Supplementary Table 4. Full list of peptides identified by mass spectrometry from SILAC experiment of wild type 3xMBT pulldown from WT (light) MEFs as compared to MLL1 KO (heavy) MEFs

ProteinId	GeneSymb	Descriptio	PeptideSequence	max_sn_heavy	max_sn_light	Ratio H_L	Ratio L_H
D3Z5T8_D3	4930407I1	Protein 493	K.NQENFR@DGNDADIQK.Q	13.09	24.79	0.53	1.89
H3BL88_H3	9930021J0	Protein 993	K.LALLSRHLR.E	1.37	28.92	0.05	21.13
Q9D2R0_A	Aacs	Acetoacety	K.GIADVPEWFR.G	6.73	7.32	0.92	1.09
Q9D2R0_A	Aacs	Acetoacety	R.IGITILGTGAK#.W	16.41	6.06	2.71	0.37
Q9D2R0_A	Aacs	Acetoacety	R.VVLFLK#.M	20.03	7.32	2.74	0.37
Q9D2R0_A	Aacs	Acetoacety	K.WLSVLEEK#.D	12.58	7.75	1.62	0.62
Q9D2R0_A	Aacs	Acetoacety	K.AQSYEYVYR.C	42.18	24.60	1.71	0.58
Q9D2R0_A	Aacs	Acetoacety	R.DIPELQDF.-	31.11	31.11	1.00	1.00
Q9D2R0_A	Aacs	Acetoacety	K.DMK#PVETHNLHTLHTILSTGSPLK#.A	9.81	5.89	1.66	0.60
Q9D2R0_A	Aacs	Acetoacety	R.FSQIQPK#.L	71.95	34.35	2.09	0.48
Q9D2R0_A	Aacs	Acetoacety	R.GAFSNPETLDLYR.D	14.40	27.18	0.53	1.89
Q9D2R0_A	Aacs	Acetoacety	K.GIADVPEWFR.G	16.31	30.68	0.53	1.88
Q9D2R0_A	Aacs	Acetoacety	R.IGITILGTGAK#.W	30.68	20.00	1.53	0.65
Q9D2R0_A	Aacs	Acetoacety	K.K#VEVAVK#.Q	43.81	23.29	1.88	0.53
Q9D2R0_A	Aacs	Acetoacety	R.LNYAENLLR.H	13.64	24.88	0.55	1.82
Q9D2R0_A	Aacs	Acetoacety	R.M*YDEVVDTSK#.G	24.34	11.20	2.17	0.46
Q9D2R0_A	Aacs	Acetoacety	R.NLGM*AVEAWDEEGK#.A	6.43	3.97	1.62	0.62
Q9D2R0_A	Aacs	Acetoacety	R.VALYVAR.E	12.22	31.99	0.38	2.62
Q9D2R0_A	Aacs	Acetoacety	K.VTFEELR.Q	17.32	31.29	0.55	1.81
Q9D2R0_A	Aacs	Acetoacety	R.VVLFLK#.M	45.56	21.01	2.17	0.46
Q9D2R0_A	Aacs	Acetoacety	K.AQSYEYVYR.C	14.47	32.31	0.45	2.23
Q9D2R0_A	Aacs	Acetoacety	R.DIPELQDF.-	40.76	40.76	1.00	1.00
Q9D2R0_A	Aacs	Acetoacety	R.FSQIQPK#.L	80.53	37.04	2.17	0.46
Q9D2R0_A	Aacs	Acetoacety	R.GAFSNPETLDLYR.D	29.11	33.43	0.87	1.15
Q9D2R0_A	Aacs	Acetoacety	K.GIADVPEWFR.G	15.02	30.97	0.48	2.06
Q9D2R0_A	Aacs	Acetoacety	R.IGITILGTGAK#.W	56.99	22.66	2.51	0.40
Q9D2R0_A	Aacs	Acetoacety	K.K#VEVAVK#.Q	54.73	17.52	3.12	0.32
Q9D2R0_A	Aacs	Acetoacety	R.LNYAENLLR.H	17.54	43.35	0.40	2.47
Q9D2R0_A	Aacs	Acetoacety	K.M*ASGHTFQPDLVK#.R	34.77	12.92	2.69	0.37
Q9D2R0_A	Aacs	Acetoacety	R.M*YDEVVDTSK#.G	32.37	12.95	2.50	0.40
Q9D2R0_A	Aacs	Acetoacety	R.NLGM*AVEAWDEEGK#.A	10.81	4.98	2.17	0.46
Q9D2R0_A	Aacs	Acetoacety	R.SDGTLNPNGVR.F	5.81	12.19	0.48	2.10
Q9D2R0_A	Aacs	Acetoacety	R.VALYVAR.E	24.36	49.26	0.49	2.02
Q9D2R0_A	Aacs	Acetoacety	R.VVLFLK#.M	57.59	28.69	2.01	0.50
Q9D2R0_A	Aacs	Acetoacety	R.VVLIPYVLPR.E	38.76	64.61	0.60	1.67
Q9D2R0_A	Aacs	Acetoacety	K.WLSVLEEK#.D	29.60	13.11	2.26	0.44
Q3UHJ0_A	Aak1	AP2-associa	K.AQATPSQPLQSSQPK#.Q	32.06	20.89	1.53	0.65
Q3UHJ0_A	Aak1	AP2-associa	R.ATVQPLPQAAGPSNQPGLLPSVSQPK#.A	14.88	10.26	1.45	0.69
Q3UHJ0_A	Aak1	AP2-associa	K.FQNPQAEGVNAVEDEIK#K#.Y	29.65	22.05	1.34	0.74
Q3UHJ0_A	Aak1	AP2-associa	R.ILSDVTHSAVFGVPASK#.S	26.47	16.58	1.60	0.63
Q3UHJ0_A	Aak1	AP2-associa	R.LTDPIPTTETSIAPR.Q	4.81	14.17	0.34	2.95
Q3UHJ0_A	Aak1	AP2-associa	K.STQLLQAAAAEASLNK#.S	13.69	9.22	1.49	0.67
Q3UHJ0_A	Aak1	AP2-associa	K.VQTTPPPTIQGQK#.V	11.07	6.16	1.80	0.56
Q3UHJ0_A	Aak1	AP2-associa	R.APEM*VNLYSGK#.I	17.60	8.99	1.96	0.51
Q3UHJ0_A	Aak1	AP2-associa	R.APEMVNLYSGK#.I	7.31	4.38	1.67	0.60
Q3UHJ0_A	Aak1	AP2-associa	K.AQATPSQPLQSSQPK#.Q	34.98	26.04	1.34	0.74
Q3UHJ0_A	Aak1	AP2-associa	R.ATVQPLPQAAGPSNQPGLLPSVSQPK#.A	20.59	12.87	1.60	0.63
Q3UHJ0_A	Aak1	AP2-associa	R.ILSDVTHSAVFGVPASK#.S	25.08	14.06	1.78	0.56
Q3UHJ0_A	Aak1	AP2-associa	R.LTDPIPTTETSIAPR.Q	6.12	20.28	0.30	3.31
Q3UHJ0_A	Aak1	AP2-associa	K.QPQAPPTPQQTPATQTQGLPTQAQATPQHQQQHLLK#.Q	11.21	5.50	2.04	0.49
Q3UHJ0_A	Aak1	AP2-associa	K.STQLLQAAAAEASLNK#.S	16.21	7.33	2.21	0.45
Q3UHJ0_A	Aak1	AP2-associa	K.TAVVVPQSQAQPATAPQAAAAQEPGQIQAPVR.Q	1.76	4.22	0.42	2.40
Q3TJ22_Q3	Aamp	Angio-asso	R.APVLLAGTADGNTWMWK.V	3.51	2.21	1.59	0.63
Q8BGQ7_S	Aars	Alanine--tR	K.ALNEALK#.L	78.40	20.24	3.87	0.26
Q8BGQ7_S	Aars	Alanine--tR	K.ASEWVQQVSGLM*DGK#.G	14.81	4.92	3.01	0.33
Q8BGQ7_S	Aars	Alanine--tR	K.ASEWVQQVSGLMDGK#.G	15.64	4.28	3.66	0.27
Q8BGQ7_S	Aars	Alanine--tR	R.AVFDETYPDPVR.V	10.00	22.53	0.44	2.25
Q8BGQ7_S	Aars	Alanine--tR	K.DIINEEEVQFLK#.T	13.72	11.19	1.23	0.82
Q8BGQ7_S	Aars	Alanine--tR	R.EIADLGEALATAVIPQWQK#.D	30.70	15.92	1.93	0.52
Q8BGQ7_S	Aars	Alanine--tR	R.ESDGVLK#PLPK#.K	18.66	8.84	2.11	0.47
Q8BGQ7_S	Aars	Alanine--tR	K.GAM*STQQIK#.K	6.07	4.84	1.25	0.80
Q8BGQ7_S	Aars	Alanine--tR	R.GGYVLHIGTIYGNLK#.V	41.63	14.21	2.93	0.34
Q8BGQ7_S	Aars	Alanine--tR	K.GLEATDDSPK#.Y	50.17	15.48	3.24	0.31
Q8BGQ7_S	Aars	Alanine--tR	R.IVAVTGAEAQK#.A	100.94	32.50	3.11	0.32
Q8BGQ7_S	Aars	Alanine--tR	K.K#DPEMVK#DIINEEEVQFLK#.T	10.21	5.69	1.79	0.56
Q8BGQ7_S	Aars	Alanine--tR	R.LFIDEPR.R	12.57	20.26	0.62	1.61
Q8BGQ7_S	Aars	Alanine--tR	R.LVSVLQNK#.M	64.38	16.17	3.98	0.25
Q8BGQ7_S	Aars	Alanine--tR	K.M*SNYDTDLFM*PYFEAIQK#.G	4.76	1.58	3.01	0.33
Q8BGQ7_S	Aars	Alanine--tR	R.NSSHAGAFVIVTEEAIAK#.G	39.43	13.31	2.96	0.34
Q8BGQ7_S	Aars	Alanine--tR	R.NSSHAGAFVIVTEEAIAK#.G	6.21	2.81	2.21	0.45
Q8BGQ7_S	Aars	Alanine--tR	K.QLIDSNPNQPLVILEM*ESGASAK#.A	8.01	3.43	2.33	0.43
Q8BGQ7_S	Aars	Alanine--tR	K.QLIDSNPNQPLVILEMESGASAK#.A	12.62	4.03	3.13	0.32
Q8BGQ7_S	Aars	Alanine--tR	R.SVLGEADQK#.G	48.28	17.05	2.83	0.35
Q8BGQ7_S	Aars	Alanine--tR	K.THSPQTSAM*LFTVDNEAGK#.I	17.78	3.62	4.92	0.20
Q8BGQ7_S	Aars	Alanine--tR	K.VGAEDADGIDM*AYR.V	8.15	9.72	0.84	1.19
Q8BGQ7_S	Aars	Alanine--tR	K.VGAEDADGIDMAYR.V	4.01	7.76	0.52	1.93
Q8BGQ7_S	Aars	Alanine--tR	K.ALNEALK#.L	39.50	7.95	4.97	0.20
Q8BGQ7_S	Aars	Alanine--tR	K.ASEWVQQVSGLM*DGK#.G	7.82	2.95	2.65	0.38
Q8BGQ7_S	Aars	Alanine--tR	R.GGYVLHIGTIYGNLK#.V	13.29	6.44	2.07	0.48
Q8BGQ7_S	Aars	Alanine--tR	R.LVSVLQNK#.M	44.33	14.43	3.07	0.33
Q8BGQ7_S	Aars	Alanine--tR	K.M*ALELLTQEFGIPVER.L	4.16	8.67	0.48	2.08
Q8BGQ7_S	Aars	Alanine--tR	K.QLIDSNPNQPLVILEM*ESGASAK#.A	8.30	4.50	1.85	0.54
Q3THG9_A	Aarsd1	Alanyl-tRN	R.SVIELDSPSVTAEQVAAIEQSVNQK#.I	6.90	4.57	1.51	0.66
Q9JKX4_AA	Aatf	Protein AAT	K.ALLTTNQLPQPDVFPVFK#.D	8.32	9.28	0.90	1.11
Q9JKX4_AA	Aatf	Protein AAT	R.DLDEEIFDDDDFYHQLLR.E	5.51	11.71	0.47	2.12
Q9JKX4_AA	Aatf	Protein AAT	R.SLVDLQEELLFQYPDTR.H	2.06	9.20	0.22	4.47
Q9JKX4_AA	Aatf	Protein AAT	R.VLGKPEPVPEPVAETLPGEPETLPQGPANAHLR.D	2.72	12.11	0.22	4.45
P61222_AB	Abce1	ATP-bindin	K.AIIK#PQYVDQIPK#.A	23.16	8.31	2.79	0.36
P61222_AB	Abce1	ATP-bindin	R.EGINIFLDGYVPTENLR.F	3.20	3.38	0.94	1.06
P61222_AB	Abce1	ATP-bindin	R.GSELQNYFTK#.I	16.43	6.05	2.71	0.37
P61222_AB	Abce1	ATP-bindin	K.ADIFM*FDEPSSYLDVK#.Q	5.67	1.94	2.92	0.34
P61222_AB	Abce1	ATP-bindin	R.VIVFDGVPSK#.N	10.73	3.35	3.21	0.31
P61222_AB	Abce1	ATP-bindin	K.ADIFM*FDEPSSYLDVK#.Q	9.00	5.03	1.79	0.56
P61222_AB	Abce1	ATP-bindin	K.AIIK#PQYVDQIPK#.A	20.52	9.55	2.15	0.47
P61222_AB	Abce1	ATP-bindin	K.VAETANEEEVK#K#.M	4.67	2.16	2.16	0.46
Q6P542_AB	Abcf1	ATP-bindin	K.AANAAENDFSVSQAEVSSR.Q	13.54	16.40	0.83	1.21
Q6P542_AB	Abcf1	ATP-bindin	K.ANDPYANLSK#.K	51.13	16.37	3.12	0.32
Q6P542_AB	Abcf1	ATP-bindin	R.ATGAAAAEAK#.A	18.38	12.94	1.42	0.70
Q6P542_AB	Abcf1	ATP-bindin	R.GNYM*TFK#.K	21.63	7.22	2.99	0.33
Q6P542_AB	Abcf1	ATP-bindin	R.GNYMTFK#.K	21.06	5.90	3.57	0.28

Q6P542_AI	Abcf1	ATP-bindin	K.IGFFNQQYAEQLHM*EETPTEYLQR.S	23.77	27.05	0.88	1.14
Q6P542_AI	Abcf1	ATP-bindin	K.IGFFNQQYAEQLHMEETPTEYLQR.S	11.84	9.87	1.20	0.83
Q6P542_AI	Abcf1	ATP-bindin	R.LQGQLEQGDDTAAEK#.L	17.53	7.72	2.27	0.44
Q6P542_AI	Abcf1	ATP-bindin	R.LQGQLEQGDDTAAEK#LEK#.V	186.76	50.04	3.73	0.27
Q6P542_AI	Abcf1	ATP-bindin	K.NLDFGIDM*DSR.I	6.78	8.17	0.83	1.20
Q6P542_AI	Abcf1	ATP-bindin	K.NQDEESQEPPELLK#.R	24.13	10.40	2.32	0.43
Q6P542_AI	Abcf1	ATP-bindin	K.QLSVPASDEEDEVPAPIPR.G	1.74	5.03	0.35	2.89
Q6P542_AI	Abcf1	ATP-bindin	K.QQPPEPEWIGDGEGTSPADK#.V	8.99	3.88	2.32	0.43
Q6P542_AI	Abcf1	ATP-bindin	R.RLQGQLEQGDDTAAEKLEK.V	15.82	24.14	0.66	1.53
Q6P542_AI	Abcf1	ATP-bindin	R.SFNLPYQDAR.K	28.55	52.48	0.54	1.84
Q6P542_AI	Abcf1	ATP-bindin	K.STLLLLLTGK#.L	145.89	40.74	3.58	0.28
Q6P542_AI	Abcf1	ATP-bindin	K.TFFEELAVEDK#.Q	23.55	10.15	2.32	0.43
Q6P542_AI	Abcf1	ATP-bindin	K.TFFEELAVEDK#QAGEEEK#LQK#.E	7.64	2.32	3.30	0.30
Q6P542_AI	Abcf1	ATP-bindin	K.AANAAENDFSVSQAEVSSR.Q	7.01	7.61	0.92	1.09
Q6P542_AI	Abcf1	ATP-bindin	K.ANDPYANLSK#.K	22.60	8.38	2.70	0.37
Q6P542_AI	Abcf1	ATP-bindin	K.AVAEEPPGLR.S	14.67	20.02	0.73	1.36
Q6P542_AI	Abcf1	ATP-bindin	K.IGFFNQQYAEQLHM*EETPTEYLQR.S	8.01	14.62	0.55	1.82
Q6P542_AI	Abcf1	ATP-bindin	R.LQGQLEQGDDTAAEK#.L	11.03	5.37	2.05	0.49
Q6P542_AI	Abcf1	ATP-bindin	R.LQGQLEQGDDTAAEK#LEK#.V	62.93	19.12	3.29	0.30
Q6P542_AI	Abcf1	ATP-bindin	K.NQDEESQEPPELLK#.R	13.76	6.12	2.25	0.44
Q6P542_AI	Abcf1	ATP-bindin	R.RLQGQLEQGDDTAAEKLEK.V	6.44	10.25	0.63	1.59
Q6P542_AI	Abcf1	ATP-bindin	K.SK#PAAADSEGEEEEEDTAK#.E	7.09	4.04	1.75	0.57
Q6P542_AI	Abcf1	ATP-bindin	K.STLLLLLTGK#.L	75.12	21.73	3.46	0.29
Q6P542_AI	Abcf1	ATP-bindin	K.TFFEELAVEDK#.Q	14.40	6.90	2.09	0.48
Q99LE6_AE	Abcf2	ATP-bindin	R.ETTGDGEVDLLTK#.E	10.92	6.36	1.72	0.58
Q99LE6_AE	Abcf2	ATP-bindin	K.YYTGNYDQYVK#.T	15.48	10.62	1.46	0.69
Q99LE6_AE	Abcf2	ATP-bindin	R.FHWEQDQIAHM*K#.N	19.60	13.80	1.42	0.70
Q99LE6_AE	Abcf2	ATP-bindin	R.FHWEQDQIAHMK#.N	19.14	11.95	1.60	0.62
Q99LE6_AE	Abcf2	ATP-bindin	K.IPPPVIM*VQNVSFK#.Y	11.88	7.89	1.51	0.66
Q99LE6_AE	Abcf2	ATP-bindin	K.IPPPVIMVQNVSFK#.Y	33.48	21.15	1.58	0.63
Q99LE6_AE	Abcf2	ATP-bindin	K.LLTGELLPTDGM*IR.K	6.74	23.96	0.28	3.56
Q99LE6_AE	Abcf2	ATP-bindin	K.LLTGELLPTDGMIR.K	7.81	22.50	0.35	2.88
Q99LE6_AE	Abcf2	ATP-bindin	K.LVDEEPQLTK#.R	71.04	48.52	1.46	0.68
Q99LE6_AE	Abcf2	ATP-bindin	K.SMLLSAIGK#.R	27.18	15.31	1.78	0.56
Q99LE6_AE	Abcf2	ATP-bindin	R.VALVGPNGAGK#.S	10.19	6.65	1.53	0.65
Q99LE6_AE	Abcf2	ATP-bindin	K.WPGDILAYK#.E	34.97	22.69	1.54	0.65
Q99LE6_AE	Abcf2	ATP-bindin	R.YHQHLQEQLDLDLSPLEYM*M*K#.C	6.19	1.85	3.34	0.30
Q99LE6_AE	Abcf2	ATP-bindin	K.YYTGNYDQYVK#.T	74.40	56.81	1.31	0.76
Q99LE6_AE	Abcf2	ATP-bindin	K.IPPPVIM*VQNVSFK#.Y	7.46	5.20	1.43	0.70
Q99LE6_AE	Abcf2	ATP-bindin	K.IPPPVIMVQNVSFK#.Y	8.66	8.53	1.02	0.98
Q99LE6_AE	Abcf2	ATP-bindin	K.LLTGELLPTDGM*IR.K	5.04	8.97	0.56	1.78
Q99LE6_AE	Abcf2	ATP-bindin	K.SM*LLSAIGK#.R	16.88	5.41	3.12	0.32
Q99LE6_AE	Abcf2	ATP-bindin	K.YYTGNYDQYVK#.T	28.41	17.17	1.65	0.60
Q8K268_AI	Abcf3	ATP-bindin	R.EYEAQQQYR.Q	2.52	9.96	0.25	3.95
Q8K268_AI	Abcf3	ATP-bindin	K.FSPPILQLDEVDFYYDPK.H	5.37	7.32	0.73	1.36
Q8K268_AI	Abcf3	ATP-bindin	K.TSNPLVLEEASASQAGSR.K	1.19	4.13	0.29	3.46
Q8VCR7_AI	Abhd14b	Alpha/beta	K.TPALIVYGDQDPM*GSSSFQHLK#.Q	3.22	1.89	1.71	0.59
Q8CBW3_A	Abi1	Abl interac	R.ALIESYQNLTR.V	6.34	7.64	0.83	1.21
Q8CBW3_A	Abi1	Abl interac	R.K#PIDYTVLDDVGHGVK#.W	50.68	11.58	4.37	0.23
Q8CBW3_A	Abi1	Abl interac	R.VTGLFPGNYVESIM*HYTD.-	5.23	5.23	1.00	1.00
Q8CBW3_A	Abi1	Abl interac	R.VTGLFPGNYVESIMHYTD.-	4.10	4.10	1.00	1.00
Q8CBW3_A	Abi1	Abl interac	R.K#PIDYTVLDDVGHGVK#.W	10.83	5.87	1.84	0.54
Q5SSL4_AB	Abr	Active brea	K.GQIQLDPQTVESK#.N	7.23	4.52	1.60	0.63
Q5SSL4_AB	Abr	Active brea	R.ISGVATDIQALK#.A	11.11	9.35	1.19	0.84
Q5SSL4_AB	Abr	Active brea	R.STLVLHDLLK#.H	11.63	8.59	1.35	0.74
Q921H8_TI	Acaa1a	3-ketoacyl-	R.LKPEQLGDISVGNVLEPGAGAVMAR.I	3.76	4.04	0.93	1.07
Q5SWU9_A	Acaca	Acetyl-CoA	K.ANAEYIK#.M	17.74	10.36	1.71	0.58
Q5SWU9_A	Acaca	Acetyl-CoA	K.AYVWDNNK#DLVEWLEK#.Q	18.16	5.88	3.09	0.32
Q5SWU9_A	Acaca	Acetyl-CoA	R.DFTVASPAEFVTR.F	11.07	19.66	0.56	1.78
Q5SWU9_A	Acaca	Acetyl-CoA	K.EASFEYLQNEGER.L	7.63	16.09	0.47	2.11
Q5SWU9_A	Acaca	Acetyl-CoA	K.FGAYIVDGLR.E	3.94	8.45	0.47	2.14
Q5SWU9_A	Acaca	Acetyl-CoA	R.FIIGSVSEDNSEDEISNLVK#.L	22.04	8.16	2.70	0.37
Q5SWU9_A	Acaca	Acetyl-CoA	R.FIIGSVSEDNSEDEISNLVK#.L	17.90	5.96	3.01	0.33
Q5SWU9_A	Acaca	Acetyl-CoA	R.FVVM*VTPEDLK#.A	29.26	14.42	2.03	0.49
Q5SWU9_A	Acaca	Acetyl-CoA	R.FVVMVTPEDLK#.A	19.68	6.37	3.09	0.32
Q5SWU9_A	Acaca	Acetyl-CoA	R.GQVLPAHTLLNTVDVELIYEGIK#.Y	9.80	11.63	0.84	1.19
Q5SWU9_A	Acaca	Acetyl-CoA	R.GSVLEPEGTVEIK#.F	46.15	23.42	1.97	0.51
Q5SWU9_A	Acaca	Acetyl-CoA	K.GVINDILDWK#.T	31.93	12.13	2.63	0.38
Q5SWU9_A	Acaca	Acetyl-CoA	R.IGSFGPQEDLLFLR.A	18.03	34.48	0.52	1.91
Q5SWU9_A	Acaca	Acetyl-CoA	R.IIEFVPTK#.A	45.29	20.59	2.20	0.45
Q5SWU9_A	Acaca	Acetyl-CoA	K.IIQQAGQVWFPDSAFK#.T	15.42	9.58	1.61	0.62
Q5SWU9_A	Acaca	Acetyl-CoA	R.ILNVPQDLYEK#.G	32.56	14.57	2.24	0.45
Q5SWU9_A	Acaca	Acetyl-CoA	R.IPVQAVWAGWGHASENPK#.L	8.33	4.83	1.73	0.58
Q5SWU9_A	Acaca	Acetyl-CoA	K.ITDIIGKEEGLGAENLR.G	13.13	22.66	0.58	1.73
Q5SWU9_A	Acaca	Acetyl-CoA	R.ITSENPDEGFKPSSGTVQELNFR.S	12.62	22.94	0.55	1.82
Q5SWU9_A	Acaca	Acetyl-CoA	R.LGGIPVGVVAVETR.T	26.09	43.27	0.60	1.66
Q5SWU9_A	Acaca	Acetyl-CoA	K.LLETESFQLNR.I	11.94	24.29	0.49	2.03
Q5SWU9_A	Acaca	Acetyl-CoA	R.LLLEDLVK#.K	44.50	18.65	2.39	0.42
Q5SWU9_A	Acaca	Acetyl-CoA	K.LPELLLK#.N	39.71	17.13	2.32	0.43
Q5SWU9_A	Acaca	Acetyl-CoA	R.LPGGNEIGM*VAWK#.M	19.28	10.96	1.76	0.57
Q5SWU9_A	Acaca	Acetyl-CoA	R.LPGGNEIGMVAWK#.M	12.68	5.90	2.15	0.47
Q5SWU9_A	Acaca	Acetyl-CoA	R.M*AALEVYVR.R	4.92	7.98	0.62	1.62
Q5SWU9_A	Acaca	Acetyl-CoA	K.SDM*NTVLNYIFSHAQVTK#.K	19.82	9.04	2.19	0.46
Q5SWU9_A	Acaca	Acetyl-CoA	K.SPEYPDGRDIIVIGNDITYR.I	3.76	4.87	0.77	1.29
Q5SWU9_A	Acaca	Acetyl-CoA	K.TLRDPSLPLLELQDIM*TSVSGR.I	2.25	10.67	0.21	4.74
Q5SWU9_A	Acaca	Acetyl-CoA	R.TVELSIPADPANLDSEAK#.I	37.94	17.01	2.23	0.45
Q5SWU9_A	Acaca	Acetyl-CoA	R.VDWQENDFSK#.R	14.39	7.80	1.84	0.54
Q5SWU9_A	Acaca	Acetyl-CoA	K.VEVGTEVTDYR.F	15.54	28.05	0.55	1.81
Q5SWU9_A	Acaca	Acetyl-CoA	K.VLIANNGIAAVK#.C	18.15	8.84	2.05	0.49
Q5SWU9_A	Acaca	Acetyl-CoA	R.VLQAELK#.I	43.06	18.57	2.32	0.43
Q5SWU9_A	Acaca	Acetyl-CoA	K.VNNADDFPNLFR.Q	2.83	7.02	0.40	2.48
Q5SWU9_A	Acaca	Acetyl-CoA	K.VQQAELHTGSLPQIQSTALR.G	15.86	30.98	0.51	1.95
P51174_A(	Acadl	Long-chain	R.VQPIYGGTNEIMK#.E	9.68	3.27	2.96	0.34
Q9DBL1_A(	Acadsb	Short/bran	K.YYASEVAGLTTSK#.C	6.12	1.57	3.89	0.26
P50544_A(	Acadvl	Very long-c	K.VPSENVLGEVGDGFK#.V	4.77	1.98	2.41	0.41
Q6ZQK5_A(	Acap2	Arf-GAP wit	R.DLAQYSSNDAVVETSLTK#.F	4.19	2.19	1.91	0.52
Q6ZQK5_A(	Acap2	Arf-GAP wit	R.SLTLDTWEPELLK#.L	11.67	41.77	0.28	3.58
Q6ZQK5_A(	Acap2	Arf-GAP wit	R.DLAQYSSNDAVVETSLTK#.F	6.15	4.10	1.50	0.67
Q6ZQK5_A(	Acap2	Arf-GAP wit	R.SLTLDTWEPELLK#.L	15.02	7.32	2.05	0.49
Q8QZT1_TI	Acat1	Acetyl-CoA	K.FASEITPITISVK#.G	16.40	3.79	4.33	0.23
Q8QZT1_TI	Acat1	Acetyl-CoA	R.TPIGSFLGSLASQPATK#.L	5.51	2.50	2.21	0.45
Q8CAY6_TI	Acat2	Acetyl-CoA	R.HGSNLEAMGK#.L	26.95	3.06	8.80	0.11
Q8CAY6_TI	Acat2	Acetyl-CoA	R.TAIGSFNGALSTVPVHEMGTTVIK#.E	13.47	1.62	8.33	0.12

Q8BMP6_G	Acbd3	Golgi resid	K.VLEPEAAEEALENGPK#.D	9.37	1.92	4.89	0.20
Q5EE38_AC	Acd	Adrenocort	K.AVFTVSGSLLHIPEGEEQILSSTGSSQK#.A	6.08	3.33	1.83	0.55
Q5EE38_AC	Acd	Adrenocort	R.ELILGSETLSSPR.T	1.66	5.19	0.32	3.13
Q9JIX8_AC	Acin1	Apoptotic	K.LLDDLFR.K	8.28	19.47	0.43	2.35
Q9JIX8_AC	Acin1	Apoptotic	K.SGVSITIDDPVR.T	3.54	14.21	0.25	4.02
Q9JIX8_AC	Acin1	Apoptotic	R.TGTLVEEAFWIDK#.I	28.46	19.10	1.49	0.67
Q9JIX8_AC	Acin1	Apoptotic	K.AEEQGAPRPLHPPPPPPVQPPPHPR.A	2.11	14.20	0.15	6.71
Q9JIX8_AC	Acin1	Apoptotic	R.GLLVDRPSETK.A	10.21	38.27	0.27	3.75
Q9JIX8_AC	Acin1	Apoptotic	K.GVQAGNSDTEGGQPGR.K	10.91	56.25	0.19	5.15
Q9JIX8_AC	Acin1	Apoptotic	K.ISVVSATK#.G	27.47	35.71	0.77	1.30
Q9JIX8_AC	Acin1	Apoptotic	R.K#ISVVSATK#.G	41.13	33.30	1.24	0.81
Q9JIX8_AC	Acin1	Apoptotic	K.K#PSISITTESLK#.S	42.44	45.69	0.93	1.08
Q9JIX8_AC	Acin1	Apoptotic	K.LLDDLFR.K	23.29	91.90	0.25	3.95
Q9JIX8_AC	Acin1	Apoptotic	R.RWGASTAATQK.K	3.92	13.99	0.28	3.56
Q9JIX8_AC	Acin1	Apoptotic	K.SAPLPLTVEEFAPAK#.G	17.58	9.99	1.76	0.57
Q9JIX8_AC	Acin1	Apoptotic	K.SGVSITIDDPVR.T	10.43	61.92	0.17	5.94
Q9JIX8_AC	Acin1	Apoptotic	R.TGTLVEEAFWIDK#.I	82.31	69.10	1.19	0.84
Q9JIX8_AC	Acin1	Apoptotic	R.TGTLVEEAFWIDK#IK#.S	41.96	38.42	1.09	0.92
Q9JIX8_AC	Acin1	Apoptotic	K.VTLGDTLTR.R	21.68	88.17	0.25	4.07
Q9JIX8_AC	Acin1	Apoptotic	R.WGASTAATQK.K	76.24	84.40	0.90	1.11
Q9JIX8_AC	Acin1	Apoptotic	K.APVVLQPEQIVSEEETPPPLLTK.E	19.68	27.85	0.71	1.42
Q9JIX8_AC	Acin1	Apoptotic	K.ETQIVSLPQEENEVK.S	18.42	26.81	0.69	1.46
Q9JIX8_AC	Acin1	Apoptotic	K.GVQAGNSDTEGGQPGR.K	6.45	27.72	0.23	4.30
Q9JIX8_AC	Acin1	Apoptotic	K.KPSISITTESLK.S	11.24	19.55	0.57	1.74
Q9JIX8_AC	Acin1	Apoptotic	K.LLDDLFR.K	34.20	36.90	0.93	1.08
Q9JIX8_AC	Acin1	Apoptotic	K.QFEDEEGEER.T	1.46	9.01	0.16	6.15
Q9JIX8_AC	Acin1	Apoptotic	K.SAPLPLTVEEFAPAK.G	44.21	66.28	0.67	1.50
Q9JIX8_AC	Acin1	Apoptotic	K.SGVSITIDDPVR.T	4.48	24.20	0.19	5.40
Q9JIX8_AC	Acin1	Apoptotic	K.SKLPEYSQTAEEEEDQETPSR.N	5.43	29.43	0.18	5.42
Q9JIX8_AC	Acin1	Apoptotic	R.VSDESVLPLAQK.S	32.14	42.51	0.76	1.32
Q9JIX8_AC	Acin1	Apoptotic	K.VTLGDTLTR.R	4.68	36.54	0.13	7.81
Q91V92_A	Acly	ATP-citrate	R.EAYPEEAYIADLDAK#.S	7.59	1.63	4.65	0.22
Q91V92_A	Acly	ATP-citrate	K.AFDSGIIPM*EFVNK#.M	17.71	2.30	7.68	0.13
Q91V92_A	Acly	ATP-citrate	K.DGVYILDLAAK#.V	19.76	2.96	6.68	0.15
Q91V92_A	Acly	ATP-citrate	R.FGGALDAAAK#.M	29.07	4.99	5.83	0.17
Q91V92_A	Acly	ATP-citrate	K.IGNTGGM*LDNILASK#.L	12.38	2.34	5.28	0.19
Q91V92_A	Acly	ATP-citrate	K.LGLVGVNLSLDGVK#.S	21.16	5.13	4.12	0.24
Q91V92_A	Acly	ATP-citrate	K.LLVGVDEK#.L	18.44	5.13	3.60	0.28
Q91V92_A	Acly	ATP-citrate	K.LTLLNPK#.G	23.80	3.74	6.36	0.16
Q91V92_A	Acly	ATP-citrate	R.TIAIIAEGIPEALTR.K	7.05	6.39	1.10	0.91
Q91V92_A	Acly	ATP-citrate	K.AFDSGIIPM*EFVNK#.M	31.21	4.23	7.38	0.14
Q91V92_A	Acly	ATP-citrate	K.AFDSGIIPMEFVNK#.M	13.85	2.86	4.84	0.21
Q91V92_A	Acly	ATP-citrate	K.DGVYILDLAAK#.V	35.67	5.67	6.29	0.16
Q91V92_A	Acly	ATP-citrate	R.EAYPEEAYIADLDAK#.S	16.68	4.58	3.64	0.27
Q91V92_A	Acly	ATP-citrate	R.EGDYVLFHHEGGVDVGDVDAK#.A	15.08	4.45	3.38	0.30
Q91V92_A	Acly	ATP-citrate	R.FGGALDAAAK#.M	60.30	9.04	6.67	0.15
Q91V92_A	Acly	ATP-citrate	K.IGNTGGM*LDNILASK#.L	22.09	4.54	4.87	0.21
Q91V92_A	Acly	ATP-citrate	K.LGLVGVNLSLDGVK#.S	25.90	5.51	4.70	0.21
Q9CQR4_A	Acot13	Acyl-coenz	K.TLAFASVDLTNK#.T	12.80	2.87	4.46	0.22
Q9CQR4_A	Acot13	Acyl-coenz	K.VTLVSAAPEK#.L	17.15	3.82	4.49	0.22
Q91V12_B	Acot7	Cytosolic a	K.ATLWYVPLSLK#.N	40.07	8.44	4.75	0.21
Q91V12_B	Acot7	Cytosolic a	K.TNIVTASVDAINFHDK#.I	23.70	3.99	5.95	0.17
Q91V12_B	Acot7	Cytosolic a	K.VLEVPPIVYLR.Q	9.07	10.09	0.90	1.11
Q91V12_B	Acot7	Cytosolic a	K.ATLWYVPLSLK#.N	14.70	5.57	2.64	0.38
Q9R0X4_A	Acot9	Acyl-coenz	R.DSENK#GPAFVNPLIPENK#EEEELFK#.Q	4.01	1.71	2.35	0.43
Q9R0X4_A	Acot9	Acyl-coenz	K.GPAFVNPLIPENK#EEEELFK#.Q	6.97	6.49	1.07	0.93
Q9R0X4_A	Acot9	Acyl-coenz	R.IAFSTSSLLK#.V	12.82	3.32	3.87	0.26
Q8VCW8_A	Acsf2	Acyl-CoA sy	R.GGENIYPAELEDFFLK#.H	11.69	4.26	2.74	0.36
Q8VCW8_A	Acsf2	Acyl-CoA sy	K.TQQYYDILK#.Q	10.98	9.90	1.11	0.90
Q9QUJ7_A	Acsl4	Long-chain	R.IGYSSPLTLSDQSSK#.I	6.54	4.98	1.31	0.76
Q9QXG4_A	Acss2	Acetyl-coe	K.IGPIATPDYIQNAPGLPK#.T	9.04	2.50	3.62	0.28
Q9QXG4_A	Acss2	Acetyl-coe	K.VAFYWEGNEPGETTK#.I	9.09	2.05	4.42	0.23
Q9QXG4_A	Acss2	Acetyl-coe	K.IGPIATPDYIQNAPGLPK#.T	7.97	4.49	1.77	0.56
Q9QXG4_A	Acss2	Acetyl-coe	K.VAFYWEGNEPGETTK#.I	5.54	2.90	1.91	0.52
P62737_A	Acta2	Actin, aorti	K.AGFAGDDAPR.A	465.69	1972.12	0.24	4.23
P62737_A	Acta2	Actin, aorti	R.AVFPSIVGRPR.H	19.53	242.77	0.08	12.43
P62737_A	Acta2	Actin, aorti	R.DLTDYLM*K#.I	685.85	663.77	1.03	0.97
P62737_A	Acta2	Actin, aorti	R.DLTDYLMK#.I	728.73	645.05	1.13	0.89
P62737_A	Acta2	Actin, aorti	K.DSYVGDEAQSK#.R	2514.21	2361.46	1.06	0.94
P62737_A	Acta2	Actin, aorti	K.DSYVGDEAQSKR.G	148.38	501.38	0.30	3.38
P62737_A	Acta2	Actin, aorti	K.EITALAPSTM*K#.I	1324.63	1383.62	0.96	1.04
P62737_A	Acta2	Actin, aorti	K.EITALAPSTMK#.I	1208.98	950.03	1.27	0.79
P62737_A	Acta2	Actin, aorti	R.GYSFVTTAER.E	9.49	34.54	0.27	3.64
P62737_A	Acta2	Actin, aorti	R.HQGVMVGMGQK#.D	265.50	226.64	1.17	0.85
P62737_A	Acta2	Actin, aorti	R.HQGVMVGMGQK.D	230.12	194.80	1.18	0.85
P62737_A	Acta2	Actin, aorti	R.HQGVM*VGM*GQK.D	471.90	449.53	1.05	0.95
P62737_A	Acta2	Actin, aorti	R.HQGVM*VGM*GQK.D	728.88	680.00	1.07	0.93
P62737_A	Acta2	Actin, aorti	R.HQGVMVGM*GQK#.D	355.71	339.52	1.05	0.95
P62737_A	Acta2	Actin, aorti	R.HQGVM*VGMGQK#.D	221.10	248.71	0.89	1.12
P62737_A	Acta2	Actin, aorti	K.IIAPPERK.Y	56.08	257.62	0.22	4.59
P62737_A	Acta2	Actin, aorti	K.SYELPDGQVITIGNER.F	239.31	1047.86	0.23	4.38
P62737_A	Acta2	Actin, aorti	K.YPIEHGIITNWDDM*EK.I	645.32	570.36	1.13	0.88
P62737_A	Acta2	Actin, aorti	K.YPIEHGIITNWDDM*EK#.I	123.99	119.82	1.03	0.97
P62737_A	Acta2	Actin, aorti	K.YPIEHGIITNWDDMEK#.I	537.36	455.56	1.18	0.85
P62737_A	Acta2	Actin, aorti	K.YPIEHGIITNWDDMEK.I	115.20	85.11	1.35	0.74
P62737_A	Acta2	Actin, aorti	K.AGFAGDDAPR.A	35.72	41.74	0.86	1.17
P62737_A	Acta2	Actin, aorti	R.DLTDYLM*K#.I	107.30	17.60	6.10	0.16
P62737_A	Acta2	Actin, aorti	R.DLTDYLMK#.I	14.75	3.42	4.32	0.23
P62737_A	Acta2	Actin, aorti	K.DSYVGDEAQSK#.R	40.57	11.44	3.55	0.28
P62737_A	Acta2	Actin, aorti	K.DSYVGDEAQSKR.G	5.92	7.86	0.75	1.33
P62737_A	Acta2	Actin, aorti	K.EITALAPSTM*K#.I	134.05	25.28	5.30	0.19
P62737_A	Acta2	Actin, aorti	K.EITALAPSTMK#.I	68.58	10.23	6.70	0.15
P62737_A	Acta2	Actin, aorti	K.SYELPDGQVITIGNER.F	69.11	56.48	1.22	0.82
P62737_A	Acta2	Actin, aorti	K.AGFAGDDAPR.A	206.36	753.82	0.27	3.65
P62737_A	Acta2	Actin, aorti	R.DLTDYLM*K#.I	355.93	280.76	1.27	0.79
P62737_A	Acta2	Actin, aorti	R.DLTDYLMK#.I	160.25	127.77	1.25	0.80
P62737_A	Acta2	Actin, aorti	K.DSYVGDEAQSK#.R	534.55	452.09	1.18	0.85
P62737_A	Acta2	Actin, aorti	K.DSYVGDEAQSKR.G	54.13	186.25	0.29	3.44
P62737_A	Acta2	Actin, aorti	K.EITALAPSTM*K#.I	487.59	445.37	1.09	0.91
P62737_A	Acta2	Actin, aorti	K.EITALAPSTMK#.I	254.03	206.55	1.23	0.81
P62737_A	Acta2	Actin, aorti	R.HQGVM*VGMGQK#.D	78.73	70.43	1.12	0.89
P62737_A	Acta2	Actin, aorti	R.HQGVMVGMGQK#.D	65.86	60.00	1.10	0.91
P62737_A	Acta2	Actin, aorti	R.HQGVM*VGM*GQK#.D	217.16	163.86	1.33	0.75

P62737_AC	Acta2	Actin, aorti	R.HQGVMVGM*GQK#.D	89.85	68.67	1.31	0.76
P62737_AC	Acta2	Actin, aorti	K.IIAPPERK.Y	34.91	126.21	0.28	3.61
P62737_AC	Acta2	Actin, aorti	K.SYELPDGQVITIGNER.F	108.49	420.28	0.26	3.87
P62737_AC	Acta2	Actin, aorti	R.VAPEEHPTLLTEAPLNPK#.A	15.43	17.76	0.87	1.15
P62737_AC	Acta2	Actin, aorti	K.YPIEHGIITNWDDM*EK#.I	242.22	187.94	1.29	0.78
P62737_AC	Acta2	Actin, aorti	K.YPIEHGIITNWDDM*EK.I	36.85	27.77	1.33	0.75
P62737_AC	Acta2	Actin, aorti	K.YPIEHGIITNWDDMEK#.I	31.87	25.95	1.23	0.81
P62737_AC	Acta2	Actin, aorti	K.AGFAGDDAPR.A	326.40	1072.08	0.30	3.28
P62737_AC	Acta2	Actin, aorti	R.DLTDYLM*K#.I	589.11	449.09	1.31	0.76
P62737_AC	Acta2	Actin, aorti	R.DLTDYLMK#.I	219.34	150.15	1.46	0.68
P62737_AC	Acta2	Actin, aorti	K.DSYVGDEAQSK#.R	875.32	631.27	1.39	0.72
P62737_AC	Acta2	Actin, aorti	K.DSYVGDEAQSKR.G	69.44	239.49	0.29	3.45
P62737_AC	Acta2	Actin, aorti	K.EITALAPSTM*K#.I	1082.81	775.91	1.40	0.72
P62737_AC	Acta2	Actin, aorti	K.EITALAPSTMK#.I	408.13	298.98	1.37	0.73
P62737_AC	Acta2	Actin, aorti	R.HQGVMVGMGQK#.D	41.79	56.79	0.74	1.36
P62737_AC	Acta2	Actin, aorti	R.HQGVM*VGM*GQK#.D	437.61	317.43	1.38	0.73
P62737_AC	Acta2	Actin, aorti	R.HQGVMVGM*GQK#.D	67.57	49.36	1.37	0.73
P62737_AC	Acta2	Actin, aorti	K.IIAPPER.K	237.90	980.78	0.24	4.12
P62737_AC	Acta2	Actin, aorti	K.IIAPPERK.Y	55.48	148.85	0.37	2.68
P62737_AC	Acta2	Actin, aorti	K.SYELPDGQVITIGNER.F	263.37	804.62	0.33	3.06
P62737_AC	Acta2	Actin, aorti	R.VAPEEHPTLLTEAPLNPK#.A	35.96	28.90	1.24	0.80
P62737_AC	Acta2	Actin, aorti	K.YPIEHGIITNWDDM*EK#.I	521.08	369.36	1.41	0.71
P62737_AC	Acta2	Actin, aorti	K.YPIEHGIITNWDDM*EK.I	47.03	35.50	1.33	0.75
P62737_AC	Acta2	Actin, aorti	K.YPIEHGIITNWDDMEK#.I	353.87	240.18	1.47	0.68
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTM*YPGIADR.M	89.09	361.00	0.25	4.05
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTM*YPGIADR.M	83.38	262.42	0.32	3.15
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTMYPGIADR.M	53.99	223.01	0.24	4.13
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTMYPGIADR.M	60.64	238.95	0.25	3.94
P60710_AC	Actb	Actin, cytop	R.GYSFTTTAER.E	419.40	1833.79	0.23	4.37
P60710_AC	Actb	Actin, cytop	K.IWHHTFYNELR.V	236.49	949.26	0.25	4.01
P60710_AC	Actb	Actin, cytop	R.KDLYANTVLSGGTTM*YPGIADR.M	61.45	256.55	0.24	4.18
P60710_AC	Actb	Actin, cytop	R.KDLYANTVLSGGTTMYPGIADR.M	31.31	134.88	0.23	4.31
P60710_AC	Actb	Actin, cytop	K.QEYDESGPSIVHR.K	179.59	852.20	0.21	4.75
P60710_AC	Actb	Actin, cytop	R.VAPEEHPVLLTEAPLNPK#.A	1328.94	1233.79	1.08	0.93
P60710_AC	Actb	Actin, cytop	R.VAPEEHPVLLTEAPLNPK#.A	195.40	149.01	1.31	0.76
P60710_AC	Actb	Actin, cytop	K.YPIEHGIVTNWDDM*EK.I	4.31	6.98	0.62	1.62
P60710_AC	Actb	Actin, cytop	K.YPIEHGIVTNWDDMEK#.I	19.22	23.70	0.81	1.23
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTM*YPGIADR.M	10.17	6.64	1.53	0.65
P60710_AC	Actb	Actin, cytop	R.GYSFTTTAER.E	38.61	28.19	1.37	0.73
P60710_AC	Actb	Actin, cytop	R.KDLYANTVLSGGTTM*YPGIADR.M	6.61	3.06	2.16	0.46
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTM*YPGIADR.M	50.05	186.81	0.27	3.73
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTMYPGIADR.M	18.12	61.41	0.30	3.39
P60710_AC	Actb	Actin, cytop	R.GYSFTTTAER.E	189.03	668.20	0.28	3.53
P60710_AC	Actb	Actin, cytop	K.IWHHTFYNELR.V	84.89	298.19	0.28	3.51
P60710_AC	Actb	Actin, cytop	R.KDLYANTVLSGGTTM*YPGIADR.M	18.24	60.49	0.30	3.32
P60710_AC	Actb	Actin, cytop	R.KDLYANTVLSGGTTMYPGIADR.M	3.22	29.31	0.11	9.10
P60710_AC	Actb	Actin, cytop	R.VAPEEHPVLLTEAPLNPK#.A	920.65	840.34	1.10	0.91
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTM*YPGIADR.M	97.31	308.34	0.32	3.17
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTMYPGIADR.M	25.45	82.28	0.31	3.23
P60710_AC	Actb	Actin, cytop	K.DLYANTVLSGGTTMYPGIADR.M	17.25	57.25	0.30	3.32
P60710_AC	Actb	Actin, cytop	R.GYSFTTTAER.E	278.39	875.55	0.32	3.15
P60710_AC	Actb	Actin, cytop	R.KDLYANTVLSGGTTM*YPGIADR.M	29.29	89.33	0.33	3.05
P60710_AC	Actb	Actin, cytop	R.KDLYANTVLSGGTTMYPGIADR.M	5.02	19.68	0.26	3.92
P60710_AC	Actb	Actin, cytop	K.QEYDESGPSIVHR.K	135.48	514.70	0.26	3.80
P60710_AC	Actb	Actin, cytop	R.VAPEEHPVLLTEAPLNPK#.A	1574.14	1164.56	1.35	0.74
P60710_AC	Actb	Actin, cytop	R.VAPEEHPVLLTEAPLNPK#.A	81.69	52.05	1.57	0.64
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	138.13	357.95	0.39	2.59
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	2.11	4.25	0.50	2.02
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	157.72	423.77	0.37	2.69
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	2.61	5.24	0.50	2.01
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.VAPDEHPILLTEAPLNPK.I	1328.94	1233.79	1.08	0.93
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3.81	2.78	1.37	0.73
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	78.16	220.49	0.35	2.82
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	71.01	167.71	0.42	2.36
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	19.26	49.43	0.39	2.57
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.VAPDEHPILLTEAPLNPK#.I	920.65	840.34	1.10	0.91
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	143.52	373.91	0.38	2.61
Q8BFZ3_AC	Actbl2	Beta-actin-l	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	24.79	67.12	0.37	2.71
Q9Z2N8_AC	Actl6a	Actin-like p	R.ENM*EAISPLK#.N	60.53	53.02	1.14	0.88
Q9Z2N8_AC	Actl6a	Actin-like p	K.LIANNTTVER.R	44.42	153.75	0.29	3.46
Q9Z2N8_AC	Actl6a	Actin-like p	K.QGGPTYYIDTNALR.V	9.96	35.07	0.28	3.52
Q9Z2N8_AC	Actl6a	Actin-like p	K.SEASLHPVLM*SEAPWNTR.A	8.69	28.88	0.30	3.32
Q9Z2N8_AC	Actl6a	Actin-like p	K.SEASLHPVLMSEAPWNTR.A	6.23	20.17	0.31	3.24
Q9Z2N8_AC	Actl6a	Actin-like p	R.STGLILDSGATHTTAIPVHDGYVLQQGIVK#.S	25.00	12.62	1.98	0.51
Q9Z2N8_AC	Actl6a	Actin-like p	K.VDFPTAIGVVLER.D	22.85	76.79	0.30	3.36
P57780_AC	Actn4	Alpha-actin	K.ALDFIASK#.G	27.60	18.83	1.47	0.68
P57780_AC	Actn4	Alpha-actin	R.ETTDTDTADQVIASFK#.V	8.67	5.21	1.66	0.60
P57780_AC	Actn4	Alpha-actin	R.FAIQDISVEETSAK#.E	33.71	24.03	1.40	0.71
P57780_AC	Actn4	Alpha-actin	K.GYEEWLLNEIR.R	15.21	8.28	1.84	0.54
P57780_AC	Actn4	Alpha-actin	K.LASDLLEWIR.R	13.12	24.48	0.54	1.87
P57780_AC	Actn4	Alpha-actin	K.LSGSNPYTTVTPQIINSK#.W	9.57	6.09	1.57	0.64
P57780_AC	Actn4	Alpha-actin	K.LVSIGAEEIVDGNAK#.M	28.86	16.63	1.74	0.58
P57780_AC	Actn4	Alpha-actin	R.M*APYQGPDAAPGALDYK.S	6.50	7.42	0.88	1.14
P57780_AC	Actn4	Alpha-actin	R.TINEVENQILTR.D	4.50	18.85	0.24	4.19
P57780_AC	Actn4	Alpha-actin	R.VGWEQLLTTIAR.T	8.97	51.76	0.17	5.77
P57780_AC	Actn4	Alpha-actin	K.ALDFIASK#.G	9.47	7.49	1.26	0.79
P57780_AC	Actn4	Alpha-actin	R.FAIQDISVEETSAK#.E	9.85	9.30	1.06	0.94
Q9QZB7_A	Actr10	Actin-relate	K.TAVVIDLGEAFTK#.C	8.08	8.02	1.01	0.99
Q9QZB7_A	Actr10	Actin-relate	R.DSVVEILFEQDNEEK#.S	5.34	5.35	1.00	1.00
Q9QZB7_A	Actr10	Actin-relate	K.FNIDGNNERPTPPPNVDYPLDGEK.I	2.97	4.95	0.60	1.66
Q9QZB7_A	Actr10	Actin-relate	K.TAVVIDLGEAFTK#.C	20.49	22.34	0.92	1.09
P61164_AC	Actr1a	Alpha-centr	K.AQYYLPDGSTIEIGPSR.F	12.25	35.74	0.34	2.92
P61164_AC	Actr1a	Alpha-centr	R.YPM*EHGIVK#.D	28.28	20.69	1.37	0.73
P61164_AC	Actr1a	Alpha-centr	K.AQYYLPDGSTIEIGPSR.F	1.96	6.50	0.30	3.32
P61164_AC	Actr1a	Alpha-centr	K.AQYYLPDGSTIEIGPSR.F	5.64	7.41	0.76	1.31
Q8R5C5_AC	Actr1b	Beta-centra	K.AGFAGDQIPK#.Y	121.47	84.58	1.44	0.70
Q8R5C5_AC	Actr1b	Beta-centra	K.DQLQTFSEEHPVLLTEAPLNPSK#.N	63.24	40.31	1.57	0.64
Q8R5C5_AC	Actr1b	Beta-centra	K.EGADFHTSAEFEVVR.T	3.07	10.89	0.28	3.54
Q8R5C5_AC	Actr1b	Beta-centra	K.ISAPQER.L	47.42	147.14	0.32	3.10
Q8R5C5_AC	Actr1b	Beta-centra	R.IWQYVYSK#.D	100.11	61.94	1.62	0.62
Q8R5C5_AC	Actr1b	Beta-centra	R.TLFSNIVLSGGSTLFK#.G	122.64	71.97	1.70	0.59
Q8R5C5_AC	Actr1b	Beta-centra	K.VQYTLPDGSTLDVGPAR.F	6.56	21.46	0.31	3.27
Q8R5C5_AC	Actr1b	Beta-centra	K.DQLQTFSEEHPVLLTEAPLNPSK#.N	5.55	3.63	1.53	0.65

Q8R5C5_A	Actr1b	Beta-centra	R.TLFSNIVLSGGSTLFK#.G	11.11	9.21	1.21	0.83
Q8R5C5_A	Actr1b	Beta-centra	R.IWQYVYSK#.D	13.09	8.78	1.49	0.67
Q8R5C5_A	Actr1b	Beta-centra	R.TLFSNIVLSGGSTLFK#.G	24.55	9.07	2.71	0.37
Q8R5C5_A	Actr1b	Beta-centra	R.VM*AGALEGDLFIGPK#.A	8.12	7.98	1.02	0.98
P61161_A	Actr2	Actin-relat	K.HLWDYTFGPEK#.L	21.94	6.13	3.58	0.28
P61161_A	Actr2	Actin-relat	K.ILLTEPPM*NPTK#.N	24.82	7.63	3.25	0.31
P61161_A	Actr2	Actin-relat	R.VLK#GDVEK#.L	16.63	5.58	2.98	0.34
P61161_A	Actr2	Actin-relat	K.HLWDYTFGPEK#.L	10.93	3.23	3.38	0.30
P61161_A	Actr2	Actin-relat	K.ILLTEPPM*NPTK#.N	15.34	4.99	3.07	0.33
P61161_A	Actr2	Actin-relat	K.ILLTEPPM*NPTK#.N	24.31	5.74	4.24	0.24
P61161_A	Actr2	Actin-relat	K.ILLTEPPMNPTK#.N	10.51	2.26	4.65	0.22
P61161_A	Actr2	Actin-relat	K.VGNIEIK#.D	38.23	7.25	5.27	0.19
Q99JY9_AR	Actr3	Actin-relat	K.EFNK#YDTDGSK#.W	9.74	1.43	6.81	0.15
Q99JY9_AR	Actr3	Actin-relat	R.FMEQVIFK#.Y	20.87	5.04	4.14	0.24
Q99JY9_AR	Actr3	Actin-relat	K.GVDDLDFFIGDEAIEK#PTYATK#.W	31.76	16.87	1.88	0.53
Q99JY9_AR	Actr3	Actin-relat	K.GVDDLDFFIGDEAIEK#PTYATK#.W	12.01	3.74	3.22	0.31
Q99JY9_AR	Actr3	Actin-relat	K.GVDDLDFFIGDEAIEK#PTYATK#.W	17.12	4.61	3.71	0.27
Q99MU3_	Adar	Double-stra	R.AIM*EM*PSFYSPTLPR.C	2.31	5.60	0.41	2.42
Q99MU3_	Adar	Double-stra	K.ALQEEAASSADDQSGGANTDSLDESM*APNK.I	9.23	7.60	1.21	0.82
Q99MU3_	Adar	Double-stra	R.DVTSVLIDLER.Q	24.69	10.15	2.43	0.41
Q99MU3_	Adar	Double-stra	R.SFQLQQIEFLK#.G	11.87	10.67	1.11	0.90
Q99MU3_	Adar	Double-stra	R.STHSAPAPTPTAVPEATR.S	5.78	25.06	0.23	4.34
Q99MU3_	Adar	Double-stra	R.YLNTNPVGGLLEYAR.S	13.49	5.94	2.27	0.44
Q99MU3_	Adar	Double-stra	K.ALQEEAASSADDQSGGANTDSLDESM*APNK#.I	13.15	9.78	1.34	0.74
Q99MU3_	Adar	Double-stra	K.ALQEEAASSADDQSGGANTDSLDESMAPNK#.I	4.81	2.31	2.08	0.48
Q99MU3_	Adar	Double-stra	R.DLLQLSYGEAK#.K	32.69	51.08	0.64	1.56
Q99MU3_	Adar	Double-stra	K.LIDQSGPPHEPK#.F	14.32	9.45	1.52	0.66
Q99MU3_	Adar	Double-stra	K.NSIFELAR.G	7.67	24.90	0.31	3.25
Q99MU3_	Adar	Double-stra	R.QGATPPIWYLTDK.K	16.50	14.95	1.10	0.91
Q99MU3_	Adar	Double-stra	R.STHSAPAPTPTAVPEATR.S	13.74	52.91	0.26	3.85
Q99MU3_	Adar	Double-stra	R.VLIGESEKAEQLGFAEVTPVTGASLR.R	2.86	11.04	0.26	3.86
Q99MU3_	Adar	Double-stra	R.YLNTNPVGGLLEYAR.S	14.00	35.31	0.40	2.52
Q9QYC0_A	Add1	Alpha-addu	R.GSDSIAYDK#GEK#.L	4.31	3.87	1.11	0.90
Q9QYC0_A	Add1	Alpha-addu	R.SPGTPAGEGSGSPPK#.W	12.71	9.06	1.40	0.71
Q9QYC0_A	Add1	Alpha-addu	R.TLASAGGPDNLVLLDPGK#.Y	10.05	7.57	1.33	0.75
Q9QYC0_A	Add1	Alpha-addu	R.TSTSAVPNLFVPLNTNPK#.E	9.21	6.93	1.33	0.75
Q9QYC0_A	Add1	Alpha-addu	R.TLASAGGPDNLVLLDPGK#.Y	7.79	6.69	1.16	0.86
Q9QYC0_A	Add1	Alpha-addu	R.TSTSAVPNLFVPLNTNPK#.E	7.88	5.23	1.51	0.66
Q9QYB5_A	Add3	Gamma-ad	R.GLSFSEATASTLVK#.V	12.51	9.22	1.36	0.74
Q9QYB5_A	Add3	Gamma-ad	K.VNIIGEVVDQGSTDLK#.I	8.65	4.84	1.79	0.56
Q9QYB5_A	Add3	Gamma-ad	R.GLSFSEATASTLVK#.V	8.34	8.93	0.93	1.07
Q9QYB5_A	Add3	Gamma-ad	K.VNIIGEVVDQGSTDLK#.I	9.47	3.85	2.46	0.41
A2BDX0_A	Adnp	Activity-de	K.NTTWEDVGLWDPSLTK.N	4.74	5.68	0.83	1.20
A2BDX0_A	Adnp	Activity-de	K.SVGQSYGVGQSVR.L	3.09	11.31	0.27	3.66
A2BDX0_A	Adnp	Activity-de	K.SYEALVQHVIEDHER.I	3.11	15.23	0.20	4.90
A2BDX0_A	Adnp	Activity-de	K.NTTWEDVGLWDPSLTK.N	4.04	4.81	0.84	1.19
A2BDX0_A	Adnp	Activity-de	K.ATVQDDTEQLK#.W	24.43	31.20	0.78	1.28
A2BDX0_A	Adnp	Activity-de	K.DQSQWENASENAER.L	2.96	13.57	0.22	4.58
A2BDX0_A	Adnp	Activity-de	R.HQVIQTVHPVEK.K	36.20	59.21	0.61	1.64
A2BDX0_A	Adnp	Activity-de	K.IPSDNLEEPVPK.V	21.94	34.52	0.64	1.57
A2BDX0_A	Adnp	Activity-de	R.LGLGGNAPVSIPQQSQSVK.Q	13.92	14.63	0.95	1.05
A2BDX0_A	Adnp	Activity-de	R.LNQSPGLAPVK.R	5.41	10.64	0.51	1.97
A2BDX0_A	Adnp	Activity-de	K.NTTWEDVGLWDPSLTK#.N	7.92	7.59	1.04	0.96
A2BDX0_A	Adnp	Activity-de	K.SPSVSQSQASR.V	3.13	23.85	0.13	7.61
A2BDX0_A	Adnp	Activity-de	K.SVGQSYGVGQSVR.L	9.36	34.95	0.27	3.73
A2BDX0_A	Adnp	Activity-de	R.TYEQM*EFPLLK.K	10.07	14.17	0.71	1.41
A2BDX0_A	Adnp	Activity-de	R.TYEQMEFPLLK#.K	9.19	10.91	0.84	1.19
A2BDX0_A	Adnp	Activity-de	K.VPAVANYIM*K#.I	10.05	12.47	0.81	1.24
A2BDX0_A	Adnp	Activity-de	K.ATVQDDTEQLK.W	13.94	20.73	0.67	1.49
A2BDX0_A	Adnp	Activity-de	K.IPSDNLEEPVPK.V	12.40	19.16	0.65	1.55
A2BDX0_A	Adnp	Activity-de	K.NTTWEDVGLWDPSLTK#.N	4.91	7.10	0.69	1.45
A2BDX0_A	Adnp	Activity-de	K.SPSVSQSQASR.V	4.18	15.60	0.27	3.73
A2BDX0_A	Adnp	Activity-de	K.SVGQSYGVGQSVR.L	3.02	22.80	0.13	7.54
Q9JKV1_A	Adrm1	Proteasom	R.LFFWM*QEPK#.T	16.85	3.26	5.16	0.19
Q9JKV1_A	Adrm1	Proteasom	R.SQSAAVTPSSSTSSAR.A	26.03	25.34	1.03	0.97
P46664_P	Adss	Adenylosu	K.SIYPTLEIDIEGELQQLK#.G	7.00	3.12	2.24	0.45
P46664_P	Adss	Adenylosu	R.VTVVLGAQWGDEGK#.G	4.16	1.60	2.60	0.38
Q80YS6_A	Afap1	Actin filam	K.ITQQGTDPLVLAVQSK#.E	9.74	6.14	1.59	0.63
Q8K2K6_A	Agfg1	Arf-GAP do	K.AGLQTADK#YAALANLDNIFSAGQGGDQGSGFGTTGK#.A	10.35	3.29	3.14	0.32
Q8K2K6_A	Agfg1	Arf-GAP do	K.GTPSQSPVVGR.S	20.01	42.21	0.47	2.11
Q8K2K6_A	Agfg1	Arf-GAP do	K.QIWLGLFDDR.S	1.65	10.05	0.16	6.08
Q8K2K6_A	Agfg1	Arf-GAP do	K.SISM*TTFTQQEIEFLQK#.H	7.16	4.80	1.49	0.67
Q8K2K6_A	Agfg1	Arf-GAP do	K.SISM*TTFTQQEIEFLQK.H	5.97	5.45	1.09	0.91
Q8K2K6_A	Agfg1	Arf-GAP do	K.SISMTTFTQQEIEFLQK#.H	14.95	9.66	1.55	0.65
Q8K2K6_A	Agfg1	Arf-GAP do	K.SISMTTFTQQEIEFLQK.H	9.31	8.14	1.14	0.87
Q8K2K6_A	Agfg1	Arf-GAP do	K.VVASVHASISGSSASSTSSTPEVK#PLK#.S	3.92	3.97	0.99	1.01
Q8K2K6_A	Agfg1	Arf-GAP do	K.YAALANLDNIFSAGQGGDQGSGFGTTGK#.A	17.35	8.79	1.97	0.51
Q8K2K6_A	Agfg1	Arf-GAP do	K.SISM*TTFTQQEIEFLQK#.H	2.78	1.67	1.66	0.60
Q80WC7_	Agfg2	Arf-GAP do	K.SISMTTFTEPEVLFLQSR.G	3.61	5.90	0.61	1.63
Q80WC7_	Agfg2	Arf-GAP do	K.VKEFLQEK.Y	15.66	12.02	1.30	0.77
A2ASQ1_A	Agrn	Agrin OS=	R.EGSLQVGNEAPVTGSSPLGATQLDTDGALWLGGLQK#.L	2.36	1.73	1.36	0.73
Q8CJF7_EL	Ahctf1	Protein ELY	K.ESVANTVADVESSGSTSSK.C	3.26	13.51	0.24	4.14
Q6PAL7_A	Ahdc1	AT-hook D	R.AFASTGLESGASGR.G	2.65	10.10	0.26	3.81
Q6PAL7_A	Ahdc1	AT-hook D	K.SGFLGPM*AEPHPEDTFTVTSL.-	3.41	3.41	1.00	1.00
Q6PAL7_A	Ahdc1	AT-hook D	K.VSSLSSSLSVEGK#.E	7.61	8.38	0.91	1.10
E9Q616_E	Ahnak	Protein Ah	R.AGAISASGPELEGAGHSK#.F	7.36	5.49	1.34	0.75
E9Q616_E	Ahnak	Protein Ah	R.HEVTEISNTDVETQPGK#.T	24.57	14.94	1.64	0.61
E9Q616_E	Ahnak	Protein Ah	K.IEGSITGPSVEIGTPDVDVHGLGGK#.L	6.71	3.42	1.96	0.51
E9Q616_E	Ahnak	Protein Ah	K.LK#GPQITGPSLEGDLGLK#.G	9.76	6.19	1.58	0.63
E9Q616_E	Ahnak	Protein Ah	R.LPSGSGPASPTTGSAVDIR.A	4.34	12.30	0.35	2.83
E9Q616_E	Ahnak	Protein Ah	R.SSEVVLSGDDEDYQR.I	3.17	9.79	0.32	3.09
E9Q616_E	Ahnak	Protein Ah	K.VGSLDVNVK#.A	37.16	18.67	1.99	0.50
E9Q616_E	Ahnak	Protein Ah	R.LRSEDGVEGDLGETQSR.T	1.28	13.50	0.09	10.57
E9Q616_E	Ahnak	Protein Ah	R.SEDGVEGDLGETQSR.T	3.39	11.33	0.30	3.34
E9Q616_E	Ahnak	Protein Ah	K.ADLDISGTK#.V	8.82	5.35	1.65	0.61
E9Q616_E	Ahnak	Protein Ah	K.EGDQIVGATIYFDNLQSGEVTQLLNTM*GHHTVGLK#.L	14.68	5.42	2.71	0.37
E9Q616_E	Ahnak	Protein Ah	R.EGVK#DIDITSPEFMIK#.I	12.97	5.31	2.45	0.41
E9Q616_E	Ahnak	Protein Ah	K.FGVSAGLDGQIPEVGLSVSAPESSVGHK#.G	9.90	5.58	1.77	0.56
E9Q616_E	Ahnak	Protein Ah	K.FSVPGVK#.G	11.92	10.44	1.14	0.88
E9Q616_E	Ahnak	Protein Ah	K.GGVDVILPNVEGK#.A	13.08	6.45	2.03	0.49
E9Q616_E	Ahnak	Protein Ah	K.GPQVSSSLNLDTSK#.L	6.94	4.13	1.68	0.59
E9Q616_E	Ahnak	Protein Ah	R.HEVTEISNTDVETQPGK#.T	67.86	43.60	1.56	0.64
E9Q616_E	Ahnak	Protein Ah	K.IEGSITGPSVEIGTPDVDVHGLGGK#.L	20.08	9.06	2.21	0.45

E9Q616_E9	Ahnak	Protein Ahr	R.ISM*ADVDLNVAAPK#.G	14.38	13.33	1.08	0.93
E9Q616_E9	Ahnak	Protein Ahr	K.LDISAPDLNLEGPEGK.L	9.19	8.30	1.11	0.90
E9Q616_E9	Ahnak	Protein Ahr	K.LKGPDINLPEVSVK.T	23.16	13.60	1.70	0.59
E9Q616_E9	Ahnak	Protein Ahr	K.LK#GPQITGPSLEGDLGLK#.G	33.94	24.45	1.39	0.72
E9Q616_E9	Ahnak	Protein Ahr	R.LPSGSGPASPTTGSAVDIR.A	5.76	11.85	0.49	2.06
E9Q616_E9	Ahnak	Protein Ahr	R.LRSEDGVEGDLGETQSR.T	4.11	22.92	0.18	5.58
E9Q616_E9	Ahnak	Protein Ahr	K.M*DISAPDVEVHGPEWNLK#.M	14.17	7.39	1.92	0.52
E9Q616_E9	Ahnak	Protein Ahr	R.SEDGVEGDLGETQSR.T	3.21	6.98	0.46	2.18
E9Q616_E9	Ahnak	Protein Ahr	R.SSEVVLSGDDEDYQR.I	10.09	25.31	0.40	2.51
E9Q616_E9	Ahnak	Protein Ahr	K.VDIDVPDVNIEGPDAK#.L	6.23	7.62	0.82	1.22
E9Q616_E9	Ahnak	Protein Ahr	R.VDIETPNLEGTLTGPK.I	30.42	17.14	1.77	0.56
E9Q616_E9	Ahnak	Protein Ahr	K.VEVSAPDVSIEGSEGK#.L	13.24	6.92	1.91	0.52
E9Q616_E9	Ahnak	Protein Ahr	K.VGSLDVNVK#.A	55.17	32.67	1.69	0.59
E9Q616_E9	Ahnak	Protein Ahr	K.VNVEAPNVNM*EGLGGK#.L	11.12	6.27	1.77	0.56
E9Q616_E9	Ahnak	Protein Ahr	K.VNVEAPNVNMEGLGGK#.L	13.10	9.94	1.32	0.76
E9Q616_E9	Ahnak	Protein Ahr	K.VQANLDTPDINIEGPEAK#.I	4.92	3.09	1.59	0.63
E9Q616_E9	Ahnak	Protein Ahr	R.VTAYTVDVTGR.E	8.32	22.85	0.36	2.75
E9Q616_E9	Ahnak	Protein Ahr	K.ADIDVSGPK#VDIDVPDVNIEGPEGK#.L	8.56	5.65	1.51	0.66
E9Q616_E9	Ahnak	Protein Ahr	K.ADLDISGTK#.V	35.78	24.74	1.45	0.69
E9Q616_E9	Ahnak	Protein Ahr	K.ADLDVSGPK#.V	203.66	131.96	1.54	0.65
E9Q616_E9	Ahnak	Protein Ahr	K.ADVDASLPEVEGGVK#.V	21.37	12.72	1.68	0.60
E9Q616_E9	Ahnak	Protein Ahr	K.ADVDISVPK#.L	74.72	40.31	1.85	0.54
E9Q616_E9	Ahnak	Protein Ahr	R.AEGEIK#VPDVELK#.S	61.37	50.74	1.21	0.83
E9Q616_E9	Ahnak	Protein Ahr	K.AEGPDVAVDLPK#.G	16.80	10.81	1.55	0.64
E9Q616_E9	Ahnak	Protein Ahr	K.AEGPEVDVNLPK#.A	300.04	218.34	1.37	0.73
E9Q616_E9	Ahnak	Protein Ahr	K.AEGPEVSLPK#.A	62.68	45.32	1.38	0.72
E9Q616_E9	Ahnak	Protein Ahr	K.AESPEM*EVNLPK#.S	25.57	15.03	1.70	0.59
E9Q616_E9	Ahnak	Protein Ahr	R.AGAISASGPELEGAGHSK#.F	143.50	97.42	1.47	0.68
E9Q616_E9	Ahnak	Protein Ahr	K.ANIDVSGPK#.V	149.62	94.12	1.59	0.63
E9Q616_E9	Ahnak	Protein Ahr	K.APDVQLNAPDVDVHGPEWNLK.M	17.13	16.48	1.04	0.96
E9Q616_E9	Ahnak	Protein Ahr	K.APEVDVQGPEWSLK#.M	27.83	23.60	1.18	0.85
E9Q616_E9	Ahnak	Protein Ahr	K.ASLGSLEGEVEAEASSPK#.G	8.86	8.37	1.06	0.95
E9Q616_E9	Ahnak	Protein Ahr	K.ATIDVSGPK#.L	58.00	39.94	1.45	0.69
E9Q616_E9	Ahnak	Protein Ahr	R.DDGVFVQEVM*QNSPAAR.T	25.57	9.51	2.69	0.37
E9Q616_E9	Ahnak	Protein Ahr	R.DDGVFVQEVMQNSPAAR.T	2.33	5.68	0.41	2.43
E9Q616_E9	Ahnak	Protein Ahr	K.DIDITSPEFMIK#.I	10.70	6.81	1.57	0.64
E9Q616_E9	Ahnak	Protein Ahr	R.EGVK#DIDITSPEFM*IK#.I	51.52	29.01	1.78	0.56
E9Q616_E9	Ahnak	Protein Ahr	K.FGM*PGFK#.A	37.60	23.29	1.61	0.62
E9Q616_E9	Ahnak	Protein Ahr	K.FGMPGFK#.A	16.27	10.32	1.58	0.63
E9Q616_E9	Ahnak	Protein Ahr	K.FGVSAGLDGQIPEVGLSVSAPESSVGHK#.G	15.61	12.19	1.28	0.78
E9Q616_E9	Ahnak	Protein Ahr	K.FK#MPEMNIK#.A	21.92	11.14	1.97	0.51
E9Q616_E9	Ahnak	Protein Ahr	K.FK#VPDVQFK#.T	17.80	16.27	1.09	0.91
E9Q616_E9	Ahnak	Protein Ahr	K.FQVTVPGAK#.V	73.55	45.79	1.61	0.62
E9Q616_E9	Ahnak	Protein Ahr	K.FSM*PGFK#.A	198.58	136.81	1.45	0.69
E9Q616_E9	Ahnak	Protein Ahr	K.FSMPGFK#.A	113.44	69.56	1.63	0.61
E9Q616_E9	Ahnak	Protein Ahr	K.FSM*PGFK#GEGAEVDVNLQK#.A	10.87	6.72	1.62	0.62
E9Q616_E9	Ahnak	Protein Ahr	K.FSM*PGFK#GEGPEVDVNLPK#.A	29.40	21.23	1.39	0.72
E9Q616_E9	Ahnak	Protein Ahr	K.FSM*PGFK#GEGPEVDVSLPK#.A	23.42	13.46	1.74	0.57
E9Q616_E9	Ahnak	Protein Ahr	K.FSMPGFK#GEGPEVDVSLPK#.A	17.77	19.46	0.91	1.10
E9Q616_E9	Ahnak	Protein Ahr	K.FSMPTLKGEGPDVDVSLPK.A	20.55	17.14	1.20	0.83
E9Q616_E9	Ahnak	Protein Ahr	K.FSVPGFK#.A	73.96	45.43	1.63	0.61
E9Q616_E9	Ahnak	Protein Ahr	K.FSVPGVK#.G	54.44	38.03	1.43	0.70
E9Q616_E9	Ahnak	Protein Ahr	K.GDVDVSLPK#.V	25.15	19.15	1.31	0.76
E9Q616_E9	Ahnak	Protein Ahr	K.GEGAEVDVNLQK#.A	43.45	24.47	1.78	0.56
E9Q616_E9	Ahnak	Protein Ahr	K.GEGPDVDVSLPK#.A	41.36	34.65	1.19	0.84
E9Q616_E9	Ahnak	Protein Ahr	K.GEGPELDVNMPK#.A	13.63	6.46	2.11	0.47
E9Q616_E9	Ahnak	Protein Ahr	K.GEGPEVDVNLPK#.A	52.80	43.22	1.22	0.82
E9Q616_E9	Ahnak	Protein Ahr	K.GEGPEVDVSLPK#.A	161.57	24.12	6.70	0.15
E9Q616_E9	Ahnak	Protein Ahr	K.GEYDVTVPR.A	7.72	36.41	0.21	4.71
E9Q616_E9	Ahnak	Protein Ahr	K.GGQTGLQGPGLSVSGPQGHLESESGK#.V	11.17	11.87	0.94	1.06
E9Q616_E9	Ahnak	Protein Ahr	K.GK#GGVDVILPNVEGK#.A	34.70	26.96	1.29	0.78
E9Q616_E9	Ahnak	Protein Ahr	K.GKGGVDVILPNVEGK.A	9.63	7.18	1.34	0.75
E9Q616_E9	Ahnak	Protein Ahr	K.GLEVDVK#.G	41.24	24.53	1.68	0.59
E9Q616_E9	Ahnak	Protein Ahr	R.GPDWHLK#.M	17.09	12.75	1.34	0.75
E9Q616_E9	Ahnak	Protein Ahr	K.GPGLDFEGPDAK#.L	13.17	9.82	1.34	0.75
E9Q616_E9	Ahnak	Protein Ahr	K.GPNVDM*SRPDIEIEGPEGK.L	2.01	4.91	0.41	2.44
E9Q616_E9	Ahnak	Protein Ahr	K.GPQVSSSLNLDTSK#.L	13.60	11.43	1.19	0.84
E9Q616_E9	Ahnak	Protein Ahr	K.GPSFNVASPESDFGVSLK#.G	8.08	8.96	0.90	1.11
E9Q616_E9	Ahnak	Protein Ahr	K.GPSLQGDLAVSGDIK#.C	18.11	6.23	2.91	0.34
E9Q616_E9	Ahnak	Protein Ahr	K.GSK#VDIDTPQVDVHGPDLK#.I	16.69	10.27	1.63	0.62
E9Q616_E9	Ahnak	Protein Ahr	R.HEVTEISNTDVETQPGK#.T	146.89	94.66	1.55	0.64
E9Q616_E9	Ahnak	Protein Ahr	R.HEVTEISNTDVETQPGK.T	24.83	17.72	1.40	0.71
E9Q616_E9	Ahnak	Protein Ahr	K.IEGEM*K#VPDVDIK#.G	37.33	25.67	1.45	0.69
E9Q616_E9	Ahnak	Protein Ahr	K.IEGSITGPSVEIGTPDVDVHGLGGK#.L	45.99	35.57	1.29	0.77
E9Q616_E9	Ahnak	Protein Ahr	K.IKAPSFSVSAPQVSIPDVNVNLK.G	3.82	5.65	0.68	1.48
E9Q616_E9	Ahnak	Protein Ahr	K.IK#GDIDVSVPK#.I	31.70	21.19	1.50	0.67
E9Q616_E9	Ahnak	Protein Ahr	K.IK#GDVPSVGLEGPNIDLQGPEGK#.I	14.73	13.86	1.06	0.94
E9Q616_E9	Ahnak	Protein Ahr	R.ISM*ADVDLNVAAPK#.G	53.02	34.43	1.54	0.65
E9Q616_E9	Ahnak	Protein Ahr	R.ISMADVDLNVAAPK#.G	22.13	29.99	0.74	1.36
E9Q616_E9	Ahnak	Protein Ahr	K.ISM*PDFDLHLK#.G	15.91	14.32	1.11	0.90
E9Q616_E9	Ahnak	Protein Ahr	K.ISM*PDIDLHLK#.S	11.36	8.25	1.38	0.73
E9Q616_E9	Ahnak	Protein Ahr	K.ISMPDIDLNLK#.G	27.09	20.07	1.35	0.74
E9Q616_E9	Ahnak	Protein Ahr	K.ISM*PDIDLNLKGPK.V	52.75	46.80	1.13	0.89
E9Q616_E9	Ahnak	Protein Ahr	K.ISM*PDVDFNLK#.G	21.04	12.74	1.65	0.61
E9Q616_E9	Ahnak	Protein Ahr	K.ISMPDVDFNLK.G	11.50	8.65	1.33	0.75
E9Q616_E9	Ahnak	Protein Ahr	K.ISM*PDVDLHIK#.G	90.28	62.28	1.45	0.69
E9Q616_E9	Ahnak	Protein Ahr	K.ISMPDVDLHIK#.G	87.78	54.57	1.61	0.62
E9Q616_E9	Ahnak	Protein Ahr	K.ISM*PDVDLHIKGPK.V	21.22	15.99	1.33	0.75
E9Q616_E9	Ahnak	Protein Ahr	K.ISM*PDVDLHIK#GPK#.V	30.15	17.20	1.75	0.57
E9Q616_E9	Ahnak	Protein Ahr	K.ISMPDVDLNIK#.G	16.79	8.67	1.94	0.52
E9Q616_E9	Ahnak	Protein Ahr	K.ISMPDVGLNLK#.G	17.71	10.85	1.63	0.61
E9Q616_E9	Ahnak	Protein Ahr	K.ISM*PDVSLNLK#.G	20.63	15.44	1.34	0.75
E9Q616_E9	Ahnak	Protein Ahr	K.ISMPDVSLNLK#.G	22.02	21.17	1.04	0.96
E9Q616_E9	Ahnak	Protein Ahr	K.LDANIPEVAVEGPEGK#.W	37.92	27.28	1.39	0.72
E9Q616_E9	Ahnak	Protein Ahr	K.LDIDVPNVDVQGPELHM*K#.M	23.42	15.67	1.49	0.67
E9Q616_E9	Ahnak	Protein Ahr	K.LDIETSDVSLEGPEGK#.L	74.55	51.31	1.45	0.69
E9Q616_E9	Ahnak	Protein Ahr	K.LDISAPDLNLEGPEGK#.L	82.84	59.68	1.39	0.72
E9Q616_E9	Ahnak	Protein Ahr	K.LDVNAPDIDVHGPEGK#.L	31.90	27.49	1.16	0.86
E9Q616_E9	Ahnak	Protein Ahr	K.LKGPDINLPEVSVK.T	85.04	60.12	1.41	0.71
E9Q616_E9	Ahnak	Protein Ahr	K.LK#GPQITGPSLEGDLGLK#.G	68.71	52.38	1.31	0.76
E9Q616_E9	Ahnak	Protein Ahr	K.LK#K#PDVDITAPK#.V	36.36	20.57	1.77	0.57
E9Q616_E9	Ahnak	Protein Ahr	R.LPSGSGPASPTTGSAVDIR.A	10.04	30.51	0.33	3.04
E9Q616_E9	Ahnak	Protein Ahr	R.LRSEDGVEGDLGETQSR.T	6.95	32.90	0.21	4.74

E9Q616_E9	Ahnak	Protein Ahr	K.M*DINAPDM*DVQGPDWHLK#.M	28.51	23.08	1.24	0.81
E9Q616_E9	Ahnak	Protein Ahr	K.MDINAPDM*DVQGPDWHLK#.M	14.49	11.04	1.31	0.76
E9Q616_E9	Ahnak	Protein Ahr	K.M*DINAPDMDVQGPDWHLK#.M	15.75	9.86	1.60	0.63
E9Q616_E9	Ahnak	Protein Ahr	K.M*DISAPDVEVHGPEWNLK#.M	36.20	26.97	1.34	0.75
E9Q616_E9	Ahnak	Protein Ahr	K.MPEMNIK#.A	15.55	12.80	1.22	0.82
E9Q616_E9	Ahnak	Protein Ahr	K.MPSLEVSVPK#.I	7.62	5.54	1.37	0.73
E9Q616_E9	Ahnak	Protein Ahr	K.SDIDVSGPNVDVK#.V	60.49	34.99	1.73	0.58
E9Q616_E9	Ahnak	Protein Ahr	K.SDIDVSGPNVDVK#VPDVNIEGPEGK#.L	8.65	8.19	1.06	0.95
E9Q616_E9	Ahnak	Protein Ahr	R.SEDGVEGDLGETQSR.T	7.22	19.50	0.37	2.70
E9Q616_E9	Ahnak	Protein Ahr	K.TPTVDVTVPEAELNVDSPEINIGGK#.S	5.46	4.20	1.30	0.77
E9Q616_E9	Ahnak	Protein Ahr	K.VDIDVPDLDIEGPEGK#.L	61.38	36.74	1.67	0.60
E9Q616_E9	Ahnak	Protein Ahr	K.VDIDVPDVDVHGPDWHLK#.M	83.94	79.61	1.05	0.95
E9Q616_E9	Ahnak	Protein Ahr	K.VDIDVPDVNIEGPDAK#.L	164.70	127.81	1.29	0.78
E9Q616_E9	Ahnak	Protein Ahr	K.VDIDVPDVNIEGPDTK#.L	33.47	25.75	1.30	0.77
E9Q616_E9	Ahnak	Protein Ahr	K.VDIDVPDVNIEGPEGK#.L	164.70	127.81	1.29	0.78
E9Q616_E9	Ahnak	Protein Ahr	K.VDIDVPDVNVEGPDM*K#.V	6.52	4.39	1.48	0.67
E9Q616_E9	Ahnak	Protein Ahr	K.VDIEAPDVSIEGPEGK#.L	53.43	45.44	1.18	0.85
E9Q616_E9	Ahnak	Protein Ahr	R.VDIETPNLEGTLTGPK#.I	76.94	55.18	1.39	0.72
E9Q616_E9	Ahnak	Protein Ahr	K.VDINAPDVDVQGPDWHLK#.M	29.89	22.83	1.31	0.76
E9Q616_E9	Ahnak	Protein Ahr	K.VDINAPDVDVR.G	25.63	81.01	0.32	3.16
E9Q616_E9	Ahnak	Protein Ahr	K.VDINAPEVEVQGK.V	38.85	33.24	1.17	0.86
E9Q616_E9	Ahnak	Protein Ahr	R.VDLK#GPEVDISAPK#.V	20.89	17.42	1.20	0.83
E9Q616_E9	Ahnak	Protein Ahr	K.VEANVQAGAGEGK#WEESEVK#.L	17.23	10.90	1.58	0.63
E9Q616_E9	Ahnak	Protein Ahr	K.VEAPDVEVHGPDWHLK#.M	77.08	48.68	1.58	0.63
E9Q616_E9	Ahnak	Protein Ahr	K.VEGDIK#GPEVDIK#GPK#.V	13.51	10.15	1.33	0.75
E9Q616_E9	Ahnak	Protein Ahr	K.VEGDLK#GPDIDIK#.G	48.70	30.30	1.61	0.62
E9Q616_E9	Ahnak	Protein Ahr	K.VEGEIK#VPEVDIK#.G	115.33	89.01	1.30	0.77
E9Q616_E9	Ahnak	Protein Ahr	K.VEVSAPDVSIEGSEGK#.L	40.82	29.63	1.38	0.73
E9Q616_E9	Ahnak	Protein Ahr	K.VGIDAPDVEVHGPDWHLK#.M	78.95	47.76	1.65	0.60
E9Q616_E9	Ahnak	Protein Ahr	K.VGSLDVNVK#.A	115.94	63.22	1.83	0.55
E9Q616_E9	Ahnak	Protein Ahr	K.VK#GDLDAAGPNLEGDFK#GPK#.V	8.19	5.66	1.45	0.69
E9Q616_E9	Ahnak	Protein Ahr	K.VK#GDM*DVTVPK#.I	33.88	22.92	1.48	0.68
E9Q616_E9	Ahnak	Protein Ahr	K.VK#GDMDVTVPK#.I	52.87	34.61	1.53	0.65
E9Q616_E9	Ahnak	Protein Ahr	K.VKGDVDM*SLPK.V	8.53	7.94	1.07	0.93
E9Q616_E9	Ahnak	Protein Ahr	K.VK#GDVDVSLPK#.V	85.03	60.35	1.41	0.71
E9Q616_E9	Ahnak	Protein Ahr	K.VKGDVDVTVPK.L	216.37	143.95	1.50	0.67
E9Q616_E9	Ahnak	Protein Ahr	K.VK#GEYDVTMPK#.L	16.36	7.33	2.23	0.45
E9Q616_E9	Ahnak	Protein Ahr	K.VNVEAPNVNM*EGLGGK#.L	28.76	18.55	1.55	0.64
E9Q616_E9	Ahnak	Protein Ahr	K.VPDVDIK#.G	54.14	32.05	1.69	0.59
E9Q616_E9	Ahnak	Protein Ahr	K.VPDVNIEGPEGK#.L	32.70	109.04	0.30	3.33
E9Q616_E9	Ahnak	Protein Ahr	K.VQANLDTPDINIEGPEAK#.I	9.51	12.58	0.76	1.32
E9Q616_E9	Ahnak	Protein Ahr	K.VQTPEVDVK#.L	29.78	20.63	1.44	0.69
E9PYB0_E9	Ahnak2	Protein Ahr	R.FGM*TSGQSPDTSEQK#.G	3.29	1.51	2.18	0.46
E9PYB0_E9	Ahnak2	Protein Ahr	K.VEADVAPPQVQGDLK#.T	12.70	2.95	4.30	0.23
F7DBB3_F7	Ahnak2	Protein Ahr	R.FSFPAPSSEADVFFPVVR.E	2.75	8.28	0.33	3.02
F7DBB3_F7	Ahnak2	Protein Ahr	K.SQTQVISIPLEAEEK#.A	7.12	4.89	1.46	0.69
E9PYB0_E9	Ahnak2	Protein Ahr	K.FKM*PSFGVSAPGKPSLEASLEVGAPK.V	10.93	6.31	1.73	0.58
E9PYB0_E9	Ahnak2	Protein Ahr	K.GEVSAPDLEVSLPGVEVDIQAPGAK#.L	38.37	20.35	1.89	0.53
E9PYB0_E9	Ahnak2	Protein Ahr	K.LEGELALADKDVAAK.D	272.68	112.28	2.43	0.41
E9PYB0_E9	Ahnak2	Protein Ahr	K.LPEGQLPEAELPAAK#.A	12.32	6.25	1.97	0.51
E9PYB0_E9	Ahnak2	Protein Ahr	K.LPEGQLPEAELPAAQAAAAAGAGLK#.G	328.97	172.31	1.91	0.52
E9PYB0_E9	Ahnak2	Protein Ahr	K.LPEGQLPEAELPAAQAAAGAGLK#.G	14.94	11.82	1.26	0.79
E9PYB0_E9	Ahnak2	Protein Ahr	K.M*PSFGVSAPGK#PSLEASLEVGAPK#.V	13.63	10.49	1.30	0.77
E9PYB0_E9	Ahnak2	Protein Ahr	K.MPSFGVSAPGK#PSLEASLEVGAPK#.V	19.32	11.75	1.64	0.61
E9PYB0_E9	Ahnak2	Protein Ahr	K.TPDLSVQLPSADLELK#.A	48.46	25.82	1.88	0.53
E9PYB0_E9	Ahnak2	Protein Ahr	K.TPDLSVQLR.S	6.27	16.88	0.37	2.69
E9PYB0_E9	Ahnak2	Protein Ahr	K.VDLK#GPHVDLK#.G	63.09	33.18	1.90	0.53
E9PYB0_E9	Ahnak2	Protein Ahr	K.VEADVAPPQVQGDLK#.T	188.12	106.63	1.76	0.57
E9PYB0_E9	Ahnak2	Protein Ahr	K.VQM*PSLK#.M	69.79	116.62	0.60	1.67
F7DBB3_F7	Ahnak2	Protein Ahr	R.LGEQEATQK#.S	6.94	5.05	1.37	0.73
F7DBB3_F7	Ahnak2	Protein Ahr	K.SQTQVISIPLEAEEK#.A	14.25	5.22	2.73	0.37
F7CVJ5_F7	Ahnak2	Protein Ahr	K.LPEGQLPEAELPAAQAAAAGAGLK#.G	32.13	20.95	1.53	0.65
Q8BK64_AI	Ahsa1	Activator o	R.EAVGIYISTLK#.T	27.85	10.07	2.77	0.36
Q8BK64_AI	Ahsa1	Activator o	K.ETFLTSPEELYR.V	6.61	9.18	0.72	1.39
Q8BK64_AI	Ahsa1	Activator o	R.VFTTQELVQAFTHAPAALEADR.G	11.80	16.88	0.70	1.43
P31230_AI	Aimp1	Aminoacyl	K.GAEADQIIEYLK#.Q	117.17	24.89	4.71	0.21
P31230_AI	Aimp1	Aminoacyl	K.GAEADQIIEYLK#.Q	12.85	13.52	0.95	1.05
Q8R010_AI	Aimp2	Aminoacyl	R.FLFSLFGQK#.H	36.22	13.60	2.66	0.38
Q8R010_AI	Aimp2	Aminoacyl	R.VLSTVHTHSSVK#.N	18.38	4.55	4.04	0.25
Q8R010_AI	Aimp2	Aminoacyl	R.FLFSLFGQK#.H	38.50	7.36	5.23	0.19
Q8R010_AI	Aimp2	Aminoacyl	K.AAVDGLSK#.M	60.34	34.09	1.77	0.56
Q8R010_AI	Aimp2	Aminoacyl	K.M*IHTPDADLDVTNILQADEPTTLATNTLDLNSVLGK#.D	33.06	7.36	4.49	0.22
Q8R010_AI	Aimp2	Aminoacyl	K.NVPENLVK#.C	36.82	4.60	8.00	0.12
Q8R010_AI	Aimp2	Aminoacyl	K.TTSPATDAGHVQETSEPSLQALESR.Q	13.97	11.06	1.26	0.79
O08915_AI	Aip	AH recepto	K.AHAAVWNAQEAQADFAK#.V	26.62	10.96	2.43	0.41
O08915_AI	Aip	AH recepto	R.GELPDFQDGTK#.A	34.08	15.37	2.22	0.45
Q9R0Y5_KA	Ak1	Adenylate k	K.IIFVVGGPGSGK#.G	16.35	8.04	2.03	0.49
Q9WTP6_K	Ak2	Adenylate k	K.LVSDEM*VVELIEK#.N	13.22	6.66	1.99	0.50
Q9WTP7_K	Ak3	GTP:AMP p	R.VYNIEFNPPK#.T	5.76	2.23	2.59	0.39
O88845_AI	Akap10	A-kinase an	K.SIEQDAVNTFTK#.Y	7.29	10.40	0.70	1.43
O88845_AI	Akap10	A-kinase an	K.SIEQDAVNTFTK#.Y	6.67	5.12	1.30	0.77
Q9WTQ5_A	Akap12	A-kinase an	K.AEVGQEGEAGQFDGEK#.V	20.13	8.40	2.40	0.42
Q9WTQ5_A	Akap12	A-kinase an	K.ALEK#VEEVEEDSEVLATEK#.E	11.14	5.11	2.18	0.46
Q9WTQ5_A	Akap12	A-kinase an	R.AQENVELPQLK#.G	24.43	24.60	0.99	1.01
Q9WTQ5_A	Akap12	A-kinase an	K.DITAEATPALAQTLPGGK#.D	8.43	4.01	2.10	0.48
Q9WTQ5_A	Akap12	A-kinase an	R.DVLEPTQALAAGAVPILAK#.A	21.34	8.64	2.47	0.40
Q9WTQ5_A	Akap12	A-kinase an	K.GAVYVSEELSK#.T	32.66	15.60	2.09	0.48
Q9WTQ5_A	Akap12	A-kinase an	K.GPSEAPQEAEAEEGATSDGEK#.K	12.97	5.54	2.34	0.43
Q9WTQ5_A	Akap12	A-kinase an	K.IVQSVIQTAVDQFAR.T	2.62	4.64	0.56	1.77
Q9WTQ5_A	Akap12	A-kinase an	K.IVQSVIQTAVDQFAR.T	3.80	6.27	0.61	1.65
Q9WTQ5_A	Akap12	A-kinase an	K.K#DEGEGAEASVGAGDHQEPGVETVGESASK#.E	11.66	5.45	2.14	0.47
Q9WTQ5_A	Akap12	A-kinase an	R.LSADYEK#VELPLEDQVGDLEALSEK#.C	11.48	2.82	4.07	0.25
Q9WTQ5_A	Akap12	A-kinase an	K.LSETGGYGTLQHGEDTVPQGPESQAESIPIIVTPAPESILHSDLQR.E	4.61	4.36	1.06	0.95
Q9WTQ5_A	Akap12	A-kinase an	R.QTQAVLQAVADK#.V	12.63	6.22	2.03	0.49
Q9WTQ5_A	Akap12	A-kinase an	K.VELPLEDQVGDLEALSEK#.C	5.45	5.97	0.91	1.10
Q9WTQ5_A	Akap12	A-kinase an	K.VELPLEDQVGDLEALSEK#.C	10.04	8.42	1.19	0.84
O54931_AI	Akap2	A-kinase an	R.DGEFTLTTLK#K#.E	11.24	9.07	1.24	0.81
O54931_AI	Akap2	A-kinase an	R.STASLLATQESDVMVGPFK.L	4.26	3.97	1.07	0.93
O54931_AI	Akap2	A-kinase an	K.YSEAAELR.S	4.07	26.50	0.15	6.51
Q9DBR0_AI	Akap8	A-kinase an	R.GGISSGGEGVQDR.D	15.87	59.41	0.27	3.74
Q9DBR0_AI	Akap8	A-kinase an	K.LPDKTVEFLQEYIINR.N	8.60	21.29	0.40	2.48
Q9DBR0_AI	Akap8	A-kinase an	K.QFPLYEEPDAK#.L	16.96	14.58	1.16	0.86
Q9DBR0_AI	Akap8	A-kinase an	R.SFEDEEIQK#.H	56.68	59.27	0.96	1.05

Q9DBR0_A	Akap8	A-kinase an	K.TVEFLQEYIINR.N	4.36	11.41	0.38	2.62
Q9R0L7_A	Akap8l	A-kinase an	K.GALTAQDESSQAK#.R	28.60	16.01	1.79	0.56
E9QQ10_E	Akap9	A-kinase an	R.LEAVSEAPVQPSLSIDSVVFK#.G	6.30	3.84	1.64	0.61
Q8CG76_A	Akr7a2	Aflatoxin B	R.FYAYNPLAGGLLTGK#.Y	26.05	5.39	4.83	0.21
P31750_A	Akt1	RAC-alpha	R.EEWATAIQTVADGLK#.R	6.09	3.06	1.99	0.50
P31750_A	Akt1	RAC-alpha	R.HPFLTALK#.Y	21.22	4.21	5.04	0.20
Q64362_A	Aktip	AKT-interac	K.IDTTSPLNPEAAVLYEK#.D	5.89	1.67	3.52	0.28
Q571I9_A1	Aldh16a1	Aldehyde d	R.LLWTLESLVTGR.A	20.18	9.13	2.21	0.45
Q571I9_A1	Aldh16a1	Aldehyde d	R.VQDQGQTLQVTGLR.G	3.96	7.94	0.50	2.01
Q571I9_A1	Aldh16a1	Aldehyde d	R.VQDQGQTLQVTGLR.G	2.94	9.58	0.31	3.26
Q9Z110_P	Aldh18a1	Delta-1-pyr	R.GPVGLEGLLTTK#.W	8.24	6.09	1.35	0.74
Q9Z110_P	Aldh18a1	Delta-1-pyr	K.FASYLTFSPSEVK#.S	23.72	10.96	2.16	0.46
Q9Z110_P	Aldh18a1	Delta-1-pyr	R.GPVGLEGLLTTK#.W	30.47	18.25	1.67	0.60
Q9Z110_P	Aldh18a1	Delta-1-pyr	R.ILHLLTQEALSIHGVK#.E	5.84	5.28	1.11	0.90
Q9Z110_P	Aldh18a1	Delta-1-pyr	R.LASIVEQVSVLQNQGR.E	3.20	6.79	0.47	2.12
Q9Z110_P	Aldh18a1	Delta-1-pyr	R.LASPLLK#.R	18.48	49.52	0.37	2.68
Q9Z110_P	Aldh18a1	Delta-1-pyr	K.LIDIFYPGDQQSVTFGTK#.S	14.33	6.88	2.08	0.48
Q9Z110_P	Aldh18a1	Delta-1-pyr	K.VSGHVITDIVEGK#.K	11.37	6.83	1.67	0.60
Q9Z110_P	Aldh18a1	Delta-1-pyr	K.FASYLTFSPSEVK#.S	9.64	5.08	1.90	0.53
Q9Z110_P	Aldh18a1	Delta-1-pyr	K.LIDIFYPGDQQSVTFGTK#.S	7.02	4.00	1.76	0.57
Q8K009_A	Aldh1l2	Mitochond	K.DLGEEALNEYLK#.I	12.62	3.67	3.44	0.29
Q8K009_A	Aldh1l2	Mitochond	R.ILSNTPVIEDSTDFFK#.S	18.87	5.14	3.67	0.27
Q8K009_A	Aldh1l2	Mitochond	K.M*IPASQYFSAGETSVVELTAEELK#.V	4.07	4.68	0.87	1.15
Q8K009_A	Aldh1l2	Mitochond	R.TPQPEEGATYEGIQK#.K	11.10	4.27	2.60	0.38
Q8K009_A	Aldh1l2	Mitochond	R.ILSNTPVIEDSTDFFK#.S	7.04	3.20	2.20	0.45
Q8K009_A	Aldh1l2	Mitochond	K.M*IPASQYFSAGETSVVELTAEELK#.V	4.35	5.24	0.83	1.20
P47738_A	Aldh2	Aldehyde d	R.TEQGPQVDETQFK#.K	6.08	2.71	2.24	0.45
Q9DBT5_A	Ampd2	AMP deami	R.HLEEIVHVEQGR.E	9.93	15.88	0.63	1.60
Q9DBT5_A	Ampd2	AMP deami	R.LQYLSSK#.F	25.73	13.98	1.84	0.54
Q9DBT5_A	Ampd2	AMP deami	R.SAPYEFPEESPIEQLEER.R	3.97	7.40	0.54	1.86
Q9DBT5_A	Ampd2	AMP deami	K.TDSDSDLQLYK#.E	23.12	5.96	3.88	0.26
Q9DBT5_A	Ampd2	AMP deami	K.YFAHIIK#.E	14.87	4.94	3.01	0.33
Q9DBT5_A	Ampd2	AMP deami	R.YLQQLAEKPLETR.T	3.10	2.96	1.05	0.95
Q9DBT5_A	Ampd2	AMP deami	R.LQYLSSK#.F	36.09	10.40	3.47	0.29
Q9DBT5_A	Ampd2	AMP deami	R.SAPYEFPEESPIEQLEER.R	4.11	6.15	0.67	1.49
Q9DBT5_A	Ampd2	AMP deami	K.TDSDSDLQLYK#.E	21.60	5.88	3.67	0.27
P53995_A	Anapc1	Anaphase-p	R.GM*FTLFSYHPVPTEPLPVPK.L	8.28	8.96	0.92	1.08
P53995_A	Anapc1	Anaphase-p	R.LAPVLLGNPQPM*VM*.-	13.89	13.89	1.00	1.00
P53995_A	Anapc1	Anaphase-p	R.NVESHLLNK#.S	11.23	11.30	0.99	1.01
P53995_A	Anapc1	Anaphase-p	R.QLQPASELWSSDGAAGLVGSLQEVTIHEK#.Q	5.02	5.38	0.93	1.07
P53995_A	Anapc1	Anaphase-p	R.SFDFEGSLSPVIAPK#.K	21.48	13.77	1.56	0.64
Q91W96_	Anapc4	Anaphase-p	R.DLIALANTTGEVLLHR.L	4.50	9.16	0.49	2.03
Q91W96_	Anapc4	Anaphase-p	R.LDEQGSIIPTR.T	3.68	8.37	0.44	2.27
Q91W96_	Anapc4	Anaphase-p	K.LGQSIESSYSSIQK#.L	11.99	6.01	2.00	0.50
Q91W96_	Anapc4	Anaphase-p	K.LLAFALADTK#.K	10.65	8.98	1.19	0.84
Q9WVM3_	Anapc7	Anaphase-p	K.AIQLNSNSVQALLLK#.G	8.58	4.03	2.13	0.47
Q8C8R3_A	Ank2	Ankyrin-2	R.DSAM*IDDTVVIPSHQVSALAK#.E	12.42	3.15	3.94	0.25
Q8C8R3_A	Ank2	Ankyrin-2	K.FVVFAK#.S	18.54	10.13	1.83	0.55
Q8C8R3_A	Ank2	Ankyrin-2	R.IK#QDSNLIGPEGGVLSSTVVSQVQAVFPEGALTK#.R	7.98	2.47	3.23	0.31
Q8C8R3_A	Ank2	Ankyrin-2	R.LGYISVVDTLK#.V	17.28	8.60	2.01	0.50
Q8C8R3_A	Ank2	Ankyrin-2	K.SGLTSLHLAAQEDK#VNVADILTK#.H	12.31	1.45	8.49	0.12
Q8C8R3_A	Ank2	Ankyrin-2	K.VVTEEVTTTTTTITEK#.H	13.63	4.71	2.89	0.35
G5E8K5_A	Ank3	Ankyrin-3	R.YLVQDGAQVEAK.A	6.95	7.98	0.87	1.15
Q810B6_A	Ankfy1	Rabankyrin	R.GDLFASTFLIK#.N	12.06	9.88	1.22	0.82
Q810B6_A	Ankfy1	Rabankyrin	R.AAGAGNEAAALFLATSGAHANHR.N	1.75	9.84	0.18	5.62
Q810B6_A	Ankfy1	Rabankyrin	K.ANALHATNNLQIIPDFSLK#.D	13.83	17.60	0.79	1.27
Q810B6_A	Ankfy1	Rabankyrin	R.ESGAAEQVDNK.G	3.57	4.05	0.88	1.13
Q810B6_A	Ankfy1	Rabankyrin	R.GDLFASTFLIK#.N	28.73	23.00	1.25	0.80
Q810B6_A	Ankfy1	Rabankyrin	R.LGVNNNQGVNIFNYQVATK#.Q	4.07	3.98	1.02	0.98
Q810B6_A	Ankfy1	Rabankyrin	K.NGALVNAATAGAQETPLHLVALYSPK.K	9.10	6.19	1.47	0.68
E9Q4F8_E9	Ankrd11	Protein An	K.VFSSIISEDFSER.K	1.90	8.71	0.22	4.59
Q99NH0_A	Ankrd17	Ankyrin rep	R.LEALLEAAGIGK#.L	10.84	6.51	1.67	0.60
Q99NH0_A	Ankrd17	Ankyrin rep	K.NASILLEELDLEK.L	6.18	6.92	0.89	1.12
Q99NH0_A	Ankrd17	Ankyrin rep	K.GADVNAPPVPSSR.D	5.43	24.69	0.22	4.55
Q99NH0_A	Ankrd17	Ankyrin rep	R.GASLEEVNDEGYTPLM*EAAR.E	2.51	6.01	0.42	2.39
Q99NH0_A	Ankrd17	Ankyrin rep	R.LEALLEAAGIGK#.L	34.35	25.23	1.36	0.73
Q99NH0_A	Ankrd17	Ankyrin rep	K.LLLSGTADGADLR.T	6.75	24.01	0.28	3.56
Q99NH0_A	Ankrd17	Ankyrin rep	K.NASILLEELDLEK#.L	22.04	15.86	1.39	0.72
Q99NH0_A	Ankrd17	Ankyrin rep	R.NVSDYTPLSLAASGGYVNIIK#.I	18.76	15.91	1.18	0.85
Q99NH0_A	Ankrd17	Ankyrin rep	R.TEVVSLLLDR.K	4.63	22.24	0.21	4.81
Q99NH0_A	Ankrd17	Ankyrin rep	K.TGLTPLM*EAASGGYAEVGR.V	2.55	8.95	0.28	3.51
Q99NH0_A	Ankrd17	Ankyrin rep	K.TPAPVQSSSASVLNVNHIK#.R	11.01	6.25	1.76	0.57
Q3UMR0_	Ankrd27	Ankyrin rep	R.LLSQDDQDK#DAM*QK#.M	9.12	1.32	6.90	0.15
Q8K298_A	Anln	Actin-bindi	R.AESADSLGSEDRDLLYSIDAYR.S	1.88	11.50	0.16	6.11
Q8K298_A	Anln	Actin-bindi	R.ALLIDELNK#.L	14.29	17.28	0.83	1.21
Q8K298_A	Anln	Actin-bindi	K.ASSPVTAATFITENR.E	2.88	9.90	0.29	3.43
Q8K298_A	Anln	Actin-bindi	R.DSNLSAASPKPGK.F	8.52	8.06	1.06	0.95
Q8K298_A	Anln	Actin-bindi	R.GLNSGSEASATSSVK#.T	17.59	9.49	1.85	0.54
Q8K298_A	Anln	Actin-bindi	K.ITLFLEEEK.S	11.06	12.95	0.85	1.17
Q8K298_A	Anln	Actin-bindi	R.LLLIATEK#.R	16.37	17.95	0.91	1.10
Q8K298_A	Anln	Actin-bindi	K.LNQVIVDIR.L	3.68	14.51	0.25	3.94
Q8K298_A	Anln	Actin-bindi	K.LSSTEPAGSTESEM*TK#.S	7.74	4.94	1.57	0.64
Q8K298_A	Anln	Actin-bindi	R.NTLELITVRPQR.E	1.60	4.54	0.35	2.83
Q8K298_A	Anln	Actin-bindi	K.RLLTSITSK.S	2.35	12.29	0.19	5.22
Q8K298_A	Anln	Actin-bindi	K.TSVISQSEFAPSK#.G	14.94	21.31	0.70	1.43
Q8K298_A	Anln	Actin-bindi	K.VASDLEVEQNTEAVR.E	3.91	17.07	0.23	4.37
P97822_A	Anp32e	Acidic leuci	K.IK#DLSTVEALQNLK#.N	16.91	4.23	3.99	0.25
P97822_A	Anp32e	Acidic leuci	K.DLSTVEALQNLK#.N	8.85	19.37	0.46	2.19
P10107_A	Anxa1	Annexin A1	K.ALLALAK#.G	140.59	26.52	5.30	0.19
P10107_A	Anxa1	Annexin A1	K.ALTGHLEEVVLAM*LK#.T	47.54	8.32	5.71	0.18
P10107_A	Anxa1	Annexin A1	K.ALTGHLEEVVLAMLK#.T	154.34	29.67	5.20	0.19
P10107_A	Anxa1	Annexin A1	K.DITSDTSGDFRK.A	25.88	22.43	1.15	0.87
P10107_A	Anxa1	Annexin A1	R.FLENQEQEYVQAVK#.S	274.68	38.98	7.05	0.14
P10107_A	Anxa1	Annexin A1	K.GGPGSAVSPYPSFNVSSDVAALHK#.A	349.74	53.84	6.50	0.15
P10107_A	Anxa1	Annexin A1	K.GLGTDEDTLIEILTTR.S	68.50	57.07	1.20	0.83
P10107_A	Anxa1	Annexin A1	K.GTDVNVFTTILTSR.S	42.44	41.95	1.01	0.99
P10107_A	Anxa1	Annexin A1	K.GVDEATIIDILTK#.R	234.15	41.92	5.59	0.18
P10107_A	Anxa1	Annexin A1	R.K#ALLALAK#.G	15.38	3.32	4.63	0.22
P10107_A	Anxa1	Annexin A1	R.K#ALTGHLEEVVLAM*LK#.T	10.66	25.46	0.42	2.39
P10107_A	Anxa1	Annexin A1	R.K#ALTGHLEEVVLAMLK#.T	32.52	4.31	7.54	0.13
P10107_A	Anxa1	Annexin A1	R.SEIDM*NEIK#.V	124.34	21.11	5.89	0.17
P10107_A	Anxa1	Annexin A1	R.SEIDMNEIK#.V	86.95	15.34	5.67	0.18
P10107_A	Anxa1	Annexin A1	K.TPAQFDADELR.G	84.83	88.40	0.96	1.04

P10107_AN	Anxa1	Annexin A1 R.VFQNYGK#.Y	121.03	19.81	6.11	0.16
P10107_AN	Anxa1	Annexin A1 R.FLENQEQEYVQAVK#.S	5.36	1.50	3.58	0.28
P10107_AN	Anxa1	Annexin A1 K.ALLALAK#.G	31.29	8.53	3.67	0.27
P10107_AN	Anxa1	Annexin A1 K.ALTGHLEEVVLAMLK#.T	14.90	2.72	5.48	0.18
P10107_AN	Anxa1	Annexin A1 R.FLENQEQEYVQAVK#.S	18.63	12.35	1.51	0.66
P10107_AN	Anxa1	Annexin A1 K.GGPGSAVSPYPSFNVSSDVAALHK#.A	23.97	10.56	2.27	0.44
P10107_AN	Anxa1	Annexin A1 K.TPAQFDADELR.G	14.39	9.30	1.55	0.65
P10107_AN	Anxa1	Annexin A1 K.ALLALAK#.G	28.68	16.91	1.70	0.59
P10107_AN	Anxa1	Annexin A1 R.FLENQEQEYVQAVK#.S	41.68	46.11	0.90	1.11
P10107_AN	Anxa1	Annexin A1 K.GGPGSAVSPYPSFNVSSDVAALHK#.A	38.05	14.05	2.71	0.37
P97384_AN	Anxa11	Annexin A1 K.TPVLFDVYEIK#.E	8.38	6.23	1.34	0.74
P07356_AN	Anxa2	Annexin A2 R.AEDGSVIDYELIDQDAR.E	4.52	18.75	0.24	4.15
P07356_AN	Anxa2	Annexin A2 R.DALNIETAVK.T	80.09	52.39	1.53	0.65
P07356_AN	Anxa2	Annexin A2 K.GVDEVTIVNILTNR.S	4.55	16.97	0.27	3.73
P07356_AN	Anxa2	Annexin A2 K.LM*VALAK#.G	17.66	10.97	1.61	0.62
P07356_AN	Anxa2	Annexin A2 K.LMVALAK#.G	36.36	30.30	1.20	0.83
P07356_AN	Anxa2	Annexin A2 R.QDIAFAYQR.R	26.28	103.37	0.25	3.93
P07356_AN	Anxa2	Annexin A2 R.RAEDGSVIDYELIDQDAR.E	4.73	43.67	0.11	9.23
P07356_AN	Anxa2	Annexin A2 K.SALSGHLETVILGLLK#.T	177.60	136.63	1.30	0.77
P07356_AN	Anxa2	Annexin A2 K.SALSGHLETVILGLLK#.T	17.83	8.32	2.14	0.47
P07356_AN	Anxa2	Annexin A2 R.SEVDMLK#.I	18.37	9.60	1.91	0.52
P07356_AN	Anxa2	Annexin A2 K.SLYYYIQQDTK#.G	62.11	46.65	1.33	0.75
P07356_AN	Anxa2	Annexin A2 K.SYSPYDMLESIK.K	6.72	7.10	0.95	1.06
P07356_AN	Anxa2	Annexin A2 K.SYSPYDM*LESIK#K#.E	11.83	7.20	1.64	0.61
P07356_AN	Anxa2	Annexin A2 K.TDLEKDIISDTSGDFRK.L	24.53	77.65	0.32	3.17
P07356_AN	Anxa2	Annexin A2 K.TKGVDEVTIVNILTNR.S	9.16	33.98	0.27	3.71
P07356_AN	Anxa2	Annexin A2 R.TNQELQEINR.V	38.41	129.39	0.30	3.37
P07356_AN	Anxa2	Annexin A2 K.TPAQYDASELK#.A	103.50	95.69	1.08	0.92
P07356_AN	Anxa2	Annexin A2 K.WISIMTER.S	2.94	7.86	0.37	2.68
P07356_AN	Anxa2	Annexin A2 R.AEDGSVIDYELIDQDAR.E	2.40	4.23	0.57	1.77
P07356_AN	Anxa2	Annexin A2 K.GVDEVTIVNILTNR.S	5.15	20.39	0.25	3.96
P07356_AN	Anxa2	Annexin A2 R.RAEDGSVIDYELIDQDAR.E	2.25	13.34	0.17	5.94
P07356_AN	Anxa2	Annexin A2 K.SALSGHLETVILGLLK#.T	49.36	43.48	1.14	0.88
P07356_AN	Anxa2	Annexin A2 K.SLYYYIQQDTK#.G	19.02	11.98	1.59	0.63
P07356_AN	Anxa2	Annexin A2 K.TKGVDEVTIVNILTNR.S	4.86	19.76	0.25	4.06
P07356_AN	Anxa2	Annexin A2 R.TNQELQEINR.V	8.07	32.75	0.25	4.06
P07356_AN	Anxa2	Annexin A2 K.TPAQYDASELK#.A	37.70	39.66	0.95	1.05
P07356_AN	Anxa2	Annexin A2 R.AEDGSVIDYELIDQDAR.E	3.47	9.06	0.38	2.61
P07356_AN	Anxa2	Annexin A2 R.DALNIETAVK#.T	25.79	27.57	0.94	1.07
P07356_AN	Anxa2	Annexin A2 K.SLYYYIQQDTK#.G	18.31	15.55	1.18	0.85
P07356_AN	Anxa2	Annexin A2 K.TKGVDEVTIVNILTNR.S	4.18	17.40	0.24	4.17
P07356_AN	Anxa2	Annexin A2 R.TNQELQEINR.V	15.08	57.43	0.26	3.81
P07356_AN	Anxa2	Annexin A2 K.TPAQYDASELK#.A	53.36	49.96	1.07	0.94
P97429_AN	Anxa4	Annexin A4 K.GLGTDEDAIIGILAYR.N	2.52	5.19	0.48	2.06
P97429_AN	Anxa4	Annexin A4 R.INQTYQQQYGR.S	2.53	4.80	0.53	1.89
P97429_AN	Anxa4	Annexin A4 K.SETSGSFEDALLAIVK#.C	12.26	6.45	1.90	0.53
P48036_AN	Anxa5	Annexin A5 K.GLGTDEDSILNLLTSR.S	11.46	14.67	0.78	1.28
P48036_AN	Anxa5	Annexin A5 R.GTVTDFPGFDGR.A	8.73	10.05	0.87	1.15
P48036_AN	Anxa5	Annexin A5 R.LYDAYELK#.H	37.97	11.92	3.18	0.31
P48036_AN	Anxa5	Annexin A5 R.TPEELSAIK#.Q	28.16	6.08	4.63	0.22
P48036_AN	Anxa5	Annexin A5 K.VLTEIIASR.T	13.75	16.65	0.83	1.21
P14824_AN	Anxa6	Annexin A6 R.ENDDVVSEDLVQQDVQDLYEAGELK#.W	12.32	3.25	3.79	0.26
P14824_AN	Anxa6	Annexin A6 K.GFGSDKESILELITSR.S	5.06	8.47	0.60	1.67
P14824_AN	Anxa6	Annexin A6 R.GSVHDFPEFDANQDAEALYTAMK#.G	5.72	2.82	2.03	0.49
P14824_AN	Anxa6	Annexin A6 R.SEIDLLNIR.R	3.73	9.52	0.39	2.55
P14824_AN	Anxa6	Annexin A6 K.TLIEILATR.T	3.08	11.79	0.26	3.84
P14824_AN	Anxa6	Annexin A6 K.DAFVAIVQSVK#.N	8.86	6.80	1.30	0.77
P14824_AN	Anxa6	Annexin A6 R.ENDDVVSEDLVQQDVQDLYEAGELK#.W	9.16	4.05	2.26	0.44
P14824_AN	Anxa6	Annexin A6 R.GSVHDFPEFDANQDAEALYTAM*K#.G	7.74	3.72	2.08	0.48
P14824_AN	Anxa6	Annexin A6 R.GSVHDFPEFDANQDAEALYTAMK#.G	5.10	1.77	2.89	0.35
O35643_AP	Ap1b1	AP-1 compl R.AAMIWIVGEYAER.I	3.07	6.73	0.46	2.20
O35643_AP	Ap1b1	AP-1 compl K.EYATEVDVDFVR.K	5.81	8.37	0.69	1.44
O35643_AP	Ap1b1	AP-1 compl R.IQPGNPSFTLSLK#.C	11.77	6.74	1.75	0.57
O35643_AP	Ap1b1	AP-1 compl K.KGEIFELK.A	77.18	18.42	4.19	0.24
O35643_AP	Ap1b1	AP-1 compl R.LASQANIAQVLAELK#.E	50.35	14.72	3.42	0.29
O35643_AP	Ap1b1	AP-1 compl K.LHDINAQLVEDQGFLDTLK#.D	6.78	2.29	2.96	0.34
O35643_AP	Ap1b1	AP-1 compl R.LSHANSAVVLSAVK#.V	92.44	24.05	3.84	0.26
O35643_AP	Ap1b1	AP-1 compl K.LVYLYLM*NYAK#.S	12.36	3.43	3.61	0.28
O35643_AP	Ap1b1	AP-1 compl K.M*EPLNNLQVAVK#.N	13.21	6.27	2.11	0.47
O35643_AP	Ap1b1	AP-1 compl R.NINLIVQK#.R	84.00	24.60	3.42	0.29
O35643_AP	Ap1b1	AP-1 compl R.NVEGQDM*LYQSLK#.L	13.62	9.65	1.41	0.71
O35643_AP	Ap1b1	AP-1 compl K.VNYVVQEAIVVIK#.D	18.25	4.00	4.57	0.22
O35643_AP	Ap1b1	AP-1 compl K.YNDPIYVK#.L	72.75	21.21	3.43	0.29
O35643_AP	Ap1b1	AP-1 compl K.DLDYYATLLK#.K	18.09	4.86	3.73	0.27
O35643_AP	Ap1b1	AP-1 compl K.FM*EM*LSK#.D	16.14	5.99	2.69	0.37
O35643_AP	Ap1b1	AP-1 compl R.IQPGNPSFTLSLK#.C	14.27	5.11	2.80	0.36
O35643_AP	Ap1b1	AP-1 compl K.K#GEIFELK#.A	84.59	21.54	3.93	0.25
O35643_AP	Ap1b1	AP-1 compl R.LASQANIAQVLAELK#.E	64.39	16.75	3.84	0.26
O35643_AP	Ap1b1	AP-1 compl K.LHDINAQLVEDQGFLDTLK#.D	5.90	2.45	2.41	0.42
O35643_AP	Ap1b1	AP-1 compl R.LLSTDPVAAK#.E	48.78	11.81	4.13	0.24
O35643_AP	Ap1b1	AP-1 compl R.LSHANSAVVLSAVK#.V	66.63	20.98	3.18	0.31
O35643_AP	Ap1b1	AP-1 compl K.M*EPLNNLQVAVK#.N	20.45	9.17	2.23	0.45
O35643_AP	Ap1b1	AP-1 compl R.NINLIVQK#.R	67.98	19.32	3.52	0.28
O35643_AP	Ap1b1	AP-1 compl R.NVEGQDM*LYQSLK#.L	13.71	3.93	3.48	0.29
O35643_AP	Ap1b1	AP-1 compl K.VNYVVQEAIVVIK#.D	12.34	4.05	3.05	0.33
P22892_AP	Ap1g1	AP-1 compl R.DLAGEVEK#.L	12.57	6.40	1.96	0.51
P22892_AP	Ap1g1	AP-1 compl R.VLAINILGR.F	5.25	12.90	0.41	2.46
P22892_AP	Ap1g1	AP-1 compl R.YVALTSLLK#.T	33.43	12.23	2.73	0.37
P22892_AP	Ap1g1	AP-1 compl R.AVEYNALFK#.K	21.88	7.81	2.80	0.36
P22892_AP	Ap1g1	AP-1 compl R.GYALTAIM*K#.L	11.06	4.26	2.59	0.39
P22892_AP	Ap1g1	AP-1 compl R.VLAINILGR.F	8.86	14.34	0.62	1.62
P22892_AP	Ap1g1	AP-1 compl R.YVALTSLLK#.T	48.65	14.35	3.39	0.30
P35585_AP	Ap1m1	AP-1 compl K.ILQEYITQEGHK#.L	7.68	3.16	2.43	0.41
P35585_AP	Ap1m1	AP-1 compl K.VVQVFSEYFK#.E	24.20	7.92	3.06	0.33
P35585_AP	Ap1m1	AP-1 compl R.STANNVEIHIPVPNDADSPK#.F	9.07	4.52	2.01	0.50
P35585_AP	Ap1m1	AP-1 compl K.VVQVFSEYFK#.E	12.30	5.98	2.06	0.49
P35585_AP	Ap1m1	AP-1 compl R.AHFGLPSVEAEDK#EGK#PPISVK#.F	12.61	5.10	2.47	0.40
P35585_AP	Ap1m1	AP-1 compl R.STANNVEIHIPVPNDADSPK#.F	13.80	6.00	2.30	0.43
P35585_AP	Ap1m1	AP-1 compl K.VVQVFSEYFK#.E	14.41	7.92	1.82	0.55
P61967_AP	Ap1s1	AP-1 compl K.AIEQADLLQEEDESPR.S	8.08	16.85	0.48	2.08
P61967_AP	Ap1s1	AP-1 compl R.FM*LLFSR.Q	7.25	10.11	0.72	1.40
P17426_AP	Ap2a1	AP-2 compl R.ALLLSTYIK#.F	56.63	16.45	3.44	0.29
P17426_AP	Ap2a1	AP-2 compl R.DFLTPPLLSVR.F	4.05	8.37	0.48	2.07

P17426_AF	Ap2a1	AP-2 compl	K.FINLFPETK#.A	20.77	6.49	3.20	0.31
P17426_AF	Ap2a1	AP-2 compl	R.GLAVFISDIR.N	19.19	15.02	1.28	0.78
P17426_AF	Ap2a1	AP-2 compl	R.IAGDYVSEEVWYR.V	12.59	12.03	1.05	0.96
P17426_AF	Ap2a1	AP-2 compl	R.ILVAGDSM*DSVK#.Q	26.65	8.56	3.11	0.32
P17426_AF	Ap2a1	AP-2 compl	R.ILVAGDSMDSVK#.Q	26.04	2.70	9.63	0.10
P17426_AF	Ap2a1	AP-2 compl	K.LPVTINK#.F	33.14	12.96	2.56	0.39
P17426_AF	Ap2a1	AP-2 compl	R.NADVELQQR.A	22.21	28.16	0.79	1.27
P17426_AF	Ap2a1	AP-2 compl	K.NSGVLFENQLLQIGVK#.S	24.91	6.21	4.01	0.25
P17426_AF	Ap2a1	AP-2 compl	K.QLSLPLQEAQK#.I	16.43	8.47	1.94	0.52
P17426_AF	Ap2a1	AP-2 compl	K.THIDTVINALK#.T	12.92	5.41	2.39	0.42
P17426_AF	Ap2a1	AP-2 compl	K.VAILAEK#.Y	53.80	16.56	3.25	0.31
P17426_AF	Ap2a1	AP-2 compl	R.YGGTAQSLTLK#.L	32.81	13.97	2.35	0.43
P17426_AF	Ap2a1	AP-2 compl	R.ALLLSTYIK#.F	30.32	8.86	3.42	0.29
P17426_AF	Ap2a1	AP-2 compl	R.ILVAGDSM*DSVK#.Q	16.73	5.97	2.80	0.36
P17426_AF	Ap2a1	AP-2 compl	K.NSGVLFENQLLQIGVK#.S	9.38	4.03	2.32	0.43
P17426_AF	Ap2a1	AP-2 compl	K.VAILAEK#.Y	57.28	11.53	4.97	0.20
P17427_AF	Ap2a2	AP-2 compl	R.EM*AEAFAGEIPK#.I	18.78	3.83	4.91	0.20
P17427_AF	Ap2a2	AP-2 compl	K.ILVAGDTM*DSVK#.Q	44.28	15.83	2.80	0.36
P17427_AF	Ap2a2	AP-2 compl	K.LPITLNK#.F	39.11	9.69	4.03	0.25
P17427_AF	Ap2a2	AP-2 compl	R.MFIFYGNK#.T	7.87	2.96	2.66	0.38
P17427_AF	Ap2a2	AP-2 compl	K.NNGVLFENQLLQIGLK#.S	10.20	4.19	2.43	0.41
P17427_AF	Ap2a2	AP-2 compl	K.QLSNPQQEVQNIFK#.A	13.34	4.47	2.98	0.34
P17427_AF	Ap2a2	AP-2 compl	K.THIETVINALK#.T	29.38	8.45	3.48	0.29
P17427_AF	Ap2a2	AP-2 compl	R.YGGTFQNVSVK#.L	56.42	19.31	2.92	0.34
P17427_AF	Ap2a2	AP-2 compl	R.EM*AEAFAGEIPK#.I	15.86	4.86	3.26	0.31
P17427_AF	Ap2a2	AP-2 compl	K.ILVAGDTM*DSVK#.Q	27.79	6.45	4.31	0.23
P17427_AF	Ap2a2	AP-2 compl	K.LPITLNK#.F	23.78	5.80	4.10	0.24
P17427_AF	Ap2a2	AP-2 compl	K.QLSNPQQEVQNIFK#.A	10.86	2.14	5.08	0.20
Q9DBG3_A	Ap2b1	AP-2 compl	K.ALQHM*TDFAIQFNK#.N	14.77	4.73	3.13	0.32
Q9DBG3_A	Ap2b1	AP-2 compl	K.DSDYYNM*LLK#.K	20.81	5.65	3.69	0.27
Q9DBG3_A	Ap2b1	AP-2 compl	K.FLELLPK#.D	40.03	13.05	3.07	0.33
Q9DBG3_A	Ap2b1	AP-2 compl	K.LHDINAQM*VEDQGFLDSLR.D	3.82	5.05	0.76	1.32
Q9DBG3_A	Ap2b1	AP-2 compl	R.LLSTDPVTAK#.E	83.01	29.18	2.84	0.35
Q9DBG3_A	Ap2b1	AP-2 compl	K.LQNNNVYTIAK#.R	24.71	8.56	2.89	0.35
Q9DBG3_A	Ap2b1	AP-2 compl	K.VNYVVQEAIVVIR.D	4.87	10.97	0.44	2.25
Q9DBG3_A	Ap2b1	AP-2 compl	K.ALQHM*TDFAIQFNK#.N	14.51	4.58	3.17	0.32
Q9DBG3_A	Ap2b1	AP-2 compl	K.AVWLPAVK#.A	18.84	8.44	2.23	0.45
Q9DBG3_A	Ap2b1	AP-2 compl	K.DSDYYNM*LLK#.K	13.73	5.51	2.49	0.40
Q9DBG3_A	Ap2b1	AP-2 compl	K.KPSETQELVQQVLSLATQDSDNPDLR.D	8.19	10.83	0.76	1.32
Q9DBG3_A	Ap2b1	AP-2 compl	R.LLSTDPVTAK#.E	83.52	22.39	3.73	0.27
Q9DBG3_A	Ap2b1	AP-2 compl	K.VIAAM*TVGK#.D	50.49	11.22	4.50	0.22
P84091_AF	Ap2m1	AP-2 compl	K.ASENAIVWK#.I	94.59	32.45	2.91	0.34
P84091_AF	Ap2m1	AP-2 compl	K.ESQISAEIELLPTNDK#.K	16.50	6.11	2.70	0.37
P84091_AF	Ap2m1	AP-2 compl	K.LNYSDHDVIK#.W	108.37	36.30	2.99	0.33
P84091_AF	Ap2m1	AP-2 compl	K.QNVNAAMVFEFLYK#.M	8.08	2.82	2.86	0.35
P84091_AF	Ap2m1	AP-2 compl	K.SNFK#PSLLAQK#.I	14.55	7.17	2.03	0.49
P84091_AF	Ap2m1	AP-2 compl	R.SNIWLAAVTK#.Q	65.12	20.49	3.18	0.31
P84091_AF	Ap2m1	AP-2 compl	R.SPVTNIAR.T	40.28	48.87	0.82	1.21
P84091_AF	Ap2m1	AP-2 compl	K.WARPPISMNFEVPFAPSGLK.V	6.20	9.85	0.63	1.59
P84091_AF	Ap2m1	AP-2 compl	R.SNIWLAAVTK#.Q	8.83	4.63	1.91	0.52
P62743_AF	Ap2s1	AP-2 compl	K.QLLM*LQSLE.-	28.74	28.74	1.00	1.00
P62743_AF	Ap2s1	AP-2 compl	K.QLLMLQSLE.-	12.12	12.12	1.00	1.00
P62743_AF	Ap2s1	AP-2 compl	K.VYTVVDEM*FLAGEIR.E	6.67	7.17	0.93	1.07
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LLTQYILNLGK#.Y	17.50	4.36	4.01	0.25
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.VVNVANLGAVPSSQDNVHR.F	4.65	10.05	0.46	2.16
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.EGSTAQLIINTEK#.T	13.07	2.84	4.61	0.22
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.EASADLSPYVR.K	7.82	21.66	0.36	2.77
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.EGSTAQLIINTEK#.T	20.51	7.13	2.88	0.35
Q9Z1T1_AF	Ap3b1	AP-3 compl	R.ELK#PVLSQG.-	13.73	8.12	1.69	0.59
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.EMLIEVIEK#.L	15.47	5.74	2.70	0.37
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LEILTNLANEANISTLLR.E	3.90	12.70	0.31	3.26
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LLDSITVPVAR.A	15.86	67.89	0.23	4.28
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LLTQYILNLGK#.Y	86.29	35.24	2.45	0.41
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LQILNLAAK#.L	61.12	21.65	2.82	0.35
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LYLTNSK#.Q	25.73	13.98	1.84	0.54
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LYSLDPEQK#.E	22.38	8.35	2.68	0.37
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.NASELFPAVVK#.N	25.95	14.34	1.81	0.55
Q9Z1T1_AF	Ap3b1	AP-3 compl	R.NVEVIESAK#.E	21.35	5.63	3.79	0.26
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.QFAAATIQTIGR.C	4.65	10.11	0.46	2.17
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.SFTSEDDLVK#.L	51.13	25.97	1.97	0.51
Q9Z1T1_AF	Ap3b1	AP-3 compl	R.VPIIVPVM*M*LAIK#.E	11.25	4.30	2.62	0.38
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.VVNVANLGAVPSSQDNVHR.F	9.48	14.75	0.64	1.56
Q9Z1T1_AF	Ap3b1	AP-3 compl	R.YAEEQQDLALLSISTFQR.A	4.71	15.03	0.31	3.19
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.EASADLSPYVR.K	16.71	17.89	0.93	1.07
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.EQGTLTGM*NETSATLIAAPQNFTPSM*ILQK#.V	7.02	3.65	1.92	0.52
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LLDSITVPVAR.A	11.96	157.38	0.08	13.16
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LLTQYILNLGK#.Y	75.57	29.37	2.57	0.39
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LQILNLAAK#.L	38.02	20.51	1.85	0.54
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LYSLDPEQK#.E	18.19	6.66	2.73	0.37
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.LYSLDPEQK#EM*LIEVIEK#.L	13.31	6.22	2.14	0.47
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.NASELFPAVVK#.N	34.56	13.18	2.62	0.38
Q9Z1T1_AF	Ap3b1	AP-3 compl	K.QFAAATIQTIGR.C	3.83	7.90	0.49	2.06
Q9Z1T1_AF	Ap3b1	AP-3 compl	R.VPIIVPVM*M*LAIK#.E	11.24	4.82	2.33	0.43
O54774_AI	Ap3d1	AP-3 compl	R.ALDLLYGMVSK#.K	9.85	3.09	3.19	0.31
O54774_AI	Ap3d1	AP-3 compl	R.ILIEDSDQNLK#.Y	18.34	13.00	1.41	0.71
O54774_AI	Ap3d1	AP-3 compl	K.LFGALTPLEPR.L	3.15	7.87	0.40	2.50
O54774_AI	Ap3d1	AP-3 compl	R.LPQFVQSADLEVQER.A	1.86	2.71	0.68	1.46
O54774_AI	Ap3d1	AP-3 compl	K.LYASILQQK#.E	14.19	75.12	0.19	5.29
O54774_AI	Ap3d1	AP-3 compl	K.NYLSLAPLFFK#.L	20.02	7.73	2.59	0.39
O54774_AI	Ap3d1	AP-3 compl	R.ALDIDLDK#PLADSEK#LPVQK#.H	17.68	6.37	2.78	0.36
O54774_AI	Ap3d1	AP-3 compl	R.ALDLLYGM*VSK#.K	21.02	12.83	1.64	0.61
O54774_AI	Ap3d1	AP-3 compl	K.EQAADTEAAQEVTQLLVER.L	14.55	31.88	0.46	2.19
O54774_AI	Ap3d1	AP-3 compl	R.ILIEDSDQNLK#.Y	80.81	43.94	1.84	0.54
O54774_AI	Ap3d1	AP-3 compl	K.LFGALTPLEPR.L	10.59	25.98	0.41	2.45
O54774_AI	Ap3d1	AP-3 compl	K.LLESGDLSM*NSIK#.V	21.97	36.29	0.61	1.65
O54774_AI	Ap3d1	AP-3 compl	R.LPQFVQSADLEVQER.A	3.52	8.79	0.40	2.49
O54774_AI	Ap3d1	AP-3 compl	K.LYASILQQK#.E	54.22	55.90	0.97	1.03
O54774_AI	Ap3d1	AP-3 compl	K.NM*ELNVLDSLNTK#.M	13.20	7.31	1.81	0.55
O54774_AI	Ap3d1	AP-3 compl	K.NYLSLAPLFFK#.L	77.60	33.83	2.29	0.44
O54774_AI	Ap3d1	AP-3 compl	R.RRQPEEDEEELAR.R	2.43	14.47	0.17	5.96
O54774_AI	Ap3d1	AP-3 compl	K.VTYDIQASLQK#.D	30.49	12.48	2.44	0.41
O54774_AI	Ap3d1	AP-3 compl	K.YLGLLAM*SK#.I	21.42	10.70	2.00	0.50
Q9JKC8_AF	Ap3m1	AP-3 compl	K.GLVNLQSGAPK#PEENPNLNIQFK#.I	20.64	20.24	1.02	0.98

Q9JKC8_AF	Ap3m1	AP-3 compl	K.IQQLAISGLK#.V	52.35	42.03	1.25	0.80
Q9JKC8_AF	Ap3m1	AP-3 compl	R.SVVNSITGSSNVGDTLPTGQLSNIPWR.R	3.75	7.00	0.54	1.87
Q9JKC8_AF	Ap3m1	AP-3 compl	R.VSSQNLVAIPVYVK#.H	28.67	19.33	1.48	0.67
Q9JKC8_AF	Ap3m1	AP-3 compl	K.GLVNLQSGAPKPEENPNLNIQFK.I	10.84	4.89	2.21	0.45
Q9JKC8_AF	Ap3m1	AP-3 compl	K.GLVNLQSGAPK#PEENPNLNIQFK#.I	13.64	5.65	2.41	0.41
Q9JKC8_AF	Ap3m1	AP-3 compl	K.IQQLAISGLK#.V	29.67	10.68	2.78	0.36
Q9JKC8_AF	Ap3m1	AP-3 compl	K.VLAWDVGK#.I	17.10	8.62	1.98	0.50
Q9DCR2_AI	Ap3s1	AP-3 compl	K.FYQPYSEDTQQQIIR.E	3.48	3.94	0.88	1.13
Q9DCR2_AI	Ap3s1	AP-3 compl	K.FYQPYSEDTQQQIIR.E	4.89	7.78	0.63	1.59
Q9DCR2_AI	Ap3s1	AP-3 compl	R.NINIGDISIK#.V	51.69	30.22	1.71	0.58
Q9DCR2_AI	Ap3s1	AP-3 compl	R.NINIGDISIK#VPNLPSFK#.-	17.53	11.65	1.50	0.66
Q9DCR2_AI	Ap3s1	AP-3 compl	K.NM*NLPEIPR.N	3.69	11.95	0.31	3.24
Q9DCR2_AI	Ap3s1	AP-3 compl	K.SEAGLAGAPAR.A	6.54	21.22	0.31	3.25
Q9DCR2_AI	Ap3s1	AP-3 compl	K.FYQPYSEDTQQQIIR.E	2.22	7.56	0.29	3.41
Q8BSZ2_AF	Ap3s2	AP-3 compl	R.NINIGDLNIK#.V	8.52	4.54	1.88	0.53
O88879_AI	Apaf1	Apoptotic p	R.GLQLIAGK#.T	13.18	5.21	2.53	0.40
O35841_AI	Api5	Apoptosis i	K.ELPQFATGENLPR.V	12.25	32.61	0.38	2.66
O35841_AI	Api5	Apoptosis i	K.EVEELILTESK#.K	51.36	23.04	2.23	0.45
O35841_AI	Api5	Apoptosis i	K.ITNNINVLIK#.D	69.11	25.70	2.69	0.37
O35841_AI	Api5	Apoptosis i	R.LAAQFIPK#.F	68.86	36.32	1.90	0.53
O35841_AI	Api5	Apoptosis i	R.QAVPLFSK#.N	31.56	16.55	1.91	0.52
O35841_AI	Api5	Apoptosis i	K.SLQTVSGR.Q	15.69	27.92	0.56	1.78
O35841_AI	Api5	Apoptosis i	K.STVTLSWK#PVQK#.V	10.79	24.82	0.43	2.30
O35841_AI	Api5	Apoptosis i	K.TGEALK#TEENK#.I	15.55	10.06	1.55	0.65
O35841_AI	Api5	Apoptosis i	K.VLEDVTGEEFVLFMK#.I	20.41	12.82	1.59	0.63
O35841_AI	Api5	Apoptosis i	K.ITNNINVLIK#.D	17.19	11.53	1.49	0.67
O35841_AI	Api5	Apoptosis i	K.YSSNLSNFNYER.S	24.11	6.09	3.96	0.25
O35841_AI	Api5	Apoptosis i	K.DAYQVILDGVK#.G	21.52	6.34	3.39	0.29
O35841_AI	Api5	Apoptosis i	K.ELPQFATGENLPR.V	4.90	12.43	0.39	2.53
O35841_AI	Api5	Apoptosis i	K.ITNNINVLIK#.D	16.39	8.65	1.90	0.53
O35841_AI	Api5	Apoptosis i	R.K#LPDFLTAK#.L	16.94	12.42	1.36	0.73
O35841_AI	Api5	Apoptosis i	R.LAAQFIPK#.F	21.91	12.19	1.80	0.56
O35841_AI	Api5	Apoptosis i	K.VLEDVTGEEFVLFMK#.I	8.59	4.30	2.00	0.50
O35841_AI	Api5	Apoptosis i	K.DAYQVILDGVK#.G	45.74	19.10	2.39	0.42
O35841_AI	Api5	Apoptosis i	K.ELPQFATGENLPR.V	7.80	16.80	0.46	2.15
O35841_AI	Api5	Apoptosis i	K.EVEELILTESK#.K	18.94	12.27	1.54	0.65
O35841_AI	Api5	Apoptosis i	K.ITNNINVLIK#.D	26.59	13.77	1.93	0.52
O35841_AI	Api5	Apoptosis i	R.LAAQFIPK#.F	32.59	16.16	2.02	0.50
O35841_AI	Api5	Apoptosis i	K.TGEALK#TEENK#IK#.V	33.37	8.73	3.82	0.26
O35841_AI	Api5	Apoptosis i	K.VLEDVTGEEFVLFM*K#.I	6.14	7.68	0.80	1.25
O35841_AI	Api5	Apoptosis i	K.VLEDVTGEEFVLFMK#.I	7.81	3.92	1.99	0.50
Q8C7I4_Q8	Apol9b	Protein Apo	R.ELTALLAIADR.G	17.23	23.48	0.73	1.36
Q8C7I4_Q8	Apol9b	Protein Apo	K.HLYEGSASESAEALRK.L	12.87	24.47	0.53	1.90
Q8C7I4_Q8	Apol9b	Protein Apo	R.ILATTGSISAQR.A	32.95	67.72	0.49	2.05
Q8C7I4_Q8	Apol9b	Protein Apo	R.ILATTGSISAQR.A	1.97	5.61	0.35	2.85
Q8CFQ3_A(	Aqr	Intron-binc	R.AAFAHFPELYDFALSNVAEVDAR.D	4.34	14.91	0.29	3.43
Q8CFQ3_A(	Aqr	Intron-binc	R.AGM*QPGLTM*VVGPPGTGK#.T	8.33	14.55	0.57	1.75
Q8CFQ3_A(	Aqr	Intron-binc	K.DADGEEDDTEEAK#.T	2.50	2.49	1.01	0.99
Q8CFQ3_A(	Aqr	Intron-binc	K.FISVLK#.S	19.08	12.99	1.47	0.68
Q8CFQ3_A(	Aqr	Intron-binc	K.M*PNQIATLDFNDTFLSIEHLK#.A	35.77	23.37	1.53	0.65
Q8CFQ3_A(	Aqr	Intron-binc	R.NFNLFR.L	4.01	15.42	0.26	3.84
Q8CFQ3_A(	Aqr	Intron-binc	R.RIELLEEVKR.L	2.97	40.41	0.07	13.61
Q8CFQ3_A(	Aqr	Intron-binc	K.TDVAVQIISNIYHNFPEQR.T	9.29	33.34	0.28	3.59
Q8CFQ3_A(	Aqr	Intron-binc	R.TLIVTHSNQALNQLFEK#.I	29.81	28.32	1.05	0.95
Q8CFQ3_A(	Aqr	Intron-binc	K.VIEEIYEK#EIVK#.S	22.82	16.02	1.42	0.70
Q8CFQ3_A(	Aqr	Intron-binc	R.VNYVLAR.R	6.72	29.19	0.23	4.34
Q8CFQ3_A(	Aqr	Intron-binc	K.YSNM*EQSLFTR.F	3.02	15.80	0.19	5.24
P04627_AF	Araf	Serine/thre	K.IGDFGLATVK#.T	14.52	8.68	1.67	0.60
Q5XJY5_CC	Arcn1	Coatomer s	R.ENVNLAQIR.T	17.77	57.40	0.31	3.23
Q5XJY5_CC	Arcn1	Coatomer s	R.FSTETTFLVDK#YEIL.-	46.12	23.85	1.93	0.52
Q5XJY5_CC	Arcn1	Coatomer s	K.GK#EVDNFVDK#.L	34.19	14.18	2.41	0.41
Q5XJY5_CC	Arcn1	Coatomer s	K.GK#EVDNFVDK#LK#.S	15.55	12.57	1.24	0.81
Q5XJY5_CC	Arcn1	Coatomer s	R.IEGLLAAFPK#.L	36.00	25.71	1.40	0.71
Q5XJY5_CC	Arcn1	Coatomer s	R.ISDDKFGR.I	7.08	15.12	0.47	2.14
Q5XJY5_CC	Arcn1	Coatomer s	K.KAPGFGGFGSSAVSGGSTAAM*ITETIIETDKPK.V	2.88	2.73	1.05	0.95
Q5XJY5_CC	Arcn1	Coatomer s	K.KAPGFGGFGSSAVSGGSTAAMITETIIETDKPK.V	6.96	4.50	1.55	0.65
Q5XJY5_CC	Arcn1	Coatomer s	K.LFTAESLIGLK#.N	166.64	83.47	2.00	0.50
Q5XJY5_CC	Arcn1	Coatomer s	R.LHVENEDK#K#.G	11.75	6.67	1.76	0.57
Q5XJY5_CC	Arcn1	Coatomer s	K.LYM*VLITTK#.N	15.79	10.03	1.57	0.64
Q5XJY5_CC	Arcn1	Coatomer s	K.NSNILEDLETLR.L	34.01	96.33	0.35	2.83
Q5XJY5_CC	Arcn1	Coatomer s	K.SEGETIMSSNM*GK#.R	13.91	9.24	1.51	0.66
Q5XJY5_CC	Arcn1	Coatomer s	K.SEGETIMSSNMGK#.R	8.41	4.78	1.76	0.57
Q5XJY5_CC	Arcn1	Coatomer s	K.SEGETIM*SSNM*GK#.R	17.93	10.83	1.65	0.60
Q5XJY5_CC	Arcn1	Coatomer s	K.SEGETIM*SSNMGK#.R	10.74	4.83	2.22	0.45
Q5XJY5_CC	Arcn1	Coatomer s	K.SFPVNSDVGVLK#.W	65.96	38.01	1.74	0.58
Q5XJY5_CC	Arcn1	Coatomer s	R.TFTEM*DSHEEK#.V	15.96	12.78	1.25	0.80
Q5XJY5_CC	Arcn1	Coatomer s	R.TFTEMDSHEEK#.V	17.11	16.27	1.05	0.95
Q5XJY5_CC	Arcn1	Coatomer s	R.TRIEGLLAAFPK.L	7.55	24.18	0.31	3.20
Q5XJY5_CC	Arcn1	Coatomer s	K.VHAPPINMESVHM*K#.I	8.21	5.27	1.56	0.64
Q5XJY5_CC	Arcn1	Coatomer s	K.VHAPPINMESVHMK#.I	11.41	4.44	2.57	0.39
Q5XJY5_CC	Arcn1	Coatomer s	K.VTQVDGNSPVR.F	42.81	102.85	0.42	2.40
Q5XJY5_CC	Arcn1	Coatomer s	R.YVYQPM*EK#.L	37.16	30.44	1.22	0.82
Q5XJY5_CC	Arcn1	Coatomer s	R.IEGLLAAFPK#.L	108.32	39.55	2.74	0.37
Q5XJY5_CC	Arcn1	Coatomer s	K.LYM*VLITTK#.N	21.37	12.61	1.69	0.59
Q5XJY5_CC	Arcn1	Coatomer s	K.LYMVLITTK#.N	58.60	17.80	3.29	0.30
Q5XJY5_CC	Arcn1	Coatomer s	K.NSNILEDLETLR.L	51.79	85.42	0.61	1.65
Q5XJY5_CC	Arcn1	Coatomer s	R.TRIEGLLAAFPK.L	24.06	37.78	0.64	1.57
Q5XJY5_CC	Arcn1	Coatomer s	R.YVYQPM*EK#.L	38.27	16.06	2.38	0.42
Q5XJY5_CC	Arcn1	Coatomer s	R.IEGLLAAFPK#.L	12.38	10.76	1.15	0.87
Q5XJY5_CC	Arcn1	Coatomer s	K.LFTAESLIGLK#.N	18.53	9.74	1.90	0.53
Q5XJY5_CC	Arcn1	Coatomer s	K.NSNILEDLETLR.L	9.66	27.82	0.35	2.88
Q5XJY5_CC	Arcn1	Coatomer s	K.SFPVNSDVGVLK#.W	17.01	19.50	0.87	1.15
Q5XJY5_CC	Arcn1	Coatomer s	K.VTQVDGNSPVR.F	4.45	17.33	0.26	3.89
Q5XJY5_CC	Arcn1	Coatomer s	R.FSTETTFLVDK#YEIL.-	11.77	5.45	2.16	0.46
Q5XJY5_CC	Arcn1	Coatomer s	K.LFTAESLIGLK#.N	19.33	9.34	2.07	0.48
Q5XJY5_CC	Arcn1	Coatomer s	K.SEGETIM*SSNM*GK#.R	4.97	2.64	1.89	0.53
Q5XJY5_CC	Arcn1	Coatomer s	R.TFTEM*DSHEEK#.V	4.94	3.18	1.55	0.64
Q5XJY5_CC	Arcn1	Coatomer s	K.VTQVDGNSPVR.F	25.53	15.96	1.60	0.63
P84078_AF	Arf1	ADP-ribosy	R.ILMVGLDAAGK#.T	16.71	8.48	1.97	0.51
P84078_AF	Arf1	ADP-ribosy	K.LGEIVTTIPTIGFNVETVEYK#.N	7.56	2.30	3.29	0.30
P84078_AF	Arf1	ADP-ribosy	K.NISFTVWDVGGQDK#.I	9.51	5.18	1.84	0.54
P84078_AF	Arf1	ADP-ribosy	R.DAVLLVFANK#.Q	763.58	326.98	2.34	0.43
P84078_AF	Arf1	ADP-ribosy	R.HYFQNTQGLIFVVDSNDR.E	7.72	18.95	0.41	2.46

