.27	2.16	0.46
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	R.HDDYLVM*LK#.A	12.52	11.96	1.05	0.96
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.HILGFDTGDAVLNEAAQILR@.L	88.99	36.07	2.47	0.41
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.INEAIVAVQAIIADPK#.T	38.24	23.87	1.60	0.62
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	R.LEYGDNAEK#.Y	30.73	15.83	1.94	0.52
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	R.LLHIEELR@.E	12.99	9.91	1.31	0.76
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.NAEPLINLDVNNPDFK#.A	47.59	19.78	2.41	0.42
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	R.NFIVWLEDQK#.I	64.27	25.10	2.56	0.39
IGKC_MOUSE		Ig kappa chain C region O	R.QNGVLNSWTDQDSK.D	1.84	73.32	0.03	39.85
Q9CXL3_CG050_MOUSE		Uncharacterized protein	R.EAGIAATQTAK#.V	19.47	12.19	1.60	0.63
Q9CXL3_CG050_MOUSE		Uncharacterized protein	K.LDEAEPEDSGGSPGK#.V	20.83	14.67	1.42	0.70
Q9CXL3_CG050_MOUSE		Uncharacterized protein	R.LR@EAGIAATQTAK#.V	3.18	2.08	1.53	0.65
Q9CXL3_CG050_MOUSE		Uncharacterized protein	R.TSEAGPDK#ETASTLVQEASPELSPEER@.R	12.67	10.53	1.20	0.83
Q9CXL3_CG050_MOUSE		Uncharacterized protein	K.VQTLPAK#PSAATLALEYLQGWAQK#.Q	9.92	11.68	0.85	1.18
Q8VDP2_CX056_MOUSE		UPF0428 protein CXorf5	K.NAPVTFIVDGAVVK#.F	4.86	2.91	1.67	0.60
P10404_ENV1_MOUSE		MLV-related proviral Env	R.GLDLLFLK#.E	27.28	6.41	4.26	0.23
P10404_ENV1_MOUSE		MLV-related proviral Env	R.ISVVQALVLTQQYHQLK#.S	11.41	4.11	2.78	0.36
P10404_ENV1_MOUSE		MLV-related proviral Env	R.R@GLDLLFLK#.E	7.87	3.70	2.13	0.47
P10404_ENV1_MOUSE		MLV-related proviral Env	K.SLTSLSEVVLQNR@.R	12.88	3.44	3.74	0.27
Q3TYS2_CQ062_MOUSE		Uncharacterized protein	R.R@SDVEAIAK#.L	31.16	13.72	2.27	0.44
Q8BZR9_CQ085_MOUSE		Uncharacterized protein	R.ADSISTSNIK#.N	25.97	5.10	5.10	0.20
Q8BZR9_CQ085_MOUSE		Uncharacterized protein	K.AEAPAGPALGLPSPEVESGLER@.G	10.92	5.51	1.98	0.50
Q8BZR9_CQ085_MOUSE		Uncharacterized protein	R.AEVNLAQR@.N	25.04	5.74	4.36	0.23
Q8BZR9_CQ085_MOUSE		Uncharacterized protein	K.AGSFITGIDVTSK#.E	35.98	8.91	4.04	0.25
Q8BZR9_CQ085_MOUSE		Uncharacterized protein	R.ALINM*SSLPAQDK#.M	24.66	7.53	3.28	0.31
Q8BZR9_CQ085_MOUSE		Uncharacterized protein	R.ASGAEEDDSELQR@.A	24.73	8.67	2.85	0.35
Q8BZR9_CQ085_MOUSE		Uncharacterized protein	K.M*TM*YADEVESQLK#.S	16.59	4.61	3.60	0.28
Q9CQE8_CN166_MOUSE		UPF0568 protein C14orf	K.HILGFDTGDAVLNEAAQILR@.L	7.92	3.34	2.37	0.42
Q6PIU9_YJ005_MOUSE		Uncharacterized protein	R.ASDDLGEPDVFATAPFR@.S	12.53	3.44	3.64	0.27
Q6PIU9_YJ005_MOUSE		Uncharacterized protein	K.GSVAPSQM*DEVDVFSR@.A	9.85	3.06	3.21	0.31
Q6PIU9_YJ005_MOUSE		Uncharacterized protein	R.SSLVPADDVDIFSK#.A	13.11	3.31	3.96	0.25
IGKC_MOUSE		Ig kappa chain C region O	R.QNGVLNSWTDQDSK.D	1.97	25.06	0.08	12.69
Q8BGA7_CG026_MOUSE		Uncharacterized protein	R.LADELNPLNASQEIELALDR@.L	7.05	3.90	1.81	0.55
Q8BGA7_CG026_MOUSE		Uncharacterized protein	R.LGLILFDHM*VPLVEEINR@.L	9.61	2.62	3.67	0.27
Q8BGA7_CG026_MOUSE		Uncharacterized protein	R.QIIFSSLFSPQGNK#.A	12.41	3.78	3.28	0.30
SjGST_Schistosoma		japonicum (Blood fluke)	R.AEISM*LEGAVLDIR.Y	2.54	4.50	0.56	1.77
SjGST_Schistosoma		japonicum (Blood fluke)	R.LLLEYLEEK.Y	3.63	17.16	0.21	4.73
Q6PIU9_YJ005_MOUSE		Uncharacterized protein	R.AIYTPAQAQYPM*TGFAPQAGLPSHSVQVADHFDGNSPR@.G	5.73	6.67	0.86	1.16
Q6PIU9_YJ005_MOUSE		Uncharacterized protein	R.ASDDLGEPDVFATAPFR@.S	12.48	3.69	3.39	0.30
Q6PIU9_YJ005_MOUSE		Uncharacterized protein	R.SSLVPADDVDIFSK#.A	18.31	5.30	3.46	0.29
Q6PIU9_YJ005_MOUSE		Uncharacterized protein	K.TQNTLASDSLAR@.E	13.53	1.69	7.99	0.13
IGKC_MOUSE		Ig kappa chain C region O	K.DSTYSM*SSTLTLTK.D	6.80	131.93	0.05	19.41
IGKC_MOUSE		Ig kappa chain C region O	K.DSTYSMSSTLTLTK.D	1.14	13.45	0.08	11.79
KV2A7_MOUSE		Ig kappa chain V-II region	R.FSGSGSGTDFTLK.I	4.29	802.43	0.01	187.17
Q8BGA7_CG026_MOUSE		Uncharacterized protein	R.LADELNPLNASQEIELALDR@.L	12.19	4.24	2.87	0.35
Q8BGA7_CG026_MOUSE		Uncharacterized protein	R.LGLILFDHM*VPLVEEINR@.L	9.85	3.19	3.09	0.32
Q8BGA7_CG026_MOUSE		Uncharacterized protein	R.QIIFSSLFSPQGNK#.A	16.84	4.29	3.92	0.26
P84750_KVM5_MOUSE		Ig kappa chain V region M	R.YSGVPDR.F	1.39	30.64	0.05	22.12