P84078_AF	Arf1	ADP-ribosy	R.HYFQNTQGLIFVVDSNDRER.V	4.23	35.01	0.12	8.28
P84078_AF	Arf1	ADP-ribosy	R.ILM*VGLDAAGK#.T	851.94	541.27	1.57	0.64
P84078_AF	Arf1	ADP-ribosy	K.LGEIVTTIPTIGFNVETVEYK#.N	167.18	72.27	2.31	0.43
P84078_AF	Arf1	ADP-ribosy	K.LK#LGEIVTTIPTIGFNVETVEYK#.N	49.03	27.99	1.75	0.57
P84078_AF	Arf1	ADP-ribosy	R.M*LAEDELR.D	28.93	67.91	0.43	2.35
P84078_AF	Arf1	ADP-ribosy	K.NISFTVWDVGGQDK#.I	247.42	93.84	2.64	0.38
P84078_AF	Arf1	ADP-ribosy	K.QDLPNAM*NAAEITDK#.L	28.37	11.64	2.44	0.41
P84078_AF	Arf1	ADP-ribosy	K.QDLPNAMNAAEITDK#.L	18.67	8.52	2.19	0.46
P84078_AF	Arf1	ADP-ribosy	K.QDLPNAM*NAAEITDKLGLHSLR.H	4.17	11.50	0.36	2.76
P84078_AF	Arf1	ADP-ribosy	K.QDLPNAMNAAEITDKLGLHSLR.H	5.25	17.00	0.31	3.24
P84078_AF	Arf1	ADP-ribosy	R.ILMVGLDAAGK#.T	17.74	11.15	1.59	0.63
P84078_AF	Arf1	ADP-ribosy	K.LGEIVTTIPTIGFNVETVEYK#.N	44.85	19.95	2.25	0.44
P84078_AF	Arf1	ADP-ribosy	K.NISFTVWDVGGQDK#.I	11.95	6.99	1.71	0.59
P84078_AF	Arf1	ADP-ribosy	R.ILMVGLDAAGK#.T	21.42	8.37	2.56	0.39
P84078_AF	Arf1	ADP-ribosy	K.LGEIVTTIPTIGFNVETVEYK#.N	39.84	16.13	2.47	0.40
P84078_AF	Arf1	ADP-ribosy	K.NISFTVWDVGGQDK#.I	11.15	8.09	1.38	0.73
P61750_AF	Arf4	ADP-ribosy	R.IQEGAAVLQK#.M	22.16	11.92	1.86	0.54
P61750_AF	Arf4	ADP-ribosy	R.IQEGAAVLQK#.M	220.05	143.40	1.53	0.65
P61750_AF	Arf4	ADP-ribosy	K.LGLQSLR.N	9.16	40.88	0.22	4.46
P61750_AF	Arf4	ADP-ribosy	K.QDLPNAM*AISEM*TDK#.L	6.07	5.38	1.13	0.89
P61750_AF	Arf4	ADP-ribosy	R.IQEGAAVLQK#.M	31.74	17.92	1.77	0.56
P84084_AF	Arf5	ADP-ribosy	K.QDM*PNAM*PVSELTDK#.L	2.37	2.01	1.18	0.85
P84084_AF	Arf5	ADP-ribosy	R.VQESADELQK#.M	85.33	48.28	1.77	0.57
P62331_AF	Arf6	ADP-ribosy	K.FNVWDVGGQDK#.I	9.94	4.20	2.37	0.42
P62331_AF	Arf6	ADP-ribosy	K.LGQSVTTIPTVGFNVETVTYK#.N	8.96	2.67	3.36	0.30
P62331_AF	Arf6	ADP-ribosy	K.LGQSVTTIPTVGFNVETVTYK#.N	3.56	2.35	1.51	0.66
P62331_AF	Arf6	ADP-ribosy	R.DAIILIFANK#.Q	120.98	53.36	2.27	0.44
P62331_AF	Arf6	ADP-ribosy	K.FNVWDVGGQDK#.I	85.82	42.08	2.04	0.49
P62331_AF	Arf6	ADP-ribosy	R.ILM*LGLDAAGK#.T	68.15	70.34	0.97	1.03
P62331_AF	Arf6	ADP-ribosy	R.ILMLGLDAAGK#.T	57.17	22.42	2.55	0.39
P62331_AF	Arf6	ADP-ribosy	K.LGQSVTTIPTVGFNVETVTYK#.N	110.21	43.50	2.53	0.39
P62331_AF	Arf6	ADP-ribosy	K.LK#LGQSVTTIPTVGFNVETVTYK#.N	12.16	6.39	1.90	0.53
P62331_AF	Arf6	ADP-ribosy	R.DAIILIFANK#.Q	14.11	5.92	2.39	0.42
P62331_AF	Arf6	ADP-ribosy	K.LGQSVTTIPTVGFNVETVTYK#.N	3.43	2.16	1.59	0.63
P62331_AF	Arf6	ADP-ribosy	K.LGQSVTTIPTVGFNVETVTYK#.N	10.08	4.12	2.45	0.41
P62331_AF	Arf6	ADP-ribosy	R.DAIILIFANK#.Q	20.88	5.96	3.50	0.29
P62331_AF	Arf6	ADP-ribosy	K.LGQSVTTIPTVGFNVETVTYK#.N	16.50	8.41	1.96	0.51
Q9EPJ9_AR	Arfgap1	ADP-ribosy	R.IFDDVSSGVSQLASK#.V	4.10	3.85	1.07	0.94
Q99K28_AI	Arfgap2	ADP-ribosy	R.EVDSEYEAR.S	2.87	17.63	0.16	6.15
Q99K28_AI	Arfgap2	ADP-ribosy	R.LGM*GLVSR.S	4.92	21.58	0.23	4.39
Q99K28_AI	Arfgap2	ADP-ribosy	R.SQLDLFDDVGTFASGPPK.Y	14.21	17.21	0.83	1.21
Q99K28_AI	Arfgap2	ADP-ribosy	R.SSISHSVLSEM*QM*IEQETPLSAK#.S	4.19	4.59	0.91	1.10
Q99K28_AI	Arfgap2	ADP-ribosy	R.STELDSNWSWLQLR.C	2.61	13.00	0.20	4.98
Q99K28_AI	Arfgap2	ADP-ribosy	K.VSNQSFTEIER.Q	7.29	37.44	0.19	5.13
Q99K28_AI	Arfgap2	ADP-ribosy	K.YKDNPFSLGETFGSR.W	3.03	15.24	0.20	5.02
Q99K28_AI	Arfgap2	ADP-ribosy	R.SQLDLFDDVGTFASGPPK.Y	4.58	5.57	0.82	1.22
Q9D8S3_AI	Arfgap3	ADP-ribosy	R.LSTSSSISSADLFDEQR.K	3.07	10.45	0.29	3.41
Q9D8S3_AI	Arfgap3	ADP-ribosy	K.LTNTSFTEIEK#.Q	31.92	17.75	1.80	0.56
Q9D8S3_AI	Arfgap3	ADP-ribosy	R.SSSFSSWDDGADSYWK#.K	6.48	3.72	1.74	0.57
Q9D8S3_AI	Arfgap3	ADP-ribosy	K.YQEDPEDSYFSSSSK#.W	13.30	8.23	1.61	0.62
Q9D8S3_AI	Arfgap3	ADP-ribosy	R.LSTSSSISSADLFDEQR.K	1.80	3.47	0.52	1.93
Q9D8S3_AI	Arfgap3	ADP-ribosy	K.LTNTSFTEIEK#.Q	17.67	9.51	1.86	0.54
A2RSX9_A2	Arfip1	Arfip1 prot	K.EGVTEAGAPQGGQR.T	16.88	30.78	0.55	1.82
G5E8V9_G5	Arfip1	MCG18094	K.GGPVILADEIK#.N	23.05	10.85	2.12	0.47
G5E8V9_G5	Arfip1	MCG18094	K.K#YENILK#.L	68.98	22.73	3.04	0.33
G5E8V9_G5	Arfip1	MCG18094	R.LK#TPGVDAPSWLEEQ.-	21.63	8.47	2.55	0.39
G5E8V9_G5	Arfip1	MCG18094	K.LTQQAGDLTVPAGGQR.T	7.85	20.30	0.39	2.59
G5E8V9_G5	Arfip1	MCG18094	R.NQLVLFHSAVAAYFAGNQK#.Q	16.14	9.88	1.63	0.61
G5E8V9_G5	Arfip1	MCG18094	K.QLGDAFADLSLK#.S	30.56	12.54	2.44	0.41
G5E8V9_G5	Arfip1	MCG18094	K.SLELHEEFGYNADTQK#.L	8.98	3.53	2.54	0.39
G5E8V9_G5	Arfip1	MCG18094	R.TDLEELNLGPR.D	20.05	34.78	0.58	1.73
G5E8V9_G5	Arfip1	MCG18094	K.TIEDTLM*TVK#.Q	47.11	13.59	3.47	0.29
G5E8V9_G5	Arfip1	MCG18094	K.TPGVDAPSWLEEQ.-	13.33	13.33	1.00	1.00
G5E8V9_G5	Arfip1	MCG18094	K.WSLNTYK#.C	24.85	9.86	2.52	0.40
A2RSX9_A2	Arfip1	Arfip1 prot	K.EGVTEAGAPQGGQR.T	1.51	4.55	0.33	3.00
Q8K221_AI	Arfip2	Arfaptin-2 (	K.QLEQTLQQFNIK#.L	6.31	12.07	0.52	1.91
Q5FWK3_R	Arhgap1	Rho GTPase	K.FLLDHQGELFPSTDAQGV.-	32.83	32.83	1.00	1.00
Q5FWK3_R	Arhgap1	Rho GTPase	K.LEQLGIPR.Q	5.93	15.98	0.37	2.69
Q5FWK3_R	Arhgap1	Rho GTPase	K.SPGQDPIPIVLR.E	4.09	12.74	0.32	3.11
Q5FWK3_R	Arhgap1	Rho GTPase	K.WDDPYYDIAR.H	5.93	5.54	1.07	0.93
Q5FWK3_R	Arhgap1	Rho GTPase	K.FLLDHQGELFPSTDAQGV.-	10.79	10.79	1.00	1.00
Q5FWK3_R	Arhgap1	Rho GTPase	K.FLLDHQGELFPSTDAQGV.-	9.17	9.17	1.00	1.00
Q8C0D4_RI	Arhgap12	Rho GTPase	R.LFGHFPGPEFLDIEK#.T	7.75	3.97	1.95	0.51
Q3UIA2_RH	Arhgap17	Rho GTPase	R.ADSSSGGGPVFSSTGILEQGLSPGDSSPPK#PK#.D	7.45	2.16	3.44	0.29
Q3UIA2_RH	Arhgap17	Rho GTPase	K.EIM*DPLYGIAEVEIPNIQK#.Q	4.91	3.79	1.30	0.77
Q3UIA2_RH	Arhgap17	Rho GTPase	K.LAQTSDVNK#.M	15.17	7.53	2.02	0.50
Q3UIA2_RH	Arhgap17	Rho GTPase	K.LPLTALAQNM*QEASAQLEESLLGK#.M	5.48	3.68	1.49	0.67
Q3UIA2_RH	Arhgap17	Rho GTPase	K.SSGTNFQGLPSK#.I	21.46	22.09	0.97	1.03
Q3UIA2_RH	Arhgap17	Rho GTPase	K.TEVLSEDLLQIER.R	4.15	11.46	0.36	2.76
Q3UIA2_RH	Arhgap17	Rho GTPase	R.ADSSSGGGPVFSSTGILEQGLSPGDSSPPK#PK#.D	3.85	2.00	1.92	0.52
Q3UIA2_RH	Arhgap17	Rho GTPase	K.EVPGHILLDIDNDTESTAL.-	5.16	5.16	1.00	1.00
Q3UIA2_RH	Arhgap17	Rho GTPase	K.SSGTNFQGLPSK#.I	15.56	7.55	2.06	0.49
Q8K0Q5_RI	Arhgap18	Rho GTPase	R.FLSQESGVAQTLK#.K	9.86	3.79	2.60	0.38
Q91YM2_R	Arhgap35	Rho GTPase	K.ESLSYVVESIEK#.S	7.69	3.22	2.39	0.42
Q91YM2_R	Arhgap35	Rho GTPase	K.FVSNLYNQLAK#.T	9.55	4.68	2.04	0.49
Q91YM2_R	Arhgap35	Rho GTPase	R.GDTSGETLHSLIQQGQQIASK#.L	5.48	4.07	1.35	0.74
Q91YM2_R	Arhgap35	Rho GTPase	R.IPTYNISVVGLSGTEK#.E	4.99	2.79	1.79	0.56
P97393_RH	Arhgap5	Rho GTPase	R.IPFDLLSTLEAEK#.V	9.09	5.19	1.75	0.57
P97393_RH	Arhgap5	Rho GTPase	R.TQSTDDEYALDGK#.I	15.84	8.54	1.85	0.54
Q61210_AI	Arhgef1	Rho guanin	R.APGPVHTQEIEENLLSLEVAIR.Q	3.01	5.97	0.50	1.98
Q61210_AI	Arhgef1	Rho guanin	R.FDGAEGSWFQK#.I	14.24	7.94	1.79	0.56
Q61210_AI	Arhgef1	Rho guanin	K.K#AFLDFYHSFLEK#.T	11.48	5.81	1.98	0.51
Q61210_AI	Arhgef1	Rho guanin	R.LLSHLEETQHTISTDEEK#.S	16.37	6.59	2.49	0.40
Q61210_AI	Arhgef1	Rho guanin	R.LRPLLSQLGGTLSPNLAAPER.S	2.23	11.70	0.19	5.25
Q61210_AI	Arhgef1	Rho guanin	R.QSFALEQLK#.A	17.11	8.87	1.93	0.52
Q61210_AI	Arhgef1	Rho guanin	R.ELVPPDTLLSLPK#.S	33.05	23.94	1.38	0.72
Q61210_AI	Arhgef1	Rho guanin	R.LLSHLEETQHTISTDEEK#.S	22.95	9.16	2.51	0.40
Q61210_AI	Arhgef1	Rho guanin	R.LRPLLSQLGGTLSPNLAAPER.S	3.15	8.55	0.37	2.71
Q61210_AI	Arhgef1	Rho guanin	R.QSFALEQLK#.A	19.51	6.18	3.16	0.32
Q61210_AI	Arhgef1	Rho guanin	R.VPVPPSVAFELDR.T	3.61	8.32	0.43	2.30
Q8C033_AI	Arhgef10	Rho guanin	K.APDGSWNSEPQQVIK#.L	5.84	3.23	1.81	0.55
Q8C033_AI	Arhgef10	Rho guanin	R.YILGSIVESEK#.N	8.86	3.91	2.27	0.44
A2AWP8_A	Arhgef10l	Rho guanin	R.LADQVAEIQQLTK#.S	9.70	3.19	3.04	0.33

Q6P9R4_AI	Arhgef18	Rho guanin	K.IGDVLVQQFSGETGER.M	3.39	6.41	0.53	1.89
Q6P9R4_AI	Arhgef18	Rho guanin	R.LSLK#DQLIAQSLLEK#.Q	13.23	29.46	0.45	2.23
Q60875_AI	Arhgef2	Rho guanin	R.FLNQLLER.R	5.30	18.65	0.28	3.52
Q60875_AI	Arhgef2	Rho guanin	K.YIFTSLDKPSVVSLQNLIVR.D	4.66	21.77	0.21	4.67
Q60875_AI	Arhgef2	Rho guanin	R.AAVASVTPEK#.Q	46.46	40.40	1.15	0.87
Q60875_AI	Arhgef2	Rho guanin	K.AGFVGM*PPPALPR.G	12.18	26.19	0.46	2.15
Q60875_AI	Arhgef2	Rho guanin	R.EAQELGSPEDR.L	3.04	10.72	0.28	3.53
Q60875_AI	Arhgef2	Rho guanin	R.FLNQLLER.R	15.68	54.76	0.29	3.49
Q60875_AI	Arhgef2	Rho guanin	R.ILQNSHGVEEEYQDLASALGLVK#.E	77.37	47.63	1.62	0.62
Q60875_AI	Arhgef2	Rho guanin	R.LGDLLISQFSGSNAEQMR.K	2.80	9.33	0.30	3.33
Q60875_AI	Arhgef2	Rho guanin	R.LM*EALFPEGPER.W	7.19	19.65	0.37	2.73
Q60875_AI	Arhgef2	Rho guanin	R.M*QDIPEETESR.D	5.09	16.89	0.30	3.32
Q60875_AI	Arhgef2	Rho guanin	R.NNTALQSVSLR.S	7.10	35.88	0.20	5.06
Q60875_AI	Arhgef2	Rho guanin	K.QATELALLQR.Q	4.98	30.58	0.16	6.14
Q60875_AI	Arhgef2	Rho guanin	K.YIFTSLDKPSVVSLQNLIVR.D	18.56	55.63	0.33	3.00
Q60875_AI	Arhgef2	Rho guanin	K.YPVLINR.I	5.00	17.35	0.29	3.47
Q3UPH7_A	Arhgef40	Rho guanin	R.AAVQLLQEQEAR.G	4.86	12.98	0.37	2.67
Q3UPH7_A	Arhgef40	Rho guanin	R.ALALDLGSPAALR.E	2.75	12.42	0.22	4.52
Q3UPH7_A	Arhgef40	Rho guanin	R.EALALEEDLTSQK#.V	7.55	10.81	0.70	1.43
Q3UPH7_A	Arhgef40	Rho guanin	R.EALLAALALR.R	4.46	15.84	0.28	3.55
Q3UPH7_A	Arhgef40	Rho guanin	R.GSPVDAEASGLSR.T	2.56	8.07	0.32	3.15
Q9ES28_AF	Arhgef7	Rho guanin	K.ELELQILTEPIR.S	3.47	16.50	0.21	4.76
Q9ES28_AF	Arhgef7	Rho guanin	K.FNFQQTNEDELSFSK#.G	11.33	6.20	1.83	0.55
Q9ES28_AF	Arhgef7	Rho guanin	R.K#STAALEEDAQILK#.V	5.14	3.29	1.56	0.64
Q9ES28_AF	Arhgef7	Rho guanin	R.LDK#YPTLLK#.E	20.68	9.43	2.19	0.46
Q9ES28_AF	Arhgef7	Rho guanin	K.LPTTGM*TITK#.L	22.61	20.91	1.08	0.92
Q9ES28_AF	Arhgef7	Rho guanin	K.NM*NDPAWDETNL.-	5.44	5.44	1.00	1.00
Q9ES28_AF	Arhgef7	Rho guanin	K.SLVDTVYALKDEVQELR.Q	8.59	34.75	0.25	4.05
Q9ES28_AF	Arhgef7	Rho guanin	K.STAALEEDAQILK#.V	14.27	9.58	1.49	0.67
A2BH40_AI	Arid1a	AT-rich inte	R.EEAGGEAAAAAAER.G	2.30	10.23	0.22	4.45
A2BH40_AI	Arid1a	AT-rich inte	K.EIGGLTQVNK#.N	25.03	11.19	2.24	0.45
A2BH40_AI	Arid1a	AT-rich inte	R.ELATNLNVGTSSSAASSLK#.K	6.86	3.09	2.22	0.45
A2BH40_AI	Arid1a	AT-rich inte	R.EM*AVVLLANLAQGDSLAAR.A	4.39	9.69	0.45	2.21
A2BH40_AI	Arid1a	AT-rich inte	R.ITATM*DDM*LSTR.S	3.74	8.45	0.44	2.26
A2BH40_AI	Arid1a	AT-rich inte	K.LSIQDNNVDLILATPPFSR.L	3.16	10.41	0.30	3.29
A2BH40_AI	Arid1a	AT-rich inte	R.RPAGGPQNQFPFQFGR.D	3.13	12.54	0.25	4.00
A2BH40_AI	Arid1a	AT-rich inte	K.VDENHSEFTLYESR.L	4.75	16.33	0.29	3.44
E9Q6R4_E9	Arid1b	Protein Ari	R.GSPVSSLPAVGK#.K	7.99	7.09	1.13	0.89
E9Q6R4_E9	Arid1b	Protein Ari	R.HM*DGM*YGPPAK#.R	2.92	3.18	0.92	1.09
E9Q6R4_E9	Arid1b	Protein Ari	K.SSPALAAPDASVDPK.E	8.17	8.85	0.92	1.08
A2CG63_AI	Arid4b	AT-rich inte	R.SANIDFQM*ALPEK#.V	9.22	2.52	3.66	0.27
Q9Z1K5_AF	Arih1	E3 ubiquiti	R.DISQDSLQDIK#.Q	15.15	3.39	4.47	0.22
Q9Z1K5_AF	Arih1	E3 ubiquiti	K.YR@YCESR.R	2.22	28.99	0.08	13.09
Q9Z1K5_AF	Arih1	E3 ubiquiti	R.DISQDSLQDIK#.Q	19.60	13.78	1.42	0.70
P61211_AF	Arl1	ADP-ribosy	K.AILVVFANK.Q	10.67	8.52	1.25	0.80
P61211_AF	Arl1	ADP-ribosy	K.GTGLDEAM*EWLVETLK#.S	8.58	6.82	1.26	0.80
Q9D0J4_AF	Arl2	ADP-ribosy	K.K#FNGEDVDTISPTLGFNIK#.T	4.15	4.23	0.98	1.02
Q9D0J4_AF	Arl2	ADP-ribosy	R.LAGATLLIFANK#.Q	31.06	9.14	3.40	0.29
Q9D0J4_AF	Arl2	ADP-ribosy	R.LLM*LGLDNAGK#.T	23.08	10.64	2.17	0.46
Q9D0J4_AF	Arl2	ADP-ribosy	K.LNIWDVGGQK#.S	16.92	5.69	2.97	0.34
Q9WUL7_A	Arl3	ADP-ribosy	R.ILLLGLDNAGK#.T	19.64	3.77	5.21	0.19
Q9JM93_AI	Arl6ip4	ADP-ribosy	R.LIK#GDGEVLEEIVTK#.E	8.62	8.79	0.98	1.02
Q9JM93_AI	Arl6ip4	ADP-ribosy	R.SAGEDNDGPVLTDEQK#.S	4.45	5.93	0.75	1.33
Q8R5J9_PF	Arl6ip5	PRA1 famil	R.AWDDFFPGSDR.F	9.63	47.17	0.20	4.90
Q8R5J9_PF	Arl6ip5	PRA1 famil	K.K#TPM*GIILDALEQQEDNINK#.F	2.79	2.43	1.15	0.87
Q8R5J9_PF	Arl6ip5	PRA1 famil	K.K#TPMGIILDALEQQEDNINK#.F	7.23	9.05	0.80	1.25
Q8R5J9_PF	Arl6ip5	PRA1 famil	K.TPM*GIILDALEQQEDNINK#.F	26.71	27.27	0.98	1.02
Q8R5J9_PF	Arl6ip5	PRA1 famil	K.TPMGIILDALEQQEDNINK#.F	7.94	7.85	1.01	0.99
Q8VEH3_AI	Arl8a	ADP-ribosy	R.DLAGALDEK#ELIEK#.M	7.50	3.26	2.30	0.43
Q8VEH3_AI	Arl8a	ADP-ribosy	K.LWDIGGQPR.F	12.11	9.78	1.24	0.81
G3X920_G	Armc8	Armadillo r	R.IVTGLSESSVK#.V	14.58	4.28	3.41	0.29
P53762_AF	Arnt	Aryl hydroc	R.FPEIYPSITADQSK.G	4.07	5.22	0.78	1.28
Q9CVB6_AI	Arpc2	Actin-relate	R.DDETM*YVESK#.K	10.81	2.28	4.73	0.21
Q9CVB6_AI	Arpc2	Actin-relate	K.DSIVHQAGM*LK#.R	8.97	2.07	4.33	0.23
Q9CVB6_AI	Arpc2	Actin-relate	K.ELQAHGADELLK#.R	5.54	5.89	0.94	1.06
Q9CVB6_AI	Arpc2	Actin-relate	R.IIEETLALK#.F	41.47	14.21	2.92	0.34
Q9JM76_AI	Arpc3	Actin-relate	K.ANVFFK#.N	26.08	7.00	3.73	0.27
Q9JM76_AI	Arpc3	Actin-relate	R.ETK#DTDIVDEAIYYFK#.A	72.86	17.86	4.08	0.25
Q9JM76_AI	Arpc3	Actin-relate	K.LIGNM*ALLPLR.S	26.71	27.36	0.98	1.02
Q9JM76_AI	Arpc3	Actin-relate	K.ANVFFK#.N	12.59	3.71	3.40	0.29
P59999_AF	Arpc4	Actin-relate	R.AENFFILR.R	45.24	47.38	0.95	1.05
P59999_AF	Arpc4	Actin-relate	R.IVAEEFLK#.N	240.59	64.01	3.76	0.27
P59999_AF	Arpc4	Actin-relate	K.VLIEGSINSVR.V	33.92	42.92	0.79	1.27
Q9D898_AI	Arpc5l	Actin-relate	K.ALAVGGLGSIIR.V	59.04	61.96	0.95	1.05
Q9D898_AI	Arpc5l	Actin-relate	R.AQGVVLK#.V	48.85	10.12	4.83	0.21
Q9D898_AI	Arpc5l	Actin-relate	K.SSEIEQAVQSLDR.N	13.52	18.20	0.74	1.35
Q9D0A3_AI	Arpin	Arpin OS=M	R.GDGPFIDSLAK#.L	10.07	6.76	1.49	0.67
Q9D0A3_AI	Arpin	Arpin OS=M	R.LPGTWDPATHQGGNGILLEGELVDVSR.H	7.92	27.72	0.29	3.50
Q9D0A3_AI	Arpin	Arpin OS=M	K.TGASWTDNIM*AQK#.S	7.18	5.21	1.38	0.73
Q9QWY8_A	Asap1	Arf-GAP wit	K.AIYNSGQDHVQNEENYAQVLDK#.F	9.87	4.91	2.01	0.50
Q9QWY8_A	Asap1	Arf-GAP wit	R.GEQSTGENSLEDLTK#.A	13.39	9.71	1.38	0.73
Q9QWY8_A	Asap1	Arf-GAP wit	K.GVDLLQNLIK#.Y	9.54	10.76	0.89	1.13
Q9QWY8_A	Asap1	Arf-GAP wit	R.IQSLELDK#LGTSELLLAK#.N	25.95	12.64	2.05	0.49
Q9QWY8_A	Asap1	Arf-GAP wit	R.NTVTLLEEALDQDR.T	2.81	6.11	0.46	2.17
E9PZJ8_AS	Ascc3	Activating s	K.AGEDGEVSGEGVLPFDPK.E	8.46	6.06	1.40	0.72
E9PZJ8_AS	Ascc3	Activating s	K.ALAAEM*TNYFSK#.R	11.74	8.55	1.37	0.73
E9PZJ8_AS	Ascc3	Activating s	R.DLADWLNIK#.Q	15.07	11.84	1.27	0.79
E9PZJ8_AS	Ascc3	Activating s	K.ELTGDM*QLSK#.S	13.89	12.51	1.11	0.90
E9PZJ8_AS	Ascc3	Activating s	K.FLNEQFQEPYTPELKPVEK.T	19.32	21.72	0.89	1.12
E9PZJ8_AS	Ascc3	Activating s	R.FRPVPLGQTFLGIK.S	2.04	9.23	0.22	4.52
E9PZJ8_AS	Ascc3	Activating s	R.GEM*DSFSLISDSAYVAQNAAR.I	3.49	8.94	0.39	2.56
E9PZJ8_AS	Ascc3	Activating s	K.QDNYNEEVADLK#.L	10.86	8.55	1.27	0.79
E9PZJ8_AS	Ascc3	Activating s	K.RLEPLGIVVK.E	4.41	18.79	0.23	4.26
E9PZJ8_AS	Ascc3	Activating s	K.TEGDIFAIVSK#.A	16.91	11.48	1.47	0.68
E9PZJ8_AS	Ascc3	Activating s	K.TVAAELAIFR.V	5.54	12.77	0.43	2.31
E9PZJ8_AS	Ascc3	Activating s	R.YVDFPITDVLQM*M*GR.A	4.71	5.31	0.89	1.13
Q9CQE6_AS	Asf1a	Histone cha	R.ENPPVK#PDFSK#.L	3.68	3.34	1.10	0.91
Q9CQE6_AS	Asf1a	Histone cha	R.VGYYVNNEYTETELR.E	2.75	8.62	0.32	3.14
Q91X20_AS	Ash2l	Set1/Ash2 I	K.FGLLDQDLSNIGPAYDNQK#.Q	8.11	4.60	1.76	0.57
O54984_AS	Asna1	ATPase Asna	R.ESVLIISTDPAHNISDAFDQK#.F	18.89	15.56	1.21	0.82
O54984_AS	Asna1	ATPase Asna	R.LLNFPTIVER.G	25.59	22.28	1.15	0.87
O54984_AS	Asna1	ATPase Asna	K.YLDQM*EDLYEDFHIVK#.L	18.85	12.03	1.57	0.64
O54984_AS	Asna1	ATPase Asna	K.YLDQMEDLYEDFHIVK#.L	20.01	13.52	1.48	0.68

Q61024_A	Asns	Asparagine	R.ASVGM*YLISK#.Y	43.23	8.98	4.82	0.21
Q61024_A	Asns	Asparagine	R.ASVGMYLISK#.Y	50.59	14.10	3.59	0.28
Q61024_A	Asns	Asparagine	K.EAFSDGITSVK#.N	169.24	38.05	4.45	0.22
Q61024_A	Asns	Asparagine	K.ELYLFDVLR.A	37.20	32.48	1.15	0.87
Q61024_A	Asns	Asparagine	K.FPFNTPK#.T	50.74	15.31	3.31	0.30
Q61024_A	Asns	Asparagine	K.HSTTPFLK#.V	151.78	35.54	4.27	0.23
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEM*M*SAASQK#.F	46.91	9.35	5.02	0.20
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEM*MSAASQK#.F	15.40	2.65	5.81	0.17
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEMMSAASQK#.F	28.91	7.12	4.06	0.25
Q61024_A	Asns	Asparagine	R.K#NTDSVVIFSGEGSDELTQGYIYFHK#.A	48.75	12.76	3.82	0.26
Q61024_A	Asns	Asparagine	R.KNTDSVVIFSGEGSDELTQGYIYFHK.A	17.85	3.89	4.59	0.22
Q61024_A	Asns	Asparagine	R.LAVVDPLFGM*QPIR.V	16.21	16.85	0.96	1.04
Q61024_A	Asns	Asparagine	R.LAVVDPLFGMQPIR.V	18.85	21.14	0.89	1.12
Q61024_A	Asns	Asparagine	K.NTDSVVIFSGEGSDELTQGYIYFHK#.A	40.46	10.61	3.81	0.26
Q61024_A	Asns	Asparagine	R.TTAAHGLELR.V	10.04	12.67	0.79	1.26
Q61024_A	Asns	Asparagine	K.VASVEMVK#.Y	79.69	15.74	5.06	0.20
Q61024_A	Asns	Asparagine	K.VASVEM*VK#.Y	50.67	15.10	3.36	0.30
Q61024_A	Asns	Asparagine	K.WINATDPSAR.T	19.25	24.76	0.78	1.29
Q61024_A	Asns	Asparagine	R.ASVGM*YLISK#.Y	20.66	5.04	4.10	0.24
Q61024_A	Asns	Asparagine	R.ASVGMYLISK#.Y	30.53	6.94	4.40	0.23
Q61024_A	Asns	Asparagine	K.EAFSDGITSVK#.N	125.21	21.62	5.79	0.17
Q61024_A	Asns	Asparagine	K.ELYLFDVLR.A	33.95	27.74	1.22	0.82
Q61024_A	Asns	Asparagine	K.HSTTPFLK#.V	105.03	19.91	5.27	0.19
Q61024_A	Asns	Asparagine	R.ILFDNAIK#.K	84.75	20.30	4.17	0.24
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEM*M*SAASQK#.F	51.85	8.54	6.07	0.16
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEM*MSAASQK#.F	6.46	1.66	3.89	0.26
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEMM*SAASQK#.F	7.53	1.03	7.32	0.14
Q61024_A	Asns	Asparagine	R.LAVVDPLFGM*QPIR.V	12.58	11.73	1.07	0.93
Q61024_A	Asns	Asparagine	K.NTDSVVIFSGEGSDELTQGYIYFHK#.A	28.57	5.63	5.08	0.20
Q61024_A	Asns	Asparagine	K.VASVEM*VK#.Y	40.93	11.81	3.47	0.29
Q61024_A	Asns	Asparagine	K.WINATDPSAR.T	12.36	14.42	0.86	1.17
Q61024_A	Asns	Asparagine	R.ASVGM*YLISK#.Y	62.45	17.55	3.56	0.28
Q61024_A	Asns	Asparagine	R.ASVGMYLISK#.Y	45.96	8.95	5.13	0.19
Q61024_A	Asns	Asparagine	R.DTYGVRPLFK.A	26.11	21.35	1.22	0.82
Q61024_A	Asns	Asparagine	K.EAFSDGITSVK#.N	209.95	38.70	5.42	0.18
Q61024_A	Asns	Asparagine	K.EAQVQYPLQTFAIGM*EDSPDLLAAR.K	16.18	16.63	0.97	1.03
Q61024_A	Asns	Asparagine	K.ELYLFDVLR.A	82.60	68.95	1.20	0.83
Q61024_A	Asns	Asparagine	K.FPFNTPK#.T	60.32	13.47	4.48	0.22
Q61024_A	Asns	Asparagine	K.HSTTPFLK#.V	310.92	49.23	6.32	0.16
Q61024_A	Asns	Asparagine	R.ILFDNAIK#.K	164.28	29.88	5.50	0.18
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEM*M*SAASQK#.F	104.03	21.56	4.82	0.21
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEM*MSAASQK#.F	12.02	4.14	2.90	0.34
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEMM*SAASQK#.F	16.85	5.49	3.07	0.33
Q61024_A	Asns	Asparagine	K.ILQDYVEHQVDDEMMSAASQK#.F	19.36	3.49	5.55	0.18
Q61024_A	Asns	Asparagine	R.LAVVDPLFGM*QPIR.V	28.55	33.38	0.86	1.17
Q61024_A	Asns	Asparagine	R.LAVVDPLFGMQPIR.V	17.02	13.42	1.27	0.79
Q61024_A	Asns	Asparagine	K.NTDSVVIFSGEGSDELTQGYIYFHK#.A	35.65	7.51	4.75	0.21
Q61024_A	Asns	Asparagine	K.VASVEM*VK#.Y	81.46	15.07	5.41	0.18
Q61024_A	Asns	Asparagine	K.WINATDPSAR.T	30.04	25.01	1.20	0.83
P16460_A	Ass1	Argininosu	K.APNSPDVLEIEFK#.K	7.85	4.35	1.80	0.55
P16460_A	Ass1	Argininosu	K.SPWSM*DENLM*HISYEAGILENPK#.N	2.89	5.66	0.51	1.96
P16460_A	Ass1	Argininosu	K.VQVSVFK#.G	44.73	11.67	3.83	0.26
Q8QZV7_A	Asun	Protein asu	R.IM*WNELETLVR.A	2.39	10.20	0.23	4.27
Q8QZV7_A	Asun	Protein asu	R.TQGIIPLAPISK#.S	16.35	12.98	1.26	0.79
G3X963_G	Atad2	ATPase fam	R.EFLFSLPDK#.N	15.21	13.47	1.13	0.89
G3X963_G	Atad2	ATPase fam	K.LITNTAEAVLQK#.M	33.37	25.97	1.28	0.78
G3X963_G	Atad2	ATPase fam	R.NQAQTSSESSFDK#.N	4.64	3.91	1.19	0.84
G3X963_G	Atad2	ATPase fam	R.STTSSATDSLDLSSEFLSLQDSGGR.R	2.46	5.37	0.46	2.18
G3X963_G	Atad2	ATPase fam	R.VFTKPVDPDEVPDYVTVIK.Q	14.18	12.62	1.12	0.89
G3X963_G	Atad2	ATPase fam	R.EFLFSLPDK.N	28.62	27.89	1.03	0.97
G3X963_G	Atad2	ATPase fam	R.GSQVEQQELISM*EQALAILSQPTPSLVLDHK#.Q	8.19	3.55	2.31	0.43
G3X963_G	Atad2	ATPase fam	K.IGASLADVDPM*QLDTSVR.F	2.47	6.81	0.36	2.75
G3X963_G	Atad2	ATPase fam	K.KLEDLGVFNETEESNLTM*YTR.G	1.65	5.37	0.31	3.26
G3X963_G	Atad2	ATPase fam	R.LDSIDPALR.R	7.49	27.51	0.27	3.67
G3X963_G	Atad2	ATPase fam	R.LEEQEEDTFR.E	4.33	17.35	0.25	4.01
G3X963_G	Atad2	ATPase fam	R.LESNIDLK#.N	27.30	22.25	1.23	0.82
G3X963_G	Atad2	ATPase fam	K.LITNTAEAVLQK#.M	60.49	52.73	1.15	0.87
G3X963_G	Atad2	ATPase fam	R.LLIVGEPGFGQSSHLAPAVIHALEK#.F	31.95	26.12	1.22	0.82
G3X963_G	Atad2	ATPase fam	R.STTSSATDSLDLSSEFLSLQDSGGR.R	2.88	12.51	0.23	4.35
G3X963_G	Atad2	ATPase fam	R.VFTK#PVDPDEVPDYVTVIK#.Q	41.23	34.61	1.19	0.84
G3X963_G	Atad2	ATPase fam	R.YSTM*NQSVLFDK#.L	12.88	12.06	1.07	0.94
E9Q166_E	Atad2b	Protein Ata	R.ARNR@CLPMNFR.A	4.53	2.50	1.82	0.55
Q4QY64_A	Atad5	ATPase fam	K.NIASPSQDLLSLLK#.H	10.40	10.49	0.99	1.01
P81269_A	Atf1	Cyclic AMP	R.TTPSATSLPQTVVMTSPVTLASQTTK#.T	6.63	4.70	1.41	0.71
Q8R0S1_A	Atf7	Cyclic AMP	K.KAEELTSQNIQLSNEVTLLR.N	2.46	5.50	0.45	2.24
Q9CPX6_A	Atg3	Ubiquitin-l	K.ALEVAEYLTPVLK#.E	6.74	3.54	1.90	0.53
Q99J83_AT	Atg5	Autophagy	R.VSYLTLVTDK#.V	14.72	3.55	4.14	0.24
Q9D906_A	Atg7	Ubiquitin-l	R.AEGVTALPYFLFK#.Y	12.81	7.32	1.75	0.57
Q9D906_A	Atg7	Ubiquitin-l	R.FDNVLPVSLAFDK#.C	11.08	4.75	2.33	0.43
Q9D906_A	Atg7	Ubiquitin-l	K.LLLEQSANEIWEAIK#.S	9.67	2.61	3.70	0.27
Q9D906_A	Atg7	Ubiquitin-l	K.LLLEQSANEIWEAIK#.S	7.52	1.64	4.58	0.22
Q9D906_A	Atg7	Ubiquitin-l	K.YDDDTVLVSLLK#.H	7.07	1.67	4.24	0.24
Q9CWJ9_P	Atic	Bifunctiona	R.DLIVATVAVK#.Y	48.81	7.46	6.54	0.15
Q9CWJ9_P	Atic	Bifunctiona	R.EVSDGIVAPGYEEEALK#.I	66.26	14.74	4.49	0.22
Q9CWJ9_P	Atic	Bifunctiona	R.GAVDIPAAASFK#.H	55.29	9.45	5.85	0.17
Q9CWJ9_P	Atic	Bifunctiona	R.LDFNLVR.V	15.15	13.58	1.12	0.90
Q9CWJ9_P	Atic	Bifunctiona	R.SGVAYIVAPSGSTADK#.V	20.84	3.88	5.37	0.19
Q9CWJ9_P	Atic	Bifunctiona	R.SLASLGLSLVASGGTAK#.A	23.94	3.50	6.83	0.15
Q9CWJ9_P	Atic	Bifunctiona	K.SLFSNIVTK#.N	76.00	14.59	5.21	0.19
Q9CWJ9_P	Atic	Bifunctiona	R.YGM*NPHQTPAQLYTLK#PK#.L	47.40	8.52	5.57	0.18
Q9CWJ9_P	Atic	Bifunctiona	R.DLIVATVAVK#.Y	12.60	5.02	2.51	0.40
Q9CWJ9_P	Atic	Bifunctiona	R.EVSDGIVAPGYEEEALK#.I	15.50	3.30	4.69	0.21
Q9CWJ9_P	Atic	Bifunctiona	R.EVSDGIVAPGYEEEALK#.I	6.32	2.43	2.60	0.38
Q91YH5_A	Atl3	Atlastin-3 C	R.ELGGAIDSGAAYVLEQASSHIGNSTQAAVR.D	3.60	6.32	0.57	1.75
Q91YH5_A	Atl3	Atlastin-3 C	K.IKKM*GGK.D	1.28	17.68	0.07	13.86
Q8VDN2_A	Atp1a1	Sodium/po	K.GVGIISEGNETVEDIAAR.L	1.85	4.83	0.38	2.61
Q8VDN2_A	Atp1a1	Sodium/po	R.AVAGDASESALLK#.C	14.30	15.45	0.93	1.08
Q8VDN2_A	Atp1a1	Sodium/po	R.AVFQANQENLPILK#.R	21.76	22.19	0.98	1.02
Q8VDN2_A	Atp1a1	Sodium/po	K.GVGIISEGNETVEDIAAR.L	6.24	12.82	0.49	2.05
Q8VDN2_A	Atp1a1	Sodium/po	K.IVEIPFNSTNK.Y	29.95	31.91	0.94	1.07
Q8VDN2_A	Atp1a1	Sodium/po	K.M*SINAEDVVVGDLVEVK#.G	7.18	8.55	0.84	1.19
Q8VDN2_A	Atp1a1	Sodium/po	R.SPDFTNENPLETR.N	4.24	16.32	0.26	3.85
Q8VDN2_A	Atp1a1	Sodium/po	K.TSATWFALSR.I	9.56	11.76	0.81	1.23

Q8VDN2_A	Atp1a1	Sodium/po	K.VDNSSLTGESEPQTR.S	6.70	13.58	0.49	2.03
O55143_A	Atp2a2	Sarcoplasm	R.IGIFGQDEDVTSK.A	7.04	7.16	0.98	1.02
Q03265_A	Atp5a1	ATP synthas	K.AVDSLVPIGR.G	24.97	23.78	1.05	0.95
Q03265_A	Atp5a1	ATP synthas	K.EIVTNFLAGFEP.-	25.31	25.31	1.00	1.00
Q03265_A	Atp5a1	ATP synthas	R.FNDGTDEK#.K	6.92	5.67	1.22	0.82
Q03265_A	Atp5a1	ATP synthas	K.GMSLNLEPDNVGVVVFGNDK#.L	12.77	5.94	2.15	0.47
Q03265_A	Atp5a1	ATP synthas	R.GYLDK#LEPSK#.I	31.15	44.54	0.70	1.43
Q03265_A	Atp5a1	ATP synthas	K.HALIIYDDLSK#.Q	95.39	16.17	5.90	0.17
Q03265_A	Atp5a1	ATP synthas	R.ILGADTSVDLEETGR.V	15.52	17.50	0.89	1.13
Q03265_A	Atp5a1	ATP synthas	K.LK#EIVTNFLAGFEP.-	74.18	16.40	4.52	0.22
Q03265_A	Atp5a1	ATP synthas	R.NVQAEEM*VEFSSGLK#.G	19.46	4.45	4.37	0.23
Q03265_A	Atp5a1	ATP synthas	R.NVQAEEMVEFSSGLK#.G	24.08	9.28	2.59	0.39
Q03265_A	Atp5a1	ATP synthas	R.STVAQLVK#.R	92.43	15.13	6.11	0.16
Q03265_A	Atp5a1	ATP synthas	K.TGTAEM*SSILEER.I	19.16	18.55	1.03	0.97
Q03265_A	Atp5a1	ATP synthas	K.TGTAEMSSILEER.I	6.09	5.02	1.21	0.82
Q03265_A	Atp5a1	ATP synthas	K.TSIAIDTIINQK#.R	102.98	21.12	4.88	0.21
Q03265_A	Atp5a1	ATP synthas	R.VVDALGNAIDGK#.G	162.35	31.83	5.10	0.20
Q03265_A	Atp5a1	ATP synthas	K.EIVTNFLAGFEP.-	4.69	4.69	1.00	1.00
Q03265_A	Atp5a1	ATP synthas	K.LK#EIVTNFLAGFEP.-	21.27	5.72	3.72	0.27
Q03265_A	Atp5a1	ATP synthas	R.LTELLK#.Q	11.08	3.82	2.90	0.34
Q03265_A	Atp5a1	ATP synthas	R.VVDALGNAIDGK#.G	10.32	2.99	3.45	0.29
P56480_A	Atp5b	ATP synthas	R.AIAELGIYPAVDPLDSTSR.I	2.42	4.26	0.57	1.76
P56480_A	Atp5b	ATP synthas	R.FTQAGSEVSALLGR.I	16.87	11.35	1.49	0.67
P56480_A	Atp5b	ATP synthas	K.IGLFGGAGVGK#.T	31.05	22.22	1.40	0.72
P56480_A	Atp5b	ATP synthas	K.QFAPIHAEAPEFIEM*SVEQEILVTGIK#.V	4.05	1.21	3.34	0.30
P56480_A	Atp5b	ATP synthas	R.VALTGLTVAEYFR.D	7.74	12.58	0.62	1.62
P56480_A	Atp5b	ATP synthas	K.VLDSGAPIKIPVGPETLGR.I	9.07	10.83	0.84	1.19
Q91VR2_A	Atp5c1	ATP synthas	K.ELIEIISGAAALD.-	11.86	11.86	1.00	1.00
Q91VR2_A	Atp5c1	ATP synthas	R.VYGTGSLALYEK#.A	15.95	5.50	2.90	0.34
Q9D3D9_A	Atp5d	ATP synthas	K.AQSELSGAADEAAR.A	2.57	6.24	0.41	2.43
P50516_V	Atp6v1a	V-type prot	K.AK#EILQEEEDLAEIVQLVGK#.A	17.02	2.60	6.55	0.15
P50516_V	Atp6v1a	V-type prot	K.FK#DPVK#DGEAK#.I	4.04	1.39	2.90	0.34
P50516_V	Atp6v1a	V-type prot	R.VGSHITGGDIYGIVNENSLIK#.H	20.89	3.78	5.53	0.18
P50516_V	Atp6v1a	V-type prot	K.AK#EILQEEEDLAEIVQLVGK#.A	73.32	9.46	7.75	0.13
P50516_V	Atp6v1a	V-type prot	R.AVETTAQSDNK#.I	5.94	1.30	4.56	0.22
P50516_V	Atp6v1a	V-type prot	R.DIK#WEFIPSK#.N	13.77	5.10	2.70	0.37
P50516_V	Atp6v1a	V-type prot	R.LAEM*PADSGYPAYLGAR.L	6.26	5.51	1.14	0.88
P50516_V	Atp6v1a	V-type prot	R.TALVANTSNM*PVAAR.E	14.90	12.48	1.19	0.84
P50516_V	Atp6v1a	V-type prot	K.TVISQSLSK#.Y	94.29	16.74	5.63	0.18
P50516_V	Atp6v1a	V-type prot	R.VGSHITGGDIYGIVNENSLIK#.H	65.57	9.96	6.59	0.15
P50516_V	Atp6v1a	V-type prot	K.AK#EILQEEEDLAEIVQLVGK#.A	16.52	5.65	2.92	0.34
P50516_V	Atp6v1a	V-type prot	K.TVISQSLSK#.Y	23.92	6.96	3.44	0.29
P62814_V	Atp6v1b2	V-type prot	K.AVVGEEALTSDDLLYLEFLQK#.F	22.84	2.77	8.25	0.12
P62814_V	Atp6v1b2	V-type prot	K.AVVQVFEGTSGIDAK#.K	110.19	21.44	5.14	0.19
P62814_V	Atp6v1b2	V-type prot	K.NFITQGPYENR.T	18.64	23.05	0.81	1.24
P62814_V	Atp6v1b2	V-type prot	R.SGQVLEVSGSK#.A	72.06	14.43	4.99	0.20
P62814_V	Atp6v1b2	V-type prot	R.TPVSEDM*LGR.V	14.43	14.65	0.99	1.02
P62814_V	Atp6v1b2	V-type prot	K.AVVGEEALTSDDLLYLEFLQK#.F	10.26	4.30	2.38	0.42
P62814_V	Atp6v1b2	V-type prot	K.AVVQVFEGTSGIDAK#.K	19.11	4.43	4.31	0.23
P62814_V	Atp6v1b2	V-type prot	K.AVVQVFEGTSGIDAK#.K	31.43	5.11	6.15	0.16
P57746_V	Atp6v1d	V-type prot	R.AAGEVM*EPANLLAEEK#.D	29.29	6.35	4.61	0.22
P57746_V	Atp6v1d	V-type prot	R.AAGEVMEPANLLAEEK#.D	11.70	5.22	2.24	0.45
P57746_V	Atp6v1d	V-type prot	R.EAAFSLAEAK#.F	17.70	5.03	3.52	0.28
P57746_V	Atp6v1d	V-type prot	K.FTAGDFSTTVIQNVNK#.A	33.02	10.54	3.13	0.32
P57746_V	Atp6v1d	V-type prot	R.AAGEVM*EPANLLAEEK#.D	3.93	2.66	1.48	0.68
P50518_V	Atp6v1e1	V-type prot	K.AEEEFNIEK#.G	35.90	9.28	3.87	0.26
P50518_V	Atp6v1e1	V-type prot	R.ARDDLITDLLNEAK.Q	20.61	16.51	1.25	0.80
P50518_V	Atp6v1e1	V-type prot	R.K#QDFPLVK#.A	28.87	5.41	5.34	0.19
P50518_V	Atp6v1e1	V-type prot	R.LDLIAQQM*M*PEVR.G	11.14	5.69	1.96	0.51
Q9D1K2_V	Atp6v1f	V-type prot	K.DTTINEIEDTFR.Q	6.66	13.70	0.49	2.05
Q9D1K2_V	Atp6v1f	V-type prot	R.SIPAVLEIPSK#.E	24.04	9.56	2.51	0.40
Q8BVE3_V	Atp6v1h	V-type prot	K.ELMEGSDLNYYFNWIK#.T	7.52	1.58	4.74	0.21
Q8BVE3_V	Atp6v1h	V-type prot	R.GAVDAAVPTNIIAAK#.A	32.12	10.71	3.00	0.33
Q8BVE3_V	Atp6v1h	V-type prot	K.LGESVQDLSSFDEYSSELK#.S	19.36	7.56	2.56	0.39
Q8BVE3_V	Atp6v1h	V-type prot	K.QLENLEQQK#YDDEDISEDIK#.F	7.62	3.42	2.23	0.45
Q8BVE3_V	Atp6v1h	V-type prot	R.VSIFFDYAK#.R	20.99	9.57	2.19	0.46
Q8BVE3_V	Atp6v1h	V-type prot	R.GAVDAAVPTNIIAAK#.A	22.91	6.74	3.40	0.29
Q8BVE3_V	Atp6v1h	V-type prot	K.LGESVQDLSSFDEYSSELK#.S	13.49	5.11	2.64	0.38
Q8BVE3_V	Atp6v1h	V-type prot	R.VSIFFDYAK#.R	15.24	4.97	3.07	0.33
Q8BVE3_V	Atp6v1h	V-type prot	R.GAVDAAVPTNIIAAK#.A	53.15	14.86	3.58	0.28
Q8BVE3_V	Atp6v1h	V-type prot	K.LGESVQDLSSFDEYSSELK#.S	32.37	11.72	2.76	0.36
Q8BVE3_V	Atp6v1h	V-type prot	K.QLENLEQQK#YDDEDISEDIK#.F	9.88	4.34	2.28	0.44
Q8BVE3_V	Atp6v1h	V-type prot	R.VSIFFDYAK#.R	29.58	8.37	3.53	0.28
Q61687_A	Atrx	Transcripti	K.LIETTSNM*NSSYIK#.F	17.75	12.78	1.39	0.72
Q61687_A	Atrx	Transcripti	K.LIETTSNMNSSYIK#.F	10.83	8.20	1.32	0.76
Q61687_A	Atrx	Transcripti	R.VVDQQQVER.H	1.79	8.76	0.20	4.89
Q61687_A	Atrx	Transcripti	K.AGSLGINLVAANR.V	1.86	9.61	0.19	5.16
Q61687_A	Atrx	Transcripti	R.EAIYNDVLTK.Q	13.85	17.30	0.80	1.25
Q61687_A	Atrx	Transcripti	R.LFIISTK#.A	13.77	12.40	1.11	0.90
Q61687_A	Atrx	Transcripti	K.LFQDFQM*LSR.I	3.46	13.40	0.26	3.87
Q61687_A	Atrx	Transcripti	K.LIETTSNM*NSSYIK#.F	9.36	10.94	0.85	1.17
Q61687_A	Atrx	Transcripti	K.LYQYYLDHLTGVGNSTEGGR.G	3.35	9.95	0.34	2.97
Q61687_A	Atrx	Transcripti	R.SRGGGDGNVDDTGNNPSVSLK.L	5.10	10.45	0.49	2.05
Q61687_A	Atrx	Transcripti	K.SVPATVDDDDDDNDPENR.I	3.63	13.22	0.27	3.64
Q61687_A	Atrx	Transcripti	R.VVDQQQVER.H	6.17	31.76	0.19	5.14
Q61687_A	Atrx	Transcripti	K.VVEATNSM*TAVR.I	3.45	12.24	0.28	3.55
P28658_A	Atxn10	Ataxin-10 C	K.AEGDIEHM*TEGFK#.S	7.88	7.67	1.03	0.97
P28658_A	Atxn10	Ataxin-10 C	R.ALTALFK#.E	40.16	15.16	2.65	0.38
P28658_A	Atxn10	Ataxin-10 C	K.ESTNIFSPSDSLK#.A	36.88	20.52	1.80	0.56
P28658_A	Atxn10	Ataxin-10 C	K.HPASEWPFLIISDHFLK#.S	21.03	9.68	2.17	0.46
P28658_A	Atxn10	Ataxin-10 C	R.ITLLDIVIAK#.L	50.28	26.35	1.91	0.52
P28658_A	Atxn10	Ataxin-10 C	R.LSGIM*VPAPIQDLEALR.A	3.41	7.34	0.46	2.15
P28658_A	Atxn10	Ataxin-10 C	K.LVGEEQLTKDDISIFVR.H	6.19	12.72	0.49	2.06
P28658_A	Atxn10	Ataxin-10 C	R.NLTEDNSQNQDVIAK#.M	49.35	28.74	1.72	0.58
P28658_A	Atxn10	Ataxin-10 C	K.SPELVEAM*YGK#.L	20.86	6.19	3.37	0.30
P28658_A	Atxn10	Ataxin-10 C	K.HPASEWPFLIISDHFLK#.S	13.30	5.22	2.55	0.39
P28658_A	Atxn10	Ataxin-10 C	R.ITLLDIVIAK#.L	30.43	13.66	2.23	0.45
P28658_A	Atxn10	Ataxin-10 C	R.NLTEDNSQNQDVIAK#.M	21.18	10.61	2.00	0.50
P28658_A	Atxn10	Ataxin-10 C	R.ALTALFK#.E	31.85	14.52	2.19	0.46
P28658_A	Atxn10	Ataxin-10 C	K.ESTNIFSPSDSLK#.A	20.80	8.70	2.39	0.42
P28658_A	Atxn10	Ataxin-10 C	R.ITLLDIVIAK#.L	25.90	4.76	5.45	0.18
P28658_A	Atxn10	Ataxin-10 C	K.LVGEEQLTK#.D	20.21	7.73	2.61	0.38
P28658_A	Atxn10	Ataxin-10 C	R.NLTEDNSQNQDVIAK#.M	50.38	19.15	2.63	0.38

P28658_A	Atxn10	Ataxin-10	K.SPELVEAM*YGK#.L	34.00	14.32	2.37	0.42
O70305_A	Atxn2	Ataxin-2 OS	R.ANQLAEEIESSAQYK#.A	15.07	6.86	2.20	0.46
O70305_A	Atxn2	Ataxin-2 OS	R.DAFTDSALSAK#.V	22.22	7.28	3.05	0.33
O70305_A	Atxn2	Ataxin-2 OS	K.GLPQPTISFDGIYANVR.M	2.54	6.03	0.42	2.37
O70305_A	Atxn2	Ataxin-2 OS	R.ANQLAEEIESSAQYK#.A	20.70	4.99	4.15	0.24
O70305_A	Atxn2	Ataxin-2 OS	K.ASETSPSFSK#.A	18.48	6.41	2.88	0.35
O70305_A	Atxn2	Ataxin-2 OS	R.DAFTDSALSAK#.V	30.85	8.15	3.78	0.26
O70305_A	Atxn2	Ataxin-2 OS	K.GLPQPTISFDGIYANVR.M	3.44	8.09	0.42	2.35
O70305_A	Atxn2	Ataxin-2 OS	R.TSPAGGTWSSVVSGVPR.L	2.40	6.56	0.37	2.74
Q7TQH0_A	Atxn2l	Ataxin-2-lik	K.TTYDSSLSSYTVPLEK#.D	3.42	2.08	1.64	0.61
Q7TQH0_A	Atxn2l	Ataxin-2-lik	K.DK#FTDSAIAM*NSK#.V	11.78	7.12	1.66	0.60
Q7TQH0_A	Atxn2l	Ataxin-2-lik	R.EIESSPQYR.L	6.46	14.88	0.43	2.30
Q7TQH0_A	Atxn2l	Ataxin-2-lik	K.FNEENYGVK#.T	51.91	24.46	2.12	0.47
Q7TQH0_A	Atxn2l	Ataxin-2-lik	K.GDEKEEGPVTEQVKK.S	18.90	14.37	1.31	0.76
Q7TQH0_A	Atxn2l	Ataxin-2-lik	K.LQPSSSPETGLDPFPSR.I	3.36	12.08	0.28	3.60
Q7TQH0_A	Atxn2l	Ataxin-2-lik	R.NVDFNYATK#.D	30.22	17.45	1.73	0.58
Q7TQH0_A	Atxn2l	Ataxin-2-lik	R.REDIVDTMVFKPSDVLLVHFR.N	2.88	7.55	0.38	2.62
Q7TQH0_A	Atxn2l	Ataxin-2-lik	K.STLNPNAK#.E	14.20	8.65	1.64	0.61
Q7TQH0_A	Atxn2l	Ataxin-2-lik	K.TTYDSSLSSYTVPLEK#.D	10.64	6.28	1.69	0.59
O70126_A	Aurkb	Aurora kina	R.DIKPENLLLGLQGELK.I	4.22	11.21	0.38	2.66
O70126_A	Aurkb	Aurora kina	K.FPSSVPSGAQDLISK.L	3.79	6.16	0.62	1.62
Q8BGF0_Q	AW551984	Protein AW	K.ELKDEWELLER.K	1.36	4.64	0.29	3.41
P01887_B	B2m	Beta-2-mic	K.TPQIQVYSR.H	14.66	100.42	0.15	6.85
P01887_B	B2m	Beta-2-mic	K.VEM*SDM*SFSK.D	11.06	20.38	0.54	1.84
Q3UI43_BA	Babam1	BRISC and	R.ALGAQASVGSR.S	12.04	25.96	0.46	2.16
Q3UI43_BA	Babam1	BRISC and	R.TNALNVSQK#.M	18.13	7.27	2.49	0.40
Q91YN9_B	Bag2	BAG family	K.FLDDLGNAK#.S	22.28	13.95	1.60	0.63
Q91YN9_B	Bag2	BAG family	R.IIDEVVSK#.F	42.36	38.77	1.09	0.92
Q91YN9_B	Bag2	BAG family	R.LLESLDQLELR.V	13.46	50.94	0.26	3.78
Q91YN9_B	Bag2	BAG family	K.SLQNTDGK#FN.-	14.80	10.93	1.35	0.74
Q9Z1R2_B	Bag6	Large proli	R.DLEAPEVQESYR.Q	4.28	7.55	0.57	1.77
Q9Z1R2_B	Bag6	Large proli	R.ESFSLVQVQPGVDIIR.T	3.67	6.72	0.55	1.83
Q9Z1R2_B	Bag6	Large proli	R.LQVVLEHMPVGPDAILR.Y	7.77	5.67	1.37	0.73
Q9Z1R2_B	Bag6	Large proli	K.VK#PQPPLSDAYLSGM*PAK#.R	4.58	1.92	2.39	0.42
Q9Z1R2_B	Bag6	Large proli	R.AGSSESIAAFIQR.L	5.97	10.07	0.59	1.69
Q9Z1R2_B	Bag6	Large proli	R.APPQTQLPSGASSGTGSASATHGGAPLPGTR.G	9.92	19.57	0.51	1.97
Q9Z1R2_B	Bag6	Large proli	R.DIQTLLSR.M	8.41	19.02	0.44	2.26
Q9Z1R2_B	Bag6	Large proli	K.EHIAASVSIPSEK#.Q	9.45	2.71	3.48	0.29
Q9Z1R2_B	Bag6	Large proli	R.LINLVGESLR.L	13.20	23.10	0.57	1.75
Q9Z1R2_B	Bag6	Large proli	R.LLGNTFVALSDLR.C	15.26	25.29	0.60	1.66
Q9Z1R2_B	Bag6	Large proli	R.LQEDPNYSPQR.F	3.24	12.44	0.26	3.84
Q9Z1R2_B	Bag6	Large proli	R.LQVVLEHMPVGPDAILR.Y	3.35	7.39	0.45	2.20
Q9Z1R2_B	Bag6	Large proli	R.TFIVGAQM*NVK#.E	16.36	4.84	3.38	0.30
Q9Z1R2_B	Bag6	Large proli	R.TFIVGAQMNVK#.E	12.59	3.81	3.31	0.30
Q9Z1R2_B	Bag6	Large proli	R.APPQTQLPSGASSGTGSASATHGGAPLPGTR.G	2.16	5.72	0.38	2.65
Q9Z1R2_B	Bag6	Large proli	R.LQEDPNYSPQR.F	1.92	9.76	0.20	5.08
Q8BKX1_B	Baiap2	Brain-speci	K.AIFSHAAGDNSTLLSFK#.E	21.69	11.62	1.87	0.54
Q8BKX1_B	Baiap2	Brain-speci	K.M*GELASESQGSK#.E	8.08	6.16	1.31	0.76
Q8BKX1_B	Baiap2	Brain-speci	K.QGELENYVSDGYK#.T	8.96	5.42	1.65	0.61
Q8BKX1_B	Baiap2	Brain-speci	K.SFHNELLTQLEQK#.V	18.70	10.95	1.71	0.59
Q8BKX1_B	Baiap2	Brain-speci	K.YSDK#ELQYIDAISNK#.Q	20.46	11.50	1.78	0.56
O54962_B	Banf1	Barrier-to-a	K.AYVVLGQFLVLK#.K	88.06	68.93	1.28	0.78
O54962_B	Banf1	Barrier-to-a	R.DFVAEPM*GEK#PVGSLAGIGDVLSK#.R	105.33	82.61	1.28	0.78
O54962_B	Banf1	Barrier-to-a	R.DFVAEPMGEK#PVGSLAGIGDVLSK#.R	36.00	34.97	1.03	0.97
Q9DCT6_B	Bap18	Chromatin	K.LGELTM*QLHPVSDSSPAGAK#.W	21.90	19.18	1.14	0.88
Q9DCT6_B	Bap18	Chromatin	K.VGEIFSAAGAAFTK#.L	36.69	29.49	1.24	0.80
Q9DCT6_B	Bap18	Chromatin	K.VYEDSGIPLPAESPK#.K	7.58	7.37	1.03	0.97
Q9DCT6_B	Bap18	Chromatin	K.WTETEIEM*LR.A	5.06	15.29	0.33	3.02
Q07813_B	Bax	Apoptosis r	R.IGDELDSNM*ELQR.M	9.33	35.01	0.27	3.75
Q07813_B	Bax	Apoptosis r	R.M*AGETPELTLEQPPQDASTK#.K	9.64	12.49	0.77	1.30
Q07813_B	Bax	Apoptosis r	R.M*IADVDTDSPR.E	8.34	23.16	0.36	2.78
Q07813_B	Bax	Apoptosis r	R.VVALFYFASK#.L	11.29	5.31	2.13	0.47
O88379_B	Baz1a	Bromodom	R.ISFGQEDSIASK.Q	6.39	7.23	0.88	1.13
O88379_B	Baz1a	Bromodom	K.DLTEALDEDADPTK.S	7.31	8.38	0.87	1.15
O88379_B	Baz1a	Bromodom	R.ISFGQEDSIASK#.Q	14.71	11.52	1.28	0.78
O88379_B	Baz1a	Bromodom	K.LGLHVSPSTVDQVSTPLAAK#.K	12.13	17.50	0.69	1.44
O88379_B	Baz1a	Bromodom	R.LSNPSLVK#.K	15.62	13.21	1.18	0.85
O88379_B	Baz1a	Bromodom	K.LSSTSVYDLTPGEK#.M	5.75	5.90	0.97	1.03
Q9Z277_B	Baz1b	Tyrosine-pr	R.AGTGENAPWVVEDELVK.K	9.78	10.81	0.90	1.11
Q9Z277_B	Baz1b	Tyrosine-pr	K.EAWEEEQEVAELLKEEFPNWYEK.L	6.97	8.13	0.86	1.17
Q9Z277_B	Baz1b	Tyrosine-pr	K.FLQGFM*APK.Q	13.59	19.43	0.70	1.43
Q9Z277_B	Baz1b	Tyrosine-pr	K.GGLGYM*EGTSEFEAR.V	2.60	14.08	0.18	5.43
Q9Z277_B	Baz1b	Tyrosine-pr	K.GGLGYMEGTSEFEAR.V	1.16	5.82	0.20	5.01
Q9Z277_B	Baz1b	Tyrosine-pr	K.IISNVPADSLIR.T	11.70	41.13	0.28	3.51
Q9Z277_B	Baz1b	Tyrosine-pr	R.KPFPLVKPLPGEEPLFTIPHTQEAFR.T	6.31	20.99	0.30	3.33
Q9Z277_B	Baz1b	Tyrosine-pr	R.LADDEGDSDSESVGQSR.G	5.30	16.53	0.32	3.12
Q9Z277_B	Baz1b	Tyrosine-pr	K.LVDSAWLEIMTK#.Y	14.58	9.53	1.53	0.65
Q9Z277_B	Baz1b	Tyrosine-pr	R.SDLIEVATR.L	6.48	31.00	0.21	4.79
Q9Z277_B	Baz1b	Tyrosine-pr	R.SRPKDDPEVDDLVLQTK.R	1.93	23.64	0.08	12.27
Q9Z277_B	Baz1b	Tyrosine-pr	K.FSDFLLDPYK.Y	3.85	5.70	0.68	1.48
Q9Z277_B	Baz1b	Tyrosine-pr	R.SDLIEVATR.L	5.71	16.64	0.34	2.91
Q9Z277_B	Baz1b	Tyrosine-pr	K.AFQEGIAK#.A	79.55	69.06	1.15	0.87
Q9Z277_B	Baz1b	Tyrosine-pr	R.AGTGENAPWVVEDELVK.K	14.16	11.34	1.25	0.80
Q9Z277_B	Baz1b	Tyrosine-pr	R.DEAEDYYDVIEHPM*DFQTIQNK#.C	4.47	4.28	1.04	0.96
Q9Z277_B	Baz1b	Tyrosine-pr	R.FEDQELGGR.N	15.94	82.21	0.19	5.16
Q9Z277_B	Baz1b	Tyrosine-pr	K.FLQGFM*APK#.Q	22.76	28.61	0.80	1.26
Q9Z277_B	Baz1b	Tyrosine-pr	K.FSDFLLDPYK#.Y	38.53	36.67	1.05	0.95
Q9Z277_B	Baz1b	Tyrosine-pr	K.FSDFLLDPYK#YM*TLNPSTK#.R	5.61	5.66	0.99	1.01
Q9Z277_B	Baz1b	Tyrosine-pr	K.GGFLYLNR.V	7.18	27.51	0.26	3.83
Q9Z277_B	Baz1b	Tyrosine-pr	K.GGLGYM*EGTSEFEAR.V	7.17	31.16	0.23	4.35
Q9Z277_B	Baz1b	Tyrosine-pr	K.GGLGYMEGTSEFEAR.V	1.83	11.57	0.16	6.34
Q9Z277_B	Baz1b	Tyrosine-pr	K.IEQQVEVEADDM*ISAVK#.S	9.73	10.82	0.90	1.11
Q9Z277_B	Baz1b	Tyrosine-pr	K.IEQQVEVEADDMISAVK#.S	11.38	12.87	0.88	1.13
Q9Z277_B	Baz1b	Tyrosine-pr	K.IEQQVEVEADDMISAVK.S	4.01	5.51	0.73	1.38
Q9Z277_B	Baz1b	Tyrosine-pr	K.IISNVPADSLIR.T	9.33	37.85	0.25	4.06
Q9Z277_B	Baz1b	Tyrosine-pr	R.KPFPLVKPLPGEEPLFTIPHTQEAFR.T	7.51	27.15	0.28	3.61
Q9Z277_B	Baz1b	Tyrosine-pr	K.LETSEFFELTSEEK#.L	20.59	21.31	0.97	1.04
Q9Z277_B	Baz1b	Tyrosine-pr	K.LVDSAWLEIMTK#.Y	19.05	23.38	0.82	1.23
Q9Z277_B	Baz1b	Tyrosine-pr	K.NASVNAHHGPALEAVETTVPK.Q	24.33	26.58	0.92	1.09
Q9Z277_B	Baz1b	Tyrosine-pr	R.SDLIEVATR.L	13.24	66.71	0.20	5.04
Q9Z277_B	Baz1b	Tyrosine-pr	R.SRPKDDPEVDDLVLQTK.R	4.16	19.32	0.22	4.64
Q9Z277_B	Baz1b	Tyrosine-pr	R.SVQEFLTDM*K#.Q	18.76	27.42	0.68	1.46
Q9Z277_B	Baz1b	Tyrosine-pr	K.WDM*SAENAR.C	1.50	7.67	0.20	5.12

Q9Z277_B	Baz1b	Tyrosine-pr	K.AFQEGIAK#.A	88.12	55.77	1.58	0.63
Q9Z277_B	Baz1b	Tyrosine-pr	R.AGTGENAPWVVEDELVK#.K	29.40	18.42	1.60	0.63
Q9Z277_B	Baz1b	Tyrosine-pr	K.DDPEVDDLVLQTK#.R	17.27	10.70	1.61	0.62
Q9Z277_B	Baz1b	Tyrosine-pr	R.DEAEDYYDVIEHPM*DFQTIQNK#.C	13.60	5.99	2.27	0.44
Q9Z277_B	Baz1b	Tyrosine-pr	R.DEAEDYYDVIEHPMDFQTIQNK#.C	7.67	4.90	1.57	0.64
Q9Z277_B	Baz1b	Tyrosine-pr	R.DSSSLSSPLNPK#.L	50.28	25.29	1.99	0.50
Q9Z277_B	Baz1b	Tyrosine-pr	R.FEDQELGGR.N	16.87	68.12	0.25	4.04
Q9Z277_B	Baz1b	Tyrosine-pr	K.FLQGFM*APK#.Q	48.02	32.74	1.47	0.68
Q9Z277_B	Baz1b	Tyrosine-pr	K.FSDFLLDPYK#.Y	52.38	33.70	1.55	0.64
Q9Z277_B	Baz1b	Tyrosine-pr	K.GGFLYLNR.V	10.07	25.29	0.40	2.51
Q9Z277_B	Baz1b	Tyrosine-pr	K.GGLGYM*EGTSEFEAR.V	12.28	31.43	0.39	2.56
Q9Z277_B	Baz1b	Tyrosine-pr	K.GGLGYMEGTSEFEAR.V	2.10	9.27	0.23	4.41
Q9Z277_B	Baz1b	Tyrosine-pr	K.IEQQVEVEADDM*ISAVK#.S	12.96	11.37	1.14	0.88
Q9Z277_B	Baz1b	Tyrosine-pr	K.IEQQVEVEADDMISAVK.S	15.03	11.55	1.30	0.77
Q9Z277_B	Baz1b	Tyrosine-pr	K.IEQQVEVEADDMISAVK#.S	5.67	4.17	1.36	0.73
Q9Z277_B	Baz1b	Tyrosine-pr	R.LADDEGDSDSESVGQSR.G	5.27	25.58	0.21	4.85
Q9Z277_B	Baz1b	Tyrosine-pr	K.LETSEFFELTSEEK#.L	31.81	23.28	1.37	0.73
Q9Z277_B	Baz1b	Tyrosine-pr	K.LQNEDKIISNVPADSLIR.T	11.32	34.50	0.33	3.05
Q9Z277_B	Baz1b	Tyrosine-pr	K.LVDSAWLEIMTK#.Y	12.95	10.47	1.24	0.81
Q9Z277_B	Baz1b	Tyrosine-pr	K.NASVNAHHGPALEAVETTVPK#.Q	56.08	28.89	1.94	0.52
Q9Z277_B	Baz1b	Tyrosine-pr	K.QM*TLLDM*AK#.G	14.76	11.91	1.24	0.81
Q9Z277_B	Baz1b	Tyrosine-pr	R.SDLIEVATR.L	25.05	61.09	0.41	2.44
Q9Z277_B	Baz1b	Tyrosine-pr	K.SLNGPPLK#.V	19.99	13.01	1.54	0.65
Q9Z277_B	Baz1b	Tyrosine-pr	K.SPEEHLEGVM*K#.I	39.21	29.37	1.34	0.75
Q9Z277_B	Baz1b	Tyrosine-pr	R.SRPKDDPEVDDLVLQTK.R	9.26	24.67	0.38	2.66
Q9Z277_B	Baz1b	Tyrosine-pr	R.SVQEFLTDM*K#.Q	34.18	20.65	1.66	0.60
Q9Z277_B	Baz1b	Tyrosine-pr	K.VDEEAVEK.K	17.80	10.61	1.68	0.60
Q9Z277_B	Baz1b	Tyrosine-pr	K.YM*TLNPSTK#.R	23.01	18.97	1.21	0.82
Q91YE5_B	Baz2a	Bromodom	R.ELTGSNASTSPAR.S	1.97	9.17	0.21	4.66
Q91YE5_B	Baz2a	Bromodom	R.GESQTPVQGQAR.N	2.25	9.48	0.24	4.22
Q61335_B	Bcap31	B-cell recep	K.AENEALAM*QK#.Q	13.74	13.07	1.05	0.95
Q9D287_S	Bcas2	Pre-mRNA-	R.TIVQLENEIYQIK#.Q	16.72	9.20	1.82	0.55
Q9D287_S	Bcas2	Pre-mRNA-	R.EM*ESNWVSLVSK#.N	25.86	14.16	1.83	0.55
Q9D287_S	Bcas2	Pre-mRNA-	K.LREM*ESNWVSLVSK.N	7.88	20.55	0.38	2.61
Q9D287_S	Bcas2	Pre-mRNA-	K.NMQLTAGSK#.L	13.63	7.46	1.83	0.55
Q9D287_S	Bcas2	Pre-mRNA-	K.NYLSYLTAPDYSAFETDIM*R.N	2.26	5.00	0.45	2.21
Q9D287_S	Bcas2	Pre-mRNA-	K.NYLSYLTAPDYSAFETDIMR.N	2.25	5.00	0.45	2.23
Q9D287_S	Bcas2	Pre-mRNA-	K.NYLSYLTAPDYSAFETDIM*RNEFER.L	1.78	11.99	0.15	6.74
Q9D287_S	Bcas2	Pre-mRNA-	R.TIVQLENEIYQIK#.Q	170.26	105.80	1.61	0.62
Q9D287_S	Bcas2	Pre-mRNA-	R.YELPAPSSGQK#.N	42.47	25.93	1.64	0.61
Q8CCN5_B	Bcas3	Breast carci	K.SAGLEEIEQELTSK#.Q	10.75	5.99	1.80	0.56
P59017_B	Bcl2l13	Bcl-2-like p	K.QQGPSPPGVQLDVAPQSLNPEVLLK#.L	4.36	3.62	1.20	0.83
Q8K019_B	Bclaf1	Bcl-2-assoc	R.SSFYPEGDQETAK.T	19.09	19.22	0.99	1.01
Q8K019_B	Bclaf1	Bcl-2-assoc	K.DRLLASTLVHSVK.K	4.08	15.37	0.27	3.77
Q8K019_B	Bclaf1	Bcl-2-assoc	K.DYSGFAGVSRPR.G	2.84	9.83	0.29	3.46
Q8K019_B	Bclaf1	Bcl-2-assoc	K.EEEWDPEYTPK#.S	11.66	9.65	1.21	0.83
Q8K019_B	Bclaf1	Bcl-2-assoc	R.ESDGFREEK.N	5.66	14.30	0.40	2.53
Q8K019_B	Bclaf1	Bcl-2-assoc	K.EVQSPEQVK#.S	20.01	18.40	1.09	0.92
Q8K019_B	Bclaf1	Bcl-2-assoc	K.EYK#PYK#DDSK#.H	8.37	4.18	2.00	0.50
Q8K019_B	Bclaf1	Bcl-2-assoc	K.FHDSEGDDTEETEDYR.Q	5.93	15.24	0.39	2.57
Q8K019_B	Bclaf1	Bcl-2-assoc	R.GFKEEIQK.G	38.60	38.81	0.99	1.01
Q8K019_B	Bclaf1	Bcl-2-assoc	R.GFKEEIQKGDK.K	32.19	26.19	1.23	0.81
Q8K019_B	Bclaf1	Bcl-2-assoc	K.KAEGEPQEESPLK.S	10.31	9.36	1.10	0.91
Q8K019_B	Bclaf1	Bcl-2-assoc	K.RPKEEEWDPEYTPK.S	5.11	27.09	0.19	5.30
Q8K019_B	Bclaf1	Bcl-2-assoc	K.SFATSSHR.N	5.02	15.18	0.33	3.03
Q8K019_B	Bclaf1	Bcl-2-assoc	K.SPAVTLNER.F	24.39	138.90	0.18	5.69
Q8K019_B	Bclaf1	Bcl-2-assoc	K.SQEEPKDTFEHDPSESIDEFNK.S	25.58	20.19	1.27	0.79
Q8K019_B	Bclaf1	Bcl-2-assoc	R.SSFYPEGDQETAK#.T	142.93	132.00	1.08	0.92
Q8K019_B	Bclaf1	Bcl-2-assoc	K.STSESFIQHIVSLVHHVK#.E	12.27	10.70	1.15	0.87
Q8K019_B	Bclaf1	Bcl-2-assoc	R.VFLLDR.G	33.92	110.57	0.31	3.26
Q8K019_B	Bclaf1	Bcl-2-assoc	K.SPAVTLNER.F	6.41	30.65	0.21	4.78
Q8K019_B	Bclaf1	Bcl-2-assoc	K.SQEEPKDTFEHDPSESIDEFNK.S	13.24	12.03	1.10	0.91
Q8K019_B	Bclaf1	Bcl-2-assoc	R.SSFYPEGDQETAK#.T	27.74	29.83	0.93	1.08
Q8K019_B	Bclaf1	Bcl-2-assoc	R.VFLLDR.G	7.18	32.74	0.22	4.56
O35623_B	Bet1	BET1 homo	K.LLAEM*DSQFDSTTGFLGK.T	5.31	3.38	1.57	0.64
P28653_P	Bgn	Biglycan O	K.IQAIELEDLLR.Y	2.66	11.95	0.22	4.49
Q921C5_B	Bicd2	Protein bic	K.ISLLEK#.A	38.42	27.75	1.38	0.72
Q921C5_B	Bicd2	Protein bic	R.LLQDYSELEEENISLQK.Q	3.45	2.76	1.25	0.80
O08539_B	Bin1	Myc box-d	K.ESDWNQHK#ELEK#.C	2.97	1.25	2.37	0.42
O08539_B	Bin1	Myc box-d	R.HHYESLQTAK#.K	16.54	2.79	5.92	0.17
O08539_B	Bin1	Myc box-d	R.LDLPPGFMFK#.V	12.64	4.37	2.89	0.35
O08539_B	Bin1	Myc box-d	K.LNQNLNDVLVSLEK#.Q	12.82	3.91	3.27	0.31
O08539_B	Bin1	Myc box-d	K.SPSPPPDGSPAATPEIR.V	3.13	2.91	1.07	0.93
O08539_B	Bin1	Myc box-d	R.VGFYVNTFQSIAGLEENFHK#.E	43.01	11.29	3.81	0.26
O08539_B	Bin1	Myc box-d	R.VNHEPEPASGASPGATIPK#.S	61.81	22.98	2.69	0.37
O08539_B	Bin1	Myc box-d	K.VQAQHDYTATDTDELQLK#.A	37.86	10.50	3.61	0.28
O88738_B	Birc6	Baculoviral	K.HFYLK#.R	18.82	5.13	3.67	0.27
O88738_B	Birc6	Baculoviral	R.LLDYVATVEDEAAAAK#.K	10.96	5.40	2.03	0.49
O55102_B	Bloc1s1	Biogenesis	R.TIATALEYVYK#.G	34.14	24.39	1.40	0.71
O55102_B	Bloc1s1	Biogenesis	K.TLQVQAAQFAK#.Q	30.79	19.69	1.56	0.64
Q9CWG9_	Bloc1s2	Biogenesis	K.M*ATYLTGELTATSEDYK#.L	6.05	11.01	0.55	1.82
Q8R015_B	Bloc1s5	Biogenesis	R.DSLGTPGAAHLIIK#.D	5.16	3.50	1.48	0.68
Q8R015_B	Bloc1s5	Biogenesis	R.LVQWEEFVSGQPQR.R	1.50	7.91	0.19	5.28
Q8R015_B	Bloc1s5	Biogenesis	K.VINDYLTASEK#.R	18.89	19.34	0.98	1.02
Q6PGF5_Q	Bms1	BMS1 hom	R.IAATGVVLDLDK#.S	8.98	7.44	1.21	0.83
Q6PGF5_Q	Bms1	BMS1 hom	K.ILAEEEELYGDFEDLETGDVHK#.G	9.46	5.13	1.84	0.54
Q6PGF5_Q	Bms1	BMS1 hom	R.IAATGVVLDLDK#.S	19.18	10.94	1.75	0.57
Q6PGF5_Q	Bms1	BMS1 hom	K.ILAEEEELYGDFEDLETGDVHK#.G	11.19	7.26	1.54	0.65
E9Q6J5_E9	Bod1l	Protein Bo	K.AAETEAQEGVTR@.Q	7.78	4.28	1.82	0.55
E9Q6J5_E9	Bod1l	Protein Bo	K.ETVEDTTISTGLVK#.G	14.71	5.62	2.62	0.38
E9Q6J5_E9	Bod1l	Protein Bo	K.GVVTEGFAESEILLTSSK#.E	7.55	1.60	4.70	0.21
E9Q6J5_E9	Bod1l	Protein Bo	K.TGDATTTSSEVGEK#.G	17.41	6.20	2.81	0.36
E9Q6J5_E9	Bod1l	Protein Bo	K.VSQADESNK#EIANLEEK#.S	12.12	4.92	2.46	0.41
A2A654_A	Bptf	Protein Bpt	K.DENVNGESQRK.T	2.40	47.58	0.05	19.82
A2A654_A	Bptf	Protein Bpt	K.ESASTQVITPR.A	4.54	13.52	0.34	2.98
A2A654_A	Bptf	Protein Bpt	R.FIAPEQGGESVESTK.C	7.95	8.79	0.90	1.11
A2A654_A	Bptf	Protein Bpt	R.K#LHSQDDSSTVVSSSK#.S	10.43	10.47	1.00	1.00
A2A654_A	Bptf	Protein Bpt	R.LIIEEDTDNENEK.K	7.67	7.08	1.08	0.92
A2A654_A	Bptf	Protein Bpt	K.LSTPSPDTGVDTISVK#.E	11.84	11.08	1.07	0.94
A2A654_A	Bptf	Protein Bpt	K.QGQSNSGM*VQVQQK#.V	2.84	2.40	1.18	0.84
A2A654_A	Bptf	Protein Bpt	R.TETSETEITTTEIIK#.R	8.90	4.91	1.81	0.55
A2A654_A	Bptf	Protein Bpt	K.VGSPATVTFQQNK#.N	14.91	16.68	0.89	1.12
A2A654_A	Bptf	Protein Bpt	R.WAAAQAEVAPK.T	6.24	7.88	0.79	1.26

Q99MP8_B	Brap	BRCA1-ass	K.FVAPFNDVIEQMK#.I	6.40	3.33	1.92	0.52
Q99MP8_B	Brap	BRCA1-ass	K.LSTELQEEQELNK#.C	6.29	7.51	0.84	1.19
Q99MP8_B	Brap	BRCA1-ass	K.LSTELQEEQELNK#.C	6.24	3.67	1.70	0.59
Q8C3R1_B	Brat1	BRCA1-ass	R.LSPIQAGPLALGTLK#.L	8.97	7.04	1.27	0.78
G5E8P1_G	Brd1	MCG7283 (	K.IFAQPVSLK#.E	23.30	16.81	1.39	0.72
G5E8P1_G	Brd1	MCG7283 (	R.IVEYSPPSAPR.R	2.34	55.94	0.04	23.88
G5E8P1_G	Brd1	MCG7283 (	R.LLIELLR.K	3.59	11.11	0.32	3.09
G5E8P1_G	Brd1	MCG7283 (	R.LTPLTVLLR.S	6.27	28.30	0.22	4.51
Q7JJ13_BR	Brd2	Bromodom	K.AGGGGSNATTLSHPGFGTSGGSSNK#.L	12.16	7.75	1.57	0.64
Q7JJ13_BR	Brd2	Bromodom	R.AVHEQLAALSQGPISK#PK#.R	28.06	14.13	1.99	0.50
Q7JJ13_BR	Brd2	Bromodom	R.LAELQEQLR.A	11.18	24.34	0.46	2.18
Q7JJ13_BR	Brd2	Bromodom	K.SLHSAGPPLLAVSAAPPAQPLAK#.K	36.39	24.39	1.49	0.67
Q7JJ13_BR	Brd2	Bromodom	K.VASM*PQEEQELVVTIPK#.N	12.19	9.69	1.26	0.80
Q7JJ13_BR	Brd2	Bromodom	K.VASMPQEEQELVVTIPK#.N	9.27	11.01	0.84	1.19
Q8K2F0_B	Brd3	Bromodom	R.LAELQEQLK#.A	84.13	37.55	2.24	0.45
Q8K2F0_B	Brd3	Bromodom	R.LQDVSGQLNSK#.K	14.69	6.01	2.44	0.41
Q9ESU6_B	Brd4	Bromodom	K.AVHEQLAALSQPQQNK#PK#.K	14.90	5.94	2.51	0.40
Q9ESU6_B	Brd4	Bromodom	R.DAQEFGADVR.L	8.41	12.54	0.67	1.49
Q9ESU6_B	Brd4	Bromodom	K.HQFAWPFQQPVDAVK#.L	14.53	6.67	2.18	0.46
Q9ESU6_B	Brd4	Bromodom	K.INELPTEETEIM*IVQAK#.G	9.91	5.45	1.82	0.55
Q9ESU6_B	Brd4	Bromodom	K.INELPTEETEIMIVQAK#.G	10.48	6.04	1.74	0.58
Q9ESU6_B	Brd4	Bromodom	K.LNLPDYYK#.I	41.81	18.27	2.29	0.44
Q9ESU6_B	Brd4	Bromodom	K.AVHEQLAALSQPQQNK#PK#.K	13.13	4.97	2.64	0.38
Q9ESU6_B	Brd4	Bromodom	R.DAQEFGADVR.L	4.23	11.30	0.37	2.67
Q9ESU6_B	Brd4	Bromodom	K.DVPDSQQHPGPEK#.S	9.56	6.68	1.43	0.70
Q9ESU6_B	Brd4	Bromodom	K.INELPTEETEIM*IVQAK#.G	5.06	3.84	1.32	0.76
Q9ESU6_B	Brd4	Bromodom	K.INELPTEETEIMIVQAK#.G	5.80	3.70	1.57	0.64
Q9ESU6_B	Brd4	Bromodom	K.LNLPDYYK#.I	28.67	24.44	1.17	0.85
O88665_B	Brd7	Bromodom	K.EAEITQIEPTGR.L	16.74	8.08	2.07	0.48
O88665_B	Brd7	Bromodom	R.LQSGVNTLQGFK.E	11.48	15.53	0.74	1.35
O88665_B	Brd7	Bromodom	K.VGGSEVTELSTGSSGHDSSLFEDR.S	3.15	7.46	0.42	2.37
Q8R3B7_B	Brd8	Bromodom	R.LLEAGPTQFTTPLPSFTTVASEPPVK.L	8.50	11.34	0.75	1.34
Q8R3B7_B	Brd8	Bromodom	K.LLSTGPTEPWSIR.E	1.54	6.14	0.25	3.99
Q8K3W0_	Bre	BRCA1-A c	K.LPVDFSNIPTYLLK#.D	24.88	10.68	2.33	0.43
Q8K3W0_	Bre	BRCA1-A c	K.LPVDFSNIPTYLLK#.D	14.67	6.02	2.44	0.41
Q8K3W0_	Bre	BRCA1-A c	K.LPVDFSNIPTYLLK#.D	17.86	10.25	1.74	0.57
Q9DCA5_B	Brix1	Ribosome	K.EFLIQIFSTPR.Y	3.05	7.55	0.40	2.48
Q9DCA5_B	Brix1	Ribosome	R.FVLNLIK#.I	44.55	17.20	2.59	0.39
Q9DCA5_B	Brix1	Ribosome	R.FVLNLIK#.I	12.50	3.87	3.23	0.31
Q91VR8_B	Brk1	Protein BR	R.EYIEIITSSIK#.K	22.55	6.43	3.51	0.29
Q3U1T3_B	Brms1l	Breast canc	K.LLLYDTVQSELEEK#.I	18.25	11.68	1.56	0.64
Q8R2Q8_B	Bst2	Bone marr	R.IK#ELENEVTK#.L	31.55	27.52	1.15	0.87
Q8R2Q8_B	Bst2	Bone marr	R.IKELENEVTK.L	45.40	34.40	1.32	0.76
Q8R2Q8_B	Bst2	Bone marr	K.KVSQALEQQAR.I	9.21	29.44	0.31	3.20
Q8R2Q8_B	Bst2	Bone marr	K.KVSQALEQQAR.I	6.84	26.51	0.26	3.88
Q8R2Q8_B	Bst2	Bone marr	K.LNQELENLR.I	18.98	65.34	0.29	3.44
Q8R2Q8_B	Bst2	Bone marr	K.VSQALEQQAR.I	10.51	49.04	0.21	4.67
Q8R2Q8_B	Bst2	Bone marr	K.KVSQALEQQAR.I	2.78	12.79	0.22	4.60
Q8R2Q8_B	Bst2	Bone marr	K.LNQELENLR.I	4.97	23.08	0.22	4.64
Q8R2Q8_B	Bst2	Bone marr	K.VSQALEQQAR.I	1.81	14.36	0.13	7.93
E9QAE3_E9	Btaf1	Protein Bta	K.AAAQQLGEVVK.L	11.53	9.88	1.17	0.86
E9QAE3_E9	Btaf1	Protein Bta	K.IPVPINAELR.K	2.68	9.96	0.27	3.72
E9QAE3_E9	Btaf1	Protein Bta	K.VANVVINQTASDSK#.V	12.77	10.74	1.19	0.84
Q64152_B	Btf3	Transcripti	K.APLATGEDDDDEVPDLVENFDEASK#.N	19.00	9.96	1.91	0.52
Q64152_B	Btf3	Transcripti	K.K#LGVNNISGIEEVNM*FTNQGTVIHFNNPK#.V	13.54	4.02	3.37	0.30
Q64152_B	Btf3	Transcripti	K.K#LGVNNISGIEEVNMFTNQGTVIHFNNPK#.V	12.57	3.53	3.56	0.28
Q64152_B	Btf3	Transcripti	K.LGVNNISGIEEVNM*FTNQGTVIHFNNPK#.V	29.31	14.85	1.97	0.51
Q64152_B	Btf3	Transcripti	K.LGVNNISGIEEVNMFTNQGTVIHFNNPK#.V	36.03	14.57	2.47	0.40
Q64152_B	Btf3	Transcripti	R.RLAEALPK.Q	7.39	10.01	0.74	1.35
Q64152_B	Btf3	Transcripti	K.VQASLAANTFTITGHAETK#.Q	48.47	21.94	2.21	0.45
Q64152_B	Btf3	Transcripti	K.VQASLAANTFTITGHAETK.Q	7.29	5.19	1.40	0.71
Q9CQH7_B	Btf3l4	Transcripti	K.APK#PEDIDEEDDDVPDLVENFDEASK#.N	7.46	4.62	1.62	0.62
Q9CQH7_B	Btf3l4	Transcripti	K.APK#PEDIDEEDDDVPDLVENFDEASK#NEAN.-	29.07	14.93	1.95	0.51
Q9CQH7_B	Btf3l4	Transcripti	K.LAVNNIAGIEEVNM*IK#DDGTVIHFNNPK#.V	11.86	5.40	2.19	0.46
Q9CQH7_B	Btf3l4	Transcripti	K.LQAQVR.I	11.52	37.14	0.31	3.22
Q9WVA3_	Bub3	Mitotic ch	R.QVTDAETK#PK#.S	5.24	1.83	2.87	0.35
Q9WVA3_	Bub3	Mitotic ch	R.VAVEYLDPSPEVQK#.K	13.48	4.59	2.93	0.34
Q8R149_B	Bud13	BUD13 ho	K.TGLVTDVQR.E	4.38	22.06	0.20	5.03
Q8R149_B	Bud13	BUD13 ho	R.YIDDEDLDR.M	2.96	19.37	0.15	6.54
Q8R149_B	Bud13	BUD13 ho	R.YLSGTDAGLEGGPEAGR.K	8.19	12.94	0.63	1.58
E0CX20_E0	Bud31	Protein BU	K.APPDGWELIEPTLDELDQK#.M	25.63	21.80	1.18	0.85
E0CX20_E0	Bud31	Protein BU	K.APPDGWELIEPTLDELDQK.M	3.45	6.06	0.57	1.76
E0CX20_E0	Bud31	Protein BU	R.KAPPDGWELIEPTLDELDQK.M	58.08	74.76	0.78	1.29
E0CX20_E0	Bud31	Protein BU	R.KVESLWPIFR.I	5.90	15.89	0.37	2.69
E0CX20_E0	Bud31	Protein BU	R.YIFDLFYK.R	40.72	42.35	0.96	1.04
O54825_B	Bysl	Bystin OS=	K.EALLELLR.L	5.85	7.41	0.79	1.27
O54825_B	Bysl	Bystin OS=	R.FYNLVLLPR.V	5.80	10.53	0.55	1.82
O54825_B	Bysl	Bystin OS=	K.IAEM*EYSGANSIFLR.L	2.46	3.62	0.68	1.47
Q9CQC6_B	Bzw1	Basic leuci	K.AEVLSEEPILK#.W	24.57	9.32	2.64	0.38
Q9CQC6_B	Bzw1	Basic leuci	K.EGVSAAFAVK#.L	23.79	3.48	6.83	0.15
Q9CQC6_B	Bzw1	Basic leuci	R.GDPFK#DIILYVK#.E	8.74	2.42	3.61	0.28
Q9CQC6_B	Bzw1	Basic leuci	K.IVVLFYK#.A	39.95	8.28	4.83	0.21
B2RQC6_P	Cad	CAD prote	R.AAFALGGLGSGFASTK#.E	32.56	16.88	1.93	0.52
B2RQC6_P	Cad	CAD prote	K.AIVHAVGQELQVTGPFNLQLIAK#.D	16.48	9.28	1.78	0.56
B2RQC6_P	Cad	CAD prote	K.ALK#EENIQTLLINPNIATVQTSQGLADK#.V	9.04	3.79	2.39	0.42
B2RQC6_P	Cad	CAD prote	R.ASDPGLPAEEPK#.E	47.63	3.33	14.29	0.07
B2RQC6_P	Cad	CAD prote	K.ATGYPLAYVAAK#.L	47.81	24.49	1.95	0.51
B2RQC6_P	Cad	CAD prote	R.EAAAGNIGGQTVR.E	29.72	50.29	0.59	1.69
B2RQC6_P	Cad	CAD prote	K.EELSALVAPAFAHTSQVLIDK#.S	38.32	21.02	1.82	0.55
B2RQC6_P	Cad	CAD prote	R.ELSDLESAR.Q	15.90	22.17	0.72	1.39
B2RQC6_P	Cad	CAD prote	R.EQGSLLGK#.L	22.06	11.61	1.90	0.53
B2RQC6_P	Cad	CAD prote	R.FLSSAAAVSK#.E	64.34	26.18	2.46	0.41
B2RQC6_P	Cad	CAD prote	R.IVTHAQLLEQHR.G	7.87	16.03	0.49	2.04
B2RQC6_P	Cad	CAD prote	K.LALGIPLPELR.N	40.66	94.05	0.43	2.31
B2RQC6_P	Cad	CAD prote	K.LFVEALGQIGPAPPLK#.V	23.26	11.68	1.99	0.50
B2RQC6_P	Cad	CAD prote	R.LGGAVLSFSEATSSVQK#.G	42.91	16.38	2.62	0.38
B2RQC6_P	Cad	CAD prote	R.LGYPVLVR.A	9.47	14.19	0.67	1.50
B2RQC6_P	Cad	CAD prote	R.LLDTIGISQPQWR.E	12.37	26.62	0.46	2.15
B2RQC6_P	Cad	CAD prote	R.LSLDDLLQR.L	15.98	21.90	0.73	1.37
B2RQC6_P	Cad	CAD prote	R.M*AEIGEHVAPSEAANSLEQAQAAAER.L	12.51	23.65	0.53	1.89
B2RQC6_P	Cad	CAD prote	R.MAEIGEHVAPSEAANSLEQAQAAAER.L	4.15	6.06	0.68	1.46
B2RQC6_P	Cad	CAD prote	R.M*ALLATVLGR.F	10.03	12.29	0.82	1.23
B2RQC6_P	Cad	CAD prote	K.NILLTIGSYK#.N	27.49	14.11	1.95	0.51

B2RQC6_P	Cad	CAD protei	K.TLGVDLVALATR.I	17.33	36.82	0.47	2.12
B2RQC6_P	Cad	CAD protei	K.VEPVGLM*TGSGVVGVK#.V	19.94	8.68	2.30	0.44
B2RQC6_P	Cad	CAD protei	R.VLGTSPEAIDSAENR.F	18.80	31.01	0.61	1.65
B2RQC6_P	Cad	CAD protei	R.VNEISVEVDSDPR.A	7.53	13.85	0.54	1.84
Q8VCQ8_Q	Cald1	Caldesmon	R.AEFLNK#.S	30.38	12.95	2.35	0.43
Q8VCQ8_Q	Cald1	Caldesmon	R.ASGDK#EAEGAPQVEAGK#.R	20.43	9.25	2.21	0.45
Q8VCQ8_Q	Cald1	Caldesmon	R.ASGDKEAEGAPQVEAGK.R	7.50	4.06	1.85	0.54
Q8VCQ8_Q	Cald1	Caldesmon	K.GSVFSAPSASGTPNK#.E	15.72	8.99	1.75	0.57
Q8VCQ8_Q	Cald1	Caldesmon	K.GSVFSAPSASGTPNK#ETAGLK#.V	23.08	14.92	1.55	0.65
Q8VCQ8_Q	Cald1	Caldesmon	R.LEQYTNAIEGTK#.A	31.50	11.59	2.72	0.37
Q8VCQ8_Q	Cald1	Caldesmon	R.SGRYEVEETEVVIK.S	8.43	8.34	1.01	0.99
Q8VCQ8_Q	Cald1	Caldesmon	K.VLEEEEQR.R	7.61	22.51	0.34	2.96
Q8VCQ8_Q	Cald1	Caldesmon	R.YEVEETEVVIK#.S	28.91	9.72	2.97	0.34
Q8VCQ8_Q	Cald1	Caldesmon	R.AEFLNK#.S	82.58	38.17	2.16	0.46
Q8VCQ8_Q	Cald1	Caldesmon	R.ASGDK#EAEGAPQVEAGK#.R	79.21	39.90	1.99	0.50
Q8VCQ8_Q	Cald1	Caldesmon	K.ASKPM*KPAASDLPVPAEGVR.N	5.97	15.83	0.38	2.65
Q8VCQ8_Q	Cald1	Caldesmon	K.DK#EPK#EEVK#.S	4.74	3.58	1.33	0.75
Q8VCQ8_Q	Cald1	Caldesmon	K.GSVFSAPSASGTPNK#.E	42.79	18.81	2.27	0.44
Q8VCQ8_Q	Cald1	Caldesmon	R.INEWLTK#.S	77.83	32.46	2.40	0.42
Q8VCQ8_Q	Cald1	Caldesmon	R.LEQYTNAIEGTK#.A	149.62	68.53	2.18	0.46
Q8VCQ8_Q	Cald1	Caldesmon	K.LKQTENAFSPSR.S	4.75	17.34	0.27	3.65
Q8VCQ8_Q	Cald1	Caldesmon	R.QKQEEESLGQVTDQVEAHVQNSVPDEESKPASSNTQVEGDEEAALLER.L	4.40	3.44	1.28	0.78
Q8VCQ8_Q	Cald1	Caldesmon	K.QSVDK#VTSPTK#V.-	7.47	5.61	1.33	0.75
Q8VCQ8_Q	Cald1	Caldesmon	R.RGETENEEFEK.L	5.27	11.33	0.47	2.15
Q8VCQ8_Q	Cald1	Caldesmon	R.SGRYEVEETEVVIK.S	20.43	36.60	0.56	1.79
Q8VCQ8_Q	Cald1	Caldesmon	R.STHQAAVVSK#.I	13.81	9.48	1.46	0.69
Q8VCQ8_Q	Cald1	Caldesmon	K.VLEEEEQR.R	21.35	35.74	0.60	1.67
Q8VCQ8_Q	Cald1	Caldesmon	R.YEVEETEVVIK#.S	46.66	18.00	2.59	0.39
F6ZAW1_F	Cald1	Protein Cal	K.GGSLGENQVEK#.M	9.71	3.25	2.98	0.34
P62204_C	Calm1	Calmodulir	K.DTDSEEEIR.E	11.20	19.78	0.57	1.77
P62204_C	Calm1	Calmodulir	R.EADIDGDGQVNYEEFVQM*M*TAK#.-	71.38	30.52	2.34	0.43
P62204_C	Calm1	Calmodulir	R.EADIDGDGQVNYEEFVQMM*TAK#.-	12.82	4.99	2.57	0.39
P62204_C	Calm1	Calmodulir	R.EADIDGDGQVNYEEFVQM*MTAK#.-	7.09	4.81	1.47	0.68
P62204_C	Calm1	Calmodulir	R.EADIDGDGQVNYEEFVQMM*TAK#.-	5.53	1.93	2.86	0.35
P62204_C	Calm1	Calmodulir	R.EADIDGDGQVNYEEFVQMMTAK#.-	7.04	3.96	1.78	0.56
P62204_C	Calm1	Calmodulir	K.ELGTVM*R.S	85.78	179.06	0.48	2.09
P62204_C	Calm1	Calmodulir	K.M*KDTDSEEEIR.E	3.66	14.36	0.25	3.93
P62204_C	Calm1	Calmodulir	R.VFDKDGNGYISAAELR.H	8.57	13.11	0.65	1.53
P14211_C	Calr	Calreticulir	K.IDNSQVESGSLEDDWDFLPPK#K#.I	6.50	4.44	1.46	0.68
P14211_C	Calr	Calreticulir	K.K#PEDWDEEM*DGEWEPPVIQNPEYK#.G	8.94	4.67	1.92	0.52
P14211_C	Calr	Calreticulir	K.K#PEDWDEEMDGEWEPPVIQNPEYK#.G	3.73	2.92	1.28	0.78
O35887_C	Calu	Calumenin	R.EQFVEFR.D	19.62	114.64	0.17	5.84
O35887_C	Calu	Calumenin	K.GHDLNEDGLVSWEEYK#.N	8.95	12.26	0.73	1.37
O35887_C	Calu	Calumenin	K.GHDLNEDGLVSWEEYK.N	3.42	5.56	0.61	1.63
O35887_C	Calu	Calumenin	R.HLVYESDQNKDGK.L	84.48	97.50	0.87	1.15
O35887_C	Calu	Calumenin	K.IDDDK#DGFVTVDELK#.G	66.57	105.47	0.63	1.58
O35887_C	Calu	Calumenin	K.IDDDKDGFVTVDELK.G	15.14	24.13	0.63	1.59
O35887_C	Calu	Calumenin	K.LTKEEIVDKYDLFVGSQATDFGEALVR.H	10.76	60.15	0.18	5.59
O35887_C	Calu	Calumenin	K.MDKEETKDWILPSDYDHAEAEAR.H	2.00	6.30	0.32	3.14
O35887_C	Calu	Calumenin	K.SFDQLTPEESK#.E	39.85	67.99	0.59	1.71
O35887_C	Calu	Calumenin	R.VHHEPQLSDK.V	15.53	32.56	0.48	2.10
O35887_C	Calu	Calumenin	K.VHNDAQNFDYDHDAFLGAEEAK#.S	12.33	17.28	0.71	1.40
Q6XLQ8_Q	Calu	Calumenin	K.IDADKDGFVTEGELK.S	3.42	6.80	0.50	1.99
Q6XLQ8_Q	Calu	Calumenin	R.LGM*IVDKIDADKDGFVTEGELK.S	18.01	20.35	0.88	1.13
Q6XLQ8_Q	Calu	Calumenin	R.LGMIVDKIDADKDGFVTEGELK.S	7.14	18.35	0.39	2.57
Q91YS8_K	Camk1	Calcium/ca	R.LIFQVLDAVK#.Y	9.49	1.85	5.13	0.20
Q6PHZ2_K	Camk2d	Calcium/ca	R.DLK#PENLLLASK#.S	13.61	23.17	0.59	1.70
Q6PHZ2_K	Camk2d	Calcium/ca	R.DLKPENLLLASK.S	15.48	33.36	0.46	2.15
Q6PHZ2_K	Camk2d	Calcium/ca	K.ESTESSNTTIEDEDVK#.A	13.88	22.78	0.61	1.64
Q6PHZ2_K	Camk2d	Calcium/ca	K.IPTGQEYAAK.I	34.39	54.17	0.63	1.58
Q6PHZ2_K	Camk2d	Calcium/ca	K.VTEQLIEAINNGDFEAYTK.I	5.82	9.83	0.59	1.69
Q6PHZ2_K	Camk2d	Calcium/ca	R.FYFENALSK.S	13.29	22.43	0.59	1.69
Q6PHZ2_K	Camk2d	Calcium/ca	R.LTQYM*DGSGM*PK.T	5.18	6.93	0.75	1.34
Q6PHZ2_K	Camk2d	Calcium/ca	K.VTEQLIEAINNGDFEAYTK.I	6.28	8.13	0.77	1.29
Q6PHZ2_K	Camk2d	Calcium/ca	R.DLK#PENLLLASK#.S	16.53	24.06	0.69	1.46
Q6PHZ2_K	Camk2d	Calcium/ca	K.ESTESSNTTIEDEDVK.A	9.56	13.91	0.69	1.45
Q6PHZ2_K	Camk2d	Calcium/ca	R.FTDEYQLFEELGK.G	16.53	19.68	0.84	1.19
Q6PHZ2_K	Camk2d	Calcium/ca	R.LTQYM*DGSGM*PK.T	6.20	9.32	0.67	1.50
Q6PHZ2_K	Camk2d	Calcium/ca	K.VTEQLIEAINNGDFEAYTK.I	5.85	7.66	0.76	1.31
Q6PHZ2_K	Camk2d	Calcium/ca	K.AGAYDFPSPEWDTVTPEAK.D	21.96	25.06	0.88	1.14
Q6PHZ2_K	Camk2d	Calcium/ca	R.DLK#PENLLLASK#.S	38.74	43.31	0.89	1.12
Q6PHZ2_K	Camk2d	Calcium/ca	K.ESTESSNTTIEDEDVK.A	18.91	28.84	0.66	1.53
Q6PHZ2_K	Camk2d	Calcium/ca	R.FTDEYQLFEELGK.G	32.57	34.86	0.93	1.07
Q6PHZ2_K	Camk2d	Calcium/ca	R.FYFENALSK#.S	20.01	24.86	0.80	1.24
Q6PHZ2_K	Camk2d	Calcium/ca	K.IPTGQEYAAK.I	33.80	38.27	0.88	1.13
Q6PHZ2_K	Camk2d	Calcium/ca	R.LTQYM*DGSGM*PK#.T	14.33	17.47	0.82	1.22
Q6PHZ2_K	Camk2d	Calcium/ca	K.VTEQLIEAINNGDFEAYTK.I	41.16	19.70	2.09	0.48
Q6ZQ38_C	Cand1	Cullin-asso	K.ALTLIAGSPLK#.I	22.35	7.44	3.00	0.33
Q6ZQ38_C	Cand1	Cullin-asso	R.AVAALLTIPEAEK#.S	10.22	4.03	2.54	0.39
Q6ZQ38_C	Cand1	Cullin-asso	K.EGPAVVGQFIQDVK#.N	21.46	6.60	3.25	0.31
Q6ZQ38_C	Cand1	Cullin-asso	R.HEM*LPEFYK#.T	12.15	3.66	3.32	0.30
Q6ZQ38_C	Cand1	Cullin-asso	K.ITSEALLVTQQLVK#.V	16.23	6.28	2.59	0.39
Q6ZQ38_C	Cand1	Cullin-asso	K.LGTLSALDILIK#.N	44.53	14.81	3.01	0.33
Q6ZQ38_C	Cand1	Cullin-asso	K.ALTLIAGSPLK#.I	51.42	13.89	3.70	0.27
Q6ZQ38_C	Cand1	Cullin-asso	R.AVAALLTIPEAEK#.S	22.71	8.14	2.79	0.36
Q6ZQ38_C	Cand1	Cullin-asso	R.DISSIGLK#.T	31.00	4.82	6.43	0.16
Q6ZQ38_C	Cand1	Cullin-asso	R.DLLDSVLPHLYNETK#.V	31.76	13.46	2.36	0.42
Q6ZQ38_C	Cand1	Cullin-asso	K.DSSSTNLESM*DTS.-	8.92	8.92	1.00	1.00
Q6ZQ38_C	Cand1	Cullin-asso	K.EGPAVVGQFIQDVK#.N	69.09	19.60	3.52	0.28
Q6ZQ38_C	Cand1	Cullin-asso	R.EVEM*GPFK#.H	19.00	6.16	3.08	0.32
Q6ZQ38_C	Cand1	Cullin-asso	R.FM*ATNDLM*TELQK#.D	7.41	3.20	2.31	0.43
Q6ZQ38_C	Cand1	Cullin-asso	K.ITSEALLVTQQLVK#.V	44.42	13.98	3.18	0.31
Q6ZQ38_C	Cand1	Cullin-asso	K.LGTLSALDILIK#.N	97.79	22.00	4.45	0.22
Q6ZQ38_C	Cand1	Cullin-asso	K.LTLIDPETLLPR.L	15.99	21.21	0.75	1.33
Q6ZQ38_C	Cand1	Cullin-asso	R.SSVVTAVK#.F	58.41	12.60	4.64	0.22
Q6ZQ38_C	Cand1	Cullin-asso	K.SVILEAFSSPSEEVK#.S	52.57	20.42	2.57	0.39
Q6ZQ38_C	Cand1	Cullin-asso	K.VIRPLDQPSSFDATPYIK.D	12.83	15.85	0.81	1.24
Q6ZQ73_C	Cand2	Cullin-asso	R.AVAALLTNPEVR.K	4.01	12.30	0.33	3.07
Q6ZQ73_C	Cand2	Cullin-asso	R.SNPELTTLFESIQK#.D	10.13	12.24	0.83	1.21
P35564_C	Canx	Calnexin O	K.APVPTGEVYFADSFDR.G	7.18	28.13	0.26	3.92
P35564_C	Canx	Calnexin O	R.GSLSGWILSK#.A	29.66	21.02	1.41	0.71
P35564_C	Canx	Calnexin O	R.K#IPNPDFFEDLEPFK#.M	23.12	17.65	1.31	0.76
P35564_C	Canx	Calnexin O	K.APVPTGEVYFADSFDR.G	2.17	10.15	0.21	4.67

P35564_C	Canx	Calnexin O	K.SDASTPPSPK#.V	10.78	7.32	1.47	0.68
P40124_C	Cap1	Adenylyl cy	K.EM*NDAAM*FYTNR.V	7.32	8.62	0.85	1.18
P40124_C	Cap1	Adenylyl cy	K.EPALLELEGK#.K	23.79	4.40	5.41	0.18
P40124_C	Cap1	Adenylyl cy	K.K#EPALLELEGK#.K	38.57	7.90	4.88	0.20
P40124_C	Cap1	Adenylyl cy	K.LVTTVTEIAG.-	35.97	35.97	1.00	1.00
P40124_C	Cap1	Adenylyl cy	R.VENQENVSNLVIDDTELK#.Q	51.48	10.48	4.91	0.20
P40124_C	Cap1	Adenylyl cy	K.VPTISINK#.T	72.93	17.15	4.25	0.24
P40124_C	Cap1	Adenylyl cy	R.VENQENVSNLVIDDTELK#.Q	6.97	1.98	3.52	0.28
Q99LB4_Q	Capg	Capping pr	K.AQVEIITDGEEPAEM*IQVLGPK#PALK#.E	19.30	7.03	2.74	0.36
Q99LB4_Q	Capg	Capping pr	K.AQVEIITDGEEPAEMIQVLGPK#PALK#.E	54.38	20.27	2.68	0.37
Q99LB4_Q	Capg	Capping pr	R.EGGVESAFHK#.T	51.76	14.52	3.56	0.28
Q99LB4_Q	Capg	Capping pr	K.EGNPEEDITADQTNAQAAALYK#.V	38.05	10.04	3.79	0.26
Q99LB4_Q	Capg	Capping pr	R.EVQGNESDLFM*SYFPR.G	8.02	7.99	1.00	1.00
Q99LB4_Q	Capg	Capping pr	R.EVQGNESDLFMSYFPR.G	6.31	7.84	0.80	1.24
Q99LB4_Q	Capg	Capping pr	R.QAALQVADGFISR.M	28.06	39.82	0.70	1.42
Q99LB4_Q	Capg	Capping pr	K.VSDATGQMNLTK#.V	101.53	29.75	3.41	0.29
Q99LB4_Q	Capg	Capping pr	K.VSDATGQM*NLTK#.V	144.36	45.71	3.16	0.32
Q99LB4_Q	Capg	Capping pr	R.YSPNTQVEILPQGR.E	19.37	28.74	0.67	1.48
O35350_C	Capn1	Calpain-1 c	K.APSDLYQIILK#.A	28.13	7.39	3.80	0.26
O35350_C	Capn1	Calpain-1 c	K.K#AGTQELDDQIQANLPDEK#.V	8.46	2.61	3.24	0.31
O35350_C	Capn1	Calpain-1 c	K.LVFVHSAQGNEFWSALLEK#.A	17.64	5.92	2.98	0.34
O35350_C	Capn1	Calpain-1 c	R.NYPATFWVNPQFK#.I	15.70	7.02	2.23	0.45
O35350_C	Capn1	Calpain-1 c	K.VLSEEEIDDNFK#.T	25.68	7.72	3.33	0.30
O35350_C	Capn1	Calpain-1 c	K.APSDLYQIILK#.A	47.07	10.42	4.52	0.22
O35350_C	Capn1	Calpain-1 c	R.GHAYSVTGAK#.Q	16.89	10.78	1.57	0.64
O35350_C	Capn1	Calpain-1 c	K.LVFVHSAQGNEFWSALLEK#.A	25.57	4.36	5.86	0.17
O35350_C	Capn1	Calpain-1 c	R.M*AIEAAGFK#.L	22.37	11.24	1.99	0.50
O35350_C	Capn1	Calpain-1 c	R.NYPATFWVNPQFK#.I	15.11	6.28	2.41	0.42
O35350_C	Capn1	Calpain-1 c	K.VLSEEEIDDNFK#.T	41.93	8.85	4.74	0.21
O08529_C	Capn2	Calpain-2 c	K.DGELLFVHSAEGSEFWSALLEK#.A	22.26	4.78	4.66	0.21
O08529_C	Capn2	Calpain-2 c	K.GHAYSVTGAEEVESSGSLQK#.L	28.46	7.44	3.83	0.26
O08529_C	Capn2	Calpain-2 c	R.LETLFK#.I	15.14	6.40	2.37	0.42
O08529_C	Capn2	Calpain-2 c	R.NPWGQVEWTGK#.W	18.92	5.89	3.21	0.31
O08529_C	Capn2	Calpain-2 c	R.NYPNTFWM*NPQYLIK#.L	6.89	2.85	2.42	0.41
O08529_C	Capn2	Calpain-2 c	R.NYPNTFWMNPQYLIK#.L	6.44	2.40	2.68	0.37
O08529_C	Capn2	Calpain-2 c	K.GHAYSVTGAEEVESSGSLQK#.L	37.82	8.32	4.55	0.22
O08529_C	Capn2	Calpain-2 c	K.LEEEDEDEEDGER.G	1.77	3.97	0.44	2.25
O08529_C	Capn2	Calpain-2 c	K.M*GEDM*HTIGFGIYEVPEELTGQTNIHLGK#.N	8.62	2.50	3.45	0.29
O08529_C	Capn2	Calpain-2 c	R.NPWGQVEWTGK#.W	17.29	8.14	2.12	0.47
O08529_C	Capn2	Calpain-2 c	R.NYPNTFWM*NPQYLIK#.L	8.02	2.84	2.82	0.35
D3YW48_D	Capns1	Calpain sm	R.ILGGVISAISEAAAQYNPEPPPPR.S	2.56	6.46	0.40	2.52
D3YW48_D	Capns1	Calpain sm	K.GGGGGGGGGGLGGGLGNVLGGLISGAAGGGGGGGGGM*GLGGGGGGGTAM*R.I	7.00	8.87	0.79	1.27
D3YW48_D	Capns1	Calpain sm	R.ILGGVISAISEAAAQYNPEPPPPR.S	8.25	20.09	0.41	2.44
D3YW48_D	Capns1	Calpain sm	K.LFVQLAGDDM*EVSATELM*NILNK#.V	7.53	4.21	1.79	0.56
D3YW48_D	Capns1	Calpain sm	K.LFVQLAGDDM*EVSATELMNILNK#.V	5.09	2.82	1.81	0.55
D3YW48_D	Capns1	Calpain sm	K.LGFEEFK#.Y	74.05	36.89	2.01	0.50
D3YW48_D	Capns1	Calpain sm	R.SHYSNIEANESEEVR.Q	18.38	41.22	0.45	2.24
D3YW48_D	Capns1	Calpain sm	R.SM*VAVMDSDTTGK#.L	7.19	2.03	3.54	0.28
D3YW48_D	Capns1	Calpain sm	R.SM*VAVM*DSDTTGK#.L	28.25	14.55	1.94	0.51
Q60865_C	Caprin1	Caprin-1 O	R.LNEQYEHASIHLWDLLEGK#.E	13.00	3.39	3.84	0.26
Q60865_C	Caprin1	Caprin-1 O	R.LNQDQLDAVSK#.Y	48.32	38.92	1.24	0.81
Q60865_C	Caprin1	Caprin-1 O	K.SSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQTEAM*K#.Q	4.29	3.25	1.32	0.76
Q60865_C	Caprin1	Caprin-1 O	K.TVLELQYVLDK.L	10.33	10.50	0.98	1.02
Q60865_C	Caprin1	Caprin-1 O	K.YQEVTNNLEFAK#.E	20.12	17.33	1.16	0.86
Q60865_C	Caprin1	Caprin-1 O	R.GGYDGYRPSFSNTPNSGYSQSQFTAPR.D	1.49	8.08	0.18	5.42
Q60865_C	Caprin1	Caprin-1 O	K.GKLDDYQER.M	14.49	64.64	0.22	4.46
Q60865_C	Caprin1	Caprin-1 O	K.LDDYQER.M	10.28	41.87	0.25	4.07
Q60865_C	Caprin1	Caprin-1 O	R.LNEQYEHASIHLWDLLEGK#.E	54.91	48.44	1.13	0.88
Q60865_C	Caprin1	Caprin-1 O	R.LNQDQLDAVSK#.Y	337.22	396.45	0.85	1.18
Q60865_C	Caprin1	Caprin-1 O	R.QFM*AETQFSSGEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQSDPLVR.R	1.71	2.54	0.67	1.49
Q60865_C	Caprin1	Caprin-1 O	K.QILGVIDK#K#.L	38.72	37.36	1.04	0.96
Q60865_C	Caprin1	Caprin-1 O	R.SFM*ALSQDIQK#.T	67.46	81.49	0.83	1.21
Q60865_C	Caprin1	Caprin-1 O	R.SFMALSQDIQK#.T	62.00	65.08	0.95	1.05
Q60865_C	Caprin1	Caprin-1 O	K.SSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQTEAMK.Q	29.97	27.49	1.09	0.92
Q60865_C	Caprin1	Caprin-1 O	K.TVLELQYVLDK#.L	67.46	69.72	0.97	1.03
Q60865_C	Caprin1	Caprin-1 O	K.TVLELQYVLDKLGDDDVR.T	13.22	79.21	0.17	5.99
Q60865_C	Caprin1	Caprin-1 O	K.YQEVTNNLEFAK#.E	184.95	202.13	0.91	1.09
Q60865_C	Caprin1	Caprin-1 O	K.LDDYQER.M	1.47	7.32	0.20	4.98
Q60865_C	Caprin1	Caprin-1 O	R.LNQDQLDAVSK#.Y	51.96	42.16	1.23	0.81
Q60865_C	Caprin1	Caprin-1 O	R.SFM*ALSQDIQK.T	12.92	18.64	0.69	1.44
Q60865_C	Caprin1	Caprin-1 O	K.TVLELQYVLDK#.L	7.46	6.56	1.14	0.88
Q60865_C	Caprin1	Caprin-1 O	K.YQEVTNNLEFAK#.E	24.09	25.29	0.95	1.05
Q5RKN9_Q	Capza1	Capping pr	K.DVQDSVTVSNEIQTTK#.E	15.61	16.67	0.94	1.07
Q5RKN9_Q	Capza1	Capping pr	K.EASDPQPEDVDGGLK#.S	27.76	45.19	0.61	1.63
Q5RKN9_Q	Capza1	Capping pr	K.FITHAPPGEFNEVFNDVR.L	8.89	44.96	0.20	5.06
Q5RKN9_Q	Capza1	Capping pr	K.FTITPPSAQVVGVLK.I	52.29	61.49	0.85	1.18
Q5RKN9_Q	Capza1	Capping pr	K.IEGYDDQVLITEHGDLGNSR.F	11.36	14.54	0.78	1.28
Q5RKN9_Q	Capza1	Capping pr	K.IIESAENEYQTAISENYQTM*SDTTFK.A	12.67	11.04	1.15	0.87
Q5RKN9_Q	Capza1	Capping pr	K.IIESAENEYQTAISENYQTMSDTTFK.A	9.07	5.64	1.61	0.62
P47754_C	Capza2	F-actin-cap	K.EATDPRPYEAENAIESWR.T	2.20	25.51	0.09	11.60
P47754_C	Capza2	F-actin-cap	R.EGAAHAFAQYNLDQFTPVK#.I	15.38	13.32	1.15	0.87
P47754_C	Capza2	F-actin-cap	K.FIIHAPPGEFNEVFNDVR.L	8.06	41.85	0.19	5.19
P47754_C	Capza2	F-actin-cap	K.FTVTPSTTQVVGILK.I	50.42	64.41	0.78	1.28
P47754_C	Capza2	F-actin-cap	K.IVEAAENEYQTAISENYQTM*SDTTFK.A	12.79	6.96	1.84	0.54
P47754_C	Capza2	F-actin-cap	R.TSVETALR.A	7.66	47.74	0.16	6.24
P47757_C	Capzb	F-actin-cap	R.KLEVEANNAFDQYR.D	6.52	41.10	0.16	6.30
P47757_C	Capzb	F-actin-cap	R.LVEDM*ENK.I	9.60	18.18	0.53	1.89
P47757_C	Capzb	F-actin-cap	R.LVEDMENK.I	22.63	30.18	0.75	1.33
P47757_C	Capzb	F-actin-cap	R.RLPPQQIEK.N	3.50	11.70	0.30	3.35
P47757_C	Capzb	F-actin-cap	K.SGSGTM*NLGGSLTR.Q	216.25	38.14	5.67	0.18
P47757_C	Capzb	F-actin-cap	R.SPWSNKYDPPLEDGAM*PSAR.L	2.74	15.87	0.17	5.79
P47757_C	Capzb	F-actin-cap	R.KLEVEANNAFDQYR.D	2.40	12.60	0.19	5.25
P47757_C	Capzb	F-actin-cap	K.LEVEANNAFDQYR.D	0.00	3.78	0.00	#DIV/0!
P47757_C	Capzb	F-actin-cap	K.SGSGTM*NLGGSLTR.Q	14.81	33.87	0.44	2.29
P47757_C	Capzb	F-actin-cap	R.STLNEIYFGK.T	42.55	58.83	0.72	1.38
P47757_C	Capzb	F-actin-cap	K.SGSGTM*NLGGSLTR.Q	22.88	7.99	2.86	0.35
Q9WVG6_	Carm1	Histone-ar	R.GAAVDEYFR.Q	5.76	14.10	0.41	2.45
Q9WVG6_	Carm1	Histone-ar	K.SSNLLDLK#.N	15.72	6.79	2.31	0.43
Q9WVG6_	Carm1	Histone-ar	K.YTVNFLEAK#.E	30.87	19.20	1.61	0.62
Q9ER72_SY	Cars	Cysteine--t	R.APVDITGQFEK#.W	33.24	2.52	13.19	0.08
Q9ER72_SY	Cars	Cysteine--t	R.FEDHEGLPTVVK#.L	39.06	2.23	17.55	0.06
Q9ER72_SY	Cars	Cysteine--t	K.FM*NEFFLNVK#.D	15.32	1.36	11.27	0.09
Q9ER72_SY	Cars	Cysteine--t	K.FMNEFFLNVK#.D	18.63	9.60	1.94	0.52

Q9ER72_SY	Cars	Cysteine--t	R.NK#DVFIPQDGK#K#.V	40.25	2.47	16.31	0.06
Q9ER72_SY	Cars	Cysteine--t	R.SPNDFALWK#.A	29.93	1.57	19.08	0.05
Q9ER72_SY	Cars	Cysteine--t	R.SSLSGEEVDSK#.V	50.66	1.42	35.68	0.03
Q9ER72_SY	Cars	Cysteine--t	K.WEAEEVELNK#.N	10.72	6.56	1.64	0.61
Q9ER72_SY	Cars	Cysteine--t	R.APVDITGQFEK#.W	48.20	2.69	17.91	0.06
Q9ER72_SY	Cars	Cysteine--t	R.APVDITGQFEK#WEAEEVELNK#.N	47.95	2.35	20.43	0.05
Q9ER72_SY	Cars	Cysteine--t	K.DLLSDWLDSTGGSEVTDNSIFSK#.L	19.08	1.32	14.45	0.07
Q9ER72_SY	Cars	Cysteine--t	K.DTLDYSSNTM*ESALQYEK#.F	13.88	2.02	6.88	0.15
Q9ER72_SY	Cars	Cysteine--t	R.FEDHEGLPTVVK#.L	62.16	3.38	18.41	0.05
Q9ER72_SY	Cars	Cysteine--t	K.FM*NEFFLNVK#.D	24.50	2.08	11.75	0.09
Q9ER72_SY	Cars	Cysteine--t	K.FMNEFFLNVK#.D	14.96	20.83	0.72	1.39
Q9ER72_SY	Cars	Cysteine--t	K.LFEAQEK#.L	38.86	9.59	4.05	0.25
Q9ER72_SY	Cars	Cysteine--t	K.LVPEAVGDQK#.A	108.06	6.27	17.22	0.06
Q9ER72_SY	Cars	Cysteine--t	R.SPNDFALWK#.A	35.96	3.24	11.10	0.09
Q9ER72_SY	Cars	Cysteine--t	R.SSLSGEEVDSK#.V	104.66	26.04	4.02	0.25
Q9ER72_SY	Cars	Cysteine--t	K.VQVLLEEAK#.D	97.66	3.10	31.49	0.03
Q9ER72_SY	Cars	Cysteine--t	R.VSEYVPEIVNFVQK#.I	49.03	2.68	18.33	0.05
P70677_C	Casp3	Caspase-3	K.SVDSGIYLDSSYK#.M	9.66	5.84	1.65	0.60
P49817_C	Cav1	Caveolin-1	K.HLNDDVVK#.I	20.29	23.02	0.88	1.13
Q9WVC3_	Cav2	Caveolin-2	R.SFSSVSMQLSHD.-	5.96	5.96	1.00	1.00
Q08024_P	Cbfb	Core-bindi	R.AQQEDALAQQAFEEAR.R	5.00	31.60	0.16	6.32
Q08024_P	Cbfb	Core-bindi	R.SKFENEEFFR.K	47.72	10.83	4.41	0.23
P22682_C	Cbl	E3 ubiquiti	R.APVPASTSVLGTASK#.A	18.46	7.70	2.40	0.42
Q9JIY2_HA	Cbll1	E3 ubiquiti	R.ASLENVHPPIAPPPTDIPDR.F	2.34	13.03	0.18	5.58
P08074_C	Cbr2	Carbonyl r	R.SASTSGGGILVDAGYLAS.-	46.29	46.29	1.00	1.00
P08074_C	Cbr2	Carbonyl r	R.SVFQVSQM*VAR.D	28.59	14.99	1.91	0.52
P08074_C	Cbr2	Carbonyl r	R.VNSVNPTVVLTDM*GK#.K	41.77	5.91	7.06	0.14
P08074_C	Cbr2	Carbonyl r	R.VNSVNPTVVLTDMGK#.K	15.09	3.14	4.81	0.21
P83917_C	Cbx1	Chromobo	R.IIGATDSSGELM*FLM*K.W	4.63	8.11	0.57	1.75
P83917_C	Cbx1	Chromobo	R.IIGATDSSGELMFLMK.W	4.87	9.86	0.49	2.02
P83917_C	Cbx1	Chromobo	K.KKVEEVLEEEEEEYVVEK.V	4.09	11.19	0.37	2.73
P83917_C	Cbx1	Chromobo	K.NSDEADLVPAK.E	17.19	27.08	0.63	1.57
P83917_C	Cbx1	Chromobo	K.GK#VEYLLK#.W	115.87	287.93	0.40	2.48
P83917_C	Cbx1	Chromobo	R.IIGATDSSGELM*FLM*K.W	122.84	267.87	0.46	2.18
P83917_C	Cbx1	Chromobo	R.IIGATDSSGELM*FLM*K#.W	46.91	113.80	0.41	2.43
P83917_C	Cbx1	Chromobo	R.IIGATDSSGELMFLM*K.W	26.98	58.28	0.46	2.16
P83917_C	Cbx1	Chromobo	R.IIGATDSSGELM*FLMK.W	99.84	212.63	0.47	2.13
P83917_C	Cbx1	Chromobo	R.IIGATDSSGELMFLMK.W	52.94	118.04	0.45	2.23
P83917_C	Cbx1	Chromobo	R.IIGATDSSGELMFLMK.W	3.70	9.95	0.37	2.69
P83917_C	Cbx1	Chromobo	K.K#K#VEEVLEEEEEEYVVEK#.V	41.36	116.19	0.36	2.81
P83917_C	Cbx1	Chromobo	K.KKVEEVLEEEEEEYVVEK.V	11.43	25.91	0.44	2.27
P83917_C	Cbx1	Chromobo	K.K#VEEVLEEEEEEYVVEK#.V	130.80	261.27	0.50	2.00
P83917_C	Cbx1	Chromobo	K.NSDEADLVPAK.E	133.36	281.61	0.47	2.11
P83917_C	Cbx1	Chromobo	K.VEEVLEEEEEEYVVEK.V	21.13	50.56	0.42	2.39
P83917_C	Cbx1	Chromobo	K.VEYLLK#.W	30.48	46.04	0.66	1.51
P83917_C	Cbx1	Chromobo	K.WKNSDEADLVPAK.E	29.28	60.11	0.49	2.05
P23198_C	Cbx3	Chromobo	K.KVEEAEPEEFVVEK.V	7.69	28.78	0.27	3.74
P23198_C	Cbx3	Chromobo	K.VEEAEPEEFVVEK.V	4.06	8.09	0.50	1.99
P23198_C	Cbx3	Chromobo	K.DSDEADLVLAK.E	50.89	131.71	0.39	2.59
P23198_C	Cbx3	Chromobo	K.KVEEAEPEEFVVEK.V	73.26	162.80	0.45	2.22
P23198_C	Cbx3	Chromobo	K.KVEEAEPEEFVVEK.V	187.68	411.60	0.46	2.19
P23198_C	Cbx3	Chromobo	K.SKKVEEAEPEEFVVEK.V	23.58	63.35	0.37	2.69
P23198_C	Cbx3	Chromobo	K.SLSDSESDDSK.S	5.93	17.52	0.34	2.95
P23198_C	Cbx3	Chromobo	K.VEEAEPEEFVVEK.V	124.76	287.42	0.43	2.30
P23198_C	Cbx3	Chromobo	K.VEYFLK#.W	110.96	248.06	0.45	2.24
P23198_C	Cbx3	Chromobo	R.VVNGKVEYFLK.W	1.39	10.61	0.13	7.63
P23198_C	Cbx3	Chromobo	K.WK#DSDEADLVLAK#.E	118.52	360.50	0.33	3.04
Q61686_C	Cbx5	Chromobo	K.SSFSNSADDIK.S	7.02	15.37	0.46	2.19
Q61686_C	Cbx5	Chromobo	K.GFSEEHNTWEPEK.N	3.39	9.54	0.36	2.82
Q61686_C	Cbx5	Chromobo	K.GQVEYLLK#.W	68.48	129.59	0.53	1.89
Q61686_C	Cbx5	Chromobo	R.KSSFSNSADDIK.S	11.10	24.18	0.46	2.18
Q61686_C	Cbx5	Chromobo	R.LTWHAYPEDAENKEK.E	1.96	5.49	0.36	2.80
Q61686_C	Cbx5	Chromobo	R.LTWHAYPEDAENK#EK#.E	20.53	57.37	0.36	2.79
Q61686_C	Cbx5	Chromobo	K.SSFSNSADDIK.S	133.82	216.13	0.62	1.62
Q61686_C	Cbx5	Chromobo	R.TADSSSSEDEEEYVVEK.V	13.18	27.43	0.48	2.08
Q61686_C	Cbx5	Chromobo	K.WK#DTDEADLVLAK#.E	79.85	167.74	0.48	2.10
Q9QXV1_C	Cbx8	Chromobo	R.ILGDPEEESWSPSLTNLEK.V	8.95	5.75	1.56	0.64
Q9QXV1_C	Cbx8	Chromobo	R.RQDSDLVQYGVTSPSSAEASSK.L	3.56	8.50	0.42	2.39
Q9QXV1_C	Cbx8	Chromobo	R.SPQDLASTSR.A	11.23	37.77	0.30	3.36
Q9QXV1_C	Cbx8	Chromobo	K.YSTWEPEENILDAR.L	1.82	7.60	0.24	4.17
Q8BRN9_C	Cc2d1b	Coiled-coil	R.K#GSEQDSVAATLATAQK#.L	12.97	15.37	0.84	1.18
Q8BRN9_C	Cc2d1b	Coiled-coil	K.LASEDAALVDDDEESDTPAQAPLAK#.K	7.08	2.36	3.00	0.33
Q8BRN9_C	Cc2d1b	Coiled-coil	K.NTNSPEFEQVFK#.L	10.35	3.32	3.12	0.32
Q8CH18_C	Ccar1	Cell divisio	K.AGLLQPPVR.I	4.10	14.19	0.29	3.46
Q8CH18_C	Ccar1	Cell divisio	R.IQTLPNQNQSQTQPLLK#.T	8.86	6.30	1.41	0.71
Q8CH18_C	Ccar1	Cell divisio	R.IVSQPQPAR.R	13.42	44.05	0.30	3.28
Q8CH18_C	Ccar1	Cell divisio	R.LLLPTPTIK#.Q	40.20	36.91	1.09	0.92
Q8CH18_C	Ccar1	Cell divisio	R.VLVEATYNPNM*PFK#.W	9.40	7.47	1.26	0.79
Q8CH18_C	Ccar1	Cell divisio	K.AGLLQPPVR.I	5.12	14.65	0.35	2.86
Q8CH18_C	Ccar1	Cell divisio	R.IVSQPQPAR.R	20.15	34.38	0.59	1.71
Q8CH18_C	Ccar1	Cell divisio	R.LLLPTPTIK#.Q	46.15	27.46	1.68	0.60
Q8CH18_C	Ccar1	Cell divisio	K.LQLLEEK#TDEDGK#TILNLENSNK#.S	5.80	3.79	1.53	0.65
Q8CH18_C	Ccar1	Cell divisio	R.VLVEATYNPNM*PFK#.W	8.96	7.04	1.27	0.79
Q8CH18_C	Ccar1	Cell divisio	R.VLVEATYNPNMPFK#.W	7.14	4.54	1.57	0.64
Q8VDP4_C	Ccar2	Cell cycle a	K.ADSWVEK#EEPTPSN.-	11.26	10.17	1.11	0.90
Q8VDP4_C	Ccar2	Cell cycle a	R.KEEEAVLVGGEWSPSLDGLDPQADPQVLVR.T	1.67	3.78	0.44	2.27
Q8VDP4_C	Ccar2	Cell cycle a	K.VQTLSNQPLLK#.S	33.32	9.13	3.65	0.27
Q8VDP4_C	Ccar2	Cell cycle a	R.FSATEVTNK#.T	14.40	1.44	9.99	0.10
Q8VDP4_C	Ccar2	Cell cycle a	R.LPQLGEK#.V	60.81	30.63	1.99	0.50
Q8VDP4_C	Ccar2	Cell cycle a	K.VQTLSNQPLLK#.S	24.88	8.21	3.03	0.33
Q9DA08_S	Ccdc101	SAGA-assoc	R.IAELLTELHQLIK#.Q	11.00	8.70	1.26	0.79
Q8R344_C	Ccdc12	Coiled-coil	R.AIAELIR.E	4.78	23.40	0.20	4.90
Q8R344_C	Ccdc12	Coiled-coil	K.EQLEAAKPEPVIEEVDLANLAPR.K	3.59	25.87	0.14	7.21
Q8CI71_CC	Ccdc132	Coiled-coil	R.DYVDEQTGDVPVK#.S	10.66	8.81	1.21	0.83
Q8CI71_CC	Ccdc132	Coiled-coil	K.SPPESLNDLGAFESLR.V	1.76	5.73	0.31	3.26
Q8C7V8_C	Ccdc134	Coiled-coil	K.LKDAFSHVVENTAFFGDVVLR.F	2.64	3.41	0.77	1.29
Q8C7V8_C	Ccdc134	Coiled-coil	K.TDQTEFIPSTDPFQK#.A	22.06	11.01	2.00	0.50
Q8C7V8_C	Ccdc134	Coiled-coil	R.TVLIAADVLPDGPVPQDEK#.L	9.50	5.33	1.78	0.56
Q8C7V8_C	Ccdc134	Coiled-coil	R.TVLIAADVLPDGPVPQDEK#LK#.D	4.93	2.39	2.06	0.49
Q8R0K4_C	Ccdc137	Coiled-coil	K.NQDEQEIPFR.L	4.24	10.92	0.39	2.58
Q8C9S4_C	Ccdc186	Coiled-coil	R.EESGTLSSEASDFNK#.V	5.49	3.90	1.41	0.71
Q8C9S4_C	Ccdc186	Coiled-coil	R.ESELLLFTEK#.L	10.38	4.52	2.30	0.44
Q9JIG7_CC	Ccdc22	Coiled-coil	K.FTFHLEPQVQAAQVADVPATSQR.L	1.62	10.82	0.15	6.67

Q9JIG7_CC	Ccdc22	Coiled-coil	R.ILEIVGNIR.K	6.75	15.82	0.43	2.34
Q9JIG7_CC	Ccdc22	Coiled-coil	R.LIHLASQWEK#.H	6.44	4.69	1.37	0.73
Q9JIG7_CC	Ccdc22	Coiled-coil	K.QLVSELETLPK#.D	10.53	6.57	1.60	0.62
Q9JIG7_CC	Ccdc22	Coiled-coil	R.QSELSVAEQEQALR.L	3.03	8.14	0.37	2.69
Q9JIG7_CC	Ccdc22	Coiled-coil	R.TVELLPDGAANLAK#.L	9.62	7.63	1.26	0.79
Q9CR29_C	Ccdc43	Coiled-coil	K.VK#K#EDEVQAIATLIEK#.Q	16.83	4.07	4.13	0.24
Q9CR29_C	Ccdc43	Coiled-coil	K.VK#K#EDEVQAIATLIEK#.Q	14.16	6.38	2.22	0.45
Q9CR27_C	Ccdc53	WASH com	R.IQQIETTLNILDAK#.L	14.57	11.06	1.32	0.76
Q9CR27_C	Ccdc53	WASH com	R.IQQIETTLNILDAK#.L	6.21	3.01	2.06	0.49
D3YZP9_CC	Ccdc6	Coiled-coil	R.AEQEEEFISNTLFK#.K	8.54	3.27	2.61	0.38
D3YZP9_CC	Ccdc6	Coiled-coil	R.AEQEEEFISNTLFK#.K	7.48	2.07	3.62	0.28
D3YZP9_CC	Ccdc6	Coiled-coil	K.K#LENDTISK#.Q	6.16	3.47	1.78	0.56
Q6NS45_C	Ccdc66	Coiled-coil	K.VSVK#MGNK#.F	4.77	4.16	1.15	0.87
Q9D541_C	Ccdc7	Coiled-coil	R.K#FEDFK.S	1.20	1.09	1.10	0.91
Q5SNZ0_GI	Ccdc88a	Girdin OS=I	R.TSELAEAPQK#.S	14.01	12.29	1.14	0.88
Q7TQK5_C	Ccdc93	Coiled-coil	R.ALVAM*NESLK#.S	9.99	5.73	1.75	0.57
Q7TQK5_C	Ccdc93	Coiled-coil	R.DQLNDQYLELLEK#.Q	13.58	7.76	1.75	0.57
Q7TQK5_C	Ccdc93	Coiled-coil	K.QSELSAEESPEK#.L	10.26	5.17	1.98	0.50
O88874_C	Ccnk	Cyclin-K OS	R.K#PPLAPALGEAEATGPVETSDLPK#.V	17.26	8.29	2.08	0.48
O88874_C	Ccnk	Cyclin-K OS	K.FDLQVEHPYQFLLK#.Y	9.96	5.82	1.71	0.58
O88874_C	Ccnk	Cyclin-K OS	R.K#PPLAPALGEAEATGPVETSDLPK#.V	16.29	6.79	2.40	0.42
Q9QWV9_	Ccnt1	Cyclin-T1 O	K.TYSLSSTLSSSSSTR.K	1.95	5.88	0.33	3.01
Q9QWV9_	Ccnt1	Cyclin-T1 O	R.TSESLALIGVDHSLQQDGSSAFGSQK#.Q	15.56	9.94	1.57	0.64
Q9QWV9_	Ccnt1	Cyclin-T1 O	K.TYSLSSTLSSSSSTR.K	5.04	7.50	0.67	1.49
Q9QWV9_	Ccnt1	Cyclin-T1 O	R.YSM*APAALFLAAK#.V	5.68	5.80	0.98	1.02
P80314_TC	Cct2	T-complex	R.AAHSEGHITAGLDMK#.E	171.23	48.53	3.53	0.28
P80314_TC	Cct2	T-complex	R.AAHSEGHITAGLDM*K#.E	220.88	61.55	3.59	0.28
P80314_TC	Cct2	T-complex	R.DAALM*VTNDGATILK#.N	161.46	50.88	3.17	0.32
P80314_TC	Cct2	T-complex	R.DAALMVTNDGATILK#.N	210.11	60.63	3.47	0.29
P80314_TC	Cct2	T-complex	R.EAESLIAK#.K	335.37	89.47	3.75	0.27
P80314_TC	Cct2	T-complex	R.EALLSSAVDHGSDEAR.F	27.18	44.35	0.61	1.63
P80314_TC	Cct2	T-complex	K.EAVAM*ESFAK#.A	348.55	94.53	3.69	0.27
P80314_TC	Cct2	T-complex	K.EAVAMESFAK#.A	211.16	65.51	3.22	0.31
P80314_TC	Cct2	T-complex	K.EGTIGDM*AVLGITESFQVK#.R	45.82	13.74	3.33	0.30
P80314_TC	Cct2	T-complex	K.EGTIGDM*AVLGITESFQVK#.R	4.34	1.91	2.28	0.44
P80314_TC	Cct2	T-complex	K.EGTIGDMAVLGITESFQVK#.R	87.18	17.86	4.88	0.20
P80314_TC	Cct2	T-complex	R.FWQDLM*NIAGTTLSSK#.L	67.83	16.97	4.00	0.25
P80314_TC	Cct2	T-complex	R.FWQDLMNIAGTTLSSK#.L	86.96	26.10	3.33	0.30
P80314_TC	Cct2	T-complex	R.GATQQILDEAER.S	140.11	179.35	0.78	1.28
P80314_TC	Cct2	T-complex	K.GSGNLEAIHVIK#K#.L	6.18	1.77	3.49	0.29
P80314_TC	Cct2	T-complex	K.ILIANTGM*DTDK#.I	122.69	40.91	3.00	0.33
P80314_TC	Cct2	T-complex	K.ILIANTGMDTDK#.I	63.20	17.32	3.65	0.27
P80314_TC	Cct2	T-complex	K.ILIANTGMDTDKIK.I	73.72	18.85	3.91	0.26
P80314_TC	Cct2	T-complex	K.ILLSSGR.D	145.74	175.45	0.83	1.20
P80314_TC	Cct2	T-complex	K.KIHPQTIISGWR.E	35.52	49.99	0.71	1.41
P80314_TC	Cct2	T-complex	K.K#LGGSLADSYLDEGFLLDK#.K	42.08	11.23	3.75	0.27
P80314_TC	Cct2	T-complex	K.K#LGGSLADSYLDEGFLLDK#K#.I	77.92	20.92	3.72	0.27
P80314_TC	Cct2	T-complex	R.LALVTGGEIASTFDHPELVK#.L	762.01	211.59	3.60	0.28
P80314_TC	Cct2	T-complex	K.LAVEAVLR.L	78.54	108.12	0.73	1.38
P80314_TC	Cct2	T-complex	K.LGGSLADSYLDEGFLLDK#.K	47.97	15.68	3.06	0.33
P80314_TC	Cct2	T-complex	K.LGGSLADSYLDEGFLLDK#K#.I	327.38	83.69	3.91	0.26
P80314_TC	Cct2	T-complex	K.LIEEVM*IGEDK#.L	81.22	27.48	2.96	0.34
P80314_TC	Cct2	T-complex	K.LIEEVMIGEDK#.L	70.40	39.34	1.79	0.56
P80314_TC	Cct2	T-complex	R.LK#GSGNLEAIHVIK#.K	248.11	52.78	4.70	0.21
P80314_TC	Cct2	T-complex	R.LK#GSGNLEAIHVIK#K#.L	10.13	3.91	2.59	0.39
P80314_TC	Cct2	T-complex	K.LLTHHKDHFTK.L	13.63	3.34	4.08	0.24
P80314_TC	Cct2	T-complex	R.LSSFIGAIAIGDLVK#.S	678.02	177.98	3.81	0.26
P80314_TC	Cct2	T-complex	R.M*LPTIIADNAGYDSADLVAQLR.A	40.97	45.19	0.91	1.10
P80314_TC	Cct2	T-complex	R.M*LPTIIADNAGYDSADLVAQLR.A	7.56	10.06	0.75	1.33
P80314_TC	Cct2	T-complex	R.MLPTIIADNAGYDSADLVAQLR.A	42.62	57.17	0.75	1.34
P80314_TC	Cct2	T-complex	K.NIGVDNPAAK#.V	391.80	119.48	3.28	0.30
P80314_TC	Cct2	T-complex	R.QLIYNYPEQLFGAAGVM*AIEHADFAGVER.L	17.37	16.84	1.03	0.97
P80314_TC	Cct2	T-complex	R.QVLLSAAEAAEVILR.V	56.90	57.55	0.99	1.01
P80314_TC	Cct2	T-complex	K.RQVLLSAAEAAEVILR.V	5.47	16.77	0.33	3.07
P80314_TC	Cct2	T-complex	K.VAEIEHAEK#EK#.M	384.64	128.75	2.99	0.33
P80314_TC	Cct2	T-complex	K.VAEIEHAEKEK.M	160.07	51.00	3.14	0.32
P80314_TC	Cct2	T-complex	K.VLVDM*SR.V	44.46	72.98	0.61	1.64
P80314_TC	Cct2	T-complex	R.VQDDEVGDGTTSVTVLAAELLR.E	64.20	88.12	0.73	1.37
P80314_TC	Cct2	T-complex	R.DAALM*VTNDGATILK#.N	8.54	2.51	3.40	0.29
P80314_TC	Cct2	T-complex	R.GATQQILDEAER.S	637.12	8.18	77.88	0.01
P80314_TC	Cct2	T-complex	R.LALVTGGEIASTFDHPELVK#.L	24.64	6.69	3.68	0.27
P80314_TC	Cct2	T-complex	K.LGGSLADSYLDEGFLLDK#K#.I	6.99	2.66	2.62	0.38
P80314_TC	Cct2	T-complex	R.DAALMVTNDGATILK#.N	11.55	5.37	2.15	0.47
P80314_TC	Cct2	T-complex	R.EAESLIAK#.K	30.21	29.18	1.04	0.97
P80314_TC	Cct2	T-complex	K.EAVAM*ESFAK#.A	27.80	7.29	3.81	0.26
P80314_TC	Cct2	T-complex	K.EGTIGDMAVLGITESFQVK#.R	8.02	1.67	4.80	0.21
P80314_TC	Cct2	T-complex	R.FWQDLM*NIAGTTLSSK#.L	4.88	2.64	1.85	0.54
P80314_TC	Cct2	T-complex	R.FWQDLMNIAGTTLSSK#.L	6.70	4.67	1.44	0.70
P80314_TC	Cct2	T-complex	R.GATQQILDEAER.S	17.05	20.66	0.83	1.21
P80314_TC	Cct2	T-complex	R.LALVTGGEIASTFDHPELVK#.L	81.64	28.52	2.86	0.35
P80314_TC	Cct2	T-complex	K.LGGSLADSYLDEGFLLDK#K#.I	29.75	8.75	3.40	0.29
P80314_TC	Cct2	T-complex	R.LSSFIGAIAIGDLVK#.S	56.49	18.57	3.04	0.33
P80314_TC	Cct2	T-complex	R.M*LPTIIADNAGYDSADLVAQLR.A	8.16	11.28	0.72	1.38
P80314_TC	Cct2	T-complex	K.NIGVDNPAAK#.V	32.26	10.48	3.08	0.32
P80314_TC	Cct2	T-complex	R.VDNIIK#.A	48.34	18.90	2.56	0.39
P80314_TC	Cct2	T-complex	R.VQDDEVGDGTTSVTVLAAELLR.E	14.70	14.86	0.99	1.01
P80314_TC	Cct2	T-complex	K.EAVAM*ESFAK#.A	11.66	4.95	2.36	0.42
P80314_TC	Cct2	T-complex	R.LSSFIGAIAIGDLVK#.S	25.83	9.33	2.77	0.36
P80318_TC	Cct3	T-complex	K.AM*TGVEQWPYR.A	45.96	61.69	0.74	1.34
P80318_TC	Cct3	T-complex	R.ANVTAIR.R	93.39	115.10	0.81	1.23
P80318_TC	Cct3	T-complex	R.AVAQALEVIPR.T	101.04	133.91	0.75	1.33
P80318_TC	Cct3	T-complex	R.EDDVGTGAGLLEIK#.K	35.18	11.48	3.07	0.33
P80318_TC	Cct3	T-complex	K.EILSEVER.N	91.05	111.99	0.81	1.23
P80318_TC	Cct3	T-complex	R.EIQVQHPAAK#.S	177.99	52.60	3.38	0.30
P80318_TC	Cct3	T-complex	K.ELGIWEPLAVK#.L	376.77	102.62	3.67	0.27
P80318_TC	Cct3	T-complex	R.EM*M*LSIINSSITTK#.V	85.76	26.60	3.22	0.31
P80318_TC	Cct3	T-complex	R.EM*MLSIINSSITTK#.V	32.49	11.58	2.81	0.36
P80318_TC	Cct3	T-complex	R.EMMLSIINSSITTK#.V	79.01	21.49	3.68	0.27
P80318_TC	Cct3	T-complex	K.GESQTDIEITR.E	3.38	9.39	0.36	2.78
P80318_TC	Cct3	T-complex	K.GISDLAQHYLM*R.A	20.29	22.29	0.91	1.10
P80318_TC	Cct3	T-complex	K.GISDLAQHYLMR.A	12.70	15.74	0.81	1.24
P80318_TC	Cct3	T-complex	R.IDDIVSGHKK.K	38.58	13.00	2.97	0.34
P80318_TC	Cct3	T-complex	R.IVLLDSSLEYK#.K	680.64	186.91	3.64	0.27

P80318_TC	Cct3	T-complex	R.IVSRPEELREDDVGTGAGLLEIK.K	25.25	60.19	0.42	2.38
P80318_TC	Cct3	T-complex	R.IVSRPEELREDDVGTGAGLLEIK.K	7.53	17.80	0.42	2.36
P80318_TC	Cct3	T-complex	K.KGESQTDIEITR.E	36.13	48.32	0.75	1.34
P80318_TC	Cct3	T-complex	K.KISTPVDVNNR.E	12.62	14.38	0.88	1.14
P80318_TC	Cct3	T-complex	R.K#VQSGNINAAK#.T	127.79	34.88	3.66	0.27
P80318_TC	Cct3	T-complex	R.M*ALDDM*ISTLK#.K	51.54	15.79	3.26	0.31
P80318_TC	Cct3	T-complex	R.MALDDM*ISTLK#.K	18.43	8.75	2.11	0.47
P80318_TC	Cct3	T-complex	R.M*ALDDMISTLK#.K	42.04	25.50	1.65	0.61
P80318_TC	Cct3	T-complex	R.M*ALDDMISTLKK.I	65.66	15.13	4.34	0.23
P80318_TC	Cct3	T-complex	R.MALDDMISTLK#K#.I	33.99	15.51	2.19	0.46
P80318_TC	Cct3	T-complex	K.M*LLDPM*GGIVM*TNDGNAILR.E	3.05	5.30	0.58	1.74
P80318_TC	Cct3	T-complex	K.M*LLDPMGGIVM*TNDGNAILR.E	3.37	2.27	1.48	0.67
P80318_TC	Cct3	T-complex	R.NVLLDPQLVPGGGASEM*AVAHALTEK#.S	197.73	58.86	3.36	0.30
P80318_TC	Cct3	T-complex	R.NVLLDPQLVPGGGASEMAVAHALTEK#.S	184.72	46.93	3.94	0.25
P80318_TC	Cct3	T-complex	K.SM*IEISR.T	44.17	61.82	0.71	1.40
P80318_TC	Cct3	T-complex	K.TAVETAVLLLR.I	143.21	186.79	0.77	1.30
P80318_TC	Cct3	T-complex	K.VQSGNINAAK#.T	110.95	35.38	3.14	0.32
P80318_TC	Cct3	T-complex	K.AM*TGVEQWPYR.A	7.56	9.97	0.76	1.32
P80318_TC	Cct3	T-complex	R.AVAQALEVIPR.T	28.01	33.74	0.83	1.20
P80318_TC	Cct3	T-complex	K.ELGIWEPLAVK#.L	88.75	48.78	1.82	0.55
P80318_TC	Cct3	T-complex	R.EM*M*LSIINSSITTK#.V	14.47	3.20	4.53	0.22
P80318_TC	Cct3	T-complex	R.EMMLSIINSSITTK#.V	28.39	7.89	3.60	0.28
P80318_TC	Cct3	T-complex	R.IDDIVSGHK#.K	30.16	73.12	0.41	2.42
P80318_TC	Cct3	T-complex	R.IVLLDSSLEYK#.K	153.44	44.40	3.46	0.29
P80318_TC	Cct3	T-complex	R.IVSRPEELREDDVGTGAGLLEIK.K	2.88	8.49	0.34	2.95
P80318_TC	Cct3	T-complex	R.K#VQSGNINAAK#.T	16.93	4.12	4.11	0.24
P80318_TC	Cct3	T-complex	K.TAVETAVLLLR.I	46.02	67.65	0.68	1.47
P80318_TC	Cct3	T-complex	K.VQSGNINAAK#.T	30.98	14.24	2.18	0.46
P80318_TC	Cct3	T-complex	K.ELGIWEPLAVK#.L	81.77	35.05	2.33	0.43
P80318_TC	Cct3	T-complex	R.EM*M*LSIINSSITTK#.V	16.88	5.58	3.02	0.33
P80318_TC	Cct3	T-complex	K.ISTPVDVNNR.E	23.75	25.22	0.94	1.06
P80318_TC	Cct3	T-complex	R.IVLLDSSLEYK#.K	170.91	21.93	7.79	0.13
P80318_TC	Cct3	T-complex	R.K#VQSGNINAAK#.T	20.79	7.18	2.90	0.35
P80318_TC	Cct3	T-complex	R.M*ALDDM*ISTLK#.K	15.67	6.81	2.30	0.43
P80318_TC	Cct3	T-complex	K.TAVETAVLLLR.I	34.85	39.19	0.89	1.12
P80318_TC	Cct3	T-complex	K.VQSGNINAAK#.T	35.97	8.74	4.12	0.24
P80315_TC	Cct4	T-complex	R.AFADAM*EVIPSTLAENAGLNPISTVTELR.N	26.02	28.26	0.92	1.09
P80315_TC	Cct4	T-complex	R.ALIAGGGAPEIELALR.L	67.33	73.91	0.91	1.10
P80315_TC	Cct4	T-complex	R.AYILNLVK#.Q	294.70	62.23	4.74	0.21
P80315_TC	Cct4	T-complex	R.ETLLNSATTSLNSK#.V	180.15	43.10	4.18	0.24
P80315_TC	Cct4	T-complex	R.FSNISAAK#.A	273.23	74.63	3.66	0.27
P80315_TC	Cct4	T-complex	K.GDVTITNDGATILK#.Q	112.89	28.62	3.94	0.25
P80315_TC	Cct4	T-complex	K.GIHPTIISESFQK#.A	257.63	86.56	2.98	0.34
P80315_TC	Cct4	T-complex	K.GIHPTIISESFQK#.A	115.37	36.24	3.18	0.31
P80315_TC	Cct4	T-complex	K.GLEILTDM*SRPVQLSDRETLLNSATTSLNSK.V	4.99	8.26	0.60	1.65
P80315_TC	Cct4	T-complex	K.IDDVVNTR.-	103.80	127.38	0.81	1.23
P80315_TC	Cct4	T-complex	K.LVIEEAER.S	96.22	115.89	0.83	1.20
P80315_TC	Cct4	T-complex	K.M*IQDGK#GDVTITNDGATILK#.Q	19.99	7.79	2.57	0.39
P80315_TC	Cct4	T-complex	K.M*IQDGKGDVTITNDGATILK.Q	188.29	44.23	4.26	0.23
P80315_TC	Cct4	T-complex	K.MIQDGK#GDVTITNDGATILK#.Q	94.16	20.30	4.64	0.22
P80315_TC	Cct4	T-complex	R.M*LVELSK#.A	190.75	33.50	5.69	0.18
P80315_TC	Cct4	T-complex	R.MLVELSK#.A	197.31	55.91	3.53	0.28
P80315_TC	Cct4	T-complex	K.TDM*DNQIVVSDYAQM*DR.V	8.85	12.76	0.69	1.44
P80315_TC	Cct4	T-complex	K.TDMDNQIVVSDYAQM*DR.V	5.32	5.70	0.93	1.07
P80315_TC	Cct4	T-complex	K.TDMDNQIVVSDYAQMDR.V	4.70	6.92	0.68	1.47
P80315_TC	Cct4	T-complex	K.TIGTK#PVAHIDQFTADMLGSAELAEEVSLNGSGK#.L	2.44	1.77	1.38	0.73
P80315_TC	Cct4	T-complex	K.VIDPATATSVDLR.D	112.13	144.45	0.78	1.29
P80315_TC	Cct4	T-complex	K.VVSQYSSLLSPM*SVNAVM*K#.V	15.84	5.60	2.83	0.35
P80315_TC	Cct4	T-complex	K.VVSQYSSLLSPM*SVNAVM*K#.V	40.53	10.93	3.71	0.27
P80315_TC	Cct4	T-complex	K.VVSQYSSLLSPMSVNAVM*K#.V	25.77	7.11	3.62	0.28
P80315_TC	Cct4	T-complex	K.VVSQYSSLLSPM*SVNAVMK#.V	10.84	2.28	4.75	0.21
P80315_TC	Cct4	T-complex	K.VVSQYSSLLSPM*SVNAVMK#.V	15.12	3.43	4.41	0.23
P80315_TC	Cct4	T-complex	K.VVSQYSSLLSPMSVNAVMK#.V	26.17	6.93	3.78	0.26
P80315_TC	Cct4	T-complex	K.VVSQYSSLLSPMSVNAVMK#.V	22.10	6.14	3.60	0.28
P80315_TC	Cct4	T-complex	R.ETLLNSATTSLNSK#.V	4.53	2.43	1.86	0.54
P80315_TC	Cct4	T-complex	R.ALIAGGGAPEIELALR.L	20.54	26.15	0.79	1.27
P80315_TC	Cct4	T-complex	R.AYILNLVK#.Q	60.22	16.84	3.58	0.28
P80315_TC	Cct4	T-complex	R.ETLLNSATTSLNSK#.V	26.32	7.02	3.75	0.27
P80315_TC	Cct4	T-complex	R.FSNISAAK#.A	67.55	24.10	2.80	0.36
P80315_TC	Cct4	T-complex	K.GDVTITNDGATILK#.Q	15.16	4.23	3.58	0.28
P80315_TC	Cct4	T-complex	K.GIHPTIISESFQK#.A	50.60	25.06	2.02	0.50
P80315_TC	Cct4	T-complex	K.IDDVVNTR.-	18.06	18.73	0.96	1.04
P80315_TC	Cct4	T-complex	K.LVIEEAER.S	24.35	23.76	1.02	0.98
P80315_TC	Cct4	T-complex	K.M*IQDGK#GDVTITNDGATILK#.Q	33.21	8.72	3.81	0.26
P80315_TC	Cct4	T-complex	K.MIQDGK#GDVTITNDGATILK#.Q	20.44	3.36	6.08	0.16
P80315_TC	Cct4	T-complex	K.VVSQYSSLLSPM*SVNAVM*K#.V	7.69	1.86	4.13	0.24
P80315_TC	Cct4	T-complex	R.ALIAGGGAPEIELALR.L	25.25	32.36	0.78	1.28
P80315_TC	Cct4	T-complex	R.AYILNLVK#.Q	111.80	25.48	4.39	0.23
P80315_TC	Cct4	T-complex	R.ETLLNSATTSLNSK#.V	48.64	11.08	4.39	0.23
P80315_TC	Cct4	T-complex	R.FSNISAAK#.A	73.24	29.24	2.50	0.40
P80315_TC	Cct4	T-complex	K.GDVTITNDGATILK#.Q	34.27	7.32	4.68	0.21
P80315_TC	Cct4	T-complex	K.GIHPTIISESFQK#.A	103.07	25.43	4.05	0.25
P80315_TC	Cct4	T-complex	K.IDDVVNTR.-	33.03	29.71	1.11	0.90
P80315_TC	Cct4	T-complex	K.LVIEEAER.S	31.07	33.02	0.94	1.06
P80315_TC	Cct4	T-complex	K.M*IQDGK#GDVTITNDGATILK#.Q	61.11	10.80	5.66	0.18
P80315_TC	Cct4	T-complex	K.MIQDGK#GDVTITNDGATILK#.Q	21.27	4.24	5.01	0.20
P80315_TC	Cct4	T-complex	R.M*LVELSK#.A	67.36	16.06	4.19	0.24
P80315_TC	Cct4	T-complex	R.MLVELSK#.A	21.10	9.00	2.35	0.43
P80315_TC	Cct4	T-complex	R.SGAPTAGPGSR.G	15.59	15.16	1.03	0.97
P80315_TC	Cct4	T-complex	K.VIDPATATSVDLR.D	40.10	33.56	1.20	0.84
P80315_TC	Cct4	T-complex	K.VVSQYSSLLSPM*SVNAVM*K#.V	16.42	3.77	4.36	0.23
P80316_TC	Cct5	T-complex	R.AFADALEVIPMALSENSGM*NPIQTM*TEVR.A	7.50	8.06	0.93	1.07
P80316_TC	Cct5	T-complex	R.AFADALEVIPM*ALSENSGM*NPIQTMTEVR.A	8.62	6.87	1.26	0.80
P80316_TC	Cct5	T-complex	R.AVTIFIR.G	47.07	67.25	0.70	1.43
P80316_TC	Cct5	T-complex	K.DGDVTITNDGATILSMMDVDHQIAK#.L	13.84	4.07	3.40	0.29
P80316_TC	Cct5	T-complex	R.DVDFELIK#.V	171.75	65.09	2.64	0.38
P80316_TC	Cct5	T-complex	R.DVDFELIKVEGK.V	74.08	21.65	3.42	0.29
P80316_TC	Cct5	T-complex	R.FSELTSEK#.L	619.77	154.35	4.02	0.25
P80316_TC	Cct5	T-complex	K.GSNDM*QYQHVIETLIGK#.K	125.26	38.12	3.29	0.30
P80316_TC	Cct5	T-complex	K.GSNDMQYQHVIETLIGK#.K	110.57	35.49	3.12	0.32
P80316_TC	Cct5	T-complex	K.GSNDMQYQHVIETLIGK#K#.Q	21.64	7.47	2.90	0.35
P80316_TC	Cct5	T-complex	K.GVIVDK#DFSHPQM*PK#.K	143.34	39.56	3.62	0.28
P80316_TC	Cct5	T-complex	K.GVIVDK#DFSHPQMPK#.K	131.98	44.85	2.94	0.34

P80316_TC	Cct5	T-complex	K.HK#LDVM*SVEDYK#.A	35.29	8.69	4.06	0.25
P80316_TC	Cct5	T-complex	K.HK#LDVMSVEDYK#.A	111.49	25.75	4.33	0.23
P80316_TC	Cct5	T-complex	R.IADGYEQAAR.I	140.74	195.05	0.72	1.39
P80316_TC	Cct5	T-complex	R.IAIQHLDK#.I	227.56	83.53	2.72	0.37
P80316_TC	Cct5	T-complex	K.IDDIRKPGESEE.-	19.55	21.90	0.89	1.12
P80316_TC	Cct5	T-complex	K.ISDK#VLVDINNPEPLIQTAK#.T	21.53	4.11	5.23	0.19
P80316_TC	Cct5	T-complex	K.KQQISLATQM*VR.M	9.27	12.99	0.71	1.40
P80316_TC	Cct5	T-complex	K.LDVM*SVEDYK#.A	49.43	15.76	3.14	0.32
P80316_TC	Cct5	T-complex	K.LDVMSVEDYK#.A	43.04	9.74	4.42	0.23
P80316_TC	Cct5	T-complex	K.LGFAGVVQEISFGTTK#.D	535.47	138.13	3.88	0.26
P80316_TC	Cct5	T-complex	R.LM*GLEALK#.S	176.12	47.49	3.71	0.27
P80316_TC	Cct5	T-complex	R.LMGLEALK#.S	159.90	43.55	3.67	0.27
P80316_TC	Cct5	T-complex	K.LM*VELSK#.S	112.02	33.28	3.37	0.30
P80316_TC	Cct5	T-complex	K.MIIEEAK#.R	46.92	10.91	4.30	0.23
P80316_TC	Cct5	T-complex	K.M*IIEEAK#.R	49.81	15.87	3.14	0.32
P80316_TC	Cct5	T-complex	K.M*LVIEK#.C	85.96	25.58	3.36	0.30
P80316_TC	Cct5	T-complex	K.MLVIEK#.C	168.99	48.35	3.50	0.29
P80316_TC	Cct5	T-complex	K.QQISLATQM*VR.M	27.10	29.75	0.91	1.10
P80316_TC	Cct5	T-complex	K.QQISLATQMVR.M	17.13	21.33	0.80	1.24
P80316_TC	Cct5	T-complex	R.TSLGPNGLDK#.M	94.43	55.49	1.70	0.59
P80316_TC	Cct5	T-complex	K.VLVDINNPEPLIQTAK#.T	437.23	135.16	3.24	0.31
P80316_TC	Cct5	T-complex	R.WVGGPEIELIAIATGGR.I	65.54	77.61	0.84	1.18
P80316_TC	Cct5	T-complex	R.DVDFELIK#.V	16.97	6.81	2.49	0.40
P80316_TC	Cct5	T-complex	R.IADGYEQAAR.I	17.11	24.29	0.70	1.42
P80316_TC	Cct5	T-complex	K.LGFAGVVQEISFGTTK#.D	67.86	18.50	3.67	0.27
P80316_TC	Cct5	T-complex	K.MLVIEK#.C	14.55	1.55	9.41	0.11
P80316_TC	Cct5	T-complex	R.TSLGPNGLDK#.M	12.62	6.54	1.93	0.52
P80316_TC	Cct5	T-complex	K.VLVDINNPEPLIQTAK#.T	50.39	16.81	3.00	0.33
P80316_TC	Cct5	T-complex	K.LGFAGVVQEISFGTTK#.D	37.11	15.87	2.34	0.43
P80316_TC	Cct5	T-complex	K.M*LVIEK#.C	35.03	19.21	1.82	0.55
P80316_TC	Cct5	T-complex	K.VLVDINNPEPLIQTAK#.T	32.41	7.95	4.08	0.25
P80317_TC	Cct6a	T-complex	R.AGM*SSLK#G.-	118.69	16.18	7.33	0.14
P80317_TC	Cct6a	T-complex	K.ALQFLEQVK#.V	563.28	161.67	3.48	0.29
P80317_TC	Cct6a	T-complex	R.AQAALAVNISAAR.G	26.68	36.47	0.73	1.37
P80317_TC	Cct6a	T-complex	R.AQLGVQAFADALLIIPK#.V	60.33	16.04	3.76	0.27
P80317_TC	Cct6a	T-complex	K.GIDPFSLDALAK#.E	842.85	237.26	3.55	0.28
P80317_TC	Cct6a	T-complex	R.GLQDVLR.T	63.19	86.77	0.73	1.37
P80317_TC	Cct6a	T-complex	K.GPNK#HTLTQIK#.D	25.73	10.06	2.56	0.39
P80317_TC	Cct6a	T-complex	K.HTLTQIK#.D	413.25	135.31	3.05	0.33
P80317_TC	Cct6a	T-complex	R.IITEGFEAAK#.E	627.15	192.63	3.26	0.31
P80317_TC	Cct6a	T-complex	R.KKDEPIDLFM*VEIM*EM*K.H	45.81	13.11	3.49	0.29
P80317_TC	Cct6a	T-complex	R.KKDEPIDLFMVEIM*EM*K.H	23.06	6.79	3.40	0.29
P80317_TC	Cct6a	T-complex	R.K#K#DEPIDLFMVEIMEMK#.H	13.13	3.85	3.41	0.29
P80317_TC	Cct6a	T-complex	K.M*LVSGAGDIK#.L	318.38	93.55	3.40	0.29
P80317_TC	Cct6a	T-complex	K.MLVSGAGDIK#.L	165.66	61.01	2.72	0.37
P80317_TC	Cct6a	T-complex	K.QADLYISEGLHPR.I	59.16	85.11	0.70	1.44
P80317_TC	Cct6a	T-complex	K.SETDTSLIR.G	82.87	127.06	0.65	1.53
P80317_TC	Cct6a	T-complex	K.TEVNSGFFYK#.S	180.24	48.09	3.75	0.27
P80317_TC	Cct6a	T-complex	K.VATAQDDITGDGTTSNVLIIGELLK#.Q	315.65	90.19	3.50	0.29
P80317_TC	Cct6a	T-complex	K.VLAQNSGFDLQETLVK#.V	401.45	117.46	3.42	0.29
P80317_TC	Cct6a	T-complex	K.ALQFLEQVK#.V	59.65	48.38	1.23	0.81
P80317_TC	Cct6a	T-complex	K.DGNVLLHEM*QIQHPTASIIAK#.V	10.18	4.16	2.45	0.41
P80317_TC	Cct6a	T-complex	K.DGNVLLHEMQIQHPTASIIAK#.V	15.86	5.18	3.06	0.33
P80317_TC	Cct6a	T-complex	K.GIDPFSLDALAK#.E	107.26	29.82	3.60	0.28
P80317_TC	Cct6a	T-complex	R.IITEGFEAAK#.E	78.30	31.65	2.47	0.40
P80317_TC	Cct6a	T-complex	K.M*LVSGAGDIK#.L	69.74	16.82	4.15	0.24
P80317_TC	Cct6a	T-complex	R.SVTLLVK#.G	57.25	13.58	4.22	0.24
P80317_TC	Cct6a	T-complex	K.TEVNSGFFYK#.S	18.53	6.90	2.69	0.37
P80317_TC	Cct6a	T-complex	K.VATAQDDITGDGTTSNVLIIGELLK#.Q	63.72	15.73	4.05	0.25
P80317_TC	Cct6a	T-complex	K.VLAQNSGFDLQETLVK#.V	50.98	17.55	2.90	0.34
P80317_TC	Cct6a	T-complex	K.DGNVLLHEM*QIQHPTASIIAK#.V	9.41	1.81	5.21	0.19
P80317_TC	Cct6a	T-complex	K.GIDPFSLDALAK#.E	47.76	16.58	2.88	0.35
P80317_TC	Cct6a	T-complex	K.M*LVSGAGDIK#.L	31.72	12.28	2.58	0.39
P80317_TC	Cct6a	T-complex	K.TEVNSGFFYK#.S	10.88	4.67	2.33	0.43
P80317_TC	Cct6a	T-complex	K.VLAQNSGFDLQETLVK#.V	27.80	8.11	3.43	0.29
P80313_TC	Cct7	T-complex	R.AIK#NDSVVAGGGAIEM*ELSK#.Y	43.75	11.14	3.93	0.25
P80313_TC	Cct7	T-complex	R.AIK#NDSVVAGGGAIEMELSK#.Y	28.59	10.00	2.86	0.35
P80313_TC	Cct7	T-complex	K.ALEIIPR.Q	50.76	59.29	0.86	1.17
P80313_TC	Cct7	T-complex	K.ATISNDGATILK#.L	635.23	187.43	3.39	0.30
P80313_TC	Cct7	T-complex	R.GGAEQFM*EETER.S	53.50	78.02	0.69	1.46
P80313_TC	Cct7	T-complex	R.GGAEQFMEETER.S	36.03	46.59	0.77	1.29
P80313_TC	Cct7	T-complex	R.HAQGGM*WYGVDINNENIADNFQAFVWEPAM*VR.I	3.75	5.96	0.63	1.59
P80313_TC	Cct7	T-complex	K.IALLNVELELK#.A	94.31	21.36	4.42	0.23
P80313_TC	Cct7	T-complex	K.IK#EIAVTVK#.K	119.23	35.81	3.33	0.30
P80313_TC	Cct7	T-complex	K.K#TFSYAGFEM*QPK#.K	15.85	6.28	2.52	0.40
P80313_TC	Cct7	T-complex	K.K#TFSYAGFEMQPK#.K	20.06	7.54	2.66	0.38
P80313_TC	Cct7	T-complex	K.K#VQGGALEESQLVAGVAFK#.K	78.75	23.99	3.28	0.30
P80313_TC	Cct7	T-complex	K.LISQQK#.V	133.41	35.89	3.72	0.27
P80313_TC	Cct7	T-complex	K.LLDVVHPAAK#.T	508.35	162.02	3.14	0.32
P80313_TC	Cct7	T-complex	K.LPIGDVATQYFADR.D	58.32	80.14	0.73	1.37
P80313_TC	Cct7	T-complex	K.NDSVVAGGGAIEM*ELSK#.Y	78.55	39.36	2.00	0.50
P80313_TC	Cct7	T-complex	K.NDSVVAGGGAIEMELSK#.Y	57.84	16.92	3.42	0.29
P80313_TC	Cct7	T-complex	K.QQLLIGAYAK#.A	240.44	61.06	3.94	0.25
P80313_TC	Cct7	T-complex	K.SQDAEVGDGTTSVTLLAAEFLK#.Q	208.71	55.88	3.73	0.27
P80313_TC	Cct7	T-complex	R.TATQLAVNK#.I	489.36	147.16	3.33	0.30
P80313_TC	Cct7	T-complex	K.TFSYAGFEM*QPK#.K	164.96	44.65	3.69	0.27
P80313_TC	Cct7	T-complex	K.TFSYAGFEMQPK#.K	111.96	35.91	3.12	0.32
P80313_TC	Cct7	T-complex	K.TLVDIAK#.S	446.84	142.55	3.13	0.32
P80313_TC	Cct7	T-complex	R.VHTVEDYQAIVDAEWNILYDK#.L	29.34	6.66	4.41	0.23
P80313_TC	Cct7	T-complex	R.VHTVEDYQAIVDAEWNILYDK#LEK#.I	202.40	52.49	3.86	0.26
P80313_TC	Cct7	T-complex	R.VPEEDLK#.R	91.00	30.32	3.00	0.33
P80313_TC	Cct7	T-complex	K.VQGGALEESQLVAGVAFK#.K	122.38	35.09	3.49	0.29
P80313_TC	Cct7	T-complex	R.AIK#NDSVVAGGGAIEMELSK#.Y	8.02	4.30	1.87	0.54
P80313_TC	Cct7	T-complex	K.ALEIIPR.Q	13.10	23.19	0.57	1.77
P80313_TC	Cct7	T-complex	K.ATISNDGATILK#.L	83.20	19.02	4.37	0.23
P80313_TC	Cct7	T-complex	R.GGAEQFM*EETER.S	8.13	14.03	0.58	1.72
P80313_TC	Cct7	T-complex	K.IALLNVELELK#.A	10.26	4.25	2.41	0.41
P80313_TC	Cct7	T-complex	K.LPIGDVATQYFADR.D	6.72	6.72	1.00	1.00
P80313_TC	Cct7	T-complex	K.NDSVVAGGGAIEM*ELSK#.Y	5.48	2.51	2.18	0.46
P80313_TC	Cct7	T-complex	K.NDSVVAGGGAIEMELSK#.Y	6.28	4.39	1.43	0.70
P80313_TC	Cct7	T-complex	K.SQDAEVGDGTTSVTLLAAEFLK#.Q	36.87	7.83	4.71	0.21
P80313_TC	Cct7	T-complex	R.TATQLAVNK#.I	74.63	24.92	2.99	0.33
P80313_TC	Cct7	T-complex	K.TFSYAGFEM*QPK#.K	26.55	9.06	2.93	0.34

P80313_TC	Cct7	T-complex	K.TLVDIAK#.S	71.50	16.35	4.37	0.23
P80313_TC	Cct7	T-complex	R.VHTVEDYQAIVDAEWNILYDK#LEK#.I	29.32	8.43	3.48	0.29
P80313_TC	Cct7	T-complex	K.VQGGALEESQLVAGVAFK#.K	12.46	5.12	2.43	0.41
P80313_TC	Cct7	T-complex	R.AIK#NDSVVAGGGAIEM*ELSK#.Y	14.90	3.12	4.78	0.21
P80313_TC	Cct7	T-complex	R.AIK#NDSVVAGGGAIEMELSK#.Y	9.31	1.96	4.74	0.21
P80313_TC	Cct7	T-complex	K.ATISNDGATILK#.L	79.57	23.24	3.42	0.29
P80313_TC	Cct7	T-complex	R.GGAEQFM*EETER.S	11.44	10.33	1.11	0.90
P80313_TC	Cct7	T-complex	K.LPIGDVATQYFADR.D	13.99	6.64	2.11	0.47
P80313_TC	Cct7	T-complex	K.NDSVVAGGGAIEM*ELSK#.Y	9.92	2.88	3.45	0.29
P80313_TC	Cct7	T-complex	K.NDSVVAGGGAIEMELSK#.Y	6.77	4.30	1.58	0.63
P80313_TC	Cct7	T-complex	K.SQDAEVGDGTTSVTLLAAEFLK#.Q	71.01	17.96	3.95	0.25
P80313_TC	Cct7	T-complex	R.TATQLAVNK#.I	85.62	25.41	3.37	0.30
P80313_TC	Cct7	T-complex	K.TFSYAGFEM*QPK#.K	33.03	7.93	4.16	0.24
P80313_TC	Cct7	T-complex	K.VQGGALEESQLVAGVAFK#.K	27.34	7.54	3.63	0.28
P42932_TC	Cct8	T-complex	K.AIAGTGANVIVTGGK#.V	450.92	132.70	3.40	0.29
P42932_TC	Cct8	T-complex	R.ALAENSGVK#.A	252.54	117.80	2.14	0.47
P42932_TC	Cct8	T-complex	K.APGFAQM*LK#.D	204.02	70.56	2.89	0.35
P42932_TC	Cct8	T-complex	K.APGFAQMLK#.D	85.88	25.75	3.33	0.30
P42932_TC	Cct8	T-complex	R.AVDDGVNTFK#.V	224.43	56.80	3.95	0.25
P42932_TC	Cct8	T-complex	K.DM*LEASILDTYLGK#.Y	36.71	41.33	0.89	1.13
P42932_TC	Cct8	T-complex	K.DMLEASILDTYLGK#.Y	64.55	19.49	3.31	0.30
P42932_TC	Cct8	T-complex	R.DVDEVSSLLR.T	56.51	67.46	0.84	1.19
P42932_TC	Cct8	T-complex	K.ETEGDVTSVK#.D	237.13	70.56	3.36	0.30
P42932_TC	Cct8	T-complex	K.ETEGDVTSVKDAK.I	8.29	2.50	3.32	0.30
P42932_TC	Cct8	T-complex	K.FAEAFEAIPR.A	51.57	84.20	0.61	1.63
P42932_TC	Cct8	T-complex	K.GEENLM*DAQVK#.A	94.68	23.46	4.04	0.25
P42932_TC	Cct8	T-complex	K.GEENLMDAQVK#.A	24.80	6.95	3.57	0.28
P42932_TC	Cct8	T-complex	R.GSTDNLM*DDIER.A	13.56	23.46	0.58	1.73
P42932_TC	Cct8	T-complex	R.GSTDNLMDDIER.A	11.51	20.20	0.57	1.75
P42932_TC	Cct8	T-complex	K.HFSGLEEAVYR.N	30.67	43.87	0.70	1.43
P42932_TC	Cct8	T-complex	K.ILGSGIYSSSVLHGM*VFK#.K	10.92	2.83	3.86	0.26
P42932_TC	Cct8	T-complex	K.K#ETEGDVTSVK#.D	24.97	6.41	3.90	0.26
P42932_TC	Cct8	T-complex	K.LATNAAVTVLR.V	98.22	119.08	0.82	1.21
P42932_TC	Cct8	T-complex	K.LFVTNDAATILR.E	120.41	158.76	0.76	1.32
P42932_TC	Cct8	T-complex	K.NVGLDIEAEVPAVK#.D	116.83	36.52	3.20	0.31
P42932_TC	Cct8	T-complex	K.QYGSETFLAK#.L	161.58	47.51	3.40	0.29
P42932_TC	Cct8	T-complex	K.TAEELM*NFSK#.G	54.79	15.76	3.48	0.29
P42932_TC	Cct8	T-complex	K.TAEELMNFSK#.G	61.29	14.77	4.15	0.24
P42932_TC	Cct8	T-complex	K.TAEELM*NFSKGEENLM*DAQVK.A	36.63	5.32	6.88	0.15
P42932_TC	Cct8	T-complex	K.TAEELMNFSK#GEENLM*DAQVK#.A	17.20	4.75	3.62	0.28
P42932_TC	Cct8	T-complex	K.TAEELMNFSK#GEENLMDAQVK#.A	13.15	4.59	2.87	0.35
P42932_TC	Cct8	T-complex	R.TAYGPNGMNK#.M	9.17	2.80	3.28	0.31
P42932_TC	Cct8	T-complex	K.TVGATALPK#.L	250.83	69.90	3.59	0.28
P42932_TC	Cct8	T-complex	K.YNIM*LVR.L	115.83	35.69	3.25	0.31
P42932_TC	Cct8	T-complex	K.AIAGTGANVIVTGGK#.V	177.53	47.22	3.76	0.27
P42932_TC	Cct8	T-complex	K.ANEVISK#.L	59.81	42.37	1.41	0.71
P42932_TC	Cct8	T-complex	K.APGFAQM*LK#.D	115.51	41.40	2.79	0.36
P42932_TC	Cct8	T-complex	K.APGFAQMLK#.D	80.41	9.83	8.18	0.12
P42932_TC	Cct8	T-complex	R.AVDDGVNTFK#.V	184.41	39.33	4.69	0.21
P42932_TC	Cct8	T-complex	K.DM*LEASILDTYLGK#.Y	13.67	5.54	2.47	0.40
P42932_TC	Cct8	T-complex	K.DMLEASILDTYLGK#.Y	25.74	7.20	3.58	0.28
P42932_TC	Cct8	T-complex	R.DVDEVSSLLR.T	27.54	33.86	0.81	1.23
P42932_TC	Cct8	T-complex	K.ETEGDVTSVK#.D	73.70	20.02	3.68	0.27
P42932_TC	Cct8	T-complex	K.FAEAFEAIPR.A	34.32	42.23	0.81	1.23
P42932_TC	Cct8	T-complex	K.GEENLM*DAQVK#.A	41.46	10.68	3.88	0.26
P42932_TC	Cct8	T-complex	R.GSTDNLM*DDIER.A	15.23	18.32	0.83	1.20
P42932_TC	Cct8	T-complex	K.HFSGLEEAVYR.N	14.73	27.33	0.54	1.86
P42932_TC	Cct8	T-complex	K.K#DWDDDQND.-	6.28	2.33	2.69	0.37
P42932_TC	Cct8	T-complex	K.LATNAAVTVLR.V	37.98	40.30	0.94	1.06
P42932_TC	Cct8	T-complex	K.LFVTNDAATILR.E	52.46	64.11	0.82	1.22
P42932_TC	Cct8	T-complex	K.NVGLDIEAEVPAVK#.D	32.57	10.33	3.15	0.32
P42932_TC	Cct8	T-complex	K.QYGSETFLAK#.L	84.66	39.10	2.17	0.46
P42932_TC	Cct8	T-complex	K.TAEELM*NFSK#.G	24.94	7.36	3.39	0.29
P42932_TC	Cct8	T-complex	K.TAEELMNFSK#GEENLM*DAQVK#.A	12.38	3.39	3.65	0.27
P42932_TC	Cct8	T-complex	K.TAEELMNFSK#GEENLMDAQVK#.A	6.44	4.02	1.60	0.62
P42932_TC	Cct8	T-complex	K.AIAGTGANVIVTGGK#.V	279.72	59.37	4.71	0.21
P42932_TC	Cct8	T-complex	K.ANEVISK#.L	96.69	26.21	3.69	0.27
P42932_TC	Cct8	T-complex	K.APGFAQM*LK#.D	188.72	48.73	3.87	0.26
P42932_TC	Cct8	T-complex	K.APGFAQMLK#.D	37.09	12.59	2.95	0.34
P42932_TC	Cct8	T-complex	R.AVDDGVNTFK#.V	271.87	62.35	4.36	0.23
P42932_TC	Cct8	T-complex	K.DM*LEASILDTYLGK#.Y	29.32	8.01	3.66	0.27
P42932_TC	Cct8	T-complex	K.DMLEASILDTYLGK#.Y	32.84	7.51	4.37	0.23
P42932_TC	Cct8	T-complex	R.DVDEVSSLLR.T	48.20	54.83	0.88	1.14
P42932_TC	Cct8	T-complex	K.EDGAISTIVLR.G	10.86	15.78	0.69	1.45
P42932_TC	Cct8	T-complex	K.ETEGDVTSVK#.D	204.95	44.23	4.63	0.22
P42932_TC	Cct8	T-complex	K.FAEAFEAIPR.A	47.56	48.02	0.99	1.01
P42932_TC	Cct8	T-complex	R.GSTDNLM*DDIER.A	26.73	21.80	1.23	0.82
P42932_TC	Cct8	T-complex	R.GSTDNLMDDIER.A	9.02	6.66	1.35	0.74
P42932_TC	Cct8	T-complex	K.HFSGLEEAVYR.N	19.41	19.49	1.00	1.00
P42932_TC	Cct8	T-complex	K.K#DWDDDQND.-	9.90	3.49	2.84	0.35
P42932_TC	Cct8	T-complex	K.LATNAAVTVLR.V	57.50	53.04	1.08	0.92
P42932_TC	Cct8	T-complex	K.LFVTNDAATILR.E	63.45	69.62	0.91	1.10
P42932_TC	Cct8	T-complex	K.NVGLDIEAEVPAVK#.D	66.58	20.14	3.31	0.30
P42932_TC	Cct8	T-complex	K.QYGSETFLAK#.L	108.39	78.21	1.39	0.72
P42932_TC	Cct8	T-complex	K.TAEELM*NFSK#.G	53.63	10.28	5.22	0.19
P42932_TC	Cct8	T-complex	K.TAEELM*NFSKGEENLM*DAQVK.A	26.64	4.89	5.44	0.18
P42932_TC	Cct8	T-complex	K.TAEELMNFSK#GEENLM*DAQVK#.A	20.88	4.62	4.52	0.22
P42932_TC	Cct8	T-complex	K.VADIALHYANK#.Y	148.76	26.29	5.66	0.18
P42932_TC	Cct8	T-complex	K.YNIM*LVR.L	16.56	21.34	0.78	1.29
Q8R422_C	Cd109	CD109 anti	R.FAEENEANLVDFEDASSVNNVHVR.K	1.95	9.72	0.20	4.98
Q8R422_C	Cd109	CD109 anti	K.IPVQLVFENK#.V	16.43	8.38	1.96	0.51
Q9JLQ0_C	Cd2ap	CD2-associ	K.LGLFPSNFVK#.E	24.74	7.49	3.30	0.30
Q9JLQ0_C	Cd2ap	CD2-associ	K.SSLSTPSSASK#.V	17.71	3.56	4.98	0.20
Q9JLQ0_C	Cd2ap	CD2-associ	K.VNTAAFLTPLELK#.A	17.76	5.41	3.29	0.30
Q9CWK3_	Cd2bp2	CD2 antige	R.DSWLDNIDWVR.I	7.08	8.63	0.82	1.22
Q9CWK3_	Cd2bp2	CD2 antige	R.GNLGVYQETR.E	2.35	9.56	0.25	4.06
Q9CWK3_	Cd2bp2	CD2 antige	K.VTFQGVGDEDGEDEISVPK#.K	15.41	6.96	2.21	0.45
Q76KJ5_R	Cd3eap	DNA-direct	R.FSAFGGSPPVTGPGSASALR.S	2.95	8.05	0.37	2.72
Q76KJ5_R	Cd3eap	DNA-direct	R.YFM*QEEM*EAK#.T	5.49	2.33	2.35	0.42
P15379_C	Cd44	CD44 antig	R.YGFIEGNVVIPR.I	6.35	33.73	0.19	5.31
Q61735_C	Cd47	Leukocyte	K.ISVSDLINGIASLK#.M	12.44	7.75	1.60	0.62
Q61735_C	Cd47	Leukocyte	R.NVEAQSTEEM*FVK#.W	10.87	8.43	1.29	0.78
Q61735_C	Cd47	Leukocyte	R.NVEAQSTEEMFVK#.W	7.98	5.96	1.34	0.75

P40240_C	Cd9	CD9 antige	K.ELQEFYKDTYQK.L	6.25	7.30	0.86	1.17
Q8R349_C	Cdc16	Cell divisio	K.ANELFYLSHK#.L	22.20	13.96	1.59	0.63
Q8R349_C	Cdc16	Cell divisio	R.TLATYSYK#.E	22.20	11.61	1.91	0.52
Q8BGZ4_C	Cdc23	Cell divisio	R.AWYGLGQTYEILK#.M	5.39	2.86	1.89	0.53
Q8BGZ4_C	Cdc23	Cell divisio	R.AYAVGDVEK#.K	13.33	5.97	2.23	0.45
Q8BGZ4_C	Cdc23	Cell divisio	K.K#K#DDETVDSLGPLEK#.G	9.49	6.23	1.52	0.66
Q8BGZ4_C	Cdc23	Cell divisio	R.AWYGLGQTYEILK#.M	11.93	3.87	3.08	0.32
Q8BGZ4_C	Cdc23	Cell divisio	R.AYAVGDVEK#.K	19.00	6.36	2.99	0.33
A2A6Q5_C	Cdc27	Cell divisio	K.LAEGEQILSGGVFNK#.Q	3.45	1.91	1.80	0.55
A2A6Q5_C	Cdc27	Cell divisio	K.ITTVTPQIQAFNLQK#.A	6.11	2.68	2.28	0.44
Q61081_C	Cdc37	Hsp90 co-c	K.DVQM*LQDAISK#.M	41.73	9.81	4.25	0.24
Q61081_C	Cdc37	Hsp90 co-c	K.DVQMLQDAISK#.M	30.88	5.48	5.63	0.18
Q61081_C	Cdc37	Hsp90 co-c	K.NM*PWNVDTLSK#.D	21.26	9.45	2.25	0.44
Q61081_C	Cdc37	Hsp90 co-c	K.TADHQYMEGFK#.Y	9.52	2.80	3.40	0.29
Q61081_C	Cdc37	Hsp90 co-c	K.TADHQYM*EGFK#.Y	22.29	4.61	4.84	0.21
Q9DC48_P	Cdc40	Pre-mRNA-	K.FKENDASNIDGFLGPWAK.Y	8.67	8.57	1.01	0.99
Q9DC48_P	Cdc40	Pre-mRNA-	R.SGEIVQEYDR.H	3.61	15.10	0.24	4.18
Q9DC48_P	Cdc40	Pre-mRNA-	K.YIGSVEEAEKNQGLTVFETGQK.K	12.28	8.39	1.46	0.68
Q9DC48_P	Cdc40	Pre-mRNA-	K.FKENDASNIDGFLGPWAK.Y	9.16	14.75	0.62	1.61
Q9DC48_P	Cdc40	Pre-mRNA-	R.SYLHIPQDVGVNLR.S	2.87	13.11	0.22	4.56
Q9DC48_P	Cdc40	Pre-mRNA-	R.TFATYGYALDPSLDNHQVSAK.Y	9.92	13.04	0.76	1.31
Q9DC48_P	Cdc40	Pre-mRNA-	R.VWEWDIPVDFK#.Y	16.45	16.30	1.01	0.99
Q9DC48_P	Cdc40	Pre-mRNA-	K.YVDEKDVAKPSEEEQKELDEITAK.R	10.18	17.85	0.57	1.75
P60766_C	Cdc42	Cell divisio	K.NVFDEAILAALEPPEPK#.K	31.34	32.23	0.97	1.03
P60766_C	Cdc42	Cell divisio	K.TPFLLVGTQIDLRDDPSTIEK.L	3.10	21.40	0.15	6.89
P60766_C	Cdc42	Cell divisio	K.NVFDEAILAALEPPEPK#.K	16.37	14.09	1.16	0.86
Q7TT50_M	Cdc42bpb	Serine/thre	R.GAFGEVAVVK#.L	408.79	61.40	6.66	0.15
Q7TT50_M	Cdc42bpb	Serine/thre	R.GYLQALASK#.M	7.55	5.10	1.48	0.68
Q7TT50_M	Cdc42bpb	Serine/thre	K.EVHDSESHQLALQK#.E	113.19	7.79	14.53	0.07
Q7TT50_M	Cdc42bpb	Serine/thre	K.FSGTILNVPDTSDNSK#.K	9.32	3.93	2.37	0.42
Q7TT50_M	Cdc42bpb	Serine/thre	R.GAFGEVAVVK#.L	439.97	70.51	6.24	0.16
Q7TT50_M	Cdc42bpb	Serine/thre	R.GYLQALASK#.M	14.01	11.00	1.27	0.79
Q7TT50_M	Cdc42bpb	Serine/thre	K.SQVVHVAQEAYDSSLPLIK#.A	27.51	12.57	2.19	0.46
Q7TT50_M	Cdc42bpb	Serine/thre	K.VYQIELAPK#.E	15.23	7.78	1.96	0.51
Q91W92_E	Cdc42ep1	Cdc42 effec	R.M*ASPAAPSPAPPPISPIIK#.N	5.94	5.46	1.09	0.92
Q91W92_E	Cdc42ep1	Cdc42 effec	R.MASPAAPSPAPPPISPIIK#.N	4.12	3.89	1.06	0.94
Q91W92_E	Cdc42ep1	Cdc42 effec	R.M*ASPAAPSPAPPPISPIIK.N	3.02	5.04	0.60	1.67
Q6A068_C	Cdc5l	Cell divisio	K.AQDALVQEM*EVVK#.Q	12.30	17.59	0.70	1.43
Q6A068_C	Cdc5l	Cell divisio	R.DK#LNINPEDGM*ADYSDPSYVK#.Q	3.58	1.56	2.30	0.44
Q6A068_C	Cdc5l	Cell divisio	R.EIDDTYIEDAADVDAR.K	2.43	4.92	0.49	2.02
Q6A068_C	Cdc5l	Cell divisio	K.ESDLPSAILQTSGVSEFTK#.K	5.89	4.20	1.40	0.71
Q6A068_C	Cdc5l	Cell divisio	R.GVDYNAEIPFEK#.K	21.08	10.03	2.10	0.48
Q6A068_C	Cdc5l	Cell divisio	R.LGLLGLPAPK#.N	40.25	12.05	3.34	0.30
Q6A068_C	Cdc5l	Cell divisio	K.LNINPEDGM*ADYSDPSYVK.Q	6.13	2.04	3.00	0.33
Q6A068_C	Cdc5l	Cell divisio	K.LVLPAPQISDAELQEVVK#.V	13.50	9.30	1.45	0.69
Q6A068_C	Cdc5l	Cell divisio	K.AQDALVQEM*EVVK#.Q	6.29	7.67	0.82	1.22
Q6A068_C	Cdc5l	Cell divisio	K.ILLGGYQSR.A	3.21	7.06	0.45	2.20
Q6A068_C	Cdc5l	Cell divisio	R.AAGIEIQK#.K	43.01	25.62	1.68	0.60
Q6A068_C	Cdc5l	Cell divisio	K.AQDALVQEM*EVVK#.Q	16.55	35.19	0.47	2.13
Q6A068_C	Cdc5l	Cell divisio	R.DK#LNINPEDGM*ADYSDPSYVK#.Q	6.85	6.80	1.01	0.99
Q6A068_C	Cdc5l	Cell divisio	R.EIDDTYIEDAADVDAR.K	4.48	14.52	0.31	3.24
Q6A068_C	Cdc5l	Cell divisio	K.ESDLPSAILQTSGVSEFTK#.K	14.67	12.19	1.20	0.83
Q6A068_C	Cdc5l	Cell divisio	R.GVDYNAEIPFEK#.K	28.51	25.36	1.12	0.89
Q6A068_C	Cdc5l	Cell divisio	K.HEDSAIPR.R	4.79	11.89	0.40	2.48
Q6A068_C	Cdc5l	Cell divisio	K.ILLGGYQSR.A	11.32	41.31	0.27	3.65
Q6A068_C	Cdc5l	Cell divisio	R.ILQEAQNLM*ALTNVDTPLK#.G	3.68	3.27	1.13	0.89
Q6A068_C	Cdc5l	Cell divisio	R.ILQEAQNLMALTNVDTPLK#.G	24.01	19.89	1.21	0.83
Q6A068_C	Cdc5l	Cell divisio	R.K#K#ESDLPSAILQTSGVSEFTK#.K	11.31	6.60	1.72	0.58
Q6A068_C	Cdc5l	Cell divisio	R.LGLLGLPAPK#.N	70.62	52.39	1.35	0.74
Q6A068_C	Cdc5l	Cell divisio	K.LNINPEDGM*ADYSDPSYVK#.Q	9.61	6.52	1.47	0.68
Q6A068_C	Cdc5l	Cell divisio	K.LVLPAPQISDAELQEVVK#.V	47.77	36.22	1.32	0.76
Q6A068_C	Cdc5l	Cell divisio	K.NDFEIVLPENAEK#.E	17.66	15.12	1.17	0.86
Q6A068_C	Cdc5l	Cell divisio	R.NTEDEILK#.A	30.43	22.19	1.37	0.73
Q6A068_C	Cdc5l	Cell divisio	K.NVGFATNNSEHITYLEHSPYEK#.F	19.32	11.35	1.70	0.59
Q6A068_C	Cdc5l	Cell divisio	R.QTAEESGITNSASSTLLSEYNVTNNSIALR.T	2.51	9.19	0.27	3.66
Q6A068_C	Cdc5l	Cell divisio	R.SGTTPKPVTNATPGR.T	4.70	17.20	0.27	3.66
Q6A068_C	Cdc5l	Cell divisio	R.SK#LVLPAPQISDAELQEVVK#.V	15.34	10.10	1.52	0.66
Q6A068_C	Cdc5l	Cell divisio	K.VGQASEVAR.Q	10.11	26.96	0.38	2.67
Q6A068_C	Cdc5l	Cell divisio	R.WYEWLDPSIK#.K	16.07	13.17	1.22	0.82
Q8JZM7_C	Cdc73	Parafibrom	R.AADEVLAEAK#.K	40.59	34.30	1.18	0.84
Q8JZM7_C	Cdc73	Parafibrom	K.EGIVQTEQIR.S	11.99	42.56	0.28	3.55
Q8JZM7_C	Cdc73	Parafibrom	R.FWETLDR.Y	2.95	15.54	0.19	5.27
Q8JZM7_C	Cdc73	Parafibrom	K.GDEVIFGEFSWPK#.N	25.07	23.81	1.05	0.95
Q8JZM7_C	Cdc73	Parafibrom	K.NIFAILQSVK#.A	39.90	20.29	1.97	0.51
Q8JZM7_C	Cdc73	Parafibrom	R.SAPLEIGLQR.S	5.98	22.16	0.27	3.70
Q8JZM7_C	Cdc73	Parafibrom	R.SFVDAEVDVTR.D	12.78	30.06	0.43	2.35
Q8JZM7_C	Cdc73	Parafibrom	R.SLSEAM*SVEK#.I	24.19	18.20	1.33	0.75
Q8JZM7_C	Cdc73	Parafibrom	K.TDLDDDITALK#.Q	35.58	24.29	1.46	0.68
Q8JZM7_C	Cdc73	Parafibrom	K.TNYVVWGTGK#.E	25.44	20.06	1.27	0.79
Q8JZM7_C	Cdc73	Parafibrom	R.TTILQSTGK#.N	27.26	25.94	1.05	0.95
Q8BHX3_B	Cdca8	Borealin O	K.EVENLYNIEILR.L	1.58	11.43	0.14	7.23
Q8BHX3_B	Cdca8	Borealin O	R.IDIAQLNPEALGNIR.K	1.78	33.44	0.05	18.82
Q8VDP6_C	Cdipt	CDP-diacyl	K.SVISVIHLITAAR.N	1.39	6.22	0.22	4.48
P11440_C	Cdk1	Cyclin-depe	R.ALGTPNNEVWPEVESLQDYK.N	12.63	13.08	0.97	1.04
P11440_C	Cdk1	Cyclin-depe	R.ALGTPNNEVWPEVESLQDYK.N	18.10	24.08	0.75	1.33
P11440_C	Cdk1	Cyclin-depe	R.DLK#PQNLLIDDK#.G	27.15	32.43	0.84	1.19
P11440_C	Cdk1	Cyclin-depe	R.DLK#PQNLLIDDK#GTIK#.L	25.97	29.64	0.88	1.14
P11440_C	Cdk1	Cyclin-depe	R.HPNIVSLQDVLMQDSR.L	6.02	20.35	0.30	3.38
P11440_C	Cdk1	Cyclin-depe	K.HPYFDDLDNQIK#.K	33.55	32.40	1.04	0.97
P11440_C	Cdk1	Cyclin-depe	K.IGEGTYGVVYK#.G	115.76	122.07	0.95	1.05
P11440_C	Cdk1	Cyclin-depe	K.KPLFHGDSEIDQLFR.I	10.95	57.45	0.19	5.25
P11440_C	Cdk1	Cyclin-depe	R.LESEEEGVPSTAIR.E	12.75	68.38	0.19	5.36
P11440_C	Cdk1	Cyclin-depe	K.M*LVYDPAK.R	12.60	12.35	1.02	0.98
P11440_C	Cdk1	Cyclin-depe	K.M*LVYDPAKR.I	3.14	12.16	0.26	3.88
P11440_C	Cdk1	Cyclin-depe	K.NLDENGLDLLSK#.M	52.48	43.72	1.20	0.83
P11440_C	Cdk1	Cyclin-depe	R.SPEVLLGSAR.Y	33.97	192.70	0.18	5.67
P11440_C	Cdk1	Cyclin-depe	R.VTGQIVAM*K#.K	22.82	28.37	0.80	1.24
P11440_C	Cdk1	Cyclin-depe	R.VTGQIVAMK#.K	38.22	41.40	0.92	1.08
P11440_C	Cdk1	Cyclin-depe	R.VTGQIVAM*KK.I	11.94	13.63	0.88	1.14
P11440_C	Cdk1	Cyclin-depe	R.VYTHEVVTLWYR.S	13.34	58.09	0.23	4.35
P11440_C	Cdk1	Cyclin-depe	K.YLDSIPPGQFM*DSSLVK#.S	10.54	9.66	1.09	0.92
P11440_C	Cdk1	Cyclin-depe	K.YLDSIPPGQFMDSSLVK#.S	5.38	5.13	1.05	0.95
P11440_C	Cdk1	Cyclin-depe	K.IGEGTYGVVYK#.G	5.02	6.54	0.77	1.30

P11440_C	Cdk1	Cyclin-depe	R.DLK#PQNLLIDDK#GTIK#.L	14.28	10.64	1.34	0.75
P11440_C	Cdk1	Cyclin-depe	K.KPLFHGDSEIDQLFR.I	2.57	14.54	0.18	5.65
P11440_C	Cdk1	Cyclin-depe	R.VYTHEVVTLWYR.S	2.69	10.96	0.25	4.07
P11440_C	Cdk1	Cyclin-depe	K.HPYFDDLDNQIK#.K	5.42	6.58	0.82	1.21
P11440_C	Cdk1	Cyclin-depe	K.IGEGTYGVVYK#.G	49.94	42.23	1.18	0.85
P11440_C	Cdk1	Cyclin-depe	K.KPLFHGDSEIDQLFR.I	2.64	13.55	0.20	5.13
P11440_C	Cdk1	Cyclin-depe	R.LESEEEGVPSTAIR.E	6.50	17.21	0.38	2.65
P11440_C	Cdk1	Cyclin-depe	R.SPEVLLGSAR.Y	6.66	40.18	0.17	6.03
P24788_C	Cdk11b	Cyclin-depe	R.APELLLGAK#.E	67.19	39.35	1.71	0.59
P24788_C	Cdk11b	Cyclin-depe	R.EIVVGSNM*DK#.I	28.50	15.63	1.82	0.55
P24788_C	Cdk11b	Cyclin-depe	R.ETPLPIDPSM*FPTWPAK.S	8.56	5.57	1.54	0.65
P24788_C	Cdk11b	Cyclin-depe	R.IEEGTYGVVYR.A	10.87	39.02	0.28	3.59
P24788_C	Cdk11b	Cyclin-depe	K.IYIVMNYVEHDLK#.S	20.64	15.99	1.29	0.77
P24788_C	Cdk11b	Cyclin-depe	K.M*TFSEYPYNNLR.K	2.73	8.97	0.30	3.28
P24788_C	Cdk11b	Cyclin-depe	K.SDIDQINK#.I	44.45	23.73	1.87	0.53
P24788_C	Cdk11b	Cyclin-depe	K.SLM*ETM*KQPFLPGEVK.T	16.60	11.18	1.48	0.67
P24788_C	Cdk11b	Cyclin-depe	K.TLMIQLLSGVK#.H	19.48	11.46	1.70	0.59
P24788_C	Cdk11b	Cyclin-depe	K.TSNLLLSHAGILK#.V	53.00	30.79	1.72	0.58
Q69ZA1_C	Cdk13	Cyclin-depe	K.EVK#K#LK#.T	22.39	4.64	4.82	0.21
Q69ZA1_C	Cdk13	Cyclin-depe	K.SLGGVQPSQTIQPK#.V	9.00	7.70	1.17	0.86
Q69ZA1_C	Cdk13	Cyclin-depe	K.SLGGVQPSQTIQPK#.V	11.26	9.74	1.16	0.86
P97377_C	Cdk2	Cyclin-depe	R.ALFPGDSEIDQLFR.I	8.01	20.23	0.40	2.53
P97377_C	Cdk2	Cyclin-depe	R.DLK#PQNLLINAEGSIK#.L	29.47	13.33	2.21	0.45
P97377_C	Cdk2	Cyclin-depe	K.FM*DASALTGIPLPLIK#.S	13.48	7.88	1.71	0.58
P97377_C	Cdk2	Cyclin-depe	R.TLGTPDEVVWPGVTSMPDYK#PSFPK#.W	4.24	3.33	1.27	0.79
P97377_C	Cdk2	Cyclin-depe	R.ALFPGDSEIDQLFR.I	5.14	10.71	0.48	2.08
P97377_C	Cdk2	Cyclin-depe	R.DLK#PQNLLINAEGSIK#.L	11.17	8.95	1.25	0.80
P97377_C	Cdk2	Cyclin-depe	R.ALFPGDSEIDQLFR.I	6.66	17.69	0.38	2.66
P97377_C	Cdk2	Cyclin-depe	R.DLK#PQNLLINAEGSIK#.L	21.23	14.75	1.44	0.70
P97377_C	Cdk2	Cyclin-depe	K.FM*DASALTGIPLPLIK#.S	11.46	6.41	1.79	0.56
P97377_C	Cdk2	Cyclin-depe	R.TLGTPDEVVWPGVTSM*PDYK#PSFPK#.W	12.24	4.65	2.63	0.38
P49615_C	Cdk5	Cyclin-depe	K.IGEGTYGTVFK#.A	17.16	8.55	2.01	0.50
P49615_C	Cdk5	Cyclin-depe	R.DLLQNLLK#.C	12.99	5.50	2.36	0.42
P49615_C	Cdk5	Cyclin-depe	K.IGEGTYGTVFK#.A	15.81	9.61	1.65	0.61
P49615_C	Cdk5	Cyclin-depe	R.LLGTPTEEQWPAM*TK#.L	4.65	2.52	1.85	0.54
Q03147_C	Cdk7	Cyclin-depe	R.APELLFGAR.M	1.54	9.97	0.15	6.49
Q03147_C	Cdk7	Cyclin-depe	R.DLKPNNLLLDENGVLK.L	7.01	6.56	1.07	0.94
Q03147_C	Cdk7	Cyclin-depe	R.VPFLPGDSDLDQLTR.I	7.21	16.38	0.44	2.27
Q99J95_C	Cdk9	Cyclin-depe	K.GSQITQQSTNQSR.N	1.36	3.84	0.36	2.82
Q99J95_C	Cdk9	Cyclin-depe	K.IGQGTFGEVFK#.A	19.09	10.02	1.90	0.53
Q99J95_C	Cdk9	Cyclin-depe	K.LLVLDPAQR.I	4.20	8.05	0.52	1.92
Q99J95_C	Cdk9	Cyclin-depe	R.NPATTNQTEFER.V	4.10	13.07	0.31	3.19
Q99J95_C	Cdk9	Cyclin-depe	K.ILQLLK#.H	13.61	4.78	2.85	0.35
Q99J95_C	Cdk9	Cyclin-depe	R.NPATTNQTEFER.V	7.46	10.85	0.69	1.45
P51480_C	Cdkn2a	Cyclin-depe	R.ALLEAGVSPNAPNSFGR.T	2.90	15.27	0.19	5.26
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.ATLDVFFVPLK#.E	14.11	5.19	2.72	0.37
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.ELADLPQNK#.S	19.87	82.87	0.24	4.17
Q8BI72_CA	Cdkn2aip	CDKN2A-in	R.GISSSNEGVEEPSK#.K	19.82	19.08	1.04	0.96
Q8BI72_CA	Cdkn2aip	CDKN2A-in	R.GSASFVSSLLK#.S	23.54	9.18	2.56	0.39
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.NSSSSGSSLLTPQSSSTNPSLLTSK#.S	9.62	3.93	2.45	0.41
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SGASLGSVSQLAAK#.S	28.02	14.64	1.91	0.52
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SGSQSSTSQLPSK#.S	64.38	34.12	1.89	0.53
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SSSEANISSSVSK#.N	45.48	12.26	3.71	0.27
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SSSETASSGLTSK#.S	33.48	12.13	2.76	0.36
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.STAQVAASLLATK#.S	40.74	15.05	2.71	0.37
Q8BI72_CA	Cdkn2aip	CDKN2A-in	R.GISSSNEGVEEPSK#.K	15.58	9.44	1.65	0.61
Q8BI72_CA	Cdkn2aip	CDKN2A-in	R.GSASFVSSLLK#.S	14.38	6.29	2.28	0.44
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.LVAVGGFSPTVNHGELLNAAIEALK#.A	8.03	2.93	2.74	0.36
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SGASLGSVSQLAAK#.S	23.74	6.25	3.80	0.26
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SGSQSSTSQLPSK#.S	40.52	12.17	3.33	0.30
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SSSEANISSSVSK#.N	21.43	6.53	3.28	0.30
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SSSETASSGLTSK#.S	18.96	7.55	2.51	0.40
Q8BI72_CA	Cdkn2aip	CDKN2A-in	R.GISSSNEGVEEPSK#.K	18.21	4.61	3.95	0.25
Q8BI72_CA	Cdkn2aip	CDKN2A-in	R.GSASFVSSLLK#.S	18.84	5.95	3.17	0.32
Q8BI72_CA	Cdkn2aip	CDKN2A-in	R.GSEIEDLVLLDEEARPVNLPPALK.H	1.59	3.77	0.42	2.38
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SGASLGSVSQLAAK#.S	17.72	7.48	2.37	0.42
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SGSQSSTSQLPSK#.S	24.68	7.88	3.13	0.32
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SSSEANISSSVSK#.N	29.20	8.15	3.58	0.28
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.SSSETASSGLTSK#.S	15.52	10.60	1.46	0.68
Q8BI72_CA	Cdkn2aip	CDKN2A-in	K.STAQVAASLLATK#.S	27.27	2.95	9.25	0.11
Q8R4E9_C	Cdt1	DNA replica	R.VQENAVEPSTPDAK#.V	12.25	4.69	2.61	0.38
Q8R4E9_C	Cdt1	DNA replica	R.FNVDEVPDIEPAELPQPPVTEK#.L	5.08	2.71	1.88	0.53
Q8R4E9_C	Cdt1	DNA replica	R.VQENAVEPSTPDAK#.V	12.02	5.98	2.01	0.50
Q9WTK2_C	Cdyl	Chromodo	K.EVQSALSTAAADDSK#.L	10.62	5.88	1.81	0.55
P28033_C	Cebpb	CCAAT/enh	K.VLELTAENER.L	2.57	7.87	0.33	3.06
P53569_C	Cebpz	CCAAT/enh	K.AIVSSGTLADR.M	14.86	9.80	1.52	0.66
P53569_C	Cebpz	CCAAT/enh	K.ELLITDLLPDSR.K	1.98	7.71	0.26	3.89
P53569_C	Cebpz	CCAAT/enh	K.K#GTIDDLQQGELESFIQNLNLAK#.Y	6.74	5.17	1.30	0.77
P53569_C	Cebpz	CCAAT/enh	K.AIVSSGTLADR.M	7.86	14.38	0.55	1.83
P53569_C	Cebpz	CCAAT/enh	K.EESQIPVDEVFFYR.Y	14.62	7.94	1.84	0.54
P28659_C	Celf1	CUGBP Elav	R.K#AALEAQNALHNM*K#.V	3.43	2.37	1.45	0.69
P28659_C	Celf1	CUGBP Elav	K.MFVGQVPR.T	4.66	16.11	0.29	3.46
O35216_C	Cenpa	Histone H3	K.STDLLFR.K	2.25	11.71	0.19	5.20
Q6RT24_C	Cenpe	Centromer	R.GSISENEAQGASTQDTAK.S	2.89	5.96	0.48	2.06
Q9CPQ5_C	Cenpq	Centromer	K.IQILTSEVEEEEQEVK#.Q	5.63	5.00	1.13	0.89
Q9CPQ5_C	Cenpq	Centromer	K.VLALPELSQK#.S	10.24	5.69	1.80	0.56
Q6A065_C	Cep170	Centrosom	R.FNPDGEEEDVTVHE.-	12.08	12.08	1.00	1.00
Q6A065_C	Cep170	Centrosom	R.FNPDGEEEDVTVHE.-	18.12	18.12	1.00	1.00
Q6A065_C	Cep170	Centrosom	R.IDLLAQPR.R	2.88	12.01	0.24	4.17
Q6A065_C	Cep170	Centrosom	R.M*QSTGSAM*PASSSFK#.H	9.92	7.47	1.33	0.75
Q6A065_C	Cep170	Centrosom	R.TLPQLPNEEK#.L	18.08	9.92	1.82	0.55
Q99NF3_C	Cep41	Centrosom	R.LEDNDSATSEADAEIAAK#.T	4.14	3.38	1.22	0.82
Q9R1K9_C	Cetn2	Centrin-2 C	R.EAFDLFDADGTGTIDIK#.E	26.42	16.02	1.65	0.61
Q9R1K9_C	Cetn2	Centrin-2 C	K.M*ISEIDKEGTGK.M	18.45	4.56	4.04	0.25
Q9R1K9_C	Cetn2	Centrin-2 C	K.M*NFSDFLTVM*TQK#.M	4.38	3.11	1.41	0.71
O35648_C	Cetn3	Centrin-3 C	R.ALGFDVK#.K	16.68	8.16	2.04	0.49
O35648_C	Cetn3	Centrin-3 C	K.DAFELFDTDKDQAIDYHELK.V	5.65	5.69	0.99	1.01
O35648_C	Cetn3	Centrin-3 C	R.ELGENM*SDEELR.A	2.35	8.21	0.29	3.50
Q8BTU1_C	Cfap20	Cilia- and fl	R.LYSEDELPAEFK#.L	11.30	8.99	1.26	0.80
O88271_C	Cfdp1	Craniofacia	R.EK#PQALVTSPATPLPAGSGIK#.R	18.38	5.06	3.63	0.28
P18760_C	Cfl1	Cofilin-1 O	K.EILVGDVGQTVDDPYTTFVK#.M	12.90	5.31	2.43	0.41
P18760_C	Cfl1	Cofilin-1 O	K.K#EDLVFIFWAPENAPLK#.S	24.75	9.45	2.62	0.38
P18760_C	Cfl1	Cofilin-1 O	K.LGGSAVISLEGK#PL.-	108.60	42.38	2.56	0.39

P18760_C	Cfl1	Cofilin-1 O	K.NIILEEGK#EILVGDVGQTVDDPYTTFVK#.M	47.58	13.88	3.43	0.29
P18760_C	Cfl1	Cofilin-1 O	R.YALYDATYETK#.E	69.05	21.56	3.20	0.31
P45591_C	Cfl2	Cofilin-2 O	K.ESK#K#EDLVFIFWAPESAPLK#.S	5.04	1.43	3.53	0.28
P45591_C	Cfl2	Cofilin-2 O	K.LGGSVVVSLEGK#PL.-	15.47	3.65	4.23	0.24
P45591_C	Cfl2	Cofilin-2 O	K.QILVGDIGDTVEDPYTSFVK#.L	10.71	2.78	3.85	0.26
Q8BHG9_C	Cggbp1	CGG triplet	K.ASVIQDFVK#.M	30.54	32.30	0.95	1.06
Q9QWF0_	Chaf1a	Chromatin	K.AK#EWDELLAK#.G	9.24	10.05	0.92	1.09
Q9QWF0_	Chaf1a	Chromatin	K.AKEWDELLAK.G	13.94	14.64	0.95	1.05
Q9QWF0_	Chaf1a	Chromatin	K.VPVVVLEDILATKPSIASLPM*M*SLDR.S	1.98	11.25	0.18	5.67
Q9D0N7_C	Chaf1b	Chromatin	K.AIVEFLSNLAR.H	1.24	11.07	0.11	8.95
Q9D0N7_C	Chaf1b	Chromatin	K.ASEEPSPELVNLPYR.M	1.93	7.54	0.26	3.91
Q9D0N7_C	Chaf1b	Chromatin	R.FSPTGEILASGGDDAVILLWK#.M	6.40	3.20	2.00	0.50
Q8K327_C	Champ1	Chromoso	K.APELSEEIQLEAVDNAK#.C	4.19	11.04	0.38	2.64
Q8K327_C	Champ1	Chromoso	K.DSQENSDAELSSSEYIR.A	5.79	2.79	2.07	0.48
Q8K327_C	Champ1	Chromoso	K.NVLQFTEEK#.E	16.95	8.31	2.04	0.49
Q8K327_C	Champ1	Chromoso	K.VASDIWKPVLSIDAEPR.K	7.07	10.24	0.69	1.45
Q8K327_C	Champ1	Chromoso	K.AFLLESLLK#.N	19.49	22.95	0.85	1.18
Q8K327_C	Champ1	Chromoso	K.APELSEEIQLEAVDNAK.C	4.64	4.73	0.98	1.02
Q8K327_C	Champ1	Chromoso	K.AVLPASPEPR.K	4.72	24.99	0.19	5.30
Q8K327_C	Champ1	Chromoso	K.KLLDEALSPSSK.K	6.27	6.94	0.90	1.11
Q8K327_C	Champ1	Chromoso	K.LM*EALESPLEEQQI.-	11.24	11.24	1.00	1.00
Q8K327_C	Champ1	Chromoso	K.LMEALESPLEEQQI.-	5.39	5.39	1.00	1.00
Q8K327_C	Champ1	Chromoso	K.NVLQFTEEKEAFISEEEIAK.Y	13.42	12.27	1.09	0.91
Q8K327_C	Champ1	Chromoso	K.TSPASLDFPEPQK#.S	10.57	7.49	1.41	0.71
P40201_C	Chd1	Chromodo	R.LLITGTPLQNSLK#.E	11.96	4.33	2.76	0.36
P40201_C	Chd1	Chromodo	K.SVVSDAPVHITASGEPVPIAEESEELDQK.T	4.14	3.30	1.25	0.80
P40201_C	Chd1	Chromodo	K.ELEPFLLR.R	4.90	13.72	0.36	2.80
P40201_C	Chd1	Chromodo	K.FGAEELFKEPEGEEQEPQEM*DIDEILK.R	4.23	4.86	0.87	1.15
P40201_C	Chd1	Chromodo	K.LILLDK#.L	26.03	17.57	1.48	0.67
P40201_C	Chd1	Chromodo	R.LK#NDDSLLYK#.T	21.71	11.18	1.94	0.52
P40201_C	Chd1	Chromodo	K.LVIAHEDELIPLHK#.S	12.28	9.41	1.31	0.77
P40201_C	Chd1	Chromodo	K.SVVSDAPVHITASGEPVPIAEESEELDQK#.T	14.43	8.69	1.66	0.60
E9PZM4_C	Chd2	Chromodo	R.ENEVSTSATDELLSQFK#.V	7.30	4.19	1.74	0.57
E9Q614_E	Chd3	Protein Ch	K.ELQGDGPPSSPTNDPTVK#.Y	5.95	5.91	1.01	0.99
E9Q614_E	Chd3	Protein Ch	R.ENEFSFEDNAIK#.G	11.56	8.60	1.34	0.74
E9Q614_E	Chd3	Protein Ch	K.SESGGSEYGTGPGR.K	1.50	6.51	0.23	4.33
Q6PDQ2_C	Chd4	Chromodo	R.APEPPPQQVAQQQ.-	19.55	19.55	1.00	1.00
Q6PDQ2_C	Chd4	Chromodo	K.GTTEVEK#VEEK#.S	15.55	10.16	1.53	0.65
Q6PDQ2_C	Chd4	Chromodo	K.IEENSLK#EEESTEGEK#EVK#.S	8.84	6.78	1.30	0.77
Q6PDQ2_C	Chd4	Chromodo	R.WQDIQNDPR.Y	7.93	9.42	0.84	1.19
Q6PDQ2_C	Chd4	Chromodo	K.AFLNAIM*R.Y	2.61	11.43	0.23	4.38
Q6PDQ2_C	Chd4	Chromodo	R.APEPPPQQVAQQQ.-	40.11	40.11	1.00	1.00
Q6PDQ2_C	Chd4	Chromodo	K.AYVSLFM*R.H	3.44	11.64	0.30	3.38
Q6PDQ2_C	Chd4	Chromodo	R.ENEFSFEDNAIR.G	4.45	22.85	0.19	5.13
Q6PDQ2_C	Chd4	Chromodo	K.FGTEELFK#DEATDGGGDNK#EGEDSSVIHYDDK#.A	9.11	6.78	1.34	0.74
Q6PDQ2_C	Chd4	Chromodo	R.FM*FNIADGGFTELHSLWQNEER.A	3.51	17.94	0.20	5.11
Q6PDQ2_C	Chd4	Chromodo	R.FSWAQGTDTILADEM*GLGK#.T	5.41	5.94	0.91	1.10
Q6PDQ2_C	Chd4	Chromodo	R.GNFLEIK.N	22.29	24.71	0.90	1.11
Q6PDQ2_C	Chd4	Chromodo	K.GTTEVEK#VEEK#.S	34.68	42.68	0.81	1.23
Q6PDQ2_C	Chd4	Chromodo	R.HHYEQQQEDLAR.N	4.25	36.47	0.12	8.58
Q6PDQ2_C	Chd4	Chromodo	K.IEENSLK#EEESTEGEK#EVK#.S	13.37	11.63	1.15	0.87
Q6PDQ2_C	Chd4	Chromodo	R.IGVMSLIR.K	5.57	25.64	0.22	4.61
Q6PDQ2_C	Chd4	Chromodo	R.NDKDKPLPPLLAR.V	4.27	28.42	0.15	6.65
Q6PDQ2_C	Chd4	Chromodo	R.NFEALNAR.G	3.25	16.96	0.19	5.21
Q6PDQ2_C	Chd4	Chromodo	R.TEEPM*ETEAK.G	11.02	6.59	1.67	0.60
Q6PDQ2_C	Chd4	Chromodo	K.TVQTAVFLYSLYK#.E	13.34	12.39	1.08	0.93
Q6PDQ2_C	Chd4	Chromodo	R.VGGNIEVLGFNAR.Q	9.75	39.44	0.25	4.05
Q6PDQ2_C	Chd4	Chromodo	R.VLIFSQM*TK.M	15.06	18.82	0.80	1.25
Q6PDQ2_C	Chd4	Chromodo	R.YAILNEPFK.G	7.59	8.70	0.87	1.15
Q6PDQ2_C	Chd4	Chromodo	R.YGM*PPQDAFTTQWLVR.D	2.95	8.58	0.34	2.91
Q6PDQ2_C	Chd4	Chromodo	R.AIIRENEFSFEDNAIR.G	3.67	17.83	0.21	4.86
Q6PDQ2_C	Chd4	Chromodo	R.APEPPPQQVAQQQ.-	112.33	112.33	1.00	1.00
Q6PDQ2_C	Chd4	Chromodo	K.AYVSLFM*R.H	13.10	32.53	0.40	2.48
Q6PDQ2_C	Chd4	Chromodo	R.EEEM*GEEEEVER.E	4.17	11.07	0.38	2.66
Q6PDQ2_C	Chd4	Chromodo	K.EGIQWEAK#.E	32.50	19.85	1.64	0.61
Q6PDQ2_C	Chd4	Chromodo	R.EIIK#QEESVDPDYWEK#.L	26.74	22.27	1.20	0.83
Q6PDQ2_C	Chd4	Chromodo	R.ENEFSFEDNAIR.G	28.44	112.45	0.25	3.95
Q6PDQ2_C	Chd4	Chromodo	K.ESM*AGNK#PANAVLHK#.V	72.96	71.43	1.02	0.98
Q6PDQ2_C	Chd4	Chromodo	K.ESM*AGNKPANAVLHK.V	8.49	8.14	1.04	0.96
Q6PDQ2_C	Chd4	Chromodo	K.FAEM*EER.F	12.65	43.09	0.29	3.41
Q6PDQ2_C	Chd4	Chromodo	K.FGTEELFK#.D	12.39	12.54	0.99	1.01
Q6PDQ2_C	Chd4	Chromodo	K.FGTEELFK#DEATDGGGDNK#EGEDSSVIHYDDK#.A	56.33	39.80	1.42	0.71
Q6PDQ2_C	Chd4	Chromodo	R.FM*FNIADGGFTELHSLWQNEER.A	6.64	13.58	0.49	2.05
Q6PDQ2_C	Chd4	Chromodo	R.FSWAQGTDTILADEM*GLGK#.T	50.77	32.73	1.55	0.64
Q6PDQ2_C	Chd4	Chromodo	R.GGGNQVSLLNVVM*DLK#.K	35.81	30.52	1.17	0.85
Q6PDQ2_C	Chd4	Chromodo	R.GGGNQVSLLNVVMDLK#K#.C	23.53	18.41	1.28	0.78
Q6PDQ2_C	Chd4	Chromodo	R.GNFLEIK#.N	66.79	47.94	1.39	0.72
Q6PDQ2_C	Chd4	Chromodo	K.GTTEVEKVEEK.S	95.03	67.16	1.42	0.71
Q6PDQ2_C	Chd4	Chromodo	R.HHYEQQQEDLAR.N	24.51	74.87	0.33	3.05
Q6PDQ2_C	Chd4	Chromodo	R.IDGGITGNM*R.Q	32.11	122.35	0.26	3.81
Q6PDQ2_C	Chd4	Chromodo	R.IDGGITGNMR.Q	16.29	25.85	0.63	1.59
Q6PDQ2_C	Chd4	Chromodo	K.IEENSLK#EEESTEGEK#EVK#.S	29.13	21.43	1.36	0.74
Q6PDQ2_C	Chd4	Chromodo	K.IEENSLKEEESTEGEKEVK.S	68.92	41.10	1.68	0.60
Q6PDQ2_C	Chd4	Chromodo	R.IGVM*SLIR.K	8.64	42.36	0.20	4.90
Q6PDQ2_C	Chd4	Chromodo	R.IGVMSLIR.K	14.38	36.50	0.39	2.54
Q6PDQ2_C	Chd4	Chromodo	R.ILNHSVDK#K#.G	27.42	19.66	1.39	0.72
Q6PDQ2_C	Chd4	Chromodo	R.K#EEEEEEDEDDDSK#EPK#.S	23.09	19.65	1.17	0.85
Q6PDQ2_C	Chd4	Chromodo	R.KLERPPETPTVDPTVK.Y	19.41	78.86	0.25	4.06
Q6PDQ2_C	Chd4	Chromodo	R.K#NDM*DEPPSGDFGGDEEK#.S	43.04	33.70	1.28	0.78
Q6PDQ2_C	Chd4	Chromodo	R.K#NDMDEPPSGDFGGDEEK#.S	14.27	12.88	1.11	0.90
Q6PDQ2_C	Chd4	Chromodo	K.LERPPETPTVDPTVK.Y	9.31	43.30	0.21	4.65
Q6PDQ2_C	Chd4	Chromodo	R.LLDRNQDETEDTELQGM*NEYLSSFK.V	3.50	10.88	0.32	3.11
Q6PDQ2_C	Chd4	Chromodo	R.LLDRNQDETEDTELQGMNEYLSSFK.V	3.37	11.08	0.30	3.29
Q6PDQ2_C	Chd4	Chromodo	K.LLEQALVIEEQLR.R	13.20	33.08	0.40	2.51
Q6PDQ2_C	Chd4	Chromodo	K.LLLLQK#.M	194.28	134.84	1.44	0.69
Q6PDQ2_C	Chd4	Chromodo	K.M*LDLLEDFLEHEGYK#.Y	39.67	25.28	1.57	0.64
Q6PDQ2_C	Chd4	Chromodo	K.M*M*LTHLVVRPGLGSK.T	2.17	16.04	0.14	7.38
Q6PDQ2_C	Chd4	Chromodo	K.M*SQPGSPSPK#.T	12.54	8.30	1.51	0.66
Q6PDQ2_C	Chd4	Chromodo	R.NFEALNAR.G	28.05	78.93	0.36	2.81
Q6PDQ2_C	Chd4	Chromodo	R.NQDETEDTELQGM*NEYLSSFK#.V	14.41	10.91	1.32	0.76
Q6PDQ2_C	Chd4	Chromodo	R.NQDETEDTELQGMNEYLSSFK#.V	13.78	8.79	1.57	0.64
Q6PDQ2_C	Chd4	Chromodo	K.QEESVDPDYWEK#.L	8.53	8.34	1.02	0.98
Q6PDQ2_C	Chd4	Chromodo	K.QELDDILK#.F	65.03	44.69	1.46	0.69

Q6PDQ2_C	Chd4	Chromodoı	K.QVNYNDGSQEDR.D	2.15	5.54	0.39	2.58
Q6PDQ2_C	Chd4	Chromodoı	K.SAVDLTPIVVEDK#.E	22.48	15.42	1.46	0.69
Q6PDQ2_C	Chd4	Chromodoı	K.SSAQLLEDWGM*EDIDHVFSEEDYR.T	11.43	42.37	0.27	3.71
Q6PDQ2_C	Chd4	Chromodoı	K.SSAQLLEDWGMEDIDHVFSEEDYR.T	4.56	12.20	0.37	2.67
Q6PDQ2_C	Chd4	Chromodoı	K.TPTPSTPGDTQPNTPAPVPPAEDGIK.I	13.53	12.84	1.05	0.95
Q6PDQ2_C	Chd4	Chromodoı	K.TVQTAVFLYSLYK#.E	79.19	54.76	1.45	0.69
Q6PDQ2_C	Chd4	Chromodoı	K.TVQTAVFLYSLYK.E	9.47	9.71	0.98	1.03
Q6PDQ2_C	Chd4	Chromodoı	K.VAQYVVREEEM*GEEEEVER.E	2.65	10.84	0.24	4.08
Q6PDQ2_C	Chd4	Chromodoı	R.VELSPM*QK#.K	71.95	53.70	1.34	0.75
Q6PDQ2_C	Chd4	Chromodoı	R.VGGNIEVLGFNAR.Q	32.44	101.83	0.32	3.14
Q6PDQ2_C	Chd4	Chromodoı	R.VLIFSQM*TK#.M	157.87	125.70	1.26	0.80
Q6PDQ2_C	Chd4	Chromodoı	R.VLIFSQMTK#.M	58.26	46.15	1.26	0.79
Q6PDQ2_C	Chd4	Chromodoı	R.WQDIQNDPR.Y	16.68	46.23	0.36	2.77
Q6PDQ2_C	Chd4	Chromodoı	R.YAILNEPFK#.G	25.63	22.49	1.14	0.88
Q6PDQ2_C	Chd4	Chromodoı	R.YGM*PPQDAFTTQWLVR.D	7.61	18.77	0.41	2.47
Q09XV5_Cl	Chd8	Chromodoı	R.DGNITGIQQFSK#.K	10.20	9.20	1.11	0.90
Q09XV5_Cl	Chd8	Chromodoı	R.LPPAAGDEPPDPNLFIEPITEER.A	18.89	12.23	1.54	0.65
Q09XV5_Cl	Chd8	Chromodoı	R.M*NYM*QNHQAGASAASLSR.C	2.69	6.82	0.39	2.54
O35280_Cl	Chek1	Serine/thre	R.ATSGGM*SESSSGFSK#.H	1.76	1.34	1.32	0.76
Q8CGZ0_Cl	Cherp	Calcium ho	K.ARDEFSTFGTR.K	5.03	9.56	0.53	1.90
Q8CGZ0_Cl	Cherp	Calcium ho	R.DEFSTFGTR.K	8.38	25.73	0.33	3.07
Q8CGZ0_Cl	Cherp	Calcium ho	R.ELLAALQK#.V	78.75	59.87	1.32	0.76
Q8CGZ0_Cl	Cherp	Calcium ho	R.LLQLWEK#.N	90.57	56.04	1.62	0.62
Q8CGZ0_Cl	Cherp	Calcium ho	K.M*GWSGSGGLGAK#.E	32.61	36.58	0.89	1.12
Q8CGZ0_Cl	Cherp	Calcium ho	K.MGWSGSGGLGAK#.E	17.99	12.01	1.50	0.67
Q8CGZ0_Cl	Cherp	Calcium ho	R.NGPEFEK#.M	23.61	19.07	1.24	0.81
Q8CGZ0_Cl	Cherp	Calcium ho	R.NSEGWEQNGLYEFFR.A	5.11	13.85	0.37	2.71
Q8CGZ0_Cl	Cherp	Calcium ho	R.QEQVTTAVAHAVEQQM*QK#.L	27.17	21.00	1.29	0.77
Q8CGZ0_Cl	Cherp	Calcium ho	R.ELLAALQK#.V	31.48	20.24	1.56	0.64
Q8CGZ0_Cl	Cherp	Calcium ho	K.GHQMLVKMGWSGSGGLGAK.E	3.64	23.83	0.15	6.55
Q9CQ10_Cl	Chmp3	Charged mı	R.ILFEITAGALGK#.A	11.68	5.47	2.13	0.47
Q9D8B3_Cl	Chmp4b	Charged mı	R.EALENANTNTEVLK#.N	21.08	10.93	1.93	0.52
Q9D8B3_Cl	Chmp4b	Charged mı	K.K#IEQELTAAK#.K	25.46	10.92	2.33	0.43
Q9D7S9_Cl	Chmp5	Charged mı	K.NK#DGVLVDEFGLPQIPAS.-	16.18	6.69	2.42	0.41
P0C0A3_Cl	Chmp6	Charged mı	R.ILDETQEAVEYQR.Q	1.84	10.02	0.18	5.45
P61022_Cl	Chp1	Calcineurin	R.ASTLLRDEELEEIKK.E	2.29	16.68	0.14	7.27
P61022_Cl	Chp1	Calcineurin	R.IINAFFSEGEDQVNFR.G	2.50	9.53	0.26	3.81
P61022_Cl	Chp1	Calcineurin	R.IPELAINPLGDR.I	4.03	15.27	0.26	3.79
P61022_Cl	Chp1	Calcineurin	R.TIQEADQDGDSAISFTEFVK#.V	5.65	6.10	0.93	1.08
Q9JKP8_Cl	Chrac1	Chromatin	R.LVSLPLSR.I	10.43	38.65	0.27	3.70
Q9JKP8_Cl	Chrac1	Chromatin	K.SSPEVSSINQEALVLTAK#.A	20.40	9.71	2.10	0.48
Q8BIW9_C	Chtf18	Chromosor	K.VVQGLFDNFLR.L	1.58	6.57	0.24	4.15
Q8BIW9_C	Chtf18	Chromosor	K.VVQGLFDNFLR.L	3.39	9.46	0.36	2.79
Q9CY57_Cl	Chtop	Chromatin	R.ASMQQQQQLASAR.N	3.57	18.91	0.19	5.29
Q9CY57_Cl	Chtop	Chromatin	K.EQLDNQLDAYMSK#.T	8.23	5.58	1.48	0.68
Q9CY57_Cl	Chtop	Chromatin	K.GHLDAELDAYM*AQTDPETND.-	3.95	3.95	1.00	1.00
Q9CY57_Cl	Chtop	Chromatin	K.EQLDNQLDAYM*SK#.T	8.49	6.04	1.41	0.71
Q9CY57_Cl	Chtop	Chromatin	K.EQLDNQLDAYMSK#.T	5.54	4.95	1.12	0.89
Q9CY57_Cl	Chtop	Chromatin	K.GHLDAELDAYM*AQTDPETND.-	2.82	2.82	1.00	1.00
Q99KN2_Cl	Ciao1	Probable cy	K.HVVWHPSQELLASASYDDTVK#.L	7.04	2.87	2.45	0.41
Q3V1H1_Cl	Ckap2	Cytoskeletc	R.IEPITSPIENIISIYEK#.A	10.70	5.44	1.97	0.51
Q3V1H1_Cl	Ckap2	Cytoskeletc	K.AQSEPANTVSVK#.A	18.29	10.68	1.71	0.58
Q3V1H1_Cl	Ckap2	Cytoskeletc	R.HIIIDILTTK#.S	15.88	5.47	2.90	0.34
Q3V1H1_Cl	Ckap2	Cytoskeletc	R.IEPITSPIENIISIYEK#.A	14.35	5.84	2.46	0.41
Q3V1H1_Cl	Ckap2	Cytoskeletc	R.IEPITSPIENIISIYEK#.A	6.84	3.65	1.87	0.53
Q8BMK4_C	Ckap4	Cytoskeletc	K.IETNENNLESAK#.G	11.79	13.86	0.85	1.17
A2AGT5_Cl	Ckap5	Cytoskeletc	R.IEDLEEGQQVIR.S	1.82	8.91	0.20	4.89
A2AGT5_Cl	Ckap5	Cytoskeletc	K.FIQPNIGELPTALK#.G	7.50	3.94	1.90	0.53
A2AGT5_Cl	Ckap5	Cytoskeletc	K.LDDIFEPVLIPEPK#.I	5.98	5.93	1.01	0.99
A2AGT5_Cl	Ckap5	Cytoskeletc	K.AFISNVK#.T	57.16	25.65	2.23	0.45
A2AGT5_Cl	Ckap5	Cytoskeletc	K.AK#VNDFLAEIFK#K#.I	14.49	9.92	1.46	0.69
A2AGT5_Cl	Ckap5	Cytoskeletc	R.DAAFEALGTALK#.V	82.00	44.89	1.83	0.55
A2AGT5_Cl	Ckap5	Cytoskeletc	K.DTNVM*LVALAAK#.C	9.87	5.67	1.74	0.57
A2AGT5_Cl	Ckap5	Cytoskeletc	K.DTNVMLVALAAK#.C	7.62	4.18	1.82	0.55
A2AGT5_Cl	Ckap5	Cytoskeletc	K.EALEAVEVLVK#.N	36.28	14.00	2.59	0.39
A2AGT5_Cl	Ckap5	Cytoskeletc	K.EGLDEVAGIINEAK#.F	51.87	22.46	2.31	0.43
A2AGT5_Cl	Ckap5	Cytoskeletc	K.ELEEEWVK#.L	17.41	7.02	2.48	0.40
A2AGT5_Cl	Ckap5	Cytoskeletc	K.ETNFQVM*QM*K#.L	21.73	10.29	2.11	0.47
A2AGT5_Cl	Ckap5	Cytoskeletc	K.FGQYAGHVVPTILEK#.F	51.41	26.81	1.92	0.52
A2AGT5_Cl	Ckap5	Cytoskeletc	K.FIQPNIGELPTALK#.G	70.73	40.16	1.76	0.57
A2AGT5_Cl	Ckap5	Cytoskeletc	K.FVTDSNAVVQLK#.G	35.05	17.81	1.97	0.51
A2AGT5_Cl	Ckap5	Cytoskeletc	K.GLEAALVYVENAHVAGK#.T	50.00	24.28	2.06	0.49
A2AGT5_Cl	Ckap5	Cytoskeletc	K.HINDSAPEVR.D	10.59	30.18	0.35	2.85
A2AGT5_Cl	Ckap5	Cytoskeletc	K.HSTSATDEGEDGEEPGEGGNDVVDLLPR.I	3.54	8.40	0.42	2.37
A2AGT5_Cl	Ckap5	Cytoskeletc	K.HTLQNINSVQLK#.E	18.44	8.93	2.07	0.48
A2AGT5_Cl	Ckap5	Cytoskeletc	R.IEDLEEGQQVIR.S	10.33	27.96	0.37	2.71
A2AGT5_Cl	Ckap5	Cytoskeletc	K.LDDIFEPVLIPEPK#.I	70.49	40.64	1.73	0.58
A2AGT5_Cl	Ckap5	Cytoskeletc	K.LEAGDYADLVK#.A	62.37	28.63	2.18	0.46
A2AGT5_Cl	Ckap5	Cytoskeletc	K.LFAIEIYR.W	3.43	11.25	0.31	3.28
A2AGT5_Cl	Ckap5	Cytoskeletc	R.LLPDTINSINLDR.I	13.90	32.82	0.42	2.36
A2AGT5_Cl	Ckap5	Cytoskeletc	R.LSGYEEALK#.I	50.01	22.55	2.22	0.45
A2AGT5_Cl	Ckap5	Cytoskeletc	R.M*IFEDEKPALLSQIDAEFQK.M	19.11	61.77	0.31	3.23
A2AGT5_Cl	Ckap5	Cytoskeletc	R.MIFEDEK#PALLSQIDAEFQK#.M	7.28	6.23	1.17	0.86
A2AGT5_Cl	Ckap5	Cytoskeletc	K.M*QGQSPPAPTR.G	12.36	34.06	0.36	2.76
A2AGT5_Cl	Ckap5	Cytoskeletc	K.MQGQSPPAPTR.G	3.80	12.06	0.31	3.18
A2AGT5_Cl	Ckap5	Cytoskeletc	K.NLGIPVITVLGDSK#.N	109.39	45.37	2.41	0.41
A2AGT5_Cl	Ckap5	Cytoskeletc	K.NQSETLNWLSNAIK#.E	21.72	9.38	2.32	0.43
A2AGT5_Cl	Ckap5	Cytoskeletc	K.NSSQFFQSYVER.G	7.26	24.21	0.30	3.33
A2AGT5_Cl	Ckap5	Cytoskeletc	R.QELLGWLAEK#.L	16.42	8.21	2.00	0.50
A2AGT5_Cl	Ckap5	Cytoskeletc	R.SQQELEAK#.L	18.51	11.37	1.63	0.61
A2AGT5_Cl	Ckap5	Cytoskeletc	K.SVNPFLADVDK#.L	18.30	9.31	1.96	0.51
A2AGT5_Cl	Ckap5	Cytoskeletc	K.TALAATNPAVR.T	17.85	42.70	0.42	2.39
A2AGT5_Cl	Ckap5	Cytoskeletc	R.TQNINSNANM*LR.K	8.36	20.22	0.41	2.42
A2AGT5_Cl	Ckap5	Cytoskeletc	K.TQPIPAPVEDSVSSTIEAK#PDLK#K#.A	37.16	29.14	1.28	0.78
A2AGT5_Cl	Ckap5	Cytoskeletc	K.TSAQIVLDGLVDK#.I	34.04	13.78	2.47	0.40
A2AGT5_Cl	Ckap5	Cytoskeletc	K.TSAQIVLDGLVDK#IGDVK#.C	44.95	22.42	2.01	0.50
A2AGT5_Cl	Ckap5	Cytoskeletc	K.TTGEVVSGVVSK#.V	76.33	34.19	2.23	0.45
A2AGT5_Cl	Ckap5	Cytoskeletc	K.VNDFLAEIFK#.K	16.77	10.54	1.59	0.63
A2AGT5_Cl	Ckap5	Cytoskeletc	K.VNDFLAEIFK#K#.I	32.76	15.91	2.06	0.49
A2AGT5_Cl	Ckap5	Cytoskeletc	K.YSDTDIEPFLK#.N	37.42	21.12	1.77	0.56
E9QKH0_E	Clasp1	CLIP-associ	R.AQTTNSNSSSSSDVSTHS.-	3.29	3.29	1.00	1.00
E9QKH0_E	Clasp1	CLIP-associ	R.FIVDQTQTPNLK#.V	8.72	6.78	1.29	0.78
E9QKH0_E	Clasp1	CLIP-associ	R.FIVDQTQTPNLK#.V	19.75	14.36	1.38	0.73

E9QKH0_E	Clasp1	CLIP-associ	R.QSSGSTTNVASTPSDSR.G	1.31	3.58	0.37	2.74
E9QKH0_E	Clasp1	CLIP-associ	R.AQTTNSNSSSSSDVSTHS.-	3.09	3.09	1.00	1.00
E9QKH0_E	Clasp1	CLIP-associ	K.EGAGAVDEEDFIK#.A	15.00	9.78	1.53	0.65
E9QKH0_E	Clasp1	CLIP-associ	R.EYNPYPYSDTINTYDK#.T	3.54	3.28	1.08	0.93
E9QKH0_E	Clasp1	CLIP-associ	R.FIVDQTQTPNLK#.V	25.14	15.18	1.66	0.60
E9QKH0_E	Clasp1	CLIP-associ	R.HISVLAETIK#.K	11.81	4.75	2.48	0.40
E9QKH0_E	Clasp1	CLIP-associ	R.IITWTTEPK#.S	22.70	11.16	2.03	0.49
E9QKH0_E	Clasp1	CLIP-associ	K.LLGSGLAGGSSR.G	6.42	18.33	0.35	2.86
E9QKH0_E	Clasp1	CLIP-associ	R.LNVIFTK#.F	34.86	14.74	2.37	0.42
E9QKH0_E	Clasp1	CLIP-associ	K.NFDDEDSVDGNRPSSASSSSSK.A	4.91	7.55	0.65	1.54
E9QKH0_E	Clasp1	CLIP-associ	K.NSSNTGVGSPSNTIGR.T	6.79	12.13	0.56	1.78
Q8BRT1_Cl	Clasp2	CLIP-associ	R.AGGDAADGSQPALDNK#.A	19.16	4.85	3.95	0.25
Q8BRT1_Cl	Clasp2	CLIP-associ	R.AQTGSAGADPTADVSGQS.-	6.77	6.77	1.00	1.00
Q8BRT1_Cl	Clasp2	CLIP-associ	K.EGLLGLQNLLK#.S	23.73	14.67	1.62	0.62
Q8BRT1_Cl	Clasp2	CLIP-associ	K.EGGAGAVDEDDFIK#.A	15.14	8.72	1.74	0.58
Q8BRT1_Cl	Clasp2	CLIP-associ	K.EGLLGLQNLLK#.S	48.90	28.16	1.74	0.58
Q8BRT1_Cl	Clasp2	CLIP-associ	R.FTVDQTQTPSLK#.V	22.60	12.97	1.74	0.57
Q8BRT1_Cl	Clasp2	CLIP-associ	K.LSTPLVAVGNAK#.T	15.36	6.59	2.33	0.43
Q8BRT1_Cl	Clasp2	CLIP-associ	R.VITWTTEPK#.S	16.72	7.30	2.29	0.44
Q9Z1Q5_Cl	Clic1	Chloride in	K.LAALNPESNTSGLDIFAK#.F	5.27	2.18	2.41	0.41
Q9Z1Q5_Cl	Clic1	Chloride in	K.LAALNPESNTSGLDIFAK#.F	5.51	2.37	2.33	0.43
Q9Z1Q5_Cl	Clic1	Chloride in	K.LAALNPESNTSGLDIFAK#.F	3.85	2.29	1.69	0.59
Q9QYB1_Cl	Clic4	Chloride in	K.NSRPEANEALER.G	1.46	4.01	0.36	2.74
Q9QYB1_Cl	Clic4	Chloride in	R.K#PADLQNLAPGTHPPFITFNSEVK#.T	4.95	1.83	2.70	0.37
Q9QYB1_Cl	Clic4	Chloride in	K.TLQK#LDEYLNSPLPDEIDENSM*EDIK#.F	2.29	2.29	1.00	1.00
Q5SUH6_Q	Clint1	Clathrin int	K.ATNVVM*NYSEIESK#.V	6.53	6.28	1.04	0.96
Q5SUH6_Q	Clint1	Clathrin int	K.GEFKDEEETVTTK.H	6.81	9.96	0.68	1.46
Q5SUH6_Q	Clint1	Clathrin int	K.ASPDQNASTHTPQSSAKPSVPSSK.S	8.83	9.23	0.96	1.05
Q5SUH6_Q	Clint1	Clathrin int	K.ATNVVM*NYSEIESK#.V	14.78	8.81	1.68	0.60
Q5SUH6_Q	Clint1	Clathrin int	K.ATNVVMNYSEIESK#.V	9.73	7.45	1.31	0.77
Q5SUH6_Q	Clint1	Clathrin int	K.GEFK#DEEETVTTK#.H	14.00	11.87	1.18	0.85
Q5SUH6_Q	Clint1	Clathrin int	K.IGSTIDDTISK#.F	31.54	26.53	1.19	0.84
Q5SUH6_Q	Clint1	Clathrin int	K.YVGVSSDSVGGFR.Y	5.93	13.16	0.45	2.22
Q922J3_CL	Clip1	CAP-Gly do	K.ANENASFLQK#.S	18.29	10.38	1.76	0.57
Q922J3_CL	Clip1	CAP-Gly do	K.ATSHVGEIEQELALAR.D	8.52	12.32	0.69	1.45
Q922J3_CL	Clip1	CAP-Gly do	R.DGHDQHVLELEAK#.M	19.48	11.62	1.68	0.60
Q922J3_CL	Clip1	CAP-Gly do	K.ELVLTGLQDSLNQVNQVK#.E	27.90	9.96	2.80	0.36
Q922J3_CL	Clip1	CAP-Gly do	K.EPSATPQISNLTK#.T	15.01	9.32	1.61	0.62
Q922J3_CL	Clip1	CAP-Gly do	K.FASTSEEAVSAQTR.M	7.13	15.23	0.47	2.14
Q922J3_CL	Clip1	CAP-Gly do	R.FLGETDFAK#.G	18.11	14.57	1.24	0.80
Q922J3_CL	Clip1	CAP-Gly do	K.GIGTDSAEFAELK#.T	22.29	15.27	1.46	0.69
Q922J3_CL	Clip1	CAP-Gly do	K.IGFPSTTPAK#.A	26.16	12.56	2.08	0.48
Q922J3_CL	Clip1	CAP-Gly do	K.MSGDNSSQLTK#.M	10.70	5.69	1.88	0.53
Q922J3_CL	Clip1	CAP-Gly do	K.SISLTSALLTEK#.D	7.37	3.36	2.19	0.46
Q922J3_CL	Clip1	CAP-Gly do	K.SLHSVVQTLESDK#VK#.L	12.83	9.28	1.38	0.72
Q922J3_CL	Clip1	CAP-Gly do	K.SQQLSALQEENVK#.L	36.70	15.10	2.43	0.41
Q922J3_CL	Clip1	CAP-Gly do	R.SVEELQLK#.L	26.97	13.93	1.94	0.52
Q922J3_CL	Clip1	CAP-Gly do	K.TASESISNLSEAGSVK#.K	22.21	8.74	2.54	0.39
Q922J3_CL	Clip1	CAP-Gly do	K.YTEQSEVIGNFTSQLSAVK#.E	5.86	2.30	2.55	0.39
Q922J3_CL	Clip1	CAP-Gly do	K.TASESISNLSEAGSVK#.K	7.27	5.76	1.26	0.79
Q922J3_CL	Clip1	CAP-Gly do	K.TPAAAAAPVEK#.T	27.09	6.75	4.01	0.25
O35492_Cl	Clk3	Dual specifi	R.YEIVGNLGEGTFGK#.V	9.32	5.33	1.75	0.57
Q61189_IC	Clns1a	Methylosor	R.LQQPDTEAVLNGK#.G	15.35	4.34	3.54	0.28
Q61189_IC	Clns1a	Methylosor	R.NYEDGM*EVETTPTVAGQFEDADVDH.-	8.08	8.08	1.00	1.00
Q9JHS4_CL	Clpx	ATP-depen	K.LLEGTIVNVPEK#.N	7.36	2.94	2.51	0.40
Q9JHS4_CL	Clpx	ATP-depen	R.LPVVVPLHSLDEK#.T	7.46	2.80	2.67	0.37
Q9JHS4_CL	Clpx	ATP-depen	K.YLGFGTPSNLGK#.G	8.12	2.24	3.63	0.28
Q6PFA2_Q	Clta	Clathrin lig	R.AAEEAFVNDIDESSPGTEWER.V	5.02	7.18	0.70	1.43
Q6PFA2_Q	Clta	Clathrin lig	K.ELEEWYAR.Q	12.44	18.23	0.68	1.47
Q6PFA2_Q	Clta	Clathrin lig	R.LEALDANSR.K	19.61	21.40	0.92	1.09
Q68FD5_Cl	Cltc	Clathrin he	R.ALEHFTDLYDIK#.R	17.81	5.42	3.28	0.30
Q68FD5_Cl	Cltc	Clathrin he	R.AVNYFSK#.V	29.36	7.23	4.06	0.25
Q68FD5_Cl	Cltc	Clathrin he	R.ESYVETELIFALAK#.T	20.60	5.66	3.64	0.27
Q68FD5_Cl	Cltc	Clathrin he	K.HDVVFLITK#.Y	24.86	6.44	3.86	0.26
Q68FD5_Cl	Cltc	Clathrin he	R.IAAYLFK#.G	24.88	8.54	2.91	0.34
Q68FD5_Cl	Cltc	Clathrin he	R.ISGETIFVTAPHEATAGIIGVNR.K	10.20	16.61	0.61	1.63
Q68FD5_Cl	Cltc	Clathrin he	K.IYIDSNNNPER.F	7.65	9.88	0.77	1.29
Q68FD5_Cl	Cltc	Clathrin he	K.K#AVDVFFPPEAQNDFPVAM*QISEK#.H	3.73	3.65	1.02	0.98
Q68FD5_Cl	Cltc	Clathrin he	K.K#DSLYK#.D	124.18	30.35	4.09	0.24
Q68FD5_Cl	Cltc	Clathrin he	R.K#FNALFAQGNYSEAAK#.V	25.02	5.30	4.72	0.21
Q68FD5_Cl	Cltc	Clathrin he	R.LASTLVHLGEYQAAVDGAR.K	17.20	18.45	0.93	1.07
Q68FD5_Cl	Cltc	Clathrin he	K.LLLPWLEAR.I	19.23	24.62	0.78	1.28
Q68FD5_Cl	Cltc	Clathrin he	R.NLQNLLILTAIK#.A	60.21	13.05	4.61	0.22
Q68FD5_Cl	Cltc	Clathrin he	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	4.79	6.39	0.75	1.33
Q68FD5_Cl	Cltc	Clathrin he	K.SVNESLNNLFITEEDYQALR.T	8.61	6.59	1.31	0.77
Q68FD5_Cl	Cltc	Clathrin he	K.TLQIFNIEM*K#.S	17.25	7.02	2.46	0.41
Q68FD5_Cl	Cltc	Clathrin he	R.TSIDAYDNFDNISLAQR.L	6.90	8.20	0.84	1.19
Q68FD5_Cl	Cltc	Clathrin he	K.VANVELYYK#.A	39.61	9.37	4.23	0.24
Q68FD5_Cl	Cltc	Clathrin he	K.ADDPSSYM*EVVQAANASGNWEELVK#.Y	35.99	4.99	7.21	0.14
Q68FD5_Cl	Cltc	Clathrin he	R.AHM*GM*FTELAILYSK#.F	76.50	48.41	1.58	0.63
Q68FD5_Cl	Cltc	Clathrin he	K.AHTM*TDDVTFWK#.W	25.72	6.00	4.29	0.23
Q68FD5_Cl	Cltc	Clathrin he	K.AHTMTDDVTFWK#.W	8.33	2.30	3.63	0.28
Q68FD5_Cl	Cltc	Clathrin he	R.ALEHFTDLYDIK#.R	61.55	20.73	2.97	0.34
Q68FD5_Cl	Cltc	Clathrin he	R.ALEHFTDLYDIKR.A	19.01	27.71	0.69	1.46
Q68FD5_Cl	Cltc	Clathrin he	K.AVDVFFPPEAQNDFPVAM*QISEK#.H	14.69	4.98	2.95	0.34
Q68FD5_Cl	Cltc	Clathrin he	R.AVNYFSK#.V	167.82	34.21	4.91	0.20
Q68FD5_Cl	Cltc	Clathrin he	R.AYEFAER.C	22.41	24.58	0.91	1.10
Q68FD5_Cl	Cltc	Clathrin he	K.DAMQYASESK#.D	12.01	4.90	2.45	0.41
Q68FD5_Cl	Cltc	Clathrin he	K.DAM*QYASESK#.D	35.80	11.50	3.11	0.32
Q68FD5_Cl	Cltc	Clathrin he	K.EAIDSYIK#.A	150.43	40.51	3.71	0.27
Q68FD5_Cl	Cltc	Clathrin he	R.ENPYYDSR.V	13.63	14.40	0.95	1.06
Q68FD5_Cl	Cltc	Clathrin he	R.ESYVETELIFALAK#.T	20.37	3.36	6.06	0.17
Q68FD5_Cl	Cltc	Clathrin he	R.FQEHLQLQNLGINPANIGFSTLTM*ESDK#.F	6.14	3.44	1.79	0.56
Q68FD5_Cl	Cltc	Clathrin he	R.GQFSTDELVAEVEK#.R	41.14	10.10	4.07	0.25
Q68FD5_Cl	Cltc	Clathrin he	K.HDVVFLITK#.Y	101.13	22.67	4.46	0.22
Q68FD5_Cl	Cltc	Clathrin he	R.IAAYLFK#.G	147.78	41.40	3.57	0.28
Q68FD5_Cl	Cltc	Clathrin he	R.ISGETIFVTAPHEATAGIIGVNR.K	64.16	69.38	0.92	1.08
Q68FD5_Cl	Cltc	Clathrin he	K.IVLYAK#.K	189.25	52.88	3.58	0.28
Q68FD5_Cl	Cltc	Clathrin he	K.IYIDSNNNPER.F	41.88	56.27	0.74	1.34
Q68FD5_Cl	Cltc	Clathrin he	K.K#AVDVFFPPEAQNDFPVAM*QISEK#.H	14.87	5.68	2.62	0.38
Q68FD5_Cl	Cltc	Clathrin he	K.KAVDVFFPPEAQNDFPVAMQISEK.H	11.49	3.67	3.13	0.32
Q68FD5_Cl	Cltc	Clathrin he	R.K#FNALFAQGNYSEAAK#.V	101.52	26.78	3.79	0.26
Q68FD5_Cl	Cltc	Clathrin he	R.K#VSQPIEGHAASFAQFK#.M	59.13	15.53	3.81	0.26

Q68FD5_C	Cltc	Clathrin he	R.LAELEEFINGPNNAHIQQVGDR.C	20.85	23.41	0.89	1.12
Q68FD5_C	Cltc	Clathrin he	R.LASTLVHLGEYQAAVDGAR.K	68.15	76.34	0.89	1.12
Q68FD5_C	Cltc	Clathrin he	R.LEKHELIEFR.R	18.01	14.18	1.27	0.79
Q68FD5_C	Cltc	Clathrin he	K.LLYNNVSNFGR.L	43.54	59.25	0.73	1.36
Q68FD5_C	Cltc	Clathrin he	R.NLQNLLILTAIK#.A	319.40	95.42	3.35	0.30
Q68FD5_C	Cltc	Clathrin he	K.NNRPSEGPLQTR.L	10.40	44.88	0.23	4.32
Q68FD5_C	Cltc	Clathrin he	R.RPISADSAIM*NPASK.V	7.80	10.29	0.76	1.32
Q68FD5_C	Cltc	Clathrin he	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	7.77	12.96	0.60	1.67
Q68FD5_C	Cltc	Clathrin he	K.SVNESLNNLFITEEDYQALR.T	38.72	43.10	0.90	1.11
Q68FD5_C	Cltc	Clathrin he	K.TLQIFNIEM*K#.S	92.60	24.92	3.72	0.27
Q68FD5_C	Cltc	Clathrin he	K.TLQIFNIEMK#.S	51.05	13.83	3.69	0.27
Q68FD5_C	Cltc	Clathrin he	R.TSIDAYDNFDNISLAQR.L	34.32	39.40	0.87	1.15
Q68FD5_C	Cltc	Clathrin he	K.VANVELYYK#.A	204.03	53.34	3.83	0.26
Q68FD5_C	Cltc	Clathrin he	R.VVGAM*QLYSVDR.K	8.83	12.61	0.70	1.43
Q68FD5_C	Cltc	Clathrin he	R.VVGAMQLYSVDR.K	9.57	14.88	0.64	1.56
Q68FD5_C	Cltc	Clathrin he	K.WISLNTVALVTDNAVYHWSM*EGESQPVK#.M	12.40	2.61	4.75	0.21
Q68FD5_C	Cltc	Clathrin he	K.YIEIYVQK#.V	72.57	24.02	3.02	0.33
Q9DBC3_C	Cmtr1	Cap-specifi	R.NTESDVNLVVPLM*VIK#.G	7.14	2.88	2.48	0.40
Q9DBC3_C	Cmtr1	Cap-specifi	R.EYLFSVNIK#.L	13.61	3.36	4.05	0.25
Q9D1A2_C	Cndp2	Cytosolic n	R.EGGSIPVTLTFQEATGK#.N	16.07	5.31	3.03	0.33
Q9D1A2_C	Cndp2	Cytosolic n	R.LNYIEGTK#.M	18.35	6.94	2.64	0.38
Q9D1A2_C	Cndp2	Cytosolic n	K.NVM*LLPVGSADDGAHSQNEK#.L	5.99	1.90	3.15	0.32
Q9D1A2_C	Cndp2	Cytosolic n	K.QK#LPDGSEIPLPPILLGK#.L	14.72	3.83	3.85	0.26
Q08093_C	Cnn2	Calponin-2	K.GLQSGVDIGVK#.Y	120.20	102.40	1.17	0.85
Q08093_C	Cnn2	Calponin-2	K.GPSYGLSAEVK#.N	398.83	242.36	1.65	0.61
Q08093_C	Cnn2	Calponin-2	R.NFDDATM*K#.A	62.02	51.98	1.19	0.84
Q08093_C	Cnn2	Calponin-2	R.SM*QNWHQLENLSNFIK#.A	67.78	42.97	1.58	0.63
Q08093_C	Cnn2	Calponin-2	R.SMQNWHQLENLSNFIK#.A	37.52	29.03	1.29	0.77
Q08093_C	Cnn2	Calponin-2	R.SMQNWHQLENLSNFIK.A	6.02	3.42	1.76	0.57
Q08093_C	Cnn2	Calponin-2	R.SWIEGLTGLSIGPDFQK#.G	121.35	96.38	1.26	0.79
Q08093_C	Cnn2	Calponin-2	R.SWIEGLTGLSIGPDFQK#.G	13.87	13.48	1.03	0.97
Q08093_C	Cnn2	Calponin-2	K.YDPQKEAELR.S	6.31	28.65	0.22	4.54
Q08093_C	Cnn2	Calponin-2	K.GLQSGVDIGVK#.Y	36.25	35.62	1.02	0.98
Q08093_C	Cnn2	Calponin-2	R.SM*QNWHQLENLSNFIK#.A	47.40	47.87	0.99	1.01
Q08093_C	Cnn2	Calponin-2	R.SWIEGLTGLSIGPDFQK#.G	70.58	63.02	1.12	0.89
Q08093_C	Cnn2	Calponin-2	K.GPSYGLSAEVK#.N	20.19	12.10	1.67	0.60
Q08093_C	Cnn2	Calponin-2	K.GPSYGLSAEVK#.N	18.79	13.14	1.43	0.70
Q9DAW9_	Cnn3	Calponin-3	K.AGQSVIGLQM*GTNK#.C	110.81	48.51	2.28	0.44
Q9DAW9_	Cnn3	Calponin-3	K.AGQSVIGLQMGTNK#.C	56.76	28.01	2.03	0.49
Q9DAW9_	Cnn3	Calponin-3	R.EYQYGDDQGIDY.-	47.14	47.14	1.00	1.00
Q9DAW9_	Cnn3	Calponin-3	K.GASQAGM*LAPGTR.R	32.28	64.67	0.50	2.00
Q9DAW9_	Cnn3	Calponin-3	K.GFHTTIDIGVK#.Y	73.96	27.64	2.68	0.37
Q9DAW9_	Cnn3	Calponin-3	K.GM*SVYGLGR.Q	23.91	37.05	0.65	1.55
Q9DAW9_	Cnn3	Calponin-3	K.GMSVYGLGR.Q	11.98	13.09	0.92	1.09
Q9DAW9_	Cnn3	Calponin-3	K.K#VNESSLNWPQLENIGNFIK#.A	29.23	12.33	2.37	0.42
Q9DAW9_	Cnn3	Calponin-3	K.LTLQPVDNSTISLQM*GTNK#.V	22.77	9.55	2.38	0.42
Q9DAW9_	Cnn3	Calponin-3	K.LTLQPVDNSTISLQMGTNK#.V	22.08	8.42	2.62	0.38
Q9DAW9_	Cnn3	Calponin-3	K.M*QTDKPFDQTTISLQM*GTNK.G	35.85	16.47	2.18	0.46
Q9DAW9_	Cnn3	Calponin-3	K.MQTDK#PFDQTTISLQM*GTNK#.G	13.66	6.82	2.00	0.50
Q9DAW9_	Cnn3	Calponin-3	K.M*QTDK#PFDQTTISLQMGTNK#.G	21.52	10.28	2.09	0.48
Q9DAW9_	Cnn3	Calponin-3	K.MQTDK#PFDQTTISLQMGTNK#.G	11.80	5.97	1.98	0.51
Q9DAW9_	Cnn3	Calponin-3	K.VNESSLNWPQLENIGNFIK#.A	52.73	21.60	2.44	0.41
Q9DAW9_	Cnn3	Calponin-3	K.YDQQAEEDLR.N	11.13	31.08	0.36	2.79
Q9DAW9_	Cnn3	Calponin-3	K.AGQSVIGLQM*GTNK#.C	26.39	10.20	2.59	0.39
Q9DAW9_	Cnn3	Calponin-3	K.AGQSVIGLQMGTNK#.C	122.52	4.66	26.31	0.04
Q9DAW9_	Cnn3	Calponin-3	K.GASQAGM*LAPGTR.R	7.50	13.59	0.55	1.81
Q9DAW9_	Cnn3	Calponin-3	K.K#VNESSLNWPQLENIGNFIK#.A	8.73	4.64	1.88	0.53
Q9DAW9_	Cnn3	Calponin-3	K.M*QTDKPFDQTTISLQM*GTNK.G	12.19	7.75	1.57	0.64
Q9DAW9_	Cnn3	Calponin-3	K.VNESSLNWPQLENIGNFIK#.A	10.33	5.37	1.93	0.52
Q9DAW9_	Cnn3	Calponin-3	K.VNESSLNWPQLENIGNFIK#.A	21.46	12.53	1.71	0.58
Q9DAW9_	Cnn3	Calponin-3	K.YDQQAEEDLR.N	2.23	3.80	0.59	1.70
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.AVEGLLDATSGADADLLLR.Y	7.17	15.52	0.46	2.17
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.DAIAALGLLQK#.A	65.79	43.35	1.52	0.66
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.DVPPSINTTNIDTLLVATDQTER.I	9.83	14.18	0.69	1.44
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.EIDDEANSYFQR.I	10.35	20.36	0.51	1.97
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.EPLLM*SISTNLK#.N	8.16	2.72	3.00	0.33
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.GAFGVGQEQIDAFLK#.T	30.97	13.03	2.38	0.42
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.GQQELLYVVPFVAK#.V	40.80	21.93	1.86	0.54
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.HSGEATNTVTK#.I	5.60	2.55	2.20	0.46
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.IAFIFNNLSQSNM*TQK#.V	9.14	5.54	1.65	0.61
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.IAFIFNNLSQSNMTQK#.V	4.85	2.75	1.76	0.57
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.ILTNFTGVM*PPQFK#.K	21.55	13.22	1.63	0.61
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.INLLNK#.V	40.65	16.91	2.40	0.42
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.LAEVGQYEQVK#.Q	71.15	34.50	2.06	0.48
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.LGTSGLNQPTFQQSK#.M	15.65	8.48	1.84	0.54
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.LIALLVK#.H	21.16	8.99	2.35	0.42
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.LPDPFTPNLK#.V	28.61	14.48	1.98	0.51
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.M*QGSITTPGSIALAQAQAQAQVPAK#.A	32.66	18.78	1.74	0.57
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.MQGSITTPGSIALAQAQAQAQVPAK#.A	9.98	5.68	1.76	0.57
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.M*VLNETYR.N	10.18	19.30	0.53	1.90
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.M*YYFGIAALDR.F	16.06	8.31	1.93	0.52
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.NLDEQLSAPK#.K	41.50	25.31	1.64	0.61
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.NLILSAFPR.N	12.30	31.41	0.39	2.55
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.NVPGFLPTNDLSQPTGFLAQPM*K#.Q	43.94	30.57	1.44	0.70
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.QAWATDDVAQIYDK#.C	5.87	3.05	1.93	0.52
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.SLDLIESLLR.L	13.23	39.89	0.33	3.01
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.SLK#PAPHLFAQLSK#.V	11.41	7.55	1.51	0.66
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.SLLLEAYVK#.G	16.11	10.18	1.58	0.63
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.SNYEAM*IDR.A	6.11	12.27	0.50	2.01
Q6ZQ08_C	Cnot1	CCR4-NOT t	R.SPVTFLSDLR.S	15.02	38.00	0.40	2.53
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.VLLTSDK#.A	65.63	23.76	2.76	0.36
Q6ZQ08_C	Cnot1	CCR4-NOT t	K.YNVEAVELLIR.N	4.53	11.16	0.41	2.46
Q8BH15_C	Cnot10	CCR4-NOT t	K.IILNTAVAEFFK.N	7.25	9.51	0.76	1.31
Q8BH15_C	Cnot10	CCR4-NOT t	K.IILNTAVAEFFK#.N	27.45	18.76	1.46	0.68
Q8BH15_C	Cnot10	CCR4-NOT t	K.SVM*NTAGNSAPSLFLK#.S	4.78	2.84	1.68	0.59
Q8BH15_C	Cnot10	CCR4-NOT t	K.AESAALIEAAK#.S	20.02	10.76	1.86	0.54
Q8BH15_C	Cnot10	CCR4-NOT t	K.IILNTAVAEFFK#.N	34.54	18.52	1.86	0.54
Q8BH15_C	Cnot10	CCR4-NOT t	R.ISDAITHLNPENVTDVSLGISSNEQDQGSDK#GENEAM*ESSGK#.R	3.20	2.39	1.34	0.75
Q9CWN7_	Cnot11	CCR4-NOT t	R.GGQEPDRPPLSGFLPPITPPEK.F	2.75	6.94	0.40	2.52
Q9CWN7_	Cnot11	CCR4-NOT t	K.TLDTGETPSETK#.I	16.75	8.37	2.00	0.50
Q8C5L3_C	Cnot2	CCR4-NOT t	R.AAETDPGM*VHLALGSDLTTLGLNLNSPENLYPK#.F	8.53	5.45	1.56	0.64
Q8C5L3_C	Cnot2	CCR4-NOT t	R.APYVGM*VTKPANEQSQDFSIHNEDFPALPGSSYKDPTSSNDDSK.S	6.12	4.63	1.32	0.76
Q8C5L3_C	Cnot2	CCR4-NOT t	R.EGSGNPTPLINPLAGR.A	7.55	22.63	0.33	3.00

Q8C5L3_C	Cnot2	CCR4-NOT t	R.GM*SNNTPQLNR.S	3.48	15.49	0.22	4.45
Q8C5L3_C	Cnot2	CCR4-NOT t	R.TNSM*SSSGLGSPNR.S	2.69	9.63	0.28	3.58
Q8C5L3_C	Cnot2	CCR4-NOT t	R.EGSGNPTPLINPLAGR.A	4.08	7.02	0.58	1.72
Q8K0V4_C	Cnot3	CCR4-NOT t	K.AAGTLLNGPPQFSTTPEIK#.A	4.19	3.28	1.28	0.78
Q8K0V4_C	Cnot3	CCR4-NOT t	K.TWVASNEIK#.D	10.73	7.44	1.44	0.69
Q60809_C	Cnot7	CCR4-NOT t	R.LFFPVIYDVK#.Y	18.59	10.29	1.81	0.55
Q60809_C	Cnot7	CCR4-NOT t	R.LFFPVIYDVK#.Y	14.78	10.38	1.42	0.70
Q60809_C	Cnot7	CCR4-NOT t	R.LFFPVIYDVK#.Y	31.68	17.55	1.81	0.55
Q9D8X5_C	Cnot8	CCR4-NOT t	R.LYGLGTGVAQK.Q	5.66	8.76	0.65	1.55
Q9QXT0_C	Cnpy2	Protein ca	R.ALVDELEWEIAR.V	15.74	15.76	1.00	1.00
Q9QXT0_C	Cnpy2	Protein ca	R.INPDGSQSVVEVPYAR.S	11.34	12.52	0.91	1.10
Q9QXT0_C	Cnpy2	Protein ca	R.NGESSELDLQGIR.I	3.58	4.00	0.89	1.12
P12960_C	Cntn1	Contactin-	K.TDPPIIEGNMESAK#.A	9.66	3.93	2.46	0.41
Q9DBL7_C	Coasy	Bifunctiona	R.ILLTNIQTK#.S	22.09	8.54	2.59	0.39
Q9DBL7_C	Coasy	Bifunctiona	K.ILTDIVWPVIAK#.L	19.63	7.13	2.75	0.36
Q9Z160_C	Cog1	Conserved	K.VK#LDDLLAYLPSSDTPLLK#.D	16.72	7.66	2.18	0.46
Q921L5_C	Cog2	Conserved	R.LQEWLPDLLETVK#.Q	11.10	4.09	2.71	0.37
Q8R1U1_C	Cog4	Conserved	K.LFSQGIGGEQAQAK#.F	8.50	7.43	1.14	0.87
Q8C0L8_C	Cog5	Conserved	R.LLEQGVETQNPTQVGTALQVFHNLGTLK#.E	6.42	1.76	3.65	0.27
Q3UM29_C	Cog7	Conserved	K.VVELVDAVYGPYK#PFQLK#.Y	11.78	6.87	1.71	0.58
Q5SU73_C	Coil	Coilin OS=	R.VVTDLISLIR.Q	2.62	13.84	0.19	5.28
Q8K297_G	Colgalt1	Procollage	R.AFSVEPLLIYPTHYTGDDGYVSDTETSVVWNNEQVK#.T	5.86	2.03	2.88	0.35
Q8K297_G	Colgalt1	Procollage	R.EGLDWDLIYVGR.K	10.90	6.54	1.67	0.60
Q8K297_G	Colgalt1	Procollage	R.FEIFFK#.R	22.51	7.11	3.17	0.32
Q8K297_G	Colgalt1	Procollage	R.NAAPALPATLGALEQLR.H	11.66	10.97	1.06	0.94
Q8K297_G	Colgalt1	Procollage	R.TPAYIPIR.K	8.74	13.63	0.64	1.56
Q8K297_G	Colgalt1	Procollage	R.WSPESPLQAPR.V	6.59	7.49	0.88	1.14
Q8K4M5_C	Commd1	COMM do	K.K#QGGITSEQAAVISK#.F	4.23	3.74	1.13	0.88
Q8K4M5_C	Commd1	COMM do	K.SIASADM*DFNQLEAFLTAQTK#.K	30.11	16.55	1.82	0.55
Q8JZY2_CO	Commd10	COMM do	K.AVPLINAIDTGR.F	7.21	18.72	0.39	2.59
Q8JZY2_CO	Commd10	COMM do	K.DK#AEAFASAWSAM*GQETVEK#.F	10.58	7.46	1.42	0.70
Q8JZY2_CO	Commd10	COMM do	K.DK#AEAFASAWSAMGQETVEK#.F	2.62	1.72	1.52	0.66
Q8JZY2_CO	Commd10	COMM do	K.LQSPQAVLQLGVSK#.E	21.27	12.90	1.65	0.61
Q8BXC6_C	Commd2	COMM do	R.IAVEFLR.R	8.09	21.38	0.38	2.64
Q8BXC6_C	Commd2	COMM do	K.LNVSSDTIQHGVEGLTYLLTESSK#.L	14.86	13.77	1.08	0.93
Q8BXC6_C	Commd2	COMM do	R.TILNELAPR.L	18.50	38.51	0.48	2.08
Q63829_C	Commd3	COMM do	R.AAFQSLLDAR.A	8.60	22.60	0.38	2.63
Q63829_C	Commd3	COMM do	K.NSLETLLGSIGR.S	14.01	29.40	0.48	2.10
Q8R395_C	Commd5	COMM do	R.SLQPSVLMQLK.L	11.62	9.95	1.17	0.86
Q8R395_C	Commd5	COMM do	R.VDVAISTSAQSR.S	2.04	5.87	0.35	2.88
Q8R395_C	Commd5	COMM do	R.VSFLGSQPSAEVTAVAQLLK#.D	8.49	7.60	1.12	0.90
Q3V4B5_C	Commd6	COMM do	K.SEVTGQLIDFQWK#.L	22.43	14.57	1.54	0.65
Q3V4B5_C	Commd6	COMM do	K.SIEM*TIPQFQNFYK#.Q	14.92	9.28	1.61	0.62
Q8BG94_C	Commd7	COMM do	R.FGVTSGSSELEK#.V	12.44	7.42	1.68	0.60
Q8BG94_C	Commd7	COMM do	R.FLAQLSEFATSNQISLGPLK#.S	3.12	1.97	1.59	0.63
Q8BG94_C	Commd7	COMM do	R.FLAQLSEFATSNQISLGPLK#.S	21.78	9.74	2.24	0.45
Q8BG94_C	Commd7	COMM do	R.TDLQTLGLSEEK#.A	35.40	22.11	1.60	0.62
Q8BG94_C	Commd7	COMM do	K.VGSIFLQLK#.L	21.76	27.36	0.80	1.26
Q8K2Q0_C	Commd9	COMM do	R.AEAQANQISLPR.L	2.96	9.08	0.33	3.06
Q8K2Q0_C	Commd9	COMM do	K.ETLDTM*LDGLGR.I	3.49	6.88	0.51	1.97
Q8CIE6_CO	Copa	Coatomer s	R.ASNLENSTYDLYTIPK#.D	13.98	12.99	1.08	0.93
Q8CIE6_CO	Copa	Coatomer s	R.DADSITLFDVQQK.R	23.75	19.57	1.21	0.82
Q8CIE6_CO	Copa	Coatomer s	K.DADSQNPDAPEGK.R	8.35	5.31	1.57	0.64
Q8CIE6_CO	Copa	Coatomer s	R.GITGVDLFGTTDAVVK#.H	30.98	22.94	1.35	0.74
Q8CIE6_CO	Copa	Coatomer s	R.GVNWAAFHPTMPLIVSGADDR.Q	2.27	6.72	0.34	2.96
Q8CIE6_CO	Copa	Coatomer s	R.LLELGPKPEVAQQTR.K	7.47	28.88	0.26	3.87
Q8CIE6_CO	Copa	Coatomer s	R.LLHDQVGVIQFGPYK#.Q	23.45	14.18	1.65	0.60
Q8CIE6_CO	Copa	Coatomer s	K.LVGQSIIAYLQK#.K	35.34	22.66	1.56	0.64
Q8CIE6_CO	Copa	Coatomer s	K.NLSPGAVESDVR.G	7.66	27.87	0.27	3.64
Q8CIE6_CO	Copa	Coatomer s	K.QLFLQTYAR.G	7.38	12.00	0.62	1.63
Q8CIE6_CO	Copa	Coatomer s	K.SLAYLSAATHGLDEEAESLK#ETFDPEK#ETIPDIDPNAK#.L	5.88	4.04	1.46	0.69
Q8CIE6_CO	Copa	Coatomer s	R.SSGLTAVWVAR.N	4.95	15.85	0.31	3.20
Q8CIE6_CO	Copa	Coatomer s	R.TALNLFFK#.L	24.02	16.72	1.44	0.70
Q8CIE6_CO	Copa	Coatomer s	R.VLTIDPTEFK#.F	37.25	27.84	1.34	0.75
Q8CIE6_CO	Copa	Coatomer s	R.ASNLENSTYDLYTIPK#.D	78.05	45.10	1.73	0.58
Q8CIE6_CO	Copa	Coatomer s	R.DADSITLFDVQQK#.R	104.29	55.63	1.87	0.53
Q8CIE6_CO	Copa	Coatomer s	K.DADSQNPDAPEGK#.R	31.07	25.37	1.22	0.82
Q8CIE6_CO	Copa	Coatomer s	K.DVAVM*QLR.S	10.11	42.91	0.24	4.25
Q8CIE6_CO	Copa	Coatomer s	K.ETIPDIDPNAK#.L	17.00	10.62	1.60	0.62
Q8CIE6_CO	Copa	Coatomer s	R.FAVLDR.M	26.03	66.27	0.39	2.55
Q8CIE6_CO	Copa	Coatomer s	K.GFFEGSIASK#.G	100.14	57.14	1.75	0.57
Q8CIE6_CO	Copa	Coatomer s	R.GITGVDLFGTTDAVVK#.H	186.16	112.26	1.66	0.60
Q8CIE6_CO	Copa	Coatomer s	K.GLSFHPK#.R	56.22	22.78	2.47	0.41
Q8CIE6_CO	Copa	Coatomer s	R.LLELGPKPEVAQQTR.K	35.69	93.91	0.38	2.63
Q8CIE6_CO	Copa	Coatomer s	R.LLHDQVGVIQFGPYK#.Q	124.82	82.02	1.52	0.66
Q8CIE6_CO	Copa	Coatomer s	K.LVGQSIIAYLQK#.K	203.56	120.34	1.69	0.59
Q8CIE6_CO	Copa	Coatomer s	K.NLK#NEITK#.K	65.83	25.01	2.63	0.38
Q8CIE6_CO	Copa	Coatomer s	K.NLSPGAVESDVR.G	27.51	82.77	0.33	3.01
Q8CIE6_CO	Copa	Coatomer s	R.QLDFNSSK#.D	45.77	35.22	1.30	0.77
Q8CIE6_CO	Copa	Coatomer s	K.QLFLQTYAR.G	17.17	39.95	0.43	2.33
Q8CIE6_CO	Copa	Coatomer s	K.QQPLFVSGGDDYK#.I	41.21	24.71	1.67	0.60
Q8CIE6_CO	Copa	Coatomer s	K.QQPLFVSGGDDYK#IK#.V	26.87	12.74	2.11	0.47
Q8CIE6_CO	Copa	Coatomer s	R.RLLELGPKPEVAQQTR.K	3.71	32.27	0.11	8.71
Q8CIE6_CO	Copa	Coatomer s	K.SGAWDESGVFIYTTSNHIK#.Y	59.80	36.01	1.66	0.60
Q8CIE6_CO	Copa	Coatomer s	K.SLAYLSAATHGLDEEAESLKETFDPEKETIPDIDPNAK.L	40.57	28.59	1.42	0.70
Q8CIE6_CO	Copa	Coatomer s	R.SSGLTAVWVAR.N	23.65	55.51	0.43	2.35
Q8CIE6_CO	Copa	Coatomer s	R.TALNLFFK#.L	123.93	74.50	1.66	0.60
Q8CIE6_CO	Copa	Coatomer s	R.TGVQTFR.R	18.12	70.15	0.26	3.87
Q8CIE6_CO	Copa	Coatomer s	R.TLDLPIYVTR.V	53.52	145.83	0.37	2.72
Q8CIE6_CO	Copa	Coatomer s	R.VLTIDPTEFK#.F	222.57	139.38	1.60	0.63
Q8CIE6_CO	Copa	Coatomer s	R.VTTVTEIGKDVIGLR.I	46.48	127.52	0.36	2.74
Q8CIE6_CO	Copa	Coatomer s	R.VWDISGLR.K	17.91	48.17	0.37	2.69
Q8CIE6_CO	Copa	Coatomer s	R.VWNWQSR.T	9.06	24.25	0.37	2.68
Q9JIF7_CO	Copb1	Coatomer s	K.EAGELK#PEEEITVGPVQK#.L	24.79	12.36	2.01	0.50
Q9JIF7_CO	Copb1	Coatomer s	K.LVEKPSPLTLAPHDFANIK.A	8.87	5.61	1.58	0.63
Q9JIF7_CO	Copb1	Coatomer s	R.NFEHLIPDAPELIHDFLVNEK#.D	7.83	2.29	3.42	0.29
Q9JIF7_CO	Copb1	Coatomer s	R.NVEELVIVLK#.K	9.64	4.28	2.25	0.44
Q9JIF7_CO	Copb1	Coatomer s	K.YEAAGTLVTLSSAPTAIK#.A	16.65	6.50	2.56	0.39
Q9JIF7_CO	Copb1	Coatomer s	K.LVEK#PSPLTLAPHDFANIK#.A	18.34	14.46	1.27	0.79
Q9JIF7_CO	Copb1	Coatomer s	R.QM*WAEFEWENK#.V	5.25	3.90	1.35	0.74
Q9JIF7_CO	Copb1	Coatomer s	K.EAGELK#PEEEITVGPVQK#.L	86.62	47.63	1.82	0.55
Q9JIF7_CO	Copb1	Coatomer s	K.LIVLDR.L	14.19	26.87	0.53	1.89
Q9JIF7_CO	Copb1	Coatomer s	K.LVEK#PSPLTLAPHDFANIK#.A	23.68	15.96	1.48	0.67

Q9JIF7_CO	Copb1	Coatomer s	R.NFEHLIPDAPELIHDFLVNEK#.D	56.99	44.89	1.27	0.79
Q9JIF7_CO	Copb1	Coatomer s	R.NVEELVIVLK#.K	23.04	15.43	1.49	0.67
Q9JIF7_CO	Copb1	Coatomer s	R.NVTVQPDDPISFM*QLTAK#.N	7.82	4.01	1.95	0.51
Q9JIF7_CO	Copb1	Coatomer s	R.NVTVQPDDPISFMQLTAK#.N	11.09	8.19	1.35	0.74
Q9JIF7_CO	Copb1	Coatomer s	R.QSLSQM*LSAK#.L	36.21	22.36	1.62	0.62
Q9JIF7_CO	Copb1	Coatomer s	R.VLQDLVM*DILR.V	11.31	21.74	0.52	1.92
Q9JIF7_CO	Copb1	Coatomer s	R.VLQDLVMDILR.V	14.69	22.84	0.64	1.55
Q9JIF7_CO	Copb1	Coatomer s	R.VLSTPDLEVR.K	22.73	44.85	0.51	1.97
Q9JIF7_CO	Copb1	Coatomer s	K.YEAAGTLVTLSSAPTAIK#.A	42.61	24.27	1.76	0.57
Q9JIF7_CO	Copb1	Coatomer s	R.YVALVQEK#.K	54.90	28.31	1.94	0.52
Q9JIF7_CO	Copb1	Coatomer s	K.EAELLEPLM*PAIR.A	3.91	11.01	0.36	2.82
Q9JIF7_CO	Copb1	Coatomer s	K.EAGELK#PEEEITVGPVQK#.L	177.79	107.66	1.65	0.61
Q9JIF7_CO	Copb1	Coatomer s	K.EDIQSVM*TEVR.R	3.88	9.61	0.40	2.48
Q9JIF7_CO	Copb1	Coatomer s	K.KPITDDDVDR.I	7.03	16.15	0.44	2.30
Q9JIF7_CO	Copb1	Coatomer s	K.LEEEK#LSQK#.K	16.86	9.34	1.81	0.55
Q9JIF7_CO	Copb1	Coatomer s	K.LIVLDR.L	23.80	52.65	0.45	2.21
Q9JIF7_CO	Copb1	Coatomer s	K.LKEAELLEPLM*PAIR.A	5.55	28.55	0.19	5.14
Q9JIF7_CO	Copb1	Coatomer s	K.LVEK#PSPLTLAPHDFANIK#.A	89.88	56.74	1.58	0.63
Q9JIF7_CO	Copb1	Coatomer s	K.LVEKPSPLTLAPHDFANIK.A	31.84	18.47	1.72	0.58
Q9JIF7_CO	Copb1	Coatomer s	K.MLEVFHAIK#.S	18.15	12.85	1.41	0.71
Q9JIF7_CO	Copb1	Coatomer s	R.NVEELVIVLK#.K	21.63	13.54	1.60	0.63
Q9JIF7_CO	Copb1	Coatomer s	R.NVTVQPDDPISFM*QLTAK#.N	12.96	9.14	1.42	0.70
Q9JIF7_CO	Copb1	Coatomer s	R.NVTVQPDDPISFMQLTAK#.N	14.08	10.79	1.30	0.77
Q9JIF7_CO	Copb1	Coatomer s	R.QSLSQM*LSAK#.L	56.71	29.62	1.91	0.52
Q9JIF7_CO	Copb1	Coatomer s	R.SLGEIPIVESEIK#.K	30.15	17.38	1.74	0.58
Q9JIF7_CO	Copb1	Coatomer s	K.VASTENGIIFGNIVYDVSGAASDR.N	4.14	11.03	0.38	2.67
Q9JIF7_CO	Copb1	Coatomer s	R.VLQDLVM*DILR.V	18.55	47.71	0.39	2.57
Q9JIF7_CO	Copb1	Coatomer s	R.VLQDLVMDILR.V	12.48	27.06	0.46	2.17
Q9JIF7_CO	Copb1	Coatomer s	R.VLSTPDLEVR.K	43.88	94.71	0.46	2.16
Q9JIF7_CO	Copb1	Coatomer s	K.YEAAGTLVTLSSAPTAIK#.A	81.08	47.51	1.71	0.59
Q9JIF7_CO	Copb1	Coatomer s	R.YVALVQEK#.K	94.64	59.81	1.58	0.63
O55029_C	Copb2	Coatomer s	K.AAESLADPTEYENLFPGLK#.E	10.54	8.49	1.24	0.81
O55029_C	Copb2	Coatomer s	K.AAESLADPTEYENLFPGLK#.E	45.70	31.52	1.45	0.69
O55029_C	Copb2	Coatomer s	K.DNNQFASASLDR.T	13.92	37.09	0.38	2.66
O55029_C	Copb2	Coatomer s	K.EAFVVEEWVK#.E	37.69	26.67	1.41	0.71
O55029_C	Copb2	Coatomer s	R.FELALQLGELK#.I	13.39	8.19	1.63	0.61
O55029_C	Copb2	Coatomer s	R.GSNNVALGYDEGSIIVK#.L	52.59	39.36	1.34	0.75
O55029_C	Copb2	Coatomer s	K.HSEVQQANLK#.A	83.18	52.01	1.60	0.63
O55029_C	Copb2	Coatomer s	K.IAYQLAVEAESEQK#.W	17.66	10.87	1.62	0.62
O55029_C	Copb2	Coatomer s	K.IWDYQNK#.T	25.25	14.80	1.71	0.59
O55029_C	Copb2	Coatomer s	R.LPEAAFLAR.T	16.64	48.38	0.34	2.91
O55029_C	Copb2	Coatomer s	K.NNVAFMSYFLQGK#.L	11.26	8.60	1.31	0.76
O55029_C	Copb2	Coatomer s	K.QLAELAISK#.C	30.92	16.27	1.90	0.53
O55029_C	Copb2	Coatomer s	K.SFGSAQEFAWAHDSSEYAIR.E	9.43	32.09	0.29	3.40
O55029_C	Copb2	Coatomer s	K.SFKPDFGAESIYGGFLLGVR.S	10.90	27.02	0.40	2.48
O55029_C	Copb2	Coatomer s	R.TMYLLGYIPK#.D	21.15	13.75	1.54	0.65
O55029_C	Copb2	Coatomer s	R.TYLPSQVSR.V	12.21	46.49	0.26	3.81
O55029_C	Copb2	Coatomer s	R.VFNYNTLER.V	22.89	59.50	0.38	2.60
O55029_C	Copb2	Coatomer s	K.AM*GDTEIKDGER.L	1.40	11.94	0.12	8.55
O55029_C	Copb2	Coatomer s	K.DNNQFASASLDR.T	28.89	73.02	0.40	2.53
O55029_C	Copb2	Coatomer s	K.EAFVVEEWVK#.E	75.20	49.88	1.51	0.66
O55029_C	Copb2	Coatomer s	R.GSNNVALGYDEGSIIVK#.L	97.81	92.34	1.06	0.94
O55029_C	Copb2	Coatomer s	K.HSEVQQANLK#.A	202.73	141.96	1.43	0.70
O55029_C	Copb2	Coatomer s	K.IAYQLAVEAESEQK#.W	40.17	22.97	1.75	0.57
O55029_C	Copb2	Coatomer s	K.IWDYQNK#.T	60.85	38.45	1.58	0.63
O55029_C	Copb2	Coatomer s	R.KNWVVTGADDM*QIR.V	7.71	19.67	0.39	2.55
O55029_C	Copb2	Coatomer s	R.LESTLNYGM*ER.V	19.32	52.48	0.37	2.72
O55029_C	Copb2	Coatomer s	R.LESTLNYGMER.V	5.39	13.85	0.39	2.57
O55029_C	Copb2	Coatomer s	R.LPEAAFLAR.T	36.63	81.79	0.45	2.23
O55029_C	Copb2	Coatomer s	K.NNVAFM*SYFLQGK#.L	10.75	7.79	1.38	0.72
O55029_C	Copb2	Coatomer s	K.NNVAFMSYFLQGK#.L	14.17	9.72	1.46	0.69
O55029_C	Copb2	Coatomer s	K.QLAELAISK#.C	49.52	30.49	1.62	0.62
O55029_C	Copb2	Coatomer s	R.SVNGLAFYDWENTELIR.R	3.08	10.72	0.29	3.48
O55029_C	Copb2	Coatomer s	R.TM*YLLGYIPK#.D	30.35	21.37	1.42	0.70
O55029_C	Copb2	Coatomer s	R.TMYLLGYIPK#.D	34.05	24.07	1.41	0.71
O55029_C	Copb2	Coatomer s	R.VAHFLEK#.Q	30.61	23.26	1.32	0.76
O55029_C	Copb2	Coatomer s	R.VFNYNTLER.V	37.59	106.53	0.35	2.83
O89079_C	Cope	Coatomer s	R.DSIVLELDR.E	6.76	18.64	0.36	2.76
O89079_C	Cope	Coatomer s	R.KYGVVLDEIKPSSAPELQAVR.M	11.26	35.03	0.32	3.11
O89079_C	Cope	Coatomer s	K.LQEAYYIFQELADK#.C	13.27	14.97	0.89	1.13
O89079_C	Cope	Coatomer s	K.LQEAYYIFQELADK#.C	12.36	6.52	1.90	0.53
O89079_C	Cope	Coatomer s	R.M*FAEYLASENQR.D	10.45	31.46	0.33	3.01
O89079_C	Cope	Coatomer s	K.YGVVLDEIKPSSAPELQAVR.M	1.51	5.96	0.25	3.95
Q9QZE5_C	Copg1	Coatomer s	K.ALQQYTLEPSEK#PFDLK#.S	21.85	15.30	1.43	0.70
Q9QZE5_C	Copg1	Coatomer s	R.SIATLAITTLLK.T	16.57	16.98	0.98	1.02
Q9QZE5_C	Copg1	Coatomer s	K.SSPEPVALTESETEYVIR.C	2.57	7.96	0.32	3.10
Q9QZE5_C	Copg1	Coatomer s	K.TLEEAVGNIVK#.F	21.35	15.65	1.36	0.73
Q9QZE5_C	Copg1	Coatomer s	K.ALQQYTLEPSEK#PFDLK#.S	55.50	37.86	1.47	0.68
Q9QZE5_C	Copg1	Coatomer s	R.ATFYLNVLEQK#.Q	35.76	21.97	1.63	0.61
Q9QZE5_C	Copg1	Coatomer s	R.ILHLLGQEGPK#.T	49.48	30.94	1.60	0.63
Q9QZE5_C	Copg1	Coatomer s	K.ILYLINQGEHLGTTEATEAFFAM*TK#.L	16.56	10.21	1.62	0.62
Q9QZE5_C	Copg1	Coatomer s	K.ILYLINQGEHLGTTEATEAFFAM*TK#.L	10.58	4.49	2.36	0.42
Q9QZE5_C	Copg1	Coatomer s	K.ILYLINQGEHLGTTEATEAFFAMTK#.L	18.42	14.45	1.27	0.78
Q9QZE5_C	Copg1	Coatomer s	K.K#DEESGGGSNPLQHLEK#.S	10.61	7.22	1.47	0.68
Q9QZE5_C	Copg1	Coatomer s	R.LLLLDTVTM*QVTAR.S	6.64	9.66	0.69	1.46
Q9QZE5_C	Copg1	Coatomer s	K.NTHTLLLAGVFR.G	6.24	20.99	0.30	3.37
Q9QZE5_C	Copg1	Coatomer s	K.SAVLQEAR.V	12.99	30.39	0.43	2.34
Q9QZE5_C	Copg1	Coatomer s	R.SIATLAITTLLK#.T	208.41	136.60	1.53	0.66
Q9QZE5_C	Copg1	Coatomer s	K.SSPEPVALTESETEYVIR.C	7.72	18.88	0.41	2.45
Q9QZE5_C	Copg1	Coatomer s	K.TLEEAVGNIVK#.F	76.78	39.90	1.92	0.52
Q9QZE5_C	Copg1	Coatomer s	R.VFNETPINPR.K	12.07	41.47	0.29	3.44
Q9QZE5_C	Copg1	Coatomer s	R.AGAVSALAK.F	112.96	70.00	1.61	0.62
Q9QZE5_C	Copg1	Coatomer s	K.ALQQYTLEPSEK#PFDLK#.S	100.89	65.61	1.54	0.65
Q9QZE5_C	Copg1	Coatomer s	R.ATFYLNVLEQK#.Q	72.26	46.52	1.55	0.64
Q9QZE5_C	Copg1	Coatomer s	K.FGAQNEEM*LPSILVLLKR.C	2.46	4.07	0.60	1.65
Q9QZE5_C	Copg1	Coatomer s	R.ILHLLGQEGPK#.T	87.05	49.98	1.74	0.57
Q9QZE5_C	Copg1	Coatomer s	K.KDEESGGGSNPLQHLEK.S	24.79	17.02	1.46	0.69
Q9QZE5_C	Copg1	Coatomer s	K.LFQSNDPTLR.R	84.70	34.52	2.45	0.41
Q9QZE5_C	Copg1	Coatomer s	R.LLLLDTVTM*QVTAR.S	5.72	21.45	0.27	3.75
Q9QZE5_C	Copg1	Coatomer s	K.NTHTLLLAGVFR.G	6.23	17.42	0.36	2.80
Q9QZE5_C	Copg1	Coatomer s	K.SAVLQEAR.V	21.51	62.75	0.34	2.92
Q9QZE5_C	Copg1	Coatomer s	R.SIATLAITTLLK#.T	187.28	128.78	1.45	0.69
Q9QZE5_C	Copg1	Coatomer s	K.SSPEPVALTESETEYVIR.C	9.17	25.78	0.36	2.81

Q9QZE5_C	Copg1	Coatomer s	K.TLEEAVGNIVK#.F	101.48	61.28	1.66	0.60
Q9QZE5_C	Copg1	Coatomer s	R.VFNETPINPR.K	16.54	64.49	0.26	3.90
Q9QZE5_C	Copg1	Coatomer s	K.VPSVSSSALVSSLHLLK#.C	35.24	17.01	2.07	0.48
Q9QXK3_C	Copg2	Coatomer s	K.SSEPVQLTEAETEYFVR.C	1.36	6.49	0.21	4.77
Q9QXK3_C	Copg2	Coatomer s	K.EM*ATISEDVIIVTSSLTK#.D	12.04	5.50	2.19	0.46
Q9QXK3_C	Copg2	Coatomer s	R.IFNETPINPR.R	4.45	12.42	0.36	2.79
Q9QXK3_C	Copg2	Coatomer s	K.SIPLAM*APVFEQK.S	14.12	13.06	1.08	0.92
Q9QXK3_C	Copg2	Coatomer s	K.SSEPVQLTEAETEYFVR.C	1.97	8.49	0.23	4.31
P61202_C	Cops2	COP9 signa	K.AALSSFQK#.V	53.76	13.02	4.13	0.24
P61202_C	Cops2	COP9 signa	K.AHTDFFEAFK#.N	34.18	6.51	5.25	0.19
P61202_C	Cops2	COP9 signa	K.GTQLLEIYALEIQM*YTAQK#.N	7.56	1.86	4.06	0.25
P61202_C	Cops2	COP9 signa	R.IDQVNQLLELDHQK#.R	7.86	1.96	4.01	0.25
P61202_C	Cops2	COP9 signa	R.IHIPFISK#.E	14.62	17.70	0.83	1.21
P61202_C	Cops2	COP9 signa	K.SINSILDYISTSK#.Q	49.51	9.77	5.07	0.20
P61202_C	Cops2	COP9 signa	K.WTNQLNSLNQAVVSK#.L	20.24	3.48	5.82	0.17
P61202_C	Cops2	COP9 signa	K.YLVLANM*LM*K#.S	9.97	2.76	3.61	0.28
P61202_C	Cops2	COP9 signa	K.YLVLANMLMK#.S	10.12	3.49	2.90	0.34
P61202_C	Cops2	COP9 signa	R.YTALDK#WTNQLNSLNQAVVSK#.L	24.21	2.98	8.13	0.12
P61202_C	Cops2	COP9 signa	K.AALSSFQK#.V	20.67	5.38	3.84	0.26
P61202_C	Cops2	COP9 signa	R.YTALDK#WTNQLNSLNQAVVSK#.L	13.14	3.36	3.91	0.26
P61202_C	Cops2	COP9 signa	K.AALSSFQK#.V	48.09	10.46	4.60	0.22
P61202_C	Cops2	COP9 signa	K.GTQLLEIYALEIQM*YTAQK#.N	5.89	1.94	3.04	0.33
P61202_C	Cops2	COP9 signa	K.SGINPFDSQEAK#PYK#NDPEILAMTNLVSAYQNNDITEFEK#.I	5.11	1.99	2.56	0.39
P61202_C	Cops2	COP9 signa	K.SINSILDYISTSK#.Q	46.81	10.53	4.44	0.23
P61202_C	Cops2	COP9 signa	R.TQVLIK#.L	61.19	38.21	1.60	0.62
P61202_C	Cops2	COP9 signa	R.YTALDK#WTNQLNSLNQAVVSK#.L	30.68	7.95	3.86	0.26
O88543_C	Cops3	COP9 signa	K.AM*DQEITVNPQFVQK#.S	26.95	7.62	3.54	0.28
O88543_C	Cops3	COP9 signa	K.AMDQEITVNPQFVQK#.S	17.59	2.70	6.51	0.15
O88543_C	Cops3	COP9 signa	R.FIKPLSNAYHELAQVYSTNNPSELR.N	5.16	3.54	1.46	0.69
O88543_C	Cops3	COP9 signa	K.SM*GSQEDDSGNK#PSSYS.-	13.69	3.51	3.90	0.26
O88543_C	Cops3	COP9 signa	K.SMGSQEDDSGNK#PSSYS.-	13.24	3.12	4.24	0.24
O88543_C	Cops3	COP9 signa	R.VQLSGPQEAEK#.Y	100.57	20.73	4.85	0.21
O88543_C	Cops3	COP9 signa	K.YTSQIVGR.F	11.41	9.03	1.26	0.79
O88543_C	Cops3	COP9 signa	R.VQLSGPQEAEK#.Y	42.83	8.49	5.04	0.20
O88543_C	Cops3	COP9 signa	K.AM*DQEITVNPQFVQK#.S	12.17	2.21	5.51	0.18
O88543_C	Cops3	COP9 signa	R.VQLSGPQEAEK#.Y	41.64	8.92	4.67	0.21
O88544_C	Cops4	COP9 signa	K.AIQLSGTEQLEALK#.A	127.18	26.43	4.81	0.21
O88544_C	Cops4	COP9 signa	R.ASLLQNESTNEQLQIHYK#.V	12.23	2.50	4.90	0.20
O88544_C	Cops4	COP9 signa	K.ATTADGSSILDR.A	28.11	27.81	1.01	0.99
O88544_C	Cops4	COP9 signa	R.AVIEHNLLSASK#.L	82.43	15.41	5.35	0.19
O88544_C	Cops4	COP9 signa	K.IASQM*ITEGR.M	22.25	24.85	0.90	1.12
O88544_C	Cops4	COP9 signa	K.ISQTAPEWTAQAM*EAQM*AQ.-	14.48	14.48	1.00	1.00
O88544_C	Cops4	COP9 signa	K.ISQTAPEWTAQAMEAQM*AQ.-	3.28	3.28	1.00	1.00
O88544_C	Cops4	COP9 signa	K.ISQTAPEWTAQAMEAQMAQ.-	4.23	4.23	1.00	1.00
O88544_C	Cops4	COP9 signa	R.LYLEDDDPVQAEAYINR.A	12.03	11.81	1.02	0.98
O88544_C	Cops4	COP9 signa	R.NAAQVLVGIPLETGQK#.Q	107.36	25.71	4.18	0.24
O88544_C	Cops4	COP9 signa	R.QDLAQLM*NSSGSHK#.D	4.95	1.77	2.80	0.36
O88544_C	Cops4	COP9 signa	K.QYNVDYK#.L	43.15	10.21	4.23	0.24
O88544_C	Cops4	COP9 signa	R.VISFEEQVASIR.Q	50.23	42.55	1.18	0.85
O88544_C	Cops4	COP9 signa	R.YNELSYK#.T	98.09	21.36	4.59	0.22
O35864_C	Cops5	COP9 signa	K.GYK#PPDEGPSEYQTIPLNK#.I	42.05	11.53	3.65	0.27
O35864_C	Cops5	COP9 signa	K.ISALALLK#.M	74.56	14.93	4.99	0.20
O35864_C	Cops5	COP9 signa	K.LEQSEAQLGR.G	15.62	14.80	1.06	0.95
O35864_C	Cops5	COP9 signa	K.LFNQINVA.-	28.49	28.49	1.00	1.00
O35864_C	Cops5	COP9 signa	K.LLELLWNK#.Y	38.70	7.17	5.40	0.19
O35864_C	Cops5	COP9 signa	K.QQQEILAAK#PWTK#.D	44.07	4.82	9.13	0.11
O35864_C	Cops5	COP9 signa	K.QYYALEVSYFK#.S	24.05	3.73	6.45	0.16
O35864_C	Cops5	COP9 signa	R.SGGNLEVM*GLM*LGK#.V	14.86	10.25	1.45	0.69
O35864_C	Cops5	COP9 signa	R.SGGNLEVMGLMLGK#.V	16.01	4.07	3.93	0.25
O35864_C	Cops5	COP9 signa	R.VNAQAAAYEYM*AAYIENAK#.Q	3.59	1.86	1.93	0.52
O35864_C	Cops5	COP9 signa	R.VNAQAAAYEYMAAYIENAK#.Q	10.18	1.91	5.32	0.19
O35864_C	Cops5	COP9 signa	K.ISALALLK#.M	17.23	1.61	10.72	0.09
O35864_C	Cops5	COP9 signa	K.QYYALEVSYFK#.S	7.77	2.73	2.85	0.35
O35864_C	Cops5	COP9 signa	K.GYK#PPDEGPSEYQTIPLNK#.I	24.66	2.86	8.62	0.12
O35864_C	Cops5	COP9 signa	K.ISALALLK#.M	17.50	2.63	6.66	0.15
O35864_C	Cops5	COP9 signa	R.VNAQAAAYEYMAAYIENAK#.Q	8.74	1.19	7.36	0.14
O88545_C	Cops6	COP9 signa	K.ASEAGEVPFNHEILR.E	18.02	22.73	0.79	1.26
O88545_C	Cops6	COP9 signa	K.ELEFLGWYTTGGPPDPSDIHVHK#.Q	17.33	9.33	1.86	0.54
O88545_C	Cops6	COP9 signa	K.FNVLYDR.Q	25.49	15.03	1.70	0.59
O88545_C	Cops6	COP9 signa	K.IIIDK#EYYYTK#.E	21.18	3.16	6.70	0.15
O88545_C	Cops6	COP9 signa	K.LILEYVK#.A	108.43	21.71	5.00	0.20
O88545_C	Cops6	COP9 signa	R.M*TATGSGENSTVAEHLIAQHSAIK#.M	22.32	2.77	8.05	0.12
O88545_C	Cops6	COP9 signa	R.MTATGSGENSTVAEHLIAQHSAIK#.M	33.18	6.23	5.33	0.19
O88545_C	Cops6	COP9 signa	R.SQEGRPMQVIGALIGK.Q	9.84	11.66	0.84	1.18
Q9CZ04_C	Cops7a	COP9 signa	R.ELAESDFASTFR.L	16.77	14.48	1.16	0.86
Q9CZ04_C	Cops7a	COP9 signa	R.HLSVVTLAAK#.V	60.43	13.61	4.44	0.23
Q9CZ04_C	Cops7a	COP9 signa	R.LEVDYSIGR.D	12.04	15.52	0.78	1.29
Q9CZ04_C	Cops7a	COP9 signa	K.VTGQNQEQFLLLAK#.S	57.21	12.11	4.72	0.21
Q9CZ04_C	Cops7a	COP9 signa	K.VTGQNQEQFLLLAK#.S	8.31	1.52	5.45	0.18
Q8BV13_C	Cops7b	COP9 signa	K.ESLPELSVAQQNK#.L	16.80	3.30	5.10	0.20
Q8BV13_C	Cops7b	COP9 signa	K.ESLPELSVAQQNK#.L	10.51	2.71	3.88	0.26
Q8BV13_C	Cops7b	COP9 signa	K.K#DINNIVK#.T	868.88	779.94	1.11	0.90
Q8VBV7_C	Cops8	COP9 signa	R.FIPLSEPAPVPPIPNEQQLAR.L	12.38	11.53	1.07	0.93
Q8VBV7_C	Cops8	COP9 signa	K.GVLEQGWQADSTTR.M	45.21	44.42	1.02	0.98
Q8VBV7_C	Cops8	COP9 signa	R.KPASGTLDVSLNR.F	32.55	21.46	1.52	0.66
Q8VBV7_C	Cops8	COP9 signa	K.SANSELGGIWSVGQR.I	10.09	9.17	1.10	0.91
P61924_C	Copz1	Coatomer s	R.GEDVPLTEQTVSQVLQSAK#.E	44.04	42.23	1.04	0.96
P61924_C	Copz1	Coatomer s	R.TDSEIALLEGLTVVYK#.S	34.82	32.79	1.06	0.94
P61924_C	Copz1	Coatomer s	R.VALRGEDVPLTEQTVSQVLQSAK.E	49.00	199.29	0.25	4.07
P61924_C	Copz1	Coatomer s	K.YYDDTYPSVK#.E	152.14	111.86	1.36	0.74
Q9JHH9_C	Copz2	Coatomer s	K.YYDDTFPSVK#.E	43.04	27.87	1.54	0.65
Q9WUM4_	Coro1c	Coronin-1	R.K#SDLFQDDLYPDTAGPEAALEAEEWFEGK#.N	3.21	1.69	1.90	0.53
Q9WUM4_	Coro1c	Coronin-1	K.NADPILISLK#.H	9.06	1.75	5.17	0.19
Q9WUM4_	Coro1c	Coronin-1	K.NADPILISLK#.H	13.25	3.45	3.84	0.26
Q9EPU4_C	Cpsf1	Cleavage an	K.AESTEQEPSAPK#.A	6.57	31.42	0.21	4.78
Q9EPU4_C	Cpsf1	Cleavage an	K.IGTTPDIILDDLLETDR.V	2.76	6.63	0.42	2.40
Q9EPU4_C	Cpsf1	Cleavage an	R.ISVLPAYLSYDAPWPVR.K	1.69	6.66	0.25	3.93
Q9EPU4_C	Cpsf1	Cleavage an	K.NFILAADVM*K#.S	8.30	8.37	0.99	1.01
Q9EPU4_C	Cpsf1	Cleavage an	R.SSFLPSYIIDVR.A	3.53	14.36	0.25	4.07
Q9EPU4_C	Cpsf1	Cleavage an	R.VLVDSSFGQPTTQGEVR.K	3.64	8.89	0.41	2.44
Q9EPU4_C	Cpsf1	Cleavage an	R.YIVQVSPLGIR.L	6.15	20.59	0.30	3.35
Q9EPU4_C	Cpsf1	Cleavage an	K.AAASVLTTSM*VTM*EPGYLFLGSR.L	2.80	6.28	0.45	2.24
Q9EPU4_C	Cpsf1	Cleavage an	R.DALLLSFK#.D	14.41	10.06	1.43	0.70

Q9EPU4_CI	Cpsf1	Cleavage an	K.EVLLVALGSR.Q	8.13	16.42	0.49	2.02
Q9EPU4_CI	Cpsf1	Cleavage an	K.IGTTPDIILDDLLETDR.V	8.33	18.96	0.44	2.28
Q9EPU4_CI	Cpsf1	Cleavage an	R.K#EEEETPK#AESTEQEPSAPK#.A	5.59	5.46	1.02	0.98
Q9EPU4_CI	Cpsf1	Cleavage an	R.NVLDGELLNR.Y	6.10	18.99	0.32	3.11
Q9EPU4_CI	Cpsf1	Cleavage an	R.SSFLPSYIIDVR.A	9.87	23.97	0.41	2.43
Q9EPU4_CI	Cpsf1	Cleavage an	K.TLSLHYFEEPELR.D	9.66	17.01	0.57	1.76
Q9EPU4_CI	Cpsf1	Cleavage an	R.VLVDSSFGQPTTQGEVR.K	5.63	23.09	0.24	4.10
Q9EPU4_CI	Cpsf1	Cleavage an	R.YIVQVSPLGIR.L	9.88	22.51	0.44	2.28
O35218_CI	Cpsf2	Cleavage an	K.FSQIVNLK#.G	24.63	17.39	1.42	0.71
O35218_CI	Cpsf2	Cleavage an	R.GDGNVLIAVDTAGR.V	3.99	15.41	0.26	3.86
O35218_CI	Cpsf2	Cleavage an	K.HVHQIDAVLLSHPDPLHLGALPFAVGK#.L	8.33	3.78	2.20	0.45
O35218_CI	Cpsf2	Cleavage an	K.HVHQIDAVLLSHPDPLHLGALPFAVGK#.L	6.80	7.26	0.94	1.07
O35218_CI	Cpsf2	Cleavage an	R.IRDLLYEQYAIV.-	3.96	17.07	0.23	4.31
O35218_CI	Cpsf2	Cleavage an	K.NSIILTYR.T	2.63	10.67	0.25	4.06
O35218_CI	Cpsf2	Cleavage an	K.VTEIELR.K	6.07	19.46	0.31	3.21
O35218_CI	Cpsf2	Cleavage an	R.FLIDNPTEK#.V	18.57	12.87	1.44	0.69
O35218_CI	Cpsf2	Cleavage an	R.GDGNVLIAVDTAGR.V	6.32	11.44	0.55	1.81
O35218_CI	Cpsf2	Cleavage an	R.IK#WDEYGEIIK#PEDFLVPELQATEEEK#.S	9.37	5.21	1.80	0.56
O35218_CI	Cpsf2	Cleavage an	R.IK#WDEYGEIIK#PEDFLVPELQATEEEK#.S	2.60	2.14	1.22	0.82
Q9QXK7_CI	Cpsf3	Cleavage an	R.GLIPVFALGR.A	10.43	33.46	0.31	3.21
Q9QXK7_CI	Cpsf3	Cleavage an	K.HIM*SEPEEITTM*SGQK#.L	17.85	13.30	1.34	0.75
Q9QXK7_CI	Cpsf3	Cleavage an	R.K#QININNPFVFK#.H	15.02	11.51	1.30	0.77
Q9QXK7_CI	Cpsf3	Cleavage an	K.LTGDVEELEIQEK#PALK#.V	64.67	38.04	1.70	0.59
Q9QXK7_CI	Cpsf3	Cleavage an	R.LYEALTPVH.-	77.17	77.17	1.00	1.00
Q9QXK7_CI	Cpsf3	Cleavage an	K.M*SVDYISFSAHTDYQQTSEFIR.A	1.73	2.25	0.77	1.30
Q9QXK7_CI	Cpsf3	Cleavage an	R.NTEAVTLNFR.G	10.99	31.78	0.35	2.89
Q9QXK7_CI	Cpsf3	Cleavage an	K.TANINLETR.A	13.52	42.53	0.32	3.15
Q9QXK7_CI	Cpsf3	Cleavage an	K.VSNISADDMLYTETDLEESMDK#IETINFHEVK#.E	4.50	2.20	2.04	0.49
Q9QXK7_CI	Cpsf3	Cleavage an	R.WLLSDYVK#.V	22.32	16.17	1.38	0.72
Q9QXK7_CI	Cpsf3	Cleavage an	R.LYEALTPVH.-	17.73	17.73	1.00	1.00
Q9CWS4_II	Cpsf3l	Integrator (	K.VLIPVFALGR.A	3.59	13.25	0.27	3.69
Q9CWS4_II	Cpsf3l	Integrator (	K.GIMQLVGQAEPESVLLVHGEAK#.K	9.70	4.81	2.02	0.50
Q9CWS4_II	Cpsf3l	Integrator (	K.VLIPVFALGR.A	12.88	33.16	0.39	2.57
Q9CWS4_II	Cpsf3l	Integrator (	K.VPIYFSTGLTEK#.A	12.26	8.78	1.40	0.72
Q8BQZ5_CI	Cpsf4	Cleavage an	R.FELPM*GTTEQPPLPQQTQPPTK.R	3.22	4.45	0.72	1.38
Q8BQZ5_CI	Cpsf4	Cleavage an	K.GHLAFLSGQ.-	16.07	16.07	1.00	1.00
Q8BQZ5_CI	Cpsf4	Cleavage an	R.FELPMGTTEQPPLPQQTQPPTK.R	6.18	5.34	1.16	0.86
Q8BQZ5_CI	Cpsf4	Cleavage an	K.GHLAFLSGQ.-	33.88	33.88	1.00	1.00
Q6NVF9_CI	Cpsf6	Cleavage an	K.GAAPNVVYTYTGK#.R	29.60	11.95	2.48	0.40
Q6NVF9_CI	Cpsf6	Cleavage an	K.GFALVGVGSEASSK#.K	33.34	8.30	4.02	0.25
Q6NVF9_CI	Cpsf6	Cleavage an	R.AISSSAISR.A	25.49	37.99	0.67	1.49
Q6NVF9_CI	Cpsf6	Cleavage an	K.GAAPNVVYTYTGK#.R	76.17	33.78	2.25	0.44
Q6NVF9_CI	Cpsf6	Cleavage an	K.GFALVGVGSEASSK#.K	66.34	30.78	2.16	0.46
Q6NVF9_CI	Cpsf6	Cleavage an	R.TPLSEAEFEEIMNR.N	10.02	16.76	0.60	1.67
Q8BTV2_CF	Cpsf7	Cleavage an	K.GYAEVVVASENSVHK#.L	32.69	10.78	3.03	0.33
Q8BTV2_CF	Cpsf7	Cleavage an	R.QNLSQFEAQAR.K	7.16	25.27	0.28	3.53
Q8BTV2_CF	Cpsf7	Cleavage an	K.SYSVGASGSSSR.K	11.55	27.26	0.42	2.36
Q8BTV2_CF	Cpsf7	Cleavage an	K.TPAILYTYSGLR.S	10.97	20.54	0.53	1.87
P45481_CE	Crebbp	CREB-bindi	R.DAFLTLAR.D	5.01	22.12	0.23	4.42
P45481_CE	Crebbp	CREB-bindi	R.KKEESTAASETPEGSQGDSK.N	2.02	3.06	0.66	1.51
P45481_CE	Crebbp	CREB-bindi	R.SALSSELSLVGDTTGDTLEK#.F	5.23	2.83	1.84	0.54
P45481_CE	Crebbp	CREB-bindi	K.TEVQTDDAEPEPTESKGEPR.S	6.24	14.96	0.42	2.40
P45481_CE	Crebbp	CREB-bindi	K.VEAKEEEENSSNDTASQSTSPSQPR.K	2.77	17.37	0.16	6.28
Q9DCT8_CI	Crip2	Cysteine-ri(	K.GVNIGGAGSYIYEKPQTEAPQVTGPIEVPVVR.T	4.26	10.97	0.39	2.57
P63154_CF	Crnkl1	Crooked ne	R.AIYELAISQPR.L	7.85	24.84	0.32	3.17
P63154_CF	Crnkl1	Crooked ne	R.ALDVDYR.N	4.83	24.32	0.20	5.04
P63154_CF	Crnkl1	Crooked ne	K.ANPHNYDAWFDYLR.L	2.94	9.68	0.30	3.30
P63154_CF	Crnkl1	Crooked ne	R.EAAEQDPDK#DIDESESSSF.-	11.89	15.61	0.76	1.31
P63154_CF	Crnkl1	Crooked ne	K.FAELETILGDIER.A	4.49	15.97	0.28	3.56
P63154_CF	Crnkl1	Crooked ne	R.GIEDIIVSK#.R	23.22	21.65	1.07	0.93
P63154_CF	Crnkl1	Crooked ne	K.ITDEEELNDYK#.L	9.11	9.09	1.00	1.00
P63154_CF	Crnkl1	Crooked ne	R.LM*LLESWR.S	13.26	15.82	0.84	1.19
P63154_CF	Crnkl1	Crooked ne	R.LVESDAEADTVR.E	6.37	31.32	0.20	4.92
P63154_CF	Crnkl1	Crooked ne	K.NKAPAEVQITAEQLLR.E	3.83	13.60	0.28	3.55
P63154_CF	Crnkl1	Crooked ne	R.VNQFWYK#.Y	10.81	9.32	1.16	0.86
P63154_CF	Crnkl1	Crooked ne	R.AIYELAISQPR.L	17.11	49.33	0.35	2.88
P63154_CF	Crnkl1	Crooked ne	R.LVESDAEADTVR.E	5.59	25.32	0.22	4.53
Q9CYD3_CI	Crtap	Cartilage-as	R.SVLADFQQR.E	5.91	14.25	0.41	2.41
Q9CYD3_CI	Crtap	Cartilage-as	K.SYESLFVR.A	5.84	11.26	0.52	1.93
P23927_CF	Cryab	Alpha-cryst	R.IPADVDPLTITSSLSSDGVLTVNGPR.K	8.33	13.63	0.61	1.64
Q921W4_C	Cryzl1	Quinone ox	K.LSAGVFRPLLDEPIPLYEAK.V	1.87	6.32	0.30	3.39
Q91W50_C	Csde1	Cold shock	K.AHSVNGITEEANPTIYSGK.V	10.34	7.94	1.30	0.77
Q91W50_C	Csde1	Cold shock	R.ATNIEVLSNTFQFTNEAR.E	2.37	9.04	0.26	3.82
Q91W50_C	Csde1	Cold shock	R.GPDNSM*GFGAER.K	6.33	15.92	0.40	2.52
Q91W50_C	Csde1	Cold shock	R.IK#VDFVIPK#.E	30.74	17.95	1.71	0.58
Q91W50_C	Csde1	Cold shock	R.LLGYVATLK#.D	20.28	17.16	1.18	0.85
Q9ERK4_XF	Cse1l	Exportin-2	K.ANIVHLM*LSSPEQIQK#.Q	4.43	2.16	2.05	0.49
Q9ERK4_XF	Cse1l	Exportin-2	K.IIIPEIQK.V	5666.33	7896.29	0.72	1.39
Q9ERK4_XF	Cse1l	Exportin-2	K.ANIVHLM*LSSPEQIQK#.Q	14.88	5.38	2.77	0.36
Q9ERK4_XF	Cse1l	Exportin-2	K.ANIVHLMLSSPEQIQK#.Q	15.85	7.77	2.04	0.49
Q9ERK4_XF	Cse1l	Exportin-2	K.FFEGPVTGIFSGYVNSM*LQEYAK#.N	11.85	2.99	3.97	0.25
Q9ERK4_XF	Cse1l	Exportin-2	R.GSSTIATAAADK#IPGLLGVFQK#.L	35.98	16.00	2.25	0.44
Q9ERK4_XF	Cse1l	Exportin-2	K.HK#DAAIYLVTSLASK#.A	40.62	8.62	4.71	0.21
Q9ERK4_XF	Cse1l	Exportin-2	K.LLQTDDEEEAGLLELLK#.S	24.21	6.12	3.96	0.25
Q9ERK4_XF	Cse1l	Exportin-2	K.SNELWTEIK#.L	15.66	4.78	3.27	0.31
Q9ERK4_XF	Cse1l	Exportin-2	K.SNNVNEFPVLK#.A	38.41	12.85	2.99	0.33
Q9ERK4_XF	Cse1l	Exportin-2	K.YGALALQEIFDGIQPK#.M	16.93	5.69	2.98	0.34
Q9ERK4_XF	Cse1l	Exportin-2	R.AADEEAFEDNSEEYIR.R	4.25	8.84	0.48	2.08
Q9ERK4_XF	Cse1l	Exportin-2	K.ALTLPGSSENEYIM*K#.A	32.10	11.00	2.92	0.34
Q9ERK4_XF	Cse1l	Exportin-2	K.ANIVHLM*LSSPEQIQK#.Q	29.63	11.70	2.53	0.40
Q9ERK4_XF	Cse1l	Exportin-2	K.ANIVHLMLSSPEQIQK#.Q	25.10	6.97	3.60	0.28
Q9ERK4_XF	Cse1l	Exportin-2	R.DLEGSDIDTR.R	16.94	22.41	0.76	1.32
Q9ERK4_XF	Cse1l	Exportin-2	K.EHDPVGQM*VNNPK#.I	53.88	18.22	2.96	0.34
Q9ERK4_XF	Cse1l	Exportin-2	K.FFEGPVTGIFSGYVNSM*LQEYAK#.N	24.82	4.67	5.31	0.19
Q9ERK4_XF	Cse1l	Exportin-2	R.GSSTIATAAADK#IPGLLGVFQK#.L	79.82	27.96	2.85	0.35
Q9ERK4_XF	Cse1l	Exportin-2	K.IPGLLGVFQK#.L	12.70	6.94	1.83	0.55
Q9ERK4_XF	Cse1l	Exportin-2	R.LLQAFLER.G	10.67	16.00	0.67	1.50
Q9ERK4_XF	Cse1l	Exportin-2	K.LLQTDDEEEAGLLELLK#.S	77.80	30.48	2.55	0.39
Q9ERK4_XF	Cse1l	Exportin-2	K.SNNVNEFPVLK#.A	54.97	15.49	3.55	0.28
Q9ERK4_XF	Cse1l	Exportin-2	R.TGNIPALVR.L	11.37	18.75	0.61	1.65
Q9ERK4_XF	Cse1l	Exportin-2	K.TLDPDPAIR.R	14.09	17.54	0.80	1.25
Q9ERK4_XF	Cse1l	Exportin-2	K.YGALALQEIFDGIQPK#.M	29.46	12.37	2.38	0.42
P41241_CS	Csk	Tyrosine-pr	R.HSNLVQLLGVIVEEK#.G	17.17	3.41	5.04	0.20

P41241_CS	Csk	Tyrosine-pr	R.LLYPPETGLFLVR.E	3.14	6.65	0.47	2.12
Q60737_CS	Csnk2a1	Casein kina	R.EYWDYESHVVEWGNQDDYQLVR.K	3.74	7.54	0.50	2.02
Q60737_CS	Csnk2a1	Casein kina	R.FNDILGR.H	12.67	41.52	0.31	3.28
Q60737_CS	Csnk2a1	Casein kina	R.GGPNIITLADIVK#.D	29.12	20.85	1.40	0.72
Q60737_CS	Csnk2a1	Casein kina	R.GK#YSEVFEAINITNNEK#.V	25.73	14.38	1.79	0.56
Q60737_CS	Csnk2a1	Casein kina	R.LIDWGLAEFYHPGQEYNVR.V	19.08	61.70	0.31	3.23
Q60737_CS	Csnk2a1	Casein kina	K.QLYQTLTDYDIR.F	3.43	17.08	0.20	4.98
Q60737_CS	Csnk2a1	Casein kina	R.TPALVFEHVNNTDFK#.Q	98.92	58.06	1.70	0.59
Q60737_CS	Csnk2a1	Casein kina	K.VLGTEDLYDYIDKYNIELDPR.F	11.57	41.23	0.28	3.56
Q60737_CS	Csnk2a1	Casein kina	K.YSEVFEAINITNNEK#.V	22.47	21.74	1.03	0.97
Q60737_CS	Csnk2a1	Casein kina	K.YSEVFEAINITNNEK#.V	14.02	6.60	2.13	0.47
O54833_CS	Csnk2a2	Casein kina	R.HLVSPEALDLLDK#.L	13.03	7.11	1.83	0.55
O54833_CS	Csnk2a2	Casein kina	R.HLVSPEALDLLDK.L	8.92	10.60	0.84	1.19
O54833_CS	Csnk2a2	Casein kina	K.LIDTVKDPVSK.T	7.64	7.53	1.01	0.99
O54833_CS	Csnk2a2	Casein kina	R.LIDWGLAEFYHPAQEYNVR.V	6.40	15.23	0.42	2.38
O54833_CS	Csnk2a2	Casein kina	K.TPALVFEYINNTDFK#.Q	16.20	12.74	1.27	0.79
O54833_CS	Csnk2a2	Casein kina	K.TPALVFEYINNTDFK#.Q	11.48	4.89	2.35	0.43
O54833_CS	Csnk2a2	Casein kina	K.VLGTDELYGYLK.K	21.47	17.45	1.23	0.81
P67871_CS	Csnk2b	Casein kina	R.GIAQM*LEK#.Y	76.95	48.06	1.60	0.62
P67871_CS	Csnk2b	Casein kina	R.GIAQMLEK#.Y	36.15	26.30	1.37	0.73
P67871_CS	Csnk2b	Casein kina	K.IHPM*AYQLQLQAASNFK#.S	56.66	35.31	1.60	0.62
P67871_CS	Csnk2b	Casein kina	K.IHPMAYQLQLQAASNFK#.S	13.38	10.09	1.33	0.75
P97315_CS	Csrp1	Cysteine an	K.GFGFGQGAGALVHSE.-	460.27	460.27	1.00	1.00
P97315_CS	Csrp1	Cysteine an	K.GLESTTLADK#.D	20.54	20.24	1.01	0.99
P97315_CS	Csrp1	Cysteine an	K.GYGYGQGAGTLSTDK#.G	28.98	19.65	1.48	0.68
P97315_CS	Csrp1	Cysteine an	K.GYGYGQGAGTLSTDK#GESLGIK#.H	115.47	101.37	1.14	0.88
P97315_CS	Csrp1	Cysteine an	K.GYGYGQGAGTLSTDKGESLGIKHEEAPGHRPTTNPNASK.F	3.05	7.27	0.42	2.38
P97314_CS	Csrp2	Cysteine an	K.GFGYGQGAGALVHAQ.-	10.91	10.91	1.00	1.00
P97314_CS	Csrp2	Cysteine an	K.GFGYGQGAGALVHAQ.-	369.02	369.02	1.00	1.00
P97314_CS	Csrp2	Cysteine an	K.GYGYGQGAGTLNM*DR.G	23.73	144.76	0.16	6.10
P97314_CS	Csrp2	Cysteine an	K.GYGYGQGAGTLNMDR.G	4.22	47.92	0.09	11.34
P97314_CS	Csrp2	Cysteine an	R.LGIKPESAQPHRPTTNPNTSK.F	5.11	60.57	0.08	11.86
P97314_CS	Csrp2	Cysteine an	K.SLESTTLTEK#.E	155.02	212.54	0.73	1.37
P97314_CS	Csrp2	Cysteine an	K.GFGYGQGAGALVHAQ.-	12.31	12.31	1.00	1.00
Q99LC2_CS	Cstf1	Cleavage sti	R.DGQLIATGSADASIK#.I	21.21	8.53	2.49	0.40
Q99LC2_CS	Cstf1	Cleavage sti	K.LGM*ENDDTAVQYAIGR.S	4.79	11.04	0.43	2.31
Q99LC2_CS	Cstf1	Cleavage sti	K.LGMENDDTAVQYAIGR.S	3.66	6.81	0.54	1.86
Q99LC2_CS	Cstf1	Cleavage sti	K.YIQEAEMLR.S	5.12	7.80	0.66	1.52
Q99LI7_CS	Cstf3	Cleavage sti	R.DYNK#YEEGINIHLAK#.K	28.69	10.58	2.71	0.37
Q99LI7_CS	Cstf3	Cleavage sti	K.GVEAVGSYAENQR.I	10.69	18.94	0.56	1.77
Q99LI7_CS	Cstf3	Cleavage sti	R.HLAPPGLHPVPGGVFPVPPAAVVLM*K#.L	3.94	3.19	1.23	0.81
Q99LI7_CS	Cstf3	Cleavage sti	R.HLAPPGLHPVPGGVFPVPPAAVVLMK#.L	5.63	2.04	2.76	0.36
Q99LI7_CS	Cstf3	Cleavage sti	K.IFELGLK#.K	21.08	9.29	2.27	0.44
Q99LI7_CS	Cstf3	Cleavage sti	K.KLEENPYDLDAWSILIR.E	11.91	27.97	0.43	2.35
Q99LI7_CS	Cstf3	Cleavage sti	K.LFSDEAANIYER.A	9.41	20.44	0.46	2.17
Q99LI7_CS	Cstf3	Cleavage sti	R.LLAIEDIDPTLVYIQYM*K#.F	13.76	5.96	2.31	0.43
Q99LI7_CS	Cstf3	Cleavage sti	R.LVAQFPSSGR.F	12.58	29.90	0.42	2.38
Q99LI7_CS	Cstf3	Cleavage sti	K.M*AQAYDFALDK#.I	24.11	7.38	3.27	0.31
Q99LI7_CS	Cstf3	Cleavage sti	K.SGEIWAR.F	11.42	13.01	0.88	1.14
Q99LI7_CS	Cstf3	Cleavage sti	R.TEDQTLITK#.R	44.66	18.52	2.41	0.41
Q99LI7_CS	Cstf3	Cleavage sti	R.VLTSGSLPPEK#.S	13.35	4.39	3.04	0.33
Q99LI7_CS	Cstf3	Cleavage sti	R.TEDQTLITK#.R	17.65	5.65	3.12	0.32
O88712_CT	Ctbp1	C-terminal-	K.ALAQALK#.E	83.54	42.54	1.96	0.51
O88712_CT	Ctbp1	C-terminal-	R.GAALDVHESEPFSFSQGPLK#.D	67.53	43.29	1.56	0.64
O88712_CT	Ctbp1	C-terminal-	R.GETLGIIGLGR.V	5.06	13.94	0.36	2.76
O88712_CT	Ctbp1	C-terminal-	R.GGLVDEK#.A	107.95	57.61	1.87	0.53
O88712_CT	Ctbp1	C-terminal-	R.IGSGFDNIDIK#.S	79.76	45.54	1.75	0.57
O88712_CT	Ctbp1	C-terminal-	R.IRGETLGIIGLGR.V	5.23	49.09	0.11	9.38
O88712_CT	Ctbp1	C-terminal-	R.QGAFLVNTAR.G	13.82	28.45	0.49	2.06
O88712_CT	Ctbp1	C-terminal-	R.VGQAVALR.A	23.43	52.62	0.45	2.25
O88712_CT	Ctbp1	C-terminal-	K.VLNEAVGALMYHTITLTR.E	10.69	19.11	0.56	1.79
O88712_CT	Ctbp1	C-terminal-	R.GAALDVHESEPFSFSQGPLK#.D	7.79	7.25	1.07	0.93
O88712_CT	Ctbp1	C-terminal-	R.IGSGFDNIDIK#.S	11.91	5.57	2.14	0.47
O88712_CT	Ctbp1	C-terminal-	R.GAALDVHESEPFSFSQGPLK#.D	8.87	7.07	1.25	0.80
O88712_CT	Ctbp1	C-terminal-	R.IGSGFDNIDIK#.S	13.34	7.62	1.75	0.57
P56546_CT	Ctbp2	C-terminal-	R.GAALDVHESEPFSFAQGPLK#.D	39.35	23.82	1.65	0.61
P56546_CT	Ctbp2	C-terminal-	R.IGSGYDNVDIK#.A	51.00	33.61	1.52	0.66
P56546_CT	Ctbp2	C-terminal-	R.NTWLYQALR.E	4.96	9.76	0.51	1.97
Q5SUQ9_CT	Ctc1	CST comple	R.VALQFTGLGGQTESASK#.T	7.40	2.43	3.04	0.33
Q5SUQ9_CT	Ctc1	CST comple	R.VALQFTGLGGQTESASK#.T	27.06	6.65	4.07	0.25
Q61164_CT	Ctcf	Transcripti	R.TVTLLR.N	5.16	35.11	0.15	6.80
Q61164_CT	Ctcf	Transcripti	R.YALIQHQK#.S	40.37	39.67	1.02	0.98
Q61164_CT	Ctcf	Transcripti	R.YTEEGKDVDVSVYDFEEEQQEGLLSEVNAEK.V	8.61	5.40	1.59	0.63
Q61164_CT	Ctcf	Transcripti	R.YTEEGK#DVDVSVYDFEEEQQEGLLSEVNAEK#.V	21.74	17.48	1.24	0.80
Q8BG15_CT	Ctdspl2	CTD small p	K.LLNILDPK#.K	18.29	8.20	2.23	0.45
P26231_CT	Ctnna1	Catenin alp	K.IAEQVASFQEEK#.S	28.91	24.61	1.17	0.85
P26231_CT	Ctnna1	Catenin alp	R.LLILADMADVYK#.L	11.83	7.75	1.53	0.65
P26231_CT	Ctnna1	Catenin alp	R.NAGNEQDLGIQYK.A	18.67	18.03	1.03	0.97
P26231_CT	Ctnna1	Catenin alp	K.NLM*NAVVQTVK.A	6.39	6.97	0.92	1.09
P26231_CT	Ctnna1	Catenin alp	K.NLMNAVVQTVK#.A	12.58	9.32	1.35	0.74
P26231_CT	Ctnna1	Catenin alp	K.QIIVDPLSFSEER.F	3.67	10.31	0.36	2.81
P26231_CT	Ctnna1	Catenin alp	R.TSVQTEDDQLIAGQSAR.A	5.16	15.30	0.34	2.97
P26231_CT	Ctnna1	Catenin alp	R.VIHVVTSEM*DNYEPGVYTEK#.V	11.13	8.25	1.35	0.74
Q02248_CT	Ctnnb1	Catenin bet	K.HAVVNLINYQDDAELATR.A	4.97	6.67	0.75	1.34
Q02248_CT	Ctnnb1	Catenin bet	K.LLNDEDQVVVNK.A	5.25	12.11	0.43	2.31
P30999_CT	Ctnnd1	Catenin del	R.FVGDADLER.Q	68.37	16.83	4.06	0.25
P30999_CT	Ctnnd1	Catenin del	R.GYELLFQPEVVR.I	4.20	19.22	0.22	4.58
P30999_CT	Ctnnd1	Catenin del	K.LNGPQDHNHLLYSTIPR@M*QEPGQIVETYTEEDPEGAMSVVSVETTDDGTTR@.R	1.76	2.80	0.63	1.59
P30999_CT	Ctnnd1	Catenin del	R.QDVYGPQPQVR.V	9.68	14.75	0.66	1.52
P30999_CT	Ctnnd1	Catenin del	R.TVQPVPM*GPDGLPVDASAVSNNYIQTLGR.D	1.98	6.62	0.30	3.34
P70698_PY	Ctps1	CTP syntha	R.FEVNPVLK#.K	17.76	9.07	1.96	0.51
P70698_PY	Ctps1	CTP syntha	K.FSDSYASVIK#.A	104.19	59.06	1.76	0.57
P70698_PY	Ctps1	CTP syntha	K.IQAIAWAR.K	16.45	54.04	0.30	3.29
P70698_PY	Ctps1	CTP syntha	K.IYQYVINK#.E	160.54	68.74	2.34	0.43
P70698_PY	Ctps1	CTP syntha	R.KLYGDTDYLEER.H	6.23	18.19	0.34	2.92
P70698_PY	Ctps1	CTP syntha	K.LYGDTDYLEER.H	11.25	20.93	0.54	1.86
P70698_PY	Ctps1	CTP syntha	R.NVLGWQDANSTEFDPK#.T	31.51	17.35	1.82	0.55
P70698_PY	Ctps1	CTP syntha	K.TVQVVPHITDAIQEWVMR.Q	6.56	17.41	0.38	2.66
P70698_PY	Ctps1	CTP syntha	K.YIDSTDLEPSTLQEEPVR.Y	7.72	18.06	0.43	2.34
P70698_PY	Ctps1	CTP syntha	K.GVIASSVGTILK.S	10.05	16.87	0.60	1.68
P70698_PY	Ctps1	CTP syntha	R.FEVNPVLK#.K	16.44	4.92	3.34	0.30
P70698_PY	Ctps1	CTP syntha	R.FEVNPVLK#K#.C	32.62	9.37	3.48	0.29
P70698_PY	Ctps1	CTP syntha	K.FSDSYASVIK#.A	162.28	69.95	2.32	0.43

P70698_P	Ctps1	CTP syntha	K.FVGQDVEGER.M	32.80	50.84	0.65	1.55
P70698_P	Ctps1	CTP syntha	K.GVIASSVGTILK#.S	135.43	50.81	2.67	0.38
P70698_P	Ctps1	CTP syntha	K.IQAIAWAR.K	29.27	47.49	0.62	1.62
P70698_P	Ctps1	CTP syntha	K.IYQYVINK#.E	174.07	72.38	2.40	0.42
P70698_P	Ctps1	CTP syntha	R.LTK#DNNLTTGK#.I	4.36	1.33	3.27	0.31
P70698_P	Ctps1	CTP syntha	K.LYGDTDYLEER.H	15.65	22.78	0.69	1.46
P70698_P	Ctps1	CTP syntha	R.NVLGWQDANSTEFDPK#.T	55.06	20.44	2.69	0.37
P70698_P	Ctps1	CTP syntha	K.TVQVVPHITDAIQEWVMR.Q	10.91	22.48	0.49	2.06
P70698_P	Ctps1	CTP syntha	K.YIDSTDLEPSTLQEEPVR.Y	13.78	24.94	0.55	1.81
P70698_P	Ctps1	CTP syntha	K.FSDSYASVIK#.A	65.14	21.08	3.09	0.32
P70698_P	Ctps1	CTP syntha	K.FVGQDVEGER.M	19.39	32.80	0.59	1.69
P70698_P	Ctps1	CTP syntha	K.IYQYVINK#.E	77.76	26.68	2.91	0.34
P70698_P	Ctps1	CTP syntha	K.LYGDTDYLEER.H	5.55	11.68	0.48	2.10
P70698_P	Ctps1	CTP syntha	R.NVLGWQDANSTEFDPK#.T	27.76	13.14	2.11	0.47
P70698_P	Ctps1	CTP syntha	K.YIDSTDLEPSTLQEEPVR.Y	5.83	12.10	0.48	2.07
P70303_P	Ctps2	CTP syntha	K.ALEHSALAINHK#.L	113.50	57.43	1.98	0.51
P70303_P	Ctps2	CTP syntha	R.VPLLLEEQGVVK#.Y	29.85	9.76	3.06	0.33
P70303_P	Ctps2	CTP syntha	K.YILVTGGVISGIGK#.G	36.43	16.08	2.27	0.44
P70303_P	Ctps2	CTP syntha	K.ALEHSALAINHK#.L	138.40	54.11	2.56	0.39
P70303_P	Ctps2	CTP syntha	K.GIIASSIGTILK#.S	20.04	4.73	4.24	0.24
P70303_P	Ctps2	CTP syntha	R.VPLLLEEQGVVK#.Y	29.16	8.28	3.52	0.28
P70303_P	Ctps2	CTP syntha	K.YILVTGGVISGIGK#.G	63.98	26.63	2.40	0.42
P70303_P	Ctps2	CTP syntha	K.ALEHSALAINHK#.L	75.37	37.08	2.03	0.49
P70303_P	Ctps2	CTP syntha	K.DNNITTGK#.I	8.52	8.67	0.98	1.02
P70303_P	Ctps2	CTP syntha	K.GIIASSIGTILK#.S	31.39	8.66	3.63	0.28
P70303_P	Ctps2	CTP syntha	K.LNLMYIDSIDLEPVTK#.A	10.23	3.56	2.87	0.35
P70303_P	Ctps2	CTP syntha	K.TVQVVPHITDAIQEWVMNQAK#.V	5.49	2.99	1.83	0.55
P70303_P	Ctps2	CTP syntha	R.VPLLLEEQGVVK#.Y	50.01	15.35	3.26	0.31
P70303_P	Ctps2	CTP syntha	K.YILVTGGVISGIGK#.G	26.54	8.48	3.13	0.32
Q62018_C	Ctr9	RNA polym	R.LATSVLK#DEK#.S	14.12	10.04	1.41	0.71
Q62018_C	Ctr9	RNA polym	K.DLITQATLLYTMADK#.I	6.97	2.34	2.98	0.34
Q62018_C	Ctr9	RNA polym	R.LATSVLK#DEK#.S	24.10	14.48	1.66	0.60
Q60598_S	Cttn	Src substra	K.ASAGHAVSITQDDGGADDWETDPDFVNDVSEK#.E	6.87	2.34	2.94	0.34
Q60598_S	Cttn	Src substra	K.NASTFEEVVQVPSAYQK#.T	7.53	2.39	3.15	0.32
Q60598_S	Cttn	Src substra	R.ANFENLAK#.E	170.08	76.18	2.23	0.45
Q60598_S	Cttn	Src substra	K.ASAGHAVSITQDDGGADDWETDPDFVNDVSEK#.E	32.69	13.37	2.44	0.41
Q60598_S	Cttn	Src substra	K.ASAGHAVSITQDDGGADDWETDPDFVNDVSEKEQR.W	9.85	14.74	0.67	1.50
Q60598_S	Cttn	Src substra	K.ASAGHAVSITQDDGGADDWETDPDFVNDVSEKEQR.W	2.76	2.57	1.07	0.93
Q60598_S	Cttn	Src substra	K.EK#ELETGPK#.A	33.09	15.43	2.14	0.47
Q60598_S	Cttn	Src substra	R.ENVFQEHQTLK#.E	19.59	11.00	1.78	0.56
Q60598_S	Cttn	Src substra	K.FGVQMDR.V	10.21	18.43	0.55	1.80
Q60598_S	Cttn	Src substra	K.FGVQTDR.Q	33.18	61.86	0.54	1.86
Q60598_S	Cttn	Src substra	K.HESQQDYAK#.G	13.22	4.00	3.31	0.30
Q60598_S	Cttn	Src substra	K.LQLHESQK#.D	47.14	21.18	2.23	0.45
Q60598_S	Cttn	Src substra	K.LRENVFQEHQTLK.E	33.57	55.96	0.60	1.67
Q60598_S	Cttn	Src substra	R.M*DK#NASTFEEVVQVPSAYQK#.T	32.38	14.67	2.21	0.45
Q60598_S	Cttn	Src substra	R.MDK#NASTFEEVVQVPSAYQK#.T	24.84	11.19	2.22	0.45
Q60598_S	Cttn	Src substra	K.NASTFEEVVQVPSAYQK#.T	66.20	26.81	2.47	0.41
Q60598_S	Cttn	Src substra	R.QDSSAVGFDYK#.E	74.50	39.45	1.89	0.53
Q60598_S	Cttn	Src substra	K.SAVGFDYQGK#.T	238.59	91.28	2.61	0.38
Q60598_S	Cttn	Src substra	K.SAVGFEYQGK#.T	285.30	105.90	2.69	0.37
Q60598_S	Cttn	Src substra	R.SAVGHEYQSK#.L	34.67	14.72	2.35	0.42
Q60598_S	Cttn	Src substra	R.VDQSAVGFEYQGK#.T	248.79	120.42	2.07	0.48
Q60598_S	Cttn	Src substra	K.YGIDK#DK#VDK#.S	226.48	121.03	1.87	0.53
Q60598_S	Cttn	Src substra	R.YGLFPANYVELR.Q	29.00	75.04	0.39	2.59
Q60598_S	Cttn	Src substra	R.YGLFPANYVELRQ.-	15.94	28.79	0.55	1.81
Q60598_S	Cttn	Src substra	K.SAVGFEYQGK#.T	11.84	4.97	2.38	0.42
Q99LJ0_CT	Cttnbp2nl	CTTNBP2 N	R.ELTSDSSTENQGPPR.E	3.57	8.06	0.44	2.26
Q99LJ0_CT	Cttnbp2nl	CTTNBP2 N	R.GLQTEAQVEK#.Q	16.20	6.77	2.39	0.42
Q99LJ0_CT	Cttnbp2nl	CTTNBP2 N	K.LTDTGLPGPTTAAYSYAK#.A	10.70	8.40	1.27	0.78
Q9WTX6_C	Cul1	Cullin-1 OS	R.AGIQQVYTR.Q	10.71	31.68	0.34	2.96
Q9WTX6_C	Cul1	Cullin-1 OS	K.ESFESQFLADTER.F	10.86	17.60	0.62	1.62
Q9WTX6_C	Cul1	Cullin-1 OS	R.ESTEFLQQNPVTEYM*K#.K	5.70	3.14	1.81	0.55
Q9WTX6_C	Cul1	Cullin-1 OS	R.ESTEFLQQNPVTEYMK#.K	7.48	3.98	1.88	0.53
Q9WTX6_C	Cul1	Cullin-1 OS	R.FINNNAVTK#.M	56.46	35.01	1.61	0.62
Q9WTX6_C	Cul1	Cullin-1 OS	R.FTAFYASR.H	5.75	16.64	0.35	2.89
Q9WTX6_C	Cul1	Cullin-1 OS	K.FYTQQWEDYR.F	6.00	15.47	0.39	2.58
Q9WTX6_C	Cul1	Cullin-1 OS	K.GQTPGGAQFVGLELYK#.R	11.90	7.33	1.62	0.62
Q9WTX6_C	Cul1	Cullin-1 OS	K.HLEIFHTEFQNLLDADKNEDLGR.M	5.53	16.87	0.33	3.05
Q9WTX6_C	Cul1	Cullin-1 OS	K.HQQLLGEVLTQLSSR.F	8.18	15.98	0.51	1.95
Q9WTX6_C	Cul1	Cullin-1 OS	R.IQDGLGELK#K#.L	15.91	5.70	2.79	0.36
Q9WTX6_C	Cul1	Cullin-1 OS	K.KGQTPGGAQFVGLELYK.R	18.79	11.51	1.63	0.61
Q9WTX6_C	Cul1	Cullin-1 OS	R.LISGVVQSYVELGLNEDDAFAK#.G	6.65	1.94	3.43	0.29
Q9WTX6_C	Cul1	Cullin-1 OS	R.LISGVVQSYVELGLNEDDAFAK#.G	1.94	2.74	0.71	1.41
Q9WTX6_C	Cul1	Cullin-1 OS	K.LLIQAAIVR.I	5.81	15.13	0.38	2.61
Q9WTX6_C	Cul1	Cullin-1 OS	K.LLVLEDENANVDEVELK#PDTLIK#.L	43.71	18.60	2.35	0.43
Q9WTX6_C	Cul1	Cullin-1 OS	K.LTWLYQLSK#.G	15.95	5.35	2.98	0.34
Q9WTX6_C	Cul1	Cullin-1 OS	R.LVHQNSASDDAEASMISK#.L	15.42	11.29	1.37	0.73
Q9WTX6_C	Cul1	Cullin-1 OS	K.M*DILAQVLQILLK#.S	60.94	33.31	1.83	0.55
Q9WTX6_C	Cul1	Cullin-1 OS	R.M*FQDIGVSK#.D	18.47	9.69	1.91	0.52
Q9WTX6_C	Cul1	Cullin-1 OS	R.MFQDIGVSK#.D	13.32	7.68	1.73	0.58
Q9WTX6_C	Cul1	Cullin-1 OS	K.NPEEAELEDTLNQVM*VVFK#.Y	8.53	4.42	1.93	0.52
Q9WTX6_C	Cul1	Cullin-1 OS	K.NYLTNLLK#.D	14.09	5.23	2.69	0.37
Q9WTX6_C	Cul1	Cullin-1 OS	K.NYLTNLLKDGEDLM*DESVLK.F	8.38	5.35	1.57	0.64
Q9WTX6_C	Cul1	Cullin-1 OS	K.SSK#NPEEAELEDTLNQVMVVFK#.Y	12.33	8.81	1.40	0.71
Q9WTX6_C	Cul1	Cullin-1 OS	R.VDGEK#DTYSYLA.-	23.05	13.52	1.70	0.59
Q9WTX6_C	Cul1	Cullin-1 OS	K.YIEDK#DVFQK#.F	19.80	10.60	1.87	0.54
Q9WTX6_C	Cul1	Cullin-1 OS	K.YNALVMSAFNNDAGFVAALDK#.A	6.14	5.20	1.18	0.85
Q9WTX6_C	Cul1	Cullin-1 OS	R.AGIQQVYTR.Q	13.57	34.23	0.40	2.52
Q9WTX6_C	Cul1	Cullin-1 OS	K.ESFESQFLADTER.F	5.29	12.71	0.42	2.40
Q9WTX6_C	Cul1	Cullin-1 OS	R.ESTEFLQQNPVTEYM*K#.K	4.79	2.55	1.88	0.53
Q9WTX6_C	Cul1	Cullin-1 OS	R.ESTEFLQQNPVTEYMK#.K	5.70	2.11	2.70	0.37
Q9WTX6_C	Cul1	Cullin-1 OS	R.FINNNAVTK#.M	67.94	35.35	1.92	0.52
Q9WTX6_C	Cul1	Cullin-1 OS	R.FTAFYASR.H	6.78	12.73	0.53	1.88
Q9WTX6_C	Cul1	Cullin-1 OS	K.GPTLTVYK#.E	29.14	14.67	1.99	0.50
Q9WTX6_C	Cul1	Cullin-1 OS	K.GQTPGGAQFVGLELYK#.R	12.51	10.38	1.21	0.83
Q9WTX6_C	Cul1	Cullin-1 OS	K.HQQLLGEVLTQLSSR.F	8.79	12.27	0.72	1.40
Q9WTX6_C	Cul1	Cullin-1 OS	R.LISGVVQSYVELGLNEDDAFAK#.G	13.72	9.52	1.44	0.69
Q9WTX6_C	Cul1	Cullin-1 OS	K.LLVLEDENANVDEVELK#PDTLIK#.L	41.19	21.27	1.94	0.52
Q9WTX6_C	Cul1	Cullin-1 OS	R.LVHQNSASDDAEASM*ISK#.L	42.41	25.46	1.67	0.60
Q9WTX6_C	Cul1	Cullin-1 OS	R.LVHQNSASDDAEASMISK#.L	14.81	6.37	2.33	0.43
Q9WTX6_C	Cul1	Cullin-1 OS	R.M*FQDIGVSK#.D	16.86	11.72	1.44	0.69
Q9WTX6_C	Cul1	Cullin-1 OS	K.NYLTNLLK#DGEDLM*DESVLK#.F	10.17	6.78	1.50	0.67

Q9WTX6_C	Cul1	Cullin-1 OS	K.QIGLDQIWDDLR.A	7.02	12.86	0.55	1.83
Q9WTX6_C	Cul1	Cullin-1 OS	R.VDGEK#DTYSYLA.-	24.67	13.62	1.81	0.55
Q9D4H8_C	Cul2	Cullin-2 OS	K.GM*TENEVEDK#LTSFITVFK#.Y	19.92	13.22	1.51	0.66
Q9D4H8_C	Cul2	Cullin-2 OS	R.YLNTQYIK#.K	16.09	5.98	2.69	0.37
Q9D4H8_C	Cul2	Cullin-2 OS	K.DTPQELEQTR.S	8.82	17.15	0.51	1.95
Q9D4H8_C	Cul2	Cullin-2 OS	K.GM*TENEVEDK#LTSFITVFK#.Y	28.59	9.37	3.05	0.33
Q9D4H8_C	Cul2	Cullin-2 OS	K.GMTENEVEDK#LTSFITVFK#.Y	8.48	5.30	1.60	0.62
Q9D4H8_C	Cul2	Cullin-2 OS	R.YLNTQYIK#.K	14.25	5.27	2.70	0.37
Q9JLV5_CU	Cul3	Cullin-3 OS	K.ALVSEEGEGKNPVDYIQGLLDLK.S	69.76	33.29	2.10	0.48
Q9JLV5_CU	Cul3	Cullin-3 OS	R.DM*SISNTTM*DEFR.Q	3.83	9.71	0.39	2.53
Q9JLV5_CU	Cul3	Cullin-3 OS	K.EDGSEVGVGGAQVTGSNTR.K	4.79	14.78	0.32	3.08
Q9JLV5_CU	Cul3	Cullin-3 OS	R.EVVTEHLINK#.V	30.38	12.34	2.46	0.41
Q9JLV5_CU	Cul3	Cullin-3 OS	K.FLAENSASVYIK#.K	33.48	12.43	2.69	0.37
Q9JLV5_CU	Cul3	Cullin-3 OS	K.GLTEQEVETILDK#.A	61.94	35.13	1.76	0.57
Q9JLV5_CU	Cul3	Cullin-3 OS	R.INEEIER.V	8.73	21.23	0.41	2.43
Q9JLV5_CU	Cul3	Cullin-3 OS	K.MQHNVLVAEVTQQLK#.A	13.42	5.42	2.47	0.40
Q9JLV5_CU	Cul3	Cullin-3 OS	K.NAIQEIQR.K	9.20	38.47	0.24	4.18
Q9JLV5_CU	Cul3	Cullin-3 OS	K.NNSGLSFEELYR.N	5.31	11.96	0.44	2.25
Q9JLV5_CU	Cul3	Cullin-3 OS	K.SK#EIESGHIFTVNDQFTSK#.L	24.20	10.09	2.40	0.42
Q9JLV5_CU	Cul3	Cullin-3 OS	R.SPEYLSLFIDDK#LK#.K	10.07	7.14	1.41	0.71
Q9JLV5_CU	Cul3	Cullin-3 OS	K.STEEPIVK#.V	37.61	12.95	2.90	0.34
Q9JLV5_CU	Cul3	Cullin-3 OS	K.SVSDDSEK#NM*ISK#.L	13.09	3.48	3.76	0.27
Q9JLV5_CU	Cul3	Cullin-3 OS	R.VLTTGYWPTQSATPK#.C	35.34	14.55	2.43	0.41
Q9JLV5_CU	Cul3	Cullin-3 OS	K.YVNSIWDLLK#.N	56.84	26.97	2.11	0.47
Q9JLV5_CU	Cul3	Cullin-3 OS	K.ALVSEEGEGK#NPVDYIQGLLDLK#.S	32.55	10.95	2.97	0.34
Q9JLV5_CU	Cul3	Cullin-3 OS	R.EVVTEHLINK#.V	14.89	5.38	2.77	0.36
Q9JLV5_CU	Cul3	Cullin-3 OS	K.GLTEQEVETILDK#.A	16.76	8.72	1.92	0.52
Q9JLV5_CU	Cul3	Cullin-3 OS	K.SVSDDSEK#NM*ISK#.L	3.43	1.29	2.65	0.38
Q9JLV5_CU	Cul3	Cullin-3 OS	R.VLTTGYWPTQSATPK#.C	9.48	4.17	2.27	0.44
Q9JLV5_CU	Cul3	Cullin-3 OS	K.YVNSIWDLLK#.N	12.88	3.93	3.27	0.31
Q3TCH7_C	Cul4a	Cullin-4A O	K.DVFEAFYK#.K	26.30	11.55	2.28	0.44
Q3TCH7_C	Cul4a	Cullin-4A O	K.DVFEAFYK#K#.D	13.70	6.89	1.99	0.50
Q3TCH7_C	Cul4a	Cullin-4A O	R.EDSLDSVLFLK#.K	21.64	9.27	2.33	0.43
Q3TCH7_C	Cul4a	Cullin-4A O	K.ETVEEQVSTTER.V	6.75	11.80	0.57	1.75
Q3TCH7_C	Cul4a	Cullin-4A O	R.LPDNYTQDTWR.K	4.04	6.86	0.59	1.70
Q3TCH7_C	Cul4a	Cullin-4A O	R.SIFLFLDR.T	8.60	19.26	0.45	2.24
Q3TCH7_C	Cul4a	Cullin-4A O	K.TLGHNLLVSELYNQLK#.F	20.80	5.56	3.74	0.27
Q3TCH7_C	Cul4a	Cullin-4A O	K.DVFEAFYK#.K	16.42	5.99	2.74	0.36
Q3TCH7_C	Cul4a	Cullin-4A O	R.EDSLDSVLFLK#.K	20.27	11.62	1.74	0.57
Q3TCH7_C	Cul4a	Cullin-4A O	K.ETVEEQVSTTER.V	6.54	11.85	0.55	1.81
Q3TCH7_C	Cul4a	Cullin-4A O	K.QLLGEHLTAILQK#.G	30.12	10.89	2.77	0.36
A2A432_C	Cul4b	Cullin-4B O	K.AFGSTIVINPEK#DK#.T	6.67	2.99	2.23	0.45
A2A432_C	Cul4b	Cullin-4B O	R.AGNK#EATDEELEK#.M	7.42	4.98	1.49	0.67
A2A432_C	Cul4b	Cullin-4B O	R.DK#ENPNQYNYIA.-	27.64	15.44	1.79	0.56
A2A432_C	Cul4b	Cullin-4B O	K.EAFETFINK#.R	15.13	10.10	1.50	0.67
A2A432_C	Cul4b	Cullin-4B O	K.ETVEEQASTTER.V	16.47	42.55	0.39	2.58
A2A432_C	Cul4b	Cullin-4B O	K.LPENYTDETWQK#.L	29.87	13.27	2.25	0.44
A2A432_C	Cul4b	Cullin-4B O	K.LQEIFK#.T	29.87	14.97	2.00	0.50
A2A432_C	Cul4b	Cullin-4B O	R.LYAAEGQK#.L	26.18	90.79	0.29	3.47
A2A432_C	Cul4b	Cullin-4B O	R.SATDGNTSTTPPTSAK#.K	14.55	8.08	1.80	0.56
A2A432_C	Cul4b	Cullin-4B O	K.TIDGILLLIER.E	7.86	18.77	0.42	2.39
A2A432_C	Cul4b	Cullin-4B O	K.TLSHNLLVSEVYNQLK#.F	40.73	32.73	1.24	0.80
A2A432_C	Cul4b	Cullin-4B O	R.AHIISDQK#.V	14.77	4.80	3.08	0.33
A2A432_C	Cul4b	Cullin-4B O	K.ETVEEQASTTER.V	14.17	32.52	0.44	2.30
A2A432_C	Cul4b	Cullin-4B O	K.LK#EAVEAIQNSTSIK#.Y	14.69	6.94	2.12	0.47
A2A432_C	Cul4b	Cullin-4B O	K.LPENYTDETWQK#.L	21.38	11.83	1.81	0.55
A2A432_C	Cul4b	Cullin-4B O	K.M*AEESSSSSSSSPTAATSQQQQQQLK#.T	8.94	5.97	1.50	0.67
A2A432_C	Cul4b	Cullin-4B O	R.SATDGNTSTTPPTSAK#.K	18.49	7.98	2.32	0.43
A2A432_C	Cul4b	Cullin-4B O	K.SLIASVEK#.Q	36.86	13.82	2.67	0.37
A2A432_C	Cul4b	Cullin-4B O	K.TLSHNLLVSEVYNQLK#.F	21.00	32.06	0.65	1.53
Q9D5V5_C	Cul5	Cullin-5 OS	K.DFTEGTLFSVNQDFSLIK#.N	13.33	3.91	3.41	0.29
Q9D5V5_C	Cul5	Cullin-5 OS	K.IHQALK#EDILEFIK#.Q	19.36	7.30	2.65	0.38
Q9D5V5_C	Cul5	Cullin-5 OS	K.ISNAQLQTELVEILK#.N	14.93	4.74	3.15	0.32
Q9D5V5_C	Cul5	Cullin-5 OS	R.K#LM*LDTWNESIFSNIK#.N	6.10	3.29	1.85	0.54
Q9D5V5_C	Cul5	Cullin-5 OS	K.K#LTSEEIEAK#.L	10.25	10.43	0.98	1.02
Q9D5V5_C	Cul5	Cullin-5 OS	K.LALPADSVNIK#.I	39.96	10.71	3.73	0.27
Q9D5V5_C	Cul5	Cullin-5 OS	R.QVLLYDPQVNSPK#.D	11.57	3.05	3.79	0.26
Q9D5V5_C	Cul5	Cullin-5 OS	R.TLWSLVAFPK#.L	18.42	5.87	3.14	0.32
Q9D5V5_C	Cul5	Cullin-5 OS	K.DFTEGTLFSVNQDFSLIK#.N	14.34	4.11	3.49	0.29
Q9D5V5_C	Cul5	Cullin-5 OS	R.TLWSLVAFPK#.L	14.52	7.17	2.03	0.49
Q9D5V5_C	Cul5	Cullin-5 OS	R.TQEAIIQIM*K#.M	14.08	4.30	3.27	0.31
P53564_C	Cux1	Homeobox	R.ASETGSDEAIK#.S	11.76	9.71	1.21	0.83
P53564_C	Cux1	Homeobox	R.EMEAQQAALDPALKPAPLSQPDLTILTPK.H	4.36	2.23	1.95	0.51
P53564_C	Cux1	Homeobox	R.LIDVPDPVPALDVGQQLEIK.V	9.97	9.60	1.04	0.96
P53564_C	Cux1	Homeobox	K.SQAETIALEK#.E	16.17	9.17	1.76	0.57
P53564_C	Cux1	Homeobox	K.SQGGLAEVAAAPADREEATQPAEK.A	3.90	12.24	0.32	3.14
P53564_C	Cux1	Homeobox	R.SSALPSTSAPANAPAR.R	4.42	12.82	0.34	2.90
P53564_C	Cux1	Homeobox	K.TPAAPETSTAALPSAPALK#K#.E	10.07	9.73	1.03	0.97
Q9JHS9_C	Cwc15	Spliceosom	R.MENILSGNPLLNLTGPSQPQANFK.V	4.69	4.37	1.07	0.93
Q8C5N3_C	Cwc22	Pre-mRNA-	R.GINAIFER.L	6.07	12.32	0.49	2.03
Q8C5N3_C	Cwc22	Pre-mRNA-	R.LKDETLQPFFEGLLPR.D	9.09	33.07	0.28	3.64
Q8C5N3_C	Cwc22	Pre-mRNA-	K.M*EFAESQTK#.E	13.68	5.99	2.28	0.44
Q8C5N3_C	Cwc22	Pre-mRNA-	R.M*M*QEQITDK#.S	17.34	11.11	1.56	0.64
Q8C5N3_C	Cwc22	Pre-mRNA-	R.TGGAYIPPAK#.L	9.72	7.87	1.24	0.81
Q8CI33_C1	Cwf19l1	CWF19-like	K.DFEPFDFTLDD.-	10.51	10.51	1.00	1.00
Q8CI33_C1	Cwf19l1	CWF19-like	R.FIALANVGNPEK#.K	19.14	11.78	1.62	0.62
Q8CI33_C1	Cwf19l1	CWF19-like	K.GVDILLTSPWPK#.Y	12.72	9.03	1.41	0.71
Q9CWW7_	Cxxc1	CXXC-type	R.IYEILPQR.I	5.67	9.27	0.61	1.63
Q9CWW7_	Cxxc1	CXXC-type	K.LDELFEQER.N	3.05	8.37	0.36	2.74
Q9CWW7_	Cxxc1	CXXC-type	R.RPPPTQQQPQQSQK.L	1.52	3.54	0.43	2.33
Q9DCN2_N	Cyb5r3	NADH-cyto	K.IGDTIEFR.G	9.01	25.98	0.35	2.88
Q9DCN2_N	Cyb5r3	NADH-cyto	K.M*SQYLENM*K#.I	11.76	6.19	1.90	0.53
Q9DCN2_N	Cyb5r3	NADH-cyto	R.STPAITLENPDIK#.Y	16.38	12.00	1.37	0.73
Q7TMB8_C	Cyfip1	Cytoplasmi	K.FQILNDEIITILDK#.Y	9.72	2.28	4.27	0.23
Q7TMB8_C	Cyfip1	Cytoplasmi	K.TVEVLEPEVTK#.L	11.03	5.51	2.00	0.50
Q7TMB8_C	Cyfip1	Cytoplasmi	K.FQILNDEIITILDK#.Y	27.81	4.88	5.70	0.18
Q7TMB8_C	Cyfip1	Cytoplasmi	K.LADQIFAYYK#.V	28.22	6.27	4.50	0.22
Q7TMB8_C	Cyfip1	Cytoplasmi	R.LGTPQQIAIAR.E	18.29	16.33	1.12	0.89
Q7TMB8_C	Cyfip1	Cytoplasmi	K.NVIQSVLQAIR.K	12.36	12.11	1.02	0.98
Q7TMB8_C	Cyfip1	Cytoplasmi	K.SLLQGTILQYVK#.T	36.34	5.34	6.80	0.15
Q7TMB8_C	Cyfip1	Cytoplasmi	R.SSLEGPTILDIEK#.F	53.12	18.34	2.90	0.35
Q7TMB8_C	Cyfip1	Cytoplasmi	K.TVEVLEPEVTK#.L	44.22	12.68	3.49	0.29
Q9D172_E	D10Jhu81e	ES1 protein	K.GVEVTVGHEQEEGGK#WPYAGTAEAIK#.A	4.12	1.31	3.14	0.32

Q9D172_E	D10Jhu81	ES1 protein	K.ITSLAQLNAANHDAAIFPGGFGAAK#.N	24.35	6.06	4.02	0.25
Q9ER88_R	Dap3	28S riboso	K.TVFPHGLPPR.Y	1.82	22.37	0.08	12.27
O54784_D	Dapk3	Death-asso	R.VLEDVAAAEQGLR.E	4.88	9.67	0.50	1.98
Q922B2_S	Dars	Aspartate--	R.ALHHGIDLEK#.I	79.20	23.11	3.43	0.29
Q922B2_S	Dars	Aspartate--	R.EAGVEM*DDEEDLSTPNEK#.L	30.59	5.71	5.36	0.19
Q922B2_S	Dars	Aspartate--	R.EAGVEMDDEEDLSTPNEK#.L	7.13	1.86	3.82	0.26
Q922B2_S	Dars	Aspartate--	R.EIVDAAEDYAK#.E	105.69	27.02	3.91	0.26
Q922B2_S	Dars	Aspartate--	K.ESIIDVEGVVR.K	24.25	21.05	1.15	0.87
Q922B2_S	Dars	Aspartate--	K.FAANINK#.E	118.81	32.86	3.62	0.28
Q922B2_S	Dars	Aspartate--	R.FQTEIQTVSK#.Q	75.19	22.32	3.37	0.30
Q922B2_S	Dars	Aspartate--	K.GFVEIQTPK#.I	61.43	16.41	3.74	0.27
Q922B2_S	Dars	Aspartate--	K.IISAASEGGANVFTVSYFK#.N	32.25	8.41	3.83	0.26
Q922B2_S	Dars	Aspartate--	K.IYVISLAEPR.L	18.08	15.29	1.18	0.85
Q922B2_S	Dars	Aspartate--	K.NNAYLAQSPQLYK#.Q	36.54	12.79	2.86	0.35
Q922B2_S	Dars	Aspartate--	R.QQQFNVQALVAVGDHASK#.Q	36.35	11.25	3.23	0.31
Q922B2_S	Dars	Aspartate--	R.ALHHGIDLEK#.I	40.71	15.70	2.59	0.39
Q922B2_S	Dars	Aspartate--	R.EAGVEM*DDEEDLSTPNEK#.L	13.31	3.02	4.42	0.23
Q922B2_S	Dars	Aspartate--	R.EIVDAAEDYAK#.E	36.84	9.62	3.83	0.26
Q922B2_S	Dars	Aspartate--	R.FQTEIQTVSK#.Q	49.07	11.59	4.23	0.24
Q922B2_S	Dars	Aspartate--	K.IISAASEGGANVFTVSYFK#.N	12.35	3.45	3.58	0.28
Q922B2_S	Dars	Aspartate--	K.NNAYLAQSPQLYK#.Q	15.85	6.28	2.53	0.40
Q922B2_S	Dars	Aspartate--	R.ALHHGIDLEK#.I	105.12	29.40	3.58	0.28
Q922B2_S	Dars	Aspartate--	R.EAGVEM*DDEEDLSTPNEK#.L	41.27	9.60	4.30	0.23
Q922B2_S	Dars	Aspartate--	R.EIVDAAEDYAK#.E	66.55	13.83	4.81	0.21
Q922B2_S	Dars	Aspartate--	K.FAANINK#.E	81.28	25.93	3.13	0.32
Q922B2_S	Dars	Aspartate--	R.FQTEIQTVSK#.Q	120.85	29.39	4.11	0.24
Q922B2_S	Dars	Aspartate--	K.GFVEIQTPK#.I	52.51	14.39	3.65	0.27
Q922B2_S	Dars	Aspartate--	K.IISAASEGGANVFTVSYFK#.N	36.77	9.95	3.70	0.27
Q922B2_S	Dars	Aspartate--	K.NNAYLAQSPQLYK#.Q	43.83	12.14	3.61	0.28
Q922B2_S	Dars	Aspartate--	R.QQQFNVQALVAVGDHASK#.Q	28.05	10.93	2.57	0.39
Q922B2_S	Dars	Aspartate--	R.VK#DLTVQK#.A	18.71	8.30	2.25	0.44
Q3UKR0_Q	Daxx	Death dom	K.ELDLSELDDPDSSYLQEAR.L	2.40	5.00	0.48	2.08
Q3UKR0_Q	Daxx	Death dom	R.LLGTAPQPSDPPK#.A	19.26	10.38	1.86	0.54
Q9QXS6_D	Dbn1	Drebrin OS	K.DSQAALPK#.Y	56.95	23.14	2.46	0.41
Q9QXS6_D	Dbn1	Drebrin OS	R.EQFWEQAK#.K	45.57	31.10	1.47	0.68
Q9QXS6_D	Dbn1	Drebrin OS	R.K#QQSLEAEEAK#.R	16.00	9.08	1.76	0.57
Q9QXS6_D	Dbn1	Drebrin OS	K.KSESEVEEAAAIIAQRPDNPR.E	2.09	27.76	0.08	13.31
Q9QXS6_D	Dbn1	Drebrin OS	K.LAASGEGGLQELSGHFENQK#.V	129.92	70.62	1.84	0.54
Q9QXS6_D	Dbn1	Drebrin OS	R.LREDENAEPVGTTYQK.T	26.48	48.18	0.55	1.82
Q9QXS6_D	Dbn1	Drebrin OS	R.M*APTPIPTR.S	8.26	27.33	0.30	3.31
Q9QXS6_D	Dbn1	Drebrin OS	K.QQSLEAEEAK#.R	33.40	18.57	1.80	0.56
Q9QXS6_D	Dbn1	Drebrin OS	K.SESEVEEAAAIIAQRPDNPR.E	4.22	39.02	0.11	9.25
Q9QXS6_D	Dbn1	Drebrin OS	R.SPSDSSTASTPIAEQIER.A	10.78	37.40	0.29	3.47
Q9QXS6_D	Dbn1	Drebrin OS	K.VAEFFQGVDVIVNASSVEDIDAGAIGQR.L	6.63	11.51	0.58	1.73
Q9QXS6_D	Dbn1	Drebrin OS	K.YVLINWVGEDVPDAR.K	10.84	28.29	0.38	2.61
Q62418_D	Dbnl	Drebrin-lik	R.AM*STTSVTSSQPGK#.L	20.62	3.09	6.68	0.15
Q62418_D	Dbnl	Drebrin-lik	K.ASGANYSFHK#.E	6.68	2.12	3.16	0.32
Q62418_D	Dbnl	Drebrin-lik	K.ESTSFQDVGPQAPVGSVYQK#.T	6.34	8.44	0.75	1.33
Q62418_D	Dbnl	Drebrin-lik	R.TGEPEQEAVSR.T	6.74	6.31	1.07	0.94
P53395_O	Dbt	Lipoamide	R.ILK#EDILSFLEK#.Q	15.01	3.23	4.65	0.21
P61963_D	Dcaf7	DDB1- and	K.GVYPDLLATSGDYLR.V	2.85	9.87	0.29	3.46
P61963_D	Dcaf7	DDB1- and	R.LALGSFVEEYNNK.V	16.87	13.93	1.21	0.83
Q9JLM8_D	Dclk1	Serine/thre	K.NVNPNWSVNVK.T	12.46	12.18	1.02	0.98
Q9JLM8_D	Dclk1	Serine/thre	R.SFEALLADLTR.T	2.77	13.66	0.20	4.94
Q9JLM8_D	Dclk1	Serine/thre	K.TAHSFEQVLTDITDAIK#.L	10.03	8.01	1.25	0.80
Q91YD3_D	Dcp1a	mRNA-deca	R.APVSLANPAGTALPSVDLLQK.L	3.48	3.80	0.91	1.09
Q9DAR7_D	Dcps	m7GpppX	R.TDDPLLQLLQK#.A	25.28	4.55	5.56	0.18
Q9DAR7_D	Dcps	m7GpppX	K.TPFQVEHVAQLLTGSPELK#.L	26.20	10.75	2.44	0.41
Q9DAR7_D	Dcps	m7GpppX	K.VNEDSGDTHGEDAVVILEK#.T	15.00	4.74	3.17	0.32
O08788_D	Dctn1	Dynactin s	K.SPSAQLM*EQVAQLK#.S	7.36	19.21	0.38	2.61
O08788_D	Dctn1	Dynactin s	R.AEITDAEGLGLK#.L	44.92	26.29	1.71	0.59
O08788_D	Dctn1	Dynactin s	R.AESLQQEVEALK#.E	10.35	6.68	1.55	0.65
O08788_D	Dctn1	Dynactin s	R.AFLQGGQEATDIALLLR.D	6.91	20.67	0.33	2.99
O08788_D	Dctn1	Dynactin s	R.AKEEQQDDTVYM*GK.V	10.03	5.39	1.86	0.54
O08788_D	Dctn1	Dynactin s	K.DFEETM*DALQADIDQLEAEK#AELK#.Q	7.13	3.58	2.00	0.50
O08788_D	Dctn1	Dynactin s	R.ELTNQQEASVER.Q	21.22	46.20	0.46	2.18
O08788_D	Dctn1	Dynactin s	K.ETVTQRPGATVPTDFATFPSSAFLR.A	5.41	16.81	0.32	3.11
O08788_D	Dctn1	Dynactin s	K.GSDGAASSYQLK#.Q	33.65	23.16	1.45	0.69
O08788_D	Dctn1	Dynactin s	K.IKGEELSEANVR.L	11.76	25.33	0.46	2.15
O08788_D	Dctn1	Dynactin s	K.IQLEQVQEWK#.S	54.33	36.74	1.48	0.68
O08788_D	Dctn1	Dynactin s	K.NQELEVVR.Q	5.92	13.30	0.44	2.25
O08788_D	Dctn1	Dynactin s	R.QQQPPPETFDFK#.I	14.42	12.89	1.12	0.89
O08788_D	Dctn1	Dynactin s	K.RVEAAQETVADYQQTIKK.Y	3.85	11.80	0.33	3.06
O08788_D	Dctn1	Dynactin s	R.SLDFLIELLHK#DQLDETVNVEPLTK#.A	12.71	6.93	1.83	0.55
O08788_D	Dctn1	Dynactin s	K.SLSDTIEK#.L	33.39	21.13	1.58	0.63
O08788_D	Dctn1	Dynactin s	K.SPSAQLM*EQVAQLK#.S	19.84	12.85	1.54	0.65
O08788_D	Dctn1	Dynactin s	R.VDELTTDLEILK#AEIEEK#.G	82.00	36.91	2.22	0.45
O08788_D	Dctn1	Dynactin s	R.VEAAQETVADYQQTIK#.K	7.36	5.92	1.24	0.80
O08788_D	Dctn1	Dynactin s	K.WVGVILDEAK#.G	29.64	17.71	1.67	0.60
O08788_D	Dctn1	Dynactin s	R.AEITDAEGLGLK#.L	64.40	34.89	1.85	0.54
O08788_D	Dctn1	Dynactin s	R.AESLQQEVEALK#.E	14.22	11.64	1.22	0.82
O08788_D	Dctn1	Dynactin s	R.AFLQGGQEATDIALLLR.D	9.27	22.40	0.41	2.42
O08788_D	Dctn1	Dynactin s	K.DFEETMDALQADIDQLEAEK#AELK#.Q	14.04	10.41	1.35	0.74
O08788_D	Dctn1	Dynactin s	K.DSPLLLQQISAM*R.L	5.37	10.58	0.51	1.97
O08788_D	Dctn1	Dynactin s	R.ELTNQQEASVER.Q	18.51	54.16	0.34	2.93
O08788_D	Dctn1	Dynactin s	K.ETVTQRPGATVPTDFATFPSSAFLR.A	8.16	22.21	0.37	2.72
O08788_D	Dctn1	Dynactin s	K.GSDGAASSYQLK#.Q	51.16	32.26	1.59	0.63
O08788_D	Dctn1	Dynactin s	K.IKGEELSEANVR.L	10.77	38.07	0.28	3.53
O08788_D	Dctn1	Dynactin s	K.IQLEQVQEWK#.S	36.27	23.08	1.57	0.64
O08788_D	Dctn1	Dynactin s	R.LDETQTLLR.K	14.47	34.96	0.41	2.42
O08788_D	Dctn1	Dynactin s	K.M*QEQQADLQR.R	11.91	20.56	0.58	1.73
O08788_D	Dctn1	Dynactin s	K.MQEQQADLQR.R	4.83	13.31	0.36	2.76
O08788_D	Dctn1	Dynactin s	K.NQELEVVR.Q	84.11	18.53	4.54	0.22
O08788_D	Dctn1	Dynactin s	R.QQQPPPETFDFK#.I	15.75	11.03	1.43	0.70
O08788_D	Dctn1	Dynactin s	K.RVEAAQETVADYQQTIKK.Y	4.49	14.52	0.31	3.23
O08788_D	Dctn1	Dynactin s	K.SLSDTIEK#.L	33.28	29.05	1.15	0.87
O08788_D	Dctn1	Dynactin s	K.SPSAQLM*EQVAQLK#.S	23.88	13.99	1.71	0.59
O08788_D	Dctn1	Dynactin s	K.SPSAQLMEQVAQLK.S	10.80	38.51	0.28	3.57
O08788_D	Dctn1	Dynactin s	R.VDELTTDLEILKAEIEEK.G	45.03	21.53	2.09	0.48
O08788_D	Dctn1	Dynactin s	R.VEAAQETVADYQQTIK#.K	11.52	6.14	1.88	0.53
O08788_D	Dctn1	Dynactin s	K.WVGVILDEAK#.G	35.23	20.36	1.73	0.58
O08788_D	Dctn1	Dynactin s	K.YYQHLYSIHLAEQPEDSTM*QLADHIK#.F	4.16	1.61	2.59	0.39
Q99KJ8_D	Dctn2	Dynactin s	K.ASVEDADTQNK#.V	31.74	24.42	1.30	0.77

Q99KJ8_D	Dctn2	Dynactin s	K.DNTALLTQVQTTMR.E	7.08	18.26	0.39	2.58
Q99KJ8_D	Dctn2	Dynactin s	R.ENLATVEGNFASIDAR.M	14.93	53.18	0.28	3.56
Q99KJ8_D	Dctn2	Dynactin s	K.LLGPDAAINLADPDGALAK#.R	29.09	14.63	1.99	0.50
Q99KJ8_D	Dctn2	Dynactin s	R.LLHEVQELTTEVEK#.I	23.10	16.62	1.39	0.72
Q99KJ8_D	Dctn2	Dynactin s	R.LLLQLEATK#.S	76.79	45.73	1.68	0.60
Q99KJ8_D	Dctn2	Dynactin s	R.LQSVLGK#.V	74.32	52.43	1.42	0.71
Q99KJ8_D	Dctn2	Dynactin s	R.LTELEATVR.C	16.39	53.47	0.31	3.26
Q99KJ8_D	Dctn2	Dynactin s	K.QQLVASHLEK#.L	35.89	28.99	1.24	0.81
Q99KJ8_D	Dctn2	Dynactin s	K.RLLLQLEATK.S	3.95	12.09	0.33	3.06
Q99KJ8_D	Dctn2	Dynactin s	R.TGYESGDYEM*LGEGLGVK#.E	18.05	10.15	1.78	0.56
Q99KJ8_D	Dctn2	Dynactin s	R.TGYESGDYEMLGEGLGVK#.E	17.03	13.01	1.31	0.76
Q99KJ8_D	Dctn2	Dynactin s	K.VSALDLAVLDQVEAR.L	19.05	61.66	0.31	3.24
Q99KJ8_D	Dctn2	Dynactin s	R.WSPVASTLPELVQR.L	16.43	52.23	0.31	3.18
Q99KJ8_D	Dctn2	Dynactin s	K.YADLPGIAR.N	16.16	54.13	0.30	3.35
Q99KJ8_D	Dctn2	Dynactin s	K.DNTALLTQVQTTM*R.E	3.32	6.22	0.53	1.87
Q99KJ8_D	Dctn2	Dynactin s	K.DNTALLTQVQTTM*RENLATVEGNFASIDAR.M	1.60	1.58	1.01	0.99
Q99KJ8_D	Dctn2	Dynactin s	R.LTELEATVR.C	5.44	13.23	0.41	2.43
Q99KJ8_D	Dctn2	Dynactin s	K.VSALDLAVLDQVEAR.L	10.44	18.76	0.56	1.80
Q99KJ8_D	Dctn2	Dynactin s	R.WSPVASTLPELVQR.L	4.29	5.23	0.82	1.22
Q9Z0Y1_D	Dctn3	Dynactin s	K.ALLEGYNK#.T	92.50	81.36	1.14	0.88
Q9Z0Y1_D	Dctn3	Dynactin s	K.IEDLIK#.Y	24.14	12.27	1.97	0.51
Q9Z0Y1_D	Dctn3	Dynactin s	R.K#VADGLVK#.V	11.97	10.63	1.13	0.89
Q9Z0Y1_D	Dctn3	Dynactin s	K.TTM*LLSK#.Q	100.51	15.80	6.36	0.16
Q9Z0Y1_D	Dctn3	Dynactin s	K.VQVALGNIASK#.R	133.53	69.46	1.92	0.52
Q9Z0Y1_D	Dctn3	Dynactin s	R.WVYGPGGTR.G	14.81	43.36	0.34	2.93
Q9Z0Y1_D	Dctn3	Dynactin s	K.YLDPEYIDR.I	21.79	81.20	0.27	3.73
Q8CBY8_D	Dctn4	Dynactin s	R.AGASISTLAGLSLR.E	4.83	21.01	0.23	4.35
Q8CBY8_D	Dctn4	Dynactin s	R.ATSISTQLPDDPAK#.T	38.70	28.19	1.37	0.73
Q8CBY8_D	Dctn4	Dynactin s	K.IEPAQAVAEVEPLPEDYYTRPVNLTEVTTLQQR.L	2.03	6.09	0.33	3.00
Q8CBY8_D	Dctn4	Dynactin s	K.IQLVAVNYIPEVR.I	6.40	17.33	0.37	2.71
Q8CBY8_D	Dctn4	Dynactin s	K.LIEYYQQLAQK#.E	40.85	32.51	1.26	0.80
Q8CBY8_D	Dctn4	Dynactin s	R.LLQPDLQPVSASQLYPR.H	87.90	93.45	0.94	1.06
Q8CBY8_D	Dctn4	Dynactin s	K.IQLVAVNYIPEVR.I	1.84	3.73	0.49	2.02
Q8CBY8_D	Dctn4	Dynactin s	K.LIEYYQQLAQK#.E	6.17	2.57	2.40	0.42
Q9CXV9_D	Dcun1d5	DCN1-like	R.K#APGVAAAVAEDAGLK#K#.C	9.66	5.69	1.70	0.59
Q9CXV9_D	Dcun1d5	DCN1-like	R.SQLNDISSFK#.N	17.88	7.54	2.37	0.42
Q9D9Z5_D	Dda1	DET1- and	R.EYPSEQIIVTEK#.T	12.06	6.15	1.96	0.51
Q3U1J4_D	Ddb1	DNA damag	K.DLLFILTAK#.Y	19.85	10.91	1.82	0.55
Q3U1J4_D	Ddb1	DNA damag	K.GESK#DLLFILTAK#.Y	13.16	3.68	3.57	0.28
Q3U1J4_D	Ddb1	DNA damag	R.IEVQDSSGGTTALRPSASTQALSSSVSSSK.L	10.23	24.03	0.43	2.35
Q3U1J4_D	Ddb1	DNA damag	R.IVVFQYSDGK#.L	59.18	20.76	2.85	0.35
Q3U1J4_D	Ddb1	DNA damag	R.LGDSQLVK#.L	50.78	26.95	1.88	0.53
Q3U1J4_D	Ddb1	DNA damag	K.LGK#DPNTYFIVGTAM*VYPEEAEPK#.Q	8.28	6.47	1.28	0.78
Q3U1J4_D	Ddb1	DNA damag	K.LGK#DPNTYFIVGTAMVYPEEAEPK#.Q	7.61	6.33	1.20	0.83
Q3U1J4_D	Ddb1	DNA damag	K.LLASINSTVR.L	11.40	24.74	0.46	2.17
Q3U1J4_D	Ddb1	DNA damag	K.LPSFELLHK#.E	28.02	19.18	1.46	0.68
Q3U1J4_D	Ddb1	DNA damag	K.LVFSNVNLK#.E	38.76	24.52	1.58	0.63
Q3U1J4_D	Ddb1	DNA damag	R.LYEWTTEK#.E	23.73	16.58	1.43	0.70
Q3U1J4_D	Ddb1	DNA damag	R.SVLLLAYKPM*EGNFEEIAR.D	4.70	15.58	0.30	3.32
Q3U1J4_D	Ddb1	DNA damag	R.SVLLLAYKPMEGNFEEIAR.D	3.10	10.57	0.29	3.41
Q3U1J4_D	Ddb1	DNA damag	K.TYEVSLR.E	11.22	22.65	0.50	2.02
Q3U1J4_D	Ddb1	DNA damag	K.VTLGTQPTVLR.T	10.13	24.04	0.42	2.37
Q3U1J4_D	Ddb1	DNA damag	K.YLAIAPPIIK#.Q	20.17	16.21	1.24	0.80
Q3U1J4_D	Ddb1	DNA damag	R.IEVQDSSGGTTALRPSASTQALSSSVSSSK.L	3.01	9.00	0.33	2.99
Q3U1J4_D	Ddb1	DNA damag	R.IVVFQYSDGK#.L	38.04	12.93	2.94	0.34
Q3U1J4_D	Ddb1	DNA damag	R.LGDSQLVK#.L	21.42	15.60	1.37	0.73
Q3U1J4_D	Ddb1	DNA damag	K.LGK#DPNTYFIVGTAM*VYPEEAEPK#.Q	4.93	4.91	1.00	1.00
Q3U1J4_D	Ddb1	DNA damag	K.LLASINSTVR.L	9.17	13.81	0.66	1.51
Q3U1J4_D	Ddb1	DNA damag	K.LVFSNVNLK#.E	24.28	8.57	2.83	0.35
Q3U1J4_D	Ddb1	DNA damag	K.YLAIAPPIIK#.Q	10.90	7.19	1.52	0.66
A2ADY9_D	Ddi2	Protein DD	R.LFSADPFDLEAQAK#.I	7.20	3.65	1.97	0.51
O54734_O	Ddost	Dolichyl-di	R.TLVLLDNLNVR.D	2.30	6.17	0.37	2.68
Q91VR5_D	Ddx1	ATP-depen	K.APDNYIVK#.S	31.29	20.92	1.50	0.67
Q91VR5_D	Ddx1	ATP-depen	K.DGFVALSK#.A	19.03	7.46	2.55	0.39
Q91VR5_D	Ddx1	ATP-depen	R.ELAEQTLNNVK#.Q	40.92	21.41	1.91	0.52
Q91VR5_D	Ddx1	ATP-depen	R.ELLIIGGVAAR.D	5.40	7.69	0.70	1.42
Q91VR5_D	Ddx1	ATP-depen	K.GHVDVLAPTVQELAALEK#.E	2.14	2.96	0.72	1.39
Q91VR5_D	Ddx1	ATP-depen	K.GHVDVLAPTVQELAALEK#.E	21.52	15.98	1.35	0.74
Q91VR5_D	Ddx1	ATP-depen	R.GIDIHGVPYVINVTLPDEK#.Q	16.10	8.55	1.88	0.53
Q91VR5_D	Ddx1	ATP-depen	R.LDDLVSTGK#.L	18.64	9.54	1.95	0.51
Q91VR5_D	Ddx1	ATP-depen	K.TGASVLNK#.W	10.72	9.15	1.17	0.85
Q91VR5_D	Ddx1	ATP-depen	R.VGWSTM*QASLDLGTDK#.F	7.84	1.81	4.33	0.23
Q91VR5_D	Ddx1	ATP-depen	K.GHVDVLAPTVQELAALEK.E	12.32	12.95	0.95	1.05
Q91VR5_D	Ddx1	ATP-depen	R.GIDIHGVPYVINVTLPDEK#.Q	7.60	2.99	2.54	0.39
Q91VR5_D	Ddx1	ATP-depen	K.ALIVEPSR.E	32.63	79.69	0.41	2.44
Q91VR5_D	Ddx1	ATP-depen	K.ALIVEPSRELAEQTLNNVK.Q	17.89	37.05	0.48	2.07
Q91VR5_D	Ddx1	ATP-depen	K.APDNYIVK#.S	185.56	111.14	1.67	0.60
Q91VR5_D	Ddx1	ATP-depen	K.DGFVALSK#.A	83.93	45.94	1.83	0.55
Q91VR5_D	Ddx1	ATP-depen	K.DLGLAFEIPAHIK#.N	91.84	72.02	1.28	0.78
Q91VR5_D	Ddx1	ATP-depen	K.DNTRPGANSPEM*WSEAIK.I	7.04	26.71	0.26	3.79
Q91VR5_D	Ddx1	ATP-depen	K.DNTRPGANSPEMWSEAIK.I	6.60	17.25	0.38	2.61
Q91VR5_D	Ddx1	ATP-depen	R.DQLSVLDNGVDIVVGTPGR.L	4.03	10.93	0.37	2.71
Q91VR5_D	Ddx1	ATP-depen	R.DQLSVLDNGVDIVVGTPGR.L	3.97	10.86	0.37	2.74
Q91VR5_D	Ddx1	ATP-depen	R.DQLSVLDNGVDIVVGTPGRLDDLVSTGK.L	7.22	17.95	0.40	2.48
Q91VR5_D	Ddx1	ATP-depen	K.EAQTSFLHLGYLPNQLFR.T	43.65	97.59	0.45	2.24
Q91VR5_D	Ddx1	ATP-depen	K.EAQTSFLHLGYLPNQLFR.T	3.16	7.57	0.42	2.39
Q91VR5_D	Ddx1	ATP-depen	R.ELAEQTLNNVK#.Q	240.87	119.04	2.02	0.49
Q91VR5_D	Ddx1	ATP-depen	R.ELLIIGGVAAR.D	33.25	72.61	0.46	2.18
Q91VR5_D	Ddx1	ATP-depen	K.FNFGEEEFK#FPPK#.D	18.29	10.50	1.74	0.57
Q91VR5_D	Ddx1	ATP-depen	K.GHVDVLAPTVQELAALEK#.E	193.03	110.99	1.74	0.57
Q91VR5_D	Ddx1	ATP-depen	R.GIDIHGVPYVINVTLPDEK#.Q	138.89	75.25	1.85	0.54
Q91VR5_D	Ddx1	ATP-depen	K.K#YIDNPK#.L	13.91	9.29	1.50	0.67
Q91VR5_D	Ddx1	ATP-depen	R.LDDLVSTGK#.L	128.21	60.74	2.11	0.47
Q91VR5_D	Ddx1	ATP-depen	K.LNLSQVR.F	41.80	112.74	0.37	2.70
Q91VR5_D	Ddx1	ATP-depen	K.SQHTGNAQVSQTK#.F	5.91	4.57	1.29	0.77
Q91VR5_D	Ddx1	ATP-depen	K.TGASVLNK#.W	98.36	66.79	1.47	0.68
Q91VR5_D	Ddx1	ATP-depen	R.VGWSTM*QASLDLGTDK#.F	25.32	13.08	1.94	0.52
Q91VR5_D	Ddx1	ATP-depen	R.VGWSTMQASLDLGTDK#.F	12.86	6.08	2.12	0.47
Q91VR5_D	Ddx1	ATP-depen	R.VGWSTM*QASLDLGTDK#FGFGFGGTGK#.K	21.27	8.82	2.41	0.41
Q91VR5_D	Ddx1	ATP-depen	K.VPVDEFDGK#.V	70.74	47.88	1.48	0.68
Q91VR5_D	Ddx1	ATP-depen	K.WQMNPYDR.G	5.10	14.25	0.36	2.80
Q91VR5_D	Ddx1	ATP-depen	K.ALIVEPSRELAEQTLNNVK.Q	2.46	8.26	0.30	3.36
Q91VR5_D	Ddx1	ATP-depen	K.DGFVALSK#.A	18.35	8.59	2.14	0.47

Q91VR5_D	Ddx1	ATP-depen	R.ELAEQTLNNVK#.Q	20.76	16.06	1.29	0.77
Q91VR5_D	Ddx1	ATP-depen	K.GHVDVLAPTVQELAALEK#.E	34.48	20.19	1.71	0.59
Q91VR5_D	Ddx1	ATP-depen	R.LDDLVSTGK#.L	25.65	13.04	1.97	0.51
Q91VR5_D	Ddx1	ATP-depen	K.LNLSQVR.F	6.31	14.73	0.43	2.34
Q91VR5_D	Ddx1	ATP-depen	K.VPVDEFDGK#.V	11.22	10.86	1.03	0.97
Q501J6_D	Ddx17	Probable A	K.APILIATDVASR.G	201.44	863.34	0.23	4.29
Q501J6_D	Ddx17	Probable A	R.DM*VGIAQTGSGK#.T	66.86	34.79	1.92	0.52
Q501J6_D	Ddx17	Probable A	R.DWVLNEFR.S	9.69	20.85	0.46	2.15
Q501J6_D	Ddx17	Probable A	R.ELAQQVQQVADDYGK.C	60.64	34.54	1.76	0.57
Q501J6_D	Ddx17	Probable A	K.FVINYDYPNSSEDYVHR.I	2.27	4.61	0.49	2.03
Q501J6_D	Ddx17	Probable A	R.GLDVEDVK#.F	372.72	330.95	1.13	0.89
Q501J6_D	Ddx17	Probable A	K.GTAYTFFTPGNLK#.Q	84.76	43.85	1.93	0.52
Q501J6_D	Ddx17	Probable A	K.LIQLM*EEIM*AEK#.E	8.87	2.94	3.02	0.33
Q501J6_D	Ddx17	Probable A	R.M*LDM*GFEPQIR.K	30.75	146.03	0.21	4.75
Q501J6_D	Ddx17	Probable A	R.MLDM*GFEPQIR.K	17.48	57.82	0.30	3.31
Q501J6_D	Ddx17	Probable A	R.M*LDMGFEPQIR.K	13.52	45.41	0.30	3.36
Q501J6_D	Ddx17	Probable A	R.MLDMGFEPQIR.K	12.67	53.07	0.24	4.19
Q501J6_D	Ddx17	Probable A	R.QLAEDFLR.D	8.54	18.32	0.47	2.15
Q501J6_D	Ddx17	Probable A	R.QTLM*WSATWPK#.E	86.04	71.19	1.21	0.83
Q501J6_D	Ddx17	Probable A	R.QTLMWSATWPK#.E	62.56	94.70	0.66	1.51
Q501J6_D	Ddx17	Probable A	R.SSQSSSQQFSGIGR.S	12.00	30.10	0.40	2.51
Q501J6_D	Ddx17	Probable A	K.VLEEANQAINPK#.L	120.89	70.41	1.72	0.58
Q501J6_D	Ddx17	Probable A	K.WDLSELPK#.F	30.42	16.23	1.87	0.53
Q501J6_D	Ddx17	Probable A	K.APILIATDVASR.G	1.15	6.81	0.17	5.93
Q501J6_D	Ddx17	Probable A	R.SSQSSSQQFSGIGR.S	13.60	6.58	2.07	0.48
Q501J6_D	Ddx17	Probable A	K.APILIATDVASR.G	138.30	364.73	0.38	2.64
Q501J6_D	Ddx17	Probable A	R.DM*VGIAQTGSGK#.T	153.46	66.25	2.32	0.43
Q501J6_D	Ddx17	Probable A	R.DMVGIAQTGSGK#.T	66.94	32.59	2.05	0.49
Q501J6_D	Ddx17	Probable A	R.DWVLNEFR.S	18.17	33.83	0.54	1.86
Q501J6_D	Ddx17	Probable A	R.ELAQQVQQVADDYGK#.C	185.46	79.19	2.34	0.43
Q501J6_D	Ddx17	Probable A	R.GLDVEDVK#.F	329.58	202.68	1.63	0.61
Q501J6_D	Ddx17	Probable A	K.GTAYTFFTPGNLK#.Q	209.11	94.28	2.22	0.45
Q501J6_D	Ddx17	Probable A	K.KKWDLSELPK.F	42.85	17.94	2.39	0.42
Q501J6_D	Ddx17	Probable A	K.K#WDLSELPK#.F	23.09	13.68	1.69	0.59
Q501J6_D	Ddx17	Probable A	R.LIDFLESGK#.T	221.17	79.52	2.78	0.36
Q501J6_D	Ddx17	Probable A	K.LIQLM*EEIM*AEK#.E	13.75	5.52	2.49	0.40
Q501J6_D	Ddx17	Probable A	K.LIQLMEEIMAEK#.E	18.26	6.34	2.88	0.35
Q501J6_D	Ddx17	Probable A	R.M*LDM*GFEPQIR.K	30.96	92.24	0.34	2.98
Q501J6_D	Ddx17	Probable A	R.MLDM*GFEPQIR.K	13.46	30.80	0.44	2.29
Q501J6_D	Ddx17	Probable A	R.MLDMGFEPQIR.K	8.50	23.43	0.36	2.76
Q501J6_D	Ddx17	Probable A	R.QLAEDFLR.D	21.88	49.26	0.44	2.25
Q501J6_D	Ddx17	Probable A	R.QTLM*WSATWPK#.E	62.88	35.00	1.80	0.56
Q501J6_D	Ddx17	Probable A	R.QTLMWSATWPK.E	42.40	31.12	1.36	0.73
Q501J6_D	Ddx17	Probable A	R.SSQSSSQQFSGIGR.S	55.04	128.09	0.43	2.33
Q501J6_D	Ddx17	Probable A	K.VLEEANQAINPK#.L	302.83	129.58	2.34	0.43
Q501J6_D	Ddx17	Probable A	K.WDLSELPK#.F	50.42	26.81	1.88	0.53
Q501J6_D	Ddx17	Probable A	K.APILIATDVASR.G	17.15	70.44	0.24	4.11
Q501J6_D	Ddx17	Probable A	R.ELAQQVQQVADDYGK#.C	11.05	10.11	1.09	0.91
Q501J6_D	Ddx17	Probable A	K.GTAYTFFTPGNLK#.Q	15.65	4.88	3.21	0.31
Q501J6_D	Ddx17	Probable A	R.M*LDM*GFEPQIR.K	5.00	10.49	0.48	2.10
Q501J6_D	Ddx17	Probable A	R.SSQSSSQQFSGIGR.S	4.33	9.38	0.46	2.17
Q501J6_D	Ddx17	Probable A	K.VLEEANQAINPK#.L	19.19	9.24	2.08	0.48
Q8K363_D	Ddx18	ATP-depen	K.VPLNQFDFSWSK#.V	17.82	19.81	0.90	1.11
Q8K363_D	Ddx18	ATP-depen	K.VSDIQSQLEK#.L	30.02	28.73	1.04	0.96
Q8K363_D	Ddx18	ATP-depen	K.VPLNQFDFSWSK#.V	11.87	9.86	1.20	0.83
Q8K363_D	Ddx18	ATP-depen	K.VSDIQSQLEK.L	15.37	20.01	0.77	1.30
Q61655_D	Ddx19a	ATP-depen	R.AAQSLLNK#.L	91.37	43.33	2.11	0.47
Q61655_D	Ddx19a	ATP-depen	R.DPSSPLYSVK#.S	112.84	41.13	2.74	0.36
Q61655_D	Ddx19a	ATP-depen	R.EEETLDTIK#.Q	72.75	36.57	1.99	0.50
Q61655_D	Ddx19a	ATP-depen	K.EGHQVALLSGEM*M*VEQR.A	9.78	11.69	0.84	1.20
Q61655_D	Ddx19a	ATP-depen	R.GLAVNMVDSK#.H	30.91	14.56	2.12	0.47
Q61655_D	Ddx19a	ATP-depen	R.IQEHFNK#.K	55.83	15.55	3.59	0.28
Q61655_D	Ddx19a	ATP-depen	R.K#TASWLAAELSK#.E	18.71	5.59	3.34	0.30
Q61655_D	Ddx19a	ATP-depen	R.LDTDDLDEIEK#.I	113.16	48.32	2.34	0.43
Q61655_D	Ddx19a	ATP-depen	R.SNLVDNTNQVEVLQR.D	24.73	46.01	0.54	1.86
Q61655_D	Ddx19a	ATP-depen	K.TAAFVLAM*LSR.V	6.91	18.78	0.37	2.72
Q61655_D	Ddx19a	ATP-depen	K.TASWLAAELSK#.E	76.58	28.32	2.70	0.37
Q61655_D	Ddx19a	ATP-depen	K.TSTTAEK#TEEEEK#.E	4.84	2.38	2.03	0.49
Q61655_D	Ddx19a	ATP-depen	K.VFVLDEADVM*IATQGHQDQSIR.I	10.31	11.36	0.91	1.10
Q61655_D	Ddx19a	ATP-depen	K.VFVLDEADVMIATQGHQDQSIR.I	9.92	16.31	0.61	1.64
Q61655_D	Ddx19a	ATP-depen	R.AAQSLLNK#.L	25.45	7.26	3.51	0.29
Q61655_D	Ddx19a	ATP-depen	R.DPSSPLYSVK#.S	30.13	14.76	2.04	0.49
Q61655_D	Ddx19a	ATP-depen	R.SNLVDNTNQVEVLQR.D	6.98	10.51	0.66	1.51
Q61655_D	Ddx19a	ATP-depen	K.TSTTAEKTEEEEKEDR.A	3.70	12.80	0.29	3.46
Q61655_D	Ddx19a	ATP-depen	R.AAQSLLNK#.L	34.47	12.81	2.69	0.37
Q61655_D	Ddx19a	ATP-depen	R.DPSSPLYSVK#.S	35.94	14.03	2.56	0.39
Q61655_D	Ddx19a	ATP-depen	K.EGHQVALLSGEM*M*VEQR.A	8.71	11.56	0.75	1.33
Q61655_D	Ddx19a	ATP-depen	K.HSM*NILNR.I	9.98	18.77	0.53	1.88
Q61655_D	Ddx19a	ATP-depen	R.LDTDDLDEIEK#.I	41.36	17.75	2.33	0.43
Q61655_D	Ddx19a	ATP-depen	R.SNLVDNTNQVEVLQR.D	6.29	12.48	0.50	1.98
Q61655_D	Ddx19a	ATP-depen	K.TASWLAAELSK#.E	25.03	5.57	4.50	0.22
Q61655_D	Ddx19a	ATP-depen	K.TSTTAEKTEEEEKEDR.A	7.89	12.98	0.61	1.65
Q9JIK5_DD	Ddx21	Nucleolar R	R.GVNFLFPIQAK.T	9.15	12.55	0.73	1.37
Q9JIK5_DD	Ddx21	Nucleolar R	R.IGVPSATEIIK#.A	15.06	11.67	1.29	0.77
Q9JIK5_DD	Ddx21	Nucleolar R	R.TEAVTEIQEK.W	16.12	17.41	0.93	1.08
Q9JIK5_DD	Ddx21	Nucleolar R	R.AAVIGDVIR.V	81.28	187.11	0.43	2.30
Q9JIK5_DD	Ddx21	Nucleolar R	R.APQVLVLAPTR.E	27.17	126.93	0.21	4.67
Q9JIK5_DD	Ddx21	Nucleolar R	K.DFSDITK#K#.L	47.65	44.32	1.08	0.93
Q9JIK5_DD	Ddx21	Nucleolar R	K.EGAFSNFPISEETVK#.L	139.94	115.29	1.21	0.82
Q9JIK5_DD	Ddx21	Nucleolar R	R.ELANQVSK#.D	209.26	125.42	1.67	0.60
Q9JIK5_DD	Ddx21	Nucleolar R	K.ELK#EQLGESIDAK#.V	49.15	45.17	1.09	0.92
Q9JIK5_DD	Ddx21	Nucleolar R	K.EQLGESIDAK#.V	38.85	36.54	1.06	0.94
Q9JIK5_DD	Ddx21	Nucleolar R	K.GAVEALAAALAHISGATSVDQR.S	52.95	229.15	0.23	4.33
Q9JIK5_DD	Ddx21	Nucleolar R	K.GM*VFLK#.G	43.15	35.18	1.23	0.82
Q9JIK5_DD	Ddx21	Nucleolar R	R.GVNFLFPIQAK#.T	329.30	296.41	1.11	0.90
Q9JIK5_DD	Ddx21	Nucleolar R	R.IGVPSATEIIK#.A	166.17	158.27	1.05	0.95
Q9JIK5_DD	Ddx21	Nucleolar R	K.KGPSEDDVDPPK.S	42.07	49.28	0.85	1.17
Q9JIK5_DD	Ddx21	Nucleolar R	K.K#QEEEPQDDTASTSK#.T	22.82	24.85	0.92	1.09
Q9JIK5_DD	Ddx21	Nucleolar R	K.LGSDGAEESM*ETLPKPSEK.K	45.42	59.86	0.76	1.32
Q9JIK5_DD	Ddx21	Nucleolar R	K.LGSDGAEESMETLPK#PSEK#.K	29.11	34.02	0.86	1.17
Q9JIK5_DD	Ddx21	Nucleolar R	R.LLDSVPPTAISHFK#.Q	60.64	58.60	1.03	0.97
Q9JIK5_DD	Ddx21	Nucleolar R	K.LQGGLQER.K	26.62	120.69	0.22	4.53
Q9JIK5_DD	Ddx21	Nucleolar R	R.NGNFGVLVATNVAAR.G	4.47	18.01	0.25	4.03

Q9JIK5_DD	Ddx21	Nucleolar R	R.RWQLTVATEQPELEGPPDGYR.G	1.14	8.96	0.13	7.85
Q9JIK5_DD	Ddx21	Nucleolar R	R.SGIDILVGTPGR.I	30.13	143.06	0.21	4.75
Q9JIK5_DD	Ddx21	Nucleolar R	K.SK#TEEATEGMEEAVSSK#.A	25.83	21.32	1.21	0.83
Q9JIK5_DD	Ddx21	Nucleolar R	K.SKTEEATEGMEEAVSSK.A	61.49	45.10	1.36	0.73
Q9JIK5_DD	Ddx21	Nucleolar R	K.SK#TEEATEGM*EEAVSSK#.A	103.68	93.54	1.11	0.90
Q9JIK5_DD	Ddx21	Nucleolar R	K.SKTEEATEGM*EEAVSSK.A	38.46	45.08	0.85	1.17
Q9JIK5_DD	Ddx21	Nucleolar R	R.SLINSQAGFVTM*ILR.C	4.39	24.65	0.18	5.61
Q9JIK5_DD	Ddx21	Nucleolar R	R.SLINSQAGFVTMILR.C	8.08	37.90	0.21	4.69
Q9JIK5_DD	Ddx21	Nucleolar R	K.SNSSDAPGEESSSETEKEIPVEQK.E	64.27	70.68	0.91	1.10
Q9JIK5_DD	Ddx21	Nucleolar R	K.STYEQVDLIGK#.K	52.40	39.21	1.34	0.75
Q9JIK5_DD	Ddx21	Nucleolar R	R.TEAVTEIQEK#.W	245.91	214.43	1.15	0.87
Q9JIK5_DD	Ddx21	Nucleolar R	K.TEEATEGMEEAVSSK#.A	11.27	7.16	1.57	0.64
Q9JIK5_DD	Ddx21	Nucleolar R	K.TEEATEGM*EEAVSSK#.A	26.10	23.46	1.11	0.90
Q9JIK5_DD	Ddx21	Nucleolar R	K.TFHHVYSGK.D	21.10	23.34	0.90	1.11
Q9JIK5_DD	Ddx21	Nucleolar R	K.TFSFAIPLIEK.L	284.53	293.54	0.97	1.03
Q9JIK5_DD	Ddx21	Nucleolar R	R.WQLTVATEQPELEGPPDGYR.G	5.38	27.73	0.19	5.15
Q9JIK5_DD	Ddx21	Nucleolar R	R.AAVIGDVIR.V	15.47	46.99	0.33	3.04
Q9JIK5_DD	Ddx21	Nucleolar R	R.APQVLVLAPTR.E	6.33	36.54	0.17	5.77
Q9JIK5_DD	Ddx21	Nucleolar R	K.ELKEQLGESIDAK.V	9.27	9.29	1.00	1.00
Q9JIK5_DD	Ddx21	Nucleolar R	K.EQLGESIDAK#.V	14.57	14.54	1.00	1.00
Q9JIK5_DD	Ddx21	Nucleolar R	K.GAVEALAAALAHISGATSVDQR.S	9.82	55.54	0.18	5.65
Q9JIK5_DD	Ddx21	Nucleolar R	R.GVNFLFPIQAK#.T	73.35	70.96	1.03	0.97
Q9JIK5_DD	Ddx21	Nucleolar R	K.KQEEEPQDDTASTSK.T	4.86	3.72	1.30	0.77
Q9JIK5_DD	Ddx21	Nucleolar R	R.SGIDILVGTPGR.I	15.15	43.81	0.35	2.89
Q9JIK5_DD	Ddx21	Nucleolar R	K.SK#TEEATEGMEEAVSSK#.A	12.21	9.09	1.34	0.74
Q9JIK5_DD	Ddx21	Nucleolar R	K.SK#TEEATEGM*EEAVSSK#.A	46.74	38.89	1.20	0.83
Q9JIK5_DD	Ddx21	Nucleolar R	K.STYEQVDLIGK#.K	17.12	7.88	2.17	0.46
Q9JIK5_DD	Ddx21	Nucleolar R	R.TEAVTEIQEK#.W	54.74	42.40	1.29	0.77
Q9JIK5_DD	Ddx21	Nucleolar R	K.TEEATEGM*EEAVSSK#.A	10.45	7.75	1.35	0.74
Q9JIK5_DD	Ddx21	Nucleolar R	K.TFSFAIPLIEK.L	93.00	88.24	1.05	0.95
D3Z0M9_D	Ddx23	MCG18410	R.DIIGVAETGSGK#.T	91.03	51.20	1.78	0.56
D3Z0M9_D	Ddx23	MCG18410	K.DILVATDVAGR.G	23.18	48.81	0.47	2.11
D3Z0M9_D	Ddx23	MCG18410	K.EDSAVFYELK#.Q	56.46	27.50	2.05	0.49
D3Z0M9_D	Ddx23	MCG18410	R.ELAQQIEEETIK#.F	71.36	40.74	1.75	0.57
D3Z0M9_D	Ddx23	MCG18410	R.FYGDLM*EK#.R	34.11	19.68	1.73	0.58
D3Z0M9_D	Ddx23	MCG18410	R.GFIAGIDLK#.Q	56.36	26.22	2.15	0.47
D3Z0M9_D	Ddx23	MCG18410	R.GIDIQDVSM*VVNYDM*AK#.N	4.39	2.38	1.84	0.54
D3Z0M9_D	Ddx23	MCG18410	R.GIDIQDVSMVVNYDMAK#.N	6.70	3.55	1.89	0.53
D3Z0M9_D	Ddx23	MCG18410	R.HQVQLLGR.G	15.80	51.79	0.31	3.28
D3Z0M9_D	Ddx23	MCG18410	K.IDRIEESDQGPYAIILAPTR.E	4.00	21.11	0.19	5.28
D3Z0M9_D	Ddx23	MCG18410	R.IEESDQGPYAIILAPTR.E	3.78	11.27	0.34	2.98
D3Z0M9_D	Ddx23	MCG18410	R.IFREDYSITTK.G	8.22	30.41	0.27	3.70
D3Z0M9_D	Ddx23	MCG18410	K.IQPLSLEELLAK#.K	146.17	76.85	1.90	0.53
D3Z0M9_D	Ddx23	MCG18410	R.LIDVLENR.Y	19.66	43.12	0.46	2.19
D3Z0M9_D	Ddx23	MCG18410	R.M*IDM*GFEPDVQK#.I	12.00	7.31	1.64	0.61
D3Z0M9_D	Ddx23	MCG18410	R.MIDM*GFEPDVQK#.I	10.41	3.24	3.22	0.31
D3Z0M9_D	Ddx23	MCG18410	R.QAIPIGLQNR.D	15.62	34.77	0.45	2.23
D3Z0M9_D	Ddx23	MCG18410	R.QTVM*FTATM*PPAVER.L	2.47	6.28	0.39	2.54
D3Z0M9_D	Ddx23	MCG18410	R.RPAVVYIGSAGKPHER.V	4.00	23.52	0.17	5.88
D3Z0M9_D	Ddx23	MCG18410	K.SGVAITFLTK#.E	54.42	25.71	2.12	0.47
D3Z0M9_D	Ddx23	MCG18410	R.TLEEKEQEEAR.L	11.55	20.30	0.57	1.76
D3Z0M9_D	Ddx23	MCG18410	R.TVAVIGGISR.E	12.49	31.03	0.40	2.48
D3Z0M9_D	Ddx23	MCG18410	K.VFLMSESEK#.R	20.69	9.06	2.28	0.44
D3Z0M9_D	Ddx23	MCG18410	K.DILVATDVAGR.G	30.98	14.50	2.14	0.47
D3Z0M9_D	Ddx23	MCG18410	K.EDSAVFYELK#.Q	18.33	9.22	1.99	0.50
D3Z0M9_D	Ddx23	MCG18410	K.IQPLSLEELLAK#.K	36.82	19.70	1.87	0.54
D3Z0M9_D	Ddx23	MCG18410	R.TLEEKEQEEAR.L	2.83	6.56	0.43	2.32
Q9ESV0_D	Ddx24	ATP-depend	R.NEGTVETLTETK.I	6.76	9.73	0.69	1.44
Q9ESV0_D	Ddx24	ATP-depend	K.TLQKDEDIPLFPVQSK.Y	4.28	7.53	0.57	1.76
Q921N6_D	Ddx27	Probable AT	R.AM*PEDEPTGPAK#.K	7.63	5.46	1.40	0.72
Q921N6_D	Ddx27	Probable AT	R.GLDIEGVK#.T	11.54	6.77	1.70	0.59
Q921N6_D	Ddx27	Probable AT	R.IFVNSNTDVAPFLR.Q	4.89	9.24	0.53	1.89
Q921N6_D	Ddx27	Probable AT	K.TAAFALPVLER.L	4.33	10.85	0.40	2.51
Q921N6_D	Ddx27	Probable AT	K.TVINFTMPNTVK#.H	7.21	1.86	3.87	0.26
Q8VDW0_D	Ddx39a	ATP-depend	R.DFLLKPELLR.A	54.17	86.41	0.63	1.60
Q8VDW0_D	Ddx39a	ATP-depend	R.DVQEIFR.L	82.04	158.79	0.52	1.94
Q8VDW0_D	Ddx39a	ATP-depend	R.FEVNVAELPEEIDISTYIEQSR.-	6.70	12.98	0.52	1.94
Q8VDW0_D	Ddx39a	ATP-depend	K.FM*QDPM*EVFVDDETK#.L	7.00	3.71	1.89	0.53
Q8VDW0_D	Ddx39a	ATP-depend	K.GLAVTFVSDENDAK#.I	151.70	56.87	2.67	0.37
Q8VDW0_D	Ddx39a	ATP-depend	K.ILNDVQDR.F	51.24	97.02	0.53	1.89
Q8VDW0_D	Ddx39a	ATP-depend	K.ILNDVQDRFEVNVAELPEEIDISTYIEQSR.-	1.36	8.01	0.17	5.89
Q8VDW0_D	Ddx39a	ATP-depend	R.ILVATNLFGR.G	137.58	289.10	0.48	2.10
Q8VDW0_D	Ddx39a	ATP-depend	K.LTLHGLQQYYVK#.L	359.97	162.61	2.21	0.45
Q8VDW0_D	Ddx39a	ATP-depend	R.RDVQEIFR.L	7.19	27.47	0.26	3.82
Q8VDW0_D	Ddx39a	ATP-depend	R.RILVATNLFGR.G	2.11	13.44	0.16	6.38
Q8VDW0_D	Ddx39a	ATP-depend	R.VNIVFNYDM*PEDSDTYLHR.V	8.54	17.56	0.49	2.06
Q8VDW0_D	Ddx39a	ATP-depend	K.VSVFFGGLSIK#.K	115.83	57.12	2.03	0.49
Q8VDW0_D	Ddx39a	ATP-depend	R.ILVATNLFGR.G	13.29	36.32	0.37	2.73
Q8VDW0_D	Ddx39a	ATP-depend	R.DVQEIFR.L	50.86	99.04	0.51	1.95
Q8VDW0_D	Ddx39a	ATP-depend	K.GLAVTFVSDENDAK#.I	78.42	33.03	2.37	0.42
Q8VDW0_D	Ddx39a	ATP-depend	K.GSYVSIHSSGFR.D	19.97	33.96	0.59	1.70
Q8VDW0_D	Ddx39a	ATP-depend	K.ILNDVQDR.F	10.75	27.85	0.39	2.59
Q8VDW0_D	Ddx39a	ATP-depend	R.ILVATNLFGR.G	83.54	153.11	0.55	1.83
Q8VDW0_D	Ddx39a	ATP-depend	K.LTLHGLQQYYVK#.L	162.09	61.49	2.64	0.38
Q8VDW0_D	Ddx39a	ATP-depend	R.VNIVFNYDM*PEDSDTYLHR.V	11.55	11.33	1.02	0.98
Q8VDW0_D	Ddx39a	ATP-depend	K.VSVFFGGLSIK#.K	60.28	25.99	2.32	0.43
Q8VDW0_D	Ddx39a	ATP-depend	R.DVQEIFR.L	51.23	115.66	0.44	2.26
Q8VDW0_D	Ddx39a	ATP-depend	K.FM*QDPM*EVFVDDETK#.L	8.49	4.67	1.82	0.55
Q8VDW0_D	Ddx39a	ATP-depend	K.GLAVTFVSDENDAK#.I	148.40	60.75	2.44	0.41
Q8VDW0_D	Ddx39a	ATP-depend	K.ILNDVQDR.F	16.03	33.37	0.48	2.08
Q8VDW0_D	Ddx39a	ATP-depend	R.ILVATNLFGR.G	111.88	209.96	0.53	1.88
Q8VDW0_D	Ddx39a	ATP-depend	K.LTLHGLQQYYVK#.L	187.07	87.36	2.14	0.47
Q8VDW0_D	Ddx39a	ATP-depend	R.VNIVFNYDM*PEDSDTYLHR.V	13.73	19.48	0.70	1.42
Q8VDW0_D	Ddx39a	ATP-depend	K.VSVFFGGLSIK#.K	105.86	42.49	2.49	0.40
Q9Z1N5_D	Ddx39b	Spliceosom	R.FEVNISELPDEIDISSYIEQTR.-	14.94	26.81	0.56	1.79
Q9Z1N5_D	Ddx39b	Spliceosom	K.FM*QDPM*EIFVDDETK#.L	18.04	11.60	1.55	0.64
Q9Z1N5_D	Ddx39b	Spliceosom	K.FMQDPM*EIFVDDETK#.L	5.98	4.07	1.47	0.68
Q9Z1N5_D	Ddx39b	Spliceosom	K.FM*QDPMEIFVDDETK#.L	8.14	3.60	2.26	0.44
Q9Z1N5_D	Ddx39b	Spliceosom	K.FMQDPMEIFVDDETK#.L	13.73	6.92	1.99	0.50
Q9Z1N5_D	Ddx39b	Spliceosom	K.FM*QDPMEIFVDDETK#LTLHGLQQYYVK#.L	12.93	3.92	3.30	0.30
Q9Z1N5_D	Ddx39b	Spliceosom	K.FMQDPMEIFVDDETK#LTLHGLQQYYVK#.L	10.42	7.43	1.40	0.71
Q9Z1N5_D	Ddx39b	Spliceosom	K.GLAITFVSDENDAK#.I	346.88	158.74	2.19	0.46
Q9Z1N5_D	Ddx39b	Spliceosom	R.KFM*QDPM*EIFVDDETK.L	12.77	7.64	1.67	0.60

Q9Z1N5_D	Ddx39b	Spliceosom	K.QVM*M*FSATLSK#.E	66.86	35.19	1.90	0.53
Q9Z1N5_D	Ddx39b	Spliceosom	K.QVMM*FSATLSK#.E	24.78	13.58	1.83	0.55
Q9Z1N5_D	Ddx39b	Spliceosom	K.QVMMFSATLSK#.E	25.70	14.96	1.72	0.58
Q9Z1N5_D	Ddx39b	Spliceosom	K.VAVFFGGLSIK#.K	286.55	135.34	2.12	0.47
Q9Z1N5_D	Ddx39b	Spliceosom	R.VNIAFNYDM*PEDSDTYLHR.V	40.03	75.84	0.53	1.89
Q9Z1N5_D	Ddx39b	Spliceosom	R.VNIAFNYDMPEDSDTYLHR.V	24.55	48.20	0.51	1.96
Q9Z1N5_D	Ddx39b	Spliceosom	K.GLAITFVSDENDAK.I	3.76	4.19	0.90	1.11
Q9Z1N5_D	Ddx39b	Spliceosom	R.FEVNISELPDEIDISSYIEQTR.-	6.90	10.94	0.63	1.59
Q9Z1N5_D	Ddx39b	Spliceosom	K.FM*QDPM*EIFVDDETK#.L	7.59	4.70	1.61	0.62
Q9Z1N5_D	Ddx39b	Spliceosom	K.FM*QDPMEIFVDDETK#LTLHGLQQYYVK#.L	7.44	2.14	3.47	0.29
Q9Z1N5_D	Ddx39b	Spliceosom	K.GLAITFVSDENDAK#.I	170.88	72.16	2.37	0.42
Q9Z1N5_D	Ddx39b	Spliceosom	K.QVMM*FSATLSK#.E	6.76	3.25	2.08	0.48
Q9Z1N5_D	Ddx39b	Spliceosom	K.VAVFFGGLSIK#.K	176.13	79.92	2.20	0.45
Q9Z1N5_D	Ddx39b	Spliceosom	R.VNIAFNYDMPEDSDTYLHR.V	11.24	17.06	0.66	1.52
Q9Z1N5_D	Ddx39b	Spliceosom	K.FM*QDPM*EIFVDDETK#.L	12.49	7.32	1.70	0.59
Q9Z1N5_D	Ddx39b	Spliceosom	K.FM*QDPMEIFVDDETK#.L	4.46	3.65	1.22	0.82
Q9Z1N5_D	Ddx39b	Spliceosom	K.GLAITFVSDENDAK#.I	281.00	128.90	2.18	0.46
Q9Z1N5_D	Ddx39b	Spliceosom	K.QVM*M*FSATLSK#.E	56.13	22.57	2.49	0.40
Q9Z1N5_D	Ddx39b	Spliceosom	K.QVMM*FSATLSK#.E	15.01	11.39	1.32	0.76
Q9Z1N5_D	Ddx39b	Spliceosom	K.VAVFFGGLSIK#.K	165.44	74.37	2.22	0.45
Q9Z1N5_D	Ddx39b	Spliceosom	R.VNIAFNYDM*PEDSDTYLHR.V	24.99	50.34	0.50	2.01
Q9Z1N5_D	Ddx39b	Spliceosom	R.VNIAFNYDMPEDSDTYLHR.V	9.42	19.55	0.48	2.07
Q9Z1N5_D	Ddx39b	Spliceosom	K.YM*PNVK#.V	77.26	39.68	1.95	0.51
Q62167_D	Ddx3x	ATP-depen	K.DLLDLLVEAK#.Q	145.29	97.78	1.49	0.67
Q62167_D	Ddx3x	ATP-depen	R.DREEALHQFR.S	6.37	82.77	0.08	13.00
Q62167_D	Ddx3x	ATP-depen	K.DSLTLVFVETK#.K	51.22	35.44	1.45	0.69
Q62167_D	Ddx3x	ATP-depen	K.EIQM*LAR.D	8.77	31.39	0.28	3.58
Q62167_D	Ddx3x	ATP-depen	R.ELAVQIYEEAR.K	58.31	124.29	0.47	2.13
Q62167_D	Ddx3x	ATP-depen	R.GLDISNVK#.H	71.29	62.86	1.13	0.88
Q62167_D	Ddx3x	ATP-depen	K.HAIPIIK#.E	74.20	65.16	1.14	0.88
Q62167_D	Ddx3x	ATP-depen	R.HTM*M*FSATFPK#.E	13.62	12.87	1.06	0.95
Q62167_D	Ddx3x	ATP-depen	K.HVINFDLPSDIEEYVHR.I	24.24	62.13	0.39	2.56
Q62167_D	Ddx3x	ATP-depen	R.IVEQDTMPPK#.G	5.40	63.91	0.08	11.84
Q62167_D	Ddx3x	ATP-depen	R.IVEQDTM*PPK#.G	43.06	31.85	1.35	0.74
Q62167_D	Ddx3x	ATP-depen	R.LEQELFSGGNTGINFEK#.Y	29.73	17.82	1.67	0.60
Q62167_D	Ddx3x	ATP-depen	R.QSSGASSSSFSSSR.A	4.04	10.57	0.38	2.61
Q62167_D	Ddx3x	ATP-depen	K.QYPISLVLAPTR.E	8.60	30.71	0.28	3.57
Q62167_D	Ddx3x	ATP-depen	R.SFLLDLLNATGK#.D	275.39	177.29	1.55	0.64
Q62167_D	Ddx3x	ATP-depen	K.SPILVATAVAAR.G	31.72	109.47	0.29	3.45
Q62167_D	Ddx3x	ATP-depen	K.SSFFGDR.G	6.53	25.03	0.26	3.83
Q62167_D	Ddx3x	ATP-depen	R.VGNLGLATSFFNER.N	17.54	46.22	0.38	2.63
Q62167_D	Ddx3x	ATP-depen	R.VGSTSENITQK#.V	231.88	171.56	1.35	0.74
Q62167_D	Ddx3x	ATP-depen	K.DLLDLLVEAK#.Q	609.24	348.90	1.75	0.57
Q62167_D	Ddx3x	ATP-depen	K.DSLTLVFVETK#.K	142.89	83.37	1.71	0.58
Q62167_D	Ddx3x	ATP-depen	K.DSLTLVFVETK#K#.G	17.16	7.63	2.25	0.44
Q62167_D	Ddx3x	ATP-depen	R.ELAVQIYEEAR.K	42.15	117.34	0.36	2.78
Q62167_D	Ddx3x	ATP-depen	R.FSGGFGAR.D	46.66	124.91	0.37	2.68
Q62167_D	Ddx3x	ATP-depen	R.GDYDGIGGR.G	10.87	29.99	0.36	2.76
Q62167_D	Ddx3x	ATP-depen	R.GLDISNVK#.H	227.15	109.54	2.07	0.48
Q62167_D	Ddx3x	ATP-depen	K.HAIPIIK#.E	272.30	166.19	1.64	0.61
Q62167_D	Ddx3x	ATP-depen	R.HTM*M*FSATFPK#.E	56.66	44.05	1.29	0.78
Q62167_D	Ddx3x	ATP-depen	R.HTM*MFSATFPK#.E	28.70	17.21	1.67	0.60
Q62167_D	Ddx3x	ATP-depen	R.HTMM*FSATFPK.E	28.70	17.21	1.67	0.60
Q62167_D	Ddx3x	ATP-depen	R.HTMMFSATFPK#.E	19.75	11.18	1.77	0.57
Q62167_D	Ddx3x	ATP-depen	K.HVINFDLPSDIEEYVHR.I	43.32	117.59	0.37	2.71
Q62167_D	Ddx3x	ATP-depen	R.IVEQDTM*PPK#.G	128.16	68.72	1.86	0.54
Q62167_D	Ddx3x	ATP-depen	R.LEQELFSGGNTGINFEK#.Y	113.22	48.01	2.36	0.42
Q62167_D	Ddx3x	ATP-depen	K.QEVPSWLENMAFEHHYK#.G	28.20	10.36	2.72	0.37
Q62167_D	Ddx3x	ATP-depen	R.QSSGASSSSFSSSR.A	13.27	35.02	0.38	2.64
Q62167_D	Ddx3x	ATP-depen	K.QYPISLVLAPTR.E	37.08	107.03	0.35	2.89
Q62167_D	Ddx3x	ATP-depen	R.SFLLDLLNATGK#.D	679.95	332.01	2.05	0.49
Q62167_D	Ddx3x	ATP-depen	K.SPILVATAVAAR.G	78.76	208.05	0.38	2.64
Q62167_D	Ddx3x	ATP-depen	K.TAAFLLPILSQIYADGPGEALR@.A	32.59	22.21	1.47	0.68
Q62167_D	Ddx3x	ATP-depen	R.VGNLGLATSFFNER.N	68.67	188.92	0.36	2.75
Q62167_D	Ddx3x	ATP-depen	R.VGSTSENITQK#.V	548.39	289.82	1.89	0.53
Q62167_D	Ddx3x	ATP-depen	K.YLVLDEADR.M	29.39	100.58	0.29	3.42
Q62167_D	Ddx3x	ATP-depen	K.YLVLDEADRM*LDM*GFEPQIR.R	3.52	22.10	0.16	6.28
Q62167_D	Ddx3x	ATP-depen	K.DKDAYSSFGSR.S	5.59	8.72	0.64	1.56
Q62167_D	Ddx3x	ATP-depen	K.DLLDLLVEAK#.Q	44.26	31.50	1.40	0.71
Q62167_D	Ddx3x	ATP-depen	K.DSLTLVFVETK#.K	23.77	12.13	1.96	0.51
Q62167_D	Ddx3x	ATP-depen	R.FSGGFGAR.D	4.99	22.46	0.22	4.50
Q62167_D	Ddx3x	ATP-depen	K.HAIPIIK#.E	67.62	39.09	1.73	0.58
Q62167_D	Ddx3x	ATP-depen	R.IVEQDTM*PPK#.G	26.23	11.95	2.19	0.46
Q62167_D	Ddx3x	ATP-depen	R.LEQELFSGGNTGINFEK#.Y	13.45	8.63	1.56	0.64
Q62167_D	Ddx3x	ATP-depen	R.QSSGASSSSFSSSR.A	4.50	11.33	0.40	2.52
Q62167_D	Ddx3x	ATP-depen	K.QYPISLVLAPTR.E	16.86	18.94	0.89	1.12
Q62167_D	Ddx3x	ATP-depen	R.SFLLDLLNATGK#.D	128.12	62.43	2.05	0.49
Q62167_D	Ddx3x	ATP-depen	K.SPILVATAVAAR.G	15.36	44.43	0.35	2.89
Q62167_D	Ddx3x	ATP-depen	R.VGNLGLATSFFNER.N	17.90	42.49	0.42	2.37
Q62167_D	Ddx3x	ATP-depen	R.VGSTSENITQK#.V	91.36	47.72	1.91	0.52
Q91VN6_D	Ddx41	Probable A	K.DYLAHSSM*DF.-	6.35	6.35	1.00	1.00
Q91VN6_D	Ddx41	Probable A	R.LLQEDSSPLLR.C	3.31	7.48	0.44	2.26
Q91VN6_D	Ddx41	Probable A	K.TPPPVLIFAEK#.K	10.45	13.90	0.75	1.33
Q91VN6_D	Ddx41	Probable A	K.DVLVATDVASK#.G	11.08	12.58	0.88	1.13
Q91VN6_D	Ddx41	Probable A	K.DYLAHSSM*DF.-	8.40	8.40	1.00	1.00
Q91VN6_D	Ddx41	Probable A	K.GILHPTPIQIQGIPTILSGR.D	2.02	8.80	0.23	4.37
Q91VN6_D	Ddx41	Probable A	K.K#ADVDAIHEYLLLK#.G	23.60	13.61	1.73	0.58
Q91VN6_D	Ddx41	Probable A	R.LLQEDSSPLLR.C	3.04	18.18	0.17	5.99
Q91VN6_D	Ddx41	Probable A	K.SALVKPVTINVGR.A	2.93	14.11	0.21	4.82
Q91VN6_D	Ddx41	Probable A	R.SGNTGIATTFINK.A	10.13	17.98	0.56	1.77
Q91VN6_D	Ddx41	Probable A	K.TPPPVLIFAEK#.K	28.08	25.29	1.11	0.90
Q810A7_D	Ddx42	ATP-depen	K.AAFQSQYK#.S	40.67	24.83	1.64	0.61
Q810A7_D	Ddx42	ATP-depen	K.DIPVLVATDVAAR.G	20.08	72.07	0.28	3.59
Q810A7_D	Ddx42	ATP-depen	R.DM*IGIAK#.T	46.96	25.94	1.81	0.55
Q810A7_D	Ddx42	ATP-depen	K.DSNFAGDLVR.N	11.51	34.73	0.33	3.02
Q810A7_D	Ddx42	ATP-depen	K.ELLDLAM*QNAWFR.K	4.50	9.84	0.46	2.19
Q810A7_D	Ddx42	ATP-depen	K.ELLDLAMQNAWFR.K	4.68	9.25	0.51	1.98
Q810A7_D	Ddx42	ATP-depen	R.GFGFGGFAISAGK#.K	38.85	18.23	2.13	0.47
Q810A7_D	Ddx42	ATP-depen	K.GIRDDIEEEDDQEAYFR.Y	2.93	8.84	0.33	3.01
Q810A7_D	Ddx42	ATP-depen	R.GLDIPSIK#.T	43.52	35.68	1.22	0.82
Q810A7_D	Ddx42	ATP-depen	K.GVAYTLLTPK#.D	50.45	31.71	1.59	0.63
Q810A7_D	Ddx42	ATP-depen	K.K#ANAEELASNLK#.Q	12.64	8.68	1.46	0.69
Q810A7_D	Ddx42	ATP-depen	K.LPQQSHSAFGAASSSSGFGK#.S	12.07	6.19	1.95	0.51

Q810A7_D	Ddx42	ATP-depen	K.NFYNEHEEITNLTPQQLIDLR.H	12.86	37.42	0.34	2.91
Q810A7_D	Ddx42	ATP-depen	K.NIPGFNNSGNISSAPVTYPSIGAQGVNNTASGNNSR.E	1.57	1.75	0.90	1.12
Q810A7_D	Ddx42	ATP-depen	R.NLEGANQHVSK#.E	27.13	15.91	1.70	0.59
Q810A7_D	Ddx42	ATP-depen	R.QTLLFSATFR.K	6.29	17.82	0.35	2.83
Q810A7_D	Ddx42	ATP-depen	R.SVAVYGGGSM*WEQAK#.A	16.55	10.60	1.56	0.64
Q810A7_D	Ddx42	ATP-depen	K.TVINYDVAR.D	31.46	61.21	0.51	1.95
Q810A7_D	Ddx42	ATP-depen	K.WNWLTR.R	5.54	14.03	0.39	2.53
Q810A7_D	Ddx42	ATP-depen	K.DIPVLVATDVAAR.G	4.54	11.30	0.40	2.49
Q810A7_D	Ddx42	ATP-depen	K.GVAYTLLTPK#.D	10.10	8.87	1.14	0.88
Q810A7_D	Ddx42	ATP-depen	K.NFYNEHEEITNLTPQQLIDLR.H	3.71	10.77	0.34	2.90
Q569Z5_D	Ddx46	Probable A	K.ALELSGTAVPPDLEK#.L	19.35	17.44	1.11	0.90
Q569Z5_D	Ddx46	Probable A	R.DLIGIAK#.T	64.66	31.67	2.04	0.49
Q569Z5_D	Ddx46	Probable A	R.ELALQITK#.E	86.30	67.93	1.27	0.79
Q569Z5_D	Ddx46	Probable A	K.FDETEQALANER.K	10.75	29.55	0.36	2.75
Q569Z5_D	Ddx46	Probable A	R.GGTILAPTVSAK#.T	96.82	54.23	1.79	0.56
Q569Z5_D	Ddx46	Probable A	K.GYAYTFITEDQAR.Y	19.14	48.21	0.40	2.52
Q569Z5_D	Ddx46	Probable A	R.ILSKPIEVQVGGR.S	17.49	49.90	0.35	2.85
Q569Z5_D	Ddx46	Probable A	R.K#IYLAIESANELAVQK#.A	19.26	13.51	1.43	0.70
Q569Z5_D	Ddx46	Probable A	R.KLLEPVDHGK.I	10.75	8.26	1.30	0.77
Q569Z5_D	Ddx46	Probable A	R.LEM*EGITVK#.G	43.45	33.20	1.31	0.76
Q569Z5_D	Ddx46	Probable A	R.LEMEGITVK#.G	12.84	194.55	0.07	15.16
Q569Z5_D	Ddx46	Probable A	K.LLVATSVAAR.G	27.58	69.65	0.40	2.53
Q569Z5_D	Ddx46	Probable A	R.LQNSYQPTNK.G	94.69	57.45	1.65	0.61
Q569Z5_D	Ddx46	Probable A	R.M*IDM*LAANSGR.V	8.46	16.05	0.53	1.90
Q569Z5_D	Ddx46	Probable A	K.MSQEEVNVFR.L	5.46	16.28	0.34	2.98
Q569Z5_D	Ddx46	Probable A	K.NFYVEVPELAK#.M	102.58	54.08	1.90	0.53
Q569Z5_D	Ddx46	Probable A	K.NLGIESQVDVM*QQATNAILR.G	8.92	9.35	0.95	1.05
Q569Z5_D	Ddx46	Probable A	K.NLGIESQVDVMQQATNAILR.G	10.18	19.51	0.52	1.92
Q569Z5_D	Ddx46	Probable A	R.SLEEGEGPIAVIMTPTR.E	7.64	15.87	0.48	2.08
Q569Z5_D	Ddx46	Probable A	K.TIAEQLAEK#.I	93.54	51.42	1.82	0.55
Q569Z5_D	Ddx46	Probable A	K.TIAFLLPM*FR.H	11.85	33.00	0.36	2.78
Q569Z5_D	Ddx46	Probable A	R.VK#DM*AAPGTSSVPAPTAGNAEK#.L	45.65	30.35	1.50	0.66
Q569Z5_D	Ddx46	Probable A	R.VK#DMAAPGTSSVPAPTAGNAEK#.L	21.46	8.85	2.42	0.41
Q569Z5_D	Ddx46	Probable A	R.VTYVVLDEADR.M	9.88	26.64	0.37	2.69
Q569Z5_D	Ddx46	Probable A	K.VVTVVTTK#.K	88.74	44.62	1.99	0.50
Q569Z5_D	Ddx46	Probable A	R.YAGDIIK#.A	85.42	48.95	1.74	0.57
Q569Z5_D	Ddx46	Probable A	R.YEEELEINDFPQTAR.W	4.39	7.77	0.57	1.77
Q569Z5_D	Ddx46	Probable A	R.GGTILAPTVSAK#.T	34.96	23.35	1.50	0.67
Q569Z5_D	Ddx46	Probable A	K.LLVATSVAAR.G	8.31	16.17	0.51	1.95
Q569Z5_D	Ddx46	Probable A	R.M*IDM*LAANSGR.V	2.73	7.48	0.36	2.74
Q569Z5_D	Ddx46	Probable A	K.NFYVEVPELAK#.M	22.51	13.14	1.71	0.58
Q569Z5_D	Ddx46	Probable A	R.SLEEGEGPIAVIMTPTR.E	4.54	4.93	0.92	1.09
Q569Z5_D	Ddx46	Probable A	K.TIAFLLPM*FR.H	4.55	14.58	0.31	3.20
Q9CWX9_	Ddx47	Probable A	R.DIIGLAETGSGK#.T	27.55	16.72	1.65	0.61
Q9CWX9_	Ddx47	Probable A	R.ILNMDFETEVDK#.I	5.92	4.76	1.24	0.80
Q9CWX9_	Ddx47	Probable A	R.LFALVLTPTR.E	5.53	20.66	0.27	3.73
Q4FZF3_D	Ddx49	Probable A	R.SRPQEPAQAEAQD.-	2.91	8.66	0.34	2.98
Q61656_D	Ddx5	Probable A	R.DGWPAM*GIHGDK#.S	41.48	38.63	1.07	0.93
Q61656_D	Ddx5	Probable A	R.DWVLNEFK#.H	218.27	197.60	1.10	0.91
Q61656_D	Ddx5	Probable A	R.EANQAINPK#.L	192.71	202.46	0.95	1.05
Q61656_D	Ddx5	Probable A	K.FGNPGEK.L	100.34	100.72	1.00	1.00
Q61656_D	Ddx5	Probable A	K.FVINYDYPNSSEDYIHR.I	76.50	373.13	0.21	4.88
Q61656_D	Ddx5	Probable A	R.GYSNLLK.R	89.21	79.09	1.13	0.89
Q61656_D	Ddx5	Probable A	K.K#K#WNLDELPK#.F	5.67	4.59	1.24	0.81
Q61656_D	Ddx5	Probable A	K.K#WNLDELPK#.F	12.37	9.52	1.30	0.77
Q61656_D	Ddx5	Probable A	K.LLQLVEDR.G	101.37	398.07	0.25	3.93
Q61656_D	Ddx5	Probable A	R.LMEEIM*SEK#.E	45.00	45.60	0.99	1.01
Q61656_D	Ddx5	Probable A	R.LM*EEIMSEK.E	36.09	36.34	0.99	1.01
Q61656_D	Ddx5	Probable A	R.LMEEIMSEK#.E	59.28	61.69	0.96	1.04
Q61656_D	Ddx5	Probable A	R.LM*EEIM*SEK#.E	86.78	80.47	1.08	0.93
Q61656_D	Ddx5	Probable A	K.NFYQEHPDLAR.R	18.62	77.26	0.24	4.15
Q61656_D	Ddx5	Probable A	R.QLAEDFLK#.D	48.70	50.83	0.96	1.04
Q61656_D	Ddx5	Probable A	R.QNFTEPTAIQAQGWPVALSGLDM*VGVAQTGSGK.T	51.53	37.39	1.38	0.73
Q61656_D	Ddx5	Probable A	K.QVSDLISVLR.E	46.28	214.28	0.22	4.63
Q61656_D	Ddx5	Probable A	R.RTAQEVDTYR.R	4.19	52.74	0.08	12.58
Q61656_D	Ddx5	Probable A	R.RTTYLVLDEADR.M	1.13	14.20	0.08	12.55
Q61656_D	Ddx5	Probable A	R.TAQEVDTYR.R	27.33	143.35	0.19	5.25
Q61656_D	Ddx5	Probable A	K.TGTAYTFFTPNNIK#.Q	230.91	214.69	1.08	0.93
Q61656_D	Ddx5	Probable A	K.TIVFVETK#.R	267.68	231.91	1.15	0.87
Q61656_D	Ddx5	Probable A	R.TTYLVLDEADR.M	55.68	226.71	0.25	4.07
Q61656_D	Ddx5	Probable A	R.TTYLVLDEADRM*LDM*GFEPQIR.K	32.61	3.71	8.80	0.11
Q61656_D	Ddx5	Probable A	R.TTYLVLDEADRM*LDMGFEPQIR.K	2.86	6.80	0.42	2.38
Q61656_D	Ddx5	Probable A	K.WNLDELPK#.F	151.78	165.02	0.92	1.09
Q61656_D	Ddx5	Probable A	K.WNLDELPK#FEK#.N	39.80	36.66	1.09	0.92
Q61656_D	Ddx5	Probable A	R.DWVLNEFK#.H	61.38	55.15	1.11	0.90
Q61656_D	Ddx5	Probable A	R.EANQAINPK.L	54.27	56.67	0.96	1.04
Q61656_D	Ddx5	Probable A	K.FGNPGEK#.L	31.73	31.85	1.00	1.00
Q61656_D	Ddx5	Probable A	R.GYSNLLK#.R	56.54	55.34	1.02	0.98
Q61656_D	Ddx5	Probable A	K.LLQLVEDR.G	32.89	132.76	0.25	4.04
Q61656_D	Ddx5	Probable A	R.LM*EEIM*SEK.E	17.40	14.68	1.19	0.84
Q61656_D	Ddx5	Probable A	R.QNFTEPTAIQAQGWPVALSGLDM*VGVAQTGSGK#.T	14.87	11.31	1.32	0.76
Q61656_D	Ddx5	Probable A	R.QNFTEPTAIQAQGWPVALSGLDM*VGVAQTGSGK.T	3.98	2.24	1.77	0.56
Q61656_D	Ddx5	Probable A	K.QVSDLISVLR.E	18.49	87.80	0.21	4.75
Q61656_D	Ddx5	Probable A	K.SQQERDWVLNEFK.H	6.08	11.64	0.52	1.91
Q61656_D	Ddx5	Probable A	K.TGTAYTFFTPNNIK#.Q	64.42	62.09	1.04	0.96
Q61656_D	Ddx5	Probable A	K.TIVFVETK#.R	79.30	72.07	1.10	0.91
Q61656_D	Ddx5	Probable A	R.TTYLVLDEADR.M	14.26	54.34	0.26	3.81
Q61656_D	Ddx5	Probable A	R.TTYLVLDEADRM*LDM*GFEPQIR.K	17.85	17.06	1.05	0.96
Q61656_D	Ddx5	Probable A	K.WNLDELPK#.F	30.04	26.90	1.12	0.90
Q61656_D	Ddx5	Probable A	K.WNLDELPKFEK.N	26.06	20.89	1.25	0.80
Q61656_D	Ddx5	Probable A	R.DWVLNEFK#.H	14.20	13.39	1.06	0.94
Q61656_D	Ddx5	Probable A	R.EANQAINPK.L	4.41	16.24	0.27	3.68
Q61656_D	Ddx5	Probable A	R.QNFTEPTAIQAQGWPVALSGLDM*VGVAQTGSGK.T	5.73	5.07	1.13	0.89
Q61656_D	Ddx5	Probable A	K.TGTAYTFFTPNNIK#.Q	14.68	15.91	0.92	1.08
Q99MJ9_D	Ddx50	ATP-depen	K.EGAFSNFSISEETIK#.L	23.32	18.82	1.24	0.81
Q99MJ9_D	Ddx50	ATP-depen	R.ELANQVAK#.D	16.33	14.16	1.15	0.87
Q99MJ9_D	Ddx50	ATP-depen	K.GAVDALAAALAHISGASSFEPR.S	14.74	55.97	0.26	3.80
Q99MJ9_D	Ddx50	ATP-depen	R.GVTYLFPIQVK#.T	27.33	30.85	0.89	1.13
Q99MJ9_D	Ddx50	ATP-depen	R.LQAEWHDSDWILSVPAK#.L	10.58	9.53	1.11	0.90
Q99MJ9_D	Ddx50	ATP-depen	K.TFSFAIPLIER.L	8.71	38.21	0.23	4.39
Q99MJ9_D	Ddx50	ATP-depen	K.VLVATNVAAR.G	8.93	43.30	0.21	4.85
Q8K301_D	Ddx52	Probable A	K.IHVQGTDLPDPIATFQQLDQEYK#.I	9.29	7.54	1.23	0.81
Q8K301_D	Ddx52	Probable A	R.NSAVETVEQELLFVGSETGK#.L	13.01	10.07	1.29	0.77

Q8K301_DI	Ddx52	Probable A	R.ELLASAPTGSGK#.T	19.13	16.14	1.19	0.84
Q8K301_DI	Ddx52	Probable A	K.IHVQGTDLPDPIATFQQLDQEYK#.I	13.67	12.12	1.13	0.89
Q8K301_DI	Ddx52	Probable A	R.NSAVETVEQELLFVGSETGK#.L	23.49	21.37	1.10	0.91
Q8K301_DI	Ddx52	Probable A	R.NSAVETVEQELLFVGSETGK#.L	8.56	7.93	1.08	0.93
Q8K301_DI	Ddx52	Probable A	R.NSAVETVEQELLFVGSETGK#.L	6.46	5.11	1.26	0.79
Q8K4L0_DI	Ddx54	ATP-depen	R.QEGPADPAPQR.E	3.48	8.98	0.39	2.58
Q9D0R4_D	Ddx56	Probable A	K.ALLFVNTLER.G	3.26	11.32	0.29	3.47
Q9D0R4_D	Ddx56	Probable A	R.LLQAVTDLGWSRPTLIQEK.A	2.89	4.97	0.58	1.72
Q9D0R4_D	Ddx56	Probable A	R.VANVSAAEDSASQR.A	4.89	22.80	0.21	4.67
Q9D0R4_D	Ddx56	Probable A	R.VLSHLQQNTLK#.L	6.53	3.17	2.06	0.49
Q6Q899_D	Ddx58	Probable A	K.FSELWIVDK#.G	9.24	6.12	1.51	0.66
Q6Q899_D	Ddx58	Probable A	K.VLQLALEK#.D	14.40	6.65	2.17	0.46
Q6Q899_D	Ddx58	Probable A	R.ALVDALK#K#.W	36.34	7.54	4.82	0.21
Q6Q899_D	Ddx58	Probable A	R.DLYLVLQEEYHLK#PETK#.T	32.78	7.41	4.42	0.23
Q6Q899_D	Ddx58	Probable A	R.DPLPQVVGLTASVGVGDAK#.T	22.63	4.82	4.70	0.21
Q6Q899_D	Ddx58	Probable A	R.DSQHK#PQPVPDK#ENK#.K	4.03	1.30	3.09	0.32
Q6Q899_D	Ddx58	Probable A	R.DSQHK#PQPVPDK#ENK#.K	25.91	9.14	2.84	0.35
Q6Q899_D	Ddx58	Probable A	K.DVSEELGK#.L	38.85	15.07	2.58	0.39
Q6Q899_D	Ddx58	Probable A	K.FSELWIVDK#.G	62.58	16.04	3.90	0.26
Q6Q899_D	Ddx58	Probable A	K.IESFVVEDIVSGVQNR.H	21.43	21.00	1.02	0.98
Q6Q899_D	Ddx58	Probable A	R.IQFDPAEM*SV.-	12.62	12.62	1.00	1.00
Q6Q899_D	Ddx58	Probable A	K.IYDNFEK#.K	39.77	10.86	3.66	0.27
Q6Q899_D	Ddx58	Probable A	R.K#YNDALIISEDAQM*TDALNYLK#.A	10.61	3.53	3.00	0.33
Q6Q899_D	Ddx58	Probable A	R.K#YNDALIISEDAQMTDALNYLK#.A	14.41	4.71	3.06	0.33
Q6Q899_D	Ddx58	Probable A	R.LQTWDEM*K#.F	19.61	5.55	3.53	0.28
Q6Q899_D	Ddx58	Probable A	R.NYQLELALPAK#.K	35.92	11.31	3.18	0.31
Q6Q899_D	Ddx58	Probable A	R.RFEEKLEELEK.V	15.16	20.08	0.75	1.32
Q6Q899_D	Ddx58	Probable A	K.TFEIPVIK#.I	43.85	13.95	3.14	0.32
Q6Q899_D	Ddx58	Probable A	K.VLQLALEK#.D	41.28	13.12	3.15	0.32
Q6Q899_D	Ddx58	Probable A	R.VVETSHYTVLGDAFK#.E	63.69	19.78	3.22	0.31
Q6Q899_D	Ddx58	Probable A	K.VVFFANQIPVYEQQATVFSR.Y	12.58	16.72	0.75	1.33
Q6Q899_D	Ddx58	Probable A	K.WIEENPALSFLKPGILTGR.G	16.27	23.54	0.69	1.45
Q6Q899_D	Ddx58	Probable A	K.YEQWIVGVHK#.A	34.65	10.84	3.20	0.31
Q6Q899_D	Ddx58	Probable A	R.ALVDALK#K#.W	41.65	7.79	5.35	0.19
Q6Q899_D	Ddx58	Probable A	R.ATGMTLPAQK#.C	34.77	35.21	0.99	1.01
Q6Q899_D	Ddx58	Probable A	R.ATGM*TLPAQK#.C	80.78	18.47	4.37	0.23
Q6Q899_D	Ddx58	Probable A	R.DLYLVLQEEYHLK#PETK#.T	10.14	3.94	2.58	0.39
Q6Q899_D	Ddx58	Probable A	R.DPLPQVVGLTASVGVGDAK#.T	28.50	7.29	3.91	0.26
Q6Q899_D	Ddx58	Probable A	K.DVSEELGK#.L	66.83	17.02	3.93	0.25
Q6Q899_D	Ddx58	Probable A	K.FSELWIVDK#.G	84.66	22.47	3.77	0.27
Q6Q899_D	Ddx58	Probable A	K.IESFVVEDIVSGVQNR.H	35.02	49.52	0.71	1.41
Q6Q899_D	Ddx58	Probable A	K.IM*NESILR.L	16.75	22.22	0.75	1.33
Q6Q899_D	Ddx58	Probable A	R.IQFDPAEM*SV.-	24.40	24.40	1.00	1.00
Q6Q899_D	Ddx58	Probable A	R.K#YNDALIISEDAQM*TDALNYLK#.A	19.08	4.82	3.96	0.25
Q6Q899_D	Ddx58	Probable A	R.K#YNDALIISEDAQMTDALNYLK#.A	9.15	4.16	2.20	0.46
Q6Q899_D	Ddx58	Probable A	K.LFQIQNR.E	16.28	27.61	0.59	1.70
Q6Q899_D	Ddx58	Probable A	R.LQTWDEM*K#.F	32.85	8.00	4.10	0.24
Q6Q899_D	Ddx58	Probable A	R.NYQLELALPAK#.K	64.82	16.84	3.85	0.26
Q6Q899_D	Ddx58	Probable A	R.RFEEKLEELEK.V	16.11	24.06	0.67	1.49
Q6Q899_D	Ddx58	Probable A	R.SDK#ENWPK#.V	18.31	7.05	2.60	0.39
Q6Q899_D	Ddx58	Probable A	K.TFEIPVIK#.I	82.34	27.16	3.03	0.33
Q6Q899_D	Ddx58	Probable A	K.TILFVK#.T	61.66	18.52	3.33	0.30
Q6Q899_D	Ddx58	Probable A	K.VLQLALEK#.D	79.90	21.94	3.64	0.27
Q6Q899_D	Ddx58	Probable A	R.VVETSHYTVLGDAFK#.E	125.73	33.63	3.74	0.27
Q6Q899_D	Ddx58	Probable A	K.VVFFANQIPVYEQQATVFSR.Y	122.74	88.74	1.38	0.72
Q6Q899_D	Ddx58	Probable A	K.WIEENPALSFLKPGILTGR.G	39.22	38.27	1.03	0.98
Q6Q899_D	Ddx58	Probable A	K.YEQWIVGVHK#.A	40.79	12.82	3.18	0.31
Q6Q899_D	Ddx58	Probable A	R.YK#TFEIPVIK#.I	16.52	4.25	3.89	0.26
P54823_DI	Ddx6	Probable A	K.DNIQAM*VIVPTR.E	124.48	29.29	4.25	0.24
P54823_DI	Ddx6	Probable A	K.FM*NSHLQK#PYEINLMEELTLK#.G	6.62	3.45	1.92	0.52
P54823_DI	Ddx6	Probable A	K.FMNSHLQK#PYEINLMEELTLK#.G	19.36	10.29	1.88	0.53
P54823_DI	Ddx6	Probable A	K.GVTQYYAYVTER.Q	33.23	80.22	0.41	2.41
P54823_DI	Ddx6	Probable A	K.LAETYLHR.I	12.83	248.36	0.05	19.36
P54823_DI	Ddx6	Probable A	R.LDDTVHVVIATPGR.I	36.41	100.37	0.36	2.76
P54823_DI	Ddx6	Probable A	K.SGAYLIPLLER.L	57.25	134.73	0.42	2.35
P54823_DI	Ddx6	Probable A	K.SIEEQLGTEIKPIPSNIDK.S	198.73	106.34	1.87	0.54
P54823_DI	Ddx6	Probable A	K.SLYVAEYHSEPAEDEK#P.-	160.92	83.49	1.93	0.52
P54823_DI	Ddx6	Probable A	K.VMATTGGTNLR.D	13.08	18.72	0.70	1.43
P54823_DI	Ddx6	Probable A	K.VM*ATTGGTNLR.D	16.81	35.56	0.47	2.12
P54823_DI	Ddx6	Probable A	R.QILLYSATFPLSVQK#.F	25.71	13.14	1.96	0.51
P54823_DI	Ddx6	Probable A	K.SGAYLIPLLER.L	10.71	28.68	0.37	2.68
P54823_DI	Ddx6	Probable A	K.SIEEQLGTEIKPIPSNIDK.S	44.79	27.21	1.65	0.61
P54823_DI	Ddx6	Probable A	K.SLYVAEYHSEPAEDEK#P.-	50.95	27.45	1.86	0.54
P54823_DI	Ddx6	Probable A	K.SLYVAEYHSEPAEDEK#P.-	11.03	3.53	3.12	0.32
P54823_DI	Ddx6	Probable A	K.DNIQAM*VIVPTR.E	5.37	10.87	0.49	2.02
P54823_DI	Ddx6	Probable A	K.GVTQYYAYVTER.Q	7.09	21.59	0.33	3.05
P54823_DI	Ddx6	Probable A	R.QILLYSATFPLSVQK#.F	33.21	13.92	2.39	0.42
P54823_DI	Ddx6	Probable A	K.SGAYLIPLLER.L	21.24	50.86	0.42	2.39
P54823_DI	Ddx6	Probable A	K.SIEEQLGTEIK#PIPSNIDK#.S	40.06	26.64	1.50	0.66
G3X9F7_G	Ddx60	MCG11385	R.FITANWIQDLK#.T	6.64	2.03	3.28	0.31
G3X9F7_G	Ddx60	MCG11385	R.K#NVDSGM*K#.K	2.90	1.51	1.91	0.52
G3X9F7_G	Ddx60	MCG11385	K.DFNLIIK#.S	19.27	4.51	4.28	0.23
G3X9F7_G	Ddx60	MCG11385	K.DLPFLM*SDDPIVTSLVK#.H	25.52	8.33	3.06	0.33
G3X9F7_G	Ddx60	MCG11385	K.ESDEGVVVYVAPTK#.A	14.37	4.48	3.21	0.31
G3X9F7_G	Ddx60	MCG11385	R.FITANWIQDLK#.T	22.77	6.02	3.78	0.26
G3X9F7_G	Ddx60	MCG11385	R.K#IPLNAYALDFYK#.H	9.15	2.85	3.21	0.31
G3X9F7_G	Ddx60	MCG11385	K.SLIQQLEK#.Y	16.90	4.67	3.62	0.28
A6H8H2_D	Dennd4c	DENN dom	K.APITDIAVIIK#.S	13.67	38.87	0.35	2.84
A6H8H2_D	Dennd4c	DENN dom	K.QLTQLGLLTLVEK#.R	11.41	4.30	2.66	0.38
P31001_DI	Des	Desmin OS	R.TNEKVELQELNDR.F	8.72	15.21	0.57	1.74
P31001_DI	Des	Desmin OS	K.VSDLTQAANK.N	1.96	143.79	0.01	73.21
Q9EQM6_D	Dgcr8	Microproc	R.ATLEILIPDFVK.Q	10.15	16.05	0.63	1.58
P00375_D	Dhfr	Dihydrofol	K.LLPEYPGVLSEVQEEK#.G	12.61	8.82	1.43	0.70
Q99LB2_DI	Dhrs4	Dehydroge	R.FSSVLWEEK#.A	8.87	3.97	2.24	0.45
Q99LB2_DI	Dhrs4	Dehydroge	R.GGGSVVIVGSVAGFTR.F	4.11	6.82	0.60	1.66
Q99LB2_DI	Dhrs4	Dehydroge	K.TALLGLTK#.N	12.88	5.82	2.22	0.45
O35286_DI	Dhx15	Putative pr	R.TLATDILM*GVLK#.E	9.13	3.81	2.40	0.42
O35286_DI	Dhx15	Putative pr	R.ASTNAMLISAGLPPLK#.A	8.49	4.19	2.03	0.49
O35286_DI	Dhx15	Putative pr	R.EAM*NDPLLER.Y	8.70	27.24	0.32	3.13
O35286_DI	Dhx15	Putative pr	R.EVDDLGPEVGDIK#.I	76.04	40.32	1.89	0.53
O35286_DI	Dhx15	Putative pr	R.FAHIDGDHLTLLNVYHAFK#.Q	33.95	24.56	1.38	0.72
O35286_DI	Dhx15	Putative pr	R.FTDILVR.H	12.96	40.84	0.32	3.15
O35286_DI	Dhx15	Putative pr	R.HQSFVLVGETGSGK#.T	39.18	25.54	1.53	0.65

O35286_D	Dhx15	Putative pr	R.HRLDLGEDYPSGK.K	13.12	33.47	0.39	2.55
O35286_D	Dhx15	Putative pr	R.IFEPPPPK#.K	48.37	34.18	1.42	0.71
O35286_D	Dhx15	Putative pr	R.IRVESLLVTAISK.A	5.68	15.44	0.37	2.72
O35286_D	Dhx15	Putative pr	R.LQLPVWEYK#.D	35.17	20.56	1.71	0.58
O35286_D	Dhx15	Putative pr	R.SNLGSVVLQLK#.K	67.35	43.27	1.56	0.64
O35286_D	Dhx15	Putative pr	K.TEM*QDNTYPEILR.S	3.77	14.26	0.26	3.78
O35286_D	Dhx15	Putative pr	R.TGHYLTVK#.D	28.77	17.08	1.68	0.59
O35286_D	Dhx15	Putative pr	R.TLATDILM*GVLK#.E	186.51	117.80	1.58	0.63
O35286_D	Dhx15	Putative pr	R.TLATDILMGVLK#.E	65.88	33.23	1.98	0.50
O35286_D	Dhx15	Putative pr	K.VIVM*SATLDAGK#.F	15.73	8.76	1.80	0.56
O35286_D	Dhx15	Putative pr	K.YM*TDGM*LLR.E	7.14	12.83	0.56	1.80
O35286_D	Dhx15	Putative pr	R.ASTNAM*LISAGLPPLK#.A	13.17	5.30	2.48	0.40
O35286_D	Dhx15	Putative pr	R.DYYINIR.K	12.39	22.42	0.55	1.81
O35286_D	Dhx15	Putative pr	R.EAM*NDPLLER.Y	15.56	20.99	0.74	1.35
O35286_D	Dhx15	Putative pr	R.EVDDLGPEVGDIK#.I	65.20	24.10	2.71	0.37
O35286_D	Dhx15	Putative pr	R.FTDILVR.H	14.80	24.85	0.60	1.68
O35286_D	Dhx15	Putative pr	R.HQSFVLVGETGSGK#.T	22.32	14.08	1.58	0.63
O35286_D	Dhx15	Putative pr	R.HRLDLGEDYPSGK.K	9.58	20.51	0.47	2.14
O35286_D	Dhx15	Putative pr	R.IFEPPPPK#.K	42.70	18.68	2.29	0.44
O35286_D	Dhx15	Putative pr	R.LQLPVWEYK#.D	36.51	19.18	1.90	0.53
O35286_D	Dhx15	Putative pr	R.SNLGSVVLQLK#.K	59.83	29.57	2.02	0.49
O35286_D	Dhx15	Putative pr	R.TLATDILM*GVLK#.E	234.39	99.91	2.35	0.43
O35286_D	Dhx15	Putative pr	R.TLATDILMGVLK#.E	63.73	30.79	2.07	0.48
O35286_D	Dhx15	Putative pr	R.VESLLVTAISK#.A	15.89	6.17	2.58	0.39
O35286_D	Dhx15	Putative pr	K.VIVM*SATLDAGK#.F	15.63	8.53	1.83	0.55
O35286_D	Dhx15	Putative pr	K.VIVMSATLDAGK#.F	11.72	202.77	0.06	17.30
O35286_D	Dhx15	Putative pr	R.YGVIILDEAHER.T	13.78	35.51	0.39	2.58
G3X8X0_G	Dhx16	DEAH (Asp-	R.TSLGNVVLLLK#.S	6.72	5.78	1.16	0.86
Q6PGC1_D	Dhx29	ATP-depen	K.IYSFNSANDSGGSANLDK#.S	4.20	2.27	1.85	0.54
Q6PGC1_D	Dhx29	ATP-depen	R.DLQTYGWLLYQEK#.V	5.48	2.54	2.15	0.46
Q6PGC1_D	Dhx29	ATP-depen	R.KLQEDGLLADVSHVIVDEVHER.S	7.83	8.05	0.97	1.03
Q6PGC1_D	Dhx29	ATP-depen	R.SVQSDFLLVILK#.E	12.49	5.48	2.28	0.44
Q6PGC1_D	Dhx29	ATP-depen	K.YQEYIPVQSGASPELNPFYQK#.Y	5.60	3.49	1.61	0.62
Q6PGC1_D	Dhx29	ATP-depen	K.AAGFSSSPSWEGR.K	4.69	7.78	0.60	1.66
Q6PGC1_D	Dhx29	ATP-depen	R.DLQTYGWLLYQEK#.V	10.88	4.02	2.71	0.37
Q6PGC1_D	Dhx29	ATP-depen	K.GPQTLSFQDIALLK#.A	9.80	5.22	1.88	0.53
Q6PGC1_D	Dhx29	ATP-depen	K.ILQIITELIK#.T	13.49	7.20	1.87	0.53
Q6PGC1_D	Dhx29	ATP-depen	K.IYSFNSANDSGGSANLDK#.S	8.05	5.10	1.58	0.63
Q6PGC1_D	Dhx29	ATP-depen	R.K#GPQTLSFQDIALLK#.A	20.03	11.26	1.78	0.56
Q6PGC1_D	Dhx29	ATP-depen	R.SAEAGAVGEAQSK#.K	18.80	11.46	1.64	0.61
Q6PGC1_D	Dhx29	ATP-depen	K.SPFITPIGR.K	6.59	20.06	0.33	3.05
Q6PGC1_D	Dhx29	ATP-depen	R.VVVVAGETGSGK#.S	44.87	16.95	2.65	0.38
Q99PU8_D	Dhx30	Putative AT	R.IPQLLLER.Y	4.39	11.77	0.37	2.68
Q99PU8_D	Dhx30	Putative AT	R.LQSDDILPLGK#.D	9.08	10.49	0.87	1.16
Q99PU8_D	Dhx30	Putative AT	R.TPLENLVLQAK#.I	14.33	10.21	1.40	0.71
Q99PU8_D	Dhx30	Putative AT	K.VIQIATSSSTAK#.N	11.61	6.97	1.67	0.60
Q99PU8_D	Dhx30	Putative AT	R.ENYLEENLLYAPSLR.F	2.91	6.35	0.46	2.18
Q99PU8_D	Dhx30	Putative AT	R.LQSDDILPLGK#.D	13.39	16.33	0.82	1.22
Q99PU8_D	Dhx30	Putative AT	R.TPLENLVLQAK#.I	28.28	11.32	2.50	0.40
Q99PU8_D	Dhx30	Putative AT	K.VIQIATSSSTAK#.N	16.32	14.71	1.11	0.90
Q8VHK9_D	Dhx36	ATP-depen	R.ASLLDDYQLPEILR.T	4.93	17.50	0.28	3.55
Q8VHK9_D	Dhx36	ATP-depen	K.DPKANINSDNEK.I	6.74	33.18	0.20	4.93
Q8VHK9_D	Dhx36	ATP-depen	K.ELDSLLQEK#.I	15.17	15.60	0.97	1.03
Q8VHK9_D	Dhx36	ATP-depen	R.SDHLTVVNAFEGWEEAK#.R	6.71	3.55	1.89	0.53
Q8VHK9_D	Dhx36	ATP-depen	K.TTQVTQFILDNYIER.G	3.64	14.92	0.24	4.10
Q8VHK9_D	Dhx36	ATP-depen	R.SDHLTVVNAFEGWEEAK#.R	8.33	4.54	1.84	0.54
Q6NZL1_Q	Dhx37	DEAH (Asp-	K.ELPEFVVYQEIVETTK#.M	11.33	5.16	2.20	0.46
Q6NZL1_Q	Dhx37	DEAH (Asp-	K.TPLLDDPVFIHPSSVLFK#.E	24.80	11.93	2.08	0.48
Q80X98_Q	Dhx38	DEAH (Asp-	K.LIVTSATM*DAEK#.F	22.49	8.96	2.51	0.40
Q80X98_Q	Dhx38	DEAH (Asp-	R.SLNTDVLFGLLR.E	3.34	20.54	0.16	6.16
Q80X98_Q	Dhx38	DEAH (Asp-	R.TNLANVVLLLK#.S	20.21	11.61	1.74	0.57
Q80X98_Q	Dhx38	DEAH (Asp-	K.TPQEDYVEAAVK#.Q	19.90	11.61	1.71	0.58
Q80X98_Q	Dhx38	DEAH (Asp-	R.LEVDEDFEEDNAAK#.V	9.84	5.13	1.92	0.52
Q80X98_Q	Dhx38	DEAH (Asp-	K.LIVTSATM*DAEK#.F	19.43	10.65	1.82	0.55
Q80X98_Q	Dhx38	DEAH (Asp-	R.LM*VEFPLDPALSK#.M	16.02	9.84	1.63	0.61
Q80X98_Q	Dhx38	DEAH (Asp-	R.LMVEFPLDPALSK#.M	8.61	3.66	2.35	0.42
Q80X98_Q	Dhx38	DEAH (Asp-	R.TNLANVVLLLK#.S	24.44	12.80	1.91	0.52
Q80X98_Q	Dhx38	DEAH (Asp-	K.TPQEDYVEAAVK#.Q	17.56	9.78	1.80	0.56
Q6PE54_D	Dhx40	Probable A	R.LGLDILEVVPISK#.S	8.28	4.87	1.70	0.59
Q99J87_D	Dhx58	Probable A	K.IGSILLETPR.G	2.97	6.81	0.44	2.29
Q99J87_D	Dhx58	Probable A	K.NIIIWLPTGAGK#.T	17.31	11.62	1.49	0.67
Q99J87_D	Dhx58	Probable A	R.ELTNEALEVLM*EK#.A	20.69	12.43	1.66	0.60
Q99J87_D	Dhx58	Probable A	K.NIIIWLPTGAGK#.T	9.70	4.51	2.15	0.47
Q99J87_D	Dhx58	Probable A	K.AEPLPQVLGLTASPGTGGATK#.L	5.77	2.91	1.98	0.50
Q99J87_D	Dhx58	Probable A	R.AGQSVYSFLATEGSR.E	8.41	12.62	0.67	1.50
Q99J87_D	Dhx58	Probable A	K.DQQEVIQEFR.D	6.31	16.82	0.38	2.67
Q99J87_D	Dhx58	Probable A	K.DTVYNTILSR.Y	5.46	8.11	0.67	1.49
Q99J87_D	Dhx58	Probable A	R.ELTNEALEVLMEK#.A	19.12	9.78	1.96	0.51
Q99J87_D	Dhx58	Probable A	K.IGSILLETPR.G	12.99	27.02	0.48	2.08
Q99J87_D	Dhx58	Probable A	K.NIIIWLPTGAGK#.T	46.78	20.63	2.27	0.44
Q99J87_D	Dhx58	Probable A	R.QTASSLLLWLR.Q	2.25	8.97	0.25	3.99
Q99J87_D	Dhx58	Probable A	K.VVVLVNR.V	9.29	17.92	0.52	1.93
Q99J87_D	Dhx58	Probable A	R.YGLLTNEISM*VQAR.G	18.20	47.42	0.38	2.61
Q99J87_D	Dhx58	Probable A	K.AEPLPQVLGLTASPGTGGATK#.L	7.29	4.59	1.59	0.63
Q99J87_D	Dhx58	Probable A	R.AESWLLK#.L	23.05	7.57	3.04	0.33
Q99J87_D	Dhx58	Probable A	R.AGQSVYSFLATEGSR.E	4.96	9.76	0.51	1.97
Q99J87_D	Dhx58	Probable A	R.AQDPFGDLIK#.K	19.80	12.06	1.64	0.61
Q99J87_D	Dhx58	Probable A	K.DQQEVIQEFR.D	5.62	12.81	0.44	2.28
Q99J87_D	Dhx58	Probable A	K.DTVYNTILSR.Y	7.80	9.53	0.82	1.22
Q99J87_D	Dhx58	Probable A	R.ELTNEALEVLM*EK#.A	15.24	7.35	2.07	0.48
Q99J87_D	Dhx58	Probable A	R.ELTNEALEVLMEK#.A	16.18	5.66	2.86	0.35
Q99J87_D	Dhx58	Probable A	K.IGSILLETPR.G	9.43	22.60	0.42	2.40
Q99J87_D	Dhx58	Probable A	K.K#AEPLPQVLGLTASPGTGGATK#.L	22.80	7.82	2.92	0.34
Q99J87_D	Dhx58	Probable A	K.NIIIWLPTGAGK#.T	64.53	23.49	2.75	0.36
A2A4P0_D	Dhx8	ATP-depen	K.FSQYFYEAPIFTIPGR.T	4.41	3.75	1.17	0.85
A2A4P0_D	Dhx8	ATP-depen	K.LIVTSATLDAVK#.F	19.41	10.76	1.80	0.55
A2A4P0_D	Dhx8	ATP-depen	K.TGIDQLVVTPISQAQAK#.Q	6.56	6.37	1.03	0.97
A2A4P0_D	Dhx8	ATP-depen	R.TNLASTVLSLK#.A	21.92	12.67	1.73	0.58
A2A4P0_D	Dhx8	ATP-depen	R.VANVADVVSK#.G	10.16	7.66	1.33	0.75
A2A4P0_D	Dhx8	ATP-depen	K.LIVTSATLDAVK#.F	17.43	10.45	1.67	0.60
A2A4P0_D	Dhx8	ATP-depen	K.TGIDQLVVTPISQAQAK#.Q	10.44	4.92	2.12	0.47
A2A4P0_D	Dhx8	ATP-depen	R.TNLASTVLSLK#.A	17.98	20.00	0.90	1.11
E9QNN1_E	Dhx9	ATP-depen	R.DFVNYLVR.I	4.48	9.79	0.46	2.19

E9QNN1_E	Dhx9	ATP-depen	R.GANLK#DYYSRK.E	2.72	3.88	0.70	1.42
E9QNN1_E	Dhx9	ATP-depen	R.AAM*EALVVEVSK#.Q	67.82	60.40	1.12	0.89
E9QNN1_E	Dhx9	ATP-depen	R.AAMEALVVEVSK#.Q	78.27	77.98	1.00	1.00
E9QNN1_E	Dhx9	ATP-depen	K.AEAENNSGVESSGYGSPGPTWDR.G	5.77	25.45	0.23	4.41
E9QNN1_E	Dhx9	ATP-depen	R.DVVLAYPEVR.I	38.62	163.30	0.24	4.23
E9QNN1_E	Dhx9	ATP-depen	K.EGERVEPYK.V	1.85	7.52	0.25	4.06
E9QNN1_E	Dhx9	ATP-depen	R.ELDALDANDELTPLGR.I	41.19	174.26	0.24	4.23
E9QNN1_E	Dhx9	ATP-depen	R.ELLPVK#K#.F	21.63	19.68	1.10	0.91
E9QNN1_E	Dhx9	ATP-depen	K.FEAEILEAISSNSVVIIR.G	2.68	12.36	0.22	4.61
E9QNN1_E	Dhx9	ATP-depen	R.FSDHVALLSVFQAWDDAR.M	44.91	157.31	0.29	3.50
E9QNN1_E	Dhx9	ATP-depen	R.GISHVIVDEIHER.D	78.51	288.11	0.27	3.67
E9QNN1_E	Dhx9	ATP-depen	K.ILTTEGR.N	24.15	103.09	0.23	4.27
E9QNN1_E	Dhx9	ATP-depen	R.ISAVAVAER.V	36.36	131.69	0.28	3.62
E9QNN1_E	Dhx9	ATP-depen	R.K#EEQEVQATLESEEVDLNAGLHGNWTLENAK#.A	12.73	8.18	1.56	0.64
E9QNN1_E	Dhx9	ATP-depen	K.KFEAEILEAISSNSVVIIR.G	7.70	31.27	0.25	4.06
E9QNN1_E	Dhx9	ATP-depen	R.KLEAGIR.G	34.01	162.96	0.21	4.79
E9QNN1_E	Dhx9	ATP-depen	R.KM*TPAYEIR.A	4.79	28.13	0.17	5.87
E9QNN1_E	Dhx9	ATP-depen	R.KMTPAYEIR.A	2.35	10.05	0.23	4.28
E9QNN1_E	Dhx9	ATP-depen	R.KVFDPVPDGVTK.V	48.76	49.40	0.99	1.01
E9QNN1_E	Dhx9	ATP-depen	K.KVQSDGQIVFIDDWIR.L	17.34	64.88	0.27	3.74
E9QNN1_E	Dhx9	ATP-depen	K.LFTAHNNM*TNYATVWASK#.T	79.52	56.92	1.40	0.72
E9QNN1_E	Dhx9	ATP-depen	K.LFTAHNNM*TNYATVWASK#.T	9.36	4.82	1.94	0.52
E9QNN1_E	Dhx9	ATP-depen	K.LFTAHNNMTNYATVWASK#.T	34.80	27.79	1.25	0.80
E9QNN1_E	Dhx9	ATP-depen	R.LGGIGQFLAK#.A	189.86	174.85	1.09	0.92
E9QNN1_E	Dhx9	ATP-depen	R.LNMATLR.M	7.42	45.33	0.16	6.11
E9QNN1_E	Dhx9	ATP-depen	R.LNQYFQK#.E	173.16	148.91	1.16	0.86
E9QNN1_E	Dhx9	ATP-depen	K.LPIEPR.F	57.07	222.77	0.26	3.90
E9QNN1_E	Dhx9	ATP-depen	K.LSM*SQLNEK.E	44.61	39.08	1.14	0.88
E9QNN1_E	Dhx9	ATP-depen	K.LSMSQLNEK#.E	17.74	16.31	1.09	0.92
E9QNN1_E	Dhx9	ATP-depen	R.MSGEEAEIR.F	7.24	31.13	0.23	4.30
E9QNN1_E	Dhx9	ATP-depen	R.M*SGEEAEIR.F	42.39	124.49	0.34	2.94
E9QNN1_E	Dhx9	ATP-depen	K.MTPAYEIR.A	6.79	29.15	0.23	4.30
E9QNN1_E	Dhx9	ATP-depen	K.NELTYQM*EQDHNLQSVLQER.E	18.92	63.72	0.30	3.37
E9QNN1_E	Dhx9	ATP-depen	K.NELTYQMEQDHNLQSVLQER.E	6.86	25.79	0.27	3.76
E9QNN1_E	Dhx9	ATP-depen	R.QISRPSAAGINLM*IGSVR.Y	11.25	28.27	0.40	2.51
E9QNN1_E	Dhx9	ATP-depen	R.QLYHLGVIEAYSGLTK#.K	120.90	108.05	1.12	0.89
E9QNN1_E	Dhx9	ATP-depen	K.RLNMATLR.M	10.19	12.58	0.81	1.23
E9QNN1_E	Dhx9	ATP-depen	R.SFIAEM*TIYIK.Q	26.21	27.99	0.94	1.07
E9QNN1_E	Dhx9	ATP-depen	R.TPLHEIALSIK#.L	55.58	47.84	1.16	0.86
E9QNN1_E	Dhx9	ATP-depen	K.TTQVPQYILDDFIQNDR.A	41.27	126.73	0.33	3.07
E9QNN1_E	Dhx9	ATP-depen	K.TTQVPQYILDDFIQNDR.A	27.55	71.51	0.39	2.60
E9QNN1_E	Dhx9	ATP-depen	K.VFDPVPDGVTK#.V	143.03	133.10	1.07	0.93
E9QNN1_E	Dhx9	ATP-depen	K.VQSDGQIVFIDDWIR.L	13.78	54.57	0.25	3.96
E9QNN1_E	Dhx9	ATP-depen	R.YGDGPRPPK.M	13.98	29.09	0.48	2.08
E9QNN1_E	Dhx9	ATP-depen	K.YPSPFFVFGEK#.I	154.15	143.80	1.07	0.93
E9QNN1_E	Dhx9	ATP-depen	K.YTQVGPDHNR.S	9.35	56.18	0.17	6.01
E9QNN1_E	Dhx9	ATP-depen	R.AAM*EALVVEVSK#.Q	73.66	57.91	1.27	0.79
E9QNN1_E	Dhx9	ATP-depen	R.AAMEALVVEVSK#.Q	110.58	82.58	1.34	0.75
E9QNN1_E	Dhx9	ATP-depen	K.AEAENNSGVESSGYGSPGPTWDR.G	10.24	39.77	0.26	3.88
E9QNN1_E	Dhx9	ATP-depen	R.DFVNYLVR.I	57.61	199.39	0.29	3.46
E9QNN1_E	Dhx9	ATP-depen	R.DVVLAYPEVR.I	62.63	218.16	0.29	3.48
E9QNN1_E	Dhx9	ATP-depen	R.ELDALDANDELTPLGR.I	70.20	244.28	0.29	3.48
E9QNN1_E	Dhx9	ATP-depen	R.FSDHVALLSVFQAWDDAR.M	18.01	52.59	0.34	2.92
E9QNN1_E	Dhx9	ATP-depen	R.GANLKDYYSR.K	10.35	32.14	0.32	3.11
E9QNN1_E	Dhx9	ATP-depen	R.GISHVIVDEIHER.D	96.08	314.43	0.31	3.27
E9QNN1_E	Dhx9	ATP-depen	K.HLENNSHFGSHR.Y	10.82	44.56	0.24	4.12
E9QNN1_E	Dhx9	ATP-depen	R.ISAVAVAER.V	49.26	200.15	0.25	4.06
E9QNN1_E	Dhx9	ATP-depen	R.K#EEQEVQATLESEEVDLNAGLHGNWTLENAK#.A	40.60	33.68	1.21	0.83
E9QNN1_E	Dhx9	ATP-depen	R.KEEQEVQATLESEEVDLNAGLHGNWTLENAK.A	11.48	8.66	1.33	0.75
E9QNN1_E	Dhx9	ATP-depen	K.KFEAEILEAISSNSVVIIR.G	4.14	8.49	0.49	2.05
E9QNN1_E	Dhx9	ATP-depen	R.KLEAGIR.G	41.73	152.42	0.27	3.65
E9QNN1_E	Dhx9	ATP-depen	R.K#VFDPVPDGVTK#.V	60.85	54.16	1.12	0.89
E9QNN1_E	Dhx9	ATP-depen	K.LFTAHNNM*TNYATVWASK#.T	138.74	85.01	1.63	0.61
E9QNN1_E	Dhx9	ATP-depen	K.LFTAHNNMTNYATVWASK#.T	36.14	27.99	1.29	0.77
E9QNN1_E	Dhx9	ATP-depen	R.LGGIGQFLAK#.A	342.81	267.03	1.28	0.78
E9QNN1_E	Dhx9	ATP-depen	R.LNM*ATLR.M	26.47	79.84	0.33	3.02
E9QNN1_E	Dhx9	ATP-depen	R.LNQYFQK#.E	306.96	226.52	1.36	0.74
E9QNN1_E	Dhx9	ATP-depen	K.LPIEPR.F	91.97	344.43	0.27	3.74
E9QNN1_E	Dhx9	ATP-depen	K.LSMSQLNEK#.E	22.16	19.06	1.16	0.86
E9QNN1_E	Dhx9	ATP-depen	K.LSM*SQLNEK#.E	103.06	69.82	1.48	0.68
E9QNN1_E	Dhx9	ATP-depen	R.M*SGEEAEIR.F	42.83	135.10	0.32	3.15
E9QNN1_E	Dhx9	ATP-depen	K.NELTYQM*EQDHNLQSVLQER.E	40.19	118.93	0.34	2.96
E9QNN1_E	Dhx9	ATP-depen	K.NELTYQMEQDHNLQSVLQER.E	42.08	35.17	1.20	0.84
E9QNN1_E	Dhx9	ATP-depen	R.QISRPSAAGINLM*IGSVR.Y	11.08	32.82	0.34	2.96
E9QNN1_E	Dhx9	ATP-depen	R.QLYHLGVIEAYSGLTK#.K	186.63	123.31	1.51	0.66
E9QNN1_E	Dhx9	ATP-depen	R.RISAVAVAER.V	9.73	160.83	0.06	16.52
E9QNN1_E	Dhx9	ATP-depen	R.SFIAEM*TIYIK#.Q	52.12	42.37	1.23	0.81
E9QNN1_E	Dhx9	ATP-depen	R.TPLHEIALSIK#.L	155.84	133.24	1.17	0.85
E9QNN1_E	Dhx9	ATP-depen	K.TTQVPQYILDDFIQNDR.A	60.85	191.92	0.32	3.15
E9QNN1_E	Dhx9	ATP-depen	R.VEGFNYAGM*GNSTNK#.K	35.26	29.16	1.21	0.83
E9QNN1_E	Dhx9	ATP-depen	R.VEGFNYAGMGNSTNK#.K	8.72	5.76	1.52	0.66
E9QNN1_E	Dhx9	ATP-depen	R.VEGFNYAGM*GNSTNKK.D	19.70	12.58	1.57	0.64
E9QNN1_E	Dhx9	ATP-depen	K.VFDPVPDGVTK#.V	248.89	224.84	1.11	0.90
E9QNN1_E	Dhx9	ATP-depen	K.VQSDGQIVFIDDWIR.L	19.33	72.57	0.27	3.75
E9QNN1_E	Dhx9	ATP-depen	K.YPSPFFVFGEK#.I	219.58	176.97	1.24	0.81
E9QNN1_E	Dhx9	ATP-depen	R.YQILPLHSQIPR.E	6.72	24.48	0.27	3.64
E9QNN1_E	Dhx9	ATP-depen	K.YTQVGPDHNR.S	21.35	70.93	0.30	3.32
O08808_D	Diaph1	Protein dia	K.ELGDYFVFDPK#.K	7.60	2.33	3.26	0.31
O08808_D	Diaph1	Protein dia	R.LNAILFK#.L	13.97	5.01	2.79	0.36
O08808_D	Diaph1	Protein dia	R.NM*FLQAVK#.E	10.71	7.68	1.39	0.72
O08808_D	Diaph1	Protein dia	R.SPDELPATGGDGGK#.H	16.74	7.21	2.32	0.43
Q9Z207_D	Diaph3	Protein dia	K.INELQAELQAFK#.S	6.34	6.85	0.93	1.08
Q8C9B9_D	Dido1	Death-indu	R.LQQEELETSVYPK#.V	3.95	2.40	1.65	0.61
Q8C9B9_D	Dido1	Death-indu	K.AK#GEDTM*SAAPLLDPIVQQFGQFSK#.D	5.19	1.79	2.90	0.34
Q8C9B9_D	Dido1	Death-indu	R.LGPVSPAPSQPNSQIR.Q	2.88	8.40	0.34	2.92
Q9D0D4_D	Dimt1	Probable di	K.AALRPTDVVLEVGPGTGNM*TVK.L	2.84	6.17	0.46	2.17
Q9D0D4_D	Dimt1	Probable di	R.LLHGFNAEGIHFS.-	20.41	20.41	1.00	1.00
Q9D0D4_D	Dimt1	Probable di	K.LQVLVGDVLK#.S	19.96	7.64	2.61	0.38
Q9D0D4_D	Dimt1	Probable di	K.SSAVQQLLEK#.N	17.62	13.18	1.34	0.75
Q9CSH3_R	Dis3	Exosome c	R.AESPDFPYLNTLLR.I	5.15	13.00	0.40	2.53
Q9CSH3_R	Dis3	Exosome c	K.ASLTYAEAQM*R.I	6.70	16.75	0.40	2.50
Q9CSH3_R	Dis3	Exosome c	R.AVHEDIVAVELLPR.S	7.64	21.83	0.35	2.86
Q9CSH3_R	Dis3	Exosome c	R.IDSAAM*NDDITTSLR.G	4.97	13.45	0.37	2.71

Q9CSH3_RI	Dis3	Exosome cc	R.IEGTVFHVFDK#.V	11.75	8.23	1.43	0.70
Q9CSH3_RI	Dis3	Exosome cc	R.IIVAIDGWPR.N	6.11	21.29	0.29	3.48
Q9CSH3_RI	Dis3	Exosome cc	R.LAYDDEIPSLR.I	10.39	19.17	0.54	1.84
Q9CSH3_RI	Dis3	Exosome cc	R.LAYLSDEM*NEIESGK#.I	11.81	9.38	1.26	0.79
Q9CSH3_RI	Dis3	Exosome cc	K.NAIVVLIPK#.Y	21.91	12.25	1.79	0.56
Q9CSH3_RI	Dis3	Exosome cc	R.NVIVLQTVM*QEVR.N	1.61	7.30	0.22	4.54
Q9CSH3_RI	Dis3	Exosome cc	R.NVIVLQTVMQEVR.N	4.36	10.63	0.41	2.44
Q9CSH3_RI	Dis3	Exosome cc	K.SLTANPELIDR.L	12.10	26.48	0.46	2.19
Q9CSH3_RI	Dis3	Exosome cc	K.YGLEGTVFFEEK#.D	9.30	8.44	1.10	0.91
Q9CSH3_RI	Dis3	Exosome cc	R.AESPDFPYLNTLLR.I	10.86	21.52	0.50	1.98
Q9CSH3_RI	Dis3	Exosome cc	K.ASLTYAEAQM*R.I	8.13	22.57	0.36	2.78
Q9CSH3_RI	Dis3	Exosome cc	R.AVHEDIVAVELLPR.S	6.77	21.80	0.31	3.22
Q9CSH3_RI	Dis3	Exosome cc	R.FHM*DSETHDPIDLQTK#.E	22.75	14.71	1.55	0.65
Q9CSH3_RI	Dis3	Exosome cc	K.GALTLSSPEIR.F	19.72	31.02	0.64	1.57
Q9CSH3_RI	Dis3	Exosome cc	R.HLFTPADK#.R	23.17	73.46	0.32	3.17
Q9CSH3_RI	Dis3	Exosome cc	R.IDSAAM*NDDITTSLR.G	11.41	25.58	0.45	2.24
Q9CSH3_RI	Dis3	Exosome cc	R.IDSAAMNDDITTSLR.G	2.89	8.26	0.35	2.86
Q9CSH3_RI	Dis3	Exosome cc	R.IEGTVFHVFDK#.V	26.61	16.06	1.66	0.60
Q9CSH3_RI	Dis3	Exosome cc	R.K#HPAPPPSNYDILVK#.A	19.50	15.17	1.29	0.78
Q9CSH3_RI	Dis3	Exosome cc	R.LAYLSDEM*NEIESGK#.I	18.65	9.84	1.90	0.53
Q9CSH3_RI	Dis3	Exosome cc	R.LAYLSDEMNEIESGK#.I	10.83	8.66	1.25	0.80
Q9CSH3_RI	Dis3	Exosome cc	R.M*PWSITEEDM*K.N	4.67	5.95	0.78	1.27
Q9CSH3_RI	Dis3	Exosome cc	K.NAIVVLIPK#.Y	34.90	21.86	1.60	0.63
Q9CSH3_RI	Dis3	Exosome cc	R.NVIVLQTVM*QEVR.N	4.60	8.91	0.52	1.94
Q9CSH3_RI	Dis3	Exosome cc	K.SGSYLQGTFR.A	10.63	29.92	0.36	2.81
Q9CSH3_RI	Dis3	Exosome cc	K.SLTANPELIDR.L	12.96	28.28	0.46	2.18
Q9CSH3_RI	Dis3	Exosome cc	K.YGLEGTVFFEEK#.D	15.96	8.55	1.87	0.54
Q9ESX5_DI	Dkc1	H/ACA ribo	R.ALETLTGALFQRPPLIAAVK.R	5.31	9.79	0.54	1.84
Q9ESX5_DI	Dkc1	H/ACA ribo	R.K#PLQEDDVAEIQHAEEFLIK#PESK#.V	8.65	4.48	1.93	0.52
Q9ESX5_DI	Dkc1	H/ACA ribo	K.NTLVTEAVQAPQLAAEAVNVIK#.R	15.26	9.10	1.68	0.60
Q9ESX5_DI	Dkc1	H/ACA ribo	K.TVLESGGETGDGDNDTTK#.K	4.78	2.33	2.05	0.49
Q9ESX5_DI	Dkc1	H/ACA ribo	K.VAQLDTSQWPLLLK#.N	7.74	4.84	1.60	0.62
Q9ESX5_DI	Dkc1	H/ACA ribo	K.NTLVTEAVQAPQLAAEAVNVIK#.R	11.99	2.82	4.25	0.24
Q9ESX5_DI	Dkc1	H/ACA ribo	K.VAQLDTSQWPLLLK#.N	8.09	2.26	3.58	0.28
Q9ESX5_DI	Dkc1	H/ACA ribo	R.ALETLTGALFQRPPLIAAVK.R	5.77	6.47	0.89	1.12
Q9ESX5_DI	Dkc1	H/ACA ribo	K.NTLVTEAVQAPQLAAEAVNVIK#.R	9.10	4.61	1.97	0.51
Q9ESX5_DI	Dkc1	H/ACA ribo	K.VAQLDTSQWPLLLK#.N	10.40	4.55	2.29	0.44
Q8BMF4_O	Dlat	Dihydrolip	K.DIDSFVPSK#.A	16.68	5.76	2.90	0.35
Q8BMF4_O	Dlat	Dihydrolip	K.GIDLTQVK#.G	39.88	3.75	10.63	0.09
Q8BMF4_O	Dlat	Dihydrolip	K.GLETIASDVVSLASK#.A	46.21	5.17	8.94	0.11
Q8BMF4_O	Dlat	Dihydrolip	K.ISVNDFIIK#.A	25.18	6.03	4.18	0.24
Q8BMF4_O	Dlat	Dihydrolip	K.LQPHEFQGGTFTISNLGMFGIK#.N	6.99	2.92	2.39	0.42
Q8BMF4_O	Dlat	Dihydrolip	R.VFVSPLAK#.K	33.46	7.38	4.53	0.22
Q8BMF4_O	Dlat	Dihydrolip	K.YLEK#PITMLL.-	10.60	4.19	2.53	0.39
Q8BMF4_O	Dlat	Dihydrolip	K.GLETIASDVVSLASK#.A	18.38	6.36	2.89	0.35
Q8BMF4_O	Dlat	Dihydrolip	K.ISVNDFIIK#.A	17.96	4.13	4.35	0.23
Q811D0_D	Dlg1	Disks large	R.AASHEQAAAALK#.N	13.00	6.84	1.90	0.53
Q811D0_D	Dlg1	Disks large	K.GLGFSIAGGVGNQHIPGDNSIYVTK#.I	11.66	4.78	2.44	0.41
Q811D0_D	Dlg1	Disks large	R.GNSGLGFSIAGGTDNPHIGDDSSIFITK#.I	11.61	6.68	1.74	0.57
Q811D0_D	Dlg1	Disks large	K.LEQEFTEHFTAIVQGDTLEDIYNQVK#.Q	8.91	4.26	2.09	0.48
Q9JI44_DM	Dmap1	DNA methy	K.DAPPLLPSDTGQGYR.T	3.98	19.84	0.20	4.99
Q9JI44_DM	Dmap1	DNA methy	R.DILELGGPEGDAASGTISK#.K	22.19	17.40	1.27	0.78
Q9JI44_DM	Dmap1	DNA methy	R.EVYALLYSDKK.D	8.56	8.46	1.01	0.99
Q9JI44_DM	Dmap1	DNA methy	K.LITAADTTAEQR.R	6.98	25.62	0.27	3.67
Q9JI44_DM	Dmap1	DNA methy	R.SDLVLLYELK#.Q	37.32	27.50	1.36	0.74
Q9JI44_DM	Dmap1	DNA methy	R.TPEQVAEEEYLLQELR.K	3.18	9.62	0.33	3.03
Q9JI44_DM	Dmap1	DNA methy	R.TPEQVAEEEYLLQELRK.I	2.29	9.44	0.24	4.13
E9Q7N9_E	Dnah11	Protein Dn	K.KIAAMVR.H	28.13	124.66	0.23	4.43
E9Q7N9_E	Dnah11	Protein Dn	R.LSPSEQEDEEDEEAAAARRVQR.F	1.62	6.23	0.26	3.85
P63037_DI	Dnaja1	DnaJ homo	K.EGGAGGGFGSPM*DIFDM*FFGGGGR.M	1.95	8.53	0.23	4.38
P63037_DI	Dnaja1	DnaJ homo	K.EVEETDEM*DQVELVDFDPNQER.R	6.77	22.99	0.29	3.39
P63037_DI	Dnaja1	DnaJ homo	K.EVEETDEMDQVELVDFDPNQER.R	3.08	10.70	0.29	3.48
P63037_DI	Dnaja1	DnaJ homo	K.ILEVHIDK#.G	43.60	23.32	1.87	0.53
P63037_DI	Dnaja1	DnaJ homo	K.ITFHGEGDQEPGLEPGDIIIVLDQK#.D	97.42	67.79	1.44	0.70
P63037_DI	Dnaja1	DnaJ homo	R.KEVEETDEM*DQVELVDFDPNQER.R	1.59	9.48	0.17	5.95
P63037_DI	Dnaja1	DnaJ homo	K.NVVHQLSVTLEDLYNGATR.K	8.31	40.08	0.21	4.83
P63037_DI	Dnaja1	DnaJ homo	K.QISQAYEVLADSK#.K	87.87	70.05	1.25	0.80
P63037_DI	Dnaja1	DnaJ homo	R.TIVITSHPGQIVK.H	48.87	49.88	0.98	1.02
P63037_DI	Dnaja1	DnaJ homo	K.VNFPENGFLSPDK.L	14.10	14.42	0.98	1.02
P63037_DI	Dnaja1	DnaJ homo	K.QISQAYEVLADSK#.K	3.47	3.43	1.01	0.99
P63037_DI	Dnaja1	DnaJ homo	K.ITFHGEGDQEPGLEPGDIIIVLDQK#.D	6.50	7.10	0.92	1.09
Q9QYJ0_DI	Dnaja2	DnaJ homo	R.DGNDLHMTYK#.I	18.15	14.23	1.28	0.78
Q9QYJ0_DI	Dnaja2	DnaJ homo	R.DGNDLHM*TYK#.I	33.55	19.09	1.76	0.57
Q9QYJ0_DI	Dnaja2	DnaJ homo	R.EGSGGGGGM*DDIFSHIFGGGLFGFM*GNQSR.S	7.58	16.75	0.45	2.21
Q9QYJ0_DI	Dnaja2	DnaJ homo	K.EISFAYEVLSNPEK#.R	15.52	10.32	1.50	0.66
Q9QYJ0_DI	Dnaja2	DnaJ homo	K.FDVQFPENNWINPDK#.L	21.48	10.69	2.01	0.50
Q9QYJ0_DI	Dnaja2	DnaJ homo	K.GDLYIK#.F	118.62	72.27	1.64	0.61
Q9QYJ0_DI	Dnaja2	DnaJ homo	R.GEGM*PQYR.N	8.21	20.96	0.39	2.55
Q9QYJ0_DI	Dnaja2	DnaJ homo	K.ILEVHVDK#.G	43.50	28.23	1.54	0.65
Q9QYJ0_DI	Dnaja2	DnaJ homo	R.ITFTGEADQAPGVEPGDIVLLLQEK#.E	166.92	100.16	1.67	0.60
Q9QYJ0_DI	Dnaja2	DnaJ homo	K.LYDILGVPPGASENELK#K#.A	33.95	31.10	1.09	0.92
Q9QYJ0_DI	Dnaja2	DnaJ homo	K.VSLEDLYNGK#.T	63.80	38.45	1.66	0.60
Q9QYJ0_DI	Dnaja2	DnaJ homo	R.YGEQGLR.E	27.90	97.79	0.29	3.51
Q9QYJ3_DI	Dnajb1	DnaJ homo	K.EGDQTSNNIPADIVFVLK#.D	14.27	12.44	1.15	0.87
Q99KV1_D.	Dnajb11	DnaJ homo	K.FQDLGAAYEVLSDSEK#.R	17.26	12.72	1.36	0.74
Q99KV1_D.	Dnajb11	DnaJ homo	K.GSLIITFDVDFPK#EQLTEEAK#.E	6.08	4.52	1.34	0.74
Q99KV1_D.	Dnajb11	DnaJ homo	R.TLEVEIEPGVR.D	6.00	15.00	0.40	2.50
Q9D832_D	Dnajb4	DnaJ homo	R.DGSNIVYTAK#.I	9.00	4.85	1.86	0.54
Q9D832_D	Dnajb4	DnaJ homo	R.EGDETPNSIPADIVFVIK#.D	16.73	34.64	0.48	2.07
Q9D832_D	Dnajb4	DnaJ homo	R.EIYDQFGEEGLK#.G	7.36	2.52	2.91	0.34
O54946_DI	Dnajb6	DnaJ homo	R.GQPTPALAPGPAPAPVR.V	1.95	4.72	0.41	2.42
O54946_DI	Dnajb6	DnaJ homo	R.VEVEEDGQLK#.S	33.05	29.85	1.11	0.90
O54946_DI	Dnajb6	DnaJ homo	K.QVAEAYEVLSDAK.K	7.41	8.43	0.88	1.14
Q9DC23_D.	Dnajc10	DnaJ homo	K.SSVLFLNSLDAK#.E	118.24	9.57	12.36	0.08
G3X922_G.	Dnajc13	MCG11560	K.AGFLAFTQLPK#.F	10.19	12.79	0.80	1.25
G3X922_G.	Dnajc13	MCG11560	K.GQGTEFNLTFR.K	2.36	9.19	0.26	3.90
G3X922_G.	Dnajc13	MCG11560	K.IVDGPDPENIILILK#.T	18.86	20.82	0.91	1.10
G3X922_G.	Dnajc13	MCG11560	K.KPVVLEVTPGGFDQINPVTNR.V	2.41	16.21	0.15	6.73
G3X922_G.	Dnajc13	MCG11560	R.LGGYLSEDQATPENPTVR.K	1.62	6.22	0.26	3.85
G3X922_G.	Dnajc13	MCG11560	K.LLEGVGLENLDSPAATK#.A	7.04	9.40	0.75	1.33
G3X922_G.	Dnajc13	MCG11560	K.NEETNQQEVANSLAK.L	8.57	8.24	1.04	0.96
G3X922_G.	Dnajc13	MCG11560	R.SNLIWNFK#.T	13.89	6.18	2.25	0.45
G3X922_G.	Dnajc13	MCG11560	R.TELLTEALR.F	3.60	13.92	0.26	3.87

G3X922_G	Dnajc13	MCG1156	K.YSTDESITSLAEFVVQK#.I	7.16	3.56	2.01	0.50
P54103_D	Dnajc2	DnaJ homo	R.AFNSVDPTFDNSVPSK#.S	10.61	1.85	5.75	0.17
P54103_D	Dnajc2	DnaJ homo	K.NWSEDDLQLLIK#.A	12.10	6.92	1.75	0.57
Q91YW3_D	Dnajc3	DnaJ homo	R.SQALDAFDGADYTAAITFLDK#.I	8.95	6.88	1.30	0.77
Q91WN1_	Dnajc9	DnaJ homo	K.AVYDEQGTVDEDSAGLNQDRDWDAYWR.L	3.63	18.44	0.20	5.08
Q91WN1_	Dnajc9	DnaJ homo	K.EIPAYSAFVK#.E	66.47	54.35	1.22	0.82
Q91WN1_	Dnajc9	DnaJ homo	K.GSEEELNDIK#.Q	44.26	48.95	0.90	1.11
Q91WN1_	Dnajc9	DnaJ homo	K.ISLEDIQAFEK#.T	54.47	61.97	0.88	1.14
Q91WN1_	Dnajc9	DnaJ homo	K.K#ISLEDIQAFEK#.T	11.83	10.76	1.10	0.91
Q91WN1_	Dnajc9	DnaJ homo	K.TYK#GSEEELNDIK#.Q	10.60	9.87	1.07	0.93
Q91WN1_	Dnajc9	DnaJ homo	R.VYAVLSDKEQK.A	33.63	18.76	1.79	0.56
P39053_D	Dnm1	Dynamin-1	R.GYIGVVNR.S	16.65	32.82	0.51	1.97
P39053_D	Dnm1	Dynamin-1	R.LQDAFSAIGQNADLDLPQIAVVGGQSAGK#.S	12.05	2.87	4.20	0.24
P39053_D	Dnm1	Dynamin-1	R.TGLFTPDMAFETIVK#.K	7.58	5.53	1.37	0.73
P39053_D	Dnm1	Dynamin-1	R.VYSPHVLNLTLVDLPGM*TK#.V	13.89	5.32	2.61	0.38
P39053_D	Dnm1	Dynamin-1	K.ALLQM*VQQFAVDFEK#.R	15.85	5.47	2.90	0.34
P39053_D	Dnm1	Dynamin-1	K.ALLQM*VQQFAVDFEK#.R	14.55	5.12	2.84	0.35
P39053_D	Dnm1	Dynamin-1	R.EISYAIK#.N	92.27	164.92	0.56	1.79
P39053_D	Dnm1	Dynamin-1	R.FPFELVK#.M	137.86	54.34	2.54	0.39
P39053_D	Dnm1	Dynamin-1	K.GISPVPINLR.V	29.48	51.60	0.57	1.75
P39053_D	Dnm1	Dynamin-1	R.GYIGVVNR.S	30.20	48.02	0.63	1.59
P39053_D	Dnm1	Dynamin-1	R.IEGSGDQIDTYELSGGAR.I	5.40	7.84	0.69	1.45
P39053_D	Dnm1	Dynamin-1	K.LDLM*DEGTDAR.D	10.98	17.99	0.61	1.64
P39053_D	Dnm1	Dynamin-1	R.LQDAFSAIGQNADLDLPQIAVVGGQSAGK#.S	53.10	16.62	3.20	0.31
P39053_D	Dnm1	Dynamin-1	K.LQSQLLSIEK#.E	45.41	15.07	3.01	0.33
P39053_D	Dnm1	Dynamin-1	R.M*GTPYLQK#.V	21.09	8.22	2.57	0.39
P39053_D	Dnm1	Dynamin-1	R.NLVDSYM*AIVNK#.T	16.09	7.87	2.04	0.49
P39053_D	Dnm1	Dynamin-1	K.RIEGSGDQIDTYELSGGAR.I	6.28	14.63	0.43	2.33
P39053_D	Dnm1	Dynamin-1	K.SSVLENFVGR.D	29.04	47.13	0.62	1.62
P39053_D	Dnm1	Dynamin-1	R.TGLFTPDM*AFETIVK#.K	29.07	10.01	2.90	0.34
P39053_D	Dnm1	Dynamin-1	R.TGLFTPDMAFETIVK#.K	17.81	7.05	2.53	0.40
P39053_D	Dnm1	Dynamin-1	K.VPVGDQPPDIEFQIR.D	6.98	14.83	0.47	2.12
P39053_D	Dnm1	Dynamin-1	R.VYSPHVLNLTLVDLPGM*TK#.V	46.19	17.01	2.72	0.37
P39053_D	Dnm1	Dynamin-1	K.YM*LSVDNLK#.L	21.53	7.32	2.94	0.34
P39053_D	Dnm1	Dynamin-1	R.FPFELVK#.M	48.92	19.21	2.55	0.39
P39053_D	Dnm1	Dynamin-1	R.LQDAFSAIGQNADLDLPQIAVVGGQSAGK#.S	11.07	11.84	0.94	1.07
P39053_D	Dnm1	Dynamin-1	R.TGLFTPDM*AFETIVK#.K	9.30	4.04	2.30	0.43
P39053_D	Dnm1	Dynamin-1	K.VPVGDQPPDIEFQIR.D	2.65	7.92	0.34	2.98
P39053_D	Dnm1	Dynamin-1	R.VYSPHVLNLTLVDLPGM*TK#.V	9.94	6.34	1.57	0.64
Q8K1M6_D	Dnm1l	Dynamin-1	R.FISNPNSIILAVTAANTDM*ATSEALK#.I	5.13	3.87	1.32	0.75
Q8K1M6_D	Dnm1l	Dynamin-1	R.TLAVITK#.L	17.54	11.76	1.49	0.67
Q8K1M6_D	Dnm1l	Dynamin-1	K.VFSPNVVNLTLVDLPGM*TK#.V	7.49	5.64	1.33	0.75
Q8K1M6_D	Dnm1l	Dynamin-1	K.VFSPNVVNLTLVDLPGM*TK#.V	5.47	4.95	1.11	0.90
Q8K1M6_D	Dnm1l	Dynamin-1	K.ALQGASQIIAEIR.E	12.27	38.48	0.32	3.14
Q8K1M6_D	Dnm1l	Dynamin-1	K.DTLQSELVGQLYK#.S	18.40	10.20	1.80	0.55
Q8K1M6_D	Dnm1l	Dynamin-1	K.ALQGASQIIAEIR.E	13.19	23.61	0.56	1.79
Q8K1M6_D	Dnm1l	Dynamin-1	K.DTLQSELVGQLYK#.S	14.05	3.20	4.39	0.23
Q8K1M6_D	Dnm1l	Dynamin-1	R.FISNPNSIILAVTAANTDM*ATSEALK#.I	32.52	12.83	2.54	0.39
Q8K1M6_D	Dnm1l	Dynamin-1	R.FISNPNSIILAVTAANTDMATSEALK#.I	24.43	9.71	2.52	0.40
Q8K1M6_D	Dnm1l	Dynamin-1	K.GHAVNLLDVPVPVAR.K	15.53	27.10	0.57	1.75
Q8K1M6_D	Dnm1l	Dynamin-1	R.K#NIQDSVPK#.A	12.22	7.55	1.62	0.62
Q8K1M6_D	Dnm1l	Dynamin-1	K.LGIIGVVNR.S	15.90	30.20	0.53	1.90
Q8K1M6_D	Dnm1l	Dynamin-1	R.LLM*HHIR.D	1.65	12.21	0.14	7.38
Q8K1M6_D	Dnm1l	Dynamin-1	R.LPVTNEM*VHNLVAIELAYINTK#.H	5.32	3.42	1.55	0.64
Q8K1M6_D	Dnm1l	Dynamin-1	K.NIQDSVPK#.A	31.03	20.97	1.48	0.68
Q8K1M6_D	Dnm1l	Dynamin-1	R.RPLILQLVHVSPEDK.R	10.65	15.84	0.67	1.49
Q8K1M6_D	Dnm1l	Dynamin-1	R.RPLILQLVHVSPEDKR.K	1.85	19.08	0.10	10.34
Q8K1M6_D	Dnm1l	Dynamin-1	K.SATLLQLITK#.F	25.28	9.50	2.66	0.38
Q8K1M6_D	Dnm1l	Dynamin-1	R.SQLDINNK#K#.S	22.15	9.30	2.38	0.42
Q8K1M6_D	Dnm1l	Dynamin-1	K.SSVLESLVGR.D	11.82	25.22	0.47	2.13
Q8K1M6_D	Dnm1l	Dynamin-1	R.TLAVITK#.L	51.44	19.76	2.60	0.38
Q8K1M6_D	Dnm1l	Dynamin-1	K.TSK#AEELLAEEK#.S	17.65	4.91	3.60	0.28
Q8K1M6_D	Dnm1l	Dynamin-1	K.VFSPNVVNLTLVDLPGM*TK#.V	30.47	11.95	2.55	0.39
Q8K1M6_D	Dnm1l	Dynamin-1	K.VFSPNVVNLTLVDLPGMTK#.V	28.19	7.04	4.00	0.25
Q8K1M6_D	Dnm1l	Dynamin-1	K.VPVGDQPK#.D	61.58	25.29	2.44	0.41
Q8K1M6_D	Dnm1l	Dynamin-1	K.AEELLAEEK#.S	23.27	9.72	2.39	0.42
Q8K1M6_D	Dnm1l	Dynamin-1	K.ALQGASQIIAEIR.E	11.35	14.32	0.79	1.26
Q8K1M6_D	Dnm1l	Dynamin-1	K.DTLQSELVGQLYK#.S	25.35	10.06	2.52	0.40
Q8K1M6_D	Dnm1l	Dynamin-1	R.FISNPNSIILAVTAANTDM*ATSEALK#.I	31.35	9.61	3.26	0.31
Q8K1M6_D	Dnm1l	Dynamin-1	R.FISNPNSIILAVTAANTDMATSEALK#.I	10.18	3.91	2.60	0.38
Q8K1M6_D	Dnm1l	Dynamin-1	R.INVLAAQYQSLLNSYGEPVDDK#.S	8.40	2.65	3.17	0.32
Q8K1M6_D	Dnm1l	Dynamin-1	R.RPLILQLVHVSPEDK.R	8.86	12.40	0.72	1.40
Q8K1M6_D	Dnm1l	Dynamin-1	K.SATLLQLITK#.F	17.54	7.63	2.30	0.44
Q8K1M6_D	Dnm1l	Dynamin-1	R.TLAVITK#.L	36.71	17.27	2.13	0.47
Q8K1M6_D	Dnm1l	Dynamin-1	K.TSK#AEELLAEEK#.S	13.50	5.76	2.35	0.43
Q8K1M6_D	Dnm1l	Dynamin-1	K.VFSPNVVNLTLVDLPGM*TK#.V	27.31	10.51	2.60	0.38
Q8K1M6_D	Dnm1l	Dynamin-1	K.VFSPNVVNLTLVDLPGMTK#.V	10.29	4.18	2.46	0.41
Q8K1M6_D	Dnm1l	Dynamin-1	K.VPVGDQPK#.D	44.88	23.04	1.95	0.51
P39054_D	Dnm2	Dynamin-2	R.AGVYPEKDQAENEDGAQENTFSM*DPQLER.Q	3.04	9.55	0.32	3.14
P39054_D	Dnm2	Dynamin-2	R.AGVYPEKDQAENEDGAQENTFSMDPQLER.Q	4.12	3.28	1.26	0.80
P39054_D	Dnm2	Dynamin-2	K.ALLQM*VQQFGVDFEK#.R	7.58	6.12	1.24	0.81
P39054_D	Dnm2	Dynamin-2	K.ALLQMVQQFGVDFEK#.R	52.67	6.74	7.82	0.13
P39054_D	Dnm2	Dynamin-2	R.ESSLILAVTPANM*DLANSDALK#.L	8.33	5.13	1.62	0.62
P39054_D	Dnm2	Dynamin-2	K.EVDPQGLR.T	16.86	32.54	0.52	1.93
P39054_D	Dnm2	Dynamin-2	R.GM*EELIPLVNK#.L	52.45	26.61	1.97	0.51
P39054_D	Dnm2	Dynamin-2	R.GMEELIPLVNK#.L	23.85	7.27	3.28	0.30
P39054_D	Dnm2	Dynamin-2	R.GWLTINNISLM*K#.G	9.20	5.11	1.80	0.56
P39054_D	Dnm2	Dynamin-2	R.IEGSGDQVDTLELSGGAR.I	6.71	10.81	0.62	1.61
P39054_D	Dnm2	Dynamin-2	R.IVTTYIR.E	22.31	23.41	0.95	1.05
P39054_D	Dnm2	Dynamin-2	R.NLVDSYVAIINK#.S	71.97	35.91	2.00	0.50
P39054_D	Dnm2	Dynamin-2	K.RIEGSGDQVDTLELSGGAR.I	2.45	17.00	0.14	6.95
P39054_D	Dnm2	Dynamin-2	R.SK#LQSQLLSLEK#.E	18.27	7.42	2.46	0.41
P39054_D	Dnm2	Dynamin-2	R.TGLFTPDLAFEAIVK#.K	86.02	39.59	2.17	0.46
P39054_D	Dnm2	Dynamin-2	K.VPVGDQPPDIEYQIK#.D	67.61	33.84	2.00	0.50
P39054_D	Dnm2	Dynamin-2	R.VYSPHVLNLTLIDLPGITK#.V	118.62	50.06	2.37	0.42
P39054_D	Dnm2	Dynamin-2	K.VPVGDQPPDIEYQIK#.D	2.45	1.42	1.72	0.58
P39054_D	Dnm2	Dynamin-2	K.ALLQM*VQQFGVDFEK#.R	9.45	3.76	2.51	0.40
P39054_D	Dnm2	Dynamin-2	K.ALLQMVQQFGVDFEK#.R	15.21	4.12	3.69	0.27
P39054_D	Dnm2	Dynamin-2	K.DMILQFISR.E	7.09	13.62	0.52	1.92
P39054_D	Dnm2	Dynamin-2	R.ESSLILAVTPANM*DLANSDALK#.L	17.75	8.51	2.08	0.48
P39054_D	Dnm2	Dynamin-2	K.FTDFDEVRQEIEAETDR.V	2.49	12.37	0.20	4.96
P39054_D	Dnm2	Dynamin-2	R.GM*EELIPLVNK#.L	54.41	21.45	2.54	0.39
P39054_D	Dnm2	Dynamin-2	R.GMEELIPLVNK#.L	23.54	8.46	2.78	0.36

P39054_D	Dnm2	Dynamin-2	R.IEGSGDQVDTLELSGGAR.I	6.66	13.60	0.49	2.04
P39054_D	Dnm2	Dynamin-2	R.IVTTYIR.E	24.85	41.50	0.60	1.67
P39054_D	Dnm2	Dynamin-2	R.NLVDSYVAIINK#.S	90.48	33.56	2.70	0.37
P39054_D	Dnm2	Dynamin-2	K.RIEGSGDQVDTLELSGGAR.I	2.47	20.24	0.12	8.21
P39054_D	Dnm2	Dynamin-2	R.SK#LQSQLLSLEK#.E	14.62	6.03	2.42	0.41
P39054_D	Dnm2	Dynamin-2	R.SK#LQSQLLSLEK#EVEEYK#.N	6.14	5.28	1.16	0.86
P39054_D	Dnm2	Dynamin-2	R.TGLFTPDLAFEAIVK#.K	78.12	34.34	2.28	0.44
P39054_D	Dnm2	Dynamin-2	K.VPVGDQPPDIEYQIK#.D	59.89	27.80	2.15	0.46
P39054_D	Dnm2	Dynamin-2	R.VYSPHVLNLTLIDLPGITK#.V	147.83	59.92	2.47	0.41
P39054_D	Dnm2	Dynamin-2	K.YMLPLDNLK#.I	19.18	6.79	2.83	0.35
P39054_D	Dnm2	Dynamin-2	R.IEGSGDQVDTLELSGGAR.I	3.07	8.23	0.37	2.68
P39054_D	Dnm2	Dynamin-2	R.NLVDSYVAIINK#.S	36.73	16.51	2.22	0.45
P39054_D	Dnm2	Dynamin-2	R.TGLFTPDLAFEAIVK#.K	27.40	13.54	2.02	0.49
P39054_D	Dnm2	Dynamin-2	K.VPVGDQPPDIEYQIK#.D	18.81	8.61	2.19	0.46
P39054_D	Dnm2	Dynamin-2	R.VYSPHVLNLTLIDLPGITK#.V	57.98	16.24	3.57	0.28
P13864_D	Dnmt1	DNA (cytosi	R.FFGNILDR.H	4.01	12.67	0.32	3.16
P13864_D	Dnmt1	DNA (cytosi	R.FFLLENVR.N	2.64	11.11	0.24	4.21
P13864_D	Dnmt1	DNA (cytosi	R.FTEDSLLR.H	3.89	13.87	0.28	3.57
P13864_D	Dnmt1	DNA (cytosi	K.GSNLDAPEPYR.I	5.24	9.66	0.54	1.84
P13864_D	Dnmt1	DNA (cytosi	K.NLGPINQWWLSGFDGGEK.V	12.62	10.74	1.17	0.85
P13864_D	Dnmt1	DNA (cytosi	K.VLEQIEEVDGR.V	4.24	23.74	0.18	5.60
P13864_D	Dnmt1	DNA (cytosi	K.AIGLEIK#.L	35.37	41.32	0.86	1.17
P13864_D	Dnmt1	DNA (cytosi	K.AIHDENPSM*EGGINGK#.N	34.80	34.89	1.00	1.00
P13864_D	Dnmt1	DNA (cytosi	R.AIILAAAPGEK#.L	74.54	86.03	0.87	1.15
P13864_D	Dnmt1	DNA (cytosi	R.AIILAAAPGEKLPLFPEPLHVFAPR.A	3.95	40.65	0.10	10.29
P13864_D	Dnmt1	DNA (cytosi	R.ALIHLAGVSLGQR.R	17.50	92.17	0.19	5.27
P13864_D	Dnmt1	DNA (cytosi	R.DLPNIQVR.L	15.07	92.83	0.16	6.16
P13864_D	Dnmt1	DNA (cytosi	K.DM*SPLVAAR.M	116.54	41.28	2.82	0.35
P13864_D	Dnmt1	DNA (cytosi	K.EADDDEEADDDVSEM*PSPK#.K	17.38	14.24	1.22	0.82
P13864_D	Dnmt1	DNA (cytosi	K.EAEPEQVAPETPEDR.D	3.66	18.96	0.19	5.19
P13864_D	Dnmt1	DNA (cytosi	R.EARPETHLDEDEDGKK.D	2.74	9.05	0.30	3.31
P13864_D	Dnmt1	DNA (cytosi	K.EESEEGNSAESAAEER.D	6.17	31.41	0.20	5.09
P13864_D	Dnmt1	DNA (cytosi	R.FESPPK#.T	69.67	90.37	0.77	1.30
P13864_D	Dnmt1	DNA (cytosi	R.FFGNILDR.H	22.76	100.00	0.23	4.39
P13864_D	Dnmt1	DNA (cytosi	R.FFLLENVR.N	18.09	100.46	0.18	5.55
P13864_D	Dnmt1	DNA (cytosi	R.FTEDSLLR.H	26.45	109.41	0.24	4.14
P13864_D	Dnmt1	DNA (cytosi	K.FVSNITR.L	18.15	95.73	0.19	5.27
P13864_D	Dnmt1	DNA (cytosi	R.FYFLEAYNSK#.T	70.34	61.14	1.15	0.87
P13864_D	Dnmt1	DNA (cytosi	K.GK#HQVSEPK#EPEAAIK#.L	30.99	30.75	1.01	0.99
P13864_D	Dnmt1	DNA (cytosi	K.GK#VNEADIK#.L	26.08	25.36	1.03	0.97
P13864_D	Dnmt1	DNA (cytosi	K.GSNLDAPEPYR.I	20.12	132.08	0.15	6.56
P13864_D	Dnmt1	DNA (cytosi	R.HAQFVVSQVESYDEAK.D	12.05	13.09	0.92	1.09
P13864_D	Dnmt1	DNA (cytosi	K.HQVSEPK#EPEAAIK#.L	98.40	95.85	1.03	0.97
P13864_D	Dnmt1	DNA (cytosi	K.IVVEFLQNNPDAVYEDLINK#.I	9.10	10.92	0.83	1.20
P13864_D	Dnmt1	DNA (cytosi	K.KDPVNETLYPEHYR.K	12.84	67.62	0.19	5.27
P13864_D	Dnmt1	DNA (cytosi	R.LEWDGFFSTTVTNPEPM*GK#.Q	31.19	30.79	1.01	0.99
P13864_D	Dnmt1	DNA (cytosi	R.LEWDGFFSTTVTNPEPM*GK.Q	24.17	27.24	0.89	1.13
P13864_D	Dnmt1	DNA (cytosi	R.LEWDGFFSTTVTNPEPMGK#.Q	10.70	7.38	1.45	0.69
P13864_D	Dnmt1	DNA (cytosi	R.LGDGVIAHK#.L	51.22	43.40	1.18	0.85
P13864_D	Dnmt1	DNA (cytosi	R.LGDSVYLPPEAFTFNIK.V	85.33	86.25	0.99	1.01
P13864_D	Dnmt1	DNA (cytosi	K.LHK#EELSEEGYLAK#.V	75.90	96.81	0.78	1.28
P13864_D	Dnmt1	DNA (cytosi	K.LNLLHEFLQTEIK#.S	39.21	40.20	0.98	1.03
P13864_D	Dnmt1	DNA (cytosi	K.LNLLHEFLQTEIK.S	9.56	10.10	0.95	1.06
P13864_D	Dnmt1	DNA (cytosi	K.LPLFPEPLHVFAPR.A	54.06	257.30	0.21	4.76
P13864_D	Dnmt1	DNA (cytosi	K.LVM*AGEVTNSLGQR.L	10.40	61.80	0.17	5.94
P13864_D	Dnmt1	DNA (cytosi	K.LVMAGEVTNSLGQR.L	4.43	29.39	0.15	6.64
P13864_D	Dnmt1	DNA (cytosi	K.NLGPINQWWLSGFDGGEK#.V	73.75	80.86	0.91	1.10
P13864_D	Dnmt1	DNA (cytosi	R.QVGNAVPPPLAK.A	32.89	37.63	0.87	1.14
P13864_D	Dnmt1	DNA (cytosi	K.SDSDTLSVETSPSSVATR.R	4.81	23.43	0.21	4.87
P13864_D	Dnmt1	DNA (cytosi	R.SKSDSDTLSVETSPSSVATR.R	7.80	36.90	0.21	4.73
P13864_D	Dnmt1	DNA (cytosi	R.SQGFPDSYR.F	7.54	56.42	0.13	7.48
P13864_D	Dnmt1	DNA (cytosi	K.VLEQIEEVDGR.V	35.54	204.08	0.17	5.74
P13864_D	Dnmt1	DNA (cytosi	K.VNEADIK#.L	39.57	38.33	1.03	0.97
P13864_D	Dnmt1	DNA (cytosi	R.VPALASPAGSLPDHVR.R	26.09	146.67	0.18	5.62
P13864_D	Dnmt1	DNA (cytosi	R.VTALWEDK.N	31.51	29.58	1.07	0.94
P13864_D	Dnmt1	DNA (cytosi	R.VVDTESGAAAAVEK#.L	97.16	114.96	0.85	1.18
P13864_D	Dnmt1	DNA (cytosi	K.YQQHPEDAVDEPQM*LTSEK#.L	113.03	127.77	0.88	1.13
J3QNW0_J	Dnmt1	DNA (cytosi	K.SDSDTLFETSPSSVATR.R	3.69	18.37	0.20	4.98
J3QNW0_J	Dnmt1	DNA (cytosi	R.SKSDSDTLFETSPSSVATR.R	3.58	19.68	0.18	5.50
Q9Z2W0_D	Dnpep	Aspartyl a	K.EAIQATAR.E	15.39	28.01	0.55	1.82
Q9Z2W0_D	Dnpep	Aspartyl a	R.ELK#ETEGWDIVPENK#.Y	38.84	20.19	1.92	0.52
Q9Z2W0_D	Dnpep	Aspartyl a	R.ELKETEGWDIVPENK.Y	13.11	6.26	2.09	0.48
Q9Z2W0_D	Dnpep	Aspartyl a	R.EVAGQVGVPLQDLM*VR.N	5.51	10.74	0.51	1.95
Q9Z2W0_D	Dnpep	Aspartyl a	R.EVAGQVGVPLQDLMVR.N	4.83	11.13	0.43	2.30
Q9Z2W0_D	Dnpep	Aspartyl a	K.GFFELFPSVSR.N	22.36	45.61	0.49	2.04
Q9Z2W0_D	Dnpep	Aspartyl a	K.GTPEPGPLGATDER.H	16.20	39.05	0.41	2.41
Q9Z2W0_D	Dnpep	Aspartyl a	R.LTAFEEAIPK#.S	107.92	45.69	2.36	0.42
Q9Z2W0_D	Dnpep	Aspartyl a	R.YASNAVSESM*IR.E	14.37	23.30	0.62	1.62
Q9Z2W0_D	Dnpep	Aspartyl a	K.GFFELFPSVSR.N	5.79	11.18	0.52	1.93
Q9Z2W0_D	Dnpep	Aspartyl a	R.LTAFEEAIPK#.S	9.86	4.19	2.35	0.43
Q9Z2W0_D	Dnpep	Aspartyl a	K.GFFELFPSVSR.N	7.59	10.07	0.75	1.33
Q9Z2W0_D	Dnpep	Aspartyl a	K.GTPEPGPLGATDER.H	8.22	13.22	0.62	1.61
Q9Z2W0_D	Dnpep	Aspartyl a	K.GFFELFPSVSR.N	10.20	18.19	0.56	1.78
Q9Z2W0_D	Dnpep	Aspartyl a	R.LLQAGFR.E	22.53	45.18	0.50	2.01
Q9Z2W0_D	Dnpep	Aspartyl a	R.LTAFEEAIPK#.S	47.79	20.99	2.28	0.44
Q99LB0_T	Dnttip1	Deoxynucle	R.AVLQPSINEEIQGVFNK#.Y	5.84	4.53	1.29	0.78
Q8BUR4_D	Dock1	Dedicator	K.IFALAFVK#.L	23.49	6.07	3.87	0.26
Q8BUR4_D	Dock1	Dedicator	K.LTQNVDLLGLLK#.W	32.61	10.97	2.97	0.34
Q8BUR4_D	Dock1	Dedicator	R.SFQM*FENEIITK#.L	6.87	1.81	3.81	0.26
Q8BUR4_D	Dock1	Dedicator	K.SVIYYQVK#.Q	18.37	6.08	3.02	0.33
A2AF47_D	Dock11	Dedicator	K.IIQINTDSLVQEK#.K	22.59	6.19	3.65	0.27
A2AF47_D	Dock11	Dedicator	K.K#QDTVETPVGFAWVPLLK#.D	32.70	11.05	2.96	0.34
A2AF47_D	Dock11	Dedicator	K.LIIPIYEK#.R	37.83	11.04	3.43	0.29
A2AF47_D	Dock11	Dedicator	K.LSNEDILK#.L	31.39	5.00	6.28	0.16
A2AF47_D	Dock11	Dedicator	R.YEVISEISK#.L	20.92	8.39	2.49	0.40
A2AF47_D	Dock11	Dedicator	R.YTAISVIK#.N	14.89	4.18	3.56	0.28
B2RY04_D	Dock5	Dedicator	R.AINQFAEVLTK#.S	11.54	4.67	2.47	0.40
B2RY04_D	Dock5	Dedicator	K.VFDYEGLGSLLK#.K	38.45	3.54	10.88	0.09
Q8R1A4_D	Dock7	Dedicator	R.DLVEFPPDDIEVVYSPR.D	2.07	3.93	0.53	1.90
Q8R1A4_D	Dock7	Dedicator	R.DVYVPNTTYR.N	8.71	22.83	0.38	2.62
Q8R1A4_D	Dock7	Dedicator	K.ELFALHPSPDEEEPIER.L	4.64	12.61	0.37	2.72
Q8R1A4_D	Dock7	Dedicator	K.ESILGGVLK#.V	22.38	13.72	1.63	0.61
Q8R1A4_D	Dock7	Dedicator	R.FGDLDEQEFVYK#EPAITK#.L	51.71	36.46	1.42	0.71

Q8R1A4_D	Dock7	Dedicator c	R.FGEDVLEVIKDSNPVDK.C	22.01	10.16	2.17	0.46
Q8R1A4_D	Dock7	Dedicator c	R.GFVFSLIK#.S	15.09	9.75	1.55	0.65
Q8R1A4_D	Dock7	Dedicator c	K.GYQTSPDLR.L	7.03	18.62	0.38	2.65
Q8R1A4_D	Dock7	Dedicator c	R.LEGFYGER.F	5.52	22.82	0.24	4.13
Q8R1A4_D	Dock7	Dedicator c	K.LGTGFNPNTLDK#.Q	36.63	24.86	1.47	0.68
Q8R1A4_D	Dock7	Dedicator c	R.NLLYIYPQSLNFANR.Q	7.79	20.88	0.37	2.68
Q8R1A4_D	Dock7	Dedicator c	K.QISGQYSGSPQLLK#.N	12.12	8.58	1.41	0.71
Q8R1A4_D	Dock7	Dedicator c	K.SLIGPDQK#.E	20.48	13.63	1.50	0.67
Q8R1A4_D	Dock7	Dedicator c	R.SPSGSAFGSQENLR.W	7.90	32.08	0.25	4.06
Q8R1A4_D	Dock7	Dedicator c	R.YSDPQIK#.A	37.63	26.21	1.44	0.70
P97465_D	Dok1	Docking pr	R.GLYDLPQEPR.D	2.81	8.96	0.31	3.19
P97465_D	Dok1	Docking pr	R.IPPGPSQDSVYSDPLGSTPAGAGEGVHSK#.K	6.14	4.88	1.26	0.79
Q8BPA8_D	Dpcd	Protein DP	K.DVYSVSVAQK#.E	30.38	12.52	2.43	0.41
Q8BPA8_D	Dpcd	Protein DP	K.NALGALGQWQLEVGEPVPSGAGSLGSELIK#.E	10.79	2.50	4.32	0.23
Q61103_R	Dpf2	Zinc finger	K.EGLISQDGSSLEALLR.T	11.95	37.95	0.31	3.18
Q61103_R	Dpf2	Zinc finger	R.GPGLASGQLYSYPAR.R	5.11	16.26	0.31	3.18
Q61103_R	Dpf2	Zinc finger	R.IIEPDDFLDDLDDEDYEEDTPK#.R	8.01	6.51	1.23	0.81
Q61103_R	Dpf2	Zinc finger	R.IIEPDDFLDDLDDEDYEEDTPKR.R	2.46	5.83	0.42	2.37
Q61103_R	Dpf2	Zinc finger	K.LLGEQYYK#.D	37.49	24.00	1.56	0.64
Q61103_R	Dpf2	Zinc finger	R.VDDDSLGEFPVSNSR.A	4.90	18.95	0.26	3.87
Q99LT0_D	Dpy30	Protein dp	K.VDLQSLPTR.A	7.45	26.94	0.28	3.62
O08553_D	Dpysl2	Dihydropy	K.DHGVNSFLVYM*AFK#.D	18.45	2.52	7.31	0.14
O08553_D	Dpysl2	Dihydropy	R.GSPLVVISQGK#.I	155.90	11.97	13.02	0.08
O08553_D	Dpysl2	Dihydropy	R.ISVGSDADLVIWDPDSVK#.T	66.29	5.07	13.07	0.08
O08553_D	Dpysl2	Dihydropy	K.IVNDDQSFYADIYM*EDGLIK#.Q	12.49	2.20	5.69	0.18
O08553_D	Dpysl2	Dihydropy	K.M*DENQFVAVTSTNAAK#.I	74.29	10.44	7.11	0.14
O08553_D	Dpysl2	Dihydropy	K.MDENQFVAVTSTNAAK#.I	36.96	5.50	6.72	0.15
O08553_D	Dpysl2	Dihydropy	R.MSVIWDK#.A	40.18	5.41	7.43	0.13
O08553_D	Dpysl2	Dihydropy	K.QIGENLIVPGGVK#.T	90.56	7.14	12.68	0.08
O08553_D	Dpysl2	Dihydropy	R.ISVGSDADLVIWDPDSVK#.T	15.11	4.41	3.42	0.29
O08553_D	Dpysl2	Dihydropy	K.M*DENQFVAVTSTNAAK#.I	13.00	2.65	4.90	0.20
O08553_D	Dpysl2	Dihydropy	R.GSPLVVISQGK#.I	53.24	5.40	9.87	0.10
O08553_D	Dpysl2	Dihydropy	R.ISVGSDADLVIWDPDSVK#.T	39.02	4.63	8.42	0.12
O08553_D	Dpysl2	Dihydropy	K.IVNDDQSFYADIYM*EDGLIK#.Q	10.94	2.39	4.59	0.22
O08553_D	Dpysl2	Dihydropy	K.IVNDDQSFYADIYMEDGLIK#.Q	9.82	1.94	5.06	0.20
O08553_D	Dpysl2	Dihydropy	K.M*DENQFVAVTSTNAAK#.I	36.12	6.74	5.36	0.19
O08553_D	Dpysl2	Dihydropy	K.MDENQFVAVTSTNAAK#.I	19.54	4.77	4.10	0.24
O08553_D	Dpysl2	Dihydropy	R.MSVIWDK#.A	21.37	5.00	4.27	0.23
O08553_D	Dpysl2	Dihydropy	K.QIGENLIVPGGVK#.T	38.20	1.88	20.33	0.05
E9PWE8_E	Dpysl3	Dihydropy	K.EVLQNLGPK#.D	33.16	4.48	7.40	0.14
E9PWE8_E	Dpysl3	Dihydropy	K.GM*TTVDDFFQGTK#.A	16.14	6.72	2.40	0.42
E9PWE8_E	Dpysl3	Dihydropy	K.GMTTVDDFFQGTK#.A	11.35	6.61	1.72	0.58
E9PWE8_E	Dpysl3	Dihydropy	R.GM*YDGPVFDLTTTPK#.G	15.38	4.99	3.08	0.32
E9PWE8_E	Dpysl3	Dihydropy	R.GMYDGPVFDLTTTPK#.G	6.27	2.60	2.41	0.42
E9PWE8_E	Dpysl3	Dihydropy	R.IAVGSDSDLVIWDPDALK#.I	22.53	8.32	2.71	0.37
E9PWE8_E	Dpysl3	Dihydropy	K.IFNLYPR.K	8.48	14.17	0.60	1.67
E9PWE8_E	Dpysl3	Dihydropy	K.QEVQSLSK#.E	27.70	8.60	3.22	0.31
E9PWE8_E	Dpysl3	Dihydropy	K.QIGDNLIVPGGVK#.T	17.44	8.91	1.96	0.51
E9PWE8_E	Dpysl3	Dihydropy	K.SAADLISQAR.K	13.60	15.15	0.90	1.11
E9PWE8_E	Dpysl3	Dihydropy	R.GMYDGPVFDLTTTPK#.G	4.08	3.76	1.08	0.92
E9PWE8_E	Dpysl3	Dihydropy	R.IAVGSDSDLVIWDPDALK#.I	9.14	1.94	4.70	0.21
E9PWE8_E	Dpysl3	Dihydropy	K.GM*TTVDDFFQGTK#.A	24.01	8.77	2.74	0.37
E9PWE8_E	Dpysl3	Dihydropy	R.GM*YDGPVFDLTTTPK#.G	22.46	9.30	2.42	0.41
E9PWE8_E	Dpysl3	Dihydropy	R.GMYDGPVFDLTTTPK#.G	9.90	2.79	3.55	0.28
E9PWE8_E	Dpysl3	Dihydropy	K.GNVVFGEPITASLGIDGTHYWSK#.N	18.86	9.18	2.05	0.49
E9PWE8_E	Dpysl3	Dihydropy	R.IAVGSDSDLVIWDPDALK#.I	35.26	12.17	2.90	0.35
E9PWE8_E	Dpysl3	Dihydropy	K.IFNLYPR.K	37.62	16.26	2.31	0.43
E9PWE8_E	Dpysl3	Dihydropy	K.QIGDNLIVPGGVK#.T	23.12	9.46	2.44	0.41
E9PWE8_E	Dpysl3	Dihydropy	K.SAADLISQAR.K	17.23	27.47	0.63	1.59
E9PWE8_E	Dpysl3	Dihydropy	R.GM*YDGPVFDLTTTPK#.G	3.36	8.15	0.41	2.43
E9PWE8_E	Dpysl3	Dihydropy	R.IAVGSDSDLVIWDPDALK#.I	5.07	3.41	1.49	0.67
O35098_D	Dpysl4	Dihydropy	K.M*DENEFVAVTSTNAAK#.I	70.68	8.44	8.37	0.12
Q91WV0_N	Dr1	Protein Dr1	R.LENLGIPEEELLR.Q	36.69	82.25	0.45	2.24
Q9D6N5_N	Drap1	Dr1-associa	K.IM*QTDEEIGK#.V	28.79	12.07	2.39	0.42
Q9D6N5_N	Drap1	Dr1-associa	K.K#IM*QTDEEIGK#.V	7.13	2.49	2.87	0.35
Q9D6N5_N	Drap1	Dr1-associa	K.VAAAVPVIISR.A	16.41	21.21	0.77	1.29
Q9D6N5_N	Drap1	Dr1-associa	K.IM*QTDEEIGK#.V	11.34	3.35	3.38	0.30
Q9D6N5_N	Drap1	Dr1-associa	K.VAAAVPVIISR.A	6.20	15.36	0.40	2.48
P32233_D	Drg1	Developme	K.GGGGGGPGEGFDVAK#.T	43.30	33.37	1.30	0.77
P32233_D	Drg1	Developme	K.GQLPDYTSPVVLPYSR.T	3.84	20.26	0.19	5.27
P32233_D	Drg1	Developme	K.IAEIEAEM*AR.T	6.24	15.44	0.40	2.48
P32233_D	Drg1	Developme	R.IGFVGFPSVGK#.S	58.57	48.04	1.22	0.82
P32233_D	Drg1	Developme	R.SDATADDLIDVVEGNR.V	8.39	13.35	0.63	1.59
P32233_D	Drg1	Developme	K.VGK#DHTLEDEDVIQIVK#.K	8.50	6.16	1.38	0.72
P32233_D	Drg1	Developme	R.WNFDDLLEK#.I	12.41	9.64	1.29	0.78
P32233_D	Drg1	Developme	K.GGGGGGPGEGFDVAK#.T	27.38	17.97	1.52	0.66
P32233_D	Drg1	Developme	K.IDQISIEELDIIYK#.V	8.32	3.26	2.55	0.39
P32233_D	Drg1	Developme	R.IGFVGFPSVGK#.S	36.84	23.85	1.55	0.65
P32233_D	Drg1	Developme	K.IIENELEGFGIR.L	3.12	15.97	0.20	5.11
P32233_D	Drg1	Developme	K.IQLLDLPGIIEGAK#.D	47.66	26.80	1.78	0.56
P32233_D	Drg1	Developme	K.GGGGGGPGEGFDVAK#.T	37.97	19.03	2.00	0.50
P32233_D	Drg1	Developme	R.IGFVGFPSVGK#.S	52.93	33.42	1.58	0.63
P32233_D	Drg1	Developme	R.SDATADDLIDVVEGNR.V	18.69	8.83	2.12	0.47
Q9QXB9_D	Drg2	Developme	K.IDQISM*EEVDR.L	6.95	11.94	0.58	1.72
Q9QXB9_D	Drg2	Developme	R.VALIGFPSVGK#.S	40.57	16.44	2.47	0.41
Q9QXB9_D	Drg2	Developme	R.VGLTHTM*EHEDVIQIVK#.K	11.67	3.67	3.18	0.31
Q9QXB9_D	Drg2	Developme	K.YALVWGTSTK#.Y	29.72	11.13	2.67	0.37
Q9QXB9_D	Drg2	Developme	R.VALIGFPSVGK#.S	45.77	12.55	3.65	0.27
Q9QXB9_D	Drg2	Developme	R.AQLLEPSK#.S	40.26	11.53	3.49	0.29
Q9QXB9_D	Drg2	Developme	K.GEGFDVM*K#.S	28.36	10.26	2.76	0.36
Q9QXB9_D	Drg2	Developme	R.VALIGFPSVGK#.S	89.98	24.03	3.74	0.27
Q9QXB9_D	Drg2	Developme	K.YALVWGTSTK#.Y	31.86	25.31	1.26	0.79
O35075_D	Dscr3	Down synd	K.LTPSPVDFTITPETLQNVK.E	3.12	3.37	0.93	1.08
O35075_D	Dscr3	Down synd	K.TEVPFEFPLLVK#.G	7.78	10.54	0.74	1.35
O35075_D	Dscr3	Down synd	K.LTPSPVDFTITPETLQNVK.E	2.74	2.35	1.17	0.86
O35075_D	Dscr3	Down synd	K.TEVPFEFPLLVK#.G	9.25	10.09	0.92	1.09
O35075_D	Dscr3	Down synd	K.TEVPFEFPLLVK.G	15.36	15.95	0.96	1.04
Q9CYC5_D	Dsn1	Kinetochor	K.AADFSLEASVAEVK#.E	9.83	7.17	1.37	0.73
Q91ZU6_D	Dst	Dystonin O	K.ALQGQISSQQVAVEK#.L	12.36	7.92	1.56	0.64
Q91ZU6_D	Dst	Dystonin O	R.DLEGIGKSLKHYR.D	1.76	4.55	0.39	2.58
Q91ZU6_D	Dst	Dystonin O	K.LANSEPIGTQAPK#.L	10.82	8.28	1.31	0.77
Q91ZU6_D	Dst	Dystonin O	R.LAQDLVVEAADSK#.G	11.89	9.68	1.23	0.81
Q91ZU6_D	Dst	Dystonin O	R.LEQDQTSAQLQVQK#.A	7.53	7.40	1.02	0.98

Q91ZU6_D	Dst	Dystonin O	K.LGAGEEDEVNGNLLETDAEGHSEATK#.G	5.05	2.16	2.33	0.43
Q91ZU6_D	Dst	Dystonin O	R.LLDPEDVDVSSPDEK#.S	7.15	4.28	1.67	0.60
Q91ZU6_D	Dst	Dystonin O	R.VGGGWM*ALDEFLVK#.N	14.62	9.91	1.48	0.68
Q9R0P5_D	Dstn	Destrin OS	K.LGGSLIVAFEGSPV.-	17.48	17.48	1.00	1.00
Q3UIR3_D	Dtx3l	E3 ubiquiti	K.LLEPELLQEISEIEQK#.F	9.85	5.10	1.93	0.52
Q3UIR3_D	Dtx3l	E3 ubiquiti	K.FGGPANFGYPDPDYLKR.V	8.39	29.95	0.28	3.57
Q3UIR3_D	Dtx3l	E3 ubiquiti	K.GNQPEGTM*SYSTQK.G	15.30	8.93	1.71	0.58
Q3UIR3_D	Dtx3l	E3 ubiquiti	K.IHHFLSEQLLER.E	16.52	30.31	0.55	1.83
Q3UIR3_D	Dtx3l	E3 ubiquiti	K.ITASGYTTGIEVDSTR.F	11.04	36.67	0.30	3.32
Q3UIR3_D	Dtx3l	E3 ubiquiti	K.LLEPELLQEISEIEQK#.F	34.79	27.16	1.28	0.78
Q3UIR3_D	Dtx3l	E3 ubiquiti	R.M*GLAPSSGEK#.L	17.92	16.18	1.11	0.90
Q3UIR3_D	Dtx3l	E3 ubiquiti	K.SEHEM*LVHNK#PVTIVLETTK#.K	8.80	7.41	1.19	0.84
Q3UIR3_D	Dtx3l	E3 ubiquiti	R.TEVLSLK#.G	44.09	31.42	1.40	0.71
Q3UIR3_D	Dtx3l	E3 ubiquiti	R.TLTLLGSPADISAATEK#.V	40.17	30.62	1.31	0.76
Q3UIR3_D	Dtx3l	E3 ubiquiti	K.VSQGLGLRPVK.I	4.84	14.41	0.34	2.97
Q3UIR3_D	Dtx3l	E3 ubiquiti	K.LLEPELLQEISEIEQK#.F	18.37	17.91	1.03	0.97
Q9D0T2_D	Dusp12	Dual specifi	K.LYEAM*GYEVDTSSAFYK#.Q	3.25	2.58	1.26	0.79
Q9D7X3_D	Dusp3	Dual specifi	R.VYVGNASVAQDITQLQK#.L	44.53	13.85	3.21	0.31
Q8VCG1_Q	Dut	Deoxyuridi	R.AAGYDLFSAYDYTISPM*EK#.A	8.45	3.10	2.72	0.37
Q8VCG1_Q	Dut	Deoxyuridi	R.GNVGVVLFNFGK#.E	41.31	8.37	4.93	0.20
Q9JHU4_D	Dync1h1	Cytoplasmi	K.VTDFGDKVEDPTFLNQLQSGVNR.W	2.64	3.35	0.79	1.27
Q9JHU4_D	Dync1h1	Cytoplasmi	R.K#LVPLLLEDGGDAPAALEAALEEK#.S	25.04	14.61	1.71	0.58
Q9JHU4_D	Dync1h1	Cytoplasmi	R.K#LVPLLLEDGGDAPAALEAALEEK#.S	9.18	5.41	1.70	0.59
Q9JHU4_D	Dync1h1	Cytoplasmi	K.VAEVLFDAADANAIEEVNLAYENVK#.E	7.10	3.03	2.34	0.43
Q9JHU4_D	Dync1h1	Cytoplasmi	K.VTDFGDKVEDPTFLNQLQSGVNR.W	2.87	4.27	0.67	1.49
Q9JHU4_D	Dync1h1	Cytoplasmi	K.ADLAAVEAK#.V	58.00	39.94	1.45	0.69
Q9JHU4_D	Dync1h1	Cytoplasmi	K.ANEVEQM*IR.D	6.97	10.92	0.64	1.57
Q9JHU4_D	Dync1h1	Cytoplasmi	K.AVDDLNLHSYSNLPIWVNK#.L	32.09	16.74	1.92	0.52
Q9JHU4_D	Dync1h1	Cytoplasmi	R.DLPPVSGSIIWAK#.Q	18.41	7.53	2.44	0.41
Q9JHU4_D	Dync1h1	Cytoplasmi	K.EDLDK#VEPAVIEAQNAVK#.S	24.62	10.23	2.41	0.42
Q9JHU4_D	Dync1h1	Cytoplasmi	K.EFGPVVIDYGK#.V	34.44	8.10	4.25	0.24
Q9JHU4_D	Dync1h1	Cytoplasmi	K.EIVLSAGSTPK#.I	17.05	4.90	3.48	0.29
Q9JHU4_D	Dync1h1	Cytoplasmi	R.ESPEVLLTLDILK#.H	16.52	5.04	3.28	0.31
Q9JHU4_D	Dync1h1	Cytoplasmi	R.EVWNTYELDLVNYQNK#.C	9.76	2.80	3.48	0.29
Q9JHU4_D	Dync1h1	Cytoplasmi	R.EYQTQLIQR.V	9.02	17.25	0.52	1.91
Q9JHU4_D	Dync1h1	Cytoplasmi	R.FGNPLLVQDVESYDPVLNPVLNR.E	8.66	15.81	0.55	1.83
Q9JHU4_D	Dync1h1	Cytoplasmi	K.FNYGFEYLGVQDK#.L	24.31	12.23	1.99	0.50
Q9JHU4_D	Dync1h1	Cytoplasmi	R.FQSISTEFLALM*K#.K	13.56	3.28	4.14	0.24
Q9JHU4_D	Dync1h1	Cytoplasmi	R.FQSISTEFLALMK#.K	13.99	5.12	2.74	0.37
Q9JHU4_D	Dync1h1	Cytoplasmi	R.IFVFEPPPGVK#.A	47.60	19.57	2.43	0.41
Q9JHU4_D	Dync1h1	Cytoplasmi	R.ILDDDTIITTLENLK#.R	13.68	4.33	3.16	0.32
Q9JHU4_D	Dync1h1	Cytoplasmi	K.INEWLTLVEK#.E	29.15	8.06	3.61	0.28
Q9JHU4_D	Dync1h1	Cytoplasmi	K.IQGLTVEQAEAVVR.L	9.82	12.20	0.80	1.24
Q9JHU4_D	Dync1h1	Cytoplasmi	R.K#LVPLLLEDGGDAPAALEAALEEK#.S	32.38	10.22	3.17	0.32
Q9JHU4_D	Dync1h1	Cytoplasmi	R.LADLLGK#.I	24.24	8.69	2.79	0.36
Q9JHU4_D	Dync1h1	Cytoplasmi	R.LAETVFNFQEK#.V	23.63	7.10	3.33	0.30
Q9JHU4_D	Dync1h1	Cytoplasmi	R.LGGSPFGPAGTGK#.T	54.77	18.55	2.95	0.34
Q9JHU4_D	Dync1h1	Cytoplasmi	K.LK#VNFLPEIITLSK#.E	18.71	6.56	2.85	0.35
Q9JHU4_D	Dync1h1	Cytoplasmi	K.LNTQEIFDDWAR.K	5.56	8.60	0.65	1.55
Q9JHU4_D	Dync1h1	Cytoplasmi	K.QLQNISQAAASGGAK#.E	28.22	9.98	2.83	0.35
Q9JHU4_D	Dync1h1	Cytoplasmi	R.QNLDGLLNQLK#.N	14.59	10.64	1.37	0.73
Q9JHU4_D	Dync1h1	Cytoplasmi	K.SLLQALNEVK#.G	53.83	21.91	2.46	0.41
Q9JHU4_D	Dync1h1	Cytoplasmi	K.SVLVSAGNVK#.R	27.80	13.79	2.02	0.50
Q9JHU4_D	Dync1h1	Cytoplasmi	R.TAEVLANK#.I	21.81	6.46	3.38	0.30
Q9JHU4_D	Dync1h1	Cytoplasmi	K.TKPVTGNLRPEEALQALTIYEGK.F	9.96	11.28	0.88	1.13
Q9JHU4_D	Dync1h1	Cytoplasmi	R.TLINELVK#.G	44.29	13.99	3.17	0.32
Q9JHU4_D	Dync1h1	Cytoplasmi	K.TLM*AQSIYGGR.V	3.83	8.45	0.45	2.21
Q9JHU4_D	Dync1h1	Cytoplasmi	R.TPNGVVLAPVQLGK#.W	7.37	3.31	2.22	0.45
Q9JHU4_D	Dync1h1	Cytoplasmi	R.TTDLLTDWEK#.T	24.24	8.57	2.83	0.35
Q9JHU4_D	Dync1h1	Cytoplasmi	K.VAEVLFDAADANAIEEVNLAYENVK#.E	30.04	9.48	3.17	0.32
Q9JHU4_D	Dync1h1	Cytoplasmi	R.VLLTTQGVDM*ISK#.M	36.00	10.60	3.40	0.29
Q9JHU4_D	Dync1h1	Cytoplasmi	K.VLQLYQITQINHGLM*M*VGPSGSGK#.S	11.03	2.95	3.74	0.27
Q9JHU4_D	Dync1h1	Cytoplasmi	R.VLRPQVTAVAQQNQGEAPEPQDM*K.V	8.59	15.33	0.56	1.79
Q9JHU4_D	Dync1h1	Cytoplasmi	K.VNFLPEIITLSK#.E	70.96	22.47	3.16	0.32
Q9JHU4_D	Dync1h1	Cytoplasmi	R.VPLAIVNK#.A	47.80	20.10	2.38	0.42
Q9JHU4_D	Dync1h1	Cytoplasmi	R.VQVALEELQDLK#.G	52.25	33.83	1.54	0.65
Q9JHU4_D	Dync1h1	Cytoplasmi	K.VTDFGDKVEDPTFLNQLQSGVNR.W	6.18	11.59	0.53	1.87
O88487_D	Dync1i2	Cytoplasmi	R.DLEDK#EGEIQAGAK#.L	7.81	51.25	0.15	6.56
O88487_D	Dync1i2	Cytoplasmi	R.ADAEEEAATR.I	8.52	11.30	0.75	1.33
O88487_D	Dync1i2	Cytoplasmi	R.ALSEQINIFFDYSGR.D	5.91	15.93	0.37	2.69
O88487_D	Dync1i2	Cytoplasmi	R.DLEDK#EGEIQAGAK#.L	119.86	39.00	3.07	0.33
O88487_D	Dync1i2	Cytoplasmi	K.EAAVSVQEESDLEK#.K	65.04	20.13	3.23	0.31
O88487_D	Dync1i2	Cytoplasmi	K.ETQTPVTAQPK#.E	27.59	10.39	2.66	0.38
O88487_D	Dync1i2	Cytoplasmi	K.SVSTPSEAGSQDSGDGAVGSR.R	22.57	38.96	0.58	1.73
O88487_D	Dync1i2	Cytoplasmi	K.EAAVSVQEESDLEK#.K	20.79	3.86	5.38	0.19
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.DAVFIPAGWDNDKK.I	16.98	6.84	2.48	0.40
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.DFQEYVEPGEDFPASPQR.R	4.17	6.02	0.69	1.44
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.DTLVMLVVDM*SK#PWTALDSLQK#.W	6.57	4.95	1.33	0.75
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.EIM*AEDDQVFLM*K#.L	15.05	6.85	2.20	0.46
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.EIM*AEDDQVFLMK#.L	11.70	5.71	2.05	0.49
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.EIMAEDDQVFLMK#.L	13.09	6.60	1.98	0.50
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.FSLDALSLR.D	22.58	40.46	0.56	1.79
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.IGILHENFQTLK#.V	208.42	65.51	3.18	0.31
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.IPAVVVEK#.D	60.59	29.74	2.04	0.49
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.IQGIEEYK#K#.G	48.50	8.32	5.83	0.17
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.K#PASVSPTTPTSPTEGEAS.-	57.16	23.85	2.40	0.42
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.K#TGSPGGPGVGGSPGGGAAGASPSLPPSAK#.K	6.32	4.22	1.50	0.67
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.LQSLLAK#.Q	88.99	33.90	2.62	0.38
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.LYGFPYK#.I	73.49	28.38	2.59	0.39
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.NVLLLGEDGAGK#.T	80.21	31.28	2.56	0.39
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.RIQGIEEYKK.G	12.67	28.43	0.45	2.24
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.SVSSNVASVSPIPAGSK#.K	60.42	84.08	0.72	1.39
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.TGSPGGPGVGGSPGGGAAGASPSLPPSAK#.K	7.67	2.78	2.76	0.36
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.VEDNFEDIITKPPVR.K	24.67	44.47	0.55	1.80
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.IPAVVVEK#.D	12.88	6.99	1.84	0.54
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.K#PASVSPTTPTSPTEGEAS.-	16.08	4.70	3.42	0.29
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.LQSLLAK#.Q	20.57	7.36	2.79	0.36
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.LYGFPYK#.I	17.27	7.47	2.31	0.43
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.NVLLLGEDGAGK#.T	19.06	9.75	1.95	0.51
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.SVSSNVASVSPIPAGSK#.K	15.09	7.90	1.91	0.52
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.K#PASVSPTTPTSPTEGEAS.-	14.24	5.84	2.44	0.41
Q8R1Q8_D	Dync1li1	Cytoplasmi	K.NVLLLGEDGAGK#.T	24.61	2.08	11.84	0.08
Q8R1Q8_D	Dync1li1	Cytoplasmi	R.SVSSNVASVSPIPAGSK#.K	11.62	5.94	1.96	0.51

Q6PDL0_D	Dync1li2	Cytoplasmi	K.FAVSAESLR.E	12.89	20.87	0.62	1.62
Q6PDL0_D	Dync1li2	Cytoplasmi	R.K#PDSM*VTNSSTENEA.-	8.79	1.73	5.07	0.20
Q6PDL0_D	Dync1li2	Cytoplasmi	R.K#PDSMVTNSSTENEA.-	10.20	4.48	2.28	0.44
Q6PDL0_D	Dync1li2	Cytoplasmi	K.K#TGSPGSPSAGGVQSTAK#.K	13.34	7.40	1.80	0.55
Q6PDL0_D	Dync1li2	Cytoplasmi	K.TYGFHFTIPALVVEK#.D	26.18	15.14	1.73	0.58
Q6PDL0_D	Dync1li2	Cytoplasmi	K.NILVFGEDGSGK#.T	10.77	5.40	2.00	0.50
P63168_D	Dynll1	Dynein ligh	K.DIAAHIK#.K	100.48	117.32	0.86	1.17
P63168_D	Dynll1	Dynein ligh	K.DIAAHIK#K#.E	5.77	4.33	1.33	0.75
P63168_D	Dynll1	Dynein ligh	K.YNIEKDIAAHIK.K	42.35	35.32	1.20	0.83
P63168_D	Dynll1	Dynein ligh	K.YNIEK#DIAAHIK#K#.E	13.01	9.11	1.43	0.70
Q9D0M5_	Dynll2	Dynein ligh	K.YNIEK#DIAAYIK#.K	37.09	29.13	1.27	0.79
Q9D0M5_	Dynll2	Dynein ligh	K.YNIEKDIAAYIK.K	11.50	8.33	1.38	0.72
Q9D0M5_	Dynll2	Dynein ligh	K.YNIEK#DIAAYIK#K#.E	20.67	12.29	1.68	0.59
P62627_D	Dynlrb1	Dynein ligh	R.EIDPQNDLTFLR.I	15.89	30.69	0.52	1.93
P62627_D	Dynlrb1	Dynein ligh	K.GVQGIIVVNTEGIPIK#.S	35.47	15.18	2.34	0.43
P62627_D	Dynlrb1	Dynein ligh	K.STM*DNPTTTQYANLM*HNFILK#.A	7.16	4.53	1.58	0.63
Q61214_D	Dyrk1a	Dual specifi	K.HINEVYYAK#.K	15.35	13.48	1.14	0.88
Q9D903_E	Ebna1bp2	Probable r	K.ESYDDVSSFR.A	11.28	23.70	0.48	2.10
Q9D903_E	Ebna1bp2	Probable r	R.GLLK#PGLNVVLEK#PK#.K	19.67	13.07	1.51	0.66
Q9D903_E	Ebna1bp2	Probable r	K.K#AVNDVSGLK#.Q	11.26	6.24	1.81	0.55
Q9D903_E	Ebna1bp2	Probable r	K.K#VQTEVLQK#.R	20.81	13.75	1.51	0.66
Q9D903_E	Ebna1bp2	Probable r	R.LDVTLGPVPEVSETQPTPQNQDQK#.K	15.36	10.94	1.40	0.71
Q9D903_E	Ebna1bp2	Probable r	R.LDVTLGPVPEVSETQPTPQNQDQK#K#.G	4.44	4.50	0.99	1.01
Q9D903_E	Ebna1bp2	Probable r	K.RPTDYFAEM*AK.S	3.99	8.47	0.47	2.12
Q9D9V3_E	Echdc1	Ethylmalon	R.VIELENWTEGK#.G	12.95	5.81	2.23	0.45
Q6PDI5_EC	Ecm29	Proteasom	R.FQEFSDIVIPLIK#.K	6.49	3.97	1.64	0.61
Q6PDI5_EC	Ecm29	Proteasom	R.ALM*SSSQATASSSNK#.S	14.92	4.16	3.59	0.28
Q6PDI5_EC	Ecm29	Proteasom	R.ALSINTLVK#.I	34.80	9.26	3.76	0.27
Q6PDI5_EC	Ecm29	Proteasom	K.AQGAIAM*ASISK#.Q	22.02	8.29	2.66	0.38
Q6PDI5_EC	Ecm29	Proteasom	K.EILQDLIK#.N	11.69	6.91	1.69	0.59
Q6PDI5_EC	Ecm29	Proteasom	K.EIQSAFVSVLSENDELSQDVASK#.G	38.65	11.80	3.28	0.31
Q6PDI5_EC	Ecm29	Proteasom	R.FQEFSDIVIPLIK#.K	31.72	10.17	3.12	0.32
Q6PDI5_EC	Ecm29	Proteasom	R.HSVATAADLELK#.S	12.41	4.68	2.65	0.38
Q6PDI5_EC	Ecm29	Proteasom	K.LLLQGLM*DSVEAK#.Q	23.73	8.31	2.85	0.35
Q6PDI5_EC	Ecm29	Proteasom	K.LLLQGLMDSVEAK#.Q	9.89	4.34	2.28	0.44
Q6PDI5_EC	Ecm29	Proteasom	K.LLSM*AYSAVGK#.L	21.16	11.67	1.81	0.55
Q6PDI5_EC	Ecm29	Proteasom	R.NGPLPIPSEGSGFTK#.L	18.65	7.44	2.50	0.40
Q6PDI5_EC	Ecm29	Proteasom	R.QAAETFPANIQVVYDGLFGTNTNSK#.L	9.64	4.22	2.28	0.44
Q6PDI5_EC	Ecm29	Proteasom	K.QSLIDWNNPAIINK#.M	16.28	5.95	2.74	0.37
Q6PDI5_EC	Ecm29	Proteasom	K.TPDGQGLSTYK#.E	24.09	9.88	2.44	0.41
Q6PDI5_EC	Ecm29	Proteasom	R.VK#HEVSGETVVFQGGGLGK#.T	24.07	5.44	4.42	0.23
Q6PDI5_EC	Ecm29	Proteasom	K.VYLGDIPLK#.T	27.85	7.79	3.57	0.28
Q6PDI5_EC	Ecm29	Proteasom	R.YQFDPNLGIR.Q	7.51	13.21	0.57	1.76
Q8K2D3_E	Edc3	Enhancer o	K.AAVFEEIDTYER.R	2.33	7.81	0.30	3.35
Q8K2D3_E	Edc3	Enhancer o	K.K#PASSSSAPQSIPK#.R	6.78	9.95	0.68	1.47
Q8K2D3_E	Edc3	Enhancer o	K.M*LESITNELSLFSK.T	7.70	6.47	1.19	0.84
Q3UJB9_E	Edc4	Enhancer o	R.EAFQSVVLPAFEK.S	4.65	5.96	0.78	1.28
Q3UJB9_E	Edc4	Enhancer o	R.ELAELWHNQEELLQR.L	1.58	5.52	0.29	3.49
Q3UJB9_E	Edc4	Enhancer o	R.SLEPVAGQLSNSVATK#.L	4.60	4.79	0.96	1.04
Q3UJB9_E	Edc4	Enhancer o	R.AAADTLQGPM*QAAYR.E	1.68	4.94	0.34	2.94
Q3UJB9_E	Edc4	Enhancer o	R.EAFQSVVLPAFEK.S	16.40	24.22	0.68	1.48
Q3UJB9_E	Edc4	Enhancer o	R.ELAELWHNQEELLQR.L	2.23	14.44	0.15	6.47
Q3UJB9_E	Edc4	Enhancer o	R.GGQLQEQLTQQLSQALSSAVAGR.L	5.77	28.27	0.20	4.90
Q3UJB9_E	Edc4	Enhancer o	R.GLVSTLQSATEQMAATVSSSVR.A	2.99	17.59	0.17	5.88
Q3UJB9_E	Edc4	Enhancer o	K.GPGQVSTAASALSLDLQEVEPLGLPQASPSR.T	1.95	7.79	0.25	4.00
Q3UJB9_E	Edc4	Enhancer o	K.LFQFLQADPHNSLSK.A	9.13	15.54	0.59	1.70
Q3UJB9_E	Edc4	Enhancer o	R.LTEHQVAEPPEDWPALIWQQQR.E	1.90	9.48	0.20	5.00
Q3UJB9_E	Edc4	Enhancer o	R.SLEPVAGQLSNSVATK#.L	18.41	19.28	0.95	1.05
Q3UJB9_E	Edc4	Enhancer o	R.SLLPGLLPGPADK.L	24.33	36.13	0.67	1.49
Q3UJB9_E	Edc4	Enhancer o	R.AAADTLQGPM*QAAYR.E	2.48	6.07	0.41	2.45
Q3UJB9_E	Edc4	Enhancer o	K.ALQDVQIR.F	5.17	21.04	0.25	4.07
Q3UJB9_E	Edc4	Enhancer o	R.DSQDTSAEQSDHDDEVASLASASGGFGSK#.I	11.28	7.27	1.55	0.64
Q3UJB9_E	Edc4	Enhancer o	R.ELAELWHNQEELLQR.L	2.73	10.33	0.26	3.78
Q3UJB9_E	Edc4	Enhancer o	K.EVEIVASSDSSISSK.A	6.41	9.52	0.67	1.49
Q3UJB9_E	Edc4	Enhancer o	R.GGQLQEQLTQQLSQALSSAVAGR.L	7.02	21.21	0.33	3.02
Q3UJB9_E	Edc4	Enhancer o	R.GLVSTLQSATEQMAATVSSSVR.A	3.47	20.71	0.17	5.97
Q3UJB9_E	Edc4	Enhancer o	R.HTEVLPAEEENDSLGTESSHGAGALESAAGVLIK#.L	27.38	14.44	1.90	0.53
Q3UJB9_E	Edc4	Enhancer o	K.LFQFLQADPHNSLSK.A	18.95	19.90	0.95	1.05
Q3UJB9_E	Edc4	Enhancer o	K.QGFIVVK#.G	12.37	8.34	1.48	0.67
Q3UJB9_E	Edc4	Enhancer o	R.SLEPVAGQLSNSVATK.L	15.42	17.32	0.89	1.12
Q3UJB9_E	Edc4	Enhancer o	R.SLLPGLLPGPADK#.L	27.55	27.22	1.01	0.99
Q8BL66_EE	Eea1	Early endos	K.AAQLATEIADIK#.S	28.86	18.52	1.56	0.64
Q8BL66_EE	Eea1	Early endos	K.AAVLDLEK#.A	22.26	12.78	1.74	0.57
Q8BL66_EE	Eea1	Early endos	R.ADLQNHLDTAQHALQDK#.Q	21.66	15.35	1.41	0.71
Q8BL66_EE	Eea1	Early endos	R.ADLQNHLDTAQHALQDK#QQELNK#.V	10.92	7.44	1.47	0.68
Q8BL66_EE	Eea1	Early endos	K.DALLAELSTTK#.E	25.79	10.84	2.38	0.42
Q8BL66_EE	Eea1	Early endos	R.DLDCQQLQAR.L	2.93	14.25	0.21	4.87
Q8BL66_EE	Eea1	Early endos	R.ENQSLQIK#.H	18.79	15.08	1.25	0.80
Q8BL66_EE	Eea1	Early endos	K.EQALQSLQQQR.Q	5.75	12.79	0.45	2.22
Q8BL66_EE	Eea1	Early endos	K.GPQEVAVYVQEIQK#.L	6.40	6.14	1.04	0.96
Q8BL66_EE	Eea1	Early endos	K.HYQAVHDAGNDSGHGGEAGLALTR.D	2.47	12.48	0.20	5.05
Q8BL66_EE	Eea1	Early endos	K.IELNSVK#GEVSQAQNTLK#.Q	12.72	8.69	1.46	0.68
Q8BL66_EE	Eea1	Early endos	K.IQAGEGETAVLNQLQEK#.N	15.15	10.86	1.40	0.72
Q8BL66_EE	Eea1	Early endos	K.IQNLEALLQK#.G	30.37	17.48	1.74	0.58
Q8BL66_EE	Eea1	Early endos	K.K#EEENVVLK#QEFEK#.L	25.42	17.53	1.45	0.69
Q8BL66_EE	Eea1	Early endos	K.K#LEADALEVK#.A	22.34	12.81	1.74	0.57
Q8BL66_EE	Eea1	Early endos	K.LQQQSSQAAQELAAEK#.G	36.55	21.18	1.73	0.58
Q8BL66_EE	Eea1	Early endos	K.LTLAQEDLISNR.N	7.70	16.67	0.46	2.16
Q8BL66_EE	Eea1	Early endos	K.LTM*QVTTLNENLGTVK#.K	7.06	4.03	1.75	0.57
Q8BL66_EE	Eea1	Early endos	K.LTMQVTTLNENLGTVK#.K	5.41	4.10	1.32	0.76
Q8BL66_EE	Eea1	Early endos	R.MQAAVTELTAVK#.A	14.90	8.21	1.81	0.55
Q8BL66_EE	Eea1	Early endos	K.NHALQQQLTQLTEK#.L	8.52	3.75	2.27	0.44
Q8BL66_EE	Eea1	Early endos	K.QQHQEQQALQQSATAK#.L	16.17	10.22	1.58	0.63
Q8BL66_EE	Eea1	Early endos	K.SDGLVTDSSAELQALEQQLEEAQTENFNIK#.Q	19.78	9.10	2.17	0.46
Q8BL66_EE	Eea1	Early endos	K.SK#QQHQEQQALQQSATAK#.L	18.62	9.18	2.03	0.49
Q8BL66_EE	Eea1	Early endos	K.VEDLEGHIK#.K	13.91	3.03	4.59	0.22
Q8BL66_EE	Eea1	Early endos	R.VLSLETSVSELSSQLNESK#.E	14.64	9.32	1.57	0.64
Q8BL66_EE	Eea1	Early endos	K.VSVQLDQLTAK#.F	40.03	20.11	1.99	0.50
Q8BL66_EE	Eea1	Early endos	K.VTHLTEDLNK#.Q	13.34	5.76	2.32	0.43
Q8BL66_EE	Eea1	Early endos	K.YQGLQQQEAK#.S	27.15	15.91	1.71	0.59
Q8BL66_EE	Eea1	Early endos	K.AAVLDLEK#.A	104.38	56.32	1.85	0.54
Q8BL66_EE	Eea1	Early endos	R.ADLQNHLDTAQHALQDK#.Q	23.59	10.65	2.21	0.45
Q8BL66_EE	Eea1	Early endos	K.EQALQSLQQQR.Q	5.87	16.37	0.36	2.79

Q8BL66_EE	Eea1	Early endos	K.EQQVADLQLK.L	9.26	25.60	0.36	2.76
Q8BL66_EE	Eea1	Early endos	K.IQAGEGETAVLNQLQEK#.N	15.16	9.96	1.52	0.66
Q8BL66_EE	Eea1	Early endos	K.IQNLEALLQK#.G	27.53	19.52	1.41	0.71
Q8BL66_EE	Eea1	Early endos	K.K#EEENVVLK#QEFEK#.L	20.11	12.66	1.59	0.63
Q8BL66_EE	Eea1	Early endos	K.LQQQSSQAAQELAAEK#.G	23.14	16.14	1.43	0.70
Q8BL66_EE	Eea1	Early endos	K.LSALQSNYEK#.C	15.56	16.50	0.94	1.06
Q8BL66_EE	Eea1	Early endos	R.LTASESSLQR.A	10.00	25.92	0.39	2.59
Q8BL66_EE	Eea1	Early endos	K.LTLAQEDLISNR.N	7.85	15.12	0.52	1.93
Q8BL66_EE	Eea1	Early endos	K.LTM*QVTTLNENLGTVK#.K	4.27	3.37	1.27	0.79
Q8BL66_EE	Eea1	Early endos	R.M*QAAVTELTAVK#.A	13.14	17.85	0.74	1.36
Q8BL66_EE	Eea1	Early endos	K.QTTVIQDLK#.T	12.20	9.40	1.30	0.77
Q8BL66_EE	Eea1	Early endos	K.SK#QQHQEQQALQQSATAK#.L	20.19	12.78	1.58	0.63
Q8BL66_EE	Eea1	Early endos	R.VLSLETSVSELSSQLNESK#.E	7.73	3.33	2.32	0.43
Q8BL66_EE	Eea1	Early endos	R.VLSLETSVSELSSQLNESK#.E	17.48	12.68	1.38	0.73
Q8BL66_EE	Eea1	Early endos	K.VSQLDIQIK#.A	18.60	8.61	2.16	0.46
Q921E6_EE	Eed	Polycomb	R.DPNLLLSVSK#.D	17.08	16.27	1.05	0.95
Q921E6_EE	Eed	Polycomb	K.EGDPLVFATVGSNR.V	3.99	13.99	0.29	3.50
Q921E6_EE	Eed	Polycomb	R.EVSTAPAGTDMPAAK#.K	6.74	5.11	1.32	0.76
Q921E6_EE	Eed	Polycomb	R.EVSTAPAGTDM*PAAK#.K	11.64	8.62	1.35	0.74
Q921E6_EE	Eed	Polycomb	R.FSM*DFWQK#.M	9.34	7.57	1.23	0.81
Q921E6_EE	Eed	Polycomb	K.HYVGHGNAINELK#.F	17.86	15.33	1.16	0.86
Q921E6_EE	Eed	Polycomb	R.WLGDLILSK#.S	17.15	21.38	0.80	1.25
Q921E6_EE	Eed	Polycomb	R.DPNLLLSVSK#.D	15.59	12.16	1.28	0.78
Q921E6_EE	Eed	Polycomb	K.EGDPLVFATVGSNR.V	4.01	9.22	0.44	2.30
Q921E6_EE	Eed	Polycomb	R.WLGDLILSK#.S	13.67	6.20	2.20	0.45
P10126_EF	Eef1a1	Elongation	R.EHALLAYTLGVK#.Q	645.48	98.92	6.52	0.15
P10126_EF	Eef1a1	Elongation	R.EHALLAYTLGVK#.Q	557.20	75.83	7.35	0.14
P10126_EF	Eef1a1	Elongation	K.EVSTYIK#.K	1582.02	260.33	6.08	0.16
P10126_EF	Eef1a1	Elongation	K.EVSTYIK#K#.I	300.53	56.94	5.28	0.19
P10126_EF	Eef1a1	Elongation	K.FEKEAAEM*GK.G	34.38	7.46	4.61	0.22
P10126_EF	Eef1a1	Elongation	K.IGGIGTVPVGR.V	705.24	545.67	1.29	0.77
P10126_EF	Eef1a1	Elongation	K.IGYNPDTVAFVPISGWNGDNM*LEPSANM*PWFK#.G	114.72	14.65	7.83	0.13
P10126_EF	Eef1a1	Elongation	K.KIGYNPDTVAFVPISGWNGDNM*LEPSANM*PWFK.G	36.28	7.81	4.65	0.22
P10126_EF	Eef1a1	Elongation	K.K#LEDGPK#.F	650.24	136.37	4.77	0.21
P10126_EF	Eef1a1	Elongation	R.LPLQDVYK#.I	2780.82	406.41	6.84	0.15
P10126_EF	Eef1a1	Elongation	K.M*DSTEPPYSQK#.R	1029.11	198.02	5.20	0.19
P10126_EF	Eef1a1	Elongation	K.MDSTEPPYSQK#.R	1192.89	230.58	5.17	0.19
P10126_EF	Eef1a1	Elongation	K.QLIVGVNK#.M	1730.31	315.22	5.49	0.18
P10126_EF	Eef1a1	Elongation	K.QLIVGVNK#M*DSTEPPYSQK#.R	140.88	18.81	7.49	0.13
P10126_EF	Eef1a1	Elongation	K.STTTGHLIYK#.C	1705.69	328.24	5.20	0.19
P10126_EF	Eef1a1	Elongation	K.THINIVVIGHVDSGK#.S	460.17	75.78	6.07	0.16
P10126_EF	Eef1a1	Elongation	R.TIEK#FEK#.E	1263.58	182.83	6.91	0.14
P10126_EF	Eef1a1	Elongation	R.VETGVLK#PGM*VVTFAPVNVTTEVK#.S	1002.91	161.75	6.20	0.16
P10126_EF	Eef1a1	Elongation	R.VETGVLKPGM*VVTFAPVNVTTEVK.S	55.29	9.06	6.10	0.16
P10126_EF	Eef1a1	Elongation	R.VETGVLK#PGMVVTFAPVNVTTEVK#.S	1252.22	207.35	6.04	0.17
P10126_EF	Eef1a1	Elongation	R.VETGVLKPGMVVTFAPVNVTTEVK.S	78.06	11.15	7.00	0.14
P10126_EF	Eef1a1	Elongation	R.YEEIVK#EVSTYIK#.K	62.16	7.65	8.13	0.12
P10126_EF	Eef1a1	Elongation	K.YYVTIIDAPGHR.D	138.98	111.59	1.25	0.80
P10126_EF	Eef1a1	Elongation	K.YYVTIIDAPGHR.D	371.04	288.85	1.28	0.78
P10126_EF	Eef1a1	Elongation	R.EHALLAYTLGVK#.Q	51.18	10.96	4.67	0.21
P10126_EF	Eef1a1	Elongation	K.IGGIGTVPVGR.V	19.56	16.19	1.21	0.83
P10126_EF	Eef1a1	Elongation	R.LPLQDVYK#.I	83.70	22.80	3.67	0.27
P10126_EF	Eef1a1	Elongation	K.M*DSTEPPYSQK#.R	39.22	9.94	3.95	0.25
P10126_EF	Eef1a1	Elongation	K.QLIVGVNK#.M	53.93	12.03	4.48	0.22
P10126_EF	Eef1a1	Elongation	R.QTVAVGVIK#.A	64.84	16.78	3.86	0.26
P10126_EF	Eef1a1	Elongation	K.STTTGHLIYK#.C	106.34	19.84	5.36	0.19
P10126_EF	Eef1a1	Elongation	K.THINIVVIGHVDSGK#.S	58.84	14.83	3.97	0.25
P10126_EF	Eef1a1	Elongation	R.TIEK#FEK#.E	43.78	8.70	5.03	0.20
P10126_EF	Eef1a1	Elongation	R.VETGVLK#PGM*VVTFAPVNVTTEVK#.S	26.57	5.16	5.15	0.19
P10126_EF	Eef1a1	Elongation	R.VETGVLK#PGMVVTFAPVNVTTEVK#.S	82.43	12.23	6.74	0.15
P10126_EF	Eef1a1	Elongation	R.YEEIVK#.E	47.25	5.61	8.42	0.12
P10126_EF	Eef1a1	Elongation	R.EHALLAYTLGVK#.Q	218.42	29.07	7.51	0.13
P10126_EF	Eef1a1	Elongation	K.EVSTYIK#K#.I	89.88	22.84	3.93	0.25
P10126_EF	Eef1a1	Elongation	K.IGGIGTVPVGR.V	250.97	192.83	1.30	0.77
P10126_EF	Eef1a1	Elongation	K.K#LEDGPK#.F	94.62	34.45	2.75	0.36
P10126_EF	Eef1a1	Elongation	R.LPLQDVYK#.I	710.82	108.16	6.57	0.15
P10126_EF	Eef1a1	Elongation	K.MDSTEPPYSQK#.R	104.68	18.37	5.70	0.18
P10126_EF	Eef1a1	Elongation	K.M*DSTEPPYSQK#.R	219.21	38.18	5.74	0.17
P10126_EF	Eef1a1	Elongation	K.QLIVGVNK#.M	431.97	80.59	5.36	0.19
P10126_EF	Eef1a1	Elongation	K.QLIVGVNK#M*DSTEPPYSQK#.R	58.20	8.56	6.80	0.15
P10126_EF	Eef1a1	Elongation	K.STTTGHLIYK#.C	504.10	94.49	5.33	0.19
P10126_EF	Eef1a1	Elongation	K.THINIVVIGHVDSGK#.S	197.01	34.97	5.63	0.18
P10126_EF	Eef1a1	Elongation	R.TIEK#FEK#.E	214.71	32.94	6.52	0.15
P10126_EF	Eef1a1	Elongation	R.VETGVLK#PGM*VVTFAPVNVTTEVK#.S	300.58	46.44	6.47	0.15
P10126_EF	Eef1a1	Elongation	R.VETGVLKPGMVVTFAPVNVTTEVK.S	373.99	52.29	7.15	0.14
P10126_EF	Eef1a1	Elongation	R.YEEIVK#.E	423.18	68.62	6.17	0.16
P10126_EF	Eef1a1	Elongation	R.YEEIVK#EVSTYIK#.K	6.61	0.95	6.98	0.14
P10126_EF	Eef1a1	Elongation	R.EHALLAYTLGVK#.Q	237.45	36.31	6.54	0.15
P10126_EF	Eef1a1	Elongation	K.EVSTYIK#K#.I	113.42	24.68	4.60	0.22
P10126_EF	Eef1a1	Elongation	K.IGGIGTVPVGR.V	326.04	241.50	1.35	0.74
P10126_EF	Eef1a1	Elongation	K.K#LEDGPK#.F	119.00	24.36	4.88	0.20
P10126_EF	Eef1a1	Elongation	R.LPLQDVYK#.I	763.68	121.58	6.28	0.16
P10126_EF	Eef1a1	Elongation	K.MDSTEPPYSQK#.R	99.96	16.17	6.18	0.16
P10126_EF	Eef1a1	Elongation	K.M*DSTEPPYSQK#.R	212.27	37.62	5.64	0.18
P10126_EF	Eef1a1	Elongation	K.QLIVGVNK#.M	513.23	80.31	6.39	0.16
P10126_EF	Eef1a1	Elongation	K.QLIVGVNK#M*DSTEPPYSQK#.R	65.10	13.12	4.96	0.20
P10126_EF	Eef1a1	Elongation	K.STTTGHLIYK#.C	463.87	91.56	5.07	0.20
P10126_EF	Eef1a1	Elongation	K.THINIVVIGHVDSGK#.S	96.56	22.44	4.30	0.23
P10126_EF	Eef1a1	Elongation	R.TIEK#FEK#.E	211.21	25.80	8.19	0.12
P10126_EF	Eef1a1	Elongation	R.VETGVLK#PGM*VVTFAPVNVTTEVK#.S	342.95	53.75	6.38	0.16
P10126_EF	Eef1a1	Elongation	R.VETGVLK#PGMVVTFAPVNVTTEVK#.S	447.93	62.03	7.22	0.14
P10126_EF	Eef1a1	Elongation	R.YEEIVK#.E	454.00	80.95	5.61	0.18
P10126_EF	Eef1a1	Elongation	R.YEEIVK#EVSTYIK#.K	28.57	4.58	6.24	0.16
P10126_EF	Eef1a1	Elongation	K.YYVTIIDAPGHR.D	24.83	19.99	1.24	0.80
O70251_E	Eef1b	Elongation	R.SIQADGLVWGSSK#.L	105.71	55.00	1.92	0.52
O70251_E	Eef1b	Elongation	K.SSILLDVK#PWDDETDM*TK#.L	6.17	1.70	3.62	0.28
O70251_E	Eef1b	Elongation	K.TPAGLQVLNDYLADK#.S	158.35	20.88	7.58	0.13
O70251_E	Eef1b	Elongation	K.YGPSSVEDTTGSGAADAK#.D	33.29	4.22	7.90	0.13
O70251_E	Eef1b	Elongation	K.TPAGLQVLNDYLADK#.S	23.18	3.43	6.77	0.15
O70251_E	Eef1b	Elongation	K.YGPSSVEDTTGSGAADAK#.D	3.72	2.98	1.25	0.80
Q80T06_Q	Eef1d	Elongation	K.AK#K#PTLVAK#.S	39.68	11.86	3.35	0.30
Q80T06_Q	Eef1d	Elongation	R.ATAPQTQHVSPM*R.Q	20.74	15.65	1.33	0.75
Q80T06_Q	Eef1d	Elongation	K.FEEHVQSVDIAAFNK#I.-	27.28	8.11	3.37	0.30

Q80T06_Q	Eef1d	Elongation	R.FYEQM*NGPVTSGSR.Q	27.74	23.70	1.17	0.85
Q80T06_Q	Eef1d	Elongation	R.FYEQMNGPVTSGSR.Q	13.32	11.67	1.14	0.88
Q80T06_Q	Eef1d	Elongation	K.GATPAEDDEDKDIDLFGSDEEEEDKEAAR.L	4.62	5.49	0.84	1.19
Q80T06_Q	Eef1d	Elongation	R.GVVQDLQQAISK#.L	454.09	92.54	4.91	0.20
Q80T06_Q	Eef1d	Elongation	R.ITSLEVENQNLR.G	133.39	121.82	1.10	0.91
Q80T06_Q	Eef1d	Elongation	K.IWFDK#FK#.Y	60.80	10.03	6.06	0.16
Q80T06_Q	Eef1d	Elongation	K.K#PTLVAK#.S	235.26	46.29	5.08	0.20
Q80T06_Q	Eef1d	Elongation	R.SIQLDGLVWGASK#.L	301.65	56.32	5.36	0.19
Q80T06_Q	Eef1d	Elongation	K.SLAGSSGPGASSGPGGDHSELIVR.I	10.49	7.44	1.41	0.71
Q80T06_Q	Eef1d	Elongation	R.GVVQDLQQAISK#.L	53.84	8.71	6.18	0.16
Q80T06_Q	Eef1d	Elongation	R.ITSLEVENQNLR.G	6.57	7.77	0.85	1.18
Q80T06_Q	Eef1d	Elongation	R.SIQLDGLVWGASK#.L	10.15	1.71	5.95	0.17
Q80T06_Q	Eef1d	Elongation	R.GVVQDLQQAISK#.L	8.28	3.41	2.43	0.41
Q9D1M4_	Eef1e1	Eukaryotic	K.DLNSYLEDK#.V	28.24	5.39	5.24	0.19
Q9D1M4_	Eef1e1	Eukaryotic	R.FIVDLTVQEK#.E	40.73	20.58	1.98	0.51
Q9D1M4_	Eef1e1	Eukaryotic	R.QHLSSIVFIK#.N	26.46	6.43	4.12	0.24
Q9D1M4_	Eef1e1	Eukaryotic	K.SLGLK#PGNK#.Y	14.15	6.16	2.30	0.44
Q9D8N0_E	Eef1g	Elongation	K.AK#DPFAHLPK#.S	137.73	12.26	11.23	0.09
Q9D8N0_E	Eef1g	Elongation	K.ALIAAQYSGAQVR.V	56.55	29.53	1.92	0.52
Q9D8N0_E	Eef1g	Elongation	R.ILGLLDTHLK#.T	129.11	12.88	10.02	0.10
Q9D8N0_E	Eef1g	Elongation	K.K#FAESQPK#.K	41.03	8.18	5.01	0.20
Q9D8N0_E	Eef1g	Elongation	R.KLDPGSEETQTLVR.E	17.13	14.34	1.19	0.84
Q9D8N0_E	Eef1g	Elongation	K.LDPGSEETQTLVR.E	12.21	12.15	1.01	0.99
Q9D8N0_E	Eef1g	Elongation	K.MAQFDAK#.K	43.76	4.35	10.06	0.10
Q9D8N0_E	Eef1g	Elongation	K.M*AQFDAK#.K	57.95	9.13	6.35	0.16
Q9D8N0_E	Eef1g	Elongation	K.STFVLDEFK#.R	22.28	4.01	5.55	0.18
Q9D8N0_E	Eef1g	Elongation	K.AK#DPFAHLPK#.S	66.33	13.97	4.75	0.21
Q9D8N0_E	Eef1g	Elongation	K.FAESQPK#.K	20.28	6.81	2.98	0.34
Q9D8N0_E	Eef1g	Elongation	R.ILGLLDTHLK#.T	67.76	8.24	8.23	0.12
Q9D8N0_E	Eef1g	Elongation	K.M*AQFDAK#.K	28.25	3.42	8.27	0.12
P58252_EF	Eef2	Elongation	K.AYLPVNESFGFTADLR.S	13.99	8.17	1.71	0.58
P58252_EF	Eef2	Elongation	R.GHVFEESQVAGTPMFVVK#.A	23.15	3.65	6.35	0.16
P58252_EF	Eef2	Elongation	K.GVQYLNEIK#DSVVAGFQWATK#.E	35.86	4.09	8.76	0.11
P58252_EF	Eef2	Elongation	R.VFSGVVSTGLK#.V	53.60	7.52	7.13	0.14
P58252_EF	Eef2	Elongation	K.YEWDVAEAR.K	18.90	12.62	1.50	0.67
P58252_EF	Eef2	Elongation	K.AGIIASAR.A	94.47	96.72	0.98	1.02
P58252_EF	Eef2	Elongation	R.ALLELQLEPEELYQTFQR.I	107.98	98.55	1.10	0.91
P58252_EF	Eef2	Elongation	K.ARPFPDGLAEDIDKGEVSAR.Q	9.00	23.68	0.38	2.63
P58252_EF	Eef2	Elongation	K.AYLPVNESFGFTADLR.S	59.91	58.31	1.03	0.97
P58252_EF	Eef2	Elongation	K.DSVVAGFQWATK#.E	37.78	8.67	4.36	0.23
P58252_EF	Eef2	Elongation	K.EGIPALDNFLDK#L.-	232.60	52.31	4.45	0.22
P58252_EF	Eef2	Elongation	K.FSVSPVVR.V	108.35	105.49	1.03	0.97
P58252_EF	Eef2	Elongation	K.GEGQLSAAER.A	121.99	114.58	1.06	0.94
P58252_EF	Eef2	Elongation	R.GGGQIIPTAR.R	90.36	145.13	0.62	1.61
P58252_EF	Eef2	Elongation	R.GHVFEESQVAGTPM*FVVK#.A	113.13	23.59	4.80	0.21
P58252_EF	Eef2	Elongation	R.GHVFEESQVAGTPMFVVK#.A	64.59	10.79	5.99	0.17
P58252_EF	Eef2	Elongation	K.GLK#EGIPALDNFLDK#L.-	68.20	22.61	3.02	0.33
P58252_EF	Eef2	Elongation	K.GPLMM*YISK#.M	38.88	8.71	4.46	0.22
P58252_EF	Eef2	Elongation	K.GPLM*MYISK#.M	32.68	8.62	3.79	0.26
P58252_EF	Eef2	Elongation	K.GPLMMYISK#.M	58.01	18.02	3.22	0.31
P58252_EF	Eef2	Elongation	K.GVQYLNEIK#DSVVAGFQWATK#.E	236.72	39.64	5.97	0.17
P58252_EF	Eef2	Elongation	R.IK#PVLM*MNK#.M	62.84	12.35	5.09	0.20
P58252_EF	Eef2	Elongation	R.IK#PVLMMNK#.M	49.08	10.41	4.72	0.21
P58252_EF	Eef2	Elongation	R.IM*GPNYTPGK#.K	109.37	26.35	4.15	0.24
P58252_EF	Eef2	Elongation	R.IMGPNYTPGK#.K	54.74	16.70	3.28	0.31
P58252_EF	Eef2	Elongation	R.IM*GPNYTPGK#K#.E	29.92	9.15	3.27	0.31
P58252_EF	Eef2	Elongation	R.IMGPNYTPGK#K#.E	8.90	3.64	2.45	0.41
P58252_EF	Eef2	Elongation	K.KEDLYLKPIQR.T	31.95	31.20	1.02	0.98
P58252_EF	Eef2	Elongation	K.K#VEDMMK#.K	25.23	6.01	4.20	0.24
P58252_EF	Eef2	Elongation	K.NPADLPK#.L	295.28	81.08	3.64	0.27
P58252_EF	Eef2	Elongation	K.QFAEM*YVAK#.F	128.33	26.33	4.87	0.21
P58252_EF	Eef2	Elongation	K.QFAEMYVAK#.F	79.23	17.13	4.62	0.22
P58252_EF	Eef2	Elongation	K.VFDAIM*NFR.K	35.91	30.73	1.17	0.86
P58252_EF	Eef2	Elongation	R.VFSGVVSTGLK#.V	652.50	135.91	4.80	0.21
P58252_EF	Eef2	Elongation	K.YEWDVAEAR.K	40.79	46.84	0.87	1.15
P58252_EF	Eef2	Elongation	R.YFDPANGK#.F	74.01	15.99	4.63	0.22
P58252_EF	Eef2	Elongation	R.YLAEKYEWDVAEAR.K	6.62	4.93	1.34	0.74
P58252_EF	Eef2	Elongation	K.AGIIASAR.A	97.92	95.19	1.03	0.97
P58252_EF	Eef2	Elongation	R.ALLELQLEPEELYQTFQR.I	11.34	9.96	1.14	0.88
P58252_EF	Eef2	Elongation	K.ARPFPDGLAEDIDKGEVSAR.Q	5.96	16.95	0.35	2.84
P58252_EF	Eef2	Elongation	K.AYLPVNESFGFTADLR.S	44.09	43.91	1.00	1.00
P58252_EF	Eef2	Elongation	K.EGIPALDNFLDK#.L	19.29	7.15	2.70	0.37
P58252_EF	Eef2	Elongation	K.FSVSPVVR.V	77.53	63.95	1.21	0.82
P58252_EF	Eef2	Elongation	K.GEGQLSAAER.A	103.55	74.65	1.39	0.72
P58252_EF	Eef2	Elongation	R.GGGQIIPTAR.R	69.70	79.98	0.87	1.15
P58252_EF	Eef2	Elongation	R.GHVFEESQVAGTPM*FVVK#.A	135.11	26.29	5.14	0.19
P58252_EF	Eef2	Elongation	R.GHVFEESQVAGTPMFVVK#.A	46.65	9.52	4.90	0.20
P58252_EF	Eef2	Elongation	K.GLK#EGIPALDNFLDK#L.-	51.26	8.21	6.24	0.16
P58252_EF	Eef2	Elongation	K.GPLM*M*YISK#.M	52.43	14.46	3.63	0.28
P58252_EF	Eef2	Elongation	K.GPLM*MYISK#.M	16.44	4.16	3.95	0.25
P58252_EF	Eef2	Elongation	K.GVQYLNEIK#.D	55.49	6.95	7.98	0.13
P58252_EF	Eef2	Elongation	K.GVQYLNEIK#DSVVAGFQWATK#.E	116.30	19.93	5.84	0.17
P58252_EF	Eef2	Elongation	R.IK#PVLMMNK#.M	15.00	2.75	5.46	0.18
P58252_EF	Eef2	Elongation	R.IM*GPNYTPGK#.K	122.28	22.17	5.52	0.18
P58252_EF	Eef2	Elongation	R.IMGPNYTPGK#.K	41.25	8.30	4.97	0.20
P58252_EF	Eef2	Elongation	K.NPADLPK#.L	322.30	86.07	3.74	0.27
P58252_EF	Eef2	Elongation	K.QFAEM*YVAK#.F	81.55	15.97	5.11	0.20
P58252_EF	Eef2	Elongation	K.SDPVVSYR.E	73.46	64.69	1.14	0.88
P58252_EF	Eef2	Elongation	K.VFDAIM*NFR.K	22.28	20.48	1.09	0.92
P58252_EF	Eef2	Elongation	R.VFSGVVSTGLK#.V	521.86	92.44	5.65	0.18
P58252_EF	Eef2	Elongation	K.YEWDVAEAR.K	26.46	25.38	1.04	0.96
P58252_EF	Eef2	Elongation	R.YFDPANGK#.F	62.63	11.46	5.47	0.18
Q9D8Y0_E	Efhd2	EF-hand do	R.DGFIDLM*ELK#.L	11.00	10.08	1.09	0.92
Q9D8Y0_E	Efhd2	EF-hand do	K.SM*IQEVDEDFDSK.L	3.85	5.89	0.65	1.53
Q9D8Y0_E	Efhd2	EF-hand do	K.SMIQEVDEDFDSK#.L	4.17	4.49	0.93	1.08
Q8C0D5_E	Eftud1	Elongation	K.IVTSLGLK#.I	43.34	19.87	2.18	0.46
Q8C0D5_E	Eftud1	Elongation	R.LIVELK#.F	26.03	17.57	1.48	0.67
O08810_U	Eftud2	116 kDa U5	K.AFIPAIDSFGFETDLR.T	29.39	72.81	0.40	2.48
O08810_U	Eftud2	116 kDa U5	K.DSIVQGFQWGTR.E	17.03	44.73	0.38	2.63
O08810_U	Eftud2	116 kDa U5	K.FFDDPM*LLELAK#.Q	32.94	29.62	1.11	0.90
O08810_U	Eftud2	116 kDa U5	K.FFDDPMLLELAK#.Q	27.51	19.06	1.44	0.69
O08810_U	Eftud2	116 kDa U5	K.FNTTSVIK#.I	98.23	59.75	1.64	0.61
O08810_U	Eftud2	116 kDa U5	K.GLAEDIENEVVQITWNR.K	26.45	89.64	0.30	3.39

O08810_U	Eftud2	116 kDa U5	K.GLSEDVSISK#.F	127.01	70.06	1.81	0.55
O08810_U	Eftud2	116 kDa U5	K.IAVEPVNPSELPK#.M	145.24	123.41	1.18	0.85
O08810_U	Eftud2	116 kDa U5	K.ILAQVVGDVDTSLPR.T	19.27	57.44	0.34	2.98
O08810_U	Eftud2	116 kDa U5	K.ILDAVVAQEPLHR.G	42.59	98.81	0.43	2.32
O08810_U	Eftud2	116 kDa U5	R.ISDGVVLFIDAAEGVM*LNTER.L	4.77	14.66	0.33	3.07
O08810_U	Eftud2	116 kDa U5	K.ITM*IAEPLEK#.G	68.59	44.83	1.53	0.65
O08810_U	Eftud2	116 kDa U5	K.ITMIAEPLEK#.G	45.37	30.30	1.50	0.67
O08810_U	Eftud2	116 kDa U5	K.IYADTFGDINYQEFAK#.R	80.24	51.57	1.56	0.64
O08810_U	Eftud2	116 kDa U5	R.K#GLSEDVSISK#.F	22.49	16.37	1.37	0.73
O08810_U	Eftud2	116 kDa U5	K.LGEFFQTK#.Y	109.95	73.67	1.49	0.67
O08810_U	Eftud2	116 kDa U5	R.LILELK#.L	73.43	38.85	1.89	0.53
O08810_U	Eftud2	116 kDa U5	K.LPPTDAYYK#.L	51.88	36.72	1.41	0.71
O08810_U	Eftud2	116 kDa U5	R.LWGDIYFNPK#.T	43.57	29.43	1.48	0.68
O08810_U	Eftud2	116 kDa U5	R.LWISVAR.Y	16.57	43.46	0.38	2.62
O08810_U	Eftud2	116 kDa U5	K.M*YSEIDIK#.V	33.03	21.88	1.51	0.66
O08810_U	Eftud2	116 kDa U5	K.RLWGDIYFNPK.T	6.35	10.67	0.60	1.68
O08810_U	Eftud2	116 kDa U5	K.STPVTVVLPDTK#.G	113.88	84.33	1.35	0.74
O08810_U	Eftud2	116 kDa U5	K.SYLFNIM*DTPGHVNFSDEVTAGLR.I	18.84	36.12	0.52	1.92
O08810_U	Eftud2	116 kDa U5	K.TATITEPR.G	23.72	82.07	0.29	3.46
O08810_U	Eftud2	116 kDa U5	R.VPAGNWVLIEGVDQPIVK#.T	60.63	41.17	1.47	0.68
O08810_U	Eftud2	116 kDa U5	R.VPAGNWVLIEGVDQPIVK.T	76.74	45.48	1.69	0.59
O08810_U	Eftud2	116 kDa U5	K.YDWDLLAAR.S	21.35	64.46	0.33	3.02
O08810_U	Eftud2	116 kDa U5	K.YYPTAEEVYGPEVETIVQEEDTQPLTEPIIKPVK.T	24.68	20.27	1.22	0.82
O08810_U	Eftud2	116 kDa U5	K.AFIPAIDSFGFETDLR.T	16.28	34.62	0.47	2.13
O08810_U	Eftud2	116 kDa U5	K.DSIVQGFQWGTR.E	9.56	21.64	0.44	2.26
O08810_U	Eftud2	116 kDa U5	K.FFDDPM*LLELAK#.Q	35.49	18.26	1.94	0.51
O08810_U	Eftud2	116 kDa U5	K.FNTTSVIK#.I	51.75	28.50	1.82	0.55
O08810_U	Eftud2	116 kDa U5	K.GLSEDVSISK#.F	65.27	33.97	1.92	0.52
O08810_U	Eftud2	116 kDa U5	K.IAVEPVNPSELPK#.M	93.02	61.30	1.52	0.66
O08810_U	Eftud2	116 kDa U5	K.ILDAVVAQEPLHR.G	25.84	47.86	0.54	1.85
O08810_U	Eftud2	116 kDa U5	K.ITM*IAEPLEK#.G	32.72	21.48	1.52	0.66
O08810_U	Eftud2	116 kDa U5	K.ITMIAEPLEK#.G	18.98	12.00	1.58	0.63
O08810_U	Eftud2	116 kDa U5	K.IYADTFGDINYQEFAK#.R	49.94	26.63	1.88	0.53
O08810_U	Eftud2	116 kDa U5	K.LGEFFQTK#.Y	54.71	34.87	1.57	0.64
O08810_U	Eftud2	116 kDa U5	R.LILELK#.L	31.72	20.17	1.57	0.64
O08810_U	Eftud2	116 kDa U5	K.M*YSEIDIK#.V	15.03	10.70	1.40	0.71
O08810_U	Eftud2	116 kDa U5	K.STPVTVVLPDTK#.G	73.37	47.22	1.55	0.64
O08810_U	Eftud2	116 kDa U5	K.SYLFNIM*DTPGHVNFSDEVTAGLR.I	10.16	23.24	0.44	2.29
O08810_U	Eftud2	116 kDa U5	R.VPAGNWVLIEGVDQPIVK#.T	38.99	21.84	1.78	0.56
O08810_U	Eftud2	116 kDa U5	K.YDWDLLAAR.S	11.99	30.51	0.39	2.55
O08810_U	Eftud2	116 kDa U5	K.YYPTAEEVYGPEVETIVQEEDTQPLTEPIIK#PVK#.T	14.04	9.37	1.50	0.67
P08046_E	Egr1	Early growt	R.TQQPSLTPLSTIK.A	4.55	5.72	0.80	1.26
Q9WVK4_E	Ehd1	EH domain	K.ADQIETQQLM*R.V	13.10	25.03	0.52	1.91
Q9WVK4_E	Ehd1	EH domain	K.ADQIETQQLMR.V	11.29	10.26	1.10	0.91
Q9WVK4_E	Ehd1	EH domain	K.DK#PTYDEIFYTLSPVNGK#.I	9.41	5.83	1.61	0.62
Q9WVK4_E	Ehd1	EH domain	R.EHQISSGDFPSLR.K	14.07	32.81	0.43	2.33
Q9WVK4_E	Ehd1	EH domain	K.ELVNNLGEIYQK#.I	78.42	33.46	2.34	0.43
Q9WVK4_E	Ehd1	EH domain	R.FHEFHSPALEDADFDNK#PM*VLLVGQYSTGK#.T	12.05	4.48	2.69	0.37
Q9WVK4_E	Ehd1	EH domain	K.GGAFDGTM*NGPFGHGYGEGAGEGIDDVEWVVGK#.D	11.86	4.93	2.41	0.42
Q9WVK4_E	Ehd1	EH domain	K.GGAFDGTMNGPFGHGYGEGAGEGIDDVEWVVGK#.D	6.45	2.47	2.61	0.38
Q9WVK4_E	Ehd1	EH domain	R.IGPEPTTDSFIAVM*HGPTEGVVPGNALVVDPR.R	3.98	5.72	0.70	1.44
Q9WVK4_E	Ehd1	EH domain	R.IILLFDAHK#LDISDEFSEVIK#.A	10.05	4.96	2.03	0.49
Q9WVK4_E	Ehd1	EH domain	K.IINTPEVVR.V	29.76	61.00	0.49	2.05
Q9WVK4_E	Ehd1	EH domain	R.K#LNDLIK#.R	49.14	22.68	2.17	0.46
Q9WVK4_E	Ehd1	EH domain	R.K#M*QELLQTQDFSK#.F	13.60	5.91	2.30	0.43
Q9WVK4_E	Ehd1	EH domain	R.K#MQELLQTQDFSK#.F	12.47	2.29	5.44	0.18
Q9WVK4_E	Ehd1	EH domain	K.LDISDEFSEVIK#.A	51.80	25.14	2.06	0.49
Q9WVK4_E	Ehd1	EH domain	K.LFEAEEQDLFK#.D	28.48	15.75	1.81	0.55
Q9WVK4_E	Ehd1	EH domain	K.LFEAEEQDLFKDIQSLPR.N	3.81	10.87	0.35	2.85
Q9WVK4_E	Ehd1	EH domain	K.LLDTVDDM*LANDIAR.L	5.97	9.00	0.66	1.51
Q9WVK4_E	Ehd1	EH domain	K.LLDTVDDMLANDIAR.L	3.77	7.58	0.50	2.01
Q9WVK4_E	Ehd1	EH domain	K.M*QELLQTQDFSK#.F	14.43	7.58	1.90	0.53
Q9WVK4_E	Ehd1	EH domain	R.QEESLM*PSQAVK#.G	20.66	8.47	2.44	0.41
Q9WVK4_E	Ehd1	EH domain	R.QEESLMPSQAVK#.G	22.70	12.28	1.85	0.54
Q9WVK4_E	Ehd1	EH domain	K.SK#LPNTVLGK#.I	49.40	20.83	2.37	0.42
Q9WVK4_E	Ehd1	EH domain	R.VYGALMWSLGK#.I	23.03	13.84	1.66	0.60
Q9WVK4_E	Ehd1	EH domain	K.ELVNNLGEIYQK#.I	18.49	10.15	1.82	0.55
Q9WVK4_E	Ehd1	EH domain	K.GGAFDGTM*NGPFGHGYGEGAGEGIDDVEWVVGK#.D	3.58	2.73	1.31	0.76
Q9WVK4_E	Ehd1	EH domain	R.IGPEPTTDSFIAVM*HGPTEGVVPGNALVVDPR.R	1.64	3.03	0.54	1.85
Q9WVK4_E	Ehd1	EH domain	R.K#LNDLIK#.R	23.04	7.47	3.08	0.32
Q9WVK4_E	Ehd1	EH domain	K.LFEAEEQDLFKDIQSLPR.N	3.66	7.89	0.46	2.15
Q9WVK4_E	Ehd1	EH domain	R.VYGALMWSLGK#.I	7.20	2.57	2.80	0.36
Q9WVK4_E	Ehd1	EH domain	K.ELVNNLGEIYQK#.I	16.44	6.48	2.54	0.39
Q9WVK4_E	Ehd1	EH domain	K.GGAFDGTM*NGPFGHGYGEGAGEGIDDVEWVVGK#.D	3.06	1.77	1.73	0.58
Q8BH64_E	Ehd2	EH domain	R.FGSFHSPALEDADFDGK#PM*VLVAGQYSTGK#.T	8.84	3.99	2.21	0.45
Q8BH64_E	Ehd2	EH domain	R.GYDFPAVLR.W	6.98	23.30	0.30	3.34
Q8BH64_E	Ehd2	EH domain	R.LFELEEQDLFR.D	7.18	24.51	0.29	3.41
Q8BH64_E	Ehd2	EH domain	K.LLEALDDM*LAQDIAK#.L	7.21	7.68	0.94	1.07
Q8BH64_E	Ehd2	EH domain	K.LPVIFAK#.I	19.06	19.30	0.99	1.01
Q8BH64_E	Ehd2	EH domain	K.SK#YDEIFYNLAPADGK#.L	11.58	10.37	1.12	0.90
Q8BH64_E	Ehd2	EH domain	K.TSFIQYLLEQEVPGSR.V	14.26	26.49	0.54	1.86
Q8BH64_E	Ehd2	EH domain	R.VHAYIISYLK#.K	27.59	12.55	2.20	0.45
Q8BH64_E	Ehd2	EH domain	K.VVGTPEVLR.V	12.32	32.99	0.37	2.68
Q8BH64_E	Ehd2	EH domain	R.GYDFPAVLR.W	5.86	11.60	0.51	1.98
Q8BH64_E	Ehd2	EH domain	R.LFELEEQDLFR.D	7.44	29.70	0.25	3.99
Q8BH64_E	Ehd2	EH domain	K.LPVIFAK#.I	15.34	13.49	1.14	0.88
Q8BH64_E	Ehd2	EH domain	K.TSFIQYLLEQEVPGSR.V	14.11	18.47	0.76	1.31
Q8BH64_E	Ehd2	EH domain	R.LFELEEQDLFR.D	4.24	17.51	0.24	4.13
Q8BH64_E	Ehd2	EH domain	K.TSFIQYLLEQEVPGSR.V	8.15	19.92	0.41	2.44
Q9EQP2_E	Ehd4	EH domain	K.ADQVDTQQLM*R.V	9.47	15.57	0.61	1.64
Q9EQP2_E	Ehd4	EH domain	K.AM*QEQLENYDFTK#.F	48.35	15.63	3.09	0.32
Q9EQP2_E	Ehd4	EH domain	K.AMQEQLENYDFTK#.F	23.13	6.34	3.65	0.27
Q9EQP2_E	Ehd4	EH domain	R.DIQSLPQK#.A	67.32	16.80	4.01	0.25
Q9EQP2_E	Ehd4	EH domain	K.DK#PVYDELFYTLSPINGK#.I	7.87	3.80	2.07	0.48
Q9EQP2_E	Ehd4	EH domain	R.EYQISAGDFPEVK#.A	58.36	23.58	2.48	0.40
Q9EQP2_E	Ehd4	EH domain	R.FGNAFLNR.F	12.85	17.14	0.75	1.33
Q9EQP2_E	Ehd4	EH domain	R.IILLFDAHK#LDISDEFSEAIK#.A	21.30	4.41	4.84	0.21
Q9EQP2_E	Ehd4	EH domain	K.LDISDEFSEAIK#.A	36.86	11.91	3.10	0.32
Q9EQP2_E	Ehd4	EH domain	R.LFEAEAQDLFR.D	16.97	21.19	0.80	1.25
Q9EQP2_E	Ehd4	EH domain	K.LIEAVDNM*LTNK#.I	35.98	12.16	2.96	0.34
Q9EQP2_E	Ehd4	EH domain	K.SISIIDSPGILSGEK#.Q	77.32	29.35	2.63	0.38
Q9EQP2_E	Ehd4	EH domain	K.AM*QEQLENYDFTK#.F	22.10	7.08	3.12	0.32
Q9EQP2_E	Ehd4	EH domain	K.AMQEQLENYDFTK#.F	9.37	2.51	3.73	0.27

Q9EQP2_E	Ehd4	EH domain	R.DIQSLPQK#.A	38.52	8.19	4.70	0.21
Q9EQP2_E	Ehd4	EH domain	R.EYQISAGDFPEVK#.A	35.98	10.56	3.41	0.29
Q9EQP2_E	Ehd4	EH domain	R.FHEFHSPALEDADFENK#PM*ILLVGQYSTGK#.T	4.33	2.56	1.70	0.59
Q9EQP2_E	Ehd4	EH domain	R.IGPEPTTDSFIAVM*YGETEGSTPGNALVVDPK#.K	5.92	2.40	2.46	0.41
Q9EQP2_E	Ehd4	EH domain	K.LDISDEFSEAIK#.A	16.09	6.11	2.63	0.38
Q9EQP2_E	Ehd4	EH domain	R.LFEAEAQDLFR.D	8.13	10.78	0.75	1.33
Q9EQP2_E	Ehd4	EH domain	K.LIEAVDNM*LTNK#.I	18.66	5.11	3.65	0.27
Q9EQP2_E	Ehd4	EH domain	K.AM*QEQLENYDFTK#.F	18.91	5.75	3.29	0.30
Q9EQP2_E	Ehd4	EH domain	K.EGADEEEWVVAK#.D	18.25	5.66	3.22	0.31
Q9EQP2_E	Ehd4	EH domain	R.EYQISAGDFPEVK#.A	25.79	8.25	3.13	0.32
Q9EQP2_E	Ehd4	EH domain	R.LFEAEAQDLFR.D	5.53	9.67	0.57	1.75
Q9EQP2_E	Ehd4	EH domain	K.LIEAVDNM*LTNK#.I	18.72	4.78	3.92	0.26
Q9EQP2_E	Ehd4	EH domain	R.SGGM*DAVQTVTGGLR.S	4.48	8.01	0.56	1.79
Q9EQP2_E	Ehd4	EH domain	K.SISIIDSPGILSGEK#.Q	49.95	16.95	2.95	0.34
Q5DW34_E	Ehmt1	Histone-lys	K.ADTTSTVTLAPGQEK#.S	11.54	12.56	0.92	1.09
Q5DW34_E	Ehmt1	Histone-lys	R.ADTTTGSIAGAPEDER.S	3.03	13.81	0.22	4.56
Q5DW34_E	Ehmt1	Histone-lys	R.DSAPDK#PVAVEK#.T	9.78	10.61	0.92	1.08
Q5DW34_E	Ehmt1	Histone-lys	R.LIQAGEQLGFDYGER.F	6.91	9.94	0.70	1.44
Q5DW34_E	Ehmt1	Histone-lys	K.ADTTSTVTLAPGQEK#.S	11.43	8.82	1.30	0.77
Q9Z148_E	Ehmt2	Histone-lys	R.LDPHPELLPDLSSLPPINT.-	27.22	27.22	1.00	1.00
Q9Z148_E	Ehmt2	Histone-lys	R.TGEELGFDYGDRFWDIK.S	1.21	6.12	0.20	5.07
Q9Z148_E	Ehmt2	Histone-lys	R.LDPHPELLPDLSSLPPINT.-	14.09	14.09	1.00	1.00
Q9CXU9_EI	Eif1b	Eukaryotic	K.TLTTVQGIADDYDK#.K	48.82	16.89	2.89	0.35
Q9CXU9_EI	Eif1b	Eukaryotic	K.TLTTVQGIADDYDK#K#K#.L	6.36	2.46	2.59	0.39
Q8BJW6_EI	Eif2a	Eukaryotic	K.AIEQLK#EQAAAGK#.Q	27.41	5.71	4.80	0.21
Q8BJW6_EI	Eif2a	Eukaryotic	K.DGTAGTPNLQLYDM*K#.T	16.23	4.51	3.60	0.28
Q8BJW6_EI	Eif2a	Eukaryotic	K.DGTAGTPNLQLYDMK#.T	15.85	3.41	4.64	0.22
Q8BJW6_EI	Eif2a	Eukaryotic	K.GLLHSFDLPK#.A	45.95	10.26	4.48	0.22
Q8BJW6_EI	Eif2a	Eukaryotic	R.GQMEVWDVK#.N	25.30	4.04	6.26	0.16
Q8BJW6_EI	Eif2a	Eukaryotic	K.IWHYTGSLLHK#.Y	31.29	7.38	4.24	0.24
Q8BJW6_EI	Eif2a	Eukaryotic	R.LYQYPNFAGPQAALANK#.S	26.54	6.00	4.43	0.23
Q8BJW6_EI	Eif2a	Eukaryotic	R.NTVTQSASGDPEVDK#K#.I	19.16	5.93	3.23	0.31
Q8BJW6_EI	Eif2a	Eukaryotic	R.NTVTQSASGDPEVDK#K#.I	77.10	19.69	3.92	0.26
Q8BJW6_EI	Eif2a	Eukaryotic	R.NVNNEVHFFENNNFNTIANK#.L	39.02	11.32	3.45	0.29
Q8BJW6_EI	Eif2a	Eukaryotic	R.SDAAPTPVPQSAPR.N	36.58	25.43	1.44	0.70
Q8BJW6_EI	Eif2a	Eukaryotic	K.VAVYVPGSK#.G	50.22	11.07	4.54	0.22
Q8BJW6_EI	Eif2a	Eukaryotic	K.VNDFNLSPGTQPYK#.V	38.51	7.34	5.25	0.19
Q8BJW6_EI	Eif2a	Eukaryotic	K.VNIINVANK#.G	121.46	23.62	5.14	0.19
Q8BJW6_EI	Eif2a	Eukaryotic	K.YQAVPSEVPSEEPK#.V	67.81	12.08	5.61	0.18
Q8BJW6_EI	Eif2a	Eukaryotic	R.LYQYPNFAGPQAALANK#.S	7.89	3.08	2.57	0.39
Q8BJW6_EI	Eif2a	Eukaryotic	K.VNDFNLSPGTQPYK#.V	10.31	3.24	3.18	0.31
Q8BJW6_EI	Eif2a	Eukaryotic	K.VNIINVANK#.G	17.33	3.08	5.62	0.18
Q8BJW6_EI	Eif2a	Eukaryotic	K.YQAVPSEVPSEEPK#.V	21.27	6.05	3.51	0.28
Q8BJW6_EI	Eif2a	Eukaryotic	R.LYQYPNFAGPQAALANK#.S	6.87	2.72	2.53	0.40
Q8BJW6_EI	Eif2a	Eukaryotic	R.NVNNEVHFFENNNFNTIANK#.L	14.03	2.20	6.38	0.16
Q8BJW6_EI	Eif2a	Eukaryotic	K.VAVYVPGSK#.G	23.87	4.55	5.24	0.19
Q8BJW6_EI	Eif2a	Eukaryotic	K.VNIINVANK#.G	15.05	4.07	3.69	0.27
Q8BJW6_EI	Eif2a	Eukaryotic	K.YQAVPSEVPSEEPK#.V	22.35	5.08	4.40	0.23
Q03963_E	Eif2ak2	Interferon-i	R.DLKPGNIFLVDER.H	10.90	34.24	0.32	3.14
Q03963_E	Eif2ak2	Interferon-i	K.DRPETSEILK.T	26.79	128.82	0.21	4.81
Q03963_E	Eif2ak2	Interferon-i	R.FTFQVLIDEK#.E	26.02	14.90	1.75	0.57
Q03963_E	Eif2ak2	Interferon-i	R.FTFQVLIDEK#EFPEAK#.G	39.98	25.25	1.58	0.63
Q03963_E	Eif2ak2	Interferon-i	K.GDFSNDIFDNK#.E	27.24	18.89	1.44	0.69
Q03963_E	Eif2ak2	Interferon-i	K.GDFSNDIFDNK#EK#.S	20.89	14.17	1.47	0.68
Q03963_E	Eif2ak2	Interferon-i	K.IGDFGLATALENDGK#.S	183.03	120.56	1.52	0.66
Q03963_E	Eif2ak2	Interferon-i	K.IGQTM*YGTGSGVTK#.Q	126.61	72.43	1.75	0.57
Q03963_E	Eif2ak2	Interferon-i	K.IGQTMYGTGSGVTK#.Q	79.32	48.38	1.64	0.61
Q03963_E	Eif2ak2	Interferon-i	R.KGDFSNDIFDNKEK.S	70.25	38.43	1.83	0.55
Q03963_E	Eif2ak2	Interferon-i	K.LAVDILDNENK#.V	15.20	8.39	1.81	0.55
Q03963_E	Eif2ak2	Interferon-i	R.RFTFQVLIDEKEFPEAK.G	5.72	11.04	0.52	1.93
Q03963_E	Eif2ak2	Interferon-i	R.TGTLQYM*SPEQLFLK#.H	28.27	39.07	0.72	1.38
Q03963_E	Eif2ak2	Interferon-i	R.TGTLQYMSPEQLFLK#.H	51.12	33.63	1.52	0.66
Q03963_E	Eif2ak2	Interferon-i	K.IGDFGLATALENDGK#.S	16.10	8.54	1.89	0.53
Q03963_E	Eif2ak2	Interferon-i	R.DLKPGNIFLVDER.H	20.30	42.87	0.47	2.11
Q03963_E	Eif2ak2	Interferon-i	K.DRPETSEILK.T	15.55	52.62	0.30	3.38
Q03963_E	Eif2ak2	Interferon-i	R.FTFQVLIDEK#EFPEAK#.G	28.21	18.93	1.49	0.67
Q03963_E	Eif2ak2	Interferon-i	K.IGDFGLATALENDGK#.S	68.26	40.14	1.70	0.59
Q03963_E	Eif2ak2	Interferon-i	K.IGQTM*YGTGSGVTK#.Q	34.65	20.53	1.69	0.59
Q03963_E	Eif2ak2	Interferon-i	K.IGQTMYGTGSGVTK#.Q	20.27	13.75	1.47	0.68
Q03963_E	Eif2ak2	Interferon-i	R.K#GDFSNDIFDNK#EK#.S	16.71	12.55	1.33	0.75
Q03963_E	Eif2ak2	Interferon-i	R.TGTLQYM*SPEQLFLK#.H	14.47	9.85	1.47	0.68
Q03963_E	Eif2ak2	Interferon-i	R.DLKPGNIFLVDER.H	15.87	38.34	0.41	2.42
Q03963_E	Eif2ak2	Interferon-i	K.DRPETSEILK.T	4.37	44.21	0.10	10.12
Q03963_E	Eif2ak2	Interferon-i	K.GDFSNDIFDNK#.E	13.67	5.75	2.38	0.42
Q03963_E	Eif2ak2	Interferon-i	K.IGDFGLATALENDGK#.S	89.05	44.88	1.98	0.50
Q03963_E	Eif2ak2	Interferon-i	K.IGQTM*YGTGSGVTK#.Q	41.32	21.96	1.88	0.53
Q03963_E	Eif2ak2	Interferon-i	K.LAVDILDNENK#.V	8.51	5.34	1.60	0.63
Q03963_E	Eif2ak2	Interferon-i	R.TGTLQYM*SPEQLFLK#.H	25.77	27.44	0.94	1.06
Q03963_E	Eif2ak2	Interferon-i	R.TGTLQYMSPEQLFLK#.H	12.10	10.25	1.18	0.85
Q03963_E	Eif2ak2	Interferon-i	K.VSPDDVQR.N	13.39	34.25	0.39	2.56
Q9QZ05_E	Eif2ak4	Eukaryotic	R.DASDNLAVQTLK#.G	8.73	5.26	1.66	0.60
Q9QZ05_E	Eif2ak4	Eukaryotic	R.DLK#PVNIFLDSDDHVK#.I	10.87	4.83	2.25	0.44
Q9QZ05_E	Eif2ak4	Eukaryotic	R.LEITSLTNQDYASK#.R	9.24	22.62	0.41	2.45
Q99LC8_EI	Eif2b1	Translation	K.ADLVIVGAEGVVENGGIINK#.I	8.80	3.72	2.36	0.42
Q99LC8_EI	Eif2b1	Translation	R.ANLTYAIK#.T	25.51	12.35	2.07	0.48
Q99LC8_EI	Eif2b1	Translation	R.FISLTSLEYSDYSK#.C	27.50	10.71	2.57	0.39
Q99LC8_EI	Eif2b1	Translation	R.FSVYITESQPDLSGK#.K	9.14	5.10	1.79	0.56
Q99LC8_EI	Eif2b1	Translation	R.FSVYITESQPDLSGK#K#.M	4.30	3.77	1.14	0.88
Q99LC8_EI	Eif2b1	Translation	R.VLEEAVAAK#.K	76.51	19.76	3.87	0.26
Q99LC8_EI	Eif2b1	Translation	R.FISLTSLEYSDYSK#.C	6.62	4.80	1.38	0.73
Q99LC8_EI	Eif2b1	Translation	K.ADLVIVGAEGVVENGGIINK#.I	4.36	1.86	2.35	0.43
Q99LC8_EI	Eif2b1	Translation	R.ANLTYAIK#.T	16.29	4.84	3.37	0.30
Q99LC8_EI	Eif2b1	Translation	K.AQNK#PFYVVAESFK#.F	13.17	6.19	2.13	0.47
Q99LC8_EI	Eif2b1	Translation	R.FISLTSLEYSDYSK#.C	13.17	8.26	1.59	0.63
Q99LC8_EI	Eif2b1	Translation	K.ADLVIVGAEGVVENGGIINK#.I	13.86	6.89	2.01	0.50
Q99LC8_EI	Eif2b1	Translation	R.ANLTYAIK#.T	21.46	8.59	2.50	0.40
Q99LC8_EI	Eif2b1	Translation	K.AQNK#PFYVVAESFK#.F	21.20	9.36	2.27	0.44
Q99LC8_EI	Eif2b1	Translation	R.FISLTSLEYSDYSK#.C	26.66	11.10	2.40	0.42
Q99LD9_EI	Eif2b2	Translation	K.FVAPEEVLPFTEGDILEK#.V	27.71	19.58	1.42	0.71
Q99LD9_EI	Eif2b2	Translation	R.M*TAAQPSETTVGNM*VR.R	3.93	10.40	0.38	2.64
Q99LD9_EI	Eif2b2	Translation	R.TVEAFLK#.E	26.84	21.64	1.24	0.81
Q99LD9_EI	Eif2b2	Translation	K.FVAPEEVLPFTEGDILEK#.V	8.32	4.90	1.70	0.59
Q99LD9_EI	Eif2b2	Translation	K.FVAPEEVLPFTEGDILEK#.V	13.96	8.94	1.56	0.64

Q3UKV0_Q	Eif2b3	Protein Eif2	R.DFIGVDSTGK#.R	10.56	6.19	1.71	0.59
Q3UKV0_Q	Eif2b3	Protein Eif2	R.K#GQESIEPVPGQK#.G	27.37	9.51	2.88	0.35
Q3UKV0_Q	Eif2b3	Protein Eif2	K.SLDIYSFIK#.K	46.58	36.09	1.29	0.77
Q3UKV0_Q	Eif2b3	Protein Eif2	R.VGFEEVIVVTTK#.D	29.09	10.37	2.80	0.36
Q3UKV0_Q	Eif2b3	Protein Eif2	K.HLIGADSLIGPDTQIGEK#.S	7.43	2.74	2.71	0.37
Q3UKV0_Q	Eif2b3	Protein Eif2	K.SLDIYSFIK#.K	14.24	7.74	1.84	0.54
Q3UKV0_Q	Eif2b3	Protein Eif2	R.VGFEEVIVVTTK#.D	8.91	4.20	2.12	0.47
Q3UKV0_Q	Eif2b3	Protein Eif2	R.AYDASLAM*LM*R@.K	18.49	60.44	0.31	3.27
Q3UKV0_Q	Eif2b3	Protein Eif2	K.GQESIEPVPGQK#.G	10.38	4.97	2.09	0.48
Q3UKV0_Q	Eif2b3	Protein Eif2	R.K#GQESIEPVPGQK#.G	9.00	2.21	4.07	0.25
Q3UKV0_Q	Eif2b3	Protein Eif2	K.SLDIYSFIK#.K	21.78	7.48	2.91	0.34
Q61749_EI	Eif2b4	Translation	R.ELPGPGSQLGGTAGEK#.L	11.61	9.49	1.22	0.82
Q61749_EI	Eif2b4	Translation	K.GADQEIGSAVSAAQR.Q	11.69	5.02	2.33	0.43
Q61749_EI	Eif2b4	Translation	K.IVLAAQAISR.F	8.36	26.91	0.31	3.22
Q61749_EI	Eif2b4	Translation	R.LGLQYSQGLISGSNAR.C	3.76	8.52	0.44	2.26
Q61749_EI	Eif2b4	Translation	R.VGTAQLALVAR.A	7.01	24.01	0.29	3.42
Q61749_EI	Eif2b4	Translation	K.GADQEIGSAVSAAQR.Q	8.33	2.45	3.40	0.29
Q61749_EI	Eif2b4	Translation	K.IVLAAQAISR.F	3.07	11.05	0.28	3.60
Q61749_EI	Eif2b4	Translation	R.VGTAQLALVAR.A	4.61	10.47	0.44	2.27
Q61749_EI	Eif2b4	Translation	K.GADQEIGSAVSAAQR.Q	3.22	8.71	0.37	2.71
Q61749_EI	Eif2b4	Translation	K.IVLAAQAISR.F	5.74	14.59	0.39	2.54
Q61749_EI	Eif2b4	Translation	R.VGTAQLALVAR.A	4.88	11.39	0.43	2.34
Q8CHW4_E	Eif2b5	Translation	R.DTTDEGQQLR.K	4.96	12.71	0.39	2.56
Q8CHW4_E	Eif2b5	Translation	R.FIQWLR.E	4.95	9.55	0.52	1.93
Q8CHW4_E	Eif2b5	Translation	K.GYNPAEVGLEGQGYLWK#.A	13.34	6.20	2.15	0.46
Q8CHW4_E	Eif2b5	Translation	K.HAYNISLK#.E	14.05	7.65	1.84	0.54
Q8CHW4_E	Eif2b5	Translation	K.LK#GYNPAEVGLEGQGYLWK#.A	12.11	6.19	1.96	0.51
Q8CHW4_E	Eif2b5	Translation	R.VFQNEVLGTLQR.G	10.95	20.57	0.53	1.88
Q8CHW4_E	Eif2b5	Translation	R.VFQNEVLGTLQR.G	8.16	15.06	0.54	1.84
Q6ZWX6_I	Eif2s1	Eukaryotic	R.ENAEVDGDDDAEEMEAK#.A	34.70	13.48	2.57	0.39
Q6ZWX6_I	Eif2s1	Eukaryotic	R.ENAEVDGDDDAEEM*EAK#.A	81.42	27.77	2.93	0.34
Q6ZWX6_I	Eif2s1	Eukaryotic	R.GVFNVQM*EPK#.V	64.04	26.52	2.41	0.41
Q6ZWX6_I	Eif2s1	Eukaryotic	R.GVFNVQMEPK#.V	31.77	11.76	2.70	0.37
Q6ZWX6_I	Eif2s1	Eukaryotic	K.GYIDLSK#.R	39.20	14.67	2.67	0.37
Q6ZWX6_I	Eif2s1	Eukaryotic	K.HAVSDPSILDSLDLNEDER.E	12.71	19.42	0.65	1.53
Q6ZWX6_I	Eif2s1	Eukaryotic	R.HVAEVLEYTKDEQLESLFQR.T	10.17	17.09	0.60	1.68
Q6ZWX6_I	Eif2s1	Eukaryotic	R.HVAEVLEYTKDEQLESLFQR.T	10.00	17.46	0.57	1.75
Q6ZWX6_I	Eif2s1	Eukaryotic	K.INLIAPPR.Y	22.38	51.91	0.43	2.32
Q6ZWX6_I	Eif2s1	Eukaryotic	R.LERENAEVDGDDDAEEM*EAK.A	6.53	12.16	0.54	1.86
Q6ZWX6_I	Eif2s1	Eukaryotic	K.RPGYGAYDAFK.H	12.07	20.06	0.60	1.66
Q6ZWX6_I	Eif2s1	Eukaryotic	R.TAWVFDDK#YK#.R	19.09	4.33	4.41	0.23
Q6ZWX6_I	Eif2s1	Eukaryotic	R.TEGLSVLNQAM*AVIK#.E	58.99	25.34	2.33	0.43
Q6ZWX6_I	Eif2s1	Eukaryotic	R.TEGLSVLNQAMAVIK#.E	72.68	26.48	2.74	0.36
Q6ZWX6_I	Eif2s1	Eukaryotic	K.VVTDTDETELAR.Q	71.79	137.07	0.52	1.91
Q6ZWX6_I	Eif2s1	Eukaryotic	R.YVMTTTTLER.T	19.88	28.01	0.71	1.41
Q6ZWX6_I	Eif2s1	Eukaryotic	R.TEGLSVLNQAMAVIK#.E	7.72	3.07	2.52	0.40
Q6ZWX6_I	Eif2s1	Eukaryotic	R.ENAEVDGDDDAEEM*EAK#.A	5.32	1.52	3.50	0.29
Q6ZWX6_I	Eif2s1	Eukaryotic	R.TEGLSVLNQAM*AVIK#.E	12.50	2.69	4.64	0.22
Q6ZWX6_I	Eif2s1	Eukaryotic	R.TEGLSVLNQAMAVIK#.E	15.79	4.43	3.56	0.28
Q6ZWX6_I	Eif2s1	Eukaryotic	K.VVTDTDETELAR.Q	16.04	12.88	1.25	0.80
Q99L45_IF	Eif2s2	Eukaryotic	R.DYTYEELLNR.V	32.37	55.42	0.58	1.71
Q99L45_IF	Eif2s2	Eukaryotic	R.EK#NPDM*VAGEK#.R	17.18	9.23	1.86	0.54
Q99L45_IF	Eif2s2	Eukaryotic	R.EK#NPDMVAGEK#.R	21.87	11.17	1.96	0.51
Q99L45_IF	Eif2s2	Eukaryotic	K.FPEEDEILEK#.D	88.80	38.88	2.28	0.44
Q99L45_IF	Eif2s2	Eukaryotic	K.IESDAQEPAEPEDDLDIM*LGNK#.K	25.42	10.38	2.45	0.41
Q99L45_IF	Eif2s2	Eukaryotic	K.IESDAQEPAEPEDDLDIMLGNK#.K	15.47	7.47	2.07	0.48
Q99L45_IF	Eif2s2	Eukaryotic	K.IESDAQEPAEPEDDLDIMLGNK#K#.K	6.81	2.29	2.97	0.34
Q99L45_IF	Eif2s2	Eukaryotic	K.IFDIDEAEEAIK#.D	31.51	15.62	2.02	0.50
Q99L45_IF	Eif2s2	Eukaryotic	K.IFDIDEAEEAIK#DVK#.I	164.93	64.71	2.55	0.39
Q99L45_IF	Eif2s2	Eukaryotic	K.K#IFDIDEAEEAIK#.D	12.34	4.33	2.85	0.35
Q99L45_IF	Eif2s2	Eukaryotic	K.KIFDIDEAEEAIKDVK.I	107.33	47.29	2.27	0.44
Q99L45_IF	Eif2s2	Eukaryotic	R.K#K#DASDDLDDLNFFNQK#.K	31.97	11.99	2.67	0.38
Q99L45_IF	Eif2s2	Eukaryotic	K.K#K#PFMLDEEGDAQTEETQPSETK#.E	2.24	1.51	1.48	0.67
Q99L45_IF	Eif2s2	Eukaryotic	R.SPDTILQK#.D	175.37	72.48	2.42	0.41
Q99L45_IF	Eif2s2	Eukaryotic	K.TGFQAVTGK#.R	250.27	84.84	2.95	0.34
Q99L45_IF	Eif2s2	Eukaryotic	R.VFNIM*R.E	24.39	50.02	0.49	2.05
Q99L45_IF	Eif2s2	Eukaryotic	R.DYTYEELLNR.V	3.12	5.71	0.55	1.83
Q99L45_IF	Eif2s2	Eukaryotic	K.TGFQAVTGK#.R	17.62	7.49	2.35	0.43
Q99L45_IF	Eif2s2	Eukaryotic	K.DASDDLDDLNFFNQK#.K	7.82	2.72	2.87	0.35
Q9Z0N1_IF	Eif2s3x	Eukaryotic	K.GGVAGGSILK#.G	19.06	7.60	2.51	0.40
Q9Z0N1_IF	Eif2s3x	Eukaryotic	R.GVTIK#PTVDDD.-	45.96	29.08	1.58	0.63
Q9Z0N1_IF	Eif2s3x	Eukaryotic	K.HILILQNK#.I	135.38	43.47	3.11	0.32
Q9Z0N1_IF	Eif2s3x	Eukaryotic	R.QATINIGTIGHVAHGK#.S	47.14	21.98	2.15	0.47
Q9Z0N1_IF	Eif2s3x	Eukaryotic	R.QDLATLDVTK#.L	120.20	50.15	2.40	0.42
Q9Z0N1_IF	Eif2s3x	Eukaryotic	R.RGVTIKPTVDDD.-	7.22	17.23	0.42	2.39
Q9Z0N1_IF	Eif2s3x	Eukaryotic	R.GVTIK#PTVDDD.-	31.47	9.52	3.30	0.30
Q9Z0N1_IF	Eif2s3x	Eukaryotic	R.QDLATLDVTK#.L	27.03	9.97	2.71	0.37
Q9Z0N1_IF	Eif2s3x	Eukaryotic	R.GVTIK#PTVDDD.-	35.12	15.19	2.31	0.43
Q9Z0N1_IF	Eif2s3x	Eukaryotic	K.HILILQNK#.I	55.70	15.83	3.52	0.28
Q9Z0N1_IF	Eif2s3x	Eukaryotic	K.IVSLFAEHNDLQYAAPGGLIGVGTK#.I	10.40	3.26	3.19	0.31
Q9Z0N1_IF	Eif2s3x	Eukaryotic	R.QDLATLDVTK#.L	60.84	16.29	3.74	0.27
Q9Z0N1_IF	Eif2s3x	Eukaryotic	K.VGQEIEVRPGIVSK.D	26.59	36.73	0.72	1.38
Q9Z0N2_IF	Eif2s3y	Eukaryotic	R.GVTIK#PTIDDE.-	16.02	5.49	2.92	0.34
P23116_EI	Eif3a	Eukaryotic	K.AFKDIDIEDLEELDPDFIM*AK.Q	34.17	9.87	3.46	0.29
P23116_EI	Eif3a	Eukaryotic	K.AFKDIDIEDLEELDPDFIMAK.Q	24.71	8.65	2.86	0.35
P23116_EI	Eif3a	Eukaryotic	R.ANEFLEVGK#.K	50.49	15.87	3.18	0.31
P23116_EI	Eif3a	Eukaryotic	R.ANEFLEVGK#K#.Q	18.55	8.62	2.15	0.46
P23116_EI	Eif3a	Eukaryotic	K.DIDIEDLEELDPDFIMAK#.Q	15.24	5.34	2.85	0.35
P23116_EI	Eif3a	Eukaryotic	K.EGLYQYK#.N	47.83	21.90	2.18	0.46
P23116_EI	Eif3a	Eukaryotic	R.EQPEKEPELQQYVPQLQNNTILR.L	9.86	20.65	0.48	2.10
P23116_EI	Eif3a	Eukaryotic	R.FSVLQYVVPEVK#.D	94.74	35.71	2.65	0.38
P23116_EI	Eif3a	Eukaryotic	R.IGLINDM*VR.F	18.75	19.39	0.97	1.03
P23116_EI	Eif3a	Eukaryotic	R.LEEIPLIK#.S	40.54	13.41	3.02	0.33
P23116_EI	Eif3a	Eukaryotic	R.LESLNIQR.E	19.75	33.88	0.58	1.72
P23116_EI	Eif3a	Eukaryotic	R.LLDM*DGIIVEK#.Q	54.07	22.87	2.36	0.42
P23116_EI	Eif3a	Eukaryotic	R.LLDMDGIIVEK#.Q	26.66	9.89	2.70	0.37
P23116_EI	Eif3a	Eukaryotic	R.LLLTPWVK#.F	80.37	32.55	2.47	0.41
P23116_EI	Eif3a	Eukaryotic	R.LVQLDSAISM*ELWQEAFK#.A	35.51	12.07	2.94	0.34
P23116_EI	Eif3a	Eukaryotic	R.LYHDIAQQAFK#.F	39.98	18.14	2.20	0.45
P23116_EI	Eif3a	Eukaryotic	R.NQLTAM*SSVLAK#.A	52.55	18.58	2.83	0.35
P23116_EI	Eif3a	Eukaryotic	K.QPALDVLYDVM*K#.S	7.26	2.66	2.73	0.37
P23116_EI	Eif3a	Eukaryotic	K.RLEEIPLIK.S	10.61	20.41	0.52	1.92
P23116_EI	Eif3a	Eukaryotic	K.SLEDVVR.A	18.09	25.65	0.71	1.42

P23116_EI	Eif3a	Eukaryotic	R.TLSFGSDLNYATR.E	16.32	26.69	0.61	1.64
P23116_EI	Eif3a	Eukaryotic	R.VKDM*DLWEQQEEER.I	9.31	19.05	0.49	2.05
P23116_EI	Eif3a	Eukaryotic	R.VKDMDLWEQQEEER.I	4.72	8.14	0.58	1.72
P23116_EI	Eif3a	Eukaryotic	R.VLLATLSIPITPER.T	20.15	42.87	0.47	2.13
P23116_EI	Eif3a	Eukaryotic	K.AFK#DIDIEDLEELDPDFIM*AK#.Q	89.45	36.68	2.44	0.41
P23116_EI	Eif3a	Eukaryotic	K.AFKDIDIEDLEELDPDFIMAK.Q	27.16	9.44	2.88	0.35
P23116_EI	Eif3a	Eukaryotic	R.ANEFLEVGK#.K	117.40	37.63	3.12	0.32
P23116_EI	Eif3a	Eukaryotic	R.ANEFLEVGKK.Q	26.04	9.89	2.63	0.38
P23116_EI	Eif3a	Eukaryotic	K.DIDIEDLEELDPDFIM*AK#.Q	73.11	26.12	2.80	0.36
P23116_EI	Eif3a	Eukaryotic	K.DIDIEDLEELDPDFIMAK#.Q	22.81	12.38	1.84	0.54
P23116_EI	Eif3a	Eukaryotic	R.EQPEKEPELQQYVPQLQNNTILR.L	27.25	39.57	0.69	1.45
P23116_EI	Eif3a	Eukaryotic	R.ESSLRPDDDRIPR.R	7.31	41.91	0.17	5.73
P23116_EI	Eif3a	Eukaryotic	K.FLWESYR.Q	4.89	10.64	0.46	2.18
P23116_EI	Eif3a	Eukaryotic	R.FSVLQYVVPEVK#.D	176.33	64.87	2.72	0.37
P23116_EI	Eif3a	Eukaryotic	R.IGLINDM*VR.F	42.20	38.81	1.09	0.92
P23116_EI	Eif3a	Eukaryotic	R.IGLINDMVR.F	12.70	21.21	0.60	1.67
P23116_EI	Eif3a	Eukaryotic	K.IHEPIMLK#.Y	11.81	3.25	3.64	0.27
P23116_EI	Eif3a	Eukaryotic	R.ILQEHEQIK#.K	257.89	70.65	3.65	0.27
P23116_EI	Eif3a	Eukaryotic	R.ITTM*QLER.E	30.02	52.88	0.57	1.76
P23116_EI	Eif3a	Eukaryotic	R.KGPEADSEWR.R	9.39	19.35	0.49	2.06
P23116_EI	Eif3a	Eukaryotic	K.K#QPALDVLYDVM*K#.S	32.85	15.69	2.09	0.48
P23116_EI	Eif3a	Eukaryotic	R.LATLLGLQAPPTR.I	19.04	28.47	0.67	1.50
P23116_EI	Eif3a	Eukaryotic	R.LESLNIQR.E	44.40	77.36	0.57	1.74
P23116_EI	Eif3a	Eukaryotic	R.LLDM*DGIIVEK#.Q	92.41	89.68	1.03	0.97
P23116_EI	Eif3a	Eukaryotic	R.LLDMDGIIVEK#.Q	48.67	16.31	2.98	0.34
P23116_EI	Eif3a	Eukaryotic	R.LLLTPWVK#.F	111.75	47.13	2.37	0.42
P23116_EI	Eif3a	Eukaryotic	R.LVQLDSAISM*ELWQEAFK#.A	112.49	46.62	2.41	0.41
P23116_EI	Eif3a	Eukaryotic	R.LYHDIAQQAFK#.F	76.21	29.91	2.55	0.39
P23116_EI	Eif3a	Eukaryotic	K.NLTQEEM*QR.M	26.85	50.88	0.53	1.90
P23116_EI	Eif3a	Eukaryotic	R.NQLTAM*SSVLAK#.A	113.04	46.06	2.45	0.41
P23116_EI	Eif3a	Eukaryotic	R.NQLTAMSSVLAK#.A	66.85	25.43	2.63	0.38
P23116_EI	Eif3a	Eukaryotic	K.QPALDVLYDVM*K#.S	12.23	3.74	3.27	0.31
P23116_EI	Eif3a	Eukaryotic	R.QSVYEEK#.L	28.83	10.17	2.83	0.35
P23116_EI	Eif3a	Eukaryotic	R.RVPPPALSR.D	1.58	17.21	0.09	10.92
P23116_EI	Eif3a	Eukaryotic	K.SGNALFHASTLHR.L	19.35	29.62	0.65	1.53
P23116_EI	Eif3a	Eukaryotic	K.SLEDVVR.A	28.37	44.50	0.64	1.57
P23116_EI	Eif3a	Eukaryotic	R.TLSFGSDLNYATR.E	39.77	66.76	0.60	1.68
P23116_EI	Eif3a	Eukaryotic	R.VKDM*DLWEQQEEER.I	15.96	22.78	0.70	1.43
P23116_EI	Eif3a	Eukaryotic	R.VLLATLSIPITPER.T	49.92	106.64	0.47	2.14
P23116_EI	Eif3a	Eukaryotic	K.VSTVFWK#.S	110.83	43.92	2.52	0.40
Q8JZQ9_EI	Eif3b	Eukaryotic	K.AEAVGEQAR.G	10.13	20.81	0.49	2.05
Q8JZQ9_EI	Eif3b	Eukaryotic	R.AKPAAQSEEETATSPAASPTPQSAER.S	23.99	41.69	0.58	1.74
Q8JZQ9_EI	Eif3b	Eukaryotic	R.DQYSVIFESGDR.T	9.69	14.85	0.65	1.53
Q8JZQ9_EI	Eif3b	Eukaryotic	K.DRPQEADGIDSVIVVDNVPQVGPDRLEK.L	2.13	12.04	0.18	5.65
Q8JZQ9_EI	Eif3b	Eukaryotic	R.GHPSAGAEEEGGSDGSAAEAEPR.A	41.60	99.85	0.42	2.40
Q8JZQ9_EI	Eif3b	Eukaryotic	R.GIALWGGDK#.F	46.90	22.84	2.05	0.49
Q8JZQ9_EI	Eif3b	Eukaryotic	R.GIALWGGDKFK.Q	58.35	25.00	2.33	0.43
Q8JZQ9_EI	Eif3b	Eukaryotic	K.GTQGVVTNFEIFR.M	67.09	129.63	0.52	1.93
Q8JZQ9_EI	Eif3b	Eukaryotic	K.GTYLATFHQR.G	21.99	43.28	0.51	1.97
Q8JZQ9_EI	Eif3b	Eukaryotic	K.GYIFLEYASPAHAVDAVK#.N	240.85	99.42	2.42	0.41
Q8JZQ9_EI	Eif3b	Eukaryotic	K.IINDYYPEEDGK#.T	38.89	20.20	1.93	0.52
Q8JZQ9_EI	Eif3b	Eukaryotic	K.M*AQELYM*K#.Q	44.20	19.86	2.23	0.45
Q8JZQ9_EI	Eif3b	Eukaryotic	R.M*TLDTLSIYETPSM*GLLDK#.K	3.91	2.62	1.49	0.67
Q8JZQ9_EI	Eif3b	Eukaryotic	R.MTLDTLSIYETPSM*GLLDK#.K	3.99	2.56	1.56	0.64
Q8JZQ9_EI	Eif3b	Eukaryotic	R.MTLDTLSIYETPSM*GLLDK#K#.S	49.57	18.27	2.71	0.37
Q8JZQ9_EI	Eif3b	Eukaryotic	R.M*TLDTLSIYETPSMGLLDK#K#.S	21.51	9.70	2.22	0.45
Q8JZQ9_EI	Eif3b	Eukaryotic	R.MTLDTLSIYETPSMGLLDK#K#.S	30.23	9.46	3.19	0.31
Q8JZQ9_EI	Eif3b	Eukaryotic	K.NADGYK#LDK#.Q	57.22	22.71	2.52	0.40
Q8JZQ9_EI	Eif3b	Eukaryotic	K.QQANTIFWSPQGQFVVLAGLR.S	6.31	17.28	0.37	2.74
Q8JZQ9_EI	Eif3b	Eukaryotic	K.QVPVDVVEM*K#.E	48.75	22.43	2.17	0.46
Q8JZQ9_EI	Eif3b	Eukaryotic	K.QVPVDVVEMK#.E	38.51	1.22	31.44	0.03
Q8JZQ9_EI	Eif3b	Eukaryotic	R.SPSQEPSAPGK#.A	84.17	34.91	2.41	0.41
Q8JZQ9_EI	Eif3b	Eukaryotic	R.SPSQEPSAPGKAEAVGEQAR.G	22.61	49.30	0.46	2.18
Q8JZQ9_EI	Eif3b	Eukaryotic	R.TSIFWNDVKDPVSIEER.A	37.91	68.59	0.55	1.81
Q8JZQ9_EI	Eif3b	Eukaryotic	K.VDNAYWLWTFQGR.L	25.34	40.18	0.63	1.59
Q8JZQ9_EI	Eif3b	Eukaryotic	K.VDNAYWLWTFQGR.L	8.20	12.14	0.68	1.48
Q8JZQ9_EI	Eif3b	Eukaryotic	R.VNLFTDFDK#.Y	43.59	21.17	2.06	0.49
Q8JZQ9_EI	Eif3b	Eukaryotic	R.VNLFTDFDK#YMTISDEWDIPEK#QPFK#.D	33.12	8.85	3.74	0.27
Q8JZQ9_EI	Eif3b	Eukaryotic	R.VTLM*QLPTR.Q	28.63	53.76	0.53	1.88
Q8JZQ9_EI	Eif3b	Eukaryotic	R.WTETYVR.W	49.10	90.41	0.54	1.84
Q8JZQ9_EI	Eif3b	Eukaryotic	R.AKPAAQSEEETATSPAASPTPQSAER.S	18.45	13.25	1.39	0.72
Q8JZQ9_EI	Eif3b	Eukaryotic	K.DRPQEADGIDSVIVVDNVPQVGPDR.L	2.94	9.83	0.30	3.35
Q8JZQ9_EI	Eif3b	Eukaryotic	R.GHPSAGAEEEGGSDGSAAEAEPR.A	8.10	29.45	0.27	3.64
Q8JZQ9_EI	Eif3b	Eukaryotic	K.GYIFLEYASPAHAVDAVK#.N	39.74	27.38	1.45	0.69
Q8JZQ9_EI	Eif3b	Eukaryotic	K.IINDYYPEEDGK#.T	9.73	5.41	1.80	0.56
Q8JZQ9_EI	Eif3b	Eukaryotic	R.SPSQEPSAPGK#.A	16.58	11.20	1.48	0.68
Q8JZQ9_EI	Eif3b	Eukaryotic	R.TSIFWNDVKDPVSIEER.A	6.84	13.37	0.51	1.95
Q8R1B4_EI	Eif3c	Eukaryotic	R.AKELLGQGLLLR.S	14.73	27.93	0.53	1.90
Q8R1B4_EI	Eif3c	Eukaryotic	K.DAHNALLDIQSSGR.A	5.15	9.09	0.57	1.76
Q8R1B4_EI	Eif3c	Eukaryotic	R.DFESHITNYK#.Q	65.43	25.10	2.61	0.38
Q8R1B4_EI	Eif3c	Eukaryotic	K.ELLGQGLLLR@.S	12.13	19.02	0.64	1.57
Q8R1B4_EI	Eif3c	Eukaryotic	R.FEELTNLIR.T	19.24	35.25	0.55	1.83
Q8R1B4_EI	Eif3c	Eukaryotic	K.GTEITHAVVIK#.K	32.12	14.96	2.15	0.47
Q8R1B4_EI	Eif3c	Eukaryotic	K.GTEITHAVVIK#K#.L	47.07	16.09	2.93	0.34
Q8R1B4_EI	Eif3c	Eukaryotic	K.KLNEILQVR.G	6.43	9.27	0.69	1.44
Q8R1B4_EI	Eif3c	Eukaryotic	K.LGSLVENNER.V	44.31	54.48	0.81	1.23
Q8R1B4_EI	Eif3c	Eukaryotic	K.LNEILQVR.G	12.99	26.24	0.50	2.02
Q8R1B4_EI	Eif3c	Eukaryotic	K.SEQDQAENEGEDSAVLM*ER.L	7.71	14.90	0.52	1.93
Q8R1B4_EI	Eif3c	Eukaryotic	K.SIVDKEGVPR.F	9.81	15.96	0.61	1.63
Q8R1B4_EI	Eif3c	Eukaryotic	R.TEPTAQQNLALQLAEK#.L	81.36	28.72	2.83	0.35
Q8R1B4_EI	Eif3c	Eukaryotic	R.AKELLGQGLLLR.S	23.22	40.35	0.58	1.74
Q8R1B4_EI	Eif3c	Eukaryotic	R.DFESHITNYK#.Q	94.16	25.49	3.69	0.27
Q8R1B4_EI	Eif3c	Eukaryotic	K.ELLGQGLLLR.S	18.41	28.48	0.65	1.55
Q8R1B4_EI	Eif3c	Eukaryotic	R.FEELTNLIR.T	30.52	45.70	0.67	1.50
Q8R1B4_EI	Eif3c	Eukaryotic	R.FFTTGSDSESESSLSGEELVTK#PVSGNYGK#.Q	7.99	2.45	3.25	0.31
Q8R1B4_EI	Eif3c	Eukaryotic	K.GTEITHAVVIK#.K	63.87	25.84	2.47	0.40
Q8R1B4_EI	Eif3c	Eukaryotic	R.ILHTYYK#.F	30.86	14.59	2.12	0.47
Q8R1B4_EI	Eif3c	Eukaryotic	R.LDEEEEDNEGGEWER.V	7.04	12.30	0.57	1.75
Q8R1B4_EI	Eif3c	Eukaryotic	K.M*IINEELM*ASLDQPTQTVVM*HR.T	7.99	2.88	2.77	0.36
Q8R1B4_EI	Eif3c	Eukaryotic	K.RLDEEEEDNEGGEWER.V	4.25	32.43	0.13	7.63
Q8R1B4_EI	Eif3c	Eukaryotic	K.SEQDQAENEGEDSAVLM*ER.L	7.11	16.32	0.44	2.30
Q8R1B4_EI	Eif3c	Eukaryotic	K.SIVDKEGVPR.F	10.87	26.04	0.42	2.39
Q8R1B4_EI	Eif3c	Eukaryotic	R.TEPTAQQNLALQLAEK#.L	123.36	47.68	2.59	0.39

Q8R1B4_EI	Eif3c	Eukaryotic	K.VWDLFPEADK#.V	15.44	6.08	2.54	0.39
O70194_EI	Eif3d	Eukaryotic	R.DM*PYQPFSK#.G	38.96	19.35	2.01	0.50
O70194_EI	Eif3d	Eukaryotic	R.DMPYQPFSK#.G	11.35	5.57	2.04	0.49
O70194_EI	Eif3d	Eukaryotic	R.GAVIATELK#.N	94.61	52.32	1.81	0.55
O70194_EI	Eif3d	Eukaryotic	R.IFHTVTTTDDPVIR.K	3.88	10.67	0.36	2.75
O70194_EI	Eif3d	Eukaryotic	R.NM*VQFNLQTLPK#.S	54.21	29.19	1.86	0.54
O70194_EI	Eif3d	Eukaryotic	R.SDWEVK#EEMDFPQLMK#.M	6.23	4.13	1.51	0.66
O70194_EI	Eif3d	Eukaryotic	R.SVYSWDIVVQR.V	25.67	36.65	0.70	1.43
O70194_EI	Eif3d	Eukaryotic	K.TLNEWDSR.H	15.50	29.04	0.53	1.87
O70194_EI	Eif3d	Eukaryotic	K.VADWTGATYQDK#.R	23.04	13.61	1.69	0.59
O70194_EI	Eif3d	Eukaryotic	K.YLILK#DPNK#.Q	31.41	11.25	2.79	0.36
O70194_EI	Eif3d	Eukaryotic	R.YNFPNPNPFVEDDM*DKNEIASVAYR.Y	6.52	18.34	0.36	2.81
O70194_EI	Eif3d	Eukaryotic	K.YSSQFGGGSQYAYFHEEDETSFQLVDTAR.T	5.68	8.02	0.71	1.41
O70194_EI	Eif3d	Eukaryotic	R.DNSDFDLLTVSETANEPPQDEGNSFNSPR.N	6.89	11.55	0.60	1.68
O70194_EI	Eif3d	Eukaryotic	R.GAVIATELK#.N	79.06	34.88	2.27	0.44
O70194_EI	Eif3d	Eukaryotic	R.IFHTVTTTDDPVIR.K	19.37	43.08	0.45	2.22
O70194_EI	Eif3d	Eukaryotic	R.NM*VQFNLQTLPK#.S	39.98	16.23	2.46	0.41
O70194_EI	Eif3d	Eukaryotic	R.SDWEVKEEM*DFPQLM*K.M	19.32	7.47	2.59	0.39
O70194_EI	Eif3d	Eukaryotic	K.TLNEWDSR.H	14.78	19.98	0.74	1.35
O70194_EI	Eif3d	Eukaryotic	K.VADWTGATYQDK#.R	13.57	6.20	2.19	0.46
O70194_EI	Eif3d	Eukaryotic	K.YLILK#DPNK#.Q	20.38	10.45	1.95	0.51
O70194_EI	Eif3d	Eukaryotic	K.YSSQFGGGSQYAYFHEEDETSFQLVDTAR.T	4.23	9.30	0.46	2.20
O70194_EI	Eif3d	Eukaryotic	R.DNSDFDLLTVSETANEPPQDEGNSFNSPR.N	9.97	16.37	0.61	1.64
O70194_EI	Eif3d	Eukaryotic	R.GAVIATELK#.N	76.52	33.19	2.31	0.43
O70194_EI	Eif3d	Eukaryotic	K.LGDDIDLIVR.C	12.07	22.67	0.53	1.88
O70194_EI	Eif3d	Eukaryotic	R.NM*VQFNLQTLPK#.S	58.06	22.30	2.60	0.38
O70194_EI	Eif3d	Eukaryotic	R.SVYSWDIVVQR.V	12.08	17.86	0.68	1.48
O70194_EI	Eif3d	Eukaryotic	K.TLNEWDSR.H	8.16	20.40	0.40	2.50
O70194_EI	Eif3d	Eukaryotic	K.VADWTGATYQDK#.R	19.59	11.63	1.68	0.59
P60229_EI	Eif3e	Eukaryotic	K.ETIDNNSVSSPLQSLQQR.T	2.08	4.41	0.47	2.12
P60229_EI	Eif3e	Eukaryotic	K.LASEILM*QNWDAAM*EDLTR.L	2.12	3.72	0.57	1.75
P60229_EI	Eif3e	Eukaryotic	K.LASEILM*QNWDAAMEDLTR.L	4.40	6.35	0.69	1.44
P60229_EI	Eif3e	Eukaryotic	K.LDLLSDTNM*VDFAM*DVYK#.N	14.86	12.11	1.23	0.81
P60229_EI	Eif3e	Eukaryotic	K.LDLLSDTNM*VDFAMDVYK#.N	4.85	1.78	2.73	0.37
P60229_EI	Eif3e	Eukaryotic	K.LDLLSDTNMVDFAM*DVYK#.N	21.13	5.58	3.79	0.26
P60229_EI	Eif3e	Eukaryotic	K.LGHVVM*GNNAVSPYQQVIEK#.T	78.34	27.70	2.83	0.35
P60229_EI	Eif3e	Eukaryotic	K.LGHVVMGNNAVSPYQQVIEK#.T	5.50	2.33	2.36	0.42
P60229_EI	Eif3e	Eukaryotic	K.M*FEDPETTR.Q	12.05	16.82	0.72	1.40
P60229_EI	Eif3e	Eukaryotic	R.M*LFDYLADK#.H	45.32	18.35	2.47	0.40
P60229_EI	Eif3e	Eukaryotic	R.MLFDYLADK#.H	28.44	9.85	2.89	0.35
P60229_EI	Eif3e	Eukaryotic	R.NALSSLWGK#.L	53.38	22.47	2.38	0.42
P60229_EI	Eif3e	Eukaryotic	K.QLQAETEPIVK#.M	125.04	55.03	2.27	0.44
P60229_EI	Eif3e	Eukaryotic	R.SQM*LAM*NIEK#.K	40.68	18.22	2.23	0.45
P60229_EI	Eif3e	Eukaryotic	R.SQMLAMNIEK#.K	26.07	11.73	2.22	0.45
P60229_EI	Eif3e	Eukaryotic	R.TTVVAQLK#.Q	87.38	28.67	3.05	0.33
P60229_EI	Eif3e	Eukaryotic	R.VLVPATDR.N	28.31	70.54	0.40	2.49
P60229_EI	Eif3e	Eukaryotic	R.WIVNLIR.N	12.04	20.66	0.58	1.72
P60229_EI	Eif3e	Eukaryotic	R.YLTTAVITNK#.D	122.55	49.80	2.46	0.41
P60229_EI	Eif3e	Eukaryotic	K.LDLLSDTNM*VDFAM*DVYK#.N	11.77	4.39	2.68	0.37
P60229_EI	Eif3e	Eukaryotic	K.LGHVVM*GNNAVSPYQQVIEK#.T	35.22	13.01	2.71	0.37
P60229_EI	Eif3e	Eukaryotic	K.LGHVVMGNNAVSPYQQVIEK#.T	17.26	6.62	2.61	0.38
P60229_EI	Eif3e	Eukaryotic	R.LKETIDNNSVSSPLQSLQQR.T	11.62	13.87	0.84	1.19
P60229_EI	Eif3e	Eukaryotic	R.M*LFDYLADK#.H	23.94	11.29	2.12	0.47
P60229_EI	Eif3e	Eukaryotic	R.NALSSLWGK#.L	37.77	16.85	2.24	0.45
P60229_EI	Eif3e	Eukaryotic	K.QLQAETEPIVK#.M	59.59	25.62	2.33	0.43
P60229_EI	Eif3e	Eukaryotic	R.SEAPNWATQDSGFY.-	18.63	18.63	1.00	1.00
P60229_EI	Eif3e	Eukaryotic	R.SQM*LAM*NIEK#.K	28.90	13.05	2.21	0.45
P60229_EI	Eif3e	Eukaryotic	R.TTVVAQLK#.Q	81.66	48.75	1.68	0.60
P60229_EI	Eif3e	Eukaryotic	R.YLTTAVITNK#.D	76.72	27.71	2.77	0.36
P60229_EI	Eif3e	Eukaryotic	K.LGHVVM*GNNAVSPYQQVIEK#.T	64.38	21.40	3.01	0.33
P60229_EI	Eif3e	Eukaryotic	R.LKETIDNNSVSSPLQSLQQR.T	15.55	27.24	0.57	1.75
P60229_EI	Eif3e	Eukaryotic	K.M*FEDPETTR.Q	10.59	13.99	0.76	1.32
P60229_EI	Eif3e	Eukaryotic	R.M*LFDYLADK#.H	39.94	14.12	2.83	0.35
P60229_EI	Eif3e	Eukaryotic	R.NALSSLWGK#.L	47.42	16.66	2.85	0.35
P60229_EI	Eif3e	Eukaryotic	K.QLQAETEPIVK#.M	81.29	28.85	2.82	0.35
P60229_EI	Eif3e	Eukaryotic	R.SEAPNWATQDSGFY.-	21.12	21.12	1.00	1.00
P60229_EI	Eif3e	Eukaryotic	R.SQM*LAM*NIEK#.K	45.78	17.85	2.57	0.39
P60229_EI	Eif3e	Eukaryotic	R.WIVNLIR.N	7.78	16.34	0.48	2.10
P60229_EI	Eif3e	Eukaryotic	R.YLTTAVITNK#.D	103.46	41.46	2.50	0.40
Q9DCH4_E	Eif3f	Eukaryotic	K.AYVSTLM*GVPGR.T	28.64	46.18	0.62	1.61
Q9DCH4_E	Eif3f	Eukaryotic	K.AYVSTLMGVPGR.T	12.04	18.28	0.66	1.52
Q9DCH4_E	Eif3f	Eukaryotic	R.EAPNPIHLTVDTGLQHGR.M	1.35	2.88	0.47	2.13
Q9DCH4_E	Eif3f	Eukaryotic	R.FLM*SLVNQVPK#.I	79.39	31.92	2.49	0.40
Q9DCH4_E	Eif3f	Eukaryotic	R.IGVDLIM*K#.T	88.20	28.36	3.11	0.32
Q9DCH4_E	Eif3f	Eukaryotic	R.IGVDLIMK#.T	63.77	18.62	3.43	0.29
Q9DCH4_E	Eif3f	Eukaryotic	R.LHPVILASIVDSYER.R	32.82	48.35	0.68	1.47
Q9DCH4_E	Eif3f	Eukaryotic	K.NMYELHK#.K	40.48	13.73	2.95	0.34
Q9DCH4_E	Eif3f	Eukaryotic	R.TM*GVM*FTPLTVK#.Y	68.08	36.26	1.88	0.53
Q9DCH4_E	Eif3f	Eukaryotic	R.TMGVM*FTPLTVK#.Y	32.94	11.53	2.86	0.35
Q9DCH4_E	Eif3f	Eukaryotic	R.TM*GVMFTPLTVK#.Y	32.94	11.53	2.86	0.35
Q9DCH4_E	Eif3f	Eukaryotic	R.TMGVMFTPLTVK#.Y	27.87	7.00	3.98	0.25
Q9DCH4_E	Eif3f	Eukaryotic	R.VIGLSSDLQQVGGASAR.I	31.61	52.13	0.61	1.65
Q9DCH4_E	Eif3f	Eukaryotic	R.VIGTLLGTVDK#.H	125.30	48.34	2.59	0.39
Q9DCH4_E	Eif3f	Eukaryotic	K.VSADNTVGR.F	28.23	37.84	0.75	1.34
Q9DCH4_E	Eif3f	Eukaryotic	R.FLM*SLVNQVPK#.I	10.93	4.47	2.45	0.41
Q9DCH4_E	Eif3f	Eukaryotic	R.FLMSLVNQVPK#.I	12.42	6.15	2.02	0.50
Q9DCH4_E	Eif3f	Eukaryotic	R.VIGTLLGTVDK#.H	31.65	9.57	3.31	0.30
Q9DCH4_E	Eif3f	Eukaryotic	R.VIGTLLGTVDK#.H	29.67	10.98	2.70	0.37
Q9Z1D1_EI	Eif3g	Eukaryotic	R.AIAGVSGFGYDHLILNVEWAK#PSTN.-	23.06	5.03	4.59	0.22
Q9Z1D1_EI	Eif3g	Eukaryotic	K.EK#LPGELEPVQAAQSK#.T	115.13	47.18	2.44	0.41
Q9Z1D1_EI	Eif3g	Eukaryotic	K.ELAEQLGLSTGEK#.E	124.48	47.93	2.60	0.39
Q9Z1D1_EI	Eif3g	Eukaryotic	K.ELAEQLGLSTGEK#EK#LPGELEPVQAAQSK#.T	14.90	5.14	2.90	0.34
Q9Z1D1_EI	Eif3g	Eukaryotic	K.FGNSEFDPPGPNVATTTVSDDVSM*TFITSK#.E	8.86	3.82	2.32	0.43
Q9Z1D1_EI	Eif3g	Eukaryotic	K.FGNSEFDPPGPNVATTTVSDDVSMTFITSK#.E	18.12	7.69	2.36	0.42
Q9Z1D1_EI	Eif3g	Eukaryotic	K.GIPLPTGDTSPEPELLPGDPLPPPK#.E	25.66	19.21	1.34	0.75
Q9Z1D1_EI	Eif3g	Eukaryotic	K.GIPLPTGDTSPEPELLPGDPLPPPK.E	3.99	2.57	1.55	0.64
Q9Z1D1_EI	Eif3g	Eukaryotic	K.GIPLPTGDTSPEPELLPGDPLPPPKEVINGNIK.T	5.46	4.16	1.31	0.76
Q9Z1D1_EI	Eif3g	Eukaryotic	K.KFGNSEFDPPGPNVATTTVSDDVSMTFITSK.E	5.17	1.95	2.65	0.38
Q9Z1D1_EI	Eif3g	Eukaryotic	K.LPGELEPVQAAQSK#.T	74.01	37.74	1.96	0.51
Q9Z1D1_EI	Eif3g	Eukaryotic	K.TVTEYK#IEEDGK#K#.F	38.50	13.52	2.85	0.35
Q9Z1D1_EI	Eif3g	Eukaryotic	R.VTNLSEDTR.E	85.78	138.74	0.62	1.62
Q91WK2_E	Eif3h	Eukaryotic	K.ASITFEHM*FEEVPIVIK#.N	108.19	46.30	2.34	0.43
Q91WK2_E	Eif3h	Eukaryotic	K.ASITFEHMFEEVPIVIK#.N	153.55	54.52	2.82	0.36

Q91WK2_E	Eif3h	Eukaryotic	K.DFSPEALK#K#.A	28.23	10.05	2.81	0.36
Q91WK2_E	Eif3h	Eukaryotic	K.EGTGSTATSSGSAGGAVGK#.G	145.74	48.71	2.99	0.33
Q91WK2_E	Eif3h	Eukaryotic	K.HELLSLASSNHLGK#.S	9.36	6.91	1.35	0.74
Q91WK2_E	Eif3h	Eukaryotic	K.HYQEEGQGTEVVQGVLLGLVVEDR.L	13.76	26.24	0.52	1.91
Q91WK2_E	Eif3h	Eukaryotic	R.K#EGTGSTATSSGSAGGAVGK#.G	16.53	9.74	1.70	0.59
Q91WK2_E	Eif3h	Eukaryotic	K.LFM*AQALQEYNN.-	60.17	60.17	1.00	1.00
Q91WK2_E	Eif3h	Eukaryotic	K.LFMAQALQEYNN.-	80.71	80.71	1.00	1.00
Q91WK2_E	Eif3h	Eukaryotic	K.NSHLINVLM*WELEK#.K	20.49	12.16	1.68	0.59
Q91WK2_E	Eif3h	Eukaryotic	K.NSHLINVLMWELEK#.K	55.58	19.61	2.83	0.35
Q91WK2_E	Eif3h	Eukaryotic	K.NSHLINVLM*WELEK#K#.S	13.58	5.19	2.62	0.38
Q91WK2_E	Eif3h	Eukaryotic	K.QVQIDGLVVLK#.I	61.21	24.44	2.50	0.40
Q91WK2_E	Eif3h	Eukaryotic	K.SAVADKHELLSLASSNHLGK.S	55.23	23.58	2.34	0.43
Q91WK2_E	Eif3h	Eukaryotic	K.TAQGSLSLK#.A	228.64	85.24	2.68	0.37
Q91WK2_E	Eif3h	Eukaryotic	R.VDEM*SQDIIK#.Y	96.10	35.95	2.67	0.37
Q91WK2_E	Eif3h	Eukaryotic	R.VDEMSQDIIK#.Y	34.26	14.18	2.42	0.41
Q91WK2_E	Eif3h	Eukaryotic	K.ASITFEHMFEEVPIVIK#.N	13.63	5.00	2.73	0.37
Q91WK2_E	Eif3h	Eukaryotic	K.EGTGSTATSSGSAGGAVGK#.G	14.56	5.29	2.75	0.36
Q91WK2_E	Eif3h	Eukaryotic	K.LFM*AQALQEYNN.-	6.72	6.72	1.00	1.00
Q91WK2_E	Eif3h	Eukaryotic	K.ASITFEHMFEEVPIVIK#.N	9.94	2.24	4.44	0.23
Q91WK2_E	Eif3h	Eukaryotic	K.EGTGSTATSSGSAGGAVGK#.G	21.07	10.87	1.94	0.52
Q91WK2_E	Eif3h	Eukaryotic	K.LFM*AQALQEYNN.-	6.96	6.96	1.00	1.00
Q9QZD9_EI	Eif3i	Eukaryotic	R.DM*TM*FVTASK#.D	54.79	24.20	2.26	0.44
Q9QZD9_EI	Eif3i	Eukaryotic	R.DM*TMFVTASK#.D	18.71	8.91	2.10	0.48
Q9QZD9_EI	Eif3i	Eukaryotic	R.DPSQIDSNEPYM*K#.I	30.32	11.70	2.59	0.39
Q9QZD9_EI	Eif3i	Eukaryotic	R.EGDLLFTVAK#.D	98.89	33.41	2.96	0.34
Q9QZD9_EI	Eif3i	Eukaryotic	R.FFHLAFEEEFGR.V	28.63	45.19	0.63	1.58
Q9QZD9_EI	Eif3i	Eukaryotic	K.GHFGPINSVAFHPDGK#.S	164.44	64.04	2.57	0.39
Q9QZD9_EI	Eif3i	Eukaryotic	R.IHYFDPQYFEFEFEA.-	19.48	19.48	1.00	1.00
Q9QZD9_EI	Eif3i	Eukaryotic	K.LFDSTTLEHQK#.T	162.68	60.31	2.70	0.37
Q9QZD9_EI	Eif3i	Eukaryotic	R.QINDIQLSR.D	36.53	60.55	0.60	1.66
Q9QZD9_EI	Eif3i	Eukaryotic	K.SGEVLVNVK#.E	177.69	66.59	2.67	0.37
Q9QZD9_EI	Eif3i	Eukaryotic	K.SYSSGGEDGYVR.I	36.96	59.97	0.62	1.62
Q9QZD9_EI	Eif3i	Eukaryotic	R.TERPVNSAALSPNYDHVVLGGGQEAM*DVTTTSTR.I	5.56	13.94	0.40	2.51
Q3UGC7_EI	Eif3j1	Eukaryotic	K.ATM*K#DDLADYGGYEGGYVQDYEDFM*.-	16.47	8.96	1.84	0.54
Q3UGC7_EI	Eif3j1	Eukaryotic	R.DDFTEFGK#.L	134.38	57.73	2.33	0.43
Q3UGC7_EI	Eif3j1	Eukaryotic	K.DNWDDDDDENK#EEAEVK#PEVK#.I	6.28	2.11	2.98	0.34
Q3UGC7_EI	Eif3j1	Eukaryotic	K.ETFGVNNTVYGIDAM*NPSSR.D	6.15	11.03	0.56	1.79
Q3UGC7_EI	Eif3j1	Eukaryotic	K.K#GVVPGGGLK#.A	52.29	24.31	2.15	0.46
Q3UGC7_EI	Eif3j1	Eukaryotic	K.LQEESDLELAK#.E	207.55	93.73	2.21	0.45
Q3UGC7_EI	Eif3j1	Eukaryotic	K.RLEEPEESK.V	17.08	37.27	0.46	2.18
Q3UGC7_EI	Eif3j1	Eukaryotic	K.VLTPEEQLADK#.L	108.99	48.36	2.25	0.44
Q9DBZ5_EI	Eif3k	Eukaryotic	K.ENAYDLEANLAVLK#.L	30.32	9.60	3.16	0.32
Q9DBZ5_EI	Eif3k	Eukaryotic	K.ENAYDLEANLAVLK#.L	158.58	57.24	2.77	0.36
Q9DBZ5_EI	Eif3k	Eukaryotic	K.GIDRYNPENLATLER.Y	4.18	34.66	0.12	8.30
Q9DBZ5_EI	Eif3k	Eukaryotic	K.IDFDSVSSIM*ASSQ.-	60.65	60.65	1.00	1.00
Q9DBZ5_EI	Eif3k	Eukaryotic	K.IDFDSVSSIMASSQ.-	7.54	7.54	1.00	1.00
Q9DBZ5_EI	Eif3k	Eukaryotic	R.YNPENLATLER.Y	38.50	84.32	0.46	2.19
Q9DBZ5_EI	Eif3k	Eukaryotic	K.ENAYDLEANLAVLK#.L	45.41	20.14	2.25	0.44
Q9DBZ5_EI	Eif3k	Eukaryotic	K.IDFDSVSSIM*ASSQ.-	16.68	16.68	1.00	1.00
Q9DBZ5_EI	Eif3k	Eukaryotic	K.IDFDSVSSIMASSQ.-	9.27	9.27	1.00	1.00
Q8QZY1_EI	Eif3l	Eukaryotic	K.EPFLQQLK#.V	32.20	17.71	1.82	0.55
Q8QZY1_EI	Eif3l	Eukaryotic	R.IQLLVFK#.H	60.25	21.53	2.80	0.36
Q8QZY1_EI	Eif3l	Eukaryotic	K.LAGFLDLTEQEFR.I	41.82	64.59	0.65	1.54
Q8QZY1_EI	Eif3l	Eukaryotic	R.LHSLLGDYYQAIK#.V	84.92	25.19	3.37	0.30
Q8QZY1_EI	Eif3l	Eukaryotic	K.LYTTMPVAK#.L	36.34	24.13	1.51	0.66
Q8QZY1_EI	Eif3l	Eukaryotic	R.QLEVYTSGGDPESVAGEYGR.H	6.42	13.39	0.48	2.08
Q8QZY1_EI	Eif3l	Eukaryotic	R.QYEQQTYQVIPEVIK#.N	21.25	7.65	2.78	0.36
Q8QZY1_EI	Eif3l	Eukaryotic	K.VFSDEVQQQAQLSTIR.S	17.19	28.55	0.60	1.66
Q8QZY1_EI	Eif3l	Eukaryotic	K.VLENIELNKK.S	39.76	17.67	2.25	0.44
Q8QZY1_EI	Eif3l	Eukaryotic	K.VSGGPSLEQR.F	38.80	62.69	0.62	1.62
Q8QZY1_EI	Eif3l	Eukaryotic	R.VSSDVIDQK#.V	143.11	53.24	2.69	0.37
Q8QZY1_EI	Eif3l	Eukaryotic	K.VYEIQDIYENSWTK#.L	73.27	26.39	2.78	0.36
Q8QZY1_EI	Eif3l	Eukaryotic	K.VYELQASR.V	22.23	43.60	0.51	1.96
Q8QZY1_EI	Eif3l	Eukaryotic	R.YGDFFIR.Q	10.83	14.81	0.73	1.37
Q8QZY1_EI	Eif3l	Eukaryotic	K.EPFLQQLK#.V	16.94	6.43	2.63	0.38
Q8QZY1_EI	Eif3l	Eukaryotic	R.IQLLVFK#.H	74.98	30.81	2.43	0.41
Q8QZY1_EI	Eif3l	Eukaryotic	K.LAGFLDLTEQEFR.I	31.47	61.70	0.51	1.96
Q8QZY1_EI	Eif3l	Eukaryotic	R.LHSLLGDYYQAIK#.V	48.72	17.46	2.79	0.36
Q8QZY1_EI	Eif3l	Eukaryotic	K.NLVWTSGISALDGEFQSASEVDFYIDK#DM*IHIADTK#.V	1.95	1.67	1.16	0.86
Q8QZY1_EI	Eif3l	Eukaryotic	R.QLEVYTSGGDPESVAGEYGR.H	5.43	7.40	0.73	1.36
Q8QZY1_EI	Eif3l	Eukaryotic	R.QYEQQTYQVIPEVIK#.N	15.43	6.14	2.51	0.40
Q8QZY1_EI	Eif3l	Eukaryotic	K.TVSDLIDQK#.V	77.63	28.98	2.68	0.37
Q8QZY1_EI	Eif3l	Eukaryotic	K.VFSDEVQQQAQLSTIR.S	10.36	14.22	0.73	1.37
Q8QZY1_EI	Eif3l	Eukaryotic	K.VLENIELNK#.K	17.38	6.53	2.66	0.38
Q8QZY1_EI	Eif3l	Eukaryotic	K.VSGGPSLEQR.F	25.67	45.10	0.57	1.76
Q8QZY1_EI	Eif3l	Eukaryotic	R.VSSDVIDQK#.V	118.54	37.11	3.19	0.31
Q8QZY1_EI	Eif3l	Eukaryotic	K.VYEIQDIYENSWTK#.L	47.26	18.98	2.49	0.40
Q8QZY1_EI	Eif3l	Eukaryotic	K.VYELQASR.V	38.47	33.77	1.14	0.88
Q8QZY1_EI	Eif3l	Eukaryotic	R.YGDFFIR.Q	8.11	16.49	0.49	2.03
Q8QZY1_EI	Eif3l	Eukaryotic	K.EPFLQQLK#.V	22.87	11.83	1.93	0.52
Q8QZY1_EI	Eif3l	Eukaryotic	R.IQLLVFK#.H	115.77	43.71	2.65	0.38
Q8QZY1_EI	Eif3l	Eukaryotic	K.LAGFLDLTEQEFR.I	30.32	51.55	0.59	1.70
Q8QZY1_EI	Eif3l	Eukaryotic	R.LHSLLGDYYQAIK#.V	78.00	23.51	3.32	0.30
Q8QZY1_EI	Eif3l	Eukaryotic	K.LYTTMPVAK#.L	17.46	11.05	1.58	0.63
Q8QZY1_EI	Eif3l	Eukaryotic	R.QLEVYTSGGDPESVAGEYGR.H	8.53	9.49	0.90	1.11
Q8QZY1_EI	Eif3l	Eukaryotic	R.QYEQQTYQVIPEVIK#.N	21.56	8.61	2.50	0.40
Q8QZY1_EI	Eif3l	Eukaryotic	K.TVSDLIDQK#.V	123.23	38.75	3.18	0.31
Q8QZY1_EI	Eif3l	Eukaryotic	K.VFSDEVQQQAQLSTIR.S	16.18	27.02	0.60	1.67
Q8QZY1_EI	Eif3l	Eukaryotic	K.VLENIELNK#.K	32.13	10.13	3.17	0.32
Q8QZY1_EI	Eif3l	Eukaryotic	K.VSGGPSLEQR.F	35.91	65.92	0.54	1.84
Q8QZY1_EI	Eif3l	Eukaryotic	R.VSSDVIDQK#.V	138.45	60.23	2.30	0.44
Q8QZY1_EI	Eif3l	Eukaryotic	K.VYEIQDIYENSWTK#.L	61.49	23.49	2.62	0.38
Q8QZY1_EI	Eif3l	Eukaryotic	K.VYELQASR.V	34.93	35.50	0.98	1.02
Q8QZY1_EI	Eif3l	Eukaryotic	R.YGDFFIR.Q	10.60	21.68	0.49	2.05
Q99JX4_EI	Eif3m	Eukaryotic	R.ALK#DPNAFLFDHLLTLK#PVK#.F	122.79	55.78	2.20	0.45
Q99JX4_EI	Eif3m	Eukaryotic	K.DFIDSLGLLHEQNM*AK#.M	24.35	8.06	3.02	0.33
Q99JX4_EI	Eif3m	Eukaryotic	K.FYQNNKDFIDSLGLLHEQNM*AK.M	16.41	5.57	2.94	0.34
Q99JX4_EI	Eif3m	Eukaryotic	K.FYQNNK#DFIDSLGLLHEQNMAK#.M	22.68	7.77	2.92	0.34
Q99JX4_EI	Eif3m	Eukaryotic	R.LLTFM*GM*AVENK#.E	49.75	21.14	2.35	0.42
Q99JX4_EI	Eif3m	Eukaryotic	R.LLTFM*GMAVENK#.E	30.10	64.93	0.46	2.16
Q99JX4_EI	Eif3m	Eukaryotic	R.LLTFMGMAVENK#.E	28.77	13.79	2.09	0.48
Q99JX4_EI	Eif3m	Eukaryotic	K.QQWQQLYDTLNAWK#.Q	41.07	17.52	2.34	0.43
Q99JX4_EI	Eif3m	Eukaryotic	K.VM*VELLGSYTEDNASQAR.V	2.93	7.24	0.41	2.47

Q99JX4_EI	Eif3m	Eukaryotic	K.WISDWK#.L	53.13	18.00	2.95	0.34
Q99JX4_EI	Eif3m	Eukaryotic	R.ALK#DPNAFLFDHLLTLK#PVK#.F	40.90	10.07	4.06	0.25
Q99JX4_EI	Eif3m	Eukaryotic	K.FYQNNK#DFIDSLGLLHEQNM*AK#.M	5.25	2.01	2.61	0.38
Q99JX4_EI	Eif3m	Eukaryotic	R.LLTFM*GM*AVENK#.E	10.65	3.71	2.87	0.35
Q99JX4_EI	Eif3m	Eukaryotic	R.LLTFM*GMAVENK#.E	14.81	51.08	0.29	3.45
Q99JX4_EI	Eif3m	Eukaryotic	R.LLTFMGM*AVENK#.E	14.81	51.08	0.29	3.45
Q99JX4_EI	Eif3m	Eukaryotic	K.QQWQQLYDTLNAWK#.Q	10.58	4.21	2.51	0.40
Q99JX4_EI	Eif3m	Eukaryotic	R.ALKDPNAFLFDHLLTLKPVK.F	52.19	18.38	2.84	0.35
Q99JX4_EI	Eif3m	Eukaryotic	R.LLTFM*GM*AVENK#.E	47.03	18.54	2.54	0.39
Q99JX4_EI	Eif3m	Eukaryotic	R.LQLLSNLFHGMDK#.N	13.01	4.41	2.95	0.34
Q99JX4_EI	Eif3m	Eukaryotic	K.QQWQQLYDTLNAWK#.Q	12.00	4.06	2.95	0.34
P60843_IF	Eif4a1	Eukaryotic	K.ATQALVLAPTR.E	106.75	228.78	0.47	2.14
P60843_IF	Eif4a1	Eukaryotic	R.DFTVSAM*HGDM*DQK#.E	7.59	3.26	2.33	0.43
P60843_IF	Eif4a1	Eukaryotic	R.DFTVSAM*HGDMDQK#.E	30.39	15.92	1.91	0.52
P60843_IF	Eif4a1	Eukaryotic	R.DFTVSAMHGDM*DQK#.E	45.98	18.43	2.50	0.40
P60843_IF	Eif4a1	Eukaryotic	K.DQIYDIFQK#.L	148.64	58.20	2.55	0.39
P60843_IF	Eif4a1	Eukaryotic	K.EELTLEGIR.Q	44.29	79.58	0.56	1.80
P60843_IF	Eif4a1	Eukaryotic	R.ELAQQIQK#.V	1325.90	603.68	2.20	0.46
P60843_IF	Eif4a1	Eukaryotic	R.ENYIHR.I	39.20	73.42	0.53	1.87
P60843_IF	Eif4a1	Eukaryotic	R.GFK#DQIYDIFQK#.L	306.63	110.02	2.79	0.36
P60843_IF	Eif4a1	Eukaryotic	R.GFKDQIYDIFQK.L	438.28	157.70	2.78	0.36
P60843_IF	Eif4a1	Eukaryotic	R.GIDVQQVSLVINYDLPTNR.E	32.16	60.45	0.53	1.88
P60843_IF	Eif4a1	Eukaryotic	R.GIDVQQVSLVINYDLPTNR.E	37.70	74.32	0.51	1.97
P60843_IF	Eif4a1	Eukaryotic	R.GIYAYGFEKPSAIQQR.A	182.49	389.12	0.47	2.13
P60843_IF	Eif4a1	Eukaryotic	K.GYDVIAQAQSGTGK#.T	649.79	232.04	2.80	0.36
P60843_IF	Eif4a1	Eukaryotic	K.KEELTLEGIR.Q	71.55	152.40	0.47	2.13
P60843_IF	Eif4a1	Eukaryotic	R.KGVAINMVTEEDKR.T	182.51	334.67	0.55	1.83
P60843_IF	Eif4a1	Eukaryotic	R.K#VDWLTEK#.M	521.68	229.83	2.27	0.44
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATM*PSDVLEVTK#.K	98.03	39.02	2.51	0.40
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATM*PSDVLEVTK#.K	35.71	13.80	2.59	0.39
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATMPSDVLEVTK#.K	43.37	16.81	2.58	0.39
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATMPSDVLEVTK#.K	155.76	54.61	2.85	0.35
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATM*PSDVLEVTK#K#.F	138.61	50.58	2.74	0.36
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATM*PSDVLEVTK#K#.F	4.69	2.80	1.68	0.60
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATMPSDVLEVTKK.F	203.14	86.44	2.35	0.43
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATMPSDVLEVTKK.F	8.05	3.04	2.65	0.38
P60843_IF	Eif4a1	Eukaryotic	K.LQM*EAPHIIVGTPGR.V	117.11	267.74	0.44	2.29
P60843_IF	Eif4a1	Eukaryotic	K.LQMEAPHIIVGTPGR.V	82.40	145.62	0.57	1.77
P60843_IF	Eif4a1	Eukaryotic	K.M*FVLDEADEM*LSR.G	84.95	160.28	0.53	1.89
P60843_IF	Eif4a1	Eukaryotic	K.MFVLDEADEM*LSR.G	30.20	55.11	0.55	1.82
P60843_IF	Eif4a1	Eukaryotic	K.M*FVLDEADEMLSR.G	42.89	78.19	0.55	1.82
P60843_IF	Eif4a1	Eukaryotic	K.MFVLDEADEMLSR.G	47.38	93.51	0.51	1.97
P60843_IF	Eif4a1	Eukaryotic	R.QFYINVER.E	123.61	206.49	0.60	1.67
P60843_IF	Eif4a1	Eukaryotic	R.RKVDWLTEK.M	72.77	46.61	1.56	0.64
P60843_IF	Eif4a1	Eukaryotic	K.VDWLTEK#.M	165.19	69.13	2.39	0.42
P60843_IF	Eif4a1	Eukaryotic	R.VFDM*LNR.R	55.15	90.56	0.61	1.64
P60843_IF	Eif4a1	Eukaryotic	R.VFDMLNR.R	48.52	108.79	0.45	2.24
P60843_IF	Eif4a1	Eukaryotic	R.VLITTDLLAR.G	257.45	486.69	0.53	1.89
P60843_IF	Eif4a1	Eukaryotic	K.ATQALVLAPTR.E	5.67	17.12	0.33	3.02
P60843_IF	Eif4a1	Eukaryotic	R.ELAQQIQK#.V	22.34	23.01	0.97	1.03
P60843_IF	Eif4a1	Eukaryotic	R.GFK#DQIYDIFQK#.L	11.64	5.31	2.19	0.46
P60843_IF	Eif4a1	Eukaryotic	R.GIYAYGFEKPSAIQQR.A	7.49	31.90	0.23	4.26
P60843_IF	Eif4a1	Eukaryotic	K.GYDVIAQAQSGTGK#.T	11.86	7.39	1.60	0.62
P60843_IF	Eif4a1	Eukaryotic	R.VLITTDLLAR.G	15.50	41.24	0.38	2.66
P60843_IF	Eif4a1	Eukaryotic	K.ATQALVLAPTR.E	48.74	74.07	0.66	1.52
P60843_IF	Eif4a1	Eukaryotic	K.DQIYDIFQK#.L	22.14	8.52	2.60	0.38
P60843_IF	Eif4a1	Eukaryotic	K.EELTLEGIR.Q	16.94	19.67	0.86	1.16
P60843_IF	Eif4a1	Eukaryotic	R.ELAQQIQK#.V	282.70	117.33	2.41	0.42
P60843_IF	Eif4a1	Eukaryotic	R.ENYIHR.I	15.68	21.46	0.73	1.37
P60843_IF	Eif4a1	Eukaryotic	R.GFK#DQIYDIFQK#.L	135.66	51.21	2.65	0.38
P60843_IF	Eif4a1	Eukaryotic	R.GIDVQQVSLVINYDLPTNR.E	11.11	20.30	0.55	1.83
P60843_IF	Eif4a1	Eukaryotic	R.GIYAYGFEKPSAIQQR.A	58.76	80.61	0.73	1.37
P60843_IF	Eif4a1	Eukaryotic	K.GYDVIAQAQSGTGK#.T	267.55	92.93	2.88	0.35
P60843_IF	Eif4a1	Eukaryotic	K.KEELTLEGIR.Q	21.03	30.04	0.70	1.43
P60843_IF	Eif4a1	Eukaryotic	R.KGVAINM*VTEEDKR.T	23.86	41.51	0.57	1.74
P60843_IF	Eif4a1	Eukaryotic	R.KGVAINMVTEEDKR.T	17.91	40.53	0.44	2.26
P60843_IF	Eif4a1	Eukaryotic	R.K#VDWLTEK#.M	131.72	62.04	2.12	0.47
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATM*PSDVLEVTK#.K	24.87	9.92	2.51	0.40
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATMPSDVLEVTK#.K	9.54	3.89	2.46	0.41
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATM*PSDVLEVTK#K#.F	34.05	11.43	2.98	0.34
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATMPSDVLEVTK#K#.F	42.60	12.13	3.51	0.28
P60843_IF	Eif4a1	Eukaryotic	K.LQM*EAPHIIVGTPGR.V	26.96	61.55	0.44	2.28
P60843_IF	Eif4a1	Eukaryotic	K.LQM*EAPHIIVGTPGR.V	2.72	6.88	0.40	2.53
P60843_IF	Eif4a1	Eukaryotic	K.M*FVLDEADEM*LSR.G	19.57	35.82	0.55	1.83
P60843_IF	Eif4a1	Eukaryotic	K.MFVLDEADEM*LSR.G	10.29	12.24	0.84	1.19
P60843_IF	Eif4a1	Eukaryotic	K.M*FVLDEADEMLSR.G	11.99	23.87	0.50	1.99
P60843_IF	Eif4a1	Eukaryotic	K.MFVLDEADEMLSR.G	9.47	13.61	0.70	1.44
P60843_IF	Eif4a1	Eukaryotic	R.QFYINVER.E	15.60	23.88	0.65	1.53
P60843_IF	Eif4a1	Eukaryotic	R.RKVDWLTEK.M	24.20	42.63	0.57	1.76
P60843_IF	Eif4a1	Eukaryotic	K.VDWLTEK#.M	29.12	16.74	1.74	0.57
P60843_IF	Eif4a1	Eukaryotic	R.VLITTDLLAR.G	91.85	152.45	0.60	1.66
P60843_IF	Eif4a1	Eukaryotic	K.ATQALVLAPTR.E	52.97	103.37	0.51	1.95
P60843_IF	Eif4a1	Eukaryotic	K.DQIYDIFQK#.L	75.07	32.04	2.34	0.43
P60843_IF	Eif4a1	Eukaryotic	K.EELTLEGIR.Q	20.17	31.96	0.63	1.58
P60843_IF	Eif4a1	Eukaryotic	R.ELAQQIQK#.V	579.22	182.12	3.18	0.31
P60843_IF	Eif4a1	Eukaryotic	R.ENYIHR.I	14.54	32.19	0.45	2.21
P60843_IF	Eif4a1	Eukaryotic	R.GFK#DQIYDIFQK#.L	191.76	66.78	2.87	0.35
P60843_IF	Eif4a1	Eukaryotic	R.GIDVQQVSLVINYDLPTNR.E	10.67	19.39	0.55	1.82
P60843_IF	Eif4a1	Eukaryotic	K.GYDVIAQAQSGTGK#.T	423.71	159.28	2.66	0.38
P60843_IF	Eif4a1	Eukaryotic	K.KEELTLEGIR.Q	28.46	55.75	0.51	1.96
P60843_IF	Eif4a1	Eukaryotic	R.KGVAINM*VTEEDKR.T	43.79	90.09	0.49	2.06
P60843_IF	Eif4a1	Eukaryotic	R.KGVAINMVTEEDKR.T	29.24	52.73	0.55	1.80
P60843_IF	Eif4a1	Eukaryotic	R.K#VDWLTEK#.M	175.11	77.81	2.25	0.44
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATM*PSDVLEVTK#.K	63.80	27.70	2.30	0.43
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATM*PSDVLEVTK#.K	10.68	5.22	2.04	0.49
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATMPSDVLEVTK#.K	68.73	23.50	2.93	0.34
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATM*PSDVLEVTK#K#.F	50.89	18.48	2.75	0.36
P60843_IF	Eif4a1	Eukaryotic	K.LNSNTQVVLLSATMPSDVLEVTK#K#.F	42.52	14.80	2.87	0.35
P60843_IF	Eif4a1	Eukaryotic	K.LQM*EAPHIIVGTPGR.V	51.27	113.18	0.45	2.21
P60843_IF	Eif4a1	Eukaryotic	K.LQMEAPHIIVGTPGR.V	36.19	69.03	0.52	1.91
P60843_IF	Eif4a1	Eukaryotic	K.M*FVLDEADEM*LSR.G	35.00	56.84	0.62	1.62
P60843_IF	Eif4a1	Eukaryotic	K.MFVLDEADEM*LSR.G	7.59	14.22	0.53	1.87
P60843_IF	Eif4a1	Eukaryotic	K.M*FVLDEADEMLSR.G	14.15	19.93	0.71	1.41

P60843_IF	Eif4a1	Eukaryotic	R.QFYINVER.E	27.77	40.76	0.68	1.47
P60843_IF	Eif4a1	Eukaryotic	K.VDWLTEK#.M	60.96	25.30	2.41	0.42
P60843_IF	Eif4a1	Eukaryotic	R.VFDM*LNR.R	23.01	38.17	0.60	1.66
P60843_IF	Eif4a1	Eukaryotic	R.VFDMLNR.R	7.63	14.55	0.52	1.91
P60843_IF	Eif4a1	Eukaryotic	R.VLITTDLLAR.G	162.95	266.71	0.61	1.64
P10630_IF	Eif4a2	Eukaryotic	R.DFTVSALHGDM*DQK#.E	22.85	10.29	2.22	0.45
P10630_IF	Eif4a2	Eukaryotic	R.DIETFYNTTVEEM*PM*NVADLI.-	9.99	9.99	1.00	1.00
P10630_IF	Eif4a2	Eukaryotic	K.DQIYEIFQK#.L	17.46	8.19	2.13	0.47
P10630_IF	Eif4a2	Eukaryotic	R.EHGGPEGMDPDGVIESNWNEIVDNFDDM*NLK#.E	14.24	3.40	4.18	0.24
P10630_IF	Eif4a2	Eukaryotic	R.EHGGPEGM*DPDGVIESNWNEIVDNFDDMNLK#.E	6.27	3.87	1.62	0.62
P10630_IF	Eif4a2	Eukaryotic	R.GFK#DQIYEIFQK#.L	97.05	27.33	3.55	0.28
P10630_IF	Eif4a2	Eukaryotic	R.GFKDQIYEIFQK.L	46.12	14.64	3.15	0.32
P10630_IF	Eif4a2	Eukaryotic	K.K#EELTLEGIK#.Q	98.52	31.49	3.13	0.32
P10630_IF	Eif4a2	Eukaryotic	K.LNTSIQVVLLSATM*PTDVLEVTK#.K	32.28	14.12	2.29	0.44
P10630_IF	Eif4a2	Eukaryotic	K.LNTSIQVVLLSATM*PTDVLEVTK#K#.F	9.65	3.78	2.55	0.39
P10630_IF	Eif4a2	Eukaryotic	K.LQAEAPHIVVGTPGR.V	39.77	75.89	0.52	1.91
P10630_IF	Eif4a2	Eukaryotic	K.LNTSIQVVLLSATM*PTDVLEVTK#.K	10.07	2.42	4.16	0.24
Q91VC3_IF	Eif4a3	Eukaryotic	R.DELTLEGIK.Q	46.44	202.41	0.23	4.36
Q91VC3_IF	Eif4a3	Eukaryotic	R.DIEQYYSTQIDEM*PM*NVADLI.-	43.13	43.13	1.00	1.00
Q91VC3_IF	Eif4a3	Eukaryotic	R.DVIAQSQSGTGK#.T	76.26	62.50	1.22	0.82
Q91VC3_IF	Eif4a3	Eukaryotic	R.ELAVQIQK#.G	221.26	140.34	1.58	0.63
Q91VC3_IF	Eif4a3	Eukaryotic	K.EQIYDVYR.Y	35.09	106.63	0.33	3.04
Q91VC3_IF	Eif4a3	Eukaryotic	R.ETQALILAPTR.E	50.03	174.44	0.29	3.49
Q91VC3_IF	Eif4a3	Eukaryotic	K.FM*TDPIR.I	27.80	100.16	0.28	3.60
Q91VC3_IF	Eif4a3	Eukaryotic	K.GFKEQIYDVYR.Y	6.27	31.30	0.20	4.99
Q91VC3_IF	Eif4a3	Eukaryotic	R.GLDVPQVSLIINYDLPNNR.E	18.28	52.39	0.35	2.87
Q91VC3_IF	Eif4a3	Eukaryotic	K.GRDVIAQSQSGTGK.T	24.87	70.10	0.35	2.82
Q91VC3_IF	Eif4a3	Eukaryotic	K.GVAINFVK#.N	57.04	44.09	1.29	0.77
Q91VC3_IF	Eif4a3	Eukaryotic	R.K#GVAINFVK#.N	144.08	114.56	1.26	0.80
Q91VC3_IF	Eif4a3	Eukaryotic	R.KLDYGQHVVAGTPGR.V	38.16	115.29	0.33	3.02
Q91VC3_IF	Eif4a3	Eukaryotic	R.LLK#EEDM*TK#.V	29.59	15.07	1.96	0.51
Q91VC3_IF	Eif4a3	Eukaryotic	K.M*LVLDEADEM*LNK#.G	59.08	48.61	1.22	0.82
Q91VC3_IF	Eif4a3	Eukaryotic	K.MLVLDEADEM*LNK#.G	29.08	26.04	1.12	0.90
Q91VC3_IF	Eif4a3	Eukaryotic	K.M*LVLDEADEMLNK#.G	28.41	24.90	1.14	0.88
Q91VC3_IF	Eif4a3	Eukaryotic	K.MLVLDEADEMLNK#.G	45.77	33.41	1.37	0.73
Q91VC3_IF	Eif4a3	Eukaryotic	K.QFFVAVER.E	28.97	112.48	0.26	3.88
Q91VC3_IF	Eif4a3	Eukaryotic	K.RDELTLEGIK.Q	52.25	171.28	0.31	3.28
Q91VC3_IF	Eif4a3	Eukaryotic	K.VEFETSEEVDVTPTFDTM*GLR.E	1.83	4.38	0.42	2.40
Q91VC3_IF	Eif4a3	Eukaryotic	R.VLISTDVWAR.G	59.25	176.79	0.34	2.98
Q91VC3_IF	Eif4a3	Eukaryotic	R.DIEQYYSTQIDEM*PM*NVADLI.-	8.45	8.45	1.00	1.00
Q91VC3_IF	Eif4a3	Eukaryotic	R.DVIAQSQSGTGK#.T	15.82	11.35	1.39	0.72
Q91VC3_IF	Eif4a3	Eukaryotic	R.K#GVAINFVK#.N	16.45	13.04	1.26	0.79
Q91VC3_IF	Eif4a3	Eukaryotic	R.KLDYGQHVVAGTPGR.V	5.60	25.27	0.22	4.52
Q91VC3_IF	Eif4a3	Eukaryotic	K.M*LVLDEADEM*LNK#.G	15.65	8.26	1.90	0.53
Q91VC3_IF	Eif4a3	Eukaryotic	K.M*LVLDEADEMLNK#.G	6.88	24.65	0.28	3.58
Q91VC3_IF	Eif4a3	Eukaryotic	R.DVIAQSQSGTGK#.T	25.59	13.81	1.85	0.54
Q91VC3_IF	Eif4a3	Eukaryotic	K.GVAINFVK#.N	14.09	9.17	1.54	0.65
Q91VC3_IF	Eif4a3	Eukaryotic	K.M*LVLDEADEM*LNK#.G	20.69	13.62	1.52	0.66
Q8BGD9_IF	Eif4b	Eukaryotic	R.AASIFGGAKPVDTAAR.E	7.56	12.54	0.60	1.66
Q8BGD9_IF	Eif4b	Eukaryotic	R.SQSSDTEQPSPTSGGGK#.V	10.18	3.81	2.67	0.37
Q8BMB3_II	Eif4e2	Eukaryotic	R.FQEDIISIWNK#.T	10.75	5.81	1.85	0.54
Q8BMB3_II	Eif4e2	Eukaryotic	K.QIGTFASVEQFWK#.F	7.20	5.03	1.43	0.70
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.EFLAEGQDVGSFVAEK#.K	17.33	8.57	2.02	0.49
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.FIGELFK#.L	19.34	9.20	2.10	0.48
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.GLPLVDDGGWNTVPISK#.G	18.15	9.13	1.99	0.50
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.GVIDLIFEK#.A	19.71	6.72	2.93	0.34
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.M*DQYFNQM*EK#.I	8.95	3.66	2.45	0.41
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.QVTQLAIDTEER.L	3.54	14.34	0.25	4.05
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.DK#DDDEVFEK#.K	8.54	2.43	3.52	0.28
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.EAVGDLLDAFK#.E	30.99	13.58	2.28	0.44
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.EFLAEGQDVGSFVAEK#.K	66.08	23.69	2.79	0.36
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.EM*DEAATAEER.G	1.99	4.69	0.42	2.35
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.FIGELFK#.L	71.18	22.77	3.13	0.32
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.FMLQDVLDLR.Q	56.11	15.28	3.67	0.27
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.GGPPGPPINR.G	8.66	19.91	0.43	2.30
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.GLPLVDDGGWNTVPISK#.G	61.56	19.72	3.12	0.32
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.GPAGLGPR.R	11.15	20.36	0.55	1.83
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.GVIDLIFEK#.A	59.30	21.34	2.78	0.36
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.IISSVIM*TEDIK#.L	13.02	5.72	2.28	0.44
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.K#IISSVIM*TEDIK#.L	20.15	80.58	0.25	4.00
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.K#IISSVIMTEDIK#.L	15.70	7.40	2.12	0.47
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.KVEYTLGEESEAPGQR.T	18.64	32.54	0.57	1.75
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.LGIESTLER.S	22.92	107.01	0.21	4.67
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.LKEELEEAR.D	18.21	304.56	0.06	16.73
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.LK#GVIDLIFEK#.A	20.21	6.35	3.18	0.31
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.LLTTIGK#.D	89.21	27.10	3.29	0.30
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.M*DQYFNQM*EK#.I	39.86	17.34	2.30	0.43
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.MDQYFNQM*EK#.I	8.94	3.50	2.55	0.39
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.M*DQYFNQMEK#.I	11.78	4.55	2.59	0.39
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.MDQYFNQMEK#.I	9.30	4.34	2.14	0.47
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.QVTQLAIDTEER.L	15.97	30.25	0.53	1.89
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.SDQWK#PLNLEEK#.K	28.13	20.40	1.38	0.73
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.SVTAFFNWLR.E	9.88	12.72	0.78	1.29
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.VDVQVLK#.V	38.07	13.23	2.88	0.35
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.VFDWIDANLNEQQIASNTLVR.A	8.53	17.98	0.47	2.11
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.VFDWIDANLNEQQIASNTLVR.A	2.77	5.00	0.55	1.81
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.EATLPPVSPPK#.A	34.31	13.87	2.47	0.40
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.EAVGDLLDAFK#.E	72.62	36.44	1.99	0.50
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.EFEK#DK#DDDEVFEK#.K	35.40	11.53	3.07	0.33
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.EFLAEGQDVGSFVAEK#.K	124.40	48.35	2.57	0.39
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.EM*DEAATAEER.G	6.14	10.95	0.56	1.78
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.EMDEAATAEER.G	5.69	7.91	0.72	1.39
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.FIGELFK#.L	126.71	51.70	2.45	0.41
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.FM*LQDVLDLR.Q	15.07	16.21	0.93	1.08
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.GGPGGELPR.G	35.55	69.87	0.51	1.97
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.GGPPGPPINR.G	20.94	33.40	0.63	1.59
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.GLPLVDDGGWNTVPISK#.G	160.94	62.48	2.58	0.39
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.GPAGLGPR.R	32.89	47.55	0.69	1.45
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.GSRPIDTSR.L	3.02	14.15	0.21	4.69
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.GVIDLIFEK#.A	89.48	36.21	2.47	0.40
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.IISSVIM*TEDIK#.L	38.42	18.01	2.13	0.47
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.ITKPGSIDSNNQLFAPGGR.L	44.19	81.64	0.54	1.85
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.K#IISSVIM*TEDIK#.L	28.73	11.81	2.43	0.41

Q6NZJ6_IF	Eif4g1	Eukaryotic	R.KIISSVIM*TEDIK.L	16.69	7.25	2.30	0.43
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.KVEYTLGEESEAPGQR.T	30.48	58.00	0.53	1.90
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.LGIESTLER.S	51.14	79.06	0.65	1.55
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.LTPQMFQQLM*K#.Q	15.31	6.66	2.30	0.43
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.LTPQM*FQQLMK#.Q	14.54	6.41	2.27	0.44
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.M*DQYFNQM*EK#.I	73.15	27.29	2.68	0.37
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.MDQYFNQM*EK#.I	12.74	3.54	3.60	0.28
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.M*DQYFNQMEK#.I	13.99	5.94	2.35	0.42
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.MDQYFNQMEK#.I	18.17	3.26	5.57	0.18
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.SDQWK#PLNLEEK#.K	59.01	27.41	2.15	0.46
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.SVTAFFNWLR.E	17.74	24.22	0.73	1.37
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.TIDQIHK#.E	32.47	13.41	2.42	0.41
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.VDVQVLK#.V	71.45	22.23	3.21	0.31
Q6NZJ6_IF	Eif4g1	Eukaryotic	K.VEYTLGEESEAPGQR.T	5.01	7.89	0.64	1.57
Q6NZJ6_IF	Eif4g1	Eukaryotic	R.VFDWIDANLNEQQIASNTLVR.A	22.29	35.85	0.62	1.61
Q62448_IF	Eif4g2	Eukaryotic	K.ASSLISLLK#.Q	33.88	12.90	2.63	0.38
Q62448_IF	Eif4g2	Eukaryotic	K.EDITQEFPGK#.G	20.27	8.93	2.27	0.44
Q62448_IF	Eif4g2	Eukaryotic	R.EWLTELFQQSK#.V	19.28	8.35	2.31	0.43
Q62448_IF	Eif4g2	Eukaryotic	K.HFLPEM*LSK#.V	15.85	10.46	1.51	0.66
Q62448_IF	Eif4g2	Eukaryotic	R.LAEDAPNFDGPAAEGQPGQK#.Q	6.78	4.38	1.55	0.65
Q62448_IF	Eif4g2	Eukaryotic	K.LEVDIPLVK#.S	31.19	13.92	2.24	0.45
Q62448_IF	Eif4g2	Eukaryotic	K.TAGNSEFLGK#.T	19.70	6.24	3.16	0.32
Q62448_IF	Eif4g2	Eukaryotic	R.TQTPPLGQTPQLGLK#.T	21.15	8.43	2.51	0.40
Q62448_IF	Eif4g2	Eukaryotic	K.ASSLISLLK#.Q	30.97	11.76	2.63	0.38
Q62448_IF	Eif4g2	Eukaryotic	R.EWLTELFQQSK#.V	10.05	6.28	1.60	0.62
Q62448_IF	Eif4g2	Eukaryotic	R.FLLQDTVELR.E	8.44	16.92	0.50	2.00
Q62448_IF	Eif4g2	Eukaryotic	K.GVILLIVDK#.A	14.19	5.21	2.72	0.37
Q62448_IF	Eif4g2	Eukaryotic	K.HFLPEM*LSK#.V	27.12	11.88	2.28	0.44
Q62448_IF	Eif4g2	Eukaryotic	R.LAEDAPNFDGPAAEGQPGQK#.Q	14.06	6.46	2.18	0.46
Q62448_IF	Eif4g2	Eukaryotic	K.LDPSPQTIYK#.W	17.44	9.72	1.79	0.56
Q62448_IF	Eif4g2	Eukaryotic	K.LEVDIPLVK#.S	33.91	14.29	2.37	0.42
Q62448_IF	Eif4g2	Eukaryotic	K.LTEAVVTDYLNSGNANDAVSGVR.E	6.13	12.54	0.49	2.05
Q62448_IF	Eif4g2	Eukaryotic	K.SQGLSQLYHNQSQGLLSQLQGQSK#.D	24.15	11.68	2.07	0.48
Q62448_IF	Eif4g2	Eukaryotic	K.TAGNSEFLGK#.T	37.56	10.49	3.58	0.28
Q62448_IF	Eif4g2	Eukaryotic	R.TQTPPLGQTPQLGLK#.T	21.57	9.25	2.33	0.43
Q62448_IF	Eif4g2	Eukaryotic	K.ASSLISLLK#.Q	36.07	12.08	2.99	0.33
Q62448_IF	Eif4g2	Eukaryotic	K.HFLPEM*LSK#.V	27.75	12.45	2.23	0.45
Q62448_IF	Eif4g2	Eukaryotic	R.LAEDAPNFDGPAAEGQPGQK#.Q	13.75	8.08	1.70	0.59
Q62448_IF	Eif4g2	Eukaryotic	K.LEVDIPLVK#.S	26.58	14.61	1.82	0.55
Q62448_IF	Eif4g2	Eukaryotic	K.LTEAVVTDYLNSGNANDAVSGVR.E	6.57	8.24	0.80	1.25
Q62448_IF	Eif4g2	Eukaryotic	R.TQTPPLGQTPQLGLK#.T	25.17	10.38	2.42	0.41
Q62448_IF	Eif4g2	Eukaryotic	K.VIILSLDR.S	5.17	9.93	0.52	1.92
Q80XI3_IF	Eif4g3	Eukaryotic	R.SPAPVQTATTAPK#.S	25.99	7.40	3.51	0.28
Q80XI3_IF	Eif4g3	Eukaryotic	K.YLDSDTEK#ELQALYALQASIVK#.L	15.44	6.13	2.52	0.40
Q80XI3_IF	Eif4g3	Eukaryotic	K.GVIDLVFEK#.A	14.98	4.10	3.66	0.27
Q80XI3_IF	Eif4g3	Eukaryotic	R.SPAPVQTATTAPK#.S	53.06	17.96	2.95	0.34
Q80XI3_IF	Eif4g3	Eukaryotic	R.TPDEVLEAEAEPK#AEEELAVDSVLEPEQEK#.M	8.84	4.74	1.86	0.54
Q80XI3_IF	Eif4g3	Eukaryotic	R.VDEGGWNTVQGAK#.N	20.45	1.37	14.96	0.07
P59325_IF	Eif5	Eukaryotic	K.AM*GPLVLTEVLFDEK#.I	20.56	4.56	4.51	0.22
P59325_IF	Eif5	Eukaryotic	K.GLTLSDDLER.T	18.23	16.38	1.11	0.90
P59325_IF	Eif5	Eukaryotic	K.SDNK#DDDIDIDAI.-	23.49	11.75	2.00	0.50
P59325_IF	Eif5	Eukaryotic	K.TVIVNM*VDVAK#.A	14.58	6.33	2.30	0.43
P59325_IF	Eif5	Eukaryotic	R.VNILFDFVK#.K	76.39	12.54	6.09	0.16
Q05D44_IF	Eif5b	Eukaryotic	R.HFEATDILVSK#.I	26.72	7.10	3.77	0.27
Q05D44_IF	Eif5b	Eukaryotic	R.HLQAQGVEVPSK#DSLPK#.K	23.87	6.13	3.89	0.26
Q05D44_IF	Eif5b	Eukaryotic	R.LKEGDTIIVPGVEGPIVTQIR.G	14.12	13.32	1.06	0.94
Q05D44_IF	Eif5b	Eukaryotic	K.NK#SEDSTK#DDTDLGALAAEIEGAGAAK#.E	4.99	4.17	1.20	0.84
Q05D44_IF	Eif5b	Eukaryotic	K.AIQEALAK#.L	51.81	14.13	3.67	0.27
Q05D44_IF	Eif5b	Eukaryotic	R.GLLLPPPM*K#.E	11.45	3.09	3.70	0.27
Q05D44_IF	Eif5b	Eukaryotic	R.HFEATDILVSK#.I	40.12	31.67	1.27	0.79
Q05D44_IF	Eif5b	Eukaryotic	R.HLQAQGVEVPSK#.D	19.93	3.19	6.25	0.16
Q05D44_IF	Eif5b	Eukaryotic	R.HLQAQGVEVPSK#DSLPK#.K	34.46	9.12	3.78	0.26
Q05D44_IF	Eif5b	Eukaryotic	K.K#SPDSDVAVTLK#K#.Q	32.89	7.71	4.27	0.23
Q05D44_IF	Eif5b	Eukaryotic	R.LKEGDTIIVPGVEGPIVTQIR.G	11.91	17.52	0.68	1.47
Q05D44_IF	Eif5b	Eukaryotic	K.SEDSTK#DDTDLGALAAEIEGAGAAK#.E	12.54	2.56	4.90	0.20
O55135_IF	Eif6	Eukaryotic	R.HGLLVPNNTTDQELQHIR.N	2.73	10.62	0.26	3.89
O55135_IF	Eif6	Eukaryotic	K.TSIEDQDELSSLLQVPLVAGTVNR.G	8.17	26.16	0.31	3.20
Q80Y81_R	Elac2	Zinc phospl	K.DATLLIHEATLEDGLEEEAVEK#.T	8.84	1.64	5.41	0.18
Q80Y81_R	Elac2	Zinc phospl	K.DATLLIHEATLEDGLEEEAVEK#.T	9.14	2.36	3.88	0.26
P70372_EL	Elavl1	ELAV-like p	R.AISTLNGLR.L	18.52	57.34	0.32	3.10
P70372_EL	Elavl1	ELAV-like p	K.DANLYISGLPR.T	54.41	165.03	0.33	3.03
P70372_EL	Elavl1	ELAV-like p	R.DK#VAGHSLGYGFVNYVTAK#.D	47.50	30.73	1.55	0.65
P70372_EL	Elavl1	ELAV-like p	K.DVEDM*FSR.F	24.17	67.58	0.36	2.80
P70372_EL	Elavl1	ELAV-like p	K.FAANPNQNK#.N	290.11	187.91	1.54	0.65
P70372_EL	Elavl1	ELAV-like p	R.FGGPVHHQAQR.F	8.19	13.34	0.61	1.63
P70372_EL	Elavl1	ELAV-like p	K.ILQVSFK#.T	234.53	109.12	2.15	0.47
P70372_EL	Elavl1	ELAV-like p	K.NMALLSQLYHSPAR.R	7.95	25.92	0.31	3.26
P70372_EL	Elavl1	ELAV-like p	R.SEAEEAITSFNGHK#PPGSSEPITVK#.F	26.76	18.91	1.41	0.71
P70372_EL	Elavl1	ELAV-like p	R.SLFSSIGEVESAK#.L	411.06	212.81	1.93	0.52
P70372_EL	Elavl1	ELAV-like p	R.TNLIVNYLPQNM*TQEELR.S	32.94	64.08	0.51	1.95
P70372_EL	Elavl1	ELAV-like p	R.TNLIVNYLPQNMTQEELR.S	11.03	24.53	0.45	2.22
P70372_EL	Elavl1	ELAV-like p	K.VAGHSLGYGFVNYVTAK#.D	146.73	88.78	1.65	0.61
P70372_EL	Elavl1	ELAV-like p	R.VLVDQTTGLSR.G	152.26	429.71	0.35	2.82
P70372_EL	Elavl1	ELAV-like p	K.DANLYISGLPR.T	1.73	6.77	0.26	3.92
P70372_EL	Elavl1	ELAV-like p	K.ILQVSFK#.T	30.78	20.59	1.49	0.67
P70372_EL	Elavl1	ELAV-like p	R.SLFSSIGEVESAK#.L	9.12	6.40	1.43	0.70
Q9JHC9_EL	Elf2	ETS-related	R.SPTTTAPVSAAAAPR.T	3.73	9.38	0.40	2.51
Q9JHC9_EL	Elf2	ETS-related	R.VSLSAESLLK#.A	11.84	9.36	1.27	0.79
Q8BHL5_EL	Elmo2	Engulfment	K.EPSSYDFVYHYG.-	9.86	9.86	1.00	1.00
Q8BHL5_EL	Elmo2	Engulfment	R.IAFDAESDPSNVPGSGTEK#.R	4.98	3.45	1.44	0.69
Q8BHL5_EL	Elmo2	Engulfment	K.VAIEWPGANAQLLEIDQK#.R	4.45	3.08	1.44	0.69
Q8BHL5_EL	Elmo2	Engulfment	K.VLHYGDLDDNPQGEVTFESLQEK#.I	7.50	5.76	1.30	0.77
E9Q2I4_E9	Elmsan1	Protein Elm	R.TVGPTEVAQVGGADEDGTGLEQYPTEHKPSVIVTR.R	3.31	6.65	0.50	2.01
E9Q2I4_E9	Elmsan1	Protein Elm	R.VPGTDAAAQAEDLNVK#.L	11.26	7.97	1.41	0.71
Q91WG4_E	Elp2	Elongator c	R.NFVENFSVISR.Q	2.45	8.50	0.29	3.46
Q91WG4_E	Elp2	Elongator c	R.TEDGSPSNELVSGGSDNR.V	6.00	8.24	0.73	1.37
Q9CZX0_EL	Elp3	Elongator c	R.GTGLYELWK#.S	10.66	9.20	1.16	0.86
Q9CZX0_EL	Elp3	Elongator c	R.ILALVPPWTR.V	4.84	24.05	0.20	4.97
Q9CZX0_EL	Elp3	Elongator c	R.LEIGVQSVYEDVAR.D	1.74	10.98	0.16	6.30
O70378_E	Emc8	ER membra	R.IAEGFGDAALIM*VDNAK#.F	6.23	9.66	0.65	1.55
O70378_E	Emc8	ER membra	R.IAEGFGDAALIMVDNAK#.F	4.54	1.95	2.32	0.43
O70378_E	Emc8	ER membra	R.VKDASPNQVAEK.V	6.48	6.90	0.94	1.06
O35130_N	Emg1	Ribosomal	R.FSVQEQDWETTPPK#.K	5.00	3.82	1.31	0.76

O35130_N	Emg1	Ribosomal	K.IGTSFSVEDISDIR.E	5.65	11.81	0.48	2.09
O35130_N	Emg1	Ribosomal	K.NVLIEVNPQTR.I	6.19	14.44	0.43	2.33
Q3UMY5_E	Eml4	Echinoderm	R.VQQQEDEITVLK#.A	3.34	3.04	1.10	0.91
Q8BMB0_E	Emsy	Protein EM	K.LSQPQLEQTQLQVK#.T	7.33	7.86	0.93	1.07
Q8BMB0_E	Emsy	Protein EM	K.SLVSGPTQILAQFPK#.Q	4.71	6.33	0.74	1.34
Q8BMB0_E	Emsy	Protein EM	R.TLLQHVAQSQTATQTSVVVK#.S	5.35	6.34	0.84	1.19
P17182_EN	Eno1	Alpha-enol	K.DATNVGDEGGFAPNILENK#.E	5.28	2.33	2.27	0.44
B2RWS6_E	Ep300	Histone ac	K.TDGK#EEEEQPSTSATQSSPAPGQSK#.K	15.22	21.65	0.70	1.42
Q8CHI8_EP	Ep400	E1A-bindin	K.FSAPSLLYGALR.D	2.41	10.93	0.22	4.54
Q8CHI8_EP	Ep400	E1A-bindin	K.IAQLASIAGPQSR.V	2.11	12.48	0.17	5.92
Q8CHI8_EP	Ep400	E1A-bindin	R.VAQPETPVTLQFQGNK.F	3.16	5.45	0.58	1.72
Q8CHI8_EP	Ep400	E1A-bindin	K.VAYAAQPALK.T	6.16	11.06	0.56	1.80
Q8CHI8_EP	Ep400	E1A-bindin	R.VPGSSFAAGSLQYK#.S	8.10	11.23	0.72	1.39
P48193_41	Epb41	Protein 4.1	K.TQTVTISDTANAVK#.S	9.42	7.93	1.19	0.84
P48193_41	Epb41	Protein 4.1	K.VVVHQETEISEE.-	11.03	11.03	1.00	1.00
P48193_41	Epb41	Protein 4.1	K.TQTVTISDTANAVK#.S	14.39	2.94	4.89	0.20
P48193_41	Epb41	Protein 4.1	K.VVVHQETEISEE.-	9.89	9.89	1.00	1.00
Q9Z2H5_E	Epb41l1	Band 4.1-li	R.VSAADSTQVDGGTPM*VK#.D	7.87	2.65	2.97	0.34
O70318_E	Epb41l2	Band 4.1-li	K.AKEVENEQTPVSEPEEEKGSQPGPPVER.Q	5.07	13.10	0.39	2.58
O70318_E	Epb41l2	Band 4.1-li	K.DK#EETIQDTQEEK#LEGGAAK#.R	30.74	15.75	1.95	0.51
O70318_E	Epb41l2	Band 4.1-li	K.EVPIVQTETK#.T	39.46	26.60	1.48	0.67
O70318_E	Epb41l2	Band 4.1-li	R.GLSPAQADSQFLENAK#.R	23.66	16.05	1.47	0.68
O70318_E	Epb41l2	Band 4.1-li	R.SLDGAPIGVVDQSPPGEGSVPGPGVISYTTIQDGR.R	2.66	6.86	0.39	2.58
O70318_E	Epb41l2	Band 4.1-li	K.AKEVENEQTPVSEPEEEKGSQPGPPVER.Q	6.06	19.64	0.31	3.24
O70318_E	Epb41l2	Band 4.1-li	K.DK#EETIQDTQEEK#.L	5.89	3.54	1.66	0.60
O70318_E	Epb41l2	Band 4.1-li	K.DK#EETIQDTQEEK#LEGGAAK#.R	30.08	17.07	1.76	0.57
O70318_E	Epb41l2	Band 4.1-li	K.EVPIVQTETK#.T	41.62	43.65	0.95	1.05
O70318_E	Epb41l2	Band 4.1-li	R.GLSPAQADSQFLENAK#.R	31.91	20.80	1.53	0.65
O70318_E	Epb41l2	Band 4.1-li	R.HSNLM*LEDLDK#AQEAILK#.H	6.21	6.92	0.90	1.11
O70318_E	Epb41l2	Band 4.1-li	R.HSNLMLEDLDK#AQEAILK#.H	5.64	4.98	1.13	0.88
O70318_E	Epb41l2	Band 4.1-li	R.IVITGDAALDHDQALAQAIR.E	11.24	17.50	0.64	1.56
O70318_E	Epb41l2	Band 4.1-li	R.SLDGAPIGVVDQSPPGEGSVPGPGVISYTTIQDGR.R	4.06	8.10	0.50	1.99
O70318_E	Epb41l2	Band 4.1-li	R.SLDGAPIGVVDQSPPGEGSVPGPGVISYTTIQDGRR.D	1.60	6.57	0.24	4.11
O70318_E	Epb41l2	Band 4.1-li	R.SYNLVVAK#.D	49.09	19.25	2.55	0.39
O70318_E	Epb41l2	Band 4.1-li	K.TEM*VTISDASQR.T	5.68	24.49	0.23	4.31
O70318_E	Epb41l2	Band 4.1-li	K.VRPAELEQFESTIGFK.L	14.60	39.91	0.37	2.73
Q9WV92_E	Epb41l3	Band 4.1-li	K.DSVSAAEVGTGQYATTK#.G	12.55	5.58	2.25	0.44
Q9WV92_E	Epb41l3	Band 4.1-li	R.GEEVDQSAPEQEQPATVSHEEEQASTIR.T	3.64	9.06	0.40	2.49
Q9WV92_E	Epb41l3	Band 4.1-li	R.VESTSVGSISPGGAK#.L	24.26	9.86	2.46	0.41
Q9WV92_E	Epb41l3	Band 4.1-li	K.VLQETILVEER.H	5.22	10.38	0.50	1.99
Q9WV92_E	Epb41l3	Band 4.1-li	K.DSVSAAEVGTGQYATTK#.G	6.52	3.49	1.87	0.54
Q03145_E	Epha2	Ephrin typ	K.FADIVSILDK#.L	7.62	6.16	1.24	0.81
Q8VEH5_E	Epm2aip1	EPM2A-int	K.DLELFSNPFSFKPEYAPISVR.V	2.55	7.47	0.34	2.93
Q8VEH5_E	Epm2aip1	EPM2A-int	R.EVLPDHVGVLEGIDLSPEITR.Q	5.21	11.15	0.47	2.14
Q8VEH5_E	Epm2aip1	EPM2A-int	K.DLELFSNPFSFKPEYAPISVR.V	4.10	20.91	0.20	5.10
Q8VEH5_E	Epm2aip1	EPM2A-int	R.EVLPDHVGVLEGIDLSPEITR.Q	5.55	15.63	0.36	2.82
Q8CGC7_S	Eprs	Bifunction	K.ASK#DQVDSAVQELLQLK#.A	25.76	8.30	3.10	0.32
Q8CGC7_S	Eprs	Bifunction	R.DQDVEPGAPSM*GAK#.S	19.75	2.86	6.90	0.15
Q8CGC7_S	Eprs	Bifunction	K.DQVDSAVQELLQLK#.A	9.45	3.27	2.89	0.35
Q8CGC7_S	Eprs	Bifunction	R.FDDTNPEK#EK#EDFEK#.V	16.43	7.40	2.22	0.45
Q8CGC7_S	Eprs	Bifunction	K.FVELPGAEM*GK#.V	28.13	8.62	3.26	0.31
Q8CGC7_S	Eprs	Bifunction	K.K#EENLAEWYSQVITK#.S	17.80	3.89	4.57	0.22
Q8CGC7_S	Eprs	Bifunction	R.LNLNNTVLSK#.R	42.81	13.16	3.25	0.31
Q8CGC7_S	Eprs	Bifunction	K.NPDVGLK#PVWYSPK#.V	23.88	6.36	3.76	0.27
Q8CGC7_S	Eprs	Bifunction	K.SQGSGLSSGGAGEGQGPK#.K	43.30	9.24	4.68	0.21
Q8CGC7_S	Eprs	Bifunction	K.SSSNTVESTSLYNK#.V	32.36	70.26	0.46	2.17
Q8CGC7_S	Eprs	Bifunction	K.TGQEYK#PGNPSAAAVQTVSTK#.S	51.82	7.63	6.79	0.15
Q8CGC7_S	Eprs	Bifunction	R.VYEELLAIPVVR.G	10.27	7.64	1.34	0.74
Q8CGC7_S	Eprs	Bifunction	K.APK#EDIDAAVK#.Q	12.26	2.72	4.51	0.22
Q8CGC7_S	Eprs	Bifunction	K.ASK#DQVDSAVQELLQLK#.A	208.07	37.46	5.55	0.18
Q8CGC7_S	Eprs	Bifunction	R.ATVAPDK#K#.Q	8.06	1.37	5.87	0.17
Q8CGC7_S	Eprs	Bifunction	K.AYVDDTPAEQM*K#.A	99.94	17.74	5.63	0.18
Q8CGC7_S	Eprs	Bifunction	R.DNYSPGWK#.F	57.21	17.14	3.34	0.30
Q8CGC7_S	Eprs	Bifunction	R.DQDVEPGAPSMGAK#.S	40.36	7.24	5.58	0.18
Q8CGC7_S	Eprs	Bifunction	R.DQDVEPGAPSM*GAK#.S	118.77	26.46	4.49	0.22
Q8CGC7_S	Eprs	Bifunction	K.DQVDSAVQELLQLK#.A	92.54	16.71	5.54	0.18
Q8CGC7_S	Eprs	Bifunction	K.EDIDAAVK#.Q	45.75	7.30	6.27	0.16
Q8CGC7_S	Eprs	Bifunction	K.EVVPVNVLDAQEEM*K#.E	18.66	4.15	4.50	0.22
Q8CGC7_S	Eprs	Bifunction	K.FAGGDYTTTIEAFISASGR.A	7.45	9.67	0.77	1.30
Q8CGC7_S	Eprs	Bifunction	R.FDDTNPEK#.E	20.56	4.64	4.43	0.23
Q8CGC7_S	Eprs	Bifunction	R.FDDTNPEK#EK#EDFEK#.V	107.74	28.55	3.77	0.26
Q8CGC7_S	Eprs	Bifunction	K.FVELPGAEM*GK#.V	154.10	27.62	5.58	0.18
Q8CGC7_S	Eprs	Bifunction	K.ITSLDAK#.L	131.30	32.05	4.10	0.24
Q8CGC7_S	Eprs	Bifunction	K.K#EENLAEWYSQVITK#.S	99.41	12.33	8.06	0.12
Q8CGC7_S	Eprs	Bifunction	R.LNLNNTVLSK#.R	174.75	28.00	6.24	0.16
Q8CGC7_S	Eprs	Bifunction	K.LTIAEK#EAEAK#.L	14.62	2.80	5.23	0.19
Q8CGC7_S	Eprs	Bifunction	K.NPDVGLK#PVWYSPK#.V	90.25	17.73	5.09	0.20
Q8CGC7_S	Eprs	Bifunction	K.SLTGIEYK#PVSATGAEDK#.D	32.58	7.52	4.33	0.23
Q8CGC7_S	Eprs	Bifunction	K.SQGSGLSSGGAGEGQGPK#.K	209.33	30.94	6.77	0.15
Q8CGC7_S	Eprs	Bifunction	K.SSSNTVESTSLYNK#.V	159.88	108.69	1.47	0.68
Q8CGC7_S	Eprs	Bifunction	R.SVVNM*EWDK#.I	18.74	2.66	7.05	0.14
Q8CGC7_S	Eprs	Bifunction	K.TGK#DYVPGQPPASQNSHSNPVSNAQPAGAEK#PEAK#.V	31.02	8.21	3.78	0.26
Q8CGC7_S	Eprs	Bifunction	K.TGQEYK#PGNPSAAAVQTVSTK#.S	211.89	41.60	5.09	0.20
Q8CGC7_S	Eprs	Bifunction	K.THM*VVSNTLEDFQK#.V	41.40	11.19	3.70	0.27
Q8CGC7_S	Eprs	Bifunction	K.THM*VVSNTLEDFQK#.V	14.59	4.40	3.32	0.30
Q8CGC7_S	Eprs	Bifunction	R.VAVQGDVVR.E	50.94	41.98	1.21	0.82
Q8CGC7_S	Eprs	Bifunction	K.VFIEGADAETFSEGEM*VTFINWGNINITK#.I	11.07	2.39	4.64	0.22
Q8CGC7_S	Eprs	Bifunction	R.VSETVAFTDVNSILR.Y	28.54	31.91	0.89	1.12
Q8CGC7_S	Eprs	Bifunction	R.VYEELLAIPVVR.G	49.51	47.92	1.03	0.97
Q8CGC7_S	Eprs	Bifunction	R.YVALLK#.K	78.73	13.06	6.03	0.17
P42567_E	Eps15	Epidermal	K.AEITSQESQISSYEEELLK#.A	5.78	3.61	1.60	0.63
P42567_E	Eps15	Epidermal	K.AEITSQESQISSYEEELLK#.A	3.28	3.57	0.92	1.09
P42567_E	Eps15	Epidermal	R.FHDSSSPLLTSGPSVAELPWAVK#.S	9.04	6.85	1.32	0.76
P42567_E	Eps15	Epidermal	K.SGLPDLILGK#.I	9.20	7.29	1.26	0.79
P42567_E	Eps15	Epidermal	R.TSEVQDLQDEVQR.E	3.48	8.30	0.42	2.38
P42567_E	Eps15	Epidermal	K.YDAIFDSLSPVDGFLSGDK#.V	8.58	5.49	1.56	0.64
Q60902_E	Eps15l1	Epidermal	K.IWDLADPEGK#.G	9.99	6.52	1.53	0.65
Q60902_E	Eps15l1	Epidermal	K.NPSLPSKLDPFESSDPFSSSSISSK.G	2.78	4.66	0.60	1.68
Q60902_E	Eps15l1	Epidermal	K.SGLSDIILGK#.I	16.68	10.51	1.59	0.63
Q60902_E	Eps15l1	Epidermal	R.SLEQYDQVPDGVSGTSLPDLATLNEGILLAER.G	5.00	7.98	0.63	1.60
Q60902_E	Eps15l1	Epidermal	K.TQIQSQESDLK#.S	13.47	9.64	1.40	0.72
Q60902_E	Eps15l1	Epidermal	K.TQIQSQESDLKSQEDDLNR.A	6.36	16.53	0.39	2.60
Q60902_E	Eps15l1	Epidermal	R.VGASEAALFLK#.K	16.27	9.59	1.70	0.59

Q08509_E	Eps8	Epidermal	K.ANLISEDIESAISDSK#.G	20.90	8.93	2.34	0.43
Q08509_E	Eps8	Epidermal	K.DTVDFLNYTATAEER.K	2.35	6.95	0.34	2.96
Q08509_E	Eps8	Epidermal	K.HGFNLLAK#.L	16.11	9.74	1.65	0.60
Q08509_E	Eps8	Epidermal	K.ISAAASDSGVESFDEGSSH.-	14.98	14.98	1.00	1.00
Q08509_E	Eps8	Epidermal	R.NASGDSGFVPNNILDIMR.T	6.46	8.23	0.79	1.27
Q99K30_E	Eps8l2	Epidermal	R.LLDVESQEELENFPLPTVQHSQTVLNQLR.Y	3.52	3.12	1.13	0.89
Q99K30_E	Eps8l2	Epidermal	R.QEDVGAPLEQSGQK#.Y	5.39	3.13	1.72	0.58
Q99K30_E	Eps8l2	Epidermal	R.SQPVHLPLTFESGPDEVR.A	4.89	9.29	0.53	1.90
Q99K30_E	Eps8l2	Epidermal	R.SVSSPLLSTDAVSFLR.G	4.58	10.20	0.45	2.23
Q99K30_E	Eps8l2	Epidermal	R.VGLPLPVPFSEPGYR.R	5.71	11.80	0.48	2.07
Q99K30_E	Eps8l2	Epidermal	R.VYSQLTVQK#.A	22.29	9.84	2.27	0.44
Q99MI1_R	Erc1	ELKS/Rab6-	R.AAILQTEVDALR.L	29.99	27.24	1.10	0.91
Q99MI1_R	Erc1	ELKS/Rab6-	K.LETLTNQFSDSK#.Q	20.22	11.50	1.76	0.57
Q99MI1_R	Erc1	ELKS/Rab6-	K.SLQADTTNTDTALTTLEEALADKER.T	6.50	10.14	0.64	1.56
Q8BHK9_E	Ercc6l	DNA excisi	K.ELFTVGDLQK#.S	10.11	2.24	4.51	0.22
Q8BHK9_E	Ercc6l	DNA excisi	R.SPLAELGVLK#.K	9.91	6.09	1.63	0.61
Q9DC16_E	Ergic1	Endoplasm	R.YDLSPITVK#.Y	6.19	5.00	1.24	0.81
Q9DC16_E	Ergic1	Endoplasm	R.YSYQYTVANK#.E	8.66	6.40	1.35	0.74
P84089_E	Erh	Enhancer o	R.ADTQTYQPYNK.D	14.78	24.03	0.62	1.63
P84089_E	Erh	Enhancer o	K.IYVLLR.R	19.55	128.77	0.15	6.59
P57759_E	Erp29	Endoplasm	K.FDTQYPYGEK#.Q	8.15	1.95	4.17	0.24
Q3U7R1_E	Esyt1	Extended s	R.ALTLGALTLPLAR.L	6.13	21.23	0.29	3.46
Q3U7R1_E	Esyt1	Extended s	K.LLAETVAPAVR.G	2.91	12.68	0.23	4.36
Q3U7R1_E	Esyt1	Extended s	R.ALTLGALTLPLAR.L	5.05	18.38	0.27	3.64
Q3U7R1_E	Esyt1	Extended s	R.LTHGDSPSEAPVGPLGQVK#.L	12.57	8.26	1.52	0.66
Q8BWY3_E	Etf1	Eukaryotic	K.FGATLEIVTDK#.S	40.72	14.17	2.87	0.35
Q8BWY3_E	Etf1	Eukaryotic	K.FGATLEIVTDK#SQEGSQFVK#.G	50.97	17.46	2.92	0.34
Q8BWY3_E	Etf1	Eukaryotic	K.FHTEALTALLSDDSK#.F	23.34	10.48	2.23	0.45
Q8BWY3_E	Etf1	Eukaryotic	K.FHTEALTALLSDDSK#.F	8.31	3.61	2.30	0.43
Q8BWY3_E	Etf1	Eukaryotic	K.FTVDLPK#.K	74.87	26.55	2.82	0.35
Q8BWY3_E	Etf1	Eukaryotic	K.ILYLTPEQEK#.D	87.51	31.74	2.76	0.36
Q8BWY3_E	Etf1	Eukaryotic	R.LSVLGAITSVQQR.L	25.23	35.82	0.70	1.42
Q8BWY3_E	Etf1	Eukaryotic	K.SQEGSQFVK#.G	39.33	14.87	2.65	0.38
Q8BWY3_E	Etf1	Eukaryotic	K.TELSQSDM*FDQR.L	8.77	12.76	0.69	1.46
Q8BWY3_E	Etf1	Eukaryotic	K.TELSQSDMFDQR.L	5.10	9.46	0.54	1.85
Q8BWY3_E	Etf1	Eukaryotic	K.VAETAVQLFISGDK#.V	14.30	3.21	4.46	0.22
Q8BWY3_E	Etf1	Eukaryotic	K.VNVAGLVLAGSADFK#.T	29.85	11.38	2.62	0.38
Q8BWY3_E	Etf1	Eukaryotic	R.YFDEISQDTGK#.Y	18.15	5.72	3.17	0.32
Q99LC5_ET	Etfa	Electron tr	K.LNVAPVSDIIEIK#.S	5.59	2.01	2.78	0.36
P97360_ET	Etv6	Transcripti	K.ALLLLTK#.E	12.58	20.10	0.63	1.60
P97360_ET	Etv6	Transcripti	K.TPDEIM*SGR.T	2.00	13.01	0.15	6.50
Q61545_E	Ewsr1	RNA-bindin	K.AAVEWFDGK.D	11.21	11.77	0.95	1.05
Q61545_E	Ewsr1	RNA-bindin	K.GDATVSYEDPPTAK#.A	75.37	78.84	0.96	1.05
Q61545_E	Ewsr1	RNA-bindin	R.GGPGGPGGPGGPM*GR.M	3.11	16.74	0.19	5.38
Q61545_E	Ewsr1	RNA-bindin	R.QDHPSSM*GVYGQESGGFSGPGENR.S	10.27	43.02	0.24	4.19
Q61545_E	Ewsr1	RNA-bindin	R.QDHPSSMGVYGQESGGFSGPGENR.S	5.97	19.64	0.30	3.29
Q8R3S6_E	Exoc1	Exocyst cor	K.DAIK#ENPEFDLHFEK#.V	14.00	11.36	1.23	0.81
Q8R3S6_E	Exoc1	Exocyst cor	K.DAIK#ENPEFDLHFEK#.V	10.45	9.92	1.05	0.95
Q8R3S6_E	Exoc1	Exocyst cor	K.LSSYEEM*LQSVK#.E	8.46	4.30	1.96	0.51
Q9D4H1_E	Exoc2	Exocyst cor	K.HNFQGIEK#.I	12.90	16.76	0.77	1.30
Q9D4H1_E	Exoc2	Exocyst cor	R.HTFLNIAEHFEK#.H	13.34	11.21	1.19	0.84
Q9D4H1_E	Exoc2	Exocyst cor	R.ASNTADTLFQEVLGR.K	5.61	12.39	0.45	2.21
Q9D4H1_E	Exoc2	Exocyst cor	R.LFENYIELK#.A	14.32	8.68	1.65	0.61
Q9D4H1_E	Exoc2	Exocyst cor	R.VVEAVSEELSR.L	4.49	18.87	0.24	4.20
O35382_E	Exoc4	Exocyst cor	K.ESEVLIGNLGDK#.L	17.77	10.47	1.70	0.59
O35382_E	Exoc4	Exocyst cor	R.SGELQGGPDDNLIEGGGTK#.F	14.59	8.05	1.81	0.55
O35382_E	Exoc4	Exocyst cor	R.SQTGVGDQTTQNTR.L	3.48	8.87	0.39	2.55
O35382_E	Exoc4	Exocyst cor	R.STTQVADSAYQR.G	3.56	9.19	0.39	2.58
Q3TPX4_E	Exoc5	Exocyst cor	K.LIQSVFEIK#.L	21.23	7.91	2.68	0.37
Q3TPX4_E	Exoc5	Exocyst cor	K.QVGDIFSNPEAVLAK#.L	6.92	3.25	2.13	0.47
A6H5Z3_E	Exoc6b	Exocyst cor	R.TLSNSLQNVIK#.R	7.18	4.05	1.78	0.56
A6H5Z3_E	Exoc6b	Exocyst cor	R.VNPVTALTLLEK#.M	13.33	4.73	2.82	0.35
A6H5Z3_E	Exoc6b	Exocyst cor	K.VVGQFPFQDIELEK#.Q	5.57	5.60	0.99	1.01
A6H5Z3_E	Exoc6b	Exocyst cor	K.VVGQFPFQDIELEK#.Q	6.78	10.41	0.65	1.54
O35250_E	Exoc7	Exocyst cor	K.AVEYFQDNSPDSPELNK#.V	7.86	4.11	1.91	0.52
O35250_E	Exoc7	Exocyst cor	K.SELIQLVAVTQK#.T	16.86	9.52	1.77	0.56
O35250_E	Exoc7	Exocyst cor	K.VLGNLQLNLLSK#.S	11.09	6.87	1.61	0.62
Q6PGF7_E	Exoc8	Exocyst cor	R.GAVQAGFLPGPAGVPR.E	1.97	7.03	0.28	3.58
Q6PGF7_E	Exoc8	Exocyst cor	R.GAVQAGFLPGPAGVPR.E	2.48	6.74	0.37	2.72
P56960_E	Exosc10	Exosome c	K.FALGSVVAVTK#.A	7.65	6.61	1.16	0.86
P56960_E	Exosc10	Exosome c	K.ASGGLPQFGDEYDFYR.S	3.02	8.08	0.37	2.68
P56960_E	Exosc10	Exosome c	K.FALGSVVAVTK#.A	38.79	15.40	2.52	0.40
P56960_E	Exosc10	Exosome c	K.HQQPVLPAGLQVPK#.T	17.20	9.61	1.79	0.56
P56960_E	Exosc10	Exosome c	R.K#PLPLALSK#.E	17.54	8.26	2.12	0.47
P56960_E	Exosc10	Exosome c	R.SDMYILNESLTDPAIVK#.V	4.41	3.26	1.35	0.74
P56960_E	Exosc10	Exosome c	K.SK#PSSQFDPNK#.L	4.77	2.78	1.72	0.58
P56960_E	Exosc10	Exosome c	R.TEDFIVDTLELR.S	7.16	10.95	0.65	1.53
P56960_E	Exosc10	Exosome c	K.VFHGADSDIEWLQK#.D	14.22	7.60	1.87	0.53
P56960_E	Exosc10	Exosome c	R.VGM*LLDEASGVNK#.H	7.89	5.58	1.42	0.71
P56960_E	Exosc10	Exosome c	K.ASGGLPQFGDEYDFYR.S	3.47	8.68	0.40	2.50
P56960_E	Exosc10	Exosome c	K.IDNSNTPFLPK#.I	19.60	12.09	1.62	0.62
P56960_E	Exosc10	Exosome c	R.K#PLPLALSK#.E	16.47	7.10	2.32	0.43
P56960_E	Exosc10	Exosome c	R.SDMYILNESLTDPAIVK#.V	8.60	4.48	1.92	0.52
P56960_E	Exosc10	Exosome c	R.VGM*LLDEASGVNK#HQQPVLPAGLQVPK#.T	7.60	3.29	2.31	0.43
Q8VBV3_E	Exosc2	Exosome c	K.LGQGVLVQVSPSLVK#.R	12.44	6.15	2.02	0.49
Q7TQK4_E	Exosc3	Exosome c	R.HK#EPSGGGGGVYWVDSQQK#.R	10.35	1.23	8.45	0.12
Q921I9_EX	Exosc4	Exosome c	R.M*GVFAQADGSAYIEQGNTK#.A	5.41	1.31	4.11	0.24
Q9CRA8_E	Exosc5	Exosome c	R.ADANLLTDTGTESSPR.S	2.82	8.58	0.33	3.04
Q9CRA8_E	Exosc5	Exosome c	K.IGLPGVAEK#.S	21.80	13.32	1.64	0.61
Q8BTW3_E	Exosc6	Exosome c	R.AGLLSQAK#.G	15.72	7.67	2.05	0.49
Q8BTW3_E	Exosc6	Exosome c	R.GSGPAGAGGEAPAALR.G	4.59	9.57	0.48	2.08
Q8BTW3_E	Exosc6	Exosome c	R.IRGPEESQPPQLYAAEDDETPAAR.D	1.27	4.91	0.26	3.85
Q9D753_E	Exosc8	Exosome c	R.ATTVNIGSISTADGSALVK#.L	11.45	4.87	2.35	0.43
Q9JHI7_EX	Exosc9	Exosome c	K.VAEITELIQK#.A	35.13	10.29	3.42	0.29
Q61188_E	Ezh2	Histone-lys	R.AIQTGEELFFDYR.Y	5.49	11.48	0.48	2.09
Q61188_E	Ezh2	Histone-lys	K.HLLLAPSDVAGWGIFIKDPVQK.N	8.74	5.61	1.56	0.64
Q61188_E	Ezh2	Histone-lys	R.TETLNQEWK#.Q	26.69	20.22	1.32	0.76
P26040_EZ	Ezr	Ezrin OS=M	K.APDFVFYAPR.L	4.13	14.73	0.28	3.57
P26040_EZ	Ezr	Ezrin OS=M	K.IGFPWSEIR.N	5.60	14.94	0.37	2.67
P26040_EZ	Ezr	Ezrin OS=M	K.LFFLQVK.D	14.12	11.26	1.25	0.80
P54731_F	Faf1	FAS-associa	K.LLSTFPR.R	9.80	24.83	0.39	2.53
P54731_F	Faf1	FAS-associa	R.LSLEQALPPEPK#.E	11.37	12.38	0.92	1.09
P54731_F	Faf1	FAS-associa	R.NVYDLTSIPVR.H	12.92	32.72	0.39	2.53

P54731_FA	Faf1	FAS-associa	R.RDVTQLDPNK.S	6.05	21.08	0.29	3.49
P54731_FA	Faf1	FAS-associa	K.TGDVEDSTVLK#.S	61.91	29.35	2.11	0.47
P54731_FA	Faf1	FAS-associa	R.TPSGEFLER.R	13.92	31.37	0.44	2.25
Q9D2L9_F1	Fam111a	Protein FAM	R.VVSVTQNSGSENR.N	3.30	14.54	0.23	4.41
Q8VE88_F1	Fam114a2	Protein FAM	K.SILSSLSGEELQTTR.L	2.26	4.72	0.48	2.08
Q6A0A9_F1	FAM120A	Constitutiv	K.SQGGVQPIPSQGGK#.L	4.72	3.72	1.27	0.79
Q6A0A9_F1	FAM120A	Constitutiv	R.EAALEAAVLNK#EE.-	14.90	10.27	1.45	0.69
Q6A0A9_F1	FAM120A	Constitutiv	R.LPPEFSPLIIK#.E	10.50	8.73	1.20	0.83
Q6A0A9_F1	FAM120A	Constitutiv	K.NLTEQNSYSNIPHEGK#.H	25.21	12.82	1.97	0.51
Q6A0A9_F1	FAM120A	Constitutiv	K.SPQTPELVEALAFR.E	6.01	14.70	0.41	2.45
Q6A0A9_F1	FAM120A	Constitutiv	K.SQGAIQGRPPYAASAEEVAK.E	8.96	27.30	0.33	3.05
Q6A0A9_F1	FAM120A	Constitutiv	K.SQGGVQPIPSQGGK#.L	18.21	16.99	1.07	0.93
Q6A0A9_F1	FAM120A	Constitutiv	K.VEGSSTASSGSQLAEGK#.G	32.14	17.45	1.84	0.54
Q6A0A9_F1	FAM120A	Constitutiv	R.EAALEAAVLNK#EE.-	25.73	14.45	1.78	0.56
Q6A0A9_F1	FAM120A	Constitutiv	R.GDPGDQVK#VEGSSTASSGSQLAEGK#.G	12.11	6.30	1.92	0.52
Q6A0A9_F1	FAM120A	Constitutiv	R.LPPEFSPLIIK#.E	25.32	13.32	1.90	0.53
Q6A0A9_F1	FAM120A	Constitutiv	K.LYEPDQLQELK#.I	58.03	30.88	1.88	0.53
Q6A0A9_F1	FAM120A	Constitutiv	K.NLTEQNSYSNIPHEGK#.H	80.30	31.91	2.52	0.40
Q6A0A9_F1	FAM120A	Constitutiv	R.QNHPLPFPPPPALPFYPASVYPR.H	5.96	22.41	0.27	3.76
Q6A0A9_F1	FAM120A	Constitutiv	K.SLTTSQYLM*HEVAK#.Q	9.06	4.06	2.23	0.45
Q6A0A9_F1	FAM120A	Constitutiv	K.SPQTPELVEALAFR.E	10.06	19.86	0.51	1.97
Q6A0A9_F1	FAM120A	Constitutiv	K.SQGGVQPIPSQGGK#.L	54.12	23.29	2.32	0.43
Q6A0A9_F1	FAM120A	Constitutiv	K.VEGSSTASSGSQLAEGK#.G	73.91	46.99	1.57	0.64
Q8R1F1_NI	Fam129b	Niban-like p	R.AVINSAGYK#.V	42.65	12.77	3.34	0.30
Q8R1F1_NI	Fam129b	Niban-like p	K.EVTDM*NLNVINEGGIDK#.L	5.74	3.80	1.51	0.66
Q8R1F1_NI	Fam129b	Niban-like p	R.FQELIFEDFAR.F	19.56	28.61	0.68	1.46
Q8R1F1_NI	Fam129b	Niban-like p	R.FSLVPHNYGLVLYENK#.V	61.51	16.82	3.66	0.27
Q8R1F1_NI	Fam129b	Niban-like p	R.FYEDQYGVSLFNSM*R.H	4.47	3.64	1.23	0.81
Q8R1F1_NI	Fam129b	Niban-like p	R.HEIEGTGPPQAQLLWR.K	8.55	14.14	0.61	1.65
Q8R1F1_NI	Fam129b	Niban-like p	K.KYDYDSSSVR.K	4.07	6.40	0.64	1.57
Q8R1F1_NI	Fam129b	Niban-like p	R.QWIQISDAVYR.L	10.34	6.20	1.67	0.60
Q8R1F1_NI	Fam129b	Niban-like p	K.VLTSVDQYLELVGNSLPGTTSK#.S	52.31	26.64	1.96	0.51
Q8R1F1_NI	Fam129b	Niban-like p	R.AVINSAGYK#.V	92.26	27.40	3.37	0.30
Q8R1F1_NI	Fam129b	Niban-like p	K.EVTDM*NLNVINEGGIDK#.L	10.39	4.49	2.32	0.43
Q8R1F1_NI	Fam129b	Niban-like p	K.EVTDMNLNVINEGGIDK#.L	6.74	2.20	3.07	0.33
Q8R1F1_NI	Fam129b	Niban-like p	R.FDVSSTSVFK#.Q	79.45	30.33	2.62	0.38
Q8R1F1_NI	Fam129b	Niban-like p	R.FSLVPHNYGLVLYENK#.V	5.64	1.98	2.86	0.35
Q8R1F1_NI	Fam129b	Niban-like p	R.FYEDQYGVSLFNSM*R.H	3.33	4.96	0.67	1.49
Q8R1F1_NI	Fam129b	Niban-like p	R.HEIEGTGPPQAQLLWR.K	6.16	15.05	0.41	2.44
Q8R1F1_NI	Fam129b	Niban-like p	K.LSQLAYHPLK#.M	79.76	31.12	2.56	0.39
Q8R1F1_NI	Fam129b	Niban-like p	R.LVFEQAK#.V	61.54	11.62	5.29	0.19
Q8R1F1_NI	Fam129b	Niban-like p	R.QWIQISDAVYR.L	11.51	5.32	2.16	0.46
Q8R1F1_NI	Fam129b	Niban-like p	K.SGSTPILK#.C	48.78	22.80	2.14	0.47
Q8R1F1_NI	Fam129b	Niban-like p	R.TDM*DQIITSK#.E	56.79	12.63	4.50	0.22
Q8R1F1_NI	Fam129b	Niban-like p	K.VEGPAFTDAIR.M	14.52	24.78	0.59	1.71
Q8R1F1_NI	Fam129b	Niban-like p	K.VLTSVDQYLELVGNSLPGTTSK#.S	80.74	22.57	3.58	0.28
Q3TCJ1_F1	Fam175b	BRISC comp	R.AIYQVYNALQEK#.V	8.02	1.73	4.64	0.22
Q3TCJ1_F1	Fam175b	BRISC comp	K.VSSVPNTSQSYAK#.V	11.58	4.59	2.52	0.40
Q9CQB2_F1	Fam195a	Protein FAM	R.TGPTQQQVESR.L	3.40	6.13	0.55	1.80
Q3UGS4_F1	Fam195b	Protein FAM	R.FIYEAWQGVER.D	3.55	9.73	0.36	2.74
P58468_F2	Fam207a	Protein FAM	R.AVEPALPQSPAGGAGAK#.D	9.81	8.51	1.15	0.87
P58468_F2	Fam207a	Protein FAM	R.DALPELQELEAGR.Q	3.44	12.21	0.28	3.55
Q69ZR9_F2	Fam208a	Protein FAM	R.LQAQNIQQR.H	7.09	20.28	0.35	2.86
Q69ZR9_F2	Fam208a	Protein FAM	K.NVSYVSAISTPIFSAQEK#.M	4.56	6.98	0.65	1.53
Q69ZR9_F2	Fam208a	Protein FAM	R.VVSISSSDFSAK.E	15.36	13.36	1.15	0.87
Q5DTT3_F2	Fam208b	Protein FAM	K.TPVSNVGQQSR.S	2.03	16.00	0.13	7.88
Q6PGL7_FA	Fam21	WASH com	K.DLYIDRPLPYLIGSK.L	4.93	17.38	0.28	3.52
Q6PGL7_FA	Fam21	WASH com	K.IPAGAVSVLLGHPDVSGSTSAPSLK#.E	16.97	10.24	1.66	0.60
Q6PGL7_FA	Fam21	WASH com	K.QTSSLQPQSQEK#.A	5.63	3.84	1.47	0.68
Q6PGL7_FA	Fam21	WASH com	R.RTPADDEEDILFPPPTLTDEDFSPFGSR.G	2.41	6.64	0.36	2.75
Q6PGL7_FA	Fam21	WASH com	K.SSHLPTPAGLFDDDDNDNDEDDNNFFM*PSSSK#PSK#.T	1.86	2.00	0.93	1.08
Q6PGL7_FA	Fam21	WASH com	R.SSVPSGGSLFGDDEDDDLFSSAK#.T	4.86	3.78	1.29	0.78
Q6PGL7_FA	Fam21	WASH com	K.STAIIFDDDEGDLFK#.E	4.71	12.13	0.39	2.57
Q6PGL7_FA	Fam21	WASH com	K.TEPAQDSSGLTPFK#.S	8.57	11.37	0.75	1.33
Q6PGL7_FA	Fam21	WASH com	K.VPLLFSDEEDSEVPSGVKPEDLK.V	20.40	13.20	1.55	0.65
Q6PGL7_FA	Fam21	WASH com	K.IPAGAVSVLLGHPDVSGSTSAPSLK#.E	9.34	7.50	1.25	0.80
Q6PGL7_FA	Fam21	WASH com	K.VPLLFSDEEDSEVPSGVKPEDLK.V	16.87	12.08	1.40	0.72
Q9D8N2_FA	Fam45a	Protein FAM	K.EIGQLIVQSAEDPEKSDSQVIQDIALK.T	4.19	8.57	0.49	2.04
Q9D8N2_FA	Fam45a	Protein FAM	K.IEAVQEFTR.T	5.33	10.95	0.49	2.05
Q9D8N2_FA	Fam45a	Protein FAM	K.VILNVEALK.Q	6.35	10.24	0.62	1.61
Q9D8N2_FA	Fam45a	Protein FAM	K.EIGQLIVQSAEDPEK#SDSQVIQDIALK#.T	4.50	3.55	1.27	0.79
Q9WTJ8_FA	Fam50b	Protein FAM	K.FSAHYDAVEAELK#.S	31.10	16.40	1.90	0.53
Q68FE6_FA	Fam65a	Protein FAM	R.LGFLYDLDK#.Q	10.33	3.20	3.23	0.31
Q922G2_FA	Fam76a	Protein FAM	K.ADFQYQESQTR.A	2.34	13.59	0.17	5.82
Q80XP8_FA	Fam76b	Protein FAM	K.ADFQYQESNLR.T	3.91	18.60	0.21	4.75
Q80XP8_FA	Fam76b	Protein FAM	K.SLGSSHSNSSSSSLTEK#.D	2.43	3.08	0.79	1.27
Q80XP8_FA	Fam76b	Protein FAM	K.SSAAIQNETPK.K	19.58	24.18	0.81	1.24
Q148V8_FA	Fam83h	Protein FAM	K.EQTVSETLGPSGEAVR.S	1.15	6.69	0.17	5.81
Q3UVG3_F9	Fam91a1	Protein FAM	R.SPSSLLIASLHL.-	12.54	12.54	1.00	1.00
Q3UVG3_F9	Fam91a1	Protein FAM	K.IIDSGPQLSGSLDYNVVHSLYNK#.G	23.41	12.83	1.82	0.55
Q3UVG3_F9	Fam91a1	Protein FAM	K.K#GQVINLDQLHSSWK#.N	12.90	5.69	2.27	0.44
Q3UVG3_F9	Fam91a1	Protein FAM	K.LSDESLDSFLIELEK#.V	23.42	9.37	2.50	0.40
Q3UVG3_F9	Fam91a1	Protein FAM	K.LYIYHVTGQGPPSLLLSK#.G	12.47	7.84	1.59	0.63
Q3UVG3_F9	Fam91a1	Protein FAM	R.SPSSLLIASLHL.-	48.84	48.84	1.00	1.00
Q3UVG3_F9	Fam91a1	Protein FAM	R.VQGDYFETLLYK#.I	27.06	11.08	2.44	0.41
Q3UVG3_F9	Fam91a1	Protein FAM	K.LSDESLDSFLIELEK#.V	21.34	10.85	1.97	0.51
Q3UVG3_F9	Fam91a1	Protein FAM	K.LYIYHVTGQGPPSLLLSK#.G	18.47	7.68	2.41	0.42
Q8BP22_F9	Fam92a1	Protein FAM	R.HLEETIDNFEK#.Q	5.17	3.65	1.41	0.71
Q9D187_M	Fam96b	Mitotic spi	R.EIFDLIR.S	10.74	18.65	0.58	1.74
Q9D187_M	Fam96b	Mitotic spi	R.SINDPEHPLTLEELNVVEQVR.I	2.33	8.57	0.27	3.68
Q3TJZ6_FA	Fam98a	Protein FAM	K.AQEGGGSEVFQELK#.G	31.07	18.87	1.65	0.61
Q3TJZ6_FA	Fam98a	Protein FAM	R.GGRPNEIEPPPPEM*PPWQK.R	5.26	15.82	0.33	3.01
Q3TJZ6_FA	Fam98a	Protein FAM	K.HQGGWTDGGSGSGGGYQDGAYR.D	2.30	11.51	0.20	5.00
Q3TJZ6_FA	Fam98a	Protein FAM	K.IEAINQAIANEYEVR.R	15.69	33.52	0.47	2.14
Q3TJZ6_FA	Fam98a	Protein FAM	K.K#AQEGGGSEVFQELK#.G	7.64	6.95	1.10	0.91
Q3TJZ6_FA	Fam98a	Protein FAM	K.K#PMGPAHWEK#.I	19.83	14.55	1.36	0.73
Q3TJZ6_FA	Fam98a	Protein FAM	R.LDVTVQSFGWSDR.A	8.66	15.39	0.56	1.78
Q3TJZ6_FA	Fam98a	Protein FAM	K.RLDVTVQSFGWSDR.A	4.18	32.61	0.13	7.80
Q80VD1_FA	Fam98b	Protein FAM	R.DDLESFQLEISGFLK#.E	24.29	14.50	1.67	0.60
Q80VD1_FA	Fam98b	Protein FAM	R.GPELGPETSM*EGDVLDTLEALGYK#.G	11.98	5.17	2.32	0.43
Q80VD1_FA	Fam98b	Protein FAM	K.GPLLEEQALSK#.A	138.11	74.81	1.85	0.54
Q80VD1_FA	Fam98b	Protein FAM	-.M*RGPELGPETSM*EGDVLDTLEALGYK.G	2.77	7.61	0.36	2.74
Q80VD1_FA	Fam98b	Protein FAM	K.SDTSDIPLLLSQVESK#.V	59.84	38.82	1.54	0.65

Q80VD1_F	Fam98b	Protein FA	K.TTVTLAHLLAAR.E	8.70	26.35	0.33	3.03
Q80VD1_F	Fam98b	Protein FA	K.VDLSSEQAEK#.L	69.26	54.39	1.27	0.79
Q8K368_F	Fanci	Fanconi an	K.LGANILLETFK#.I	8.72	4.70	1.85	0.54
F8VPU2_FA	Farp1	FERM, Rho	R.LGAPENSGISTLER.G	3.24	7.39	0.44	2.28
F8VPU2_FA	Farp1	FERM, Rho	R.LGAPENSGISTLER.G	5.29	12.38	0.43	2.34
F8VPU2_FA	Farp1	FERM, Rho	R.SLVSQPTAPNSEVPK#.Q	11.23	11.62	0.97	1.03
F8VPU2_FA	Farp1	FERM, Rho	R.AALAEITEMVAQLHGTM*IK#.M	9.46	6.54	1.45	0.69
F8VPU2_FA	Farp1	FERM, Rho	K.HSEALEALETSIK#.G	15.95	8.81	1.81	0.55
F8VPU2_FA	Farp1	FERM, Rho	R.LGAPENSGISTLER.G	10.55	34.37	0.31	3.26
F8VPU2_FA	Farp1	FERM, Rho	R.SLVSQPTAPNSEVPK#.Q	35.47	24.84	1.43	0.70
F8VPU2_FA	Farp1	FERM, Rho	R.YLFALQVK#.Q	13.70	19.74	0.69	1.44
Q8C0C7_SY	Farsa	Phenylalan	R.DRPFKPYNFSAR.G	6.50	40.42	0.16	6.22
Q8C0C7_SY	Farsa	Phenylalan	R.K#LLTEVILK#.T	52.80	27.98	1.89	0.53
Q8C0C7_SY	Farsa	Phenylalan	R.LDIEPR.S	11.71	33.22	0.35	2.84
Q8C0C7_SY	Farsa	Phenylalan	R.LEVADGGLDSAELATQLGVEHQAVVGAVK#.S	4.39	2.98	1.47	0.68
Q8C0C7_SY	Farsa	Phenylalan	K.LGITQLR.F	28.76	61.15	0.47	2.13
Q8C0C7_SY	Farsa	Phenylalan	K.LLTEVILK#.T	41.57	25.55	1.63	0.61
Q8C0C7_SY	Farsa	Phenylalan	K.QEAELSPEM*ISSGSWR.D	2.66	7.05	0.38	2.65
Q8C0C7_SY	Farsa	Phenylalan	R.RLEVADGGLDSAELATQLGVEHQAVVGAVK.S	16.80	30.23	0.56	1.80
Q8C0C7_SY	Farsa	Phenylalan	K.SLQALGEVIEAELR.S	20.23	51.53	0.39	2.55
Q8C0C7_SY	Farsa	Phenylalan	R.THSQGGYGSQGYK#.Y	17.59	6.26	2.81	0.36
Q8C0C7_SY	Farsa	Phenylalan	K.TYWVSK#.G	48.25	27.90	1.73	0.58
Q8C0C7_SY	Farsa	Phenylalan	R.VVDSIEDEVQK#.R	18.26	11.42	1.60	0.63
Q8C0C7_SY	Farsa	Phenylalan	K.YGINNIR.E	17.98	60.62	0.30	3.37
Q8C0C7_SY	Farsa	Phenylalan	R.ALYQLAQK#.K	8.03	5.25	1.53	0.65
Q8C0C7_SY	Farsa	Phenylalan	K.LLTEVILK#.T	22.23	7.65	2.91	0.34
Q8C0C7_SY	Farsa	Phenylalan	K.SLQALGEVIEAELR.S	5.19	9.24	0.56	1.78
Q8C0C7_SY	Farsa	Phenylalan	R.VVDSIEDEVQK#.R	6.89	3.37	2.04	0.49
Q8C0C7_SY	Farsa	Phenylalan	K.SLQALGEVIEAELR.S	3.36	8.27	0.41	2.46
Q9WUA2_S	Farsb	Phenylalan	R.ADLINK#K#.V	28.17	13.92	2.02	0.49
Q9WUA2_S	Farsb	Phenylalan	R.ALVAIGTHDLDTLSGPFTYTAK#.R	67.39	24.30	2.77	0.36
Q9WUA2_S	Farsb	Phenylalan	K.AQGASDVVLYK#.I	101.48	39.64	2.56	0.39
Q9WUA2_S	Farsb	Phenylalan	K.AVHISNPK#.T	18.60	10.70	1.74	0.58
Q9WUA2_S	Farsb	Phenylalan	R.DLLFQALGR.T	13.11	31.91	0.41	2.43
Q9WUA2_S	Farsb	Phenylalan	K.DRYDSFIELQEK.L	4.87	6.87	0.71	1.41
Q9WUA2_S	Farsb	Phenylalan	K.IDVPANR.Y	13.60	29.33	0.46	2.16
Q9WUA2_S	Farsb	Phenylalan	K.LFEISDVVVK#.D	97.30	45.79	2.13	0.47
Q9WUA2_S	Farsb	Phenylalan	K.LGLDISATK#.A	27.69	13.35	2.07	0.48
Q9WUA2_S	Farsb	Phenylalan	K.LGVLHPDVITK#.F	115.22	45.63	2.53	0.40
Q9WUA2_S	Farsb	Phenylalan	K.LVITEETAK#.V	87.83	39.25	2.24	0.45
Q9WUA2_S	Farsb	Phenylalan	K.TAEFQVAR.T	18.67	34.37	0.54	1.84
Q9WUA2_S	Farsb	Phenylalan	K.TPGFEIIHGLLDR.I	22.83	34.79	0.66	1.52
Q9WUA2_S	Farsb	Phenylalan	R.TTLLPGLLK#.T	82.78	38.50	2.15	0.47
Q9WUA2_S	Farsb	Phenylalan	K.TYTIANQFPLNK#.L	57.54	27.58	2.09	0.48
Q9WUA2_S	Farsb	Phenylalan	R.ALVAIGTHDLDTLSGPFTYTAK#.R	50.78	15.31	3.32	0.30
Q9WUA2_S	Farsb	Phenylalan	K.AQGASDVVLYK#.I	75.36	24.85	3.03	0.33
Q9WUA2_S	Farsb	Phenylalan	K.ASAGSAFFPGR.C	12.85	15.98	0.80	1.24
Q9WUA2_S	Farsb	Phenylalan	R.DLLFQALGR.T	12.77	22.02	0.58	1.72
Q9WUA2_S	Farsb	Phenylalan	K.LFEISDVVVK#.D	70.85	28.05	2.53	0.40
Q9WUA2_S	Farsb	Phenylalan	K.LVITEETAK#.V	80.14	29.20	2.74	0.36
Q9WUA2_S	Farsb	Phenylalan	R.TTLLPGLLK#.T	52.93	17.94	2.95	0.34
Q9WUA2_S	Farsb	Phenylalan	K.TYTIANQFPLNK#.L	33.07	12.70	2.60	0.38
Q9WUA2_S	Farsb	Phenylalan	R.ALVAIGTHDLDTLSGPFTYTAK#.R	66.92	18.37	3.64	0.27
Q9WUA2_S	Farsb	Phenylalan	K.ASAGSAFFPGR.C	13.93	14.93	0.93	1.07
Q9WUA2_S	Farsb	Phenylalan	R.DLLFQALGR.T	13.79	22.75	0.61	1.65
Q9WUA2_S	Farsb	Phenylalan	K.LFEISDVVVK#.D	67.50	26.39	2.56	0.39
Q9WUA2_S	Farsb	Phenylalan	K.LGLDISATK#.A	20.33	7.33	2.77	0.36
Q9WUA2_S	Farsb	Phenylalan	K.LVITEETAK#.V	76.21	23.55	3.24	0.31
Q9WUA2_S	Farsb	Phenylalan	K.TPGFEIIHGLLDR.I	12.01	21.36	0.56	1.78
Q9WUA2_S	Farsb	Phenylalan	R.TTLLPGLLK#.T	65.17	23.37	2.79	0.36
Q9WUA2_S	Farsb	Phenylalan	K.TYTIANQFPLNK#.L	46.74	16.34	2.86	0.35
P19096_FA	Fasn	Fatty acid s	R.VAASVDLITK#.S	18.39	4.58	4.01	0.25
P19096_FA	Fasn	Fatty acid s	K.VLEALLPLK#.S	16.63	7.13	2.33	0.43
P19096_FA	Fasn	Fatty acid s	R.AADQYK#PK#.A	10.88	3.03	3.58	0.28
P19096_FA	Fasn	Fatty acid s	K.AGLYGLPK#.R	160.64	62.01	2.59	0.39
P19096_FA	Fasn	Fatty acid s	R.AIPQEK#PIFLSVEDTSFQWVDSLK#.S	144.31	67.70	2.13	0.47
P19096_FA	Fasn	Fatty acid s	R.ALIAEATK#.L	183.73	67.73	2.71	0.37
P19096_FA	Fasn	Fatty acid s	K.AQVEDAFR.Y	29.02	57.47	0.51	1.98
P19096_FA	Fasn	Fatty acid s	R.DAM*LENQTPELFQDVNK#PK#.Y	80.01	30.33	2.64	0.38
P19096_FA	Fasn	Fatty acid s	R.DGAWGAFR.H	21.51	33.27	0.65	1.55
P19096_FA	Fasn	Fatty acid s	R.DGVVK#PLK#.C	98.71	38.32	2.58	0.39
P19096_FA	Fasn	Fatty acid s	R.DHK#DNLEFFLTNLGK#.V	112.25	31.30	3.59	0.28
P19096_FA	Fasn	Fatty acid s	R.DIM*LATGK#.L	58.57	19.32	3.03	0.33
P19096_FA	Fasn	Fatty acid s	K.DNLEFFLTNLGK#.V	74.38	23.73	3.13	0.32
P19096_FA	Fasn	Fatty acid s	R.EAVLAAYWR.G	16.43	34.14	0.48	2.08
P19096_FA	Fasn	Fatty acid s	R.EHDLVLPM*R.E	5.09	9.66	0.53	1.90
P19096_FA	Fasn	Fatty acid s	K.FDASFFGVHPK#.Q	221.27	78.55	2.82	0.36
P19096_FA	Fasn	Fatty acid s	K.FDLSNNHPLGM*AIFLK#.N	75.65	29.79	2.54	0.39
P19096_FA	Fasn	Fatty acid s	K.FDLSNNHPLGMAIFLK#.N	24.84	9.43	2.64	0.38
P19096_FA	Fasn	Fatty acid s	R.FLEIGK#.F	83.74	31.60	2.65	0.38
P19096_FA	Fasn	Fatty acid s	R.GNAGQTNYGFANSTM*ER.I	10.90	13.48	0.81	1.24
P19096_FA	Fasn	Fatty acid s	R.GNAGQTNYGFANSTMER.I	4.93	5.71	0.86	1.16
P19096_FA	Fasn	Fatty acid s	R.GTNTGVWVGVSGSEASEALSR.D	5.65	10.71	0.53	1.89
P19096_FA	Fasn	Fatty acid s	K.GVDLVLNSLAEEK#.L	267.99	79.20	3.38	0.30
P19096_FA	Fasn	Fatty acid s	R.GYTVLGVEGR.V	44.52	60.02	0.74	1.35
P19096_FA	Fasn	Fatty acid s	K.HDLVMNVYR.D	9.28	15.99	0.58	1.72
P19096_FA	Fasn	Fatty acid s	R.HFQLEQDK#PK#.E	144.66	83.03	1.74	0.57
P19096_FA	Fasn	Fatty acid s	R.IPALLNTQPMLQLEYTATDR.H	8.26	10.74	0.77	1.30
P19096_FA	Fasn	Fatty acid s	R.IPALLNTQPMLQLEYTATDRHPQALK.D	6.58	10.48	0.63	1.59
P19096_FA	Fasn	Fatty acid s	K.LDPGSPELQQVLK#.H	231.45	77.72	2.98	0.34
P19096_FA	Fasn	Fatty acid s	K.LGPVGGVFNLAM*VLR.D	94.10	130.38	0.72	1.39
P19096_FA	Fasn	Fatty acid s	R.LKEDTQVADVTTSR.C	20.67	32.17	0.64	1.56
P19096_FA	Fasn	Fatty acid s	R.LLEASHAFEVSDTGNLIVSGK#.V	121.95	42.13	2.89	0.35
P19096_FA	Fasn	Fatty acid s	K.LSPDAIPGK#.W	161.47	59.31	2.72	0.37
P19096_FA	Fasn	Fatty acid s	R.LTQGEVYK#.E	236.74	83.83	2.82	0.35
P19096_FA	Fasn	Fatty acid s	R.QGIQVLVSTSNVSSLEGAR.A	7.52	6.99	1.08	0.93
P19096_FA	Fasn	Fatty acid s	R.QHSQDLAFVSM*LNDIAATPTAAMPFR.G	6.48	5.30	1.22	0.82
P19096_FA	Fasn	Fatty acid s	R.QQEQLVPTLEK#.F	40.17	12.77	3.14	0.32
P19096_FA	Fasn	Fatty acid s	K.QVQPEGPYR.I	33.66	52.38	0.64	1.56
P19096_FA	Fasn	Fatty acid s	R.RVYATILNAGTNTDGSK.E	14.20	17.94	0.79	1.26
P19096_FA	Fasn	Fatty acid s	R.SDEAVK#PLGVK#.V	228.54	85.08	2.69	0.37
P19096_FA	Fasn	Fatty acid s	R.SDEAVKPLGVK.V	90.22	33.97	2.66	0.38
P19096_FA	Fasn	Fatty acid s	R.SEAVVAVLLTK#.K	141.76	47.23	3.00	0.33

P19096_FA	Fasn	Fatty acid s	R.SLGLSLEETPVVFENVSFHQATILPK#.T	253.84	83.33	3.05	0.33
P19096_FA	Fasn	Fatty acid s	R.SLGLSLEETPVVFENVSFHQATILPK#.T	9.03	6.48	1.39	0.72
P19096_FA	Fasn	Fatty acid s	K.SNM*GHPEPASGLAALTK#.V	154.48	53.03	2.91	0.34
P19096_FA	Fasn	Fatty acid s	K.SNM*GHPEPASGLAALTK#.V	17.92	6.57	2.73	0.37
P19096_FA	Fasn	Fatty acid s	K.SNMGHPEPASGLAALTK#.V	51.91	18.86	2.75	0.36
P19096_FA	Fasn	Fatty acid s	K.SYIITGGLGGFGLELAR.W	20.47	27.23	0.75	1.33
P19096_FA	Fasn	Fatty acid s	K.TDSATDTTAPK#.S	83.09	27.82	2.99	0.33
P19096_FA	Fasn	Fatty acid s	R.TGGLAFHSYFM*EGIAPTLLQALK#K#.V	7.98	4.01	1.99	0.50
P19096_FA	Fasn	Fatty acid s	K.TGTVALEVR.L	46.58	72.14	0.65	1.55
P19096_FA	Fasn	Fatty acid s	R.TLEAVQDLLEQGR.Q	32.81	110.23	0.30	3.36
P19096_FA	Fasn	Fatty acid s	R.VAASVDLITK#.S	175.03	56.08	3.12	0.32
P19096_FA	Fasn	Fatty acid s	K.VAEVLAGEGHLYSR.I	63.10	86.39	0.73	1.37
P19096_FA	Fasn	Fatty acid s	R.VFTTVGSAEK#.R	147.39	50.09	2.94	0.34
P19096_FA	Fasn	Fatty acid s	K.VGDPQELNGITR.S	26.21	39.17	0.67	1.49
P19096_FA	Fasn	Fatty acid s	K.VHLTGINVNPNALFPPVEFPAPR.G	72.32	127.91	0.57	1.77
P19096_FA	Fasn	Fatty acid s	K.VLEALLPLK#.S	238.04	76.65	3.11	0.32
P19096_FA	Fasn	Fatty acid s	K.VLVQVREEEPEAVLPGAQPTLISAISK.T	5.26	8.31	0.63	1.58
P19096_FA	Fasn	Fatty acid s	R.VQEVQQVSTNK#.R	359.57	96.56	3.72	0.27
P19096_FA	Fasn	Fatty acid s	K.VSDLLLSTDER.T	45.54	52.91	0.86	1.16
P19096_FA	Fasn	Fatty acid s	R.VYATILNAGTNTDGSK#.E	48.99	16.91	2.90	0.35
P19096_FA	Fasn	Fatty acid s	R.WLSTSIPEAQWQSSLAR.T	11.80	18.88	0.62	1.60
P62862_RS	Fau	40S ribosor	R.FVNVVPTFGK#.K	429.29	156.97	2.73	0.37
P35550_FE	Fbl	rRNA 2'-O-n	R.DHAVVVGVYRPPPK.S	47.05	134.63	0.35	2.86
P35550_FE	Fbl	rRNA 2'-O-n	R.GK#EDALVTK#.N	340.68	240.63	1.42	0.71
P35550_FE	Fbl	rRNA 2'-O-n	K.LAAAILGGVDQIHIK#PGAK#.V	181.27	108.27	1.67	0.60
P35550_FE	Fbl	rRNA 2'-O-n	R.M*LIAM*VDVIFADVAQPDQTR.I	5.50	9.43	0.58	1.71
P35550_FE	Fbl	rRNA 2'-O-n	K.M*QQENM*KPQEQLTLEPYER.D	24.01	68.70	0.35	2.86
P35550_FE	Fbl	rRNA 2'-O-n	K.MQQENM*KPQEQLTLEPYER.D	8.78	19.64	0.45	2.24
P35550_FE	Fbl	rRNA 2'-O-n	K.M*QQENMKPQEQLTLEPYER.D	3.94	11.89	0.33	3.02
P35550_FE	Fbl	rRNA 2'-O-n	R.NGGHFVISIK#.A	25.40	13.28	1.91	0.52
P35550_FE	Fbl	rRNA 2'-O-n	K.NLVPGESVYGEK#.R	262.33	186.14	1.41	0.71
P35550_FE	Fbl	rRNA 2'-O-n	K.RVSISEGDDKIEYR.A	10.17	97.47	0.10	9.58
P35550_FE	Fbl	rRNA 2'-O-n	K.VLYLGAASGTTVSHVSDIVGPDGLVYAVEFSHR.S	31.52	60.84	0.52	1.93
P35550_FE	Fbl	rRNA 2'-O-n	K.VLYLGAASGTTVSHVSDIVGPDGLVYAVEFSHR.S	4.17	8.27	0.50	1.98
P35550_FE	Fbl	rRNA 2'-O-n	R.DLINLAK#.K	35.67	30.38	1.17	0.85
P35550_FE	Fbl	rRNA 2'-O-n	R.GKEDALVTK.N	33.33	26.20	1.27	0.79
P35550_FE	Fbl	rRNA 2'-O-n	K.LAAAILGGVDQIHIKPGAK.V	15.16	12.64	1.20	0.83
P35550_FE	Fbl	rRNA 2'-O-n	R.M*LIAM*VDVIFADVAQPDQTR.I	4.50	6.00	0.75	1.33
P35550_FE	Fbl	rRNA 2'-O-n	K.M*QQENM*KPQEQLTLEPYER.D	6.42	26.13	0.25	4.07
P35550_FE	Fbl	rRNA 2'-O-n	R.GKEDALVTK.N	27.58	17.85	1.54	0.65
Q08879_FE	Fbln1	Fibulin-1 O	R.DSFDIIKR.Y	41.80	20.09	2.08	0.48
P37889_FE	Fbln2	Fibulin-2 O	R.IGPAPAFAGDTISLTITK#.G	18.44	9.27	1.99	0.50
P37889_FE	Fbln2	Fibulin-2 O	R.QGSVTTFLAK#.M	18.89	8.78	2.15	0.46
P37889_FE	Fbln2	Fibulin-2 O	R.FRAEEDIDPNSVHSVPR.G	1.60	17.47	0.09	10.93
P37889_FE	Fbln2	Fibulin-2 O	R.IGPAPAFAGDTISLTITK#.G	51.76	30.52	1.70	0.59
P37889_FE	Fbln2	Fibulin-2 O	R.IGPAPAFAGDTISLTITK#.G	6.72	5.90	1.14	0.88
P37889_FE	Fbln2	Fibulin-2 O	R.DFALDVEM*K#.L	23.00	13.34	1.72	0.58
P37889_FE	Fbln2	Fibulin-2 O	R.FRAEEDIDPNSVHSVPR.G	3.03	35.94	0.08	11.84
P37889_FE	Fbln2	Fibulin-2 O	K.GNEEGYFVTR.R	28.33	78.36	0.36	2.77
P37889_FE	Fbln2	Fibulin-2 O	R.IGPAPAFAGDTISLTITK#.G	139.09	81.76	1.70	0.59
P37889_FE	Fbln2	Fibulin-2 O	K.M*YIFFTTFAP.-	26.48	26.48	1.00	1.00
P37889_FE	Fbln2	Fibulin-2 O	R.RPPEPEAAPR.R	3.44	47.36	0.07	13.76
P37889_FE	Fbln2	Fibulin-2 O	R.SVM*QEGAAPLPR.S	14.79	49.16	0.30	3.32
Q8C7B6_FX	Fbxl22	F-box and l	-.M*HITQLNR.E	9.80	15.80	0.62	1.61
Q8BIA4_FB	Fbxw8	F-box/WD r	R.DLNELDDVPFFDVR.L	4.50	6.36	0.71	1.41
Q3UQN2_F	Fcho2	F-BAR doma	K.TK#EEVAGTLEAVQAIQNITQALQK#.S	11.13	1.84	6.05	0.17
Q91Z50_Q9	Fen1	Flap endon	K.EAQQLFLEPEVLDPESVELK#.W	43.16	10.50	4.11	0.24
Q91Z50_Q9	Fen1	Flap endon	K.EAQQLFLEPEVLDPESVELK#.W	98.53	23.46	4.20	0.24
Q91Z50_Q9	Fen1	Flap endon	R.HLTASEAK#.K	48.25	11.07	4.36	0.23
Q91Z50_Q9	Fen1	Flap endon	R.LDDFFK#.V	132.03	29.52	4.47	0.22
Q91Z50_Q9	Fen1	Flap endon	K.LIADVAPSAIR.E	61.34	69.38	0.88	1.13
Q91Z50_Q9	Fen1	Flap endon	K.QLQQAQEAGM*EEEVEK#.F	77.03	19.25	4.00	0.25
Q91Z50_Q9	Fen1	Flap endon	K.SIEEIVR.R	27.65	32.11	0.86	1.16
Q91Z50_Q9	Fen1	Flap endon	K.WSEPNEEELVK#.F	156.57	38.39	4.08	0.25
Q91Z50_Q9	Fen1	Flap endon	K.EAQQLFLEPEVLDPESVELK#.W	5.71	2.91	1.96	0.51
Q91Z50_Q9	Fen1	Flap endon	K.WSEPNEEELVK#.F	8.72	3.00	2.90	0.34
Q91Z50_Q9	Fen1	Flap endon	K.EAQQLFLEPEVLDPESVELK#.W	17.81	5.12	3.48	0.29
Q8CIB5_FE	Fermt2	Fermitin fa	R.INQLYEQAK#.W	15.19	4.93	3.08	0.32
Q8CIB5_FE	Fermt2	Fermitin fa	R.AK#DQNESLDEEM*FYK#.L	25.72	10.25	2.51	0.40
Q8CIB5_FE	Fermt2	Fermitin fa	R.FIQAWQSLPEFGITHFIAR.F	7.68	21.06	0.36	2.74
Q8CIB5_FE	Fermt2	Fermitin fa	K.GK#TM*ADSSYNLEVQNILSFLK#.M	11.78	4.98	2.37	0.42
Q8CIB5_FE	Fermt2	Fermitin fa	R.HPEELSLLK#.K	87.45	34.43	2.54	0.39
Q8CIB5_FE	Fermt2	Fermitin fa	R.ILEAHQNVAQM*SLIEAK#.M	72.71	24.75	2.94	0.34
Q8CIB5_FE	Fermt2	Fermitin fa	R.ILEAHQNVAQMSLIEAK#.M	36.73	13.92	2.64	0.38
Q8CIB5_FE	Fermt2	Fermitin fa	R.INQLYEQAK#.W	121.76	43.76	2.78	0.36
Q8CIB5_FE	Fermt2	Fermitin fa	K.K#LDDQSEDEALELEGPLIM*PGSGSIYSSPGLYSK#.T	9.20	4.17	2.21	0.45
Q8CIB5_FE	Fermt2	Fermitin fa	K.KLDDQSEDEALELEGPLIMPGSGSIYSSPGLYSK.T	4.79	2.57	1.87	0.54
Q8CIB5_FE	Fermt2	Fermitin fa	R.LQLPNMK#.Y	19.49	16.58	1.18	0.85
Q8CIB5_FE	Fermt2	Fermitin fa	K.LSIM*TSENHLNNSDK#EVDEVDAALSDLEITLEGGK#.T	33.83	8.54	3.96	0.25
Q8CIB5_FE	Fermt2	Fermitin fa	R.M*DASTGDAIK#.T	35.53	18.89	1.88	0.53
Q8CIB5_FE	Fermt2	Fermitin fa	K.M*FK#PQALLDK#.A	10.22	5.46	1.87	0.53
Q8CIB5_FE	Fermt2	Fermitin fa	R.SLM*EQDVKENEALLLR.F	14.60	25.29	0.58	1.73
Q8CIB5_FE	Fermt2	Fermitin fa	R.SLMEQDVKENEALLLR.F	7.86	10.17	0.77	1.29
Q8CIB5_FE	Fermt2	Fermitin fa	K.TM*TPTYDAHDGSPLSPTSAWFGDSALSEGNPGILAVSQPVTSPEILAK#.M	23.77	4.27	5.56	0.18
Q8CIB5_FE	Fermt2	Fermitin fa	K.TNQGWLDSSR.S	12.88	22.04	0.58	1.71
Q8CIB5_FE	Fermt2	Fermitin fa	K.YYSFFDLNPK#.Y	71.66	26.74	2.68	0.37
Q8CIB5_FE	Fermt2	Fermitin fa	R.AK#DQNESLDEEM*FYK#.L	21.47	7.36	2.92	0.34
Q8CIB5_FE	Fermt2	Fermitin fa	R.FIQAWQSLPEFGITHFIAR.F	8.49	19.57	0.43	2.31
Q8CIB5_FE	Fermt2	Fermitin fa	R.HPEELSLLK#.K	55.44	27.78	2.00	0.50
Q8CIB5_FE	Fermt2	Fermitin fa	R.ILEAHQNVAQM*SLIEAK#.M	57.89	24.49	2.36	0.42
Q8CIB5_FE	Fermt2	Fermitin fa	R.ILEAHQNVAQMSLIEAK#.M	35.99	11.79	3.05	0.33
Q8CIB5_FE	Fermt2	Fermitin fa	R.INQLYEQAK#.W	86.65	44.71	1.94	0.52
Q8CIB5_FE	Fermt2	Fermitin fa	K.K#LDDQSEDEALELEGPLIM*PGSGSIYSSPGLYSK#.T	8.84	5.23	1.69	0.59
Q8CIB5_FE	Fermt2	Fermitin fa	K.LDDQSEDEALELEGPLIM*PGSGSIYSSPGLYSK#.T	7.35	4.28	1.72	0.58
Q8CIB5_FE	Fermt2	Fermitin fa	K.LDDQSEDEALELEGPLIMPGSGSIYSSPGLYSK#.T	3.54	3.90	0.91	1.10
Q8CIB5_FE	Fermt2	Fermitin fa	K.LLIPVAEGM*NEIWLR.C	8.60	14.10	0.61	1.64
Q8CIB5_FE	Fermt2	Fermitin fa	R.LQLPNM*K#.Y	29.47	22.47	1.31	0.76
Q8CIB5_FE	Fermt2	Fermitin fa	R.MDASTGDAIK#.T	13.76	8.73	1.58	0.63
Q8CIB5_FE	Fermt2	Fermitin fa	R.M*DASTGDAIK#.T	25.29	11.83	2.14	0.47
Q8CIB5_FE	Fermt2	Fermitin fa	R.VTGEVHIGGVMLK#.L	7.42	1.10	6.76	0.15
Q8CIB5_FE	Fermt2	Fermitin fa	K.YYSFFDLNPK#.Y	63.11	22.33	2.83	0.35
Q6TYB5_FE	Fez2	Fasciculati	K.SGPPSVEDLQILTK#.I	10.16	7.65	1.33	0.75
Q69ZL1_FG	Fgd6	FYVE, RhoG	K.SLSAVDADR.C	13.19	12.80	1.03	0.97

P97807_F	Fh	Fumarate h	K.LM*NESLM*LVTALNPHIGYDK#.A	8.59	2.13	4.03	0.25
P97807_F	Fh	Fumarate h	K.LM*NESLMLVTALNPHIGYDK#.A	8.76	1.94	4.52	0.22
P97807_F	Fh	Fumarate h	R.M*PIPVIQAFGILK#.R	29.15	2.70	10.80	0.09
P97807_F	Fh	Fumarate h	R.SGLGELILPENEPGSSIM*PGK#.V	15.73	2.97	5.30	0.19
P97807_F	Fh	Fumarate h	K.VLLPGLQK#.L	48.66	5.30	9.18	0.11
P97447_F	Fhl1	Four and a	K.AIVAGDQNVEYK#.G	22.05	13.04	1.69	0.59
P97447_F	Fhl1	Four and a	K.AIVAGDQNVEYK#.G	19.18	9.49	2.02	0.49
O70433_F	Fhl2	Four and a	K.KPITTGGVTYR.E	1.96	4.96	0.40	2.53
Q9R059_F	Fhl3	Four and a	K.RPITGGSGGGEGAGLGGGK.Y	3.47	11.47	0.30	3.30
Q9R059_F	Fhl3	Four and a	K.TLTQGGVTYR.D	17.61	50.26	0.35	2.85
Q9R059_F	Fhl3	Four and a	K.TPLAGQQFTSR.D	11.86	39.12	0.30	3.30
Q9R059_F	Fhl3	Four and a	K.RPITGGSGGGEGAGLGGGK.Y	3.72	20.65	0.18	5.56
Q9R059_F	Fhl3	Four and a	K.TLTQGGVTYR.D	5.09	17.97	0.28	3.53
Q9R059_F	Fhl3	Four and a	K.TPLAGQQFTSR.D	17.77	21.83	0.81	1.23
Q6P9Q4_F	Fhod1	FH1/FH2 d	R.AETLAGATVDDTDGSSGTR.E	6.23	7.83	0.80	1.26
Q6P9Q4_F	Fhod1	FH1/FH2 d	R.EIAEPLFDLK#.V	23.14	6.17	3.75	0.27
Q6P9Q4_F	Fhod1	FH1/FH2 d	K.FSGVAGEAPNNLSVPVAVGSGPGQGDTDNHASM*K#.S	4.54	2.11	2.15	0.47
Q6P6L0_F	Filip1l	Filamin A-i	K.LQSTTSQLQAEQNK.V	8.52	7.55	1.13	0.89
Q9D824_F	Fip1l1	Pre-mRNA	K.AEFTSPPSLFK#.T	15.89	19.28	0.82	1.21
Q9D824_F	Fip1l1	Pre-mRNA	R.AFPYGNVAFPHLTSSAPSWPSLVDTTK.Q	11.52	8.95	1.29	0.78
Q9D824_F	Fip1l1	Pre-mRNA	R.ANENSNIQVLSDR.S	3.58	14.10	0.25	3.94
Q9D824_F	Fip1l1	Pre-mRNA	R.KPGADLSDYFNYGFNEDTWK.A	6.65	6.23	1.07	0.94
Q9D824_F	Fip1l1	Pre-mRNA	R.M*GLEVIPVTSTTNK#.I	4.38	5.64	0.78	1.29
Q9D824_F	Fip1l1	Pre-mRNA	R.RLPGAIDVIGQTITISR.V	1.26	21.20	0.06	16.82
Q9D824_F	Fip1l1	Pre-mRNA	K.TGAPQYGSYGTAPVNLNIK#.A	4.32	5.79	0.75	1.34
Q9D824_F	Fip1l1	Pre-mRNA	K.AEFTSPPSLFK.T	60.22	74.96	0.80	1.24
Q9D824_F	Fip1l1	Pre-mRNA	R.ANENSNIQVLSDR.S	14.26	55.77	0.26	3.91
Q9D824_F	Fip1l1	Pre-mRNA	K.DLDENEVERPEEENASANPPSGIEEEAAENGVAKPK.V	1.68	6.60	0.25	3.94
Q9D824_F	Fip1l1	Pre-mRNA	R.K#PGADLSDYFNYGFNEDTWK#.A	31.88	29.49	1.08	0.93
Q9D824_F	Fip1l1	Pre-mRNA	R.KPGADLSDYFNYGFNEDTWK.A	4.89	3.41	1.43	0.70
Q9D824_F	Fip1l1	Pre-mRNA	R.LPGAIDVIGQTITISR.V	8.43	13.07	0.64	1.55
Q9D824_F	Fip1l1	Pre-mRNA	R.M*GLEVIPVTSTTNK.I	21.02	23.24	0.90	1.11
Q9D824_F	Fip1l1	Pre-mRNA	R.MGLEVIPVTSTTNK#.I	24.63	18.40	1.34	0.75
Q9D824_F	Fip1l1	Pre-mRNA	R.RLPGAIDVIGQTITISR.V	3.13	57.93	0.05	18.49
Q9D824_F	Fip1l1	Pre-mRNA	K.TGAPQYGSYGTAPVNLNIK#.A	39.03	36.26	1.08	0.93
Q9D824_F	Fip1l1	Pre-mRNA	R.TGNSEKEAALPSTK.A	14.59	11.10	1.31	0.76
Q9CQ92_F	Fis1	Mitochond	K.FQSEQAAGSVSK#.S	8.61	5.72	1.51	0.66
Q9CQ92_F	Fis1	Mitochond	R.GLLQTEPQNNQAK.E	22.13	22.72	0.97	1.03
Q61576_F	Fkbp10	Peptidyl-pr	R.GGTYDTYIGSGWLIK#.G	9.07	4.92	1.84	0.54
Q61576_F	Fkbp10	Peptidyl-pr	K.IIIPPFLAYGEK#.G	39.25	21.98	1.79	0.56
Q61576_F	Fkbp10	Peptidyl-pr	R.LFSSHDYEAPQEITLGANK#.V	20.47	9.29	2.20	0.45
Q6P9Q6_F	Fkbp15	FK506-bin	R.ETLLDTELASAAAGTSLR.H	2.55	5.90	0.43	2.31
Q6P9Q6_F	Fkbp15	FK506-bin	R.NNSLQTATENTQAR.I	1.47	8.77	0.17	5.98
Q6P9Q6_F	Fkbp15	FK506-bin	R.YVEQSNLM*M*EK#.R	11.63	6.81	1.71	0.59
P30416_F	Fkbp4	Peptidyl-pr	K.ALELDSNNEK#.G	16.01	1.83	8.76	0.11
P30416_F	Fkbp4	Peptidyl-pr	K.QALLQYK#.K	20.21	16.51	1.22	0.82
P30416_F	Fkbp4	Peptidyl-pr	K.VLQLYPSNK#.A	24.64	3.45	7.14	0.14
Q9Z247_F	Fkbp9	Peptidyl-pr	R.YHYVGTFLDGQK#.F	7.69	8.81	0.87	1.15
Q9JJ28_FLI	Flii	Protein flig	K.ADLTALFLPR.Q	14.57	28.64	0.51	1.97
Q9JJ28_FLI	Flii	Protein flig	R.ASDPDEAK#LAEDILNTM*FDASYSK#.Q	10.90	6.31	1.73	0.58
Q9JJ28_FLI	Flii	Protein flig	R.EGEEAAAEAEEK#.Q	8.46	4.14	2.04	0.49
Q9JJ28_FLI	Flii	Protein flig	R.GAQATLSNTTK#.A	48.63	19.54	2.49	0.40
Q9JJ28_FLI	Flii	Protein flig	R.GVDLSGNDFK#.G	31.87	15.24	2.09	0.48
Q9JJ28_FLI	Flii	Protein flig	K.GYFAVTEK#.C	32.77	13.97	2.34	0.43
Q9JJ28_FLI	Flii	Protein flig	K.LDFDGLPSGIGK#.L	10.91	6.06	1.80	0.56
Q9JJ28_FLI	Flii	Protein flig	R.LLQSLLDTR.C	8.97	16.14	0.56	1.80
Q9JJ28_FLI	Flii	Protein flig	K.LYLNSNK#LDFDGLPSGIGK#.L	23.42	12.89	1.82	0.55
Q9JJ28_FLI	Flii	Protein flig	R.NAEAVLQGQGLSGK#.V	55.07	18.91	2.91	0.34
Q9JJ28_FLI	Flii	Protein flig	R.TAEWYNIDFSLQNQLR.L	13.00	7.42	1.75	0.57
Q9JJ28_FLI	Flii	Protein flig	K.VPFESEDNQGIVYAWVGR.A	2.65	4.43	0.60	1.67
Q9JJ28_FLI	Flii	Protein flig	K.VTQGTLQPTLYQIR.T	3.58	7.73	0.46	2.16
Q9JJ28_FLI	Flii	Protein flig	K.ADLTALFLPR.Q	18.27	42.36	0.43	2.32
Q9JJ28_FLI	Flii	Protein flig	R.ASDPDEAK#LAEDILNTM*FDASYSK#.Q	9.11	4.26	2.14	0.47
Q9JJ28_FLI	Flii	Protein flig	R.EGEEAAAEAEEK#.Q	19.44	7.81	2.49	0.40
Q9JJ28_FLI	Flii	Protein flig	R.GAQATLSNTTK#.A	70.72	24.72	2.86	0.35
Q9JJ28_FLI	Flii	Protein flig	K.GGYFPENVK#.A	17.95	6.06	2.96	0.34
Q9JJ28_FLI	Flii	Protein flig	R.GVDLSGNDFK#.G	43.98	21.23	2.07	0.48
Q9JJ28_FLI	Flii	Protein flig	K.K#FESLFPGK#.L	16.87	10.69	1.58	0.63
Q9JJ28_FLI	Flii	Protein flig	K.LAEDILNTMFDASYSK#.Q	7.00	2.48	2.82	0.35
Q9JJ28_FLI	Flii	Protein flig	R.LAGASPATVAAAAAVGSGSK#.D	14.20	2.75	5.17	0.19
Q9JJ28_FLI	Flii	Protein flig	K.LDFDGLPSGIGK#.L	16.64	7.08	2.35	0.43
Q9JJ28_FLI	Flii	Protein flig	R.LLQSLLDTR.C	11.46	19.08	0.60	1.66
Q9JJ28_FLI	Flii	Protein flig	K.LYLNSNK#LDFDGLPSGIGK#.L	28.95	23.45	1.23	0.81
Q9JJ28_FLI	Flii	Protein flig	R.NAEAVLQGQGLSGK#.V	59.19	25.17	2.35	0.43
Q9JJ28_FLI	Flii	Protein flig	K.NSGVPDDIFK#.L	10.10	3.75	2.69	0.37
Q9JJ28_FLI	Flii	Protein flig	K.QVINEGEEPENFFWVGIGAQK#PYDDDAEYM*K#.H	4.81	2.01	2.40	0.42
Q9JJ28_FLI	Flii	Protein flig	K.VGLGLGYLELPQINYK#.L	27.11	9.04	3.00	0.33
Q9JJ28_FLI	Flii	Protein flig	K.VPFESEDNQGIVYAWVGR.A	4.98	6.74	0.74	1.36
Q8BTM8_F	Flna	Filamin-A C	R.LTVSSLQESGLK#.V	8.80	1.01	8.72	0.11
Q8BTM8_F	Flna	Filamin-A C	R.LYSVSYLLK#.D	12.47	3.43	3.64	0.27
Q8BTM8_F	Flna	Filamin-A C	K.VATVPQHATSGPGPADVSK#.V	39.18	12.82	3.06	0.33
Q8BTM8_F	Flna	Filamin-A C	R.AEFTVETR.S	39.28	46.54	0.84	1.18
Q8BTM8_F	Flna	Filamin-A C	K.AEISFEDR.K	19.94	24.93	0.80	1.25
Q8BTM8_F	Flna	Filamin-A C	R.AEVGVPAEFGIWTR.E	78.99	95.84	0.82	1.21
Q8BTM8_F	Flna	Filamin-A C	K.AFGPGLQGGNAGSPAR.F	95.69	139.21	0.69	1.45
Q8BTM8_F	Flna	Filamin-A C	K.AGNNM*LLVGVHGPR.T	34.38	48.01	0.72	1.40
Q8BTM8_F	Flna	Filamin-A C	K.AGVAPLQVK#.V	390.35	119.31	3.27	0.31
Q8BTM8_F	Flna	Filamin-A C	R.ALTQTGGPHVK#.A	228.71	58.39	3.92	0.26
Q8BTM8_F	Flna	Filamin-A C	R.ANLPQSFQVDTSK#.A	406.56	119.72	3.40	0.29
Q8BTM8_F	Flna	Filamin-A C	K.ASGPGLNTTGVPASLPVEFTIDAK#.D	241.35	69.28	3.48	0.29
Q8BTM8_F	Flna	Filamin-A C	R.AWGPGLEGGIVGK#.S	422.55	131.26	3.22	0.31
Q8BTM8_F	Flna	Filamin-A C	R.AYGPGIEPTGNM*VK#.K	180.97	50.20	3.60	0.28
Q8BTM8_F	Flna	Filamin-A C	R.AYGPGIEPTGNMVK#.K	110.88	36.01	3.08	0.32
Q8BTM8_F	Flna	Filamin-A C	K.DAGEGGLSLAIEGPSK#.A	226.18	71.94	3.14	0.32
Q8BTM8_F	Flna	Filamin-A C	K.DAGEGLLAVQITDPEGK#PK#.K	238.10	77.52	3.07	0.33
Q8BTM8_F	Flna	Filamin-A C	R.DAGYGGLSLSIEGPSK#.V	27.57	11.68	2.36	0.42
Q8BTM8_F	Flna	Filamin-A C	K.DKGEYTLVVK.W	289.14	97.15	2.98	0.34
Q8BTM8_F	Flna	Filamin-A C	K.DLAEDAPWK#K#.I	41.70	15.52	2.69	0.37
Q8BTM8_F	Flna	Filamin-A C	R.DVDIIDHHDNTYTVK#.Y	417.33	113.57	3.67	0.27
Q8BTM8_F	Flna	Filamin-A C	R.EAGAGGLAIAVEGPSK#.A	302.52	91.07	3.32	0.30
Q8BTM8_F	Flna	Filamin-A C	R.EATTEFSVDAR.A	105.68	145.95	0.72	1.38
Q8BTM8_F	Flna	Filamin-A C	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTK#PSK#.V	88.70	28.13	3.15	0.32
Q8BTM8_F	Flna	Filamin-A C	R.EGSYSISVLYGEEEVPR.S	50.47	60.20	0.84	1.19

Q8BTM8_Fl	Flna	Filamin-A C	R.ENGIYLIDVK#.F	69.96	26.96	2.59	0.39
Q8BTM8_Fl	Flna	Filamin-A C	K.FADQHVPGSPFSVK#.V	92.36	32.79	2.82	0.36
Q8BTM8_Fl	Flna	Filamin-A C	R.FGGEHVPNSPFQVTALAGDQPTVQTPLR.S	41.46	55.34	0.75	1.33
Q8BTM8_Fl	Flna	Filamin-A C	K.FNEEHIPDSPFVVPVASPSGDAR.R	91.20	126.36	0.72	1.39
Q8BTM8_Fl	Flna	Filamin-A C	K.GAGSGELK#.V	16.16	5.60	2.89	0.35
Q8BTM8_Fl	Flna	Filamin-A C	R.GAGTGGLGLAVEGPSEAK#.M	384.48	109.24	3.52	0.28
Q8BTM8_Fl	Flna	Filamin-A C	K.GEITGEVR.M	27.07	63.47	0.43	2.34
Q8BTM8_Fl	Flna	Filamin-A C	K.GK#LDVQFSGLAK#.G	182.57	42.88	4.26	0.23
Q8BTM8_Fl	Flna	Filamin-A C	K.GLVEPVDVVDNADGTQTVNYVPSR.E	68.83	89.48	0.77	1.30
Q8BTM8_Fl	Flna	Filamin-A C	K.GQHVPGSPFQFTVGPLGEGGAHK#.V	243.78	101.37	2.40	0.42
Q8BTM8_Fl	Flna	Filamin-A C	K.GTVEPQLEAR.G	90.66	132.03	0.69	1.46
Q8BTM8_Fl	Flna	Filamin-A C	K.HTAM*VSWGGVSIPNSPFR.V	18.04	19.07	0.95	1.06
Q8BTM8_Fl	Flna	Filamin-A C	R.IANLQTDLSDGLR.L	79.02	100.77	0.78	1.28
Q8BTM8_Fl	Flna	Filamin-A C	K.IPEISIQDM*TAQVTSPSGK#.T	16.14	5.56	2.90	0.34
Q8BTM8_Fl	Flna	Filamin-A C	K.IPEISIQDM*TAQVTSPSGK#.T	21.10	10.59	1.99	0.50
Q8BTM8_Fl	Flna	Filamin-A C	K.IPEISIQDMTAQVTSPSGK#.T	20.19	8.74	2.31	0.43
Q8BTM8_Fl	Flna	Filamin-A C	K.IQQNTFTR.W	134.98	207.62	0.65	1.54
Q8BTM8_Fl	Flna	Filamin-A C	K.KGEITGEVR.M	45.56	57.06	0.80	1.25
Q8BTM8_Fl	Flna	Filamin-A C	K.LDVQFSGLAK#.G	125.24	33.85	3.70	0.27
Q8BTM8_Fl	Flna	Filamin-A C	R.LIALLEVLSQK#.K	474.20	172.47	2.75	0.36
Q8BTM8_Fl	Flna	Filamin-A C	R.LLGWIQNK#.L	287.90	117.91	2.44	0.41
Q8BTM8_Fl	Flna	Filamin-A C	K.LPQLPITNFSR.D	95.50	143.84	0.66	1.51
Q8BTM8_Fl	Flna	Filamin-A C	R.LTVSSLQESGLK#.V	272.81	62.09	4.39	0.23
Q8BTM8_Fl	Flna	Filamin-A C	K.LVSIDSK#.A	696.56	209.45	3.33	0.30
Q8BTM8_Fl	Flna	Filamin-A C	R.LVSNHSLHETSSVFVDSLTK#.V	225.84	62.24	3.63	0.28
Q8BTM8_Fl	Flna	Filamin-A C	R.LYSVSYLLK#.D	282.90	72.95	3.88	0.26
Q8BTM8_Fl	Flna	Filamin-A C	R.NDNDTFTVK#.Y	164.51	50.60	3.25	0.31
Q8BTM8_Fl	Flna	Filamin-A C	R.NGHVGISFVPK#.E	83.99	27.51	3.05	0.33
Q8BTM8_Fl	Flna	Filamin-A C	K.NGQHVASSPIPVVISQSEIGDASR.V	4.71	6.30	0.75	1.34
Q8BTM8_Fl	Flna	Filamin-A C	R.QM*QLENVSVALEFLDR.E	4.88	8.84	0.55	1.81
Q8BTM8_Fl	Flna	Filamin-A C	R.RLTVSSLQESGLK.V	10.04	8.87	1.13	0.88
Q8BTM8_Fl	Flna	Filamin-A C	K.SADFVVEAIGDDVGTLGFSVEGPSQAK#.I	225.43	80.17	2.81	0.36
Q8BTM8_Fl	Flna	Filamin-A C	R.SAGQGEVLVYVEDPAGHQEEAK#.V	269.38	76.88	3.50	0.29
Q8BTM8_Fl	Flna	Filamin-A C	R.SPFEVK#.V	337.75	85.13	3.97	0.25
Q8BTM8_Fl	Flna	Filamin-A C	K.SPFEVYVDK#.S	256.61	80.01	3.21	0.31
Q8BTM8_Fl	Flna	Filamin-A C	K.SPFEVYVDK#SQGDASK#.V	83.11	25.38	3.27	0.31
Q8BTM8_Fl	Flna	Filamin-A C	K.SPFSVGVSPSLDLSK#.I	522.51	148.35	3.52	0.28
Q8BTM8_Fl	Flna	Filamin-A C	R.TFSVWYVPEVTGTHK#.V	265.91	71.00	3.75	0.27
Q8BTM8_Fl	Flna	Filamin-A C	K.TGVAVNK#PAEFTVDAK#.H	617.42	157.51	3.92	0.26
Q8BTM8_Fl	Flna	Filamin-A C	K.VAQPSITDNK#.D	214.02	56.61	3.78	0.26
Q8BTM8_Fl	Flna	Filamin-A C	K.VATVPQHATSGPGPADVSK#.V	1147.53	330.10	3.48	0.29
Q8BTM8_Fl	Flna	Filamin-A C	K.VDVGK#DQEFTVK#.S	124.03	35.63	3.48	0.29
Q8BTM8_Fl	Flna	Filamin-A C	K.VEPGLGADNSVVR.F	50.94	68.58	0.74	1.35
Q8BTM8_Fl	Flna	Filamin-A C	R.VGEPGHGGDPGLVSAYGAGLEGGVTGSPAEFIVNTSNAGAGALSVTIDGPSK#.V	19.77	3.77	5.25	0.19
Q8BTM8_Fl	Flna	Filamin-A C	R.VHGPGIQSGTTNKPNK.F	357.30	113.14	3.16	0.32
Q8BTM8_Fl	Flna	Filamin-A C	K.VKAEGPGLNR.T	27.30	37.19	0.73	1.36
Q8BTM8_Fl	Flna	Filamin-A C	R.VK#ETADFK#.V	99.82	26.53	3.76	0.27
Q8BTM8_Fl	Flna	Filamin-A C	R.VK#VEPSHDASK#.V	42.97	14.49	2.96	0.34
Q8BTM8_Fl	Flna	Filamin-A C	K.VNQPASFAVSLNGAK#.G	65.26	18.91	3.45	0.29
Q8BTM8_Fl	Flna	Filamin-A C	R.VNVGAGSHPNK#.V	229.18	76.73	2.99	0.33
Q8BTM8_Fl	Flna	Filamin-A C	R.VSGQGLHEGHTFEPAEFIIDTR.D	6.92	7.88	0.88	1.14
Q8BTM8_Fl	Flna	Filamin-A C	K.VTAQGPGLEPSGNIANK#.T	386.65	106.40	3.63	0.28
Q8BTM8_Fl	Flna	Filamin-A C	K.VTVLFAGQHIAK#.S	253.05	83.97	3.01	0.33
Q8BTM8_Fl	Flna	Filamin-A C	R.VTYTPM*APGSYLISIK#.Y	101.94	31.78	3.21	0.31
Q8BTM8_Fl	Flna	Filamin-A C	R.VTYTPM*APGSYLISIK#.Y	42.51	11.87	3.58	0.28
Q8BTM8_Fl	Flna	Filamin-A C	R.VTYTPMAPGSYLISIK#.Y	107.87	28.49	3.79	0.26
Q8BTM8_Fl	Flna	Filamin-A C	K.VYGPGVAK#.T	372.48	116.38	3.20	0.31
Q8BTM8_Fl	Flna	Filamin-A C	K.YGGDEIPFSPYR.V	52.50	69.80	0.75	1.33
Q8BTM8_Fl	Flna	Filamin-A C	K.YGGQPVPNFPSK#.L	266.77	80.85	3.30	0.30
Q8BTM8_Fl	Flna	Filamin-A C	K.YNDQHIPGSPFTAR.V	8.53	8.91	0.96	1.04
Q80X90_FL	Flnb	Filamin-B C	R.IGNLQTDLSDGLR.L	2.12	4.92	0.43	2.32
Q80X90_FL	Flnb	Filamin-B C	K.AAGSGELGVTVK#.G	58.88	62.93	0.94	1.07
Q80X90_FL	Flnb	Filamin-B C	K.ADIEM*PFDPSK#.V	13.35	7.34	1.82	0.55
Q80X90_FL	Flnb	Filamin-B C	K.ADIEMPFDPSK#.V	10.18	4.91	2.07	0.48
Q80X90_FL	Flnb	Filamin-B C	K.AEVSIQNNK#.D	24.00	11.57	2.07	0.48
Q80X90_FL	Flnb	Filamin-B C	K.AGLAPLEVR.V	8.61	23.03	0.37	2.67
Q80X90_FL	Flnb	Filamin-B C	K.APLNVQFSSPLPGEAVK#.D	24.49	16.18	1.51	0.66
Q80X90_FL	Flnb	Filamin-B C	K.APLNVQFSSPLPGEAVK#DLDIIDNYDYSHTVK#.Y	9.94	5.40	1.84	0.54
Q80X90_FL	Flnb	Filamin-B C	R.ATVHDNKDGTYAVTYIPDK.T	13.83	5.16	2.68	0.37
Q80X90_FL	Flnb	Filamin-B C	R.DAGYGGISLAVEGPSK#.V	17.12	10.91	1.57	0.64
Q80X90_FL	Flnb	Filamin-B C	K.DNADGTYQVEYTPFEK#.G	14.44	6.91	2.09	0.48
Q80X90_FL	Flnb	Filamin-B C	R.EAGAGGLSIAVEGPSK#.A	201.26	91.63	2.20	0.46
Q80X90_FL	Flnb	Filamin-B C	K.FADEHVPGSPFTVK#.I	57.64	36.67	1.57	0.64
Q80X90_FL	Flnb	Filamin-B C	K.FNDEHIPDSPYLVPVIAPSDDAR.C	8.10	20.87	0.39	2.58
Q80X90_FL	Flnb	Filamin-B C	R.GAGIGGLGITVEGPSESK#.I	42.12	24.05	1.75	0.57
Q80X90_FL	Flnb	Filamin-B C	R.GEAGIPAEFSIWTR.E	10.25	27.08	0.38	2.64
Q80X90_FL	Flnb	Filamin-B C	K.GFLDGVYSFEYYPSTPGK#.Y	19.68	9.60	2.05	0.49
Q80X90_FL	Flnb	Filamin-B C	R.GSHIPESPLQFYVNYPNSGSVSAYGPGLVYGVANK.T	6.20	2.46	2.53	0.40
Q80X90_FL	Flnb	Filamin-B C	K.ILAQDGEGQPIDIQM*K#.S	9.19	4.72	1.95	0.51
Q80X90_FL	Flnb	Filamin-B C	K.ILAQDGEGQPIDIQMK#.S	7.17	5.37	1.33	0.75
Q80X90_FL	Flnb	Filamin-B C	K.IPEINSSDM*SAHVTSPSGHVTEAEIVPM*GK#.N	7.05	6.21	1.14	0.88
Q80X90_FL	Flnb	Filamin-B C	K.IPYLPITNFNQNWQDGK#.A	21.61	18.90	1.14	0.87
Q80X90_FL	Flnb	Filamin-B C	R.K#GEITGTVHM*PSGK#.K	21.56	12.53	1.72	0.58
Q80X90_FL	Flnb	Filamin-B C	K.LENVSVALEFLDHESIK#.L	28.95	23.09	1.25	0.80
Q80X90_FL	Flnb	Filamin-B C	K.LENVSVALEFLDHESIK#.L	6.61	4.62	1.43	0.70
Q80X90_FL	Flnb	Filamin-B C	R.LPNNHIGISFIPR.E	5.76	12.59	0.46	2.19
Q80X90_FL	Flnb	Filamin-B C	R.LVSPGSANETSSILVESVTR.S	11.29	26.39	0.43	2.34
Q80X90_FL	Flnb	Filamin-B C	K.QQYNVTYVVK#.E	29.39	19.03	1.54	0.65
Q80X90_FL	Flnb	Filamin-B C	R.SADFVVESIGSEVGTLGFAIEGPSQAK#.I	36.31	20.15	1.80	0.56
Q80X90_FL	Flnb	Filamin-B C	K.SPFEVNVDK#.A	36.97	21.65	1.71	0.59
Q80X90_FL	Flnb	Filamin-B C	K.SPFEVQVGPEAGM*QK#.V	19.82	10.50	1.89	0.53
Q80X90_FL	Flnb	Filamin-B C	K.SPFEVQVGPEAGMQK#.V	9.94	13.51	0.74	1.36
Q80X90_FL	Flnb	Filamin-B C	K.SPFTVGVAAPLDLSK#.I	67.71	41.84	1.62	0.62
Q80X90_FL	Flnb	Filamin-B C	K.TGEEVGFVVDAK#.T	63.57	25.98	2.45	0.41
Q80X90_FL	Flnb	Filamin-B C	K.TYSVEYLPK#.V	31.18	16.72	1.87	0.54
Q80X90_FL	Flnb	Filamin-B C	R.VEVGK#DQEFAIDTNGAGGQGK#.L	8.91	11.83	0.75	1.33
Q80X90_FL	Flnb	Filamin-B C	K.VFGPGVER.S	12.16	22.69	0.54	1.87
Q80X90_FL	Flnb	Filamin-B C	R.VHAQGPGLK#.E	28.39	12.40	2.29	0.44
Q80X90_FL	Flnb	Filamin-B C	K.VLFASQEIPASPFR.V	12.58	46.10	0.27	3.66
Q80X90_FL	Flnb	Filamin-B C	R.VLSDDEEDVDFDIIHNANDTFTVK#.Y	31.75	18.60	1.71	0.59
Q80X90_FL	Flnb	Filamin-B C	R.VNIGQGSHPQK#.V	12.59	6.55	1.92	0.52
Q80X90_FL	Flnb	Filamin-B C	K.VNQPASFAIR.L	10.85	22.76	0.48	2.10
Q80X90_FL	Flnb	Filamin-B C	K.VSFAGDAIPK#.S	54.52	33.02	1.65	0.61

Q80X90_Fl	Flnb	Filamin-B C	K.VSYFPTVPGVYIVSTK#.F	57.14	32.52	1.76	0.57
Q80X90_Fl	Flnb	Filamin-B C	K.VSYFPTVPGVYIVSTK#.F	11.98	6.03	1.99	0.50
Q80X90_Fl	Flnb	Filamin-B C	K.VTASGPGLSAYGVPASLPVEFAIDAR.D	14.54	46.11	0.32	3.17
Q80X90_Fl	Flnb	Filamin-B C	K.VYGQGLSEGR.T	16.58	35.00	0.47	2.11
Q80X90_Fl	Flnb	Filamin-B C	K.YADEEIPR.S	12.36	24.36	0.51	1.97
Q80X90_Fl	Flnb	Filamin-B C	K.YGGELVPHFPAWVK#.V	36.63	20.93	1.75	0.57
Q80X90_Fl	Flnb	Filamin-B C	R.YM*IGVTYGGDNIPLSPYR.I	2.11	6.37	0.33	3.02
Q80X90_Fl	Flnb	Filamin-B C	K.YTPTQQGNM*QVLVTYGGDPIPK#.S	7.40	5.47	1.35	0.74
Q8VHX6_Fl	Flnc	Filamin-C C	K.AEIAFEDR.K	15.07	24.68	0.61	1.64
Q8VHX6_Fl	Flnc	Filamin-C C	R.AFGPGLEGGLVNK#.A	330.46	144.29	2.29	0.44
Q8VHX6_Fl	Flnc	Filamin-C C	R.AGGTGLER.G	28.92	59.47	0.49	2.06
Q8VHX6_Fl	Flnc	Filamin-C C	R.APLQVAVLGPTGVAEPVEVR.D	17.36	36.00	0.48	2.07
Q8VHX6_Fl	Flnc	Filamin-C C	R.APLQVAVLGPTGVAEPVEVR.D	23.47	48.68	0.48	2.07
Q8VHX6_Fl	Flnc	Filamin-C C	R.ASGPGLNASGIPASLPVEFTIDAR.D	24.44	37.47	0.65	1.53
Q8VHX6_Fl	Flnc	Filamin-C C	K.ATIQPVFDPSK#.V	134.78	67.20	2.01	0.50
Q8VHX6_Fl	Flnc	Filamin-C C	R.AWGPGLETGQVGK#.S	122.22	50.26	2.43	0.41
Q8VHX6_Fl	Flnc	Filamin-C C	K.DAGEGGLSLAVEGPSK#.A	125.79	65.70	1.91	0.52
Q8VHX6_Fl	Flnc	Filamin-C C	R.DTVEVALEDK#.G	17.84	8.56	2.08	0.48
Q8VHX6_Fl	Flnc	Filamin-C C	R.DTVEVALEDKGDNTFR.C	6.53	9.03	0.72	1.38
Q8VHX6_Fl	Flnc	Filamin-C C	R.EAGAGGLSIAVEGPSKAEIAFEDRK.D	3.50	7.41	0.47	2.12
Q8VHX6_Fl	Flnc	Filamin-C C	K.EK#GDYILIVK#.W	111.36	48.58	2.29	0.44
Q8VHX6_Fl	Flnc	Filamin-C C	K.EVGEHVVSVR.K	21.45	57.52	0.37	2.68
Q8VHX6_Fl	Flnc	Filamin-C C	R.EVRVEESTQVGGDPFPAVFGDFLGR.E	4.50	5.42	0.83	1.21
Q8VHX6_Fl	Flnc	Filamin-C C	R.EVTTEFTVDAR.S	8.80	20.49	0.43	2.33
Q8VHX6_Fl	Flnc	Filamin-C C	R.FDDKHIPGSPFTAK.I	89.65	41.26	2.17	0.46
Q8VHX6_Fl	Flnc	Filamin-C C	K.FNDEHIPDSPFVVPVASLSDDAR.R	60.24	126.58	0.48	2.10
Q8VHX6_Fl	Flnc	Filamin-C C	R.GAGGQGQLDVR.M	75.53	173.08	0.44	2.29
Q8VHX6_Fl	Flnc	Filamin-C C	R.GAGTGGLGLAIEGPSEAK#.M	226.44	97.40	2.32	0.43
Q8VHX6_Fl	Flnc	Filamin-C C	R.GASYSSIPK#.F	163.82	83.76	1.96	0.51
Q8VHX6_Fl	Flnc	Filamin-C C	K.GDYILIVK#.W	30.28	12.10	2.50	0.40
Q8VHX6_Fl	Flnc	Filamin-C C	K.GGLVGTPAPFSIDTK#.G	292.91	139.90	2.09	0.48
Q8VHX6_Fl	Flnc	Filamin-C C	K.GLHQM*GIK#.Y	31.73	15.14	2.10	0.48
Q8VHX6_Fl	Flnc	Filamin-C C	K.GLSEGQTFQVAEFIVDTR.N	22.75	51.43	0.44	2.26
Q8VHX6_Fl	Flnc	Filamin-C C	R.GPGLEPVGNVANKPTYFDIYTAGAGTGDVAVVIVDPQGR.R	2.70	4.48	0.60	1.66
Q8VHX6_Fl	Flnc	Filamin-C C	R.GPGLSQAFVGQK#.N	282.50	121.69	2.32	0.43
Q8VHX6_Fl	Flnc	Filamin-C C	R.GVAGVPAEFSIWTR.E	54.54	128.15	0.43	2.35
Q8VHX6_Fl	Flnc	Filamin-C C	R.HIGISFTPK#.E	234.56	104.73	2.24	0.45
Q8VHX6_Fl	Flnc	Filamin-C C	R.HVSAYGPGLSHGM*VNK#PATFTIVTK#.D	60.69	28.46	2.13	0.47
Q8VHX6_Fl	Flnc	Filamin-C C	R.HVSAYGPGLSHGMVNK#PATFTIVTK#.D	43.29	21.71	1.99	0.50
Q8VHX6_Fl	Flnc	Filamin-C C	K.HVTNSPFK#.I	325.85	137.41	2.37	0.42
Q8VHX6_Fl	Flnc	Filamin-C C	K.ILVGPSEIGDASK#.V	171.60	75.85	2.26	0.44
Q8VHX6_Fl	Flnc	Filamin-C C	K.IPGNWFQMVSAQER.L	5.40	18.62	0.29	3.45
Q8VHX6_Fl	Flnc	Filamin-C C	R.IQIGEETVITVDAK#.A	29.02	14.75	1.97	0.51
Q8VHX6_Fl	Flnc	Filamin-C C	K.ITEGDLSQLTASIR.A	45.63	90.52	0.50	1.98
Q8VHX6_Fl	Flnc	Filamin-C C	K.LDVHFAGAAK#.G	25.17	10.65	2.36	0.42
Q8VHX6_Fl	Flnc	Filamin-C C	K.LEPGGGAEAQAVR.Y	193.53	117.90	1.64	0.61
Q8VHX6_Fl	Flnc	Filamin-C C	R.LGSFGSITR.Q	49.53	123.50	0.40	2.49
Q8VHX6_Fl	Flnc	Filamin-C C	R.LSGGHSLHETSTVLVETVTK#.S	149.67	57.69	2.59	0.39
Q8VHX6_Fl	Flnc	Filamin-C C	R.LTVTSLQETGLK#.V	208.76	85.90	2.43	0.41
Q8VHX6_Fl	Flnc	Filamin-C C	R.NAGYGGLGLSIEGPSK#.V	39.41	16.42	2.40	0.42
Q8VHX6_Fl	Flnc	Filamin-C C	R.QQEGEASSQDMTAQVTSPSGK#.T	25.10	11.81	2.13	0.47
Q8VHX6_Fl	Flnc	Filamin-C C	R.QQEGEASSQDM*TAQVTSPSGK#.T	40.70	17.68	2.30	0.43
Q8VHX6_Fl	Flnc	Filamin-C C	R.RDTVEVALEDKGDNTFR.C	2.63	24.31	0.11	9.23
Q8VHX6_Fl	Flnc	Filamin-C C	R.SPFEVQVSPEAGAQK#.V	69.18	35.48	1.95	0.51
Q8VHX6_Fl	Flnc	Filamin-C C	K.SPFVVNVAPPLDLSK#.V	289.42	150.81	1.92	0.52
Q8VHX6_Fl	Flnc	Filamin-C C	K.TARPNITDNKDGTITVR.Y	4.66	50.08	0.09	10.74
Q8VHX6_Fl	Flnc	Filamin-C C	K.TEAAEIVEGEDSAYSVR.F	45.12	113.19	0.40	2.51
Q8VHX6_Fl	Flnc	Filamin-C C	R.TGVEVGKPTHFTVLTK.G	103.56	36.49	2.84	0.35
Q8VHX6_Fl	Flnc	Filamin-C C	R.TSQLNVGTSTDVSLK#.I	158.28	62.68	2.53	0.40
Q8VHX6_Fl	Flnc	Filamin-C C	R.TYAVSYVPK#.V	27.05	15.63	1.73	0.58
Q8VHX6_Fl	Flnc	Filamin-C C	K.VAVGQEQAFSVNTR.G	74.54	145.05	0.51	1.95
Q8VHX6_Fl	Flnc	Filamin-C C	K.VDITYDGHPVPGSPFAVEGVLPPDPSK#.V	17.93	7.75	2.31	0.43
Q8VHX6_Fl	Flnc	Filamin-C C	R.VHVQPAVDTSGIK#.V	42.54	21.95	1.94	0.52
Q8VHX6_Fl	Flnc	Filamin-C C	R.VK#EVADFK#.V	33.19	14.36	2.31	0.43
Q8VHX6_Fl	Flnc	Filamin-C C	K.VK#VQGLNSK#.V	51.33	14.93	3.44	0.29
Q8VHX6_Fl	Flnc	Filamin-C C	K.VNQPASFAVQLNGAR.G	8.41	16.21	0.52	1.93
Q8VHX6_Fl	Flnc	Filamin-C C	K.VPQLPITNFNR.D	56.79	118.01	0.48	2.08
Q8VHX6_Fl	Flnc	Filamin-C C	K.VSGPGVEPHGVLR.E	18.93	41.35	0.46	2.18
Q8VHX6_Fl	Flnc	Filamin-C C	R.VYNVTYTVK#.E	286.67	99.90	2.87	0.35
Q8VHX6_Fl	Flnc	Filamin-C C	K.WGDESVPGSPFK#.V	127.54	52.89	2.41	0.41
Q8VHX6_Fl	Flnc	Filamin-C C	K.YADQEVPR.S	27.96	64.02	0.44	2.29
Q8VHX6_Fl	Flnc	Filamin-C C	K.YDGNHIPGSPLQFYVDAINSR.H	25.64	53.49	0.48	2.09
Q8VHX6_Fl	Flnc	Filamin-C C	K.YGGDEIPYSPFR.I	13.02	31.27	0.42	2.40
Q8VHX6_Fl	Flnc	Filamin-C C	K.YGGHPIPK#.F	37.34	15.20	2.46	0.41
Q8VHX6_Fl	Flnc	Filamin-C C	K.YTAVQQGNM*AVTVTYGGDPVPK#.S	17.15	6.34	2.70	0.37
Q8VHX6_Fl	Flnc	Filamin-C C	K.YTAVQQGNMAVTVTYGGDPVPK#.S	14.65	7.76	1.89	0.53
E9QNF5_E9	Fmr1	Fragile X m	K.DINESDEVEVYSR.A	1.84	7.20	0.26	3.91
E9QNF5_E9	Fmr1	Fragile X m	K.DSIANATVLLDYHLNYLK#.E	11.57	14.17	0.82	1.22
E9QNF5_E9	Fmr1	Fragile X m	R.SFLEFAEDVIQVPR.N	4.20	11.98	0.35	2.85
E9QNF5_E9	Fmr1	Fragile X m	R.TADGSLQSASSEGSR.L	1.72	5.40	0.32	3.14
E9QNF5_E9	Fmr1	Fragile X m	K.DINESDEVEVYSR.A	6.25	21.31	0.29	3.41
E9QNF5_E9	Fmr1	Fragile X m	K.ENTHFSQPNSTK.V	22.50	16.29	1.38	0.72
E9QNF5_E9	Fmr1	Fragile X m	R.GM*VPFVFVGTK#.D	16.09	10.91	1.47	0.68
E9QNF5_E9	Fmr1	Fragile X m	R.GMVPFVFVGTK#.D	11.05	9.26	1.19	0.84
E9QNF5_E9	Fmr1	Fragile X m	K.GYVTDDGQGM*GR.G	3.26	7.49	0.44	2.29
E9QNF5_E9	Fmr1	Fragile X m	R.SFLEFAEDVIQVPR.N	9.47	34.54	0.27	3.65
P11276_FI	Fn1	Fibronectir	R.APITGYIIR.H	8.28	32.32	0.26	3.90
P11276_FI	Fn1	Fibronectir	K.ATGVFTTLQPLR.S	4.23	17.12	0.25	4.05
P11276_FI	Fn1	Fibronectir	K.GLAFTDVDVDSIK#.I	13.53	12.24	1.11	0.90
P11276_FI	Fn1	Fibronectir	R.GVTYNIIVEALQNQR.R	3.74	15.53	0.24	4.16
P11276_FI	Fn1	Fibronectir	R.NLQPGSEYTVTLVAVK#.G	13.86	10.05	1.38	0.72
P11276_FI	Fn1	Fibronectir	R.NTFAEITGLSPGVTYLFK.V	18.25	20.14	0.91	1.10
P11276_FI	Fn1	Fibronectir	R.SDNVPPPTDLQFVELTDVK.V	5.02	6.35	0.79	1.27
P11276_FI	Fn1	Fibronectir	K.TGLDSPTGFDSSDITANSFTVHWVAPR.A	3.56	11.57	0.31	3.25
P11276_FI	Fn1	Fibronectir	R.VVTPLSPPTNLHLEANPDTGVLTVSWER.S	1.94	6.49	0.30	3.34
P11276_FI	Fn1	Fibronectir	K.YIVNVYQISEEGK.Q	14.03	10.88	1.29	0.78
P11276_FI	Fn1	Fibronectir	R.APITGYIIR.H	60.06	265.91	0.23	4.43
P11276_FI	Fn1	Fibronectir	K.ATGVFTTLQPLR.S	47.27	187.57	0.25	3.97
P11276_FI	Fn1	Fibronectir	R.EESPPLIGQQATVSDIPR.D	5.13	18.96	0.27	3.70
P11276_FI	Fn1	Fibronectir	K.EINLSPDSSSVIVSGLM*VATK#.Y	11.28	7.42	1.52	0.66
P11276_FI	Fn1	Fibronectir	R.ESNPLTAQQTTK#.L	122.48	119.36	1.03	0.97
P11276_FI	Fn1	Fibronectir	R.EVTSDSGSIVVSGLTPGVEYTYTIQVLR.D	7.58	22.08	0.34	2.91
P11276_FI	Fn1	Fibronectir	R.FLTTTPNSLLVSWQAPR.A	15.09	66.83	0.23	4.43

P11276_FI	Fn1	Fibronectir	K.FSQVTPTSFTAQWIAPSVQLTGYR.V	23.22	65.34	0.36	2.81
P11276_FI	Fn1	Fibronectir	R.FTNIGPDTM*R.V	37.01	104.85	0.35	2.83
P11276_FI	Fn1	Fibronectir	K.GLAFTDVDVDSIK#.I	210.65	179.18	1.18	0.85
P11276_FI	Fn1	Fibronectir	R.GVTYNIIVEALQNQR.R	21.45	69.07	0.31	3.22
P11276_FI	Fn1	Fibronectir	R.HALQSASAGSGSFTDVR.T	16.19	107.42	0.15	6.63
P11276_FI	Fn1	Fibronectir	K.IAWESPQGQVSR.Y	27.20	124.72	0.22	4.59
P11276_FI	Fn1	Fibronectir	R.IGDTWSK#.K	106.74	93.13	1.15	0.87
P11276_FI	Fn1	Fibronectir	R.ITGYIIK#.Y	118.64	112.85	1.05	0.95
P11276_FI	Fn1	Fibronectir	R.ITYGETGGNSPVQEFTVPGSK#.S	46.55	45.17	1.03	0.97
P11276_FI	Fn1	Fibronectir	R.K#K#TDELPQLVTLPHPNLHGPEILDVPSTVQK#.T	12.75	19.93	0.64	1.56
P11276_FI	Fn1	Fibronectir	K.KTDELPQLVTLPHPNLHGPEILDVPSTVQK.T	13.56	14.92	0.91	1.10
P11276_FI	Fn1	Fibronectir	R.LRPRPYLPNVDEEVQIGHVPR.G	12.54	30.22	0.41	2.41
P11276_FI	Fn1	Fibronectir	R.NLQPGSEYTVTLVAVK#.G	121.06	90.84	1.33	0.75
P11276_FI	Fn1	Fibronectir	R.NTFAEITGLSPGVTYLFK#.V	264.60	216.87	1.22	0.82
P11276_FI	Fn1	Fibronectir	K.QSLILSTSQTTAPDAPPDPTVDQVDDTSIVVR.W	5.89	19.29	0.31	3.27
P11276_FI	Fn1	Fibronectir	R.SDNVPPPTDLQFVELTDVK#.V	97.78	85.28	1.15	0.87
P11276_FI	Fn1	Fibronectir	R.SDNVPPPTDLQFVELTDVK#.V	64.34	60.79	1.06	0.94
P11276_FI	Fn1	Fibronectir	R.SIPPYNTEVTETTIVITWTPAPR.I	4.80	9.37	0.51	1.95
P11276_FI	Fn1	Fibronectir	R.SSPVIIDASTAIDAPSNLR.F	24.38	114.79	0.21	4.71
P11276_FI	Fn1	Fibronectir	K.STATINNIKPGADYTITLYAVTGR.G	8.38	35.85	0.23	4.28
P11276_FI	Fn1	Fibronectir	R.SYTITGLQPGTDYK#.I	175.70	149.78	1.17	0.85
P11276_FI	Fn1	Fibronectir	K.TASPDQTEM*TIEGLQPTVEYVVSVYAQNR.N	12.05	59.63	0.20	4.95
P11276_FI	Fn1	Fibronectir	K.TASPDQTEMTIEGLQPTVEYVVSVYAQNR.N	12.06	35.41	0.34	2.94
P11276_FI	Fn1	Fibronectir	K.TEIDKPSQM*QVTDVQDNSISVR.W	17.20	65.30	0.26	3.80
P11276_FI	Fn1	Fibronectir	K.TEIDKPSQMQVTDVQDNSISVR.W	14.38	63.97	0.22	4.45
P11276_FI	Fn1	Fibronectir	K.TGLDSPTGFDSSDITANSFTVHWVAPR.A	34.46	116.81	0.30	3.39
P11276_FI	Fn1	Fibronectir	R.TKTETITGFQVDAIPANGQTPVQR.S	9.23	36.36	0.25	3.94
P11276_FI	Fn1	Fibronectir	K.TPFITNPGYDTENGIQLPGTTHQQPSVGQQM*IFEEHGFR.R	4.04	6.09	0.66	1.51
P11276_FI	Fn1	Fibronectir	R.TVLVTWTPPR.A	14.69	63.28	0.23	4.31
P11276_FI	Fn1	Fibronectir	R.VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGR.K	5.61	20.09	0.28	3.58
P11276_FI	Fn1	Fibronectir	R.VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK.Y	4.40	19.11	0.23	4.34
P11276_FI	Fn1	Fibronectir	K.VFAVHQGR.E	82.63	41.72	1.98	0.50
P11276_FI	Fn1	Fibronectir	K.VGDTYERPK.D	12.07	48.48	0.25	4.02
P11276_FI	Fn1	Fibronectir	K.VTIM*WTPPDSVVSGYR.V	5.85	27.79	0.21	4.75
P11276_FI	Fn1	Fibronectir	K.VTIMWTPPDSVVSGYR.V	5.43	18.60	0.29	3.42
P11276_FI	Fn1	Fibronectir	R.VTYSSPEDGIR.E	37.17	142.66	0.26	3.84
P11276_FI	Fn1	Fibronectir	R.VVTPLSPPTNLHLEANPDTGVLTVSWER.S	14.73	48.90	0.30	3.32
P11276_FI	Fn1	Fibronectir	R.WLPSTSPVTGYR.V	31.79	119.69	0.27	3.77
P11276_FI	Fn1	Fibronectir	K.YEVSVYALK#.D	97.58	97.78	1.00	1.00
P11276_FI	Fn1	Fibronectir	K.YIVNVYQISEEGK#.Q	122.84	106.26	1.16	0.87
Q8K012_FE	Fnbp1l	Formin-bin	R.IEIEQNYAK#.Q	28.62	17.55	1.63	0.61
Q8K012_FE	Fnbp1l	Formin-bin	R.K#VIPIISK#.C	15.91	10.87	1.46	0.68
Q8K012_FE	Fnbp1l	Formin-bin	R.TISDGTISAAK#.Q	22.31	9.97	2.24	0.45
Q6ZQ03_FN	Fnbp4	Formin-bin	K.FEFLGINR.Q	4.25	9.81	0.43	2.31
Q6ZQ03_FN	Fnbp4	Formin-bin	K.FQIGELANTLTSK#.F	23.13	9.18	2.52	0.40
Q6ZQ03_FN	Fnbp4	Formin-bin	K.VEEEQDLK#FQIGELANTLTSK#.F	7.43	3.51	2.11	0.47
P47930_FC	Fosl2	Fos-related	R.GTGSAVGPVVVK.Q	11.29	17.77	0.64	1.57
P47930_FC	Fosl2	Fos-related	K.LQAETEELEEEK#.S	8.01	11.62	0.69	1.45
P42128_FC	Foxk1	Forkhead b	R.FVQNVTSDLQLAAEFAAK#.A	11.25	5.98	1.88	0.53
P42128_FC	Foxk1	Forkhead b	R.TPFGPLSSR.S	6.79	13.02	0.52	1.92
P58462_FC	Foxp1	Forkhead b	K.AAPQPLNLVSSVTLSK.S	6.70	13.29	0.50	1.99
P58462_FC	Foxp1	Forkhead b	K.NAEVRPPFTYASLIR.Q	2.27	19.15	0.12	8.44
P58462_FC	Foxp1	Forkhead b	R.YSDKYNVPISSADIAQNQEFYK.N	3.66	7.37	0.50	2.01
P58462_FC	Foxp1	Forkhead b	K.AAPQPLNLVSSVTLSK.S	11.95	22.34	0.54	1.87
P58462_FC	Foxp1	Forkhead b	K.NAEVRPPFTYASLIR.Q	11.22	20.09	0.56	1.79
P58462_FC	Foxp1	Forkhead b	R.YSDKYNVPISSADIAQNQEFYK.N	4.89	8.09	0.61	1.65
P97376_FR	Frg1	Protein FR	K.YLGINSDGLVVGR.S	1.75	8.84	0.20	5.05
P29391_FR	Ftl1	Ferritin ligl	R.QNYSTEVEAAVNR.L	2.20	3.43	0.64	1.56
Q8BGW1_F	Fto	Alpha-keto	K.DDEFYQQWQLK#.Y	2.41	2.42	1.00	1.00
Q91WJ8_F	Fubp1	Far upstrea	K.AWEEYYK#.K	27.22	12.90	2.11	0.47
Q91WJ8_F	Fubp1	Far upstrea	K.IGGDAGTSLNSNDYGYGGQK#.R	14.74	4.67	3.15	0.32
Q91WJ8_F	Fubp1	Far upstrea	R.LLDQIVEK#.G	20.01	8.78	2.28	0.44
Q91WJ8_F	Fubp1	Far upstrea	K.TGLIIGK#.G	64.38	45.75	1.41	0.71
A2AJ72_A2	Fubp3	MCG13045	R.EILGGLTVTR.G	16.39	49.45	0.33	3.02
A2AJ72_A2	Fubp3	MCG13045	R.GAPQQMEVAR.H	6.65	27.21	0.24	4.09
A2AJ72_A2	Fubp3	MCG13045	K.IDSIPHLNNSTPLVDPSVYGYGVQK#.R	49.98	28.41	1.76	0.57
A2AJ72_A2	Fubp3	MCG13045	R.IINELILTAQER.E	13.78	34.60	0.40	2.51
A2AJ72_A2	Fubp3	MCG13045	R.IQFKPDDGISPER.A	16.22	62.24	0.26	3.84
A2AJ72_A2	Fubp3	MCG13045	K.M*VGFIIGR.G	4.78	16.09	0.30	3.37
A2AJ72_A2	Fubp3	MCG13045	K.MVGFIIGR.G	4.51	10.45	0.43	2.32
A2AJ72_A2	Fubp3	MCG13045	K.M*VM*IQDGPLPTGADKPLR.I	4.63	9.56	0.48	2.06
A2AJ72_A2	Fubp3	MCG13045	R.NGPGFHNDM*DGNSTIQELLIPASK#.V	13.37	8.06	1.66	0.60
A2AJ72_A2	Fubp3	MCG13045	R.NGPGFHNDMDGNSTIQELLIPASK#.V	8.46	6.36	1.33	0.75
A2AJ72_A2	Fubp3	MCG13045	R.NPPPNTDPNLR.I	7.08	21.48	0.33	3.03
A2AJ72_A2	Fubp3	MCG13045	R.QQAAFYGQTLGQAQAHSQEQ.-	15.04	15.04	1.00	1.00
A2AJ72_A2	Fubp3	MCG13045	R.SDWSVGTPGGVQEITYTVPADK#.C	23.80	8.87	2.68	0.37
A2AJ72_A2	Fubp3	MCG13045	K.VGGASLGAPAAFGQSPFSQPPAAPHQNTFPPR.G	1.53	3.77	0.41	2.46
Q9D6K8_F	Fundc2	FUN14 don	R.K#LFGQESGPSAEK#.Y	3.02	6.35	0.48	2.10
P56959_FL	Fus	RNA-bindin	K.AAIDWFDGK#.E	93.26	26.79	3.48	0.29
P56959_FL	Fus	RNA-bindin	K.AAIDWFDGKEFSGNPIK.V	18.45	14.83	1.24	0.80
P56959_FL	Fus	RNA-bindin	R.HDSEQDNSDNNTIFVQGLGENVTIESVADYFK#.Q	8.73	5.95	1.47	0.68
P56959_FL	Fus	RNA-bindin	K.AAIDWFDGK#.E	15.19	8.53	1.78	0.56
P56959_FL	Fus	RNA-bindin	K.GEATVSFDDPPSAK#.A	55.28	28.71	1.93	0.52
P56959_FL	Fus	RNA-bindin	R.HDSEQDNSDNNTIFVQGLGENVTIESVADYFK#.Q	7.24	2.87	2.52	0.40
Q61584_F	Fxr1	Fragile X m	R.EDGM*VPFVFVGTK#.E	20.96	13.97	1.50	0.67
Q61584_F	Fxr1	Fragile X m	R.IFYHPETTQLM*ILSASEATVK#.R	9.81	7.78	1.26	0.79
Q61584_F	Fxr1	Fragile X m	R.IFYHPETTQLMILSASEATVK#.R	8.66	7.70	1.12	0.89
Q61584_F	Fxr1	Fragile X m	R.IYGESAEAVK#.K	15.77	10.75	1.47	0.68
Q61584_F	Fxr1	Fragile X m	R.IYGESAEAVK#K#.A	21.68	9.79	2.21	0.45
Q61584_F	Fxr1	Fragile X m	R.KVPGVTAIELDEDTGTFR.I	4.71	36.57	0.13	7.76
Q61584_F	Fxr1	Fragile X m	R.LQIDEQLR.Q	18.90	57.69	0.33	3.05
Q61584_F	Fxr1	Fragile X m	K.VIQEIVDK#.S	58.62	32.22	1.82	0.55
Q61584_F	Fxr1	Fragile X m	K.AINGPTSASGDEIPK#.L	5.75	4.58	1.26	0.80
Q61584_F	Fxr1	Fragile X m	K.DVHEDSLTVVFENNWQPER.Q	5.71	13.31	0.43	2.33
Q61584_F	Fxr1	Fragile X m	R.EDGM*VPFVFVGTK#.E	32.16	21.15	1.52	0.66
Q61584_F	Fxr1	Fragile X m	R.EDGMVPFVFVGTK#.E	27.98	17.17	1.63	0.61
Q61584_F	Fxr1	Fragile X m	K.EMAKDVIEEHGPSEK.A	25.47	11.86	2.15	0.47
Q61584_F	Fxr1	Fragile X m	K.ESIGNVQVLLEYHIAYLK#.E	43.66	23.39	1.87	0.54
Q61584_F	Fxr1	Fragile X m	K.GYATDESTVSSVQGSR.S	5.84	17.54	0.33	3.01
Q61584_F	Fxr1	Fragile X m	R.IFYHPETTQLM*ILSASEATVK#.R	21.40	11.24	1.90	0.53
Q61584_F	Fxr1	Fragile X m	R.IFYHPETTQLMILSASEATVK#.R	36.11	20.39	1.77	0.56
Q61584_F	Fxr1	Fragile X m	R.IYGESAEAVK#.K	66.12	28.34	2.33	0.43
Q61584_F	Fxr1	Fragile X m	R.KVPGVTAIELDEDTGTFR.I	22.62	69.92	0.32	3.09

Q61584_F	Fxr1	Fragile X m	R.LQIDEQLR.Q	63.00	189.92	0.33	3.01
Q61584_F	Fxr1	Fragile X m	R.LRPVNQNK.T	4.38	11.04	0.40	2.52
Q61584_F	Fxr1	Fragile X m	K.SSISSVLKDPDSNPYSLLDNTESDQTADTDASESHHSTNR.R	2.46	4.81	0.51	1.96
Q61584_F	Fxr1	Fragile X m	K.TLK#EDSTQEAAVLNGVS.-	3.68	3.42	1.08	0.93
Q61584_F	Fxr1	Fragile X m	K.VIQEIVDK#.S	248.47	149.03	1.67	0.60
Q61584_F	Fxr1	Fragile X m	R.VRIEGDNENKLPR.E	1.27	37.46	0.03	29.43
Q61584_F	Fxr1	Fragile X m	R.EDGM*VPFVFVGTK#.E	13.95	6.20	2.25	0.44
Q9WVR4_F	Fxr2	Fragile X m	R.SYLEFSEDSVQVPR.D	2.22	4.98	0.45	2.25
Q9WVR4_F	Fxr2	Fragile X m	R.EDLM*GLAIGTHGANIQQAR.K	7.90	23.27	0.34	2.95
Q9WVR4_F	Fxr2	Fragile X m	R.SYLEFSEDSVQVPR.D	9.05	19.78	0.46	2.19
Q91Z49_U	Fyttd1	UAP56-int	K.GVPLQFDINSVGK#.Q	23.82	26.67	0.89	1.12
Q91Z49_U	Fyttd1	UAP56-int	R.LVGATATPPPPPK#.A	16.26	22.29	0.73	1.37
Q91Z49_U	Fyttd1	UAP56-int	K.VQTQLNTEQLIDDVVAK.R	4.70	7.86	0.60	1.67
Q91Z49_U	Fyttd1	UAP56-int	R.LVGATATPPPPPK.A	1.96	3.49	0.56	1.78
P97855_G	G3bp1	Ras GTPase	K.DFFQNFGNVVELR.I	6.29	15.22	0.41	2.42
P97855_G	G3bp1	Ras GTPase	R.EAGEPGDVEPR.R	18.22	38.28	0.48	2.10
P97855_G	G3bp1	Ras GTPase	R.FM*QTFVLAPEGSVANK#.F	27.10	14.67	1.85	0.54
P97855_G	G3bp1	Ras GTPase	R.FMQTFVLAPEGSVANK#.F	20.89	9.60	2.18	0.46
P97855_G	G3bp1	Ras GTPase	R.HPDSHQLFIGNLPHEVDK#SELK#.D	8.97	7.51	1.20	0.84
P97855_G	G3bp1	Ras GTPase	K.STSPAPADVAPAQEDLR.T	4.99	11.42	0.44	2.29
P97855_G	G3bp1	Ras GTPase	R.FM*QTFVLAPEGSVANK#.F	9.29	4.49	2.07	0.48
P97855_G	G3bp1	Ras GTPase	R.FMQTFVLAPEGSVANK#.F	13.72	5.50	2.49	0.40
P97855_G	G3bp1	Ras GTPase	R.QYYTLLNQAPDM*LHR.F	13.22	28.77	0.46	2.18
P97855_G	G3bp1	Ras GTPase	R.EAGEPGDVEPR.R	37.46	93.86	0.40	2.51
P97855_G	G3bp1	Ras GTPase	R.FM*QTFVLAPEGSVANK#.F	31.50	16.05	1.96	0.51
P97855_G	G3bp1	Ras GTPase	R.FMQTFVLAPEGSVANK#.F	42.14	17.84	2.36	0.42
P97855_G	G3bp1	Ras GTPase	R.HPDSHQLFIGNLPHEVDK#SELK#.D	18.34	7.40	2.48	0.40
P97855_G	G3bp1	Ras GTPase	R.LNVEEK#.K	142.30	65.18	2.18	0.46
P97855_G	G3bp1	Ras GTPase	K.LPNFGFVVFDDSEPVQK#.V	60.16	35.04	1.72	0.58
P97855_G	G3bp1	Ras GTPase	K.NSSYAHGGLDSNGK#PADAVYGQK#.E	17.24	6.01	2.87	0.35
P97855_G	G3bp1	Ras GTPase	K.STSPAPADVAPAQEDLR.T	6.68	19.92	0.34	2.98
P97855_G	G3bp1	Ras GTPase	R.TFSWASVTSK#.N	92.32	44.20	2.09	0.48
P97379_G	G3bp2	Ras GTPase	K.FM*QTFVLAPEGSVPNK#.F	17.15	7.42	2.31	0.43
P97379_G	G3bp2	Ras GTPase	K.FMQTFVLAPEGSVPNK#.F	13.52	5.53	2.44	0.41
P97379_G	G3bp2	Ras GTPase	K.HLEELEEK#.S	53.38	22.63	2.36	0.42
P97379_G	G3bp2	Ras GTPase	K.TEELKPQVEEK.H	19.28	8.88	2.17	0.46
P97379_G	G3bp2	Ras GTPase	R.VDAKPEVQSQPPR.V	23.03	47.51	0.48	2.06
P97379_G	G3bp2	Ras GTPase	K.APEYLHR.F	8.24	11.26	0.73	1.37
P97379_G	G3bp2	Ras GTPase	K.FM*QTFVLAPEGSVPNK#.F	20.05	9.44	2.12	0.47
P97379_G	G3bp2	Ras GTPase	K.FMQTFVLAPEGSVPNK#.F	7.26	4.80	1.51	0.66
P97379_G	G3bp2	Ras GTPase	R.NSSYVHGGVDASGK#PQEAVYGQNDIHHK#.V	17.19	6.01	2.86	0.35
P97379_G	G3bp2	Ras GTPase	K.AFSWASVTSK#.N	27.96	13.13	2.13	0.47
P97379_G	G3bp2	Ras GTPase	K.FM*QTFVLAPEGSVPNK#.F	20.57	11.65	1.77	0.57
P97379_G	G3bp2	Ras GTPase	K.FMQTFVLAPEGSVPNK#.F	13.71	8.53	1.61	0.62
P97379_G	G3bp2	Ras GTPase	K.HLEELEEK#.S	77.76	38.61	2.01	0.50
P97379_G	G3bp2	Ras GTPase	K.LPNFGFVVFDDSEPVQR.I	11.76	23.39	0.50	1.99
P97379_G	G3bp2	Ras GTPase	K.TEELK#PQVEEK#.H	13.76	5.79	2.38	0.42
P97379_G	G3bp2	Ras GTPase	R.VDAKPEVQSQPPR.V	35.65	63.47	0.56	1.78
Q00422_G	Gabpa	GA-binding	K.HITTISDETSEQVTR.W	5.14	24.75	0.21	4.81
Q00422_G	Gabpa	GA-binding	K.LNILEIVK#.T	46.76	32.61	1.43	0.70
Q00422_G	Gabpa	GA-binding	K.LNQPELVAQK#.W	36.73	208.28	0.18	5.67
Q00422_G	Gabpa	GA-binding	R.MQLHGIAQPVTAVALAATSLQADK#EI.-	17.43	8.91	1.96	0.51
P81069_G	Gabpb2	GA-binding	K.ATSAHLEEMEEGNSLDSSTQQVVGSGGQR.V	1.51	2.45	0.62	1.62
P81069_G	Gabpb2	GA-binding	R.TTEPHTNVSIETISS.-	25.79	25.79	1.00	1.00
Q99KY4_G	Gak	Cyclin-G-as	R.DQSDFVGQTVELGELR.L	1.68	6.40	0.26	3.81
Q99KY4_G	Gak	Cyclin-G-as	K.VSENDFEDLLPNQGFSK#.S	3.70	3.34	1.11	0.90
Q99KY4_G	Gak	Cyclin-G-as	K.VIQSVANYAK#.G	12.35	9.29	1.33	0.75
Q99KY4_G	Gak	Cyclin-G-as	K.VSENDFEDLLPNQGFSK#.S	4.13	4.20	0.98	1.02
Q8BHN3_G	Ganab	Neutral alp	R.DDNSVELTVAEGPYK#.I	3.24	4.64	0.70	1.43
P16858_G	Gapdh	Glyceralde	R.GAAQNIIPASTGAAK#.A	168.09	245.81	0.68	1.46
P16858_G	Gapdh	Glyceralde	K.LISWYDNEYGYSNR.V	19.53	104.08	0.19	5.33
P16858_G	Gapdh	Glyceralde	K.LVINGKPITIFQER.D	3.67	29.51	0.12	8.05
P16858_G	Gapdh	Glyceralde	K.VIHDNFGIVEGLM*TTVHAITATQK#.T	42.86	39.63	1.08	0.92
P16858_G	Gapdh	Glyceralde	K.VIHDNFGIVEGLM*TTVHAITATQK.T	15.69	13.93	1.13	0.89
P16858_G	Gapdh	Glyceralde	K.VIHDNFGIVEGLMTTVHAITATQK.T	63.91	63.57	1.01	0.99
P16858_G	Gapdh	Glyceralde	R.VVDLM*AYM*ASK.E	77.94	11.92	6.54	0.15
P16858_G	Gapdh	Glyceralde	R.VVDLM*AYM*ASK#E.-	22.98	31.23	0.74	1.36
P16858_G	Gapdh	Glyceralde	R.VVDLMAYMASKE.-	10.58	13.88	0.76	1.31
P16858_G	Gapdh	Glyceralde	K.WGEAGAEYVVESTGVFTTM*EK#.A	10.09	10.09	1.00	1.00
P16858_G	Gapdh	Glyceralde	K.WGEAGAEYVVESTGVFTTMEK.A	18.56	26.39	0.70	1.42
P16858_G	Gapdh	Glyceralde	R.GAAQNIIPASTGAAK.A	12.32	21.62	0.57	1.75
P16858_G	Gapdh	Glyceralde	K.LISWYDNEYGYSNR.V	1.93	10.38	0.19	5.39
P16858_G	Gapdh	Glyceralde	R.VVDLM*AYM*ASKE.-	9.10	10.56	0.86	1.16
P16858_G	Gapdh	Glyceralde	K.WGEAGAEYVVESTGVFTTM*EK.A	8.05	7.10	1.13	0.88
P16858_G	Gapdh	Glyceralde	K.WGEAGAEYVVESTGVFTTMEK#.A	3.75	3.73	1.00	1.00
P16858_G	Gapdh	Glyceralde	R.GAAQNIIPASTGAAK#.A	10.56	12.84	0.82	1.22
Q6PAR5_G	Gapvd1	GTPase-acti	K.ILEDTQFVDGYK#.Q	12.67	2.95	4.30	0.23
Q6PAR5_G	Gapvd1	GTPase-acti	R.M*ALDNLLANLPQAK#PGK#.S	9.44	3.59	2.63	0.38
Q6PAR5_G	Gapvd1	GTPase-acti	R.LIASSLVAGEK#.L	30.29	8.35	3.63	0.28
Q6PAR5_G	Gapvd1	GTPase-acti	R.LPNFGSHVLTAAEM*EAFK#.Q	10.54	3.80	2.78	0.36
Q6PAR5_G	Gapvd1	GTPase-acti	R.LPNFGSHVLTAAEMEAFK#.Q	11.73	2.21	5.32	0.19
Q6PAR5_G	Gapvd1	GTPase-acti	K.VQEM*VDSNEAK#.L	8.67	4.39	1.98	0.51
Q6PAR5_G	Gapvd1	GTPase-acti	K.VQIAEAINLQDK#.S	13.65	12.86	1.06	0.94
Q9CY66_G	Gar1	H/ACA ribo	K.VDEIFGQLR.D	4.48	8.61	0.52	1.92
Q9CZD3_S	Gars	Glycine--tR	K.FADFM*VK#.D	15.44	4.25	3.63	0.28
Q9CZD3_S	Gars	Glycine--tR	K.GEFTIETEGK#.T	16.48	3.59	4.60	0.22
Q9CZD3_S	Gars	Glycine--tR	R.IYLYLTK#.V	24.08	2.32	10.39	0.10
Q9CZD3_S	Gars	Glycine--tR	R.LLEFNQGK#.L	32.29	4.73	6.82	0.15
Q9CZD3_S	Gars	Glycine--tR	R.TFFSFPAVVAPFK#.C	46.56	8.94	5.21	0.19
Q9CZD3_S	Gars	Glycine--tR	K.TVNVVQFEPNK#.G	25.96	9.75	2.66	0.38
Q9CZD3_S	Gars	Glycine--tR	R.YPLFEGQETGK#K#.E	34.08	5.66	6.02	0.17
Q9CZD3_S	Gars	Glycine--tR	R.TFFSFPAVVAPFK#.C	33.50	3.79	8.83	0.11
Q64737_P	Gart	Trifunction	K.AAGFK#DPLLASGTDGVGTK#.L	29.13	4.86	6.00	0.17
Q64737_P	Gart	Trifunction	R.AVDGM*QQEGAPYTGILYAGIMLTK#.D	5.46	2.27	2.40	0.42
Q64737_P	Gart	Trifunction	R.AVQEIM*QEK#.S	26.02	5.37	4.84	0.21
Q64737_P	Gart	Trifunction	K.DSGVDIAAGNM*LVK#.K	27.06	5.55	4.88	0.21
Q64737_P	Gart	Trifunction	K.GVEITGFPEAQALGLQVFHAGTALK#.D	42.10	10.86	3.88	0.26
Q64737_P	Gart	Trifunction	K.K#IQPLAK#.A	14.93	10.49	1.42	0.70
Q64737_P	Gart	Trifunction	K.M*LNIHPSLLPSFK#.G	25.15	5.89	4.27	0.23
Q64737_P	Gart	Trifunction	K.SSSHIVLVISNK#.A	23.94	4.33	5.52	0.18
P11862_G	Gas2	Growth arr	R.VGGGWETFAGYLLK#.H	5.53	6.40	0.86	1.16
Q8CHY6_P	Gatad2a	Transcripti	K.ALQQEQEM*EQR.L	3.76	10.20	0.37	2.71
Q8CHY6_P	Gatad2a	Transcripti	K.ALQQEQEMEQR.L	5.08	19.83	0.26	3.90

Q8CHY6_P	Gatad2a	Transcripti	R.ISATAAAAVLSR.E	38.74	42.42	0.91	1.10
Q8CHY6_P	Gatad2a	Transcripti	R.LLQQGVGTASIK#.A	44.55	36.08	1.23	0.81
Q8CHY6_P	Gatad2a	Transcripti	K.LQNAASATALVSR.T	5.39	24.27	0.22	4.50
Q8CHY6_P	Gatad2a	Transcripti	K.TPLSTGGTLAFVSPSLAVHK#.T	23.73	16.33	1.45	0.69
Q8CHY6_P	Gatad2a	Transcripti	R.IIQQGLIR.V	2.78	15.83	0.18	5.70
Q8CHY6_P	Gatad2a	Transcripti	R.IPGSIIPPPLVR.G	3.42	13.61	0.25	3.98
Q8CHY6_P	Gatad2a	Transcripti	R.ISATAAAAVLSR.E	5.05	14.77	0.34	2.93
Q8CHY6_P	Gatad2a	Transcripti	K.LQNAASATALVSR.T	4.66	21.57	0.22	4.63
Q8CHY6_P	Gatad2a	Transcripti	K.TPLSTGGTLAFVSPSLAVHK#.T	15.56	19.84	0.78	1.28
Q8VHR5_P	Gatad2b	Transcripti	K.ALQQEQEIEQR.L	11.99	53.99	0.22	4.50
Q8VHR5_P	Gatad2b	Transcripti	K.DLANLEVPHELPTK#.Q	4.38	4.05	1.08	0.92
Q8VHR5_P	Gatad2b	Transcripti	R.LQQQAALSPTTAPAVSSVSK.Q	12.89	12.31	1.05	0.95
Q8VHR5_P	Gatad2b	Transcripti	R.QAPQPQSSLQR.G	5.73	34.56	0.17	6.04
Q8VHR5_P	Gatad2b	Transcripti	K.TPVVQNAASIVQPSPAHVGQQGLSK.L	19.93	20.90	0.95	1.05
Q8VHR5_P	Gatad2b	Transcripti	R.VIAPNPAQLQGQR.G	16.90	28.97	0.58	1.71
Q8VHR5_P	Gatad2b	Transcripti	R.VSSPLPSPSAM*SDAANSQAAAK.L	7.24	7.87	0.92	1.09
Q8VHR5_P	Gatad2b	Transcripti	K.ALQQEQEIEQR.L	4.44	20.02	0.22	4.51
Q8VHR5_P	Gatad2b	Transcripti	R.LQQQAALSPTTAPAVSSVSK.Q	7.01	7.03	1.00	1.00
Q8VHR5_P	Gatad2b	Transcripti	K.ALQQEQEIEQR.L	11.84	25.50	0.46	2.15
Q8VHR5_P	Gatad2b	Transcripti	R.QAPQPQSSLQR.G	4.21	17.54	0.24	4.17
Q8VHR5_P	Gatad2b	Transcripti	R.VIAPNPAQLQGQR.G	6.37	21.25	0.30	3.33
Q6A099_Q	Gbf1	MKIAA024	K.FLQLESLQELMK#.A	9.31	4.70	1.98	0.50
Q6A099_Q	Gbf1	MKIAA024	R.ADAPDAGAQSDSELPSYHQNDVSLDR.G	2.90	6.84	0.42	2.36
Q6A099_Q	Gbf1	MKIAA024	R.ALLVHDLQK#.L	18.68	7.33	2.55	0.39
Q6A099_Q	Gbf1	MKIAA024	R.APSSSSPGSPMASSPSK#.L	9.23	4.99	1.85	0.54
Q6A099_Q	Gbf1	MKIAA024	R.APSSSSPGSPM*ASSPSK#.L	26.83	14.00	1.92	0.52
Q6A099_Q	Gbf1	MKIAA024	R.DLEEAGDSGADKK.F	8.83	3.46	2.55	0.39
Q6A099_Q	Gbf1	MKIAA024	R.EITTSEPGSSEM*GASDQLDPQEGAHVEK#.A	18.60	8.76	2.12	0.47
Q6A099_Q	Gbf1	MKIAA024	K.FLQLESLQELM*K#.A	13.92	4.58	3.04	0.33
Q6A099_Q	Gbf1	MKIAA024	K.FLQLESLQELMK#.A	15.83	5.59	2.83	0.35
Q6A099_Q	Gbf1	MKIAA024	K.FTALSSESIENLPSVFGSNPK#.A	9.64	3.92	2.46	0.41
Q6A099_Q	Gbf1	MKIAA024	R.FVGTDPASDEVVLM*K#.I	13.31	5.05	2.64	0.38
Q6A099_Q	Gbf1	MKIAA024	K.LMEIITVENPK#.M	9.64	2.10	4.59	0.22
Q6A099_Q	Gbf1	MKIAA024	K.SLEETIIQK#.A	43.10	17.63	2.44	0.41
Q6A099_Q	Gbf1	MKIAA024	K.VLFPLLTK#.L	37.27	19.84	1.88	0.53
Q6A099_Q	Gbf1	MKIAA024	K.VLNTLNQQEK#.K	49.29	15.94	3.09	0.32
Q91Z40_Q	Gbp7	Gbp6 prot	K.ANHVLQSFLQSQISIEDSIM*QSDK#.A	6.60	2.82	2.34	0.43
Q91Z40_Q	Gbp7	Gbp6 prot	R.DFVLELK#.L	15.26	4.39	3.48	0.29
Q91Z40_Q	Gbp7	Gbp6 prot	K.DK#ELLVHVEEM*PEDQLDHSFQVQSK#.E	5.38	2.60	2.07	0.48
Q91Z40_Q	Gbp7	Gbp6 prot	K.FTLVLLDTEGLGDVEK#.G	10.85	3.47	3.12	0.32
Q91Z40_Q	Gbp7	Gbp6 prot	K.FTLVLLDTEGLGDVEK#GDPK#.N	10.79	4.41	2.45	0.41
Q91Z40_Q	Gbp7	Gbp6 prot	R.VITADEYLENALK#.L	25.59	2.43	10.55	0.09
Q91Z40_Q	Gbp7	Gbp6 prot	R.DFVLELK#.L	10.49	3.44	3.05	0.33
Q91Z40_Q	Gbp7	Gbp6 prot	K.FTLVLLDTEGLGDVEK#.G	12.21	3.62	3.38	0.30
Q91Z40_Q	Gbp7	Gbp6 prot	R.VITADEYLENALK#.L	20.01	4.63	4.32	0.23
Q8BKT3_G	Gcfc2	GC-rich seq	R.VAFEQFASENEVSK#.N	8.50	3.24	2.62	0.38
Q8BKT3_G	Gcfc2	GC-rich seq	K.SIEDDIFIPLYPK#.S	7.95	5.49	1.45	0.69
Q8BKT3_G	Gcfc2	GC-rich seq	R.VAFEQFASENEVSK#.N	7.73	2.36	3.28	0.31
O09172_G	Gclm	Glutamate-	K.LFIVGSNSSSSTR.S	2.99	3.19	0.94	1.07
E9PVA8_E9	Gcn1l1	Protein Gc	K.LSVADAQAEAK#.L	11.97	8.07	1.48	0.67
E9PVA8_E9	Gcn1l1	Protein Gc	K.SNSPR@LMDEAVLALR.N	1.80	135.57	0.01	75.18
E9PVA8_E9	Gcn1l1	Protein Gc	K.AASQGTQVPTVTEGVAAALLLSK#.L	53.31	33.94	1.57	0.64
E9PVA8_E9	Gcn1l1	Protein Gc	R.ALQAAIQQLAEAQPEATAK#.N	30.96	16.11	1.92	0.52
E9PVA8_E9	Gcn1l1	Protein Gc	R.AYSDQAIVNLLK#.M	53.82	20.33	2.65	0.38
E9PVA8_E9	Gcn1l1	Protein Gc	K.DAPNDASYDAVR.Q	4.17	9.93	0.42	2.38
E9PVA8_E9	Gcn1l1	Protein Gc	R.DAVLFFSESLVPTAR.K	11.99	27.26	0.44	2.27
E9PVA8_E9	Gcn1l1	Protein Gc	K.DLAPYLPSVTPGLK#.A	30.34	18.95	1.60	0.62
E9PVA8_E9	Gcn1l1	Protein Gc	K.DLILPTIQK#.S	16.44	10.47	1.57	0.64
E9PVA8_E9	Gcn1l1	Protein Gc	R.EEFSIM*QTPAGELFDK#.S	7.55	5.91	1.28	0.78
E9PVA8_E9	Gcn1l1	Protein Gc	K.FVHFIDAPSLALIM*PIVQR.A	13.76	19.11	0.72	1.39
E9PVA8_E9	Gcn1l1	Protein Gc	K.GAAYGLAGLVK#.G	27.23	16.63	1.64	0.61
E9PVA8_E9	Gcn1l1	Protein Gc	R.GEELLQSLSK#.I	13.87	7.72	1.80	0.56
E9PVA8_E9	Gcn1l1	Protein Gc	K.GIK#EEVQLTSK#.Q	14.64	8.53	1.72	0.58
E9PVA8_E9	Gcn1l1	Protein Gc	K.GLGILSLK#.Q	38.74	10.90	3.55	0.28
E9PVA8_E9	Gcn1l1	Protein Gc	R.IIIEDLLEATR.S	16.85	35.08	0.48	2.08
E9PVA8_E9	Gcn1l1	Protein Gc	K.K#LDAGNQLALIEELHK#.E	42.37	18.80	2.25	0.44
E9PVA8_E9	Gcn1l1	Protein Gc	K.LANGLLDELK#.T	19.77	8.89	2.22	0.45
E9PVA8_E9	Gcn1l1	Protein Gc	K.LSGFWQLVVDEK#.R	17.30	15.12	1.14	0.87
E9PVA8_E9	Gcn1l1	Protein Gc	K.LSVADAQAEAK#.L	76.36	42.79	1.78	0.56
E9PVA8_E9	Gcn1l1	Protein Gc	K.LTEVLTDSHVK#.V	56.12	25.54	2.20	0.46
E9PVA8_E9	Gcn1l1	Protein Gc	K.LTIIAQK#.M	36.47	20.11	1.81	0.55
E9PVA8_E9	Gcn1l1	Protein Gc	R.LTSADALRPSVVSITGPLIR.I	2.72	30.86	0.09	11.33
E9PVA8_E9	Gcn1l1	Protein Gc	K.LYRPPPVLDALGR.V	1.82	15.88	0.11	8.74
E9PVA8_E9	Gcn1l1	Protein Gc	K.M*TTETASEDDNFGTAQSNK#.A	14.35	7.04	2.04	0.49
E9PVA8_E9	Gcn1l1	Protein Gc	K.QLDDEEVSEFALDGLK#.Q	31.94	4.18	7.64	0.13
E9PVA8_E9	Gcn1l1	Protein Gc	R.SDTQLVVR.Q	8.02	22.89	0.35	2.86
E9PVA8_E9	Gcn1l1	Protein Gc	R.SGAAQGLAEVM*AGLGVEK#.L	6.71	5.99	1.12	0.89
E9PVA8_E9	Gcn1l1	Protein Gc	R.SGAAQGLAEVMAGLGVEK#.L	12.00	7.15	1.68	0.60
E9PVA8_E9	Gcn1l1	Protein Gc	R.VDENGPELLPR.V	3.35	9.63	0.35	2.88
E9PVA8_E9	Gcn1l1	Protein Gc	K.VGIALK#PFLPQLQTTFTK#.A	13.56	6.54	2.07	0.48
E9PVA8_E9	Gcn1l1	Protein Gc	R.VGK#GEPDAAPLSAPAFSLVFPM*LK#.M	41.70	16.82	2.48	0.40
E9PVA8_E9	Gcn1l1	Protein Gc	R.VISESPPDQWEAR.C	4.45	10.30	0.43	2.32
E9PVA8_E9	Gcn1l1	Protein Gc	R.VLAFLSSVAGDALTR.H	9.70	14.47	0.67	1.49
E9PVA8_E9	Gcn1l1	Protein Gc	K.VLPLEALVTDAGEVTEM*GK#.T	125.02	57.50	2.17	0.46
E9PVA8_E9	Gcn1l1	Protein Gc	R.VVLPYLVPK#.L	60.06	35.55	1.69	0.59
Q9CQQ4_G	Gemin2	Gem-associ	K.SQQLDSNVAM*PK#.S	9.69	4.37	2.22	0.45
Q6P6L6_Q	Gemin4	Gem (Nucl	K.SNPSVSSLLQK#.V	14.52	5.11	2.84	0.35
Q6P6L6_Q	Gemin4	Gem (Nucl	K.VLQPSPVSPSDTDTR.W	3.69	10.20	0.36	2.77
Q8BX17_G	Gemin5	Gem-associ	R.GPSSIYHQWATGSEGTLVQR.V	2.44	7.20	0.34	2.95
Q8BX17_G	Gemin5	Gem-associ	K.LIAETPITK#.G	18.59	18.39	1.01	0.99
Q8BX17_G	Gemin5	Gem-associ	K.VLALGNEDGSIEIFQVPNLR.L	11.02	10.96	1.00	1.00
Q8BX17_G	Gemin5	Gem-associ	R.VWNTLSIK#.N	8.32	5.62	1.48	0.68
Q8BX17_G	Gemin5	Gem-associ	K.VYEAVELLK#.S	16.71	11.82	1.41	0.71
Q9D1H7_G	Get4	Golgi to ER	K.AEVDVADELLENLAK#.V	35.57	7.91	4.50	0.22
Q9D1H7_G	Get4	Golgi to ER	R.IGQLFFGVPPK#.Q	11.43	4.45	2.57	0.39
Q9D1H7_G	Get4	Golgi to ER	K.AEVDVADELLENLAK#.V	4.80	1.42	3.37	0.30
Q9D1H7_G	Get4	Golgi to ER	K.AEVDVADELLENLAK#.V	14.37	3.96	3.63	0.28
P47856_G	Gfpt1	Glutamine-	K.EIFEQPESVVNTM*R.G	1.92	6.10	0.31	3.19
P47856_G	Gfpt1	Glutamine-	K.EVLSM*DDEIQK#.L	6.87	6.07	1.13	0.88
P47856_G	Gfpt1	Glutamine-	R.GALTVGITNTVGSSISR.E	2.08	9.16	0.23	4.41
P47856_G	Gfpt1	Glutamine-	K.GYDFESETDTETIAK#.L	11.54	8.48	1.36	0.74
P47856_G	Gfpt1	Glutamine-	R.VIQQLEGAFALVFK#.S	12.75	28.60	0.45	2.24
P47856_G	Gfpt1	Glutamine-	R.AVQTLQMELQQIM*K#.G	4.19	3.61	1.16	0.86

P47856_G	Gfpt1	Glutamine-	K.EIFEQPESVVNTM*R.G	6.43	18.18	0.35	2.83
P47856_G	Gfpt1	Glutamine-	R.EILETLIK#.G	46.84	27.40	1.71	0.58
P47856_G	Gfpt1	Glutamine-	K.EVLSM*DDEIQK#.L	39.55	23.43	1.69	0.59
P47856_G	Gfpt1	Glutamine-	R.GALTVGITNTVGSSISR.E	9.34	19.99	0.47	2.14
P47856_G	Gfpt1	Glutamine-	K.GNFSSFM*QK#.E	21.97	10.97	2.00	0.50
P47856_G	Gfpt1	Glutamine-	R.GSPLLIGVR.S	8.07	20.04	0.40	2.48
P47856_G	Gfpt1	Glutamine-	K.GYDFESETDTETIAK#.L	51.15	29.92	1.71	0.58
P47856_G	Gfpt1	Glutamine-	K.LSTDHIPILYR.T	8.95	35.99	0.25	4.02
P47856_G	Gfpt1	Glutamine-	R.VIFLEDDDVAAVVDGR.L	14.54	36.75	0.40	2.53
P47856_G	Gfpt1	Glutamine-	R.VIQQLEGAFALVFK#.S	41.68	26.89	1.55	0.65
P47856_G	Gfpt1	Glutamine-	R.VNFDDYTVNLGGLK.D	8.16	6.56	1.24	0.80
P47856_G	Gfpt1	Glutamine-	K.EIFEQPESVVNTM*R.G	8.96	25.12	0.36	2.80
P47856_G	Gfpt1	Glutamine-	K.EIFEQPESVVNTMR.G	2.17	6.97	0.31	3.22
P47856_G	Gfpt1	Glutamine-	R.EILETLIK#.G	31.23	18.47	1.69	0.59
P47856_G	Gfpt1	Glutamine-	K.EIM*LGLK#.R	18.15	11.78	1.54	0.65
P47856_G	Gfpt1	Glutamine-	K.EVLSM*DDEIQK#.L	32.85	18.78	1.75	0.57
P47856_G	Gfpt1	Glutamine-	R.GALTVGITNTVGSSISR.E	4.06	13.15	0.31	3.24
P47856_G	Gfpt1	Glutamine-	K.GNFSSFM*QK#.E	16.85	13.08	1.29	0.78
P47856_G	Gfpt1	Glutamine-	R.GSPLLIGVR.S	8.24	18.78	0.44	2.28
P47856_G	Gfpt1	Glutamine-	K.GYDFESETDTETIAK#.L	42.55	26.42	1.61	0.62
P47856_G	Gfpt1	Glutamine-	K.HGPLALVDK#.L	29.98	17.37	1.73	0.58
P47856_G	Gfpt1	Glutamine-	K.LSTDHIPILYR.T	9.59	22.55	0.43	2.35
P47856_G	Gfpt1	Glutamine-	R.VIFLEDDDVAAVVDGR.L	3.91	15.77	0.25	4.04
Q9CPY6_G	Gid4	Glucose-in	K.FLAFYQYAK#.S	10.90	6.62	1.65	0.61
Q9D7M1_	Gid8	Glucose-in	R.LIMNYLVTEGFK#.E	18.04	10.62	1.70	0.59
Q9D7M1_	Gid8	Glucose-in	K.LLLWAQNELDQK#.K	11.29	6.42	1.76	0.57
Q9D7M1_	Gid8	Glucose-in	R.LIM*NYLVTEGFK#.E	8.08	3.75	2.16	0.46
Q6Y7W8_P	Gigyf2	PERQ amin	R.ALSSGGSITSPPLSPALPK#.Y	4.22	4.16	1.01	0.99
Q6Y7W8_P	Gigyf2	PERQ amin	K.ALQQQQQQQQQK#.L	3.24	1.65	1.97	0.51
Q6Y7W8_P	Gigyf2	PERQ amin	R.ALSSGGSITSPPLSPALPK#.Y	6.11	4.13	1.48	0.68
Q6Y7W8_P	Gigyf2	PERQ amin	R.M*SDQNIIPSVTR.S	15.31	8.35	1.83	0.54
Q6Y7W8_P	Gigyf2	PERQ amin	R.VPFSPGPAPPPHM*GELDQER.L	3.76	14.62	0.26	3.89
Q9CZ15_P	Gins1	DNA replica	K.ALYEQNQSDVNEAK#.S	3.19	1.41	2.27	0.44
Q9Z0G0_G	Gipc1	PDZ domai	R.GPATVEDLPSAFEEK#.A	12.43	4.87	2.55	0.39
Q9Z0G0_G	Gipc1	PDZ domai	R.NPDELAEALDER.L	6.56	12.50	0.53	1.90
Q68FF6_G	Git1	ARF GTPase	K.SLSSPTDNLELSAR.S	3.60	9.25	0.39	2.57
Q80XR8_Q	Git2	ARF GTPase	R.ADSSLDLSELAK#.A	9.05	7.61	1.19	0.84
Q80XR8_Q	Git2	ARF GTPase	R.LIEIQYELTDR.L	4.19	6.94	0.60	1.66
Q9JMB0_G	Gkap1	G kinase-an	K.EQQQSEANELR.N	2.52	4.96	0.51	1.97
Q9JMB0_G	Gkap1	G kinase-an	K.KEQQQSEANELR.N	1.67	142.08	0.01	85.17
Q61602_G	Gli3	Transcripti	K.ISEEPSTSSDER.A	1.41	6.84	0.21	4.86
Q9CYL5_G	Glipr2	Golgi-assoc	K.ASASDGSSFVVAR.Y	15.27	75.12	0.20	4.92
Q9CYL5_G	Glipr2	Golgi-assoc	R.EAQQYSEALASTR.I	16.91	76.81	0.22	4.54
Q9CYL5_G	Glipr2	Golgi-assoc	K.QFNNEVLK#.A	25.68	25.21	1.02	0.98
Q9CYL5_G	Glipr2	Golgi-assoc	K.SYNFQQPGFTSGTGHFTAMVWK.N	12.51	9.17	1.36	0.73
Q9CYL5_G	Glipr2	Golgi-assoc	R.YFPAGNIVNQGFFEENVPPPK.K	5.49	6.40	0.86	1.17
Q9CYL5_G	Glipr2	Golgi-assoc	R.YFPAGNIVNQGFFEENVPPPKK.-	38.82	45.86	0.85	1.18
Q9CQM9_	Glrx3	Glutaredox	R.GDLVGGLDIVK#.E	51.50	17.09	3.01	0.33
Q9CQM9_	Glrx3	Glutaredox	K.HNIQFSSFDIFSDEEVR.Q	7.77	8.92	0.87	1.15
Q9CQM9_	Glrx3	Glutaredox	K.LEAEAVPEVSEK#.Y	35.32	9.70	3.64	0.27
Q9CQM9_	Glrx3	Glutaredox	K.LEAEAVPEVSEK#YEISSVPTFLFFK#.N	23.08	8.73	2.65	0.38
Q9CQM9_	Glrx3	Glutaredox	K.TFSNWPTYPQLYVR.G	5.42	9.54	0.57	1.76
Q9CQM9_	Glrx3	Glutaredox	K.YEISSVPTFLFFK#.N	31.34	7.76	4.04	0.25
D3Z7P3_G	Gls	Glutaminas	K.DSPGETDAFGNSEGK#.E	12.47	4.71	2.65	0.38
D3Z7P3_G	Gls	Glutaminas	K.VADYIPQLAK#.F	26.71	12.42	2.15	0.47
Q922P9_G	Glyr1	Putative ox	K.ALDQSDNDM*SAVYR.A	14.12	36.01	0.39	2.55
Q922P9_G	Glyr1	Putative ox	K.ALDQSDNDMSAVYR.A	5.80	12.99	0.45	2.24
Q922P9_G	Glyr1	Putative ox	R.FLEAPVSGNQQLSNDGMLVILAAGDR.G	2.95	9.53	0.31	3.23
Q922P9_G	Glyr1	Putative ox	R.FQQAVDAVEEFLR.R	10.09	28.55	0.35	2.83
Q922P9_G	Glyr1	Putative ox	R.LAIALGDAVNHPTPM*AAAANEVYK#.R	17.55	10.77	1.63	0.61
Q922P9_G	Glyr1	Putative ox	R.LAIALGDAVNHPTPMAAAANEVYK#.R	20.11	10.52	1.91	0.52
Q922P9_G	Glyr1	Putative ox	R.LGDLVWGK#.L	30.46	17.10	1.78	0.56
Q922P9_G	Glyr1	Putative ox	K.TSFFLGEVGNAAK#.M	65.64	78.45	0.84	1.20
Q922P9_G	Glyr1	Putative ox	K.TSFFLGEVGNAAK#.M	15.91	5.18	3.07	0.33
A6PWE0_A	Gm15698	Protein Gm	-.MDVFLMIR@YK#.K	28.74	4.91	5.85	0.17
A2A9Z5_A2	Gm53	Protein Gm	R.QTPSLSPSFHAR.D	1.72	11.34	0.15	6.61
E9Q070_E9	Gm8730	Uncharacte	R.VLALSVETEYTFPLAEK#.V	294.61	164.55	1.79	0.56
E9Q070_E9	Gm8730	Uncharacte	R.VLALSVETEYTFPLAEK#.V	224.00	82.92	2.70	0.37
E9Q070_E9	Gm8730	Uncharacte	R.VLALSVETEYTFPLAEK#.V	84.32	29.38	2.87	0.35
E9Q070_E9	Gm8730	Uncharacte	R.VLALSVETEYTFPLAEK#.V	52.73	18.41	2.87	0.35
Q922H4_G	Gmppa	Mannose-1	K.AVILIGGPQK#.G	3.99	1.32	3.03	0.33
Q3THK7_G	Gmps	GMP synth	R.GLQK#EEIVLLTHGDSVDK#VADGFK#.V	16.07	5.59	2.88	0.35
Q3THK7_G	Gmps	GMP synth	K.IANEVIGEM*SLKPEEVFLAQGTLRPDLIESASLVASGK.A	5.40	2.69	2.01	0.50
Q3THK7_G	Gmps	GMP synth	R.IM*YDLTSK#PPGTTEWE.-	8.01	2.66	3.01	0.33
Q3THK7_G	Gmps	GMP synth	K.IVADFSASVK#.K	28.79	7.73	3.72	0.27
Q3THK7_G	Gmps	GMP synth	K.LM*QITSLHSLNAFLLPIK#.T	12.21	3.41	3.58	0.28
Q3THK7_G	Gmps	GMP synth	R.SGNIVAGIANESK#K#.L	4.99	1.39	3.59	0.28
Q3THK7_G	Gmps	GMP synth	K.TLNM*TTSPEEK#.R	14.79	5.53	2.67	0.37
Q3THK7_G	Gmps	GMP synth	R.VVYIFGPPVK#.E	16.94	41.48	0.41	2.45
P27600_G	Gna12	Guanine nu	R.DIDALLARER@R@.A	101.01	300.91	0.34	2.98
P08752_G	Gnai2	Guanine nu	R.IAQSDYIPTQQDVLR.T	1.91	10.50	0.18	5.50
P08752_G	Gnai2	Guanine nu	R.IAQSDYIPTQQDVLR.T	2.42	11.71	0.21	4.84
P08752_G	Gnai2	Guanine nu	K.TTGIVETHFTFK.D	4.05	12.24	0.33	3.02
P08752_G	Gnai2	Guanine nu	R.AVVYSNTIQSIMAIVK#.A	7.37	7.26	1.02	0.98
P08752_G	Gnai2	Guanine nu	R.EYQLNDSAAYYLNDLER.I	1.58	5.40	0.29	3.43
P08752_G	Gnai2	Guanine nu	R.IAQSDYIPTQQDVLR.T	4.18	27.99	0.15	6.69
P08752_G	Gnai2	Guanine nu	K.YDEAASYIQSK.F	9.19	12.49	0.74	1.36
Q9DC51_G	Gnai3	Guanine nu	R.ISQTNYIPTQQDVLR.T	2.42	9.85	0.25	4.06
P62874_G	Gnb1	Guanine nu	K.IYAM*HWGTDSR.L	1.52	5.96	0.25	3.93
P62874_G	Gnb1	Guanine nu	K.LIIWDSYTTNK.V	71.59	47.58	1.50	0.66
P62874_G	Gnb1	Guanine nu	R.LLVSASQDGK#.L	98.19	75.86	1.29	0.77
P62874_G	Gnb1	Guanine nu	K.LIIWDSYTTNK#.V	17.08	16.59	1.03	0.97
P62874_G	Gnb1	Guanine nu	R.AGVLAGHDNR.V	3.45	8.95	0.38	2.60
P62874_G	Gnb1	Guanine nu	K.LIIWDSYTTNK#.V	29.81	31.51	0.95	1.06
P62874_G	Gnb1	Guanine nu	R.LLVSASQDGK#.L	72.42	64.67	1.12	0.89
P68040_G	Gnb2l1	Guanine nu	R.DETNYGIPQR.A	213.76	469.00	0.46	2.19
P68040_G	Gnb2l1	Guanine nu	K.DGQAM*LWDLNEGK#.H	163.08	69.29	2.35	0.42
P68040_G	Gnb2l1	Guanine nu	K.DGQAMLWDLNEGK#.H	136.86	63.03	2.17	0.46
P68040_G	Gnb2l1	Guanine nu	R.DK#TIIM*WK#.L	85.20	42.04	2.03	0.49
P68040_G	Gnb2l1	Guanine nu	R.DK#TIIMWK#.L	190.73	66.65	2.86	0.35
P68040_G	Gnb2l1	Guanine nu	K.DVLSVAFSSDNR.Q	121.42	235.23	0.52	1.94
P68040_G	Gnb2l1	Guanine nu	K.GHNGWVTQIATTPQFPDM*ILSASR.D	10.26	15.14	0.68	1.48
P68040_G	Gnb2l1	Guanine nu	K.GHNGWVTQIATTPQFPDMILSASR.D	7.82	14.53	0.54	1.86

P68040_GI	Gnb2l1	Guanine nu	K.IIVDELK#.Q	230.16	97.27	2.37	0.42
P68040_GI	Gnb2l1	Guanine nu	K.IIVDELK#QEVISTSSK#.A	802.07	336.22	2.39	0.42
P68040_GI	Gnb2l1	Guanine nu	K.IIVDELK#QEVISTSSK#.A	4.54	3.10	1.47	0.68
P68040_GI	Gnb2l1	Guanine nu	K.IWDLEGK#.I	553.28	232.03	2.38	0.42
P68040_GI	Gnb2l1	Guanine nu	K.LTRDETNYGIPQR.A	14.45	115.62	0.12	8.00
P68040_GI	Gnb2l1	Guanine nu	R.LWDLTTGTTTR.R	149.15	298.68	0.50	2.00
P68040_GI	Gnb2l1	Guanine nu	K.QEVISTSSK#.A	136.32	31.26	4.36	0.23
P68040_GI	Gnb2l1	Guanine nu	K.TIIMWK#.L	56.49	26.32	2.15	0.47
P68040_GI	Gnb2l1	Guanine nu	R.VWQVTIGTR.-	106.62	192.04	0.56	1.80
P68040_GI	Gnb2l1	Guanine nu	R.DETNYGIPQR.A	24.51	51.33	0.48	2.09
P68040_GI	Gnb2l1	Guanine nu	K.DGQAM*LWDLNEGK#.H	23.60	12.37	1.91	0.52
P68040_GI	Gnb2l1	Guanine nu	K.DGQAMLWDLNEGK#.H	11.50	5.09	2.26	0.44
P68040_GI	Gnb2l1	Guanine nu	R.DK#TIIMWK#.L	23.15	10.22	2.27	0.44
P68040_GI	Gnb2l1	Guanine nu	K.DVLSVAFSSDNR.Q	51.08	104.06	0.49	2.04
P68040_GI	Gnb2l1	Guanine nu	K.IIVDELK#QEVISTSSK#.A	298.26	120.17	2.48	0.40
P68040_GI	Gnb2l1	Guanine nu	K.IWDLEGK#.I	98.02	42.96	2.28	0.44
P68040_GI	Gnb2l1	Guanine nu	R.LWDLTTGTTTR.R	23.54	45.19	0.52	1.92
P68040_GI	Gnb2l1	Guanine nu	R.VWQVTIGTR.-	15.70	28.29	0.55	1.80
P68040_GI	Gnb2l1	Guanine nu	R.DETNYGIPQR.A	29.37	56.05	0.52	1.91
P68040_GI	Gnb2l1	Guanine nu	K.DGQAM*LWDLNEGK#.H	21.88	8.85	2.47	0.40
P68040_GI	Gnb2l1	Guanine nu	K.DGQAMLWDLNEGK#.H	16.97	8.21	2.07	0.48
P68040_GI	Gnb2l1	Guanine nu	R.DK#TIIM*WK#.L	23.71	7.17	3.31	0.30
P68040_GI	Gnb2l1	Guanine nu	R.DK#TIIMWK#.L	36.43	15.15	2.40	0.42
P68040_GI	Gnb2l1	Guanine nu	K.DVLSVAFSSDNR.Q	33.89	55.87	0.61	1.65
P68040_GI	Gnb2l1	Guanine nu	K.IIVDELK#QEVISTSSK#.A	280.87	102.79	2.73	0.37
P68040_GI	Gnb2l1	Guanine nu	K.IWDLEGK#.I	123.86	45.89	2.70	0.37
P68040_GI	Gnb2l1	Guanine nu	K.LTRDETNYGIPQR.A	2.12	25.30	0.08	11.91
P68040_GI	Gnb2l1	Guanine nu	R.LWDLTTGTTTR.R	35.90	60.62	0.59	1.69
P68040_GI	Gnb2l1	Guanine nu	R.VWQVTIGTR.-	57.39	56.70	1.01	0.99
P68040_GI	Gnb2l1	Guanine nu	R.DETNYGIPQR.A	50.73	99.74	0.51	1.97
P68040_GI	Gnb2l1	Guanine nu	K.DGQAM*LWDLNEGK#.H	52.37	21.50	2.44	0.41
P68040_GI	Gnb2l1	Guanine nu	K.DGQAMLWDLNEGK#.H	26.22	10.15	2.58	0.39
P68040_GI	Gnb2l1	Guanine nu	R.DK#TIIM*WK#.L	32.03	12.18	2.63	0.38
P68040_GI	Gnb2l1	Guanine nu	R.DK#TIIMWK#.L	24.29	14.21	1.71	0.58
P68040_GI	Gnb2l1	Guanine nu	K.GHNGWVTQIATTPQFPDM*ILSASR.D	5.79	8.94	0.65	1.54
P68040_GI	Gnb2l1	Guanine nu	K.GHNGWVTQIATTPQFPDMILSASR.D	5.22	9.06	0.58	1.73
P68040_GI	Gnb2l1	Guanine nu	K.IIVDELK#QEVISTSSK#.A	379.68	171.54	2.21	0.45
P68040_GI	Gnb2l1	Guanine nu	K.IWDLEGK#.I	207.92	79.48	2.62	0.38
P68040_GI	Gnb2l1	Guanine nu	K.LTRDETNYGIPQR.A	4.67	59.23	0.08	12.68
P68040_GI	Gnb2l1	Guanine nu	R.LWDLTTGTTTR.R	60.82	110.44	0.55	1.82
P68040_GI	Gnb2l1	Guanine nu	K.TIIM*WK#.L	15.65	7.51	2.08	0.48
P68040_GI	Gnb2l1	Guanine nu	R.VWQVTIGTR.-	31.11	55.76	0.56	1.79
Q91WG8_	Gne	Bifunctiona	R.TLVLFPNIDAGSK#.E	8.85	5.28	1.68	0.60
Q9DAS9_GI	Gng12	Guanine nu	K.TASTNSIAQAR.R	8.20	34.60	0.24	4.22
P36916_GI	Gnl1	Guanine nu	R.ACEAITVGK#.V	32.62	11.87	2.75	0.36
P36916_GI	Gnl1	Guanine nu	R.EQVLQPVSAEVLELDIR.E	7.61	12.42	0.61	1.63
P36916_GI	Gnl1	Guanine nu	R.EVYQPGSVLDFPR.R	10.66	12.00	0.89	1.13
P36916_GI	Gnl1	Guanine nu	R.LNQQPSQGLGPR.G	4.87	13.53	0.36	2.78
P36916_GI	Gnl1	Guanine nu	R.SFQEYLGK#.I	29.71	15.90	1.87	0.54
P36916_GI	Gnl1	Guanine nu	R.TPQEPGGVLK#.K	13.14	6.47	2.03	0.49
P36916_GI	Gnl1	Guanine nu	K.VDLSSWR.E	6.90	12.66	0.55	1.83
P36916_GI	Gnl1	Guanine nu	R.YFQTYFLTPSVK#.L	21.69	9.43	2.30	0.43
P36916_GI	Gnl1	Guanine nu	R.EQVLQPVSAEVLELDIR.E	9.27	4.87	1.90	0.52
P36916_GI	Gnl1	Guanine nu	R.EVYQPGSVLDFPR.R	6.24	8.01	0.78	1.28
P36916_GI	Gnl1	Guanine nu	R.GTWESHPETAELVLSQGR.V	9.61	10.94	0.88	1.14
P36916_GI	Gnl1	Guanine nu	R.TPQEPGGVLK#K#.N	9.95	3.00	3.31	0.30
P36916_GI	Gnl1	Guanine nu	R.YFQTYFLTPSVK#.L	22.42	13.04	1.72	0.58
Q8CI11_GN	Gnl3	Guanine nu	R.ASQEDETYDFTTDYI.-	8.55	8.55	1.00	1.00
Q8CI11_GN	Gnl3	Guanine nu	K.DIQVGVIGFPNVGK#.S	14.82	7.82	1.89	0.53
Q8CI11_GN	Gnl3	Guanine nu	K.ENLENWLNYLNK#.E	10.60	8.24	1.29	0.78
Q8CI11_GN	Gnl3	Guanine nu	R.K#DPGVPNSAPFK#.E	5.21	4.74	1.10	0.91
Q8CI11_GN	Gnl3	Guanine nu	K.LILVLNK#.S	10.16	5.50	1.85	0.54
Q8CI11_GN	Gnl3	Guanine nu	R.NAEISDVAPVEETR.E	5.60	11.59	0.48	2.07
Q8CI11_GN	Gnl3	Guanine nu	R.SPASIEELRPLEAASAILSQADNEQVVLK.Y	4.31	10.05	0.43	2.33
Q8CI11_GN	Gnl3	Guanine nu	K.DIQVGVIGFPNVGK#.S	10.75	8.19	1.31	0.76
Q8CI11_GN	Gnl3	Guanine nu	K.ELPTVVFK#.A	17.47	11.43	1.53	0.65
Q8CI11_GN	Gnl3	Guanine nu	K.GGSPNVESAAK#.L	22.62	18.53	1.22	0.82
Q8CI11_GN	Gnl3	Guanine nu	R.NAEISDVAPVEETR.E	2.81	9.06	0.31	3.23
Q921M4_G	Golga2	Golgin subf	K.SQEAQGLQEQR.D	1.32	9.27	0.14	7.03
P55937_G	Golga3	Golgin subf	K.ELEGTQQTLQTIK#.S	14.18	5.74	2.47	0.40
P55937_G	Golga3	Golgin subf	R.LGSDLTSAQK#.E	18.21	7.38	2.47	0.41
P55937_G	Golga3	Golgin subf	K.QDSLSSEVDTLK#.Q	8.18	5.76	1.42	0.70
P55937_G	Golga3	Golgin subf	K.QLTSTQEALQAK#.G	12.39	3.86	3.21	0.31
P55937_G	Golga3	Golgin subf	R.ALEVELQNVGQSK#.I	7.17	4.65	1.54	0.65
P55937_G	Golga3	Golgin subf	K.QDSLSSEVDTLK#.Q	9.27	36.75	0.25	3.96
P55937_G	Golga3	Golgin subf	K.TLLQQNQQLK#.L	10.90	4.99	2.18	0.46
P55937_G	Golga3	Golgin subf	K.VLELEDELQESR.G	3.86	7.12	0.54	1.85
Q8R088_GI	Golph3l	Golgi phos	K.SDSPTGDVLLDETLK#.H	8.04	6.84	1.18	0.85
Q9CR60_G	Golt1b	Vesicle tran	R.SFVDK#VGESNNM*V.-	4.80	5.31	0.91	1.10
Q99JX3_G	Gorasp2	Golgi reass	K.ADASSLTVDVTSPASK#.V	17.06	7.37	2.31	0.43
Q99JX3_G	Gorasp2	Golgi reass	K.ISLPGQM*TGTPITPLK#.D	13.01	7.58	1.72	0.58
Q3UFS4_GI	Gpatch11	G patch do	K.SGDGIVEPIPLNVK#.T	12.69	7.37	1.72	0.58
Q3TFK5_GF	Gpatch4	G patch do	K.ALGTSQPLTDSEPSQK.K	8.81	10.16	0.87	1.15
Q3TFK5_GF	Gpatch4	G patch do	K.TAASLVVDSGK#.D	14.96	9.06	1.65	0.61
A2A6A1_GI	Gpatch8	G patch do	K.DISQATPATK.A	9.73	17.88	0.54	1.84
A2A6A1_GI	Gpatch8	G patch do	K.GAGLPSQNSNTGTGR.G	2.85	15.57	0.18	5.46
A2A6A1_GI	Gpatch8	G patch do	R.TVSEASELQK.E	17.05	23.45	0.73	1.38
P51655_GI	Gpc4	Glypican-4	R.LEGPFNIESVM*DPIDVK.I	7.35	9.98	0.74	1.36
P51655_GI	Gpc4	Glypican-4	R.LEGPFNIESVMDPIDVK.I	4.95	5.06	0.98	1.02
P51655_GI	Gpc4	Glypican-4	R.TFAQGLAVAR.D	4.34	21.29	0.20	4.91
P51655_GI	Gpc4	Glypican-4	R.LEGPFNIESVM*DPIDVK.I	4.49	5.54	0.81	1.24
P06745_G	Gpi	Glucose-6-	K.EVMQMLVELAK#.S	14.06	1.67	8.42	0.12
P06745_G	Gpi	Glucose-6-	K.ILLANFLAQTEALM*K#.G	38.54	3.61	10.68	0.09
P06745_G	Gpi	Glucose-6-	R.SNTPIK#VDGK#.D	14.97	5.57	2.69	0.37
P06745_G	Gpi	Glucose-6-	K.TFTTQETITNAETAK#.E	14.93	2.87	5.20	0.19
P06745_G	Gpi	Glucose-6-	K.TLASLSPETSLFIIASK#.T	30.30	4.32	7.01	0.14
P06745_G	Gpi	Glucose-6-	K.ILLANFLAQTEALM*K#.G	16.17	3.30	4.91	0.20
P06745_G	Gpi	Glucose-6-	K.TLASLSPETSLFIIASK#.T	17.08	2.55	6.70	0.15
P06745_G	Gpi	Glucose-6-	R.VWFVSNIDGTHIAK#.T	15.84	2.70	5.87	0.17
P06745_G	Gpi	Glucose-6-	K.ILLANFLAQTEALM*K#.G	10.03	2.48	4.05	0.25
P06745_G	Gpi	Glucose-6-	K.TLASLSPETSLFIIASK#.T	17.79	4.01	4.44	0.23
Q8VHN7_G	Gpr98	G-protein c	R.RSGGHFGR.L	8.95	29.27	0.31	3.27
Q99LD4_C	Gps1	COP9 signa	K.AESTPEIAEQR.G	14.33	11.08	1.29	0.77

Q99LD4_C	Gps1	COP9 signa	R.DSQTQAILTK#.L	41.27	8.25	5.00	0.20
Q99LD4_C	Gps1	COP9 signa	R.DSQTQAILTK#.L	32.13	5.70	5.64	0.18
Q99LD4_C	Gps1	COP9 signa	R.ALIQYFSPYVSADM*HK#.M	60.97	6.40	9.52	0.11
Q99LD4_C	Gps1	COP9 signa	R.DSQTQAILTK#.L	70.13	10.84	6.47	0.15
Q99LD4_C	Gps1	COP9 signa	R.EGSQGELTPANSQSR.M	11.80	15.40	0.77	1.31
Q99LD4_C	Gps1	COP9 signa	K.LFLELEPQVR.D	26.24	13.02	2.01	0.50
Q99LD4_C	Gps1	COP9 signa	R.NVISSSSFK#.L	62.81	8.58	7.32	0.14
P11352_G	Gpx1	Glutathion	R.DYTEM*NDLQK#.R	7.66	2.48	3.09	0.32
P11352_G	Gpx1	Glutathion	K.FLVGPDGVPVR.R	2.31	5.78	0.40	2.50
P11352_G	Gpx1	Glutathion	R.NALPTPSDDPTALM*TDPK#.Y	8.60	4.24	2.03	0.49
P11352_G	Gpx1	Glutathion	R.NDIAWNFEK#.F	9.25	2.52	3.68	0.27
P11352_G	Gpx1	Glutathion	R.TIDIEPDIETLLSQQSGNS.-	9.35	9.35	1.00	1.00
P11352_G	Gpx1	Glutathion	K.YVRPGGGFEPNFTLFEK.C	6.84	7.61	0.90	1.11
O35127_C	Grcc10	Protein C1	K.M*LQFVLPVATQIQQEVIK#.A	2.55	2.94	0.87	1.15
Q99LP6_G	Grpel1	GrpE protei	K.DLLEVADILEK#.A	13.07	3.66	3.57	0.28
Q99LP6_G	Grpel1	GrpE protei	K.SLYEGLVMTEVQIQK#.V	6.16	1.49	4.13	0.24
Q8C5Q4_G	Grsf1	G-rich sequ	K.LGDEVDDVYLIR.A	7.06	7.12	0.99	1.01
Q810D6_G	Grwd1	Glutamate-	R.DPESGETETDPGLAALPQQLLFVHQGETDLK#.E	4.55	1.75	2.60	0.38
Q810D6_G	Grwd1	Glutamate-	R.EPFLLSGGDDGALK#.V	9.25	7.91	1.17	0.86
Q810D6_G	Grwd1	Glutamate-	R.LLQVVDDPQALAIFLRDEQAR.I	3.71	13.53	0.27	3.65
Q810D6_G	Grwd1	Glutamate-	R.REPFLLSGGDDGALK.V	1.82	8.47	0.21	4.67
Q810D6_G	Grwd1	Glutamate-	K.SGSPVATFK#.Q	31.89	17.24	1.85	0.54
Q810D6_G	Grwd1	Glutamate-	R.VSWLGEEPVAGVWSEK#.G	23.19	23.26	1.00	1.00
Q2NL51_G	Gsk3a	Glycogen s	R.DIK#PQNLLVDPDTAVLK#.L	15.73	4.07	3.86	0.26
Q9WV60_G	Gsk3b	Glycogen s	R.DIK#PQNLLLDPDTAVLK#.L	29.44	11.23	2.62	0.38
Q9WV60_G	Gsk3b	Glycogen s	K.VTTVVATPGQGPDRPQEVSYTDTK.V	9.22	18.01	0.51	1.95
P13020_G	Gsn	Gelsolin OS	K.SGALNSNDAFVLK#.T	5.99	3.69	1.63	0.62
P13020_G	Gsn	Gelsolin OS	K.AGKEPGLQIWR.V	33.85	71.76	0.47	2.12
P13020_G	Gsn	Gelsolin OS	R.AQVHVSEEGGEPEAM*LQVLGPK#PALPEGTEDTAK#.E	3.60	6.08	0.59	1.69
P13020_G	Gsn	Gelsolin OS	R.AVEVMPK#.S	59.24	29.88	1.98	0.50
P13020_G	Gsn	Gelsolin OS	R.DGGQTAPASIR.L	55.76	126.70	0.44	2.27
P13020_G	Gsn	Gelsolin OS	K.DSQEEEK#TEALTSAK#.R	245.68	127.55	1.93	0.52
P13020_G	Gsn	Gelsolin OS	R.EVQGFESSTFSGYFK#.S	117.65	59.14	1.99	0.50
P13020_G	Gsn	Gelsolin OS	K.GGVASGFK#.H	76.38	37.21	2.05	0.49
P13020_G	Gsn	Gelsolin OS	K.HVVPNEVVVQR.L	32.59	70.53	0.46	2.16
P13020_G	Gsn	Gelsolin OS	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	10.07	14.03	0.72	1.39
P13020_G	Gsn	Gelsolin OS	K.K#GGVASGFK#.H	83.85	38.81	2.16	0.46
P13020_G	Gsn	Gelsolin OS	K.NWRDPDQTDGPGLGYLSSHIANVER.V	12.11	43.25	0.28	3.57
P13020_G	Gsn	Gelsolin OS	R.QTQVSVLPEGGETPLFK#.Q	107.08	47.40	2.26	0.44
P13020_G	Gsn	Gelsolin OS	R.RTPITVVR.Q	8.54	45.47	0.19	5.32
P13020_G	Gsn	Gelsolin OS	K.SGALNSNDAFVLK#.T	178.22	77.67	2.29	0.44
P13020_G	Gsn	Gelsolin OS	R.SQHVQVEEGSEPDAFWEALGGK#.T	138.12	61.49	2.25	0.45
P13020_G	Gsn	Gelsolin OS	K.TASDFISK#.M	233.36	102.66	2.27	0.44
P13020_G	Gsn	Gelsolin OS	K.TGAQELLK#.V	184.04	94.02	1.96	0.51
P13020_G	Gsn	Gelsolin OS	K.TPSAAYLWVGAGASEAEK#.T	92.80	46.38	2.00	0.50
P13020_G	Gsn	Gelsolin OS	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK#.Q	14.44	3.41	4.24	0.24
P13020_G	Gsn	Gelsolin OS	K.VPVDPATYGQFYGGDSYIILYNYR.H	13.60	18.06	0.75	1.33
P13020_G	Gsn	Gelsolin OS	K.VSNGAGSMSVSLVADENPFAQGALR.S	4.03	7.41	0.54	1.84
P13020_G	Gsn	Gelsolin OS	R.YIETDPANR.D	25.93	44.23	0.59	1.71
Q8R050_E	Gspt1	Eukaryotic	R.AYFETEK#.K	15.92	13.10	1.21	0.82
Q8R050_E	Gspt1	Eukaryotic	K.GQQLVM*M*PNK#.H	35.74	6.36	5.62	0.18
Q8R050_E	Gspt1	Eukaryotic	K.GQQLVMM*PNK#.H	15.42	3.35	4.61	0.22
Q8R050_E	Gspt1	Eukaryotic	K.GQQLVMMPNK#.H	9.57	2.29	4.18	0.24
Q8R050_E	Gspt1	Eukaryotic	K.HFTILDAPGHK#.S	55.72	9.91	5.62	0.18
Q8R050_E	Gspt1	Eukaryotic	K.HLIVLINK#.M	91.64	14.93	6.14	0.16
Q8R050_E	Gspt1	Eukaryotic	K.K#EHVNVVFIGHVDAGK#.S	11.15	1.66	6.70	0.15
Q8R050_E	Gspt1	Eukaryotic	R.K#GEFETGFEK#.G	75.38	18.63	4.05	0.25
Q8R050_E	Gspt1	Eukaryotic	K.SAVAPPGAPK#.K	98.84	23.95	4.13	0.24
Q8R050_E	Gspt1	Eukaryotic	K.SFVPNM*IGGASQADLAVLVISAR.K	9.65	10.17	0.95	1.05
Q8R050_E	Gspt1	Eukaryotic	K.DM*GTVVLGK#.L	14.16	1.61	8.79	0.11
Q8R050_E	Gspt1	Eukaryotic	K.HFTILDAPGHK#.S	16.91	69.31	0.24	4.10
Q8R050_E	Gspt1	Eukaryotic	K.HLIVLINK#.M	23.49	3.24	7.26	0.14
Q8R050_E	Gspt1	Eukaryotic	K.HNVEVLGILSDDVETDSVAPGENLK#.I	27.91	5.24	5.33	0.19
Q8R050_E	Gspt1	Eukaryotic	K.SAVAPPGAPK#.K	34.11	10.93	3.12	0.32
P19157_G	Gstp1	Glutathion	K.ALPGHLK#PFETLLSQNQGGK#.A	3.23	3.38	0.95	1.05
P19157_G	Gstp1	Glutathion	K.FEDGDLTLYQSNAILR.H	2.35	8.72	0.27	3.72
Q99L20_G	Gstt3	Glutathion	K.GQQYTDSFAQVNPLR.K	2.10	3.61	0.58	1.72
P62915_TF	Gtf2b	Transcripti	R.APDLFPSDFK.F	24.54	14.87	1.65	0.61
P62915_TF	Gtf2b	Transcripti	R.APDLFPSDFK#FDTPVDK#LPQL.-	7.60	4.77	1.59	0.63
P62915_TF	Gtf2b	Transcripti	K.EIGDIAGVADVTIR.Q	3.55	11.00	0.32	3.10
P62915_TF	Gtf2b	Transcripti	K.FDTPVDK#LPQL.-	20.68	17.07	1.21	0.83
P62915_TF	Gtf2b	Transcripti	R.KAVELDLVPGR.S	2.57	11.72	0.22	4.56
P62915_TF	Gtf2b	Transcripti	R.SPISVAAAAIYM*ASQASAEK#.R	4.58	2.42	1.89	0.53
P62915_TF	Gtf2b	Transcripti	R.SPISVAAAAIYMASQASAEK#.R	9.99	5.09	1.96	0.51
P62915_TF	Gtf2b	Transcripti	R.VGDSQNPLLSDGDLSTMIGK.G	5.44	5.96	0.91	1.10
P62915_TF	Gtf2b	Transcripti	R.VIDVGSEWR.T	3.59	9.37	0.38	2.61
Q9D0D5_T	Gtf2e1	General tra	R.AGPDDNEEVM*R.A	2.54	8.60	0.30	3.39
Q9D0D5_T	Gtf2e1	General tra	R.ESTVQGAYSSEEM*K#.E	4.66	2.28	2.04	0.49
Q9D0D5_T	Gtf2e1	General tra	R.FNEQIEPIYALLR.E	6.44	20.72	0.31	3.22
Q9D902_T	Gtf2e2	General tra	R.GLGGILLEDIEEGLPNSQK#.A	15.42	20.45	0.75	1.33
Q9D902_T	Gtf2e2	General tra	R.GLGGILLEDIEEGLPNSQK#.A	12.98	3.00	4.32	0.23
Q9D902_T	Gtf2e2	General tra	K.QWLM*TEALVNNPK#.I	5.11	5.91	0.87	1.16
Q9D902_T	Gtf2e2	General tra	R.SVTVDSM*DEEK#.I	6.93	4.21	1.65	0.61
Q9JIB4_TF	Gtf2h2	General tra	K.ATIEDILFK#.A	10.13	6.00	1.69	0.59
Q9ESZ8_GT	Gtf2i	General tra	K.AGISFIIK#.R	13.42	13.04	1.03	0.97
Q9ESZ8_GT	Gtf2i	General tra	R.DQSAVVVQGLPEGVAFK#.H	17.90	10.04	1.78	0.56
Q9ESZ8_GT	Gtf2i	General tra	K.FEAHPNDLYVEGLPENIPFR.S	4.55	7.26	0.63	1.60
Q9ESZ8_GT	Gtf2i	General tra	K.HPEHYDLATLK#.W	12.02	46.87	0.26	3.90
Q9ESZ8_GT	Gtf2i	General tra	K.RPELLTHSTTEVTQPR.T	1.28	6.36	0.20	4.99
Q9ESZ8_GT	Gtf2i	General tra	K.STVVPVPYEK#.M	27.31	16.66	1.64	0.61
Q9ESZ8_GT	Gtf2i	General tra	K.AGISFIIK#.R	47.39	17.13	2.77	0.36
Q9ESZ8_GT	Gtf2i	General tra	K.APSYLEISSM*R.R	9.54	12.34	0.77	1.29
Q9ESZ8_GT	Gtf2i	General tra	K.DFQK#DFVK#.Y	9.54	6.12	1.56	0.64
Q9ESZ8_GT	Gtf2i	General tra	R.DQSAVVVQGLPEGVAFK#.H	46.29	23.19	2.00	0.50
Q9ESZ8_GT	Gtf2i	General tra	R.EFSFEAWNAK#.I	17.77	7.45	2.39	0.42
Q9ESZ8_GT	Gtf2i	General tra	R.EQVNDLFSR.K	11.77	23.02	0.51	1.96
Q9ESZ8_GT	Gtf2i	General tra	K.FAQALGLTEAVK#.V	116.72	51.26	2.28	0.44
Q9ESZ8_GT	Gtf2i	General tra	K.FEAHPNDLYVEGLPENIPFR.S	17.99	47.88	0.38	2.66
Q9ESZ8_GT	Gtf2i	General tra	R.ILDSAEFIK#.F	63.09	31.98	1.97	0.51
Q9ESZ8_GT	Gtf2i	General tra	R.K#FGEAIGM*GFPVK#.V	11.11	5.48	2.03	0.49
Q9ESZ8_GT	Gtf2i	General tra	K.K#PEM*FETAIK#.E	16.21	63.94	0.25	3.94
Q9ESZ8_GT	Gtf2i	General tra	R.K#QVEEIFNLK#.F	19.07	7.45	2.56	0.39
Q9ESZ8_GT	Gtf2i	General tra	R.LK#STEPPPPPPVPEPANAGK#.R	8.66	7.51	1.15	0.87

Q9ESZ8_GT	Gtf2i	General tra	R.M*SVDAVEIETLR.K	2.91	7.24	0.40	2.49
Q9ESZ8_GT	Gtf2i	General tra	K.RPELLTHSTTEVTQPR.T	6.38	47.92	0.13	7.51
Q9ESZ8_GT	Gtf2i	General tra	R.RPSTYGIPR.L	3.30	26.46	0.12	8.01
Q9ESZ8_GT	Gtf2i	General tra	R.SPSWYGIPR.L	11.47	27.62	0.42	2.41
Q9ESZ8_GT	Gtf2i	General tra	R.SPTWFGIPR.L	17.37	37.28	0.47	2.15
Q9ESZ8_GT	Gtf2i	General tra	K.STEPPPPPPVPEPANAGK#.R	7.38	5.29	1.39	0.72
Q9ESZ8_GT	Gtf2i	General tra	K.STVVPVPYEK#.M	76.14	37.06	2.05	0.49
Q9ESZ8_GT	Gtf2i	General tra	R.TNTPVKEDWNVR.I	4.87	13.34	0.37	2.74
Q9ESZ8_GT	Gtf2i	General tra	R.VLAAEAER.S	22.85	49.97	0.46	2.19
Q9ESZ8_GT	Gtf2i	General tra	K.VPEIEVTVEGPNNSSPQTSAVR.T	3.84	10.39	0.37	2.70
Q9ESZ8_GT	Gtf2i	General tra	K.AGISFIIK#.R	13.42	7.45	1.80	0.55
Q9ESZ8_GT	Gtf2i	General tra	R.DQSAVVVQGLPEGVAFK#.H	16.87	12.98	1.30	0.77
Q9ESZ8_GT	Gtf2i	General tra	K.FAEALGSTEAK#.A	30.73	12.79	2.40	0.42
Q9ESZ8_GT	Gtf2i	General tra	K.FAQALGLTEAVK#.V	33.22	46.52	0.71	1.40
Q9ESZ8_GT	Gtf2i	General tra	K.RPELLTHSTTEVTQPR.T	1.36	15.98	0.08	11.77
Q9ESZ8_GT	Gtf2i	General tra	R.SPTWFGIPR.L	4.75	11.57	0.41	2.43
Q9JI57_GT	Gtf2ird1	General tra	R.LLREPGLLAVQGLPEGLAFR.R	4.30	4.92	0.87	1.14
Q9JI57_GT	Gtf2ird1	General tra	R.LLREPGLLAVQGLPEGLAFR.R	3.63	4.41	0.82	1.21
Q8K284_T	Gtf3c1	General tra	R.ALATHPGISFYEEPR.E	4.77	10.59	0.45	2.22
Q8K284_T	Gtf3c1	General tra	R.LIESLFTIQK#.M	20.81	15.53	1.34	0.75
Q8BL74_T	Gtf3c2	General tra	R.KPPSTPLVPGLLDQSNPLSTPM*PK.K	7.37	7.94	0.93	1.08
Q8BL74_T	Gtf3c2	General tra	R.LEQQDLSSEM*SK#.V	8.71	8.38	1.04	0.96
Q3TMP1_Q	Gtf3c3	General tra	R.DK#ISDNNEQETSNYDAK#.A	6.03	4.25	1.42	0.71
Q3TMP1_Q	Gtf3c3	General tra	K.ETLEEGTSEENK#.A	8.66	6.95	1.25	0.80
Q3TMP1_Q	Gtf3c3	General tra	R.LAEM*SLEQDNIK#.Q	11.69	5.94	1.97	0.51
Q3TMP1_Q	Gtf3c3	General tra	R.STLLFSQGK#.M	9.16	6.75	1.36	0.74
Q3TMP1_Q	Gtf3c3	General tra	K.SYYEANDSASAINIIEEAFSK#.H	9.66	9.93	0.97	1.03
Q8BMQ2_T	Gtf3c4	General tra	K.LQYAVSGLEPLSWSEDHR.V	3.78	7.82	0.48	2.07
Q8BMQ2_T	Gtf3c4	General tra	K.NYQVQFVTLK#.T	16.07	7.28	2.21	0.45
Q8BMQ2_T	Gtf3c4	General tra	K.SKEGDTEETPEDSLTAGGDTGGREPVEEK.L	8.79	10.17	0.86	1.16
Q8BMQ2_T	Gtf3c4	General tra	K.M*SGLIVGSAFGPVK#.I	7.29	3.95	1.85	0.54
Q8BMQ2_T	Gtf3c4	General tra	K.NYQVQFVTLK#.T	14.21	6.43	2.21	0.45
Q8R2T8_T	Gtf3c5	General tra	R.EGYHNPTISGENLIGLSR.A	3.70	10.47	0.35	2.83
Q8R2T8_T	Gtf3c5	General tra	R.STYNYSLPITVK#.K	9.58	9.49	1.01	0.99
O08582_G	Gtpbp1	GTP-bindin	K.LVLVSPTSEQYDSLLR.Q	7.46	15.13	0.49	2.03
O08582_G	Gtpbp1	GTP-bindin	R.VAVVGNVDAGK#.S	61.57	19.40	3.17	0.32
O08582_G	Gtpbp1	GTP-bindin	R.VGDNDFLEVR.V	6.55	11.65	0.56	1.78
O08582_G	Gtpbp1	GTP-bindin	K.LVLVSPTSEQYDSLLR.Q	9.00	14.37	0.63	1.60
O08582_G	Gtpbp1	GTP-bindin	R.TSYREEEPAEFQIDDTYSVPGVGTVVSGTTLR.G	1.95	2.95	0.66	1.51
O08582_G	Gtpbp1	GTP-bindin	R.VAVVGNVDAGK#.S	39.38	15.29	2.58	0.39
O08582_G	Gtpbp1	GTP-bindin	K.VITFIDLAGHEK#.Y	23.57	8.74	2.70	0.37
Q3UJK4_G	Gtpbp2	GTP-bindin	R.VAVLGNVDSGK#.S	12.88	3.01	4.27	0.23
Q99ME9_N	Gtpbp4	Nucleolar	R.ADVDVQPYAFTTK#.S	10.27	4.86	2.11	0.47
Q99ME9_N	Gtpbp4	Nucleolar	R.IAELSEEDQK#.I	11.85	10.80	1.10	0.91
Q99ME9_N	Gtpbp4	Nucleolar	K.LALGQINIAK#.N	14.71	8.03	1.83	0.55
Q99ME9_N	Gtpbp4	Nucleolar	R.IAELSEEDQK#.I	23.45	8.84	2.65	0.38
Q99ME9_N	Gtpbp4	Nucleolar	K.LALGQINIAK#.N	26.50	9.93	2.67	0.37
Q8R080_G	Gtse1	G2 and S p	R.LDPDTETPQLNK#.T	7.73	7.51	1.03	0.97
Q8R080_G	Gtse1	G2 and S p	K.TEAVSTTTNPFK#.V	16.63	52.20	0.32	3.14
Q80SU7_G	Gvin1	Interferon-i	R.AQAFLVLTALR.T	3.38	20.36	0.17	6.02
Q80SU7_G	Gvin1	Interferon-i	R.ELGFIIDEDQR.D	2.99	8.19	0.37	2.73
Q80SU7_G	Gvin1	Interferon-i	K.ELPFYFLQK#.L	15.22	16.94	0.90	1.11
Q80SU7_G	Gvin1	Interferon-i	R.EVGQIYEALEETSSSR.D	4.04	12.79	0.32	3.17
Q80SU7_G	Gvin1	Interferon-i	K.FTETLTNIWK#.Q	23.33	18.97	1.23	0.81
Q80SU7_G	Gvin1	Interferon-i	K.GK#ELSDEELHEK#.F	27.60	31.37	0.88	1.14
Q80SU7_G	Gvin1	Interferon-i	K.HIDEIVPDIEK#.I	9.90	10.80	0.92	1.09
Q80SU7_G	Gvin1	Interferon-i	K.ILTLTSNLLEEPLSR.K	6.76	32.66	0.21	4.83
Q80SU7_G	Gvin1	Interferon-i	R.LGLDNYYPK#.R	19.43	20.99	0.93	1.08
Q80SU7_G	Gvin1	Interferon-i	K.LLDFMQTLSQK#.I	14.38	6.76	2.13	0.47
Q80SU7_G	Gvin1	Interferon-i	K.LLDFSQPNSVAELQETPR.E	2.59	10.14	0.26	3.91
Q80SU7_G	Gvin1	Interferon-i	R.LLIEGDYK#.A	37.62	34.29	1.10	0.91
Q80SU7_G	Gvin1	Interferon-i	K.LLM*LDYGFR.H	4.11	10.39	0.40	2.53
Q80SU7_G	Gvin1	Interferon-i	K.LQEDLGVTSAQALQYLDRNDLQK.L	4.06	11.91	0.34	2.93
Q80SU7_G	Gvin1	Interferon-i	K.NEAPETVEEAER.T	5.14	22.49	0.23	4.37
Q80SU7_G	Gvin1	Interferon-i	R.NEILSTAQQESR.G	10.15	30.00	0.34	2.96
Q80SU7_G	Gvin1	Interferon-i	K.NSQEILDNQK#.S	29.34	19.28	1.52	0.66
Q80SU7_G	Gvin1	Interferon-i	R.NTQEVIAM*SK#.L	20.68	16.26	1.27	0.79
Q80SU7_G	Gvin1	Interferon-i	R.QAGQALQALK#.A	27.03	16.39	1.65	0.61
Q80SU7_G	Gvin1	Interferon-i	R.SEK#ELPFYFLQK#.L	12.65	12.99	0.97	1.03
Q80SU7_G	Gvin1	Interferon-i	R.SNLEENYGKK.F	4.32	3.41	1.27	0.79
Q80SU7_G	Gvin1	Interferon-i	K.SQIM*NSLLSK#.R	15.48	10.80	1.43	0.70
Q80SU7_G	Gvin1	Interferon-i	K.TANDPVNYLER.K	8.04	22.63	0.36	2.82
Q80SU7_G	Gvin1	Interferon-i	R.TATYEVTTALSSFLK#.Y	27.55	27.04	1.02	0.98
Q80SU7_G	Gvin1	Interferon-i	K.TTNNIQLK#.F	18.36	20.30	0.90	1.11
Q80SU7_G	Gvin1	Interferon-i	R.TTVEITDISTEEK.R	7.78	9.91	0.78	1.27
Q80SU7_G	Gvin1	Interferon-i	K.VTNFPEAHSIIQWINQSEYGEEQVK#.I	17.74	9.70	1.83	0.55
Q80SU7_G	Gvin1	Interferon-i	R.WASGGLALQGIYK#.T	12.71	15.95	0.80	1.25
Q80SU7_G	Gvin1	Interferon-i	R.YSYNVQELR.N	7.05	22.36	0.32	3.17
P10922_H	H1f0	Histone H1	K.GVGASGSFR.L	324.62	607.02	0.53	1.87
P10922_H	H1f0	Histone H1	K.RLVTTGVLK.Q	104.57	175.61	0.60	1.68
P10922_H	H1f0	Histone H1	K.VGENADSQIK#.L	2838.48	1067.11	2.66	0.38
P10922_H	H1f0	Histone H1	K.YSDM*IVAAIQAEK#.N	390.72	130.97	2.98	0.34
P10922_H	H1f0	Histone H1	K.YSDM*IVAAIQAEK#.N	29.76	11.97	2.49	0.40
P10922_H	H1f0	Histone H1	K.YSDMIVAAIQAEK#.N	567.71	207.26	2.74	0.37
P10922_H	H1f0	Histone H1	K.VGENADSQIK#.L	40.82	22.39	1.82	0.55
P10922_H	H1f0	Histone H1	K.YSDM*IVAAIQAEK#.N	32.27	13.50	2.39	0.42
P10922_H	H1f0	Histone H1	K.YSDMIVAAIQAEK#.N	66.99	24.61	2.72	0.37
P10922_H	H1f0	Histone H1	K.VGENADSQIK#.L	60.95	24.37	2.50	0.40
P10922_H	H1f0	Histone H1	K.YSDMIVAAIQAEK#.N	18.81	3.85	4.89	0.20
Q80ZM5_Q	H1fx	H1 histone	K.AGGSAAPTQPK#.R	15.62	7.05	2.22	0.45
Q80ZM5_Q	H1fx	H1 histone	R.ALVQNDTLLQVK#.G	54.51	26.50	2.06	0.49
Q80ZM5_Q	H1fx	H1 histone	K.AGGSAAPTQPK#.R	49.60	25.57	1.94	0.52
Q80ZM5_Q	H1fx	H1 histone	R.ALVQNDTLLQVK#.G	372.53	179.55	2.07	0.48
Q80ZM5_Q	H1fx	H1 histone	K.YSQLVVETIR.K	45.52	87.98	0.52	1.93
Q3THW5_H	H2afv	Histone H2	R.GDEELDSLIK.A	32.81	45.33	0.72	1.38
Q3THW5_H	H2afv	Histone H2	R.GDEELDSLIK#.A	1083.58	1640.77	0.66	1.51
Q3THW5_H	H2afv	Histone H2	R.HLQLAIRGDEELDSLIK.A	86.63	505.46	0.17	5.83
P27661_H	H2afx	Histone H2	K.ASQASQEY.-	52.50	52.50	1.00	1.00
P27661_H	H2afx	Histone H2	K.K#ASQASQEY.-	13.46	13.30	1.01	0.99
P27661_H	H2afx	Histone H2	K.KSSATVGPK.A	77.15	108.93	0.71	1.41
P27661_H	H2afx	Histone H2	K.SSATVGPK#.A	111.22	165.64	0.67	1.49
Q9QZQ8_H	H2afy	Core histon	K.AASADSTTEGTPTDGFTVLSTK#.S	78.46	70.95	1.11	0.90
Q9QZQ8_H	H2afy	Core histon	K.AISSYFVSTM*SSSIK#.T	39.58	40.19	0.98	1.02

Q9QZQ8_H	H2afy	Core histon	K.AISSYFVSTMSSSIK#.T	26.90	26.42	1.02	0.98
Q9QZQ8_H	H2afy	Core histon	K.DDLGNTLEK.K	11.46	13.81	0.83	1.20
Q9QZQ8_H	H2afy	Core histon	K.EFVEAVLELR.K	28.82	98.57	0.29	3.42
Q9QZQ8_H	H2afy	Core histon	K.GKLEAIITPPPAK.K	36.79	44.97	0.82	1.22
Q9QZQ8_H	H2afy	Core histon	K.GKLEAIITPPPAK.K	58.69	73.95	0.79	1.26
Q9QZQ8_H	H2afy	Core histon	K.GVTIASGGVLPNIHPELLAK#.K	195.43	171.89	1.14	0.88
Q9QZQ8_H	H2afy	Core histon	K.LEAIITPPPAK#.K	12.15	14.89	0.82	1.23
Q9QZQ8_H	H2afy	Core histon	K.NGPLEVAGAAISAGHGLPAK#.F	86.79	86.71	1.00	1.00
Q9QZQ8_H	H2afy	Core histon	K.QTAAQLILK#.A	137.96	137.66	1.00	1.00
Q9QZQ8_H	H2afy	Core histon	K.SIAFPSIGSGR.N	44.11	177.93	0.25	4.03
Q9QZQ8_H	H2afy	Core histon	K.AISSYFVSTM*SSSIK#.T	4.15	2.13	1.95	0.51
Q9QZQ8_H	H2afy	Core histon	K.GVTIASGGVLPNIHPELLAK#.K	54.69	23.07	2.37	0.42
Q9QZQ8_H	H2afy	Core histon	K.AASADSTTEGTPTDGFTVLSTK#.S	17.79	18.56	0.96	1.04
Q9QZQ8_H	H2afy	Core histon	K.AASADSTTEGTPTDGFTVLSTK.S	10.46	14.38	0.73	1.37
Q9QZQ8_H	H2afy	Core histon	K.AISSYFVSTM*SSSIK#.T	9.94	10.80	0.92	1.09
Q9QZQ8_H	H2afy	Core histon	K.AISSYFVSTMSSSIK#.T	5.54	5.76	0.96	1.04
Q9QZQ8_H	H2afy	Core histon	K.EFVEAVLELR.K	6.71	23.58	0.28	3.52
Q9QZQ8_H	H2afy	Core histon	K.GVTIASGGVLPNIHPELLAK.K	52.51	61.16	0.86	1.16
Q9QZQ8_H	H2afy	Core histon	R.IGVGAPVYM*AAVLEYLTAEILELAGNAAR.D	10.80	22.25	0.49	2.06
Q9QZQ8_H	H2afy	Core histon	K.QTAAQLILK#.A	26.72	25.96	1.03	0.97
Q9QZQ8_H	H2afy	Core histon	K.SIAFPSIGSGR.N	8.48	31.25	0.27	3.69
Q9QZQ8_H	H2afy	Core histon	K.SLFLGQK#.L	31.16	27.84	1.12	0.89
Q9QZQ8_H	H2afy	Core histon	K.AASADSTTEGTPTDGFTVLSTK#.S	18.37	24.23	0.76	1.32
Q9QZQ8_H	H2afy	Core histon	K.AISSYFVSTM*SSSIK#.T	30.47	16.89	1.80	0.55
Q9QZQ8_H	H2afy	Core histon	K.GVTIASGGVLPNIHPELLAK#.K	91.49	83.35	1.10	0.91
Q9QZQ8_H	H2afy	Core histon	K.QTAAQLILK#.A	34.82	42.16	0.83	1.21
Q9QZQ8_H	H2afy	Core histon	K.SIAFPSIGSGR.N	12.03	46.34	0.26	3.85
Q9QZQ8_H	H2afy	Core histon	K.SLFLGQK#.L	41.35	39.26	1.05	0.95
Q8CCK0_H	H2afy2	Core histon	R.AGVIFPVGR.L	62.19	278.16	0.22	4.47
Q8CCK0_H	H2afy2	Core histon	K.AISAHFDDSSSSSLK#.N	28.37	25.52	1.11	0.90
Q8CCK0_H	H2afy2	Core histon	K.DSDK#EGTSNSTSEDGPGDGFTILSSK#.S	25.57	20.32	1.26	0.79
Q8CCK0_H	H2afy2	Core histon	K.EGTSNSTSEDGPGDGFTILSSK.S	4.16	4.07	1.02	0.98
Q8CCK0_H	H2afy2	Core histon	K.GVTIASGGVLPR.I	14.69	52.22	0.28	3.55
Q8CCK0_H	H2afy2	Core histon	R.HILLAVANDEELNQLLK#.G	129.70	110.40	1.17	0.85
Q8CCK0_H	H2afy2	Core histon	R.HILLAVANDEELNQLLK.G	32.58	26.21	1.24	0.80
Q8CCK0_H	H2afy2	Core histon	R.KSQGPLEVAEAAVSQSSGLAAK.F	11.93	13.22	0.90	1.11
Q8CCK0_H	H2afy2	Core histon	K.QTAAQVTLK.A	64.77	77.62	0.83	1.20
Q8CCK0_H	H2afy2	Core histon	K.SQGPLEVAEAAVSQSSGLAAK.F	19.63	22.02	0.89	1.12
Q8CCK0_H	H2afy2	Core histon	K.SVAFPPFPSGR.N	3.07	12.05	0.26	3.92
Q8CCK0_H	H2afy2	Core histon	R.VEGIVHPTTAEIDLK#EEIGK#.A	33.74	27.03	1.25	0.80
Q8CCK0_H	H2afy2	Core histon	R.HILLAVANDEELNQLLK.G	13.49	8.19	1.65	0.61
Q8CCK0_H	H2afy2	Core histon	R.AGVIFPVGR.L	10.22	50.57	0.20	4.95
Q8CCK0_H	H2afy2	Core histon	R.HILLAVANDEELNQLLK.G	24.05	22.87	1.05	0.95
P01899_H	H2-D1	H-2 class I h	R.APWM*EQEGPEYWER.E	1.94	6.01	0.32	3.09
P01899_H	H2-D1	H-2 class I h	R.APWMEQEGPEYWER.E	12.09	8.28	1.46	0.69
P01899_H	H2-D1	H-2 class I h	R.DYIALNEDLK#.T	20.32	27.77	0.73	1.37
P01899_H	H2-D1	H-2 class I h	R.FDSDAENPR.Y	6.90	47.28	0.15	6.85
P01899_H	H2-D1	H-2 class I h	K.GGDYALAPGSQSSEM*SLR.D	1.93	10.02	0.19	5.18
P01899_H	H2-D1	H-2 class I h	K.TWTAADM*AAQITR.R	2.71	13.00	0.21	4.80
P01899_H	H2-D1	H-2 class I h	K.TWTAADMAAQITR.R	2.83	17.02	0.17	6.01
P01899_H	H2-D1	H-2 class I h	K.WASVVVPLGK#.E	45.17	46.81	0.96	1.04
P01899_H	H2-D1	H-2 class I h	R.YISVGYVDNK.E	15.09	29.71	0.51	1.97
P01899_H	H2-D1	H-2 class I h	R.DYIALNEDLK.T	6.83	10.59	0.64	1.55
P01899_H	H2-D1	H-2 class I h	R.DYIALNEDLK.T	10.71	21.33	0.50	1.99
P01899_H	H2-D1	H-2 class I h	R.FDSDAENPR.Y	5.89	35.67	0.17	6.05
P01899_H	H2-D1	H-2 class I h	K.GGDYALAPGSQSSEM*SLR.D	1.41	7.52	0.19	5.33
P01899_H	H2-D1	H-2 class I h	K.TWTAADM*AAQITR.R	4.45	7.73	0.58	1.74
P01899_H	H2-D1	H-2 class I h	K.TWTAADMAAQITR.R	2.25	9.39	0.24	4.17
P01899_H	H2-D1	H-2 class I h	K.WASVVVPLGK.E	25.77	26.24	0.98	1.02
P01899_H	H2-D1	H-2 class I h	R.YFETAVSRPGLEEPR.Y	3.04	37.47	0.08	12.31
P01899_H	H2-D1	H-2 class I h	R.APWM*EQEGPEYWER.E	1.74	4.24	0.41	2.44
P01899_H	H2-D1	H-2 class I h	R.DYIALNEDLK.T	17.47	25.98	0.67	1.49
P01899_H	H2-D1	H-2 class I h	R.FDSDAENPR.Y	4.80	25.61	0.19	5.34
P01899_H	H2-D1	H-2 class I h	K.GGDYALAPGSQSSEM*SLR.D	2.14	12.53	0.17	5.87
P01899_H	H2-D1	H-2 class I h	K.WASVVVPLGK.E	19.42	29.71	0.65	1.53
P01899_H	H2-D1	H-2 class I h	R.YFETAVSRPGLEEPR.Y	4.20	37.24	0.11	8.87
Q8BMS1_E	Hadha	Trifunction	K.AGLEQGSDAGYLAESQK#.F	32.70	7.73	4.23	0.24
Q8BMS1_E	Hadha	Trifunction	R.DSIFSNLIGQLDYK#.G	41.31	11.07	3.73	0.27
Q8BMS1_E	Hadha	Trifunction	K.FGELALTK#.E	39.38	10.70	3.68	0.27
Q8BMS1_E	Hadha	Trifunction	R.FGGGSVELLK#.Q	49.40	9.86	5.01	0.20
Q8BMS1_E	Hadha	Trifunction	R.FVDLYGAQK#.V	50.89	10.85	4.69	0.21
Q8BMS1_E	Hadha	Trifunction	K.GFYIYQEGSK#.N	33.31	6.05	5.50	0.18
Q8BMS1_E	Hadha	Trifunction	R.LPAKPEVSSDEDVQYR.V	20.30	17.43	1.16	0.86
Q8BMS1_E	Hadha	Trifunction	K.M*QLLEIITTDK#.T	13.09	6.62	1.98	0.51
Q8BMS1_E	Hadha	Trifunction	K.MQLLEIITTDK#.T	21.45	3.89	5.51	0.18
Q99JY0_EC	Hadhb	Trifunction	K.DQLLLGPTYATPK#.V	19.22	4.61	4.17	0.24
Q99JY0_EC	Hadhb	Trifunction	R.EAALGAGFSDK#.T	28.88	7.77	3.72	0.27
Q99JY0_EC	Hadhb	Trifunction	R.IPFLLSGTSYK#.D	15.75	19.01	0.83	1.21
Q61035_S	Hars	Histidine--t	R.IGDYVQQHGGVSLVEQLLQDPK#.L	9.21	1.45	6.37	0.16
Q8BY71_H	Hat1	Histone ac	R.LLVTDM*SDAEQYR.S	5.72	16.21	0.35	2.83
Q8BY71_H	Hat1	Histone ac	R.TFFPEYTHQLFGDDETAFGYK#.G	24.55	13.25	1.85	0.54
Q8BY71_H	Hat1	Histone ac	R.YYISFPTVLDITAEDPSR.S	2.14	14.56	0.15	6.79
Q8BY71_H	Hat1	Histone ac	R.LLVTDM*SDAEQYR.S	4.55	13.53	0.34	2.97
Q8BY71_H	Hat1	Histone ac	R.YYISFPTVLDITAEDPSR.S	2.89	8.62	0.34	2.98
Q9CQS9_H	Haus2	HAUS augm	R.LQQISDIQAEIYQNNLELELLK.L	7.52	10.30	0.73	1.37
Q9CQS9_H	Haus2	HAUS augm	R.LQQISDIQAEIYQNNLELELLK#LEK#.D	6.20	4.70	1.32	0.76
Q9CQS9_H	Haus2	HAUS augm	K.M*DILVNKTEELAENILK.W	10.62	14.07	0.75	1.33
Q9CQS9_H	Haus2	HAUS augm	K.MDILVNKTEELAENILK.W	3.78	7.18	0.53	1.90
Q9D786_H	Haus5	HAUS augm	K.LVPTSEAVAPQSQELLR.C	1.72	5.47	0.31	3.19
Q9D786_H	Haus5	HAUS augm	R.VLLGPLLPYHVK.G	11.97	14.34	0.84	1.20
Q99L00_H	Haus8	HAUS augm	R.LVSQVVELSSQASK#.E	18.46	18.93	0.98	1.03
Q69ZS7_H	Hbs1l	HBS1-like p	R.ILVFNIEVPITK#.G	13.59	5.02	2.71	0.37
Q69ZS7_H	Hbs1l	HBS1-like p	R.SQSSDLTTWYK#.G	8.27	3.61	2.30	0.44
Q69ZS7_H	Hbs1l	HBS1-like p	R.YGGSTVAAGVVTEIK#E.-	11.29	2.40	4.71	0.21
Q61191_H	Hcfc1	Host cell fa	R.GPFSEISAFK#.T	13.34	5.95	2.24	0.45
Q61191_H	Hcfc1	Host cell fa	K.K#QELQPGTAYK#.F	10.51	2.54	4.14	0.24
Q61191_H	Hcfc1	Host cell fa	R.ANTNSLEVSWGAVATADSYLLQLQK#.Y	27.71	6.96	3.98	0.25
Q61191_H	Hcfc1	Host cell fa	K.ENQWFDVGVIK#.G	27.66	17.50	1.58	0.63
Q61191_H	Hcfc1	Host cell fa	R.ESHTAVVYTEK#.D	12.37	5.23	2.36	0.42
Q61191_H	Hcfc1	Host cell fa	R.GPFSEISAFK#.T	25.71	8.99	2.86	0.35
Q61191_H	Hcfc1	Host cell fa	K.GPLPAGTILK#.L	29.31	20.50	1.43	0.70
Q61191_H	Hcfc1	Host cell fa	K.IATGHGQQGVTQVVLK#.G	75.23	27.52	2.73	0.37
Q61191_H	Hcfc1	Host cell fa	K.IITAVPK#.I	56.10	111.58	0.50	1.99

Q61191_H	Hcfc1	Host cell fa	K.K#QELQPGTAYK#.F	14.87	7.62	1.95	0.51
Q61191_H	Hcfc1	Host cell fa	R.LLVFGGM*VEYGK#.Y	9.35	6.05	1.55	0.65
Q61191_H	Hcfc1	Host cell fa	R.LLVFGGMVEYGK#.Y	12.87	4.99	2.58	0.39
Q61191_H	Hcfc1	Host cell fa	K.M*YVFGGWVPLVM*DDVK#.V	8.42	6.07	1.39	0.72
Q61191_H	Hcfc1	Host cell fa	R.SLHSATTIGNK#.M	15.73	5.84	2.69	0.37
Q61191_H	Hcfc1	Host cell fa	K.SPISVPGGSALISNLGK#.V	67.19	20.65	3.25	0.31
Q61191_H	Hcfc1	Host cell fa	K.GPLPAGTILK#.L	19.00	8.90	2.13	0.47
Q61191_H	Hcfc1	Host cell fa	K.IATGHGQQGVTQVVLK#.G	38.11	20.78	1.83	0.55
Q61191_H	Hcfc1	Host cell fa	K.SPISVPGGSALISNLGK#.V	24.65	14.10	1.75	0.57
O09106_H	Hdac1	Histone de	K.LHISPSNM*TNQNTNEYLEK#.I	6.55	3.92	1.67	0.60
O09106_H	Hdac1	Histone de	K.SFNLPM*LM*LGGGGYTIR.N	3.49	4.23	0.82	1.21
O09106_H	Hdac1	Histone de	R.SIRPDNMSEYSK.Q	3.35	9.21	0.36	2.75
O09106_H	Hdac1	Histone de	R.SIRPDNM*SEYSK.Q	10.02	27.17	0.37	2.71
O09106_H	Hdac1	Histone de	K.YGEYFPGTGDLR.D	22.16	73.86	0.30	3.33
O09106_H	Hdac1	Histone de	K.YHSDDYIK#.F	26.77	13.64	1.96	0.51
O09106_H	Hdac1	Histone de	R.LFENLR.M	30.86	72.28	0.43	2.34
O09106_H	Hdac1	Histone de	K.LHISPSNM*TNQNTNEYLEK#.I	53.68	4.30	12.49	0.08
O09106_H	Hdac1	Histone de	K.LHISPSNMTNQNTNEYLEK#.I	19.42	12.78	1.52	0.66
O09106_H	Hdac1	Histone de	K.SFNLPM*LM*LGGGGYTIR.N	2.83	6.51	0.43	2.30
O09106_H	Hdac1	Histone de	R.SIRPDNMSEYSK.Q	2.00	6.93	0.29	3.46
O09106_H	Hdac1	Histone de	R.SIRPDNM*SEYSK.Q	4.79	13.47	0.36	2.81
O09106_H	Hdac1	Histone de	R.SIRPDNM*SEYSK.Q	20.35	48.32	0.42	2.37
O09106_H	Hdac1	Histone de	K.YGEYFPGTGDLR.D	18.70	52.34	0.36	2.80
O09106_H	Hdac1	Histone de	K.YHSDDYIK#.F	26.44	17.33	1.53	0.66
O09106_H	Hdac1	Histone de	K.YYAVNYPLR.D	5.10	14.60	0.35	2.86
O09106_H	Hdac1	Histone de	R.DGIDDESYEAIFK#PVM*SK#.V	27.72	13.34	2.08	0.48
O09106_H	Hdac1	Histone de	K.LHISPSNM*TNQNTNEYLEK#.I	69.27	33.50	2.07	0.48
O09106_H	Hdac1	Histone de	K.LHISPSNMTNQNTNEYLEK#.I	35.53	19.71	1.80	0.55
O09106_H	Hdac1	Histone de	R.M*THNLLLNYGLYR.K	6.89	18.45	0.37	2.68
O09106_H	Hdac1	Histone de	K.SFNLPM*LM*LGGGGYTIR.N	4.65	7.68	0.61	1.65
O09106_H	Hdac1	Histone de	R.SIRPDNM*SEYSK.Q	6.86	27.73	0.25	4.04
O09106_H	Hdac1	Histone de	K.YGEYFPGTGDLR.D	30.55	62.94	0.49	2.06
O09106_H	Hdac1	Histone de	K.YHSDDYIK#.F	41.83	19.99	2.09	0.48
O09106_H	Hdac1	Histone de	K.YYAVNYPLR.D	8.40	17.73	0.47	2.11
P70288_H	Hdac2	Histone de	K.LHISPSNM*TNQNTPEYM*EK#.I	6.55	5.34	1.23	0.81
Q9Z2V5_H	Hdac6	Histone de	K.AVLAQGQSSEQAAK#.G	28.60	9.71	2.95	0.34
Q9Z2V5_H	Hdac6	Histone de	K.AVLAQGQSSEQAAK#.G	33.65	13.71	2.45	0.41
Q3UMU9_	Hdgfrp2	Hepatoma-	R.ADNEKLEEQPGEQAPR.E	5.28	14.09	0.37	2.67
Q3UMU9_	Hdgfrp2	Hepatoma-	R.ELAEDEPSTDR.S	3.66	10.38	0.35	2.84
Q3UMU9_	Hdgfrp2	Hepatoma-	R.IDDIADGAVKPPPNKYPIFFFGTHETAFLGPK.D	2.92	7.17	0.41	2.45
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.IEGDPQGVQQAK#.R	10.90	8.63	1.26	0.79
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.LEHEVNIQFPDK#DDGNQPQDQITITGYEK#.N	7.97	2.52	3.16	0.32
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.LGQALTEVYAK#.A	11.19	5.79	1.93	0.52
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.LQTQASATVPIPK#.E	12.41	9.65	1.29	0.78
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.LSVTVDPK#.Y	14.48	5.18	2.80	0.36
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.AFHPFIAGPYNR.L	27.67	48.70	0.57	1.76
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.ANSFTVSSVSAPSWLHR.F	14.95	31.05	0.48	2.08
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.APDM*SSSEEFPSFGAQVAPK#.T	12.11	8.20	1.48	0.68
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.APDMSSSEEFPSFGAQVAPK#.T	6.21	4.10	1.51	0.66
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.ARHEVLLISAEQDKR.A	3.45	23.59	0.15	6.84
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.ASVITQVFHVPLEER.K	59.80	125.82	0.48	2.10
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.DAPWTSNSSEK#.A	25.85	17.34	1.49	0.67
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.DAPWTSNSSEK#APDM*SSSEEFPSFGAQVAPK#.T	13.64	8.26	1.65	0.61
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.DAPWTSNSSEK#APDMSSSEEFPSFGAQVAPK#.T	5.41	3.93	1.38	0.73
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.DK#FPEVIINFPDPAQK#.S	93.70	50.37	1.86	0.54
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.DLANIAEVEVSIPAK#.L	91.66	42.91	2.14	0.47
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.DM*NQFGEGEQAK#.I	169.47	8.01	21.15	0.05
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.DQGLSIM*VSGK#.L	81.34	38.54	2.11	0.47
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.EIAEEYGGVM*VSFPR.S	11.48	23.82	0.48	2.07
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.EIAEEYGGVMVSFPR.S	5.21	15.96	0.33	3.06
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.ELLELASR.M	22.12	48.77	0.45	2.20
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.ELQAEQEDR.A	6.14	11.74	0.52	1.91
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.GEPEKLGQALTEVYAK.A	15.43	8.27	1.86	0.54
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.GNSLQEILER.T	35.36	77.79	0.45	2.20
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.HEVLLISAEQDKR.A	10.29	34.42	0.30	3.35
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.IDLPAENSNSETIIITGK#.R	81.80	38.11	2.15	0.47
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.IEGDPQGVQQAK#.R	296.17	127.65	2.32	0.43
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.IIFPAAEDKDQDLITIIGKEDAVR.E	3.38	12.45	0.27	3.69
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.ILSIQK#.D	129.36	49.64	2.61	0.38
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.ITQQMPK#.V	45.73	22.68	2.02	0.50
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.K#IM*DEFK#.V	30.88	14.54	2.12	0.47
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.LGQALTEVYAK#.A	208.96	96.33	2.17	0.46
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.LHNSLIGTK#.G	74.32	45.98	1.62	0.62
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.LQDLELK#.T	127.27	60.17	2.11	0.47
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.LQTQASATVPIPK#.E	216.70	112.88	1.92	0.52
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.LSVTVDPK#.Y	91.03	41.40	2.20	0.45
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.LVGEIM*QETGTR.I	25.24	48.18	0.52	1.91
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.LVGEIMQETGTR.I	21.11	41.94	0.50	1.99
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.M*DYVEINIDHK#.F	39.36	19.23	2.05	0.49
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.MDYVEINIDHK#.F	22.19	12.12	1.83	0.55
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.M*M*DEFEVNIHVPAPELQSDTIAITGLAANLDR.A	3.92	7.61	0.52	1.94
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.M*VADLVENSYSISVPIFK#.Q	46.52	24.65	1.89	0.53
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.MVADLVENSYSISVPIFK#.Q	28.54	12.72	2.24	0.45
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.SDIVQLR.G	29.66	64.49	0.46	2.17
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.SGLVPQQIK#.V	175.12	86.60	2.02	0.49
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.SGTQSDKVTLK.G	60.40	24.68	2.45	0.41
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.TEIVFTGEK#.E	27.72	20.20	1.37	0.73
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.TEIVFTGEKEQLAQAVAR.I	32.26	61.25	0.53	1.90
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.TGAHLELSLAK#.D	67.78	35.69	1.90	0.53
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.TGVSVEIPPSDSISETVILR.G	4.00	12.25	0.33	3.06
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.TKDLIIEQR.F	15.17	27.74	0.55	1.83
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.TTTIAVEVK#.K	78.61	44.40	1.77	0.56
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.TTTIAVEVK#K#.S	32.70	14.46	2.26	0.44
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.VATLNSEEENDPPTYK#.D	51.54	23.13	2.23	0.45
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.VATLNSEEENDPPTYK#DAFPPLPEK#.A	8.61	8.60	1.00	1.00
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.VHIEFTEGEDK#ITLEGPTEDVNVAQEQIEGMVK#.D	13.12	5.03	2.61	0.38
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.VKELQAEQEDR.A	11.57	29.91	0.39	2.59
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.VKELQAEQEDR.A	26.16	74.87	0.35	2.86
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.DAPWTSNSSEK#APDM*SSSEEFPSFGAQVAPK#.T	5.31	2.59	2.05	0.49
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.DK#FPEVIINFPDPAQK#.S	40.23	18.24	2.21	0.45
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.EIAEEYGGVM*VSFPR.S	6.53	7.96	0.82	1.22
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.IDLPAENSNSETIIITGK#.R	27.25	13.95	1.95	0.51
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.IEGDPQGVQQAK#.R	90.96	55.36	1.64	0.61

Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.IVGELEQM*VSEDVPLDHR.V	7.36	14.24	0.52	1.93
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.LGQALTEVYAK#.A	57.90	25.56	2.27	0.44
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.LQDLELK#.T	26.39	10.89	2.42	0.41
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.LQTQASATVPIPK#.E	41.89	19.87	2.11	0.47
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.LSVTVDPK#.Y	23.05	11.77	1.96	0.51
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.LVGEIM*QETGTR.I	7.78	14.14	0.55	1.82
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.LVGEIMQETGTR.I	3.36	10.80	0.31	3.22
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.M*VADLVENSYSISVPIFK#.Q	18.10	10.69	1.69	0.59
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.M*VADLVENSYSISVPIFK#.Q	14.53	6.73	2.16	0.46
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.SGLVPQQIK#.V	45.72	20.10	2.27	0.44
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.TEIVFTGEKEQLAQAVAR.I	11.61	25.34	0.46	2.18
Q8VDJ3_VI	Hdlbp	Vigilin OS=	R.TGAHLELSLAK#.D	18.97	8.06	2.35	0.43
Q8VDJ3_VI	Hdlbp	Vigilin OS=	K.VATLNSEEENDPPTYK#.D	18.20	9.60	1.90	0.53
G3X9B1_G	Heatr1	HEAT repea	R.EAEDEQAINR.Q	2.13	13.02	0.16	6.12
Q8BQM4_	Heatr3	HEAT repea	R.FIAYQETVEK#.R	12.04	3.84	3.13	0.32
Q8BQM4_	Heatr3	HEAT repea	R.LGPLLLDSSLAVR.E	6.50	9.66	0.67	1.49
Q8BQM4_	Heatr3	HEAT repea	K.DDGTLDTLK#.T	20.14	7.56	2.66	0.38
Q8BQM4_	Heatr3	HEAT repea	R.LGPLLLDSSLAVR.E	13.69	15.59	0.88	1.14
Q5PRF0_H	Heatr5a	HEAT repea	K.DVEGDSVPK#PLPPALSVISSASK#.L	6.55	4.00	1.64	0.61
Q5PRF0_H	Heatr5a	HEAT repea	R.IGSDQDLGIELLNVLHR.V	10.61	16.35	0.65	1.54
Q5PRF0_H	Heatr5a	HEAT repea	R.ILANGFTDTVVNILK#.A	5.23	3.72	1.41	0.71
Q5PRF0_H	Heatr5a	HEAT repea	R.SAEVDDGASEK#ETLPEFGEGK#.D	9.39	6.41	1.46	0.68
Q8C547_H	Heatr5b	HEAT repea	K.AVEAVVNDTSSENK#.S	8.42	3.94	2.14	0.47
Q6P1G0_H	Heatr6	HEAT repea	R.EQASLPFASSSWK#.R	12.04	5.14	2.34	0.43
Q6P1G0_H	Heatr6	HEAT repea	K.LLEELGAGLIQQYKPDSNIAPEQR.V	1.59	5.80	0.27	3.65
Q6P1G0_H	Heatr6	HEAT repea	R.LTQTEHLGALLAVLK#.K	10.13	5.31	1.91	0.52
Q6P1G0_H	Heatr6	HEAT repea	R.SYILQFLK#.S	15.72	8.86	1.77	0.56
Q69ZR2_H	Hectd1	E3 ubiquiti	R.LPLHLYDTPGSTYNLQILTR.R	2.20	4.42	0.50	2.01
Q69ZR2_H	Hectd1	E3 ubiquiti	R.STTGAPSAAADSK#.L	6.49	3.57	1.82	0.55
Q6NVF4_H	Helb	DNA helica	R.TESQLIVDNATR.I	3.80	7.02	0.54	1.85
Q6NVF4_H	Helb	DNA helica	R.TIHTFQGSEENTVVYVVGK#.A	18.93	6.79	2.79	0.36
Q6NVF4_H	Helb	DNA helica	R.VSIPDEYTK#.E	33.25	5.28	6.29	0.16
Q60848_H	Hells	Lymphocyt	K.LISQIQPEVNR.E	5.00	24.00	0.21	4.80
Q60848_H	Hells	Lymphocyt	R.LVTANTIDQK#.I	34.14	35.58	0.96	1.04
Q60848_H	Hells	Lymphocyt	R.TVVEGNIPIESEVNLK#.L	16.67	14.18	1.18	0.85
Q60848_H	Hells	Lymphocyt	K.IDEELVTNSGK.F	16.44	17.99	0.91	1.09
Q60848_H	Hells	Lymphocyt	R.IGQTKPVVVYR.L	6.83	32.38	0.21	4.74
Q60848_H	Hells	Lymphocyt	K.LISQIQPEVNR.E	8.58	35.37	0.24	4.12
Q60848_H	Hells	Lymphocyt	K.M*EQQQLEEQK#.K	11.40	9.87	1.16	0.87
Q60848_H	Hells	Lymphocyt	K.NFLDAK#.E	38.72	12.65	3.06	0.33
Q60848_H	Hells	Lymphocyt	R.TVVEGNIPIESEVNLK#.L	20.62	25.18	0.82	1.22
Q60848_H	Hells	Lymphocyt	K.VISDEDLELLLDR.S	1.61	8.74	0.18	5.43
Q6PAV2_H	Herc4	Probable E	K.LIQAIDHNEGFSLI.-	12.40	12.40	1.00	1.00
Q6PAV2_H	Herc4	Probable E	K.LIQAIDHNEGFSLI.-	29.77	29.77	1.00	1.00
Q6PAV2_H	Herc4	Probable E	K.LIQPDHPQISQQVAASLEK#.N	32.47	11.37	2.86	0.35
F2Z461_HE	Herc6	E3 ISG15--	K.AIISQIQYGVATEQYITNIK#.V	9.00	3.23	2.79	0.36
F2Z461_HE	Herc6	E3 ISG15--	K.M*SSPPYLILK#.V	9.74	5.63	1.73	0.58
F2Z461_HE	Herc6	E3 ISG15--	R.NSEGQLGLGK#.N	14.08	87.43	0.16	6.21
F2Z461_HE	Herc6	E3 ISG15--	R.SGQLALSGNK#.V	16.21	6.39	2.54	0.39
Q99LI8_HG	Hgs	Hepatocyt	K.KQEYLEVQR.Q	1.26	7.32	0.17	5.82
Q99LI8_HG	Hgs	Hepatocyt	R.RLYYEGLQDK.L	15.14	10.51	1.44	0.69
Q99LI8_HG	Hgs	Hepatocyt	K.VEGHVFPEFK#.E	22.01	16.06	1.37	0.73
Q99LI8_HG	Hgs	Hepatocyt	K.VNDK#NPHVALYALEVMESVVK#.N	6.97	6.87	1.01	0.99
Q99LI8_HG	Hgs	Hepatocyt	K.VVQDTYQIM*K#.V	16.47	12.28	1.34	0.75
Q8R1F6_HI	Hid1	Protein HI	R.LLQVLVPQVEK#.I	12.98	4.62	2.81	0.36
Q8R1F6_HI	Hid1	Protein HI	R.LLSNPLLQTYLPNSTK#.K	12.16	3.99	3.05	0.33
Q8R1F6_HI	Hid1	Protein HI	R.LLQVLVPQVEK#.I	16.56	5.50	3.01	0.33
Q8R1F6_HI	Hid1	Protein HI	R.LLSNPLLQTYLPNSTK#.K	16.35	4.45	3.67	0.27
Q8R1F6_HI	Hid1	Protein HI	R.NVDPPIWYDTDVK#.L	9.43	1.86	5.07	0.20
Q8R1F6_HI	Hid1	Protein HI	K.TSLVATPGIDK#LTEK#.S	20.55	8.51	2.42	0.41
P70349_HI	Hint1	Histidine tr	K.AQVAQPGGDTIFGK#.I	258.07	85.23	3.03	0.33
Q8VD75_H	Hip1	Huntingtin	R.EIAASTAQLVAASK.V	7.97	8.40	0.95	1.05
Q8VD75_H	Hip1	Huntingtin	R.LIQIPQLPENPPNFLR.A	3.74	7.32	0.51	1.96
P43275_H	Hist1h1a	Histone H1	K.ERSGVSLAALK.K	5.17	10.58	0.49	2.04
P43275_H	Hist1h1a	Histone H1	K.GTGAAGSFK.L	335.14	288.41	1.16	0.86
P43275_H	Hist1h1a	Histone H1	K.GTLVQTK#.G	3124.39	1647.19	1.90	0.53
P43275_H	Hist1h1a	Histone H1	R.K#K#PAGPSVSELIVQAVSSSK#.E	308.59	265.19	1.16	0.86
P43275_H	Hist1h1a	Histone H1	R.K#K#PAGPSVSELIVQAVSSSK#.E	275.12	186.05	1.48	0.68
P43275_H	Hist1h1a	Histone H1	K.K#PAGPSVSELIVQAVSSSK#.E	25.72	29.85	0.86	1.16
P43275_H	Hist1h1a	Histone H1	K.K#SLAAAGYDVEK#.N	32.25	36.58	0.88	1.13
P43275_H	Hist1h1a	Histone H1	R.SGVSLAALK#.K	1702.49	680.48	2.50	0.40
P43275_H	Hist1h1a	Histone H1	R.SGVSLAALK#K#.S	2220.24	798.94	2.78	0.36
P43275_H	Hist1h1a	Histone H1	K.SLAAAGYDVEK#.N	191.83	185.02	1.04	0.96
P43275_H	Hist1h1a	Histone H1	K.SLAAAGYDVEKNNSR.I	3.53	8.43	0.42	2.39
P43275_H	Hist1h1a	Histone H1	R.KKPAGPSVSELIVQAVSSSK.E	7.36	4.50	1.64	0.61
P43275_H	Hist1h1a	Histone H1	R.SGVSLAALK#.K	71.11	17.05	4.17	0.24
P43275_H	Hist1h1a	Histone H1	R.SGVSLAALK#.K	27.27	18.88	1.44	0.69
P43275_H	Hist1h1a	Histone H1	R.SGVSLAALK#K#.S	29.18	16.33	1.79	0.56
P43275_H	Hist1h1a	Histone H1	R.K#K#PAGPSVSELIVQAVSSSK#.E	5.14	7.17	0.72	1.39
P43275_H	Hist1h1a	Histone H1	R.SGVSLAALK#.K	85.24	38.24	2.23	0.45
P43275_H	Hist1h1a	Histone H1	R.SGVSLAALK#K#.S	94.00	42.45	2.21	0.45
P43276_H	Hist1h1b	Histone H1	K.AK#K#PAAAGVK#.K	8.59	4.86	1.77	0.57
P43276_H	Hist1h1b	Histone H1	K.ALAAGGYDVEK#.N	1947.36	993.68	1.96	0.51
P43276_H	Hist1h1b	Histone H1	K.ATGPPVSELITK#.A	1458.74	804.15	1.81	0.55
P43276_H	Hist1h1b	Histone H1	K.ERGGVSLPALK.K	12.47	33.94	0.37	2.72
P43276_H	Hist1h1b	Histone H1	R.GGVSLPALK#.K	719.85	345.54	2.08	0.48
P43276_H	Hist1h1b	Histone H1	R.GGVSLPALK#K#.A	274.08	122.26	2.24	0.45
P43276_H	Hist1h1b	Histone H1	K.K#ALAAGGYDVEK#.N	152.59	91.02	1.68	0.60
P43276_H	Hist1h1b	Histone H1	R.K#ATGPPVSELITK#.A	400.81	201.54	1.99	0.50
P43276_H	Hist1h1b	Histone H1	R.K#ATGPPVSELITK#.A	689.79	334.70	2.06	0.49
P43276_H	Hist1h1b	Histone H1	K.K#PAGATPK#.K	47.66	29.38	1.62	0.62
P43276_H	Hist1h1b	Histone H1	K.ATGPPVSELITK#.A	32.08	12.78	2.51	0.40
P43276_H	Hist1h1b	Histone H1	R.K#ATGPPVSELITK#.A	14.91	241.65	0.06	16.20
P43276_H	Hist1h1b	Histone H1	K.ATGPPVSELITK#.A	11.87	7.16	1.66	0.60
P43276_H	Hist1h1b	Histone H1	K.ATGPPVSELITK#.A	43.92	26.16	1.68	0.60
P43276_H	Hist1h1b	Histone H1	R.GGVSLPALK#.K	13.64	7.07	1.93	0.52
P43276_H	Hist1h1b	Histone H1	R.K#ATGPPVSELITK#.A	31.09	20.24	1.54	0.65
P15864_H	Hist1h1c	Histone H1	K.AK#K#PAAAAVTK#.K	28.28	19.83	1.43	0.70
P15864_H	Hist1h1c	Histone H1	K.ALAAAGYDVEK#.N	3028.28	1306.70	2.32	0.43
P15864_H	Hist1h1c	Histone H1	K.ASGPPVSELITK#.A	1983.02	1080.22	1.84	0.54
P15864_H	Hist1h1c	Histone H1	K.GTGASGSFK#.L	1560.15	806.20	1.94	0.52
P15864_H	Hist1h1c	Histone H1	K.K#ALAAAGYDVEK#.N	573.71	195.41	2.94	0.34
P15864_H	Hist1h1c	Histone H1	K.KALAAAGYDVEKNNSR.I	19.77	37.09	0.53	1.88

P15864_H	Hist1h1c	Histone H1	R.K#ASGPPVSELITK#.A	1048.07	693.51	1.51	0.66
P15864_H	Hist1h1c	Histone H1	R.KASGPPVSELITK.A	631.18	378.07	1.67	0.60
P15864_H	Hist1h1c	Histone H1	K.KATGAATPK.K	324.64	176.91	1.84	0.54
P15864_H	Hist1h1c	Histone H1	K.K#PAAAAVTK#.K	711.68	423.96	1.68	0.60
P15864_H	Hist1h1c	Histone H1	K.K#PAAAAVTK#K#.V	17.41	10.74	1.62	0.62
P15864_H	Hist1h1c	Histone H1	K.ASGPPVSELITK#.A	78.06	25.92	3.01	0.33
P15864_H	Hist1h1c	Histone H1	R.K#ASGPPVSELITK#.A	7.92	4.73	1.67	0.60
P15864_H	Hist1h1c	Histone H1	K.KATGAATPK.K	7.99	6.00	1.33	0.75
P15864_H	Hist1h1c	Histone H1	K.ALAAAGYDVEK#.N	64.32	31.67	2.03	0.49
P15864_H	Hist1h1c	Histone H1	K.ALAAAGYDVEK#.N	237.19	140.40	1.69	0.59
P15864_H	Hist1h1c	Histone H1	K.ASGPPVSELITK#.A	91.42	52.10	1.75	0.57
P15864_H	Hist1h1c	Histone H1	K.GTGASGSFK#.L	61.80	31.10	1.99	0.50
P15864_H	Hist1h1c	Histone H1	K.K#ALAAAGYDVEK#.N	12.00	9.58	1.25	0.80
P15864_H	Hist1h1c	Histone H1	R.K#ASGPPVSELITK#.A	21.41	11.25	1.90	0.53
P43274_H	Hist1h1e	Histone H1	K.AASGEAK#PK#.A	50.99	28.90	1.76	0.57
P43274_H	Hist1h1e	Histone H1	K.K#AAGTATAK#.K	98.37	50.28	1.96	0.51
P43274_H	Hist1h1e	Histone H1	K.K#AASGEAK#PK#.A	12.98	6.76	1.92	0.52
P43274_H	Hist1h1e	Histone H1	K.K#PAAAAGAK#.K	224.11	147.24	1.52	0.66
P43274_H	Hist1h1e	Histone H1	R.K#TSGPPVSELITK#.A	468.41	253.20	1.85	0.54
P43274_H	Hist1h1e	Histone H1	K.SLVSK#GTLVQTK#.G	11.52	10.37	1.11	0.90
P43274_H	Hist1h1e	Histone H1	K.TSGPPVSELITK#.A	2783.51	1329.30	2.09	0.48
P43274_H	Hist1h1e	Histone H1	K.TSGPPVSELITK#.A	43.28	7.70	5.62	0.18
P43274_H	Hist1h1e	Histone H1	K.TSGPPVSELITK#.A	28.56	16.75	1.71	0.59
P43274_H	Hist1h1e	Histone H1	R.K#TSGPPVSELITK#.A	26.62	12.71	2.09	0.48
P43274_H	Hist1h1e	Histone H1	K.TSGPPVSELITK#.A	169.90	96.97	1.75	0.57
Q8CGP6_H	Hist1h2ah	Histone H2	R.AGLQFPVGR.V	143.92	815.90	0.18	5.67
Q8CGP6_H	Hist1h2ah	Histone H2	R.HLQLAIR.N	214.11	723.72	0.30	3.38
Q8CGP6_H	Hist1h2ah	Histone H2	R.NDEELNK.L	42.15	60.69	0.69	1.44
Q8CGP6_H	Hist1h2ah	Histone H2	R.NDEELNKLLGR.V	7.20	35.57	0.20	4.94
Q8CGP6_H	Hist1h2ah	Histone H2	R.VTIAQGGVLPNIQAVLLPK.K	253.14	356.15	0.71	1.41
Q8CGP6_H	Hist1h2ah	Histone H2	R.VTIAQGGVLPNIQAVLLPK#.K	254.30	357.11	0.71	1.40
Q8CGP6_H	Hist1h2ah	Histone H2	R.AGLQFPVGR.V	1219.82	7020.59	0.17	5.76
Q8CGP6_H	Hist1h2ah	Histone H2	R.HLQLAIR.N	1279.35	7615.01	0.17	5.95
Q8CGP6_H	Hist1h2ah	Histone H2	R.HLQLAIRNDEELNK.L	255.48	1329.51	0.19	5.20
Q8CGP6_H	Hist1h2ah	Histone H2	R.HLQLAIRNDEELNK.L	1.22	4.94	0.25	4.06
Q8CGP6_H	Hist1h2ah	Histone H2	R.HLQLAIRNDEELNKLLGR.V	35.10	681.79	0.05	19.43
Q8CGP6_H	Hist1h2ah	Histone H2	R.KGNYSER.V	35.35	203.22	0.17	5.75
Q8CGP6_H	Hist1h2ah	Histone H2	K.K#TESHHK#.A	108.93	22.07	4.94	0.20
Q8CGP6_H	Hist1h2ah	Histone H2	R.NDEELNK#.L	700.76	989.96	0.71	1.41
Q8CGP6_H	Hist1h2ah	Histone H2	R.NDEELNKLLGR.V	405.04	2191.28	0.18	5.41
Q8CGP6_H	Hist1h2ah	Histone H2	R.NDEELNKLLGR.V	245.65	1395.32	0.18	5.68
Q8CGP6_H	Hist1h2ah	Histone H2	R.VTIAQGGVLPNIQAVLLPK.K	2817.40	3162.40	0.89	1.12
Q8CGP6_H	Hist1h2ah	Histone H2	R.VTIAQGGVLPNIQAVLLPK.K	1834.67	2429.63	0.76	1.32
Q8CGP6_H	Hist1h2ah	Histone H2	R.VTIAQGGVLPNIQAVLLPKK.T	253.87	367.17	0.69	1.45
Q8CGP6_H	Hist1h2ah	Histone H2	R.VTIAQGGVLPNIQAVLLPK#K#TESHHK#.A	18.38	20.80	0.88	1.13
Q8CGP6_H	Hist1h2ah	Histone H2	R.AGLQFPVGR.V	29.02	165.14	0.18	5.69
Q8CGP6_H	Hist1h2ah	Histone H2	R.HLQLAIR.N	5.95	141.11	0.04	23.70
Q8CGP6_H	Hist1h2ah	Histone H2	R.VTIAQGGVLPNIQAVLLPK.K	65.61	82.28	0.80	1.25
Q8CGP6_H	Hist1h2ah	Histone H2	R.AGLQFPVGR.V	41.94	193.17	0.22	4.61
Q8CGP6_H	Hist1h2ah	Histone H2	R.HLQLAIR.N	18.63	57.51	0.32	3.09
Q8CGP6_H	Hist1h2ah	Histone H2	R.VTIAQGGVLPNIQAVLLPK.K	77.33	98.01	0.79	1.27
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIM*NSFVNDIFER.I	26.73	104.34	0.26	3.90
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIM*NSFVNDIFER.I	5.54	9.94	0.56	1.79
Q64475_H	Hist1h2bb	Histone H2	K.AMGIM*NSFVNDIFER.I	8.08	25.08	0.32	3.10
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIMNSFVNDIFER.I	10.92	47.32	0.23	4.33
Q64475_H	Hist1h2bb	Histone H2	K.AMGIMNSFVNDIFER.I	18.51	104.18	0.18	5.63
Q64475_H	Hist1h2bb	Histone H2	R.EIQTAVR.L	64.47	389.08	0.17	6.03
Q64475_H	Hist1h2bb	Histone H2	K.ESYSVYVYK.V	132.29	128.72	1.03	0.97
Q64475_H	Hist1h2bb	Histone H2	R.KESYSVYVYK.V	119.43	142.94	0.84	1.20
Q64475_H	Hist1h2bb	Histone H2	R.LLLPGELAK.H	490.46	566.93	0.87	1.16
Q64475_H	Hist1h2bb	Histone H2	K.QVHPDTGISSK#.A	172.45	203.28	0.85	1.18
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIM*NSFVNDIFER.I	860.89	4194.39	0.21	4.87
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIM*NSFVNDIFER.I	3.20	12.02	0.27	3.76
Q64475_H	Hist1h2bb	Histone H2	K.AMGIM*NSFVNDIFER.I	475.85	2425.26	0.20	5.10
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIMNSFVNDIFER.I	475.85	2425.26	0.20	5.10
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIMNSFVNDIFER.I	3.64	10.33	0.35	2.84
Q64475_H	Hist1h2bb	Histone H2	K.AMGIMNSFVNDIFER.I	399.99	2032.42	0.20	5.08
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIM*NSFVNDIFERIASEASR.L	1.84	7.23	0.25	3.92
Q64475_H	Hist1h2bb	Histone H2	K.AVTKYTSSK.-	20.73	27.69	0.75	1.34
Q64475_H	Hist1h2bb	Histone H2	R.EIQTAVR.L	1058.82	5964.56	0.18	5.63
Q64475_H	Hist1h2bb	Histone H2	K.ESYSVYVYK#.V	4834.22	4722.61	1.02	0.98
Q64475_H	Hist1h2bb	Histone H2	K.HAVSEGTK#.A	1533.92	1970.29	0.78	1.28
Q64475_H	Hist1h2bb	Histone H2	K.HAVSEGTK#AVTK#.Y	26.90	29.66	0.91	1.10
Q64475_H	Hist1h2bb	Histone H2	R.IASEASR.L	212.00	1140.15	0.19	5.38
Q64475_H	Hist1h2bb	Histone H2	R.K#ESYSVYVYK#.V	2717.77	2326.87	1.17	0.86
Q64475_H	Hist1h2bb	Histone H2	R.K#ESYSVYVYK#VLK#.Q	99.18	108.92	0.91	1.10
Q64475_H	Hist1h2bb	Histone H2	R.LAHYNK#.R	105.04	192.05	0.55	1.83
Q64475_H	Hist1h2bb	Histone H2	R.LAHYNKR.S	65.63	321.79	0.20	4.90
Q64475_H	Hist1h2bb	Histone H2	R.LLLPGELAK#.H	5666.33	7896.29	0.72	1.39
Q64475_H	Hist1h2bb	Histone H2	K.QVHPDTGISSK.A	2195.14	2774.25	0.79	1.26
Q64475_H	Hist1h2bb	Histone H2	K.QVHPDTGISSK.A	2136.25	2966.46	0.72	1.39
Q64475_H	Hist1h2bb	Histone H2	K.QVHPDTGISSKAM*GIM*NSFVNDIFER.I	24.98	127.97	0.20	5.12
Q64475_H	Hist1h2bb	Histone H2	K.QVHPDTGISSKAM*GIM*NSFVNDIFER.I	6.45	30.79	0.21	4.77
Q64475_H	Hist1h2bb	Histone H2	K.QVHPDTGISSKAMGIMNSFVNDIFER.I	5.54	33.48	0.17	6.04
Q64475_H	Hist1h2bb	Histone H2	R.SRKESYSVYVYK.V	135.73	779.15	0.17	5.74
Q64475_H	Hist1h2bb	Histone H2	R.SRKESYSVYVYK.V	14.27	61.40	0.23	4.30
Q64475_H	Hist1h2bb	Histone H2	K.VLK#QVHPDTGISSK#.A	450.03	630.55	0.71	1.40
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIM*NSFVNDIFER.I	11.46	36.80	0.31	3.21
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIMNSFVNDIFER.I	3.26	12.05	0.27	3.70
Q64475_H	Hist1h2bb	Histone H2	K.AMGIMNSFVNDIFER.I	7.69	24.06	0.32	3.13
Q64475_H	Hist1h2bb	Histone H2	K.ESYSVYVYK#.V	74.03	82.04	0.90	1.11
Q64475_H	Hist1h2bb	Histone H2	R.K#ESYSVYVYK#.V	24.07	30.22	0.80	1.26
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIM*NSFVNDIFER.I	25.07	128.08	0.20	5.11
Q64475_H	Hist1h2bb	Histone H2	K.AMGIM*NSFVNDIFER.I	5.66	13.09	0.43	2.31
Q64475_H	Hist1h2bb	Histone H2	K.AM*GIMNSFVNDIFER.I	11.63	27.52	0.42	2.37
Q64475_H	Hist1h2bb	Histone H2	K.AMGIMNSFVNDIFER.I	5.95	21.74	0.27	3.65
Q64475_H	Hist1h2bb	Histone H2	R.EIQTAVR.L	68.94	349.48	0.20	5.07
Q64475_H	Hist1h2bb	Histone H2	K.ESYSVYVYK#.V	239.22	230.40	1.04	0.96
Q64475_H	Hist1h2bb	Histone H2	K.HAVSEGTK.A	19.49	20.00	0.97	1.03
Q64475_H	Hist1h2bb	Histone H2	R.K#ESYSVYVYK#.V	49.74	65.06	0.76	1.31
Q64475_H	Hist1h2bb	Histone H2	R.LLLPGELAK.H	503.56	600.99	0.84	1.19
Q6ZWY9_H	Hist1h2bc	Histone H2	R.IAGEASR.L	178.98	944.48	0.19	5.28
P68433_H	Hist1h3a	Histone H3	R.EIAQDFK#.T	779.90	621.86	1.25	0.80

P68433_H	Hist1h3a	Histone H3	K.STELLIR.K	136.55	557.08	0.25	4.08
P68433_H	Hist1h3a	Histone H3	R.EIAQDFK#.T	4889.38	3621.73	1.35	0.74
P68433_H	Hist1h3a	Histone H3	R.EIAQDFKTDLR.F	260.14	877.64	0.30	3.37
P68433_H	Hist1h3a	Histone H3	R.KLPFQR.L	604.27	2455.45	0.25	4.06
P68433_H	Hist1h3a	Histone H3	R.KSAPATGGVK.K	25.50	96.87	0.26	3.80
P68433_H	Hist1h3a	Histone H3	K.RVTIM*PK.D	455.89	2156.75	0.21	4.73
P68433_H	Hist1h3a	Histone H3	K.RVTIMPKDIQLAR.R	1.48	40.24	0.04	27.27
P68433_H	Hist1h3a	Histone H3	R.RYQKSTELLIR.K	4.97	65.60	0.08	13.20
P68433_H	Hist1h3a	Histone H3	K.STELLIR.K	1079.97	4120.69	0.26	3.82
P68433_H	Hist1h3a	Histone H3	K.STELLIRK.L	45.93	128.15	0.36	2.79
P68433_H	Hist1h3a	Histone H3	R.VTIM*PK#.D	2931.70	2682.01	1.09	0.91
P68433_H	Hist1h3a	Histone H3	R.VTIM*PKDIQLAR.R	33.10	106.55	0.31	3.22
P68433_H	Hist1h3a	Histone H3	R.VTIMPKDIQLAR.R	8.37	34.14	0.25	4.08
P68433_H	Hist1h3a	Histone H3	R.YQKSTELLIR.K	26.08	106.05	0.25	4.07
P68433_H	Hist1h3a	Histone H3	R.YRPGTVALR.E	134.89	2113.48	0.06	15.67
P68433_H	Hist1h3a	Histone H3	R.KLPFQR.L	28.13	124.66	0.23	4.43
P68433_H	Hist1h3a	Histone H3	K.STELLIR.K	77.83	296.65	0.26	3.81
P68433_H	Hist1h3a	Histone H3	R.EIAQDFK.T	191.84	164.49	1.17	0.86
P68433_H	Hist1h3a	Histone H3	K.STELLIR.K	48.74	242.57	0.20	4.98
P68433_H	Hist1h3a	Histone H3	R.YRPGTVALR.E	11.77	179.64	0.07	15.27
P62806_H	Hist1h4a	Histone H4	R.DAVTYTEHAK#.R	59.98	50.46	1.19	0.84
P62806_H	Hist1h4a	Histone H4	R.DNIQGITKPAIR.R	6.37	27.70	0.23	4.35
P62806_H	Hist1h4a	Histone H4	R.ISGLIYEETR.G	24.07	95.75	0.25	3.98
P62806_H	Hist1h4a	Histone H4	K.TVTAMDVVYALK#.R	19.17	17.07	1.12	0.89
P62806_H	Hist1h4a	Histone H4	K.VFLENVIR.D	26.64	96.36	0.28	3.62
P62806_H	Hist1h4a	Histone H4	R.DAVTYTEHAK#.R	1463.20	1371.58	1.07	0.94
P62806_H	Hist1h4a	Histone H4	R.DAVTYTEHAKR.K	15.83	46.42	0.34	2.93
P62806_H	Hist1h4a	Histone H4	R.DNIQGITKPAIR.R	815.21	3423.04	0.24	4.20
P62806_H	Hist1h4a	Histone H4	R.DNIQGITKPAIR.R	743.99	2930.26	0.25	3.94
P62806_H	Hist1h4a	Histone H4	R.GVLKVFLENVIR.D	9.13	46.35	0.20	5.08
P62806_H	Hist1h4a	Histone H4	R.ISGLIYEETR.G	1169.25	4650.72	0.25	3.98
P62806_H	Hist1h4a	Histone H4	R.K#TVTAM*DVVYALK#.R	392.96	310.68	1.26	0.79
P62806_H	Hist1h4a	Histone H4	R.KTVTAM*DVVYALK.R	352.48	284.94	1.24	0.81
P62806_H	Hist1h4a	Histone H4	R.K#TVTAMDVVYALK#.R	397.64	401.65	0.99	1.01
P62806_H	Hist1h4a	Histone H4	R.KTVTAMDVVYALK.R	115.47	105.83	1.09	0.92
P62806_H	Hist1h4a	Histone H4	R.KTVTAM*DVVYALKR.Q	393.21	1212.55	0.32	3.08
P62806_H	Hist1h4a	Histone H4	R.KTVTAMDVVYALKR.Q	158.51	474.90	0.33	3.00
P62806_H	Hist1h4a	Histone H4	K.RISGLIYEETR.G	19.73	286.54	0.07	14.52
P62806_H	Hist1h4a	Histone H4	K.RKTVTAM*DVVYALK.R	3.46	11.81	0.29	3.42
P62806_H	Hist1h4a	Histone H4	K.TVTAM*DVVYALK#.R	4112.10	3220.85	1.28	0.78
P62806_H	Hist1h4a	Histone H4	K.TVTAMDVVYALK#.R	2011.82	1840.20	1.09	0.91
P62806_H	Hist1h4a	Histone H4	K.VFLENVIR.D	1272.41	4870.59	0.26	3.83
P62806_H	Hist1h4a	Histone H4	R.DAVTYTEHAK#.R	23.63	19.54	1.21	0.83
P62806_H	Hist1h4a	Histone H4	R.DNIQGITKPAIR.R	2.47	15.75	0.16	6.38
P62806_H	Hist1h4a	Histone H4	K.VFLENVIR.D	5.36	23.28	0.23	4.34
P62806_H	Hist1h4a	Histone H4	R.DAVTYTEHAK#.R	25.70	24.89	1.03	0.97
P62806_H	Hist1h4a	Histone H4	R.ISGLIYEETR.G	13.60	39.96	0.34	2.94
P62806_H	Hist1h4a	Histone H4	K.TVTAMDVVYALK#.R	7.19	5.87	1.22	0.82
P62806_H	Hist1h4a	Histone H4	K.VFLENVIR.D	8.56	45.80	0.19	5.35
Q6GSS7_H	Hist2h2aa1	Histone H2	R.NDEELNKLLGK.V	15.31	13.15	1.16	0.86
Q6GSS7_H	Hist2h2aa1	Histone H2	R.VGAGAPVYM*AAVLEYLTAEILELAGNAAR.D	26.17	77.15	0.34	2.95
Q6GSS7_H	Hist2h2aa1	Histone H2	R.HLQLAIRNDEELNKLLGK.V	14.84	82.65	0.18	5.57
Q6GSS7_H	Hist2h2aa1	Histone H2	R.KGNYAER.V	19.68	102.12	0.19	5.19
Q6GSS7_H	Hist2h2aa1	Histone H2	K.LLGKVTIAQGGVLPNIQAVLLPK.K	8.47	13.50	0.63	1.59
Q6GSS7_H	Hist2h2aa1	Histone H2	R.NDEELNKLLGK.V	1085.87	1167.54	0.93	1.08
Q6GSS7_H	Hist2h2aa1	Histone H2	R.NDEELNKLLGKVTIAQGGVLPNIQAVLLPK.K	42.35	42.61	0.99	1.01
Q6GSS7_H	Hist2h2aa1	Histone H2	R.VGAGAPVYM*AAVLEYLTAEILELAGNAAR.D	93.32	347.39	0.27	3.72
Q64522_H	Hist2h2ab	Histone H2	R.HLQLAVR.N	32.06	153.42	0.21	4.79
Q64522_H	Hist2h2ab	Histone H2	K.LLGGVTIAQGGVLPNIQAVLLPKK.T	29.86	35.88	0.83	1.20
Q64522_H	Hist2h2ab	Histone H2	R.NDEELNKLLGGVTIAQGGVLPNIQAVLLPK.K	419.04	538.17	0.78	1.28
O08528_H	Hk2	Hexokinase	K.GLGATTHPTAAVK#.M	13.05	3.15	4.15	0.24
O08528_H	Hk2	Hexokinase	K.LSPELLTTGSFETK#.D	12.83	4.83	2.66	0.38
O08528_H	Hk2	Hexokinase	K.VTVGVDGTLYK#.L	12.27	4.13	2.97	0.34
Q9Z104_H	Hmg20b	SWI/SNF-re	K.EDSSSGLM*NTLLNGHK#.G	4.57	1.69	2.70	0.37
P52927_H	Hmga2	High mobil	R.GEGAGQPSTSAQGQPAAPVPQK.R	6.88	17.84	0.39	2.59
P63158_H	Hmgb1	High mobil	K.LGEM*WNNTAADDK#QPYEK#.K	4.62	1.79	2.59	0.39
Q8JZK9_H	Hmgcs1	Hydroxyme	K.VTQDATPGSALDK#.I	8.03	4.97	1.62	0.62
P09602_H	Hmgn2	Non-histon	K.AEGDAK#GDK#.T	10.64	2.54	4.20	0.24
Q9CX86_R	Hnrnpa0	Heterogene	K.AEIIADK#.Q	196.55	127.35	1.54	0.65
Q9CX86_R	Hnrnpa0	Heterogene	K.GDVAEGDLIEHFSQFGAVEK#.A	246.92	137.07	1.80	0.56
Q9CX86_R	Hnrnpa0	Heterogene	R.GFGFVYFQSHDAADK.A	22.38	14.66	1.53	0.66
Q9CX86_R	Hnrnpa0	Heterogene	K.LFIGGLNVQTSESGLR.G	60.33	179.10	0.34	2.97
Q9CX86_R	Hnrnpa0	Heterogene	K.RGFGFVYFQSHDAADK.A	3.04	7.67	0.40	2.52
Q9CX86_R	Hnrnpa0	Heterogene	K.AEIIADK#.Q	16.56	6.13	2.70	0.37
Q9CX86_R	Hnrnpa0	Heterogene	K.GDVAEGDLIEHFSQFGAVEK#.A	83.11	37.87	2.19	0.46
Q9CX86_R	Hnrnpa0	Heterogene	K.LFIGGLNVQTSESGLR.G	8.68	20.32	0.43	2.34
Q9CX86_R	Hnrnpa0	Heterogene	K.LFVGGLK#.G	40.43	14.10	2.87	0.35
Q9CX86_R	Hnrnpa0	Heterogene	K.LFVGGLK#GDVAEGDLIEHFSQFGAVEK#.A	1.93	1.53	1.26	0.79
P49312_R	Hnrnpa1	Heterogene	R.GFAFVTFDDHDSVDK#IVIQK#.Y	55.17	18.44	2.99	0.33
P49312_R	Hnrnpa1	Heterogene	R.GFGFVTYATVEEVDAAM*NARPHK.V	14.89	21.20	0.70	1.42
P49312_R	Hnrnpa1	Heterogene	K.IEVIEIM*TDR.G	27.01	41.07	0.66	1.52
P49312_R	Hnrnpa1	Heterogene	R.KLFIGGLSFETTDESLR.S	4.07	7.25	0.56	1.78
P49312_R	Hnrnpa1	Heterogene	K.LFIGGLSFETTDESLR.S	37.88	54.39	0.70	1.44
P49312_R	Hnrnpa1	Heterogene	R.NQGGYGGSSSSSSYGSGR.R	21.76	32.98	0.66	1.52
P49312_R	Hnrnpa1	Heterogene	K.RGFAFVTFDDHDSVDK.I	3.56	8.47	0.42	2.38
P49312_R	Hnrnpa1	Heterogene	K.SESPKEPEQLR.K	15.99	34.43	0.46	2.15
P49312_R	Hnrnpa1	Heterogene	R.SSGPYGGGGQYFAKPR.N	7.41	15.45	0.48	2.09
P49312_R	Hnrnpa1	Heterogene	R.GFAFVTFDDHDSVDKIVIQK.Y	14.12	6.29	2.25	0.45
P49312_R	Hnrnpa1	Heterogene	K.IEVIEIMTDR.G	4.24	8.49	0.50	2.00
O88569_R	Hnrnpa2b1	Heterogene	R.DYFEEYGK#.I	106.48	46.81	2.27	0.44
O88569_R	Hnrnpa2b1	Heterogene	R.DYFEEYGKIDTIEIITDR.Q	36.59	58.30	0.63	1.59
O88569_R	Hnrnpa2b1	Heterogene	R.EESGK#PGAHVTVK#.K	138.99	53.67	2.59	0.39
O88569_R	Hnrnpa2b1	Heterogene	R.GFGFVTFDDHDPVDK#.I	85.21	35.04	2.43	0.41
O88569_R	Hnrnpa2b1	Heterogene	R.GFGFVTFDDHDPVDK#IVLQK#.Y	141.82	48.28	2.94	0.34
O88569_R	Hnrnpa2b1	Heterogene	R.GFGFVTFSSM*AEVDAAM*AARPHSIDGR.V	1.88	4.27	0.44	2.27
O88569_R	Hnrnpa2b1	Heterogene	R.GGGGNFGPGPGSNFR.G	137.26	293.02	0.47	2.13
O88569_R	Hnrnpa2b1	Heterogene	R.GGNFGFGDSR.G	109.40	202.61	0.54	1.85
O88569_R	Hnrnpa2b1	Heterogene	R.GGSDGYGSGR.G	5.12	9.88	0.52	1.93
O88569_R	Hnrnpa2b1	Heterogene	K.IDTIEIITDR.Q	132.73	210.75	0.63	1.59
O88569_R	Hnrnpa2b1	Heterogene	R.KLFIGGLSFETTEESLR.N	31.83	62.62	0.51	1.97
O88569_R	Hnrnpa2b1	Heterogene	K.LFIGGLSFETTEESLR.N	128.18	218.35	0.59	1.70
O88569_R	Hnrnpa2b1	Heterogene	R.NM*GGPYGGGNYGPGGSGGSGGYGGR.S	30.52	51.92	0.59	1.70
O88569_R	Hnrnpa2b1	Heterogene	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S	7.95	12.10	0.66	1.52

O88569_R	Hnrnpa2b1	Heterogene	R.NYYEQWGK#.L	352.99	115.32	3.06	0.33
O88569_R	Hnrnpa2b1	Heterogene	R.QEM*QEVQSSR.S	21.87	44.86	0.49	2.05
O88569_R	Hnrnpa2b1	Heterogene	R.QEMQEVQSSR.S	70.91	96.50	0.73	1.36
O88569_R	Hnrnpa2b1	Heterogene	K.RGFGFVTFDDHDPVDK.I	8.06	14.34	0.56	1.78
O88569_R	Hnrnpa2b1	Heterogene	K.SGNFGGSR.N	14.47	29.60	0.49	2.04
O88569_R	Hnrnpa2b1	Heterogene	K.TLETVPLER.K	29.15	75.66	0.39	2.60
O88569_R	Hnrnpa2b1	Heterogene	R.GFGFVTFDDHDPVDK#IVLQK#.Y	40.08	13.51	2.97	0.34
O88569_R	Hnrnpa2b1	Heterogene	R.GFGFVTFSSM*AEVDAAM*AARPHSIDGR.V	1.93	4.65	0.41	2.41
O88569_R	Hnrnpa2b1	Heterogene	R.GGGGNFGPGPGSNFR.G	6.14	17.01	0.36	2.77
O88569_R	Hnrnpa2b1	Heterogene	R.GGNFGFGDSR.G	7.18	18.12	0.40	2.53
O88569_R	Hnrnpa2b1	Heterogene	R.KLFIGGLSFETTEESLR.N	2.13	5.65	0.38	2.66
O88569_R	Hnrnpa2b1	Heterogene	K.LFIGGLSFETTEESLR.N	10.04	19.98	0.50	1.99
Q8BG05_R	Hnrnpa3	Heterogene	R.GFAFVTFDDHDTVDK#.I	7.17	8.91	0.81	1.24
Q8BG05_R	Hnrnpa3	Heterogene	K.IETIEVM*EDR.Q	8.21	37.42	0.22	4.56
Q8BG05_R	Hnrnpa3	Heterogene	K.IETIEVMEDR.Q	6.54	20.62	0.32	3.15
Q8BG05_R	Hnrnpa3	Heterogene	K.IFVGGIKEDTEEYNLR.D	16.69	66.41	0.25	3.98
Q8BG05_R	Hnrnpa3	Heterogene	R.SSGSPYGGGYGSGGGSGGYGSR.R	6.01	23.27	0.26	3.87
Q99020_R	Hnrnpab	Heterogene	R.EYFGQFGEIEAIELPIDPK.L	21.92	45.30	0.48	2.07
Q99020_R	Hnrnpab	Heterogene	R.GFGFILFK.D	59.35	163.29	0.36	2.75
Q99020_R	Hnrnpab	Heterogene	R.GFVFITFK.E	6.85	19.57	0.35	2.86
Q99020_R	Hnrnpab	Heterogene	R.GFVFITFK#EEDPVK#K#.V	26.83	78.36	0.34	2.92
Q99020_R	Hnrnpab	Heterogene	K.IFVGGLNPEATEEK.I	140.51	254.16	0.55	1.81
Q99020_R	Hnrnpab	Heterogene	K.IREYFGQFGEIEAIELPIDPK.L	1.35	68.03	0.02	50.28
Q99020_R	Hnrnpab	Heterogene	K.M*FVGGLSWDTSKK.D	4.77	9.18	0.52	1.93
Q99020_R	Hnrnpab	Heterogene	K.IFVGGLNPEATEEK.I	13.72	9.26	1.48	0.68
Q9Z204_H	Hnrnpc	Heterogene	R.AAVAGEDGR.M	36.02	136.52	0.26	3.79
Q9Z204_H	Hnrnpc	Heterogene	K.GDDLQAIKK.E	32.02	25.84	1.24	0.81
Q9Z204_H	Hnrnpc	Heterogene	K.GFAFVQYVNER.N	175.43	669.36	0.26	3.82
Q9Z204_H	Hnrnpc	Heterogene	K.K#SDVEAIFSK#.Y	514.41	455.28	1.13	0.89
Q9Z204_H	Hnrnpc	Heterogene	K.LK#GDDLQAIK#.K	150.65	176.62	0.85	1.17
Q9Z204_H	Hnrnpc	Heterogene	K.LK#GDDLQAIK#K#.E	1080.84	867.34	1.25	0.80
Q9Z204_H	Hnrnpc	Heterogene	K.M*ESEAGADDSAEEGDLLDDDDNEDRGDDQLELK.D	2.30	4.57	0.50	1.99
Q9Z204_H	Hnrnpc	Heterogene	R.M*IAGQVLDINLAAEPK#.V	338.29	284.17	1.19	0.84
Q9Z204_H	Hnrnpc	Heterogene	R.M*IAGQVLDINLAAEPK.V	98.13	82.82	1.18	0.84
Q9Z204_H	Hnrnpc	Heterogene	R.MIAGQVLDINLAAEPK#.V	317.83	238.76	1.33	0.75
Q9Z204_H	Hnrnpc	Heterogene	R.MIAGQVLDINLAAEPK#.V	143.73	137.90	1.04	0.96
Q9Z204_H	Hnrnpc	Heterogene	R.MYSYPAR.V	33.08	151.08	0.22	4.57
Q9Z204_H	Hnrnpc	Heterogene	R.M*YSYPAR.V	44.96	168.77	0.27	3.75
Q9Z204_H	Hnrnpc	Heterogene	K.NEKSEEEQSSASVK.K	124.23	109.71	1.13	0.88
Q9Z204_H	Hnrnpc	Heterogene	K.NEK#SEEEQSSASVK#.K	142.50	127.22	1.12	0.89
Q9Z204_H	Hnrnpc	Heterogene	K.QADLSFSSPVEM*K#.N	129.05	113.86	1.13	0.88
Q9Z204_H	Hnrnpc	Heterogene	K.QADLSFSSPVEMK#.N	129.18	103.31	1.25	0.80
Q9Z204_H	Hnrnpc	Heterogene	K.QK#VDSLLESLEK#.I	102.19	84.08	1.22	0.82
Q9Z204_H	Hnrnpc	Heterogene	K.QK#VDSLLESLEK#IEK#.E	20.71	17.21	1.20	0.83
Q9Z204_H	Hnrnpc	Heterogene	R.SAAEM*YGSVPEHPSPSPLLSSSFDLDYDFQR.D	21.33	44.62	0.48	2.09
Q9Z204_H	Hnrnpc	Heterogene	R.SAAEMYGSVPEHPSPSPLLSSSFDLDYDFQR.D	12.64	28.55	0.44	2.26
Q9Z204_H	Hnrnpc	Heterogene	K.SDVEAIFSK#.Y	349.62	267.64	1.31	0.77
Q9Z204_H	Hnrnpc	Heterogene	K.SEEEQSSASVK#.K	153.88	137.16	1.12	0.89
Q9Z204_H	Hnrnpc	Heterogene	K.VDSLLESLEK#.I	146.26	132.91	1.10	0.91
Q9Z204_H	Hnrnpc	Heterogene	R.VFIGNLNTLVVK#.K	935.48	777.98	1.20	0.83
Q9Z204_H	Hnrnpc	Heterogene	R.VFIGNLNTLVVK.K	12.40	10.19	1.22	0.82
Q9Z204_H	Hnrnpc	Heterogene	K.GFAFVQYVNER.N	12.71	20.57	0.62	1.62
Q9Z204_H	Hnrnpc	Heterogene	K.LK#GDDLQAIK#K#.E	84.82	96.13	0.88	1.13
Q9Z204_H	Hnrnpc	Heterogene	R.M*IAGQVLDINLAAEPK#.V	25.44	30.74	0.83	1.21
Q9Z204_H	Hnrnpc	Heterogene	K.QADLSFSSPVEM*K#.N	9.27	11.33	0.82	1.22
Q9Z204_H	Hnrnpc	Heterogene	K.QADLSFSSPVEMK#.N	10.57	10.04	1.05	0.95
Q9Z204_H	Hnrnpc	Heterogene	K.QK#VDSLLESLEK#.I	18.62	22.52	0.83	1.21
Q9Z204_H	Hnrnpc	Heterogene	K.VDSLLESLEK#.I	9.11	9.68	0.94	1.06
Q9Z204_H	Hnrnpc	Heterogene	R.VFIGNLNTLVVK#.K	10.15	10.39	0.98	1.02
Q9Z204_H	Hnrnpc	Heterogene	K.GFAFVQYVNER.N	4.76	22.13	0.22	4.65
Q9Z204_H	Hnrnpc	Heterogene	R.M*IAGQVLDINLAAEPK#.V	11.38	10.75	1.06	0.95
Q9Z204_H	Hnrnpc	Heterogene	K.NEKSEEEQSSASVK.K	2.45	3.24	0.76	1.32
Q9Z204_H	Hnrnpc	Heterogene	K.QK#VDSLLESLEK#.I	7.25	5.47	1.33	0.75
Q9Z204_H	Hnrnpc	Heterogene	K.SEEEQSSASVK#.K	2.84	2.70	1.05	0.95
Q9Z204_H	Hnrnpc	Heterogene	R.VFIGNLNTLVVK#.K	41.95	38.21	1.10	0.91
Q9Z204_H	Hnrnpc	Heterogene	R.VFIGNLNTLVVK#.K	12.39	10.27	1.21	0.83
Q60668_H	Hnrnpd	Heterogene	K.DLKDYFSK.F	38.77	74.43	0.52	1.92
Q60668_H	Hnrnpd	Heterogene	K.ESESVDKVMDQK.E	9.67	17.95	0.54	1.86
Q60668_H	Hnrnpd	Heterogene	K.ESESVDKVM*DQK.E	20.40	49.32	0.41	2.42
Q60668_H	Hnrnpd	Heterogene	R.EYFGGFGEVESIELPM*DNK.T	24.87	29.10	0.85	1.17
Q60668_H	Hnrnpd	Heterogene	R.EYFGGFGEVESIELPMDNK.T	14.46	29.27	0.49	2.02
Q60668_H	Hnrnpd	Heterogene	K.IDASKNEEDEGHSNSSPR.H	2.57	39.96	0.06	15.55
Q60668_H	Hnrnpd	Heterogene	K.IFVGGLSPDTPEEK.I	120.39	236.35	0.51	1.96
Q60668_H	Hnrnpd	Heterogene	K.IREYFGGFGEVESIELPM*DNK.T	3.30	30.16	0.11	9.13
Q60668_H	Hnrnpd	Heterogene	K.IREYFGGFGEVESIELPMDNK.T	4.19	29.01	0.14	6.92
Q60668_H	Hnrnpd	Heterogene	K.KYHNVGLSK.C	21.23	41.11	0.52	1.94
Q60668_H	Hnrnpd	Heterogene	K.M*FIGGLSWDTTK.K	7.74	19.99	0.39	2.58
Q60668_H	Hnrnpd	Heterogene	K.MFIGGLSWDTTK.K	9.70	18.27	0.53	1.88
G3X9W0_	Hnrnpd	Heterogene	K.IDASKNEEDEGK.M	8.44	16.03	0.53	1.90
Q60668_H	Hnrnpd	Heterogene	K.IFVGGLSPDTPEEK.I	9.17	15.85	0.58	1.73
Q9Z130_H	Hnrnpdl	Heterogene	K.DAASVDK#VLELK#.E	8.53	8.06	1.06	0.94
Q9Z130_H	Hnrnpdl	Heterogene	K.DLTEYLSR.F	16.80	76.42	0.22	4.55
Q9Z130_H	Hnrnpdl	Heterogene	K.EYFGAFGEIENIELPM*DTK.T	4.41	6.30	0.70	1.43
Q9Z130_H	Hnrnpdl	Heterogene	R.GFGFVLFK#.D	239.40	334.03	0.72	1.40
Q9Z130_H	Hnrnpdl	Heterogene	K.MFIGGLSWDTSK.K	7.30	10.49	0.70	1.44
Q9Z130_H	Hnrnpdl	Heterogene	K.M*FIGGLSWDTSK#K#.D	7.73	10.12	0.76	1.31
Q9Z130_H	Hnrnpdl	Heterogene	K.VFVGGLSPDTSEEQIK#.E	20.97	23.92	0.88	1.14
Q9Z130_H	Hnrnpdl	Heterogene	K.VFVGGLSPDTSEEQIK#EYFGAFGEIENIELPM*DTK#.T	11.18	12.65	0.88	1.13
Q9Z130_H	Hnrnpdl	Heterogene	R.GFGFVLFK.D	7.68	18.45	0.42	2.40
Q9Z2X1_H	Hnrnpf	Heterogene	K.HSGPNSADSANDGFVR.L	67.73	289.80	0.23	4.28
Q9Z2X1_H	Hnrnpf	Heterogene	K.ITGEAFVQFASQELAEK#.A	222.49	170.43	1.31	0.77
Q9Z2X1_H	Hnrnpf	Heterogene	K.ITGEAFVQFASQELAEK.A	520.71	457.84	1.14	0.88
Q9Z2X1_H	Hnrnpf	Heterogene	R.QSGEAFVELESEDDVK#.L	115.84	107.64	1.08	0.93
Q9Z2X1_H	Hnrnpf	Heterogene	R.QSGEAFVELESEDDVK#.L	13.70	10.01	1.37	0.73
Q9Z2X1_H	Hnrnpf	Heterogene	R.RYIGIVK.Q	40.56	169.89	0.24	4.19
Q9Z2X1_H	Hnrnpf	Heterogene	R.SGAYSAGYGGYEEYSGLSDGYGFTTDLFGR.D	19.99	60.75	0.33	3.04
Q9Z2X1_H	Hnrnpf	Heterogene	R.SYSDPPLK#.F	303.86	284.61	1.07	0.94
Q9Z2X1_H	Hnrnpf	Heterogene	R.TEM*DWVLK#.H	169.02	133.21	1.27	0.79
Q9Z2X1_H	Hnrnpf	Heterogene	R.TEMDWVLK#.H	164.46	117.01	1.41	0.71
Q9Z2X1_H	Hnrnpf	Heterogene	R.VTGEADVEFATHEEAVAAM*SK#.D	93.38	78.00	1.20	0.84
Q9Z2X1_H	Hnrnpf	Heterogene	R.VTGEADVEFATHEEAVAAM*SK#.D	10.50	9.25	1.14	0.88
Q9Z2X1_H	Hnrnpf	Heterogene	R.VTGEADVEFATHEEAVAAMSK.D	7.68	6.40	1.20	0.83
Q9Z2X1_H	Hnrnpf	Heterogene	R.VTGEADVEFATHEEAVAAMSK#.D	74.19	60.51	1.23	0.82

Q9Z2X1_H	Hnrnpf	Heterogene	R.YIEVFK#.S	686.28	541.71	1.27	0.79
Q9Z2X1_H	Hnrnpf	Heterogene	K.HSGPNSADSANDGFVR.L	3.55	9.80	0.36	2.76
Q9Z2X1_H	Hnrnpf	Heterogene	K.ITGEAFVQFASQELAEK#.A	48.02	36.99	1.30	0.77
Q9Z2X1_H	Hnrnpf	Heterogene	R.QSGEAFVELESEDDVK#.L	12.62	10.30	1.23	0.82
Q9Z2X1_H	Hnrnpf	Heterogene	K.ITGEAFVQFASQELAEK#.A	23.22	13.58	1.71	0.58
Q9Z2X1_H	Hnrnpf	Heterogene	K.ITGEAFVQFASQELAEK.A	16.55	13.33	1.24	0.81
Q9Z2X1_H	Hnrnpf	Heterogene	R.QSGEAFVELESEDDVK#.L	8.50	6.05	1.41	0.71
O35737_H	Hnrnph1	Heterogene	R.ATENDIYNFFSPLNPVR.V	56.65	224.49	0.25	3.96
O35737_H	Hnrnph1	Heterogene	R.EGRPSGEAFVELESEDEVK.L	39.67	164.06	0.24	4.14
O35737_H	Hnrnph1	Heterogene	K.HTGPNSPDTANDGFVR.L	97.71	383.47	0.25	3.92
O35737_H	Hnrnph1	Heterogene	K.IQNGAQGIR.F	33.28	54.78	0.61	1.65
O35737_H	Hnrnph1	Heterogene	K.SNNVEM*DWVLK#.H	51.97	41.57	1.25	0.80
O35737_H	Hnrnph1	Heterogene	K.SNNVEMDWVLK#.H	63.36	59.53	1.06	0.94
O35737_H	Hnrnph1	Heterogene	R.STGEAFVQFASQEIAEK#.A	415.28	322.26	1.29	0.78
O35737_H	Hnrnph1	Heterogene	R.VHIEIGPDGR.V	64.16	328.14	0.20	5.11
O35737_H	Hnrnph1	Heterogene	R.VTGEADVEFATHEDAVAAM*SK#.D	82.18	63.25	1.30	0.77
O35737_H	Hnrnph1	Heterogene	R.VTGEADVEFATHEDAVAAM*SK#.D	7.22	6.27	1.15	0.87
O35737_H	Hnrnph1	Heterogene	R.YVELFLNSTAGASGGAYEHR.Y	14.37	55.70	0.26	3.87
O35737_H	Hnrnph1	Heterogene	R.ATENDIYNFFSPLNPVR.V	6.65	16.03	0.42	2.41
O35737_H	Hnrnph1	Heterogene	R.STGEAFVQFASQEIAEK#.A	5.95	4.53	1.31	0.76
O35737_H	Hnrnph1	Heterogene	R.VTGEADVEFATHEDAVAAM*SK#.D	6.89	4.30	1.60	0.62
O35737_H	Hnrnph1	Heterogene	R.ATENDIYNFFSPLNPVR.V	11.25	39.03	0.29	3.47
O35737_H	Hnrnph1	Heterogene	K.HTGPNSPDTANDGFVR.L	2.31	7.71	0.30	3.34
O35737_H	Hnrnph1	Heterogene	R.STGEAFVQFASQEIAEK#.A	23.88	18.11	1.32	0.76
O35737_H	Hnrnph1	Heterogene	R.VHIEIGPDGR.V	9.92	23.92	0.41	2.41
O35737_H	Hnrnph1	Heterogene	R.ATENDIYNFFSPLNPVR.V	6.30	24.28	0.26	3.86
O35737_H	Hnrnph1	Heterogene	R.STGEAFVQFASQEIAEK#.A	31.73	12.05	2.63	0.38
P70333_H	Hnrnph2	Heterogene	R.ATENDIYNFFSPLNPM*R.V	6.41	23.49	0.27	3.66
P70333_H	Hnrnph2	Heterogene	R.ATENDIYNFFSPLNPMR.V	6.08	23.09	0.26	3.80
P70333_H	Hnrnph2	Heterogene	K.SNSVEM*DWVLK#.H	36.54	30.05	1.22	0.82
P70333_H	Hnrnph2	Heterogene	R.VTGEADVEFATHEDAVAAMAK#.D	33.96	25.20	1.35	0.74
D3YWT1_D	Hnrnph3	MCG11326	R.ATENDIANFFSPLNPIR.V	4.19	21.65	0.19	5.17
D3YWT1_D	Hnrnph3	MCG11326	R.DGM*DNQGGYGSVGR.M	4.93	19.65	0.25	3.99
D3YWT1_D	Hnrnph3	MCG11326	K.EIAENALGK#.H	25.94	26.19	0.99	1.01
D3YWT1_D	Hnrnph3	MCG11326	R.STGEAFVQFASK#.E	43.20	46.17	0.94	1.07
D3YWT1_D	Hnrnph3	MCG11326	R.VHIDIGADGR.A	3.53	12.35	0.29	3.50
B2M1R6_B	Hnrnpk	Heterogene	R.AQPYDPNFYDETYDYGGFTM*M*FDDR.R	11.97	17.09	0.70	1.43
B2M1R6_B	Hnrnpk	Heterogene	K.DLAGSIIGK#.G	1098.19	559.23	1.96	0.51
B2M1R6_B	Hnrnpk	Heterogene	R.DYDDMSPR.R	21.93	57.10	0.38	2.60
B2M1R6_B	Hnrnpk	Heterogene	R.DYDDM*SPR.R	33.87	90.67	0.37	2.68
B2M1R6_B	Hnrnpk	Heterogene	R.ENTQTTIK#.L	265.10	157.89	1.68	0.60
B2M1R6_B	Hnrnpk	Heterogene	R.GGDLM*AYDR.R	106.33	316.51	0.34	2.98
B2M1R6_B	Hnrnpk	Heterogene	R.GGDLMAYDR.R	12.74	37.67	0.34	2.96
B2M1R6_B	Hnrnpk	Heterogene	R.GSYGDLGGPIITTQVTIPK#.D	576.17	295.98	1.95	0.51
B2M1R6_B	Hnrnpk	Heterogene	R.HESGASIK#.I	113.97	74.48	1.53	0.65
B2M1R6_B	Hnrnpk	Heterogene	R.HESGASIKIDEPLEGSEDR.I	27.37	71.42	0.38	2.61
B2M1R6_B	Hnrnpk	Heterogene	K.IDEPLEGSEDR.I	257.93	711.83	0.36	2.76
B2M1R6_B	Hnrnpk	Heterogene	K.IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK.Q	3.11	10.36	0.30	3.34
B2M1R6_B	Hnrnpk	Heterogene	K.IILDLISESPIK#.G	1118.63	675.40	1.66	0.60
B2M1R6_B	Hnrnpk	Heterogene	K.IIPTLEEYQHYK#.G	16.82	8.56	1.96	0.51
B2M1R6_B	Hnrnpk	Heterogene	R.IITITGTQDQIQNAQYLLQNSVK#.Q	1199.69	597.67	2.01	0.50
B2M1R6_B	Hnrnpk	Heterogene	R.IITITGTQDQIQNAQYLLQNSVK#.Q	80.53	41.17	1.96	0.51
B2M1R6_B	Hnrnpk	Heterogene	K.K#IIPTLEEYQHYK#.G	8.13	4.20	1.94	0.52
B2M1R6_B	Hnrnpk	Heterogene	R.LLIHQSLAGGIIGVK#.G	485.34	264.90	1.83	0.55
B2M1R6_B	Hnrnpk	Heterogene	K.NAGAVIGK#.G	687.64	272.88	2.52	0.40
B2M1R6_B	Hnrnpk	Heterogene	R.NLPLPPPPPPR.G	78.30	270.05	0.29	3.45
B2M1R6_B	Hnrnpk	Heterogene	R.NTDEM*VELR.I	97.05	258.94	0.37	2.67
B2M1R6_B	Hnrnpk	Heterogene	R.NTDEMVELR.I	68.65	175.75	0.39	2.56
B2M1R6_B	Hnrnpk	Heterogene	R.RDYDDM*SPR.R	2.41	8.36	0.29	3.46
B2M1R6_B	Hnrnpk	Heterogene	K.RPAEDMEEEQAFK.R	5.00	21.02	0.24	4.20
B2M1R6_B	Hnrnpk	Heterogene	K.RPAEDM*EEEQAFK.R	14.97	50.84	0.29	3.40
B2M1R6_B	Hnrnpk	Heterogene	K.RPAEDMEEEQAFKR.S	19.48	269.16	0.07	13.82
B2M1R6_B	Hnrnpk	Heterogene	K.RPAEDM*EEEQAFKR.S	30.70	429.42	0.07	13.99
B2M1R6_B	Hnrnpk	Heterogene	R.SRNTDEM*VELR.I	4.15	51.40	0.08	12.38
B2M1R6_B	Hnrnpk	Heterogene	R.TDYNASVSVPDSSGPER.I	127.96	383.95	0.33	3.00
B2M1R6_B	Hnrnpk	Heterogene	R.GSYGDLGGPIITTQVTIPK#.D	38.99	20.60	1.89	0.53
B2M1R6_B	Hnrnpk	Heterogene	R.IITITGTQDQIQNAQYLLQNSVK#.Q	72.72	40.32	1.80	0.55
B2M1R6_B	Hnrnpk	Heterogene	R.LLIHQSLAGGIIGVK#.G	20.96	9.28	2.26	0.44
B2M1R6_B	Hnrnpk	Heterogene	R.NTDEM*VELR.I	2.94	8.57	0.34	2.92
B2M1R6_B	Hnrnpk	Heterogene	R.TDYNASVSVPDSSGPER.I	14.11	33.34	0.42	2.36
B2M1R6_B	Hnrnpk	Heterogene	K.DLAGSIIGK#.G	166.83	113.49	1.47	0.68
B2M1R6_B	Hnrnpk	Heterogene	R.ENTQTTIK#.L	32.76	20.80	1.58	0.63
B2M1R6_B	Hnrnpk	Heterogene	R.GGDLM*AYDR.R	14.06	40.68	0.35	2.89
B2M1R6_B	Hnrnpk	Heterogene	R.GSYGDLGGPIITTQVTIPK#.D	129.33	70.27	1.84	0.54
B2M1R6_B	Hnrnpk	Heterogene	R.GSYGDLGGPIITTQVTIPK#.D	40.92	26.42	1.55	0.65
B2M1R6_B	Hnrnpk	Heterogene	R.HESGASIKIDEPLEGSEDR.I	9.61	28.72	0.33	2.99
B2M1R6_B	Hnrnpk	Heterogene	K.IDEPLEGSEDR.I	33.43	109.46	0.31	3.27
B2M1R6_B	Hnrnpk	Heterogene	K.IILDLISESPIK#.G	218.02	134.42	1.62	0.62
B2M1R6_B	Hnrnpk	Heterogene	R.IITITGTQDQIQNAQYLLQNSVK#.Q	373.69	188.20	1.99	0.50
B2M1R6_B	Hnrnpk	Heterogene	R.IITITGTQDQIQNAQYLLQNSVK#.Q	17.26	10.29	1.68	0.60
B2M1R6_B	Hnrnpk	Heterogene	R.LLIHQSLAGGIIGVK#.G	171.19	103.94	1.65	0.61
B2M1R6_B	Hnrnpk	Heterogene	R.NLPLPPPPPPR.G	11.82	49.72	0.24	4.21
B2M1R6_B	Hnrnpk	Heterogene	R.NTDEM*VELR.I	21.37	49.52	0.43	2.32
B2M1R6_B	Hnrnpk	Heterogene	R.NTDEMVELR.I	11.72	30.96	0.38	2.64
B2M1R6_B	Hnrnpk	Heterogene	K.RPAEDM*EEEQAFKR.S	2.73	59.60	0.05	21.85
B2M1R6_B	Hnrnpk	Heterogene	K.RPAEDMEEEQAFKR.S	4.56	69.31	0.07	15.18
B2M1R6_B	Hnrnpk	Heterogene	R.TDYNASVSVPDSSGPER.I	54.52	162.41	0.34	2.98
B2M1R6_B	Hnrnpk	Heterogene	K.DLAGSIIGK.G	63.20	53.05	1.19	0.84
B2M1R6_B	Hnrnpk	Heterogene	R.GSYGDLGGPIITTQVTIPK#.D	39.64	34.09	1.16	0.86
B2M1R6_B	Hnrnpk	Heterogene	K.IDEPLEGSEDR.I	9.29	38.26	0.24	4.12
B2M1R6_B	Hnrnpk	Heterogene	K.IILDLISESPIK#.G	64.71	36.64	1.77	0.57
B2M1R6_B	Hnrnpk	Heterogene	R.LLIHQSLAGGIIGVK#.G	39.23	23.59	1.66	0.60
B2M1R6_B	Hnrnpk	Heterogene	R.TDYNASVSVPDSSGPER.I	13.39	42.96	0.31	3.21
Q8R081_H	Hnrnpl	Heterogene	R.AITHLNNNFM*FGQK#.M	10.67	6.26	1.70	0.59
Q8R081_H	Hnrnpl	Heterogene	R.AITHLNNNFMFGQK#.M	42.16	27.57	1.53	0.65
Q8R081_H	Hnrnpl	Heterogene	K.IEYAKPTR.L	25.39	82.96	0.31	3.27
Q8R081_H	Hnrnpl	Heterogene	K.ISRPGDSDDSR.S	3.55	48.01	0.07	13.53
Q8R081_H	Hnrnpl	Heterogene	R.MGPPVGGHR.R	11.68	6.78	1.72	0.58
Q8R081_H	Hnrnpl	Heterogene	K.NDQDTWDYTNPNLSGQGDPGSNPNKR.Q	15.34	62.76	0.24	4.09
Q8R081_H	Hnrnpl	Heterogene	K.NGVQAMVEFDSVQSAQR.A	2.22	5.36	0.41	2.41
Q8R081_H	Hnrnpl	Heterogene	K.NPNGPYPYTLK#.L	78.06	48.36	1.61	0.62
Q8R081_H	Hnrnpl	Heterogene	K.SDALETLGFLNHYQM*K#.N	16.68	9.35	1.78	0.56
Q8R081_H	Hnrnpl	Heterogene	K.SDALETLGFLNHYQMK#.N	73.50	48.59	1.51	0.66

Q8R081_H	Hnrnpl	Heterogene	K.SKPGAAM*VEM*ADGYAVDR.A	18.25	58.41	0.31	3.20
Q8R081_H	Hnrnpl	Heterogene	K.SKPGAAM*VEMADGYAVDR.A	5.84	20.25	0.29	3.47
Q8R081_H	Hnrnpl	Heterogene	K.SKPGAAMVEM*ADGYAVDR.A	13.67	33.68	0.41	2.46
Q8R081_H	Hnrnpl	Heterogene	R.SSSGLLEWDSK#.S	126.97	87.02	1.46	0.69
Q8R081_H	Hnrnpl	Heterogene	K.TPASPVVHIR.G	15.55	61.43	0.25	3.95
Q8R081_H	Hnrnpl	Heterogene	R.YGPQYGHPPPPPPPPDYGPHADSPVLM*VYGLDQSK#.M	23.66	11.45	2.07	0.48
Q8R081_H	Hnrnpl	Heterogene	R.AITHLNNNFM*FGQK#.M	131.19	24.25	5.41	0.18
Q8R081_H	Hnrnpl	Heterogene	R.AITHLNNNFMFGQK#.M	24.60	13.66	1.80	0.56
Q8R081_H	Hnrnpl	Heterogene	K.IEYAKPTR.L	11.67	29.15	0.40	2.50
Q8R081_H	Hnrnpl	Heterogene	K.ISRPGDSDDSR.S	1.37	18.84	0.07	13.74
Q8R081_H	Hnrnpl	Heterogene	R.LKTENAGDQHGGGGGGGSGAAGGGGGENYDDPHKTPASPVVHIR.G	5.80	7.93	0.73	1.37
Q8R081_H	Hnrnpl	Heterogene	K.NDQDTWDYTNPNLSGQGDPGSNPNKR.Q	10.22	24.71	0.41	2.42
Q8R081_H	Hnrnpl	Heterogene	K.NPNGPYPYTLK#.L	32.09	20.07	1.60	0.63
Q8R081_H	Hnrnpl	Heterogene	K.SDALETLGFLNHYQMK#.N	7.02	2.43	2.89	0.35
Q8R081_H	Hnrnpl	Heterogene	K.SKPGAAM*VEM*ADGYAVDR.A	10.97	26.03	0.42	2.37
Q8R081_H	Hnrnpl	Heterogene	R.YGPQYGHPPPPPPPPDYGPHADSPVLM*VYGLDQSK#.M	12.07	2.52	4.80	0.21
Q8R081_H	Hnrnpl	Heterogene	R.YGPQYGHPPPPPPPPDYGPHADSPVLMVYGLDQSK#.M	24.60	9.39	2.62	0.38
Q921F4_H	Hnrnpll	Heterogene	R.HDGYGSHGPLLPLPSR.Y	8.91	28.26	0.32	3.17
Q921F4_H	Hnrnpll	Heterogene	R.ITRPGNTDDPSGGNK.V	7.22	8.18	0.88	1.13
Q921F4_H	Hnrnpll	Heterogene	R.QALVEFENIDSAK#.E	11.93	7.02	1.70	0.59
Q921F4_H	Hnrnpll	Heterogene	K.TDAVEALTALNHYQIR.V	7.72	16.13	0.48	2.09
Q921F4_H	Hnrnpll	Heterogene	K.TLSGLLEWK#.C	21.79	11.18	1.95	0.51
Q921F4_H	Hnrnpll	Heterogene	R.HDGYGSHGPLLPLPSR.Y	22.94	37.20	0.62	1.62
Q921F4_H	Hnrnpll	Heterogene	R.ITRPGNTDDPSGGNK.V	22.18	35.45	0.63	1.60
Q921F4_H	Hnrnpll	Heterogene	R.LKTEEGEIVYSAEESENR.Q	18.31	30.14	0.61	1.65
Q921F4_H	Hnrnpll	Heterogene	R.QALVEFENIDSAK#.E	22.81	8.81	2.59	0.39
Q921F4_H	Hnrnpll	Heterogene	K.QHSVVPSQIFELEDGTSSYK#.D	20.33	8.43	2.41	0.41
Q921F4_H	Hnrnpll	Heterogene	R.SMPLSTEGGGSHHK#.V	16.65	4.60	3.62	0.28
Q921F4_H	Hnrnpll	Heterogene	K.TDAVEALTALNHYQIR.V	18.44	34.33	0.54	1.86
Q921F4_H	Hnrnpll	Heterogene	K.TIPGTALVEM*GDEYAVER.A	11.61	17.51	0.66	1.51
Q921F4_H	Hnrnpll	Heterogene	K.TIPGTALVEMGDEYAVER.A	8.53	17.25	0.49	2.02
Q921F4_H	Hnrnpll	Heterogene	K.TLSGLLEWK#.C	86.45	31.04	2.79	0.36
Q921F4_H	Hnrnpll	Heterogene	K.YK#VFDAK#.A	24.48	13.32	1.84	0.54
Q921F4_H	Hnrnpll	Heterogene	K.TIPGTALVEM*GDEYAVER.A	1.77	3.66	0.48	2.07
Q9D0E1_H	Hnrnpm	Heterogene	K.AAEVLNK#.H	181.60	178.84	1.02	0.98
Q9D0E1_H	Hnrnpm	Heterogene	R.ADILEDK#DGK#.S	77.32	95.90	0.81	1.24
Q9D0E1_H	Hnrnpm	Heterogene	R.AFITNIPFDVK#.W	169.83	187.58	0.91	1.10
Q9D0E1_H	Hnrnpm	Heterogene	K.EKVGEVTYVELLM*DAEGK.S	10.01	15.96	0.63	1.60
Q9D0E1_H	Hnrnpm	Heterogene	K.EKVGEVTYVELLMDAEGK.S	12.97	13.13	0.99	1.01
Q9D0E1_H	Hnrnpm	Heterogene	K.EVFSM*AGVVVR.A	3.34	18.17	0.18	5.43
Q9D0E1_H	Hnrnpm	Heterogene	R.FEPYSNPTK.R	36.36	53.70	0.68	1.48
Q9D0E1_H	Hnrnpm	Heterogene	K.FESPEVAER.A	40.02	129.86	0.31	3.24
Q9D0E1_H	Hnrnpm	Heterogene	K.GDFFPPERPQQLPHGLGGIGM*GLGPGGQPIDANHLSK.G	5.99	22.64	0.26	3.78
Q9D0E1_H	Hnrnpm	Heterogene	K.GDFFPPERPQQLPHGLGGIGMGLGPGGQPIDANHLSK.G	1.74	6.89	0.25	3.95
Q9D0E1_H	Hnrnpm	Heterogene	R.GGNRFEPYSNPTKR.Y	1.67	52.69	0.03	31.63
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGM*GNLGPAGM*GM*EGIGFGINK.I	17.45	16.35	1.07	0.94
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGM*GNLGPAGMGM*EGIGFGINK.I	8.73	9.22	0.95	1.06
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGM*GNLGPAGM*GMEGIGFGINK.I	12.26	10.70	1.15	0.87
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGM*GNLGPAGMGMEGIGFGINK.I	4.20	5.59	0.75	1.33
Q9D0E1_H	Hnrnpm	Heterogene	R.GNFGGSFAGSFGGAGGHAPGVAR.K	20.18	85.85	0.24	4.25
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGM*EGPFGGGM*ENM*GR.F	5.34	28.32	0.19	5.30
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGM*EGPFGGGM*ENMGR.F	2.59	6.01	0.43	2.32
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGMEGPFGGGM*ENM*GR.F	2.08	10.40	0.20	5.01
Q9D0E1_H	Hnrnpm	Heterogene	R.INEILSNALK.R	181.12	206.32	0.88	1.14
Q9D0E1_H	Hnrnpm	Heterogene	R.ISGAGM*ER.M	5.29	16.45	0.32	3.11
Q9D0E1_H	Hnrnpm	Heterogene	R.ISGAGMER.M	11.51	62.66	0.18	5.44
Q9D0E1_H	Hnrnpm	Heterogene	R.LGSTVFVANLDYK#.V	127.79	127.85	1.00	1.00
Q9D0E1_H	Hnrnpm	Heterogene	K.LKEVFSM*AGVVVR.A	11.66	39.28	0.30	3.37
Q9D0E1_H	Hnrnpm	Heterogene	K.LKEVFSMAGVVVR.A	3.34	15.86	0.21	4.74
Q9D0E1_H	Hnrnpm	Heterogene	R.M*AAPIDR.V	14.83	109.09	0.14	7.35
Q9D0E1_H	Hnrnpm	Heterogene	R.MATGLER.M	11.10	45.82	0.24	4.13
Q9D0E1_H	Hnrnpm	Heterogene	R.MGAGLGHGM*DR.V	3.15	12.02	0.26	3.82
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GAGM*GFGLER.M	26.83	131.16	0.20	4.89
Q9D0E1_H	Hnrnpm	Heterogene	R.MGAGMGFGLER.M	3.80	21.44	0.18	5.65
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GANNLER.M	6.49	29.43	0.22	4.53
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GANSLER.M	9.94	58.77	0.17	5.91
Q9D0E1_H	Hnrnpm	Heterogene	R.MGANSLER.M	8.72	53.27	0.16	6.11
Q9D0E1_H	Hnrnpm	Heterogene	R.MGLAM*GGAGGASFDR.A	3.37	27.25	0.12	8.08
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GLAMGGAGGASFDR.A	2.86	14.87	0.19	5.20
Q9D0E1_H	Hnrnpm	Heterogene	R.MGLAMGGAGGASFDR.A	3.14	11.30	0.28	3.60
Q9D0E1_H	Hnrnpm	Heterogene	R.MGLVM*DR.M	6.36	24.07	0.26	3.79
Q9D0E1_H	Hnrnpm	Heterogene	R.MGPAIER.M	23.88	146.98	0.16	6.16
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPAIER.M	23.76	121.01	0.20	5.09
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPAM*GPALGAGIER.M	29.81	165.60	0.18	5.56
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPAMGPALGAGIER.M	2.24	25.34	0.09	11.32
Q9D0E1_H	Hnrnpm	Heterogene	R.MGPGIDR.I	10.74	74.03	0.15	6.89
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPGIDR.I	60.45	79.15	0.76	1.31
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPLGLDHM*ASSIER.M	3.82	14.56	0.26	3.81
Q9D0E1_H	Hnrnpm	Heterogene	R.M*VPTGM*GASLER.M	11.69	56.79	0.21	4.86
Q9D0E1_H	Hnrnpm	Heterogene	R.MVPTGMGASLER.M	4.61	18.70	0.25	4.06
Q9D0E1_H	Hnrnpm	Heterogene	R.NLPFDFTWK.M	105.02	122.05	0.86	1.16
Q9D0E1_H	Hnrnpm	Heterogene	K.QGGGGAGGSVPGIER.M	25.72	125.74	0.20	4.89
Q9D0E1_H	Hnrnpm	Heterogene	K.VGEVTYVELLM*DAEGK.S	23.26	19.42	1.20	0.84
Q9D0E1_H	Hnrnpm	Heterogene	K.VGEVTYVELLMDAEGK#.S	14.25	15.40	0.93	1.08
Q9D0E1_H	Hnrnpm	Heterogene	R.VGQTIER.M	16.59	92.51	0.18	5.58
Q9D0E1_H	Hnrnpm	Heterogene	R.VGSEIER.M	23.79	133.77	0.18	5.62
Q9D0E1_H	Hnrnpm	Heterogene	K.VKEDPDGEHAR.R	1.65	3.78	0.44	2.29
Q9D0E1_H	Hnrnpm	Heterogene	K.AAEVLNK#.H	188.80	197.79	0.95	1.05
Q9D0E1_H	Hnrnpm	Heterogene	R.ADILEDKDGK.S	183.93	205.67	0.89	1.12
Q9D0E1_H	Hnrnpm	Heterogene	R.AFITNIPFDVK#.W	546.68	556.68	0.98	1.02
Q9D0E1_H	Hnrnpm	Heterogene	K.EK#VGEVTYVELLM*DAEGK#.S	33.76	34.62	0.98	1.03
Q9D0E1_H	Hnrnpm	Heterogene	K.EKVGEVTYVELLMDAEGK.S	60.47	58.24	1.04	0.96
Q9D0E1_H	Hnrnpm	Heterogene	K.EVFSM*AGVVVR.A	7.95	31.35	0.25	3.94
Q9D0E1_H	Hnrnpm	Heterogene	K.FESPEVAER.A	71.27	369.05	0.19	5.18
Q9D0E1_H	Hnrnpm	Heterogene	R.FGSGMNMGR.I	11.22	40.17	0.28	3.58
Q9D0E1_H	Hnrnpm	Heterogene	R.FGSGM*NM*GR.I	16.19	61.94	0.26	3.83
Q9D0E1_H	Hnrnpm	Heterogene	K.GDFFPPERPQQLPHGLGGIGM*GLGPGGQPIDANHLSK.G	4.35	20.54	0.21	4.72
Q9D0E1_H	Hnrnpm	Heterogene	K.GDFFPPERPQQLPHGLGGIGMGLGPGGQPIDANHLSK.G	3.05	10.43	0.29	3.42
Q9D0E1_H	Hnrnpm	Heterogene	K.GEERPTQNEK.R	1.47	9.81	0.15	6.65
Q9D0E1_H	Hnrnpm	Heterogene	R.GGNRFEPYSNPTK.R	11.83	64.77	0.18	5.48
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGM*GNLGPAGM*GM*EGIGFGINK.I	121.48	113.08	1.07	0.93
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGM*GNLGPAGMGM*EGIGFGINK#.I	22.16	20.18	1.10	0.91
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGMGNLGPAGM*GM*EGIGFGINK#.I	27.47	28.20	0.97	1.03

Q9D0E1_H	Hnrnpm	Heterogene	K.GIGMGNLGPAGM*GM*EGIGFGINK.I	12.28	11.47	1.07	0.93
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGM*GNLGPAGM*GMEGIGFGINK#.I	11.83	10.27	1.15	0.87
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGMGNLGPAGMGM*EGIGFGINK.I	5.38	7.47	0.72	1.39
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGMGNLGPAGM*GMEGIGFGINK.I	16.81	18.59	0.90	1.11
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGMGNLGPAGM*GMEGIGFGINK#.I	8.34	9.06	0.92	1.09
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGM*GNLGPAGMGMEGIGFGINK.I	16.81	18.59	0.90	1.11
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGMGNLGPAGMGMEGIGFGINK.I	12.40	13.75	0.90	1.11
Q9D0E1_H	Hnrnpm	Heterogene	K.GIGMGNLGPAGMGMEGIGFGINK#.I	7.01	6.90	1.02	0.99
Q9D0E1_H	Hnrnpm	Heterogene	R.GNFGGSFAGSFGGAGGHAPGVAR.K	76.04	357.60	0.21	4.70
Q9D0E1_H	Hnrnpm	Heterogene	K.HSLSGRPLK.V	13.15	76.69	0.17	5.83
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGM*EGPFGGGM*ENM*GR.F	20.82	106.11	0.20	5.10
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGM*EGPFGGGM*ENMGR.F	3.42	16.40	0.21	4.79
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGM*EGPFGGGMENM*GR.F	2.98	14.60	0.20	4.89
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGMEGPFGGGM*ENM*GR.F	5.61	26.72	0.21	4.76
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGMEGPFGGGM*ENMGR.F	2.03	7.66	0.26	3.78
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGM*EGPFGGGMENMGR.F	2.25	7.66	0.29	3.40
Q9D0E1_H	Hnrnpm	Heterogene	K.IGGMEGPFGGGMENM*GR.F	1.44	6.28	0.23	4.35
Q9D0E1_H	Hnrnpm	Heterogene	R.IGSGVER.M	33.48	178.88	0.19	5.34
Q9D0E1_H	Hnrnpm	Heterogene	R.INEILSNALK#.R	478.56	454.81	1.05	0.95
Q9D0E1_H	Hnrnpm	Heterogene	R.ISGAGM*ER.M	11.62	49.09	0.24	4.23
Q9D0E1_H	Hnrnpm	Heterogene	K.K#AAEVLNK#.H	27.85	34.75	0.80	1.25
Q9D0E1_H	Hnrnpm	Heterogene	R.LGSTVFVANLDYK#.V	366.22	359.80	1.02	0.98
Q9D0E1_H	Hnrnpm	Heterogene	K.LKEVFSM*AGVVVR.A	23.15	96.85	0.24	4.18
Q9D0E1_H	Hnrnpm	Heterogene	K.LKEVFSMAGVVVR.A	11.33	62.43	0.18	5.51
Q9D0E1_H	Hnrnpm	Heterogene	R.M*AAPIDR.V	60.34	323.55	0.19	5.36
Q9D0E1_H	Hnrnpm	Heterogene	R.M*ATGLER.M	28.87	131.97	0.22	4.57
Q9D0E1_H	Hnrnpm	Heterogene	R.MGAGLGHGMDR.V	2.35	17.16	0.14	7.29
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GAGLGHGM*DR.V	10.41	39.38	0.26	3.78
Q9D0E1_H	Hnrnpm	Heterogene	R.MGAGLGHGM*DR.V	2.77	20.26	0.14	7.32
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GAGM*GFGLER.M	40.92	199.82	0.20	4.88
Q9D0E1_H	Hnrnpm	Heterogene	R.MGAGM*GFGLER.M	15.82	70.03	0.23	4.43
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GAGMGFGLER.M	7.84	38.04	0.21	4.85
Q9D0E1_H	Hnrnpm	Heterogene	R.MGAGMGFGLER.M	6.57	38.26	0.17	5.82
Q9D0E1_H	Hnrnpm	Heterogene	R.MGANNLER.M	28.73	113.64	0.25	3.96
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GANNLER.M	14.86	72.93	0.20	4.91
Q9D0E1_H	Hnrnpm	Heterogene	R.MGANSLER.M	45.66	199.30	0.23	4.37
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GANSLER.M	49.25	214.49	0.23	4.35
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GLAM*GGAGGASFDR.A	53.32	227.34	0.23	4.26
Q9D0E1_H	Hnrnpm	Heterogene	R.MGLAM*GGAGGASFDR.A	20.68	81.40	0.25	3.94
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GLAMGGAGGASFDR.A	6.78	28.24	0.24	4.16
Q9D0E1_H	Hnrnpm	Heterogene	R.MGLAMGGAGGASFDR.A	6.06	29.12	0.21	4.81
Q9D0E1_H	Hnrnpm	Heterogene	R.MGLSM*DR.M	6.06	27.97	0.22	4.61
Q9D0E1_H	Hnrnpm	Heterogene	R.MGLSMDR.M	6.40	34.06	0.19	5.32
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GLSM*DR.M	11.30	42.62	0.27	3.77
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GLVM*DR.M	16.27	98.36	0.17	6.05
Q9D0E1_H	Hnrnpm	Heterogene	R.MGLVM*DR.M	12.86	58.47	0.22	4.55
Q9D0E1_H	Hnrnpm	Heterogene	R.MGLVMDR.M	7.40	37.14	0.20	5.02
Q9D0E1_H	Hnrnpm	Heterogene	R.MGPAIER.M	45.73	257.46	0.18	5.63
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPAIER.M	60.93	273.32	0.22	4.49
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPAM*GPALGAGIER.M	75.41	371.86	0.20	4.93
Q9D0E1_H	Hnrnpm	Heterogene	R.MGPAM*GPALGAGIER.M	14.91	64.10	0.23	4.30
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPAMGPALGAGIER.M	11.11	58.87	0.19	5.30
Q9D0E1_H	Hnrnpm	Heterogene	R.MGPAMGPALGAGIER.M	9.76	48.00	0.20	4.92
Q9D0E1_H	Hnrnpm	Heterogene	R.MGPGIDR.I	24.18	114.51	0.21	4.74
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPGIDR.I	72.85	300.67	0.24	4.13
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPLGLDHM*ASSIER.M	53.72	259.81	0.21	4.84
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GPVM*DR.M	12.07	57.34	0.21	4.75
Q9D0E1_H	Hnrnpm	Heterogene	R.M*GSSIER.M	10.65	48.69	0.22	4.57
Q9D0E1_H	Hnrnpm	Heterogene	R.MGSSIER.M	15.30	82.20	0.19	5.37
Q9D0E1_H	Hnrnpm	Heterogene	R.M*VPTGM*GASLER.M	43.71	189.40	0.23	4.33
Q9D0E1_H	Hnrnpm	Heterogene	R.M*VPTGMGASLER.M	9.27	42.81	0.22	4.62
Q9D0E1_H	Hnrnpm	Heterogene	R.NLPFDFTWK#.M	405.66	441.06	0.92	1.09
Q9D0E1_H	Hnrnpm	Heterogene	K.QGGGGAGGSVPGIER.M	104.25	501.61	0.21	4.81
Q9D0E1_H	Hnrnpm	Heterogene	K.VGEVTYVELLM*DAEGK#.S	74.81	70.10	1.07	0.94
Q9D0E1_H	Hnrnpm	Heterogene	K.VGEVTYVELLM*DAEGK.S	25.00	27.56	0.91	1.10
Q9D0E1_H	Hnrnpm	Heterogene	K.VGEVTYVELLMDAEGK#.S	70.80	63.91	1.11	0.90
Q9D0E1_H	Hnrnpm	Heterogene	R.VGQTIER.M	70.43	342.94	0.21	4.87
Q9D0E1_H	Hnrnpm	Heterogene	R.VGSEIER.M	84.62	430.46	0.20	5.09
Q9D0E1_H	Hnrnpm	Heterogene	K.VKEDPDGEHAR.R	2.43	8.88	0.27	3.66
Q9D0E1_H	Hnrnpm	Heterogene	K.WQSLKDLVK.E	22.71	28.73	0.79	1.26
Q8VHM5_	Hnrnpr	Heterogene	R.LM*M*DPLSGQNR.G	2.84	7.48	0.38	2.63
Q8VHM5_	Hnrnpr	Heterogene	R.NLATTVTEEILEK#.S	24.28	17.18	1.41	0.71
Q8VHM5_	Hnrnpr	Heterogene	K.VQESTK#GPDEAK#.I	4.07	2.45	1.66	0.60
Q8VHM5_	Hnrnpr	Heterogene	R.DLYEDELVPLFEK#.A	24.11	17.65	1.37	0.73
Q8VHM5_	Hnrnpr	Heterogene	R.K#YGGPPPDSVYSGVQPGIGTEVFVGK#.I	12.06	6.78	1.78	0.56
Q8VHM5_	Hnrnpr	Heterogene	R.LM*M*DPLSGQNR.G	4.15	11.56	0.36	2.79
Q8VHM5_	Hnrnpr	Heterogene	R.NLATTVTEEILEK#.S	57.49	40.29	1.43	0.70
Q8VHM5_	Hnrnpr	Heterogene	K.TLIEAGLPQK#.V	22.45	11.16	2.01	0.50
Q8VHM5_	Hnrnpr	Heterogene	K.VQESTK#GPDEAK#.I	5.69	4.08	1.39	0.72
Q8VEK3_H	Hnrnpu	Heterogene	R.GYFEYIEENK#.Y	16.53	5.42	3.05	0.33
Q8VEK3_H	Hnrnpu	Heterogene	K.LLEQYK#EESK#.K	26.36	12.68	2.08	0.48
Q8VEK3_H	Hnrnpu	Heterogene	K.MM*VAGFK#.K	17.39	6.43	2.70	0.37
Q8VEK3_H	Hnrnpu	Heterogene	K.NGQDLGVAFK#.I	56.52	13.07	4.32	0.23
Q8VEK3_H	Hnrnpu	Heterogene	K.YNILGTNTIM*DK#.M	68.03	21.07	3.23	0.31
Q8VEK3_H	Hnrnpu	Heterogene	K.YNILGTNTIMDK#.M	32.83	11.86	2.77	0.36
Q8VEK3_H	Hnrnpu	Heterogene	K.DLPEHAVLK#.M	50.06	21.80	2.30	0.44
Q8VEK3_H	Hnrnpu	Heterogene	R.NFILDQTNVSAAAQR.R	5.34	10.46	0.51	1.96
Q8VEK3_H	Hnrnpu	Heterogene	K.DIDIHEVR.I	102.57	143.47	0.71	1.40
Q8VEK3_H	Hnrnpu	Heterogene	K.DLPEHAVLK#.M	786.16	179.12	4.39	0.23
Q8VEK3_H	Hnrnpu	Heterogene	R.DRLSASSLTM*ESFAFLWAGGR.A	8.59	36.58	0.23	4.26
Q8VEK3_H	Hnrnpu	Heterogene	K.FIEIAAR.K	196.40	257.62	0.76	1.31
Q8VEK3_H	Hnrnpu	Heterogene	R.GYFEYIEENK#.Y	268.63	77.72	3.46	0.29
Q8VEK3_H	Hnrnpu	Heterogene	K.HAAENPGK#.Y	19.95	8.98	2.22	0.45
Q8VEK3_H	Hnrnpu	Heterogene	K.HAAENPGK#YNILGTNTIM*DK#.M	40.68	12.11	3.36	0.30
Q8VEK3_H	Hnrnpu	Heterogene	K.HAAENPGK#YNILGTNTIMDK#.M	28.92	7.58	3.81	0.26
Q8VEK3_H	Hnrnpu	Heterogene	R.IGWSLTTSGM*LLGEEEFSYGYSLK#.G	4.43	3.15	1.41	0.71
Q8VEK3_H	Hnrnpu	Heterogene	R.IGWSLTTSGM*LLGEEEFSYGYSLK#.G	23.06	8.36	2.76	0.36
Q8VEK3_H	Hnrnpu	Heterogene	R.IGWSLTTSGMLLGEEEFSYGYSLK#.G	13.99	2.86	4.90	0.20
Q8VEK3_H	Hnrnpu	Heterogene	K.LK#VSELK#EELK#.K	73.35	13.56	5.41	0.18
Q8VEK3_H	Hnrnpu	Heterogene	K.LLEQYK#EESK#.K	154.35	60.26	2.56	0.39
Q8VEK3_H	Hnrnpu	Heterogene	K.LLEQYK#EESK#K#.A	209.84	58.50	3.59	0.28
Q8VEK3_H	Hnrnpu	Heterogene	K.LNTLLQR.A	179.20	263.38	0.68	1.47
Q8VEK3_H	Hnrnpu	Heterogene	R.LQAALDNEAGGRPAM*EPGNGSLDLGGDAAGR.S	9.77	25.96	0.38	2.66

Q8VEK3_H	Hnrnpu	Heterogen	R.LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR.S	6.73	18.58	0.36	2.76
Q8VEK3_H	Hnrnpu	Heterogen	R.LSASSLTM*ESFAFLWAGGR.A	39.59	54.14	0.73	1.37
Q8VEK3_H	Hnrnpu	Heterogen	K.M*M*VAGFK#.K	173.25	56.26	3.08	0.32
Q8VEK3_H	Hnrnpu	Heterogen	K.MM*VAGFK#.K	62.67	26.20	2.39	0.42
Q8VEK3_H	Hnrnpu	Heterogen	K.MMVAGFK#.K	84.97	26.84	3.17	0.32
Q8VEK3_H	Hnrnpu	Heterogen	K.M*MVAGFK#K#.Q	30.20	8.17	3.70	0.27
Q8VEK3_H	Hnrnpu	Heterogen	K.MM*VAGFK#K#.Q	39.54	22.41	1.76	0.57
Q8VEK3_H	Hnrnpu	Heterogen	R.NFILDQTNVSAAAQR.R	145.95	204.28	0.71	1.40
Q8VEK3_H	Hnrnpu	Heterogen	K.NGQDLGVAFK#.I	444.84	127.39	3.49	0.29
Q8VEK3_H	Hnrnpu	Heterogen	R.QGQQQAGGDGK#.T	5.78	2.36	2.45	0.41
Q8VEK3_H	Hnrnpu	Heterogen	R.QGQQQAGGDGK#TEQK#.G	11.95	4.72	2.53	0.40
Q8VEK3_H	Hnrnpu	Heterogen	K.RNFILDQTNVSAAAQR.R	3.56	22.97	0.16	6.45
Q8VEK3_H	Hnrnpu	Heterogen	K.SSGPTSLFAVTVAPPGAR.Q	131.95	210.46	0.63	1.59
Q8VEK3_H	Hnrnpu	Heterogen	K.VSELK#EELK#.K	206.08	74.10	2.78	0.36
Q8VEK3_H	Hnrnpu	Heterogen	K.VSELK#EELK#K#.R	495.38	120.91	4.10	0.24
Q8VEK3_H	Hnrnpu	Heterogen	K.VTEKIPVR.H	19.53	34.00	0.57	1.74
Q8VEK3_H	Hnrnpu	Heterogen	K.YNILGTNTIM*DK#.M	485.53	143.91	3.37	0.30
Q8VEK3_H	Hnrnpu	Heterogen	K.YNILGTNTIMDK#.M	249.24	79.28	3.14	0.32
Q8VEK3_H	Hnrnpu	Heterogen	K.DIDIHEVR.I	29.40	37.65	0.78	1.28
Q8VEK3_H	Hnrnpu	Heterogen	R.GYFEYIEENK#.Y	47.25	14.28	3.31	0.30
Q8VEK3_H	Hnrnpu	Heterogen	K.HAAENPGK#YNILGTNTIM*DK#.M	7.44	2.16	3.44	0.29
Q8VEK3_H	Hnrnpu	Heterogen	R.LQAALDNEAGGRPAM*EPGNGSLDLGGDAAGR.S	1.91	5.38	0.35	2.82
Q8VEK3_H	Hnrnpu	Heterogen	R.LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR.S	1.69	2.83	0.60	1.67
Q8VEK3_H	Hnrnpu	Heterogen	K.M*M*VAGFK#.K	34.06	9.06	3.76	0.27
Q8VEK3_H	Hnrnpu	Heterogen	R.NFILDQTNVSAAAQR.R	36.93	51.03	0.72	1.38
Q8VEK3_H	Hnrnpu	Heterogen	K.NGQDLGVAFK#.I	75.14	22.88	3.28	0.30
Q8VEK3_H	Hnrnpu	Heterogen	K.SSGPTSLFAVTVAPPGAR.Q	28.51	56.84	0.50	1.99
Q8VEK3_H	Hnrnpu	Heterogen	K.VSELK#EELK#.K	27.13	8.95	3.03	0.33
Q8VEK3_H	Hnrnpu	Heterogen	K.YNILGTNTIM*DK#.M	91.02	29.87	3.05	0.33
Q8VEK3_H	Hnrnpu	Heterogen	K.YNILGTNTIMDK#.M	34.12	11.24	3.04	0.33
Q8VDM6_	Hnrnpul1	Heterogen	K.HLPSTEPDPHVVR.I	14.29	52.09	0.27	3.65
Q8VDM6_	Hnrnpul1	Heterogen	K.QEAPPSFLPPEASQLK#.T	6.06	3.51	1.73	0.58
Q8VDM6_	Hnrnpul1	Heterogen	R.TDEEGK#DVPDHAVLEMK#.A	8.92	41.78	0.21	4.68
Q8VDM6_	Hnrnpul1	Heterogen	K.TEM*KQEAPPSFLPPEASQLK.T	8.31	8.17	1.02	0.98
Q8VDM6_	Hnrnpul1	Heterogen	K.YNILGTNAIM*DK#.M	24.89	19.48	1.28	0.78
Q00PI9_H	Hnrnpul2	Heterogen	K.ANFSLPEK#.C	62.18	44.88	1.39	0.72
Q00PI9_H	Hnrnpul2	Heterogen	K.AVEEQGDDQDSEK#.S	13.17	8.42	1.56	0.64
Q00PI9_H	Hnrnpul2	Heterogen	R.AYYEFR.E	24.34	51.58	0.47	2.12
Q00PI9_H	Hnrnpul2	Heterogen	K.DRYGGQPLFSEK.F	4.92	14.28	0.34	2.90
Q00PI9_H	Hnrnpul2	Heterogen	K.EVEGDDVPESIMLEMK#.A	7.74	6.41	1.21	0.83
Q00PI9_H	Hnrnpul2	Heterogen	K.FPTLWSGAR.S	36.09	99.43	0.36	2.75
Q00PI9_H	Hnrnpul2	Heterogen	K.GLEEPEMDPK#.S	17.26	10.80	1.60	0.63
Q00PI9_H	Hnrnpul2	Heterogen	R.K#LLLFK#.T	33.90	21.70	1.56	0.64
Q00PI9_H	Hnrnpul2	Heterogen	R.KVVVVVPNEEDWKR.R	25.90	76.79	0.34	2.96
Q00PI9_H	Hnrnpul2	Heterogen	R.LKVTELR.S	11.74	27.84	0.42	2.37
Q00PI9_H	Hnrnpul2	Heterogen	K.LVQIASR.S	82.76	213.08	0.39	2.57
Q00PI9_H	Hnrnpul2	Heterogen	K.NGEDLGVAFR.I	17.85	64.76	0.28	3.63
Q00PI9_H	Hnrnpul2	Heterogen	R.NYYGYQGYR.-	37.48	74.53	0.50	1.99
Q00PI9_H	Hnrnpul2	Heterogen	R.RYNVLGAETVLTQM*R.M	1.35	16.71	0.08	12.35
Q00PI9_H	Hnrnpul2	Heterogen	R.SGDETPGSEAPGDK#.A	33.61	28.14	1.19	0.84
Q00PI9_H	Hnrnpul2	Heterogen	R.SGDETPGSEAPGDKAVEEQGDDQDSEK.S	76.50	53.29	1.44	0.70
Q00PI9_H	Hnrnpul2	Heterogen	K.TQWALK#.Y	144.51	61.37	2.35	0.42
Q00PI9_H	Hnrnpul2	Heterogen	K.VTQNLPM*K#.E	36.37	28.27	1.29	0.78
Q00PI9_H	Hnrnpul2	Heterogen	K.VVVVVPNEEDWK#.R	15.87	9.01	1.76	0.57
Q00PI9_H	Hnrnpul2	Heterogen	R.YGGQPLFSEK#.F	80.41	66.84	1.20	0.83
Q00PI9_H	Hnrnpul2	Heterogen	R.YNVLGAETVLTQM*R.M	18.20	47.42	0.38	2.61
Q00PI9_H	Hnrnpul2	Heterogen	R.YNVLGAETVLTQMR.M	17.66	39.91	0.44	2.26
Q00PI9_H	Hnrnpul2	Heterogen	R.YRDYYR.Q	2.15	19.82	0.11	9.21
Q00PI9_H	Hnrnpul2	Heterogen	K.AVEEQGDDQDSEK#.S	3.42	1.58	2.17	0.46
Q00PI9_H	Hnrnpul2	Heterogen	K.FPTLWSGAR.S	7.18	17.83	0.40	2.48
Q00PI9_H	Hnrnpul2	Heterogen	R.KVVVVVPNEEDWKR.R	2.99	11.72	0.25	3.92
Q00PI9_H	Hnrnpul2	Heterogen	R.SGDETPGSEAPGDK.A	12.85	9.31	1.38	0.72
Q00PI9_H	Hnrnpul2	Heterogen	R.YNVLGAETVLTQM*R.M	6.12	15.19	0.40	2.48
Q99JP6_H	Homer3	Homer pro	R.ANTVYGLGFASEQQLTQFAEK#.F	7.54	3.67	2.05	0.49
Q8BUK6_H	Hook3	Protein Ho	R.HLQLQTQLEQLQEETFR.L	3.65	10.03	0.36	2.75
Q8BUK6_H	Hook3	Protein Ho	R.IEELQEALR.K	8.07	21.55	0.37	2.67
Q8BUK6_H	Hook3	Protein Ho	R.LASTGSGQSFLAR.Q	7.97	19.02	0.42	2.39
Q8BUK6_H	Hook3	Protein Ho	R.LLEVQSQVEELQK#.S	30.73	14.03	2.19	0.46
Q8BUK6_H	Hook3	Protein Ho	K.LNQEDSDNEKIALLQSLLDDANLR.K	3.68	6.73	0.55	1.83
Q8BUK6_H	Hook3	Protein Ho	R.LNQSDSIEDPNSPAGR.R	6.15	14.79	0.42	2.40
Q8BUK6_H	Hook3	Protein Ho	K.QNQGAAPEIQALK#.N	16.86	8.85	1.90	0.53
Q8BUK6_H	Hook3	Protein Ho	R.QQNDELTTLADEAQSLKDEIDVLR.H	4.51	8.96	0.50	1.99
Q8BUK6_H	Hook3	Protein Ho	K.TTEELNEALSAK#.E	13.89	6.84	2.03	0.49
Q3TEA8_H	Hp1bp3	Heterochr	K.GASGSFVVVQK#.S	29.24	15.08	1.94	0.52
Q3TEA8_H	Hp1bp3	Heterochr	R.GQLEQITGK#.G	53.35	30.21	1.77	0.57
Q3TEA8_H	Hp1bp3	Heterochr	R.K#YVSQYYPK#.L	16.89	9.74	1.73	0.58
Q3TEA8_H	Hp1bp3	Heterochr	K.LEDVLPLAFTR.L	11.46	28.70	0.40	2.50
Q3TEA8_H	Hp1bp3	Heterochr	K.GASGSFVVVQK#.S	129.49	55.62	2.33	0.43
Q3TEA8_H	Hp1bp3	Heterochr	K.GK#GASGSFVVVQK#.S	57.72	27.03	2.14	0.47
Q3TEA8_H	Hp1bp3	Heterochr	R.GQLEQITGK#.G	199.00	94.29	2.11	0.47
Q3TEA8_H	Hp1bp3	Heterochr	K.KGSALDPEPQVK.L	16.33	9.55	1.71	0.59
Q3TEA8_H	Hp1bp3	Heterochr	R.K#YVSQYYPK#.L	63.54	33.78	1.88	0.53
Q3TEA8_H	Hp1bp3	Heterochr	K.LEDVLPLAFTR.L	61.43	139.19	0.44	2.27
Q3TEA8_H	Hp1bp3	Heterochr	K.M*DAILTEAIK#.A	80.61	47.73	1.69	0.59
Q3TEA8_H	Hp1bp3	Heterochr	K.MDAILTEAIK#.A	68.85	32.06	2.15	0.47
Q3TEA8_H	Hp1bp3	Heterochr	K.NGWLEQISGK#.G	25.37	14.73	1.72	0.58
Q3TEA8_H	Hp1bp3	Heterochr	K.SGEKPLLGGSLM*EYAILSAIAAM*NEPK.T	17.97	9.40	1.91	0.52
Q3TEA8_H	Hp1bp3	Heterochr	K.TGASVVAIR.K	35.03	80.49	0.44	2.30
Q3TEA8_H	Hp1bp3	Heterochr	K.TIPAWATLSASQLAR.A	19.76	47.76	0.41	2.42
Q3TEA8_H	Hp1bp3	Heterochr	K.YPSLGLER.R	24.12	61.66	0.39	2.56
Q3TEA8_H	Hp1bp3	Heterochr	K.YVLENHPGANSNYQMHLLK#.K	18.99	18.72	1.01	0.99
Q3TEA8_H	Hp1bp3	Heterochr	K.YVSQYYPK#.L	52.65	25.48	2.07	0.48
Q3TEA8_H	Hp1bp3	Heterochr	K.LEDVLPLAFTR.L	4.15	11.88	0.35	2.87
P62748_H	Hpcal1	Hippocalci	K.IYANFFPYGDASK#.F	11.97	5.38	2.23	0.45
P62748_H	Hpcal1	Hippocalci	K.LSLEEFIK#.G	14.50	7.21	2.01	0.50
Q8VCC1_P	Hpgd	15-hydroxy	K.EENMGQYIEYK#.D	27.69	10.68	2.59	0.39
Q9CQZ1_H	Hsbp1	Heat shock	K.NIADLM*TQAGVEELDPENK#IPTAQK#.S	2.58	4.31	0.60	1.67
Q99N15_Q	Hsd17b10	17beta-hyd	K.GLVAVVTGGASGLGLATAK#.R	15.95	1.96	8.13	0.12
Q99N15_Q	Hsd17b10	17beta-hyd	R.GVIINTASVAAFEGQVGQAAYSASK#.G	27.54	2.88	9.57	0.10
Q99N15_Q	Hsd17b10	17beta-hyd	R.LVGQGATAVLLDVPDSEGEAQAK#.K	44.61	6.90	6.46	0.15
P51660_D	Hsd17b4	Peroxisom	K.AVANYDSVEAGEK#.L	112.52	71.94	1.56	0.64
P51660_D	Hsd17b4	Peroxisom	R.GALVIVNDLGGDFK#.G	15.98	5.22	3.06	0.33
P07901_H	Hsp90aa1	Heat shock	K.ADLINNLGTIAK#.S	156.22	27.07	5.77	0.17

P07901_H	Hsp90aa1	Heat shock	K.EDQTEYLEER.R	15.59	13.19	1.18	0.85
P07901_H	Hsp90aa1	Heat shock	K.EK#YIDQEELNK#.T	8.85	1.28	6.90	0.14
P07901_H	Hsp90aa1	Heat shock	K.HIYFITGETK#.D	30.68	5.66	5.42	0.18
P07901_H	Hsp90aa1	Heat shock	K.HLEINPDHSIIETLR@.Q	57.72	7.40	7.80	0.13
P07901_H	Hsp90aa1	Heat shock	K.HNDDEQYAWESSAGGSFTVR.T	5.25	5.37	0.98	1.02
P07901_H	Hsp90aa1	Heat shock	K.HSQFIGYPITLFVEK#.E	7.59	2.30	3.30	0.30
P07901_H	Hsp90aa1	Heat shock	R.NPDDITNEEYGEFYK#.S	25.85	4.04	6.40	0.16
P07901_H	Hsp90aa1	Heat shock	R.YESLTDPSK#.L	26.22	7.42	3.53	0.28
P07901_H	Hsp90aa1	Heat shock	K.YIDQEELNK#.T	253.05	63.56	3.98	0.25
P07901_H	Hsp90aa1	Heat shock	K.ADLINNLGTIAK#.S	93.75	27.48	3.41	0.29
P07901_H	Hsp90aa1	Heat shock	R.ELISNSSDALDK#.I	5.43	1.93	2.81	0.36
P07901_H	Hsp90aa1	Heat shock	R.GVVDSEDLPLNISR.E	1.58	3.78	0.42	2.39
P07901_H	Hsp90aa1	Heat shock	R.TLTIVDTGIGM*TK#.A	48.36	15.45	3.13	0.32
P07901_H	Hsp90aa1	Heat shock	R.TLTIVDTGIGMTK#.A	9.30	3.63	2.56	0.39
P07901_H	Hsp90aa1	Heat shock	R.YESLTDPSK#.L	19.99	6.95	2.88	0.35
P07901_H	Hsp90aa1	Heat shock	K.ADLINNLGTIAK#.S	1834.53	342.28	5.36	0.19
P07901_H	Hsp90aa1	Heat shock	K.AEADK#NDK#.S	6.85	1.27	5.38	0.19
P07901_H	Hsp90aa1	Heat shock	K.AFM*EALQAGADISM*IGQFGVGFYSAYLVAEK#.V	2.59	1.60	1.62	0.62
P07901_H	Hsp90aa1	Heat shock	R.ALLFVPR.R	132.27	78.58	1.68	0.59
P07901_H	Hsp90aa1	Heat shock	R.APFDLFENR.K	31.23	17.10	1.83	0.55
P07901_H	Hsp90aa1	Heat shock	R.DNSTMGYM*AAK#.K	42.50	6.19	6.87	0.15
P07901_H	Hsp90aa1	Heat shock	R.DNSTMGYMAAK#.K	34.46	5.26	6.55	0.15
P07901_H	Hsp90aa1	Heat shock	R.DNSTM*GYM*AAK#.K	85.85	14.90	5.76	0.17
P07901_H	Hsp90aa1	Heat shock	K.DQVANSAFVER.L	193.42	122.69	1.58	0.63
P07901_H	Hsp90aa1	Heat shock	K.EDQTEYLEER.R	189.51	160.96	1.18	0.85
P07901_H	Hsp90aa1	Heat shock	K.EGLELPEDEEEK#.K	133.57	28.01	4.77	0.21
P07901_H	Hsp90aa1	Heat shock	K.EK#YIDQEELNK#.T	104.50	27.80	3.76	0.27
P07901_H	Hsp90aa1	Heat shock	R.ELISNSSDALDK#.I	360.02	61.09	5.89	0.17
P07901_H	Hsp90aa1	Heat shock	R.EM*LQQSK#.I	146.35	27.03	5.42	0.18
P07901_H	Hsp90aa1	Heat shock	R.EMLQQSK#.I	220.19	50.59	4.35	0.23
P07901_H	Hsp90aa1	Heat shock	K.FYEQFSK#.N	540.69	66.94	8.08	0.12
P07901_H	Hsp90aa1	Heat shock	R.GVVDSEDLPLNISR.E	272.52	254.96	1.07	0.94
P07901_H	Hsp90aa1	Heat shock	K.HFSVEGQLEFR.A	76.30	69.08	1.10	0.91
P07901_H	Hsp90aa1	Heat shock	K.HIYFITGETK#.D	642.04	80.73	7.95	0.13
P07901_H	Hsp90aa1	Heat shock	K.HLEINPDHSIIETLR@.Q	21.87	18.51	1.18	0.85
P07901_H	Hsp90aa1	Heat shock	K.HNDDEQYAWESSAGGSFTVR.T	25.03	24.99	1.00	1.00
P07901_H	Hsp90aa1	Heat shock	K.HNDDEQYAWESSAGGSFTVR.T	127.11	104.66	1.21	0.82
P07901_H	Hsp90aa1	Heat shock	K.HSQFIGYPITLFVEK#.E	326.85	47.39	6.90	0.14
P07901_H	Hsp90aa1	Heat shock	K.HSQFIGYPITLFVEKER.D	23.79	12.66	1.88	0.53
P07901_H	Hsp90aa1	Heat shock	K.IMK#DILEK#.K	57.40	7.07	8.12	0.12
P07901_H	Hsp90aa1	Heat shock	K.IRYESLTDPSKLDSGK.E	26.27	25.97	1.01	0.99
P07901_H	Hsp90aa1	Heat shock	K.KHLEINPDHSIIETLR.Q	37.79	20.17	1.87	0.53
P07901_H	Hsp90aa1	Heat shock	K.K#HSQFIGYPITLFVEK#.E	51.72	5.70	9.08	0.11
P07901_H	Hsp90aa1	Heat shock	K.LDSGK#ELHINLIPSK#.Q	20.74	1.66	12.50	0.08
P07901_H	Hsp90aa1	Heat shock	K.LGIHEDSQNR.K	66.99	44.29	1.51	0.66
P07901_H	Hsp90aa1	Heat shock	K.LSELLR@.Y	284.23	258.62	1.10	0.91
P07901_H	Hsp90aa1	Heat shock	R.NPDDITNEEYGEFYK#.S	490.08	65.10	7.53	0.13
P07901_H	Hsp90aa1	Heat shock	R.TDTGEPM*GR.G	12.74	7.50	1.70	0.59
P07901_H	Hsp90aa1	Heat shock	R.TLTIVDTGIGM*TK#.A	769.96	179.43	4.29	0.23
P07901_H	Hsp90aa1	Heat shock	R.TLTIVDTGIGMTK#.A	508.21	114.63	4.43	0.23
P07901_H	Hsp90aa1	Heat shock	K.VILHLK#.E	278.48	58.52	4.76	0.21
P07901_H	Hsp90aa1	Heat shock	K.VILHLKEDQTEYLEER.R	160.46	119.65	1.34	0.75
P07901_H	Hsp90aa1	Heat shock	R.YESLTDPSK#.L	622.27	140.69	4.42	0.23
P07901_H	Hsp90aa1	Heat shock	R.YESLTDPSKLDSGK.E	236.21	49.47	4.77	0.21
P07901_H	Hsp90aa1	Heat shock	K.YIDQEELNK#.T	2141.58	418.21	5.12	0.20
P07901_H	Hsp90aa1	Heat shock	R.YYTSASGDEM*VSLK#.D	101.40	14.39	7.05	0.14
P07901_H	Hsp90aa1	Heat shock	R.YYTSASGDEMVSLK#.D	36.89	5.37	6.87	0.15
P07901_H	Hsp90aa1	Heat shock	K.ADLINNLGTIAK#.S	1131.43	216.71	5.22	0.19
P07901_H	Hsp90aa1	Heat shock	K.AEADKNDKSVK.D	17.11	8.78	1.95	0.51
P07901_H	Hsp90aa1	Heat shock	R.ALLFVPR.R	53.33	29.41	1.81	0.55
P07901_H	Hsp90aa1	Heat shock	R.DNSTM*GYM*AAK#.K	70.75	8.33	8.49	0.12
P07901_H	Hsp90aa1	Heat shock	K.DQVANSAFVER.L	101.24	48.46	2.09	0.48
P07901_H	Hsp90aa1	Heat shock	K.EDQTEYLEER.R	61.73	60.10	1.03	0.97
P07901_H	Hsp90aa1	Heat shock	K.EGLELPEDEEEK#.K	135.80	30.84	4.40	0.23
P07901_H	Hsp90aa1	Heat shock	R.ELISNSSDALDK#.I	183.39	17.32	10.59	0.09
P07901_H	Hsp90aa1	Heat shock	R.EM*LQQSK#.I	84.91	14.85	5.72	0.17
P07901_H	Hsp90aa1	Heat shock	R.EMLQQSK#.I	27.83	10.40	2.68	0.37
P07901_H	Hsp90aa1	Heat shock	K.FYEQFSK#.N	203.96	23.62	8.64	0.12
P07901_H	Hsp90aa1	Heat shock	R.GVVDSEDLPLNISR.E	210.71	184.50	1.14	0.88
P07901_H	Hsp90aa1	Heat shock	K.HFSVEGQLEFR.A	13.63	12.62	1.08	0.93
P07901_H	Hsp90aa1	Heat shock	K.HIYFITGETK#.D	294.22	29.90	9.84	0.10
P07901_H	Hsp90aa1	Heat shock	K.HLEINPDHSIIETLR@.Q	246.99	1.19	207.48	0.00
P07901_H	Hsp90aa1	Heat shock	K.HNDDEQYAWESSAGGSFTVR.T	54.07	44.03	1.23	0.81
P07901_H	Hsp90aa1	Heat shock	K.HSQFIGYPITLFVEK#.E	93.98	8.90	10.56	0.09
P07901_H	Hsp90aa1	Heat shock	K.LSELLR@.Y	145.27	130.61	1.11	0.90
P07901_H	Hsp90aa1	Heat shock	R.NPDDITNEEYGEFYK#.S	204.95	26.15	7.84	0.13
P07901_H	Hsp90aa1	Heat shock	R.TLTIVDTGIGM*TK#.A	520.97	122.65	4.25	0.24
P07901_H	Hsp90aa1	Heat shock	R.TLTIVDTGIGMTK#.A	200.76	40.86	4.91	0.20
P07901_H	Hsp90aa1	Heat shock	K.VILHLK#.E	114.86	21.96	5.23	0.19
P07901_H	Hsp90aa1	Heat shock	K.VILHLKEDQTEYLEER.R	68.96	61.62	1.12	0.89
P07901_H	Hsp90aa1	Heat shock	R.YESLTDPSK#.L	276.78	50.37	5.49	0.18
P07901_H	Hsp90aa1	Heat shock	R.YESLTDPSKLDSGK.E	95.00	17.57	5.41	0.18
P07901_H	Hsp90aa1	Heat shock	K.YIDQEELNK#.T	1248.39	248.81	5.02	0.20
P07901_H	Hsp90aa1	Heat shock	R.YYTSASGDEMVSLK#.D	13.23	2.05	6.44	0.16
P11499_H	Hsp90ab1	Heat shock	R.ALLFIPR.R	26.37	25.61	1.03	0.97
P11499_H	Hsp90ab1	Heat shock	K.EQVANSAFVER.V	37.58	35.56	1.06	0.95
P11499_H	Hsp90ab1	Heat shock	K.FYEAFSK#.N	143.73	28.68	5.01	0.20
P11499_H	Hsp90ab1	Heat shock	K.HSQFIGYPITLYLEK#.E	62.61	14.49	4.32	0.23
P11499_H	Hsp90ab1	Heat shock	K.K#HSQFIGYPITLYLEK#.E	5.54	3.91	1.42	0.71
P11499_H	Hsp90ab1	Heat shock	R.NPDDITQEEYGEFYK#.S	92.38	22.31	4.14	0.24
P11499_H	Hsp90ab1	Heat shock	R.RAPFDLFENK.K	12.06	12.10	1.00	1.00
P11499_H	Hsp90ab1	Heat shock	K.SIYYITGESK#.E	137.88	29.23	4.72	0.21
P11499_H	Hsp90ab1	Heat shock	K.SLVSVTK#.E	170.54	34.41	4.96	0.20
P11499_H	Hsp90ab1	Heat shock	R.YHTSQSGDEM*TSLSEYVSR.M	10.85	13.22	0.82	1.22
P11499_H	Hsp90ab1	Heat shock	K.HLEINPDHPIVETLR.Q	17.16	42.25	0.41	2.46
P11499_H	Hsp90ab1	Heat shock	K.LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR.M	16.92	18.99	0.89	1.12
P11499_H	Hsp90ab1	Heat shock	R.ALLFIPR.R	255.81	255.79	1.00	1.00
P11499_H	Hsp90ab1	Heat shock	R.APFDLFENK#.K	187.54	40.90	4.58	0.22
P11499_H	Hsp90ab1	Heat shock	R.DNSTMGYM*M*AK#.K	45.34	9.83	4.61	0.22
P11499_H	Hsp90ab1	Heat shock	R.DNSTM*GYM*MAK#.K	48.29	11.99	4.03	0.25
P11499_H	Hsp90ab1	Heat shock	R.DNSTM*GYMM*AK#.K	92.63	20.75	4.46	0.22
P11499_H	Hsp90ab1	Heat shock	R.DNSTMGYM*MAK#.K	55.40	12.81	4.32	0.23
P11499_H	Hsp90ab1	Heat shock	R.DNSTMGYMM*AK#.K	28.10	6.62	4.24	0.24

P11499_HS	Hsp90ab1	Heat shock	R.DNSTMGYMMAK#.K	38.31	8.02	4.78	0.21
P11499_HS	Hsp90ab1	Heat shock	K.EQVANSAFVER.V	327.64	359.11	0.91	1.10
P11499_HS	Hsp90ab1	Heat shock	K.FYEAFSK#.N	1335.26	260.72	5.12	0.20
P11499_HS	Hsp90ab1	Heat shock	K.HLEINPDHPIVETLR.Q	159.97	179.93	0.89	1.12
P11499_HS	Hsp90ab1	Heat shock	K.HSQFIGYPITLYLEK#.E	757.78	162.95	4.65	0.22
P11499_HS	Hsp90ab1	Heat shock	K.HSQFIGYPITLYLEK#.E	182.22	42.47	4.29	0.23
P11499_HS	Hsp90ab1	Heat shock	K.HSQFIGYPITLYLEKER.E	26.94	21.48	1.25	0.80
P11499_HS	Hsp90ab1	Heat shock	K.IDIIPNPQER.T	235.76	291.47	0.81	1.24
P11499_HS	Hsp90ab1	Heat shock	K.IEDVGSDEEDDSGK#.D	39.21	9.90	3.96	0.25
P11499_HS	Hsp90ab1	Heat shock	K.IEDVGSDEEDDSGK#DK#.K	10.24	1.97	5.20	0.19
P11499_HS	Hsp90ab1	Heat shock	K.K#FYEAFSK#.N	51.86	14.24	3.64	0.27
P11499_HS	Hsp90ab1	Heat shock	K.KHLEINPDHPIVETLR.Q	129.30	138.14	0.94	1.07
P11499_HS	Hsp90ab1	Heat shock	K.K#HSQFIGYPITLYLEK#.E	113.42	32.51	3.49	0.29
P11499_HS	Hsp90ab1	Heat shock	K.K#HSQFIGYPITLYLEK#.E	36.13	7.99	4.52	0.22
P11499_HS	Hsp90ab1	Heat shock	K.LGIHEDSTNR.R	134.19	130.67	1.03	0.97
P11499_HS	Hsp90ab1	Heat shock	K.LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR.M	23.04	28.45	0.81	1.24
P11499_HS	Hsp90ab1	Heat shock	K.LM*K#EILDK#.K	66.52	17.38	3.83	0.26
P11499_HS	Hsp90ab1	Heat shock	R.NPDDITQEEYGEFYK#.S	825.88	169.64	4.87	0.21
P11499_HS	Hsp90ab1	Heat shock	R.RAPFDLFENK.K	113.98	120.94	0.94	1.06
P11499_HS	Hsp90ab1	Heat shock	R.RAPFDLFENKK.K	59.03	62.69	0.94	1.06
P11499_HS	Hsp90ab1	Heat shock	R.RLSELLR.Y	22.60	98.91	0.23	4.38
P11499_HS	Hsp90ab1	Heat shock	K.SIYYITGESK#.E	1191.31	259.83	4.58	0.22
P11499_HS	Hsp90ab1	Heat shock	R.YHTSQSGDEM*TSLSEYVSR.M	182.21	185.69	0.98	1.02
P11499_HS	Hsp90ab1	Heat shock	R.YHTSQSGDEMTSLSEYVSR.M	66.57	60.07	1.11	0.90
P11499_HS	Hsp90ab1	Heat shock	R.ADHGEPIGR.G	30.34	35.30	0.86	1.16
P11499_HS	Hsp90ab1	Heat shock	R.ALLFIPR.R	174.00	157.38	1.11	0.90
P11499_HS	Hsp90ab1	Heat shock	R.APFDLFENK#.K	127.92	32.10	3.99	0.25
P11499_HS	Hsp90ab1	Heat shock	R.DNSTM*GYMM*AK#.K	35.39	6.38	5.55	0.18
P11499_HS	Hsp90ab1	Heat shock	R.DNSTM*GYMMAK#.K	8.79	2.12	4.14	0.24
P11499_HS	Hsp90ab1	Heat shock	K.EQVANSAFVER.V	132.20	125.75	1.05	0.95
P11499_HS	Hsp90ab1	Heat shock	K.FYEAFSK#.N	561.62	120.10	4.68	0.21
P11499_HS	Hsp90ab1	Heat shock	K.HLEINPDHPIVETLR.Q	107.59	97.93	1.10	0.91
P11499_HS	Hsp90ab1	Heat shock	K.HSQFIGYPITLYLEK#.E	241.30	53.05	4.55	0.22
P11499_HS	Hsp90ab1	Heat shock	K.HSQFIGYPITLYLEK#.E	35.77	7.48	4.78	0.21
P11499_HS	Hsp90ab1	Heat shock	K.IDIIPNPQER.T	96.12	97.96	0.98	1.02
P11499_HS	Hsp90ab1	Heat shock	K.IEDVGSDEEDDSGK#.D	54.13	13.19	4.11	0.24
P11499_HS	Hsp90ab1	Heat shock	K.KHLEINPDHPIVETLR.Q	44.47	45.54	0.98	1.02
P11499_HS	Hsp90ab1	Heat shock	K.LGIHEDSTNR.R	55.64	59.18	0.94	1.06
P11499_HS	Hsp90ab1	Heat shock	R.NPDDITQEEYGEFYK#.S	411.25	92.52	4.44	0.22
P11499_HS	Hsp90ab1	Heat shock	R.RAPFDLFENK.K	47.30	51.08	0.93	1.08
P11499_HS	Hsp90ab1	Heat shock	K.SIYYITGESK#.E	574.95	124.37	4.62	0.22
P11499_HS	Hsp90ab1	Heat shock	K.SLVSVTK#.E	736.30	152.48	4.83	0.21
P11499_HS	Hsp90ab1	Heat shock	R.YHTSQSGDEM*TSLSEYVSR.M	117.73	113.31	1.04	0.96
P08113_EN	Hsp90b1	Endoplasm	K.DISTNYYASQK#.K	13.34	3.87	3.45	0.29
P08113_EN	Hsp90b1	Endoplasm	R.ELISNASDALDK#.I	116.08	27.17	4.27	0.23
P08113_EN	Hsp90b1	Endoplasm	K.SGTSEFLNK#.M	19.67	4.06	4.85	0.21
P08113_EN	Hsp90b1	Endoplasm	K.DISTNYYASQK#.K	14.13	5.31	2.66	0.38
P08113_EN	Hsp90b1	Endoplasm	R.ELISNASDALDK#.I	32.86	13.89	2.37	0.42
P08113_EN	Hsp90b1	Endoplasm	R.LISLTDENALAGNEELTVK#.I	7.00	2.37	2.96	0.34
P08113_EN	Hsp90b1	Endoplasm	R.TDDEVVQREEEAIQLDGLNASQIR.E	2.26	8.72	0.26	3.86
P08113_EN	Hsp90b1	Endoplasm	K.ALK#DK#IEK#.A	101.04	27.83	3.63	0.28
P08113_EN	Hsp90b1	Endoplasm	K.AQAYQTGK#.D	45.80	16.29	2.81	0.36
P08113_EN	Hsp90b1	Endoplasm	K.DISTNYYASQK#.K	546.75	143.47	3.81	0.26
P08113_EN	Hsp90b1	Endoplasm	K.EAESSPFVER.L	129.18	161.66	0.80	1.25
P08113_EN	Hsp90b1	Endoplasm	R.EATEK#EFEPLLNWM*K#.D	128.93	30.64	4.21	0.24
P08113_EN	Hsp90b1	Endoplasm	R.EATEKEFEPLLNWM*K.D	22.33	8.90	2.51	0.40
P08113_EN	Hsp90b1	Endoplasm	R.EATEK#EFEPLLNWMK#.D	333.35	76.94	4.33	0.23
P08113_EN	Hsp90b1	Endoplasm	K.EEASDYLELDTIK#.N	177.23	43.82	4.04	0.25
P08113_EN	Hsp90b1	Endoplasm	R.EEEAIQLDGLNASQIR.E	8.95	13.77	0.65	1.54
P08113_EN	Hsp90b1	Endoplasm	K.EESDDEAAVEEEEEEK#.K	14.93	5.43	2.75	0.36
P08113_EN	Hsp90b1	Endoplasm	K.EFEPLLNWM*K#.D	32.51	7.95	4.09	0.24
P08113_EN	Hsp90b1	Endoplasm	K.EFEPLLNWMK#.D	57.26	12.28	4.66	0.21
P08113_EN	Hsp90b1	Endoplasm	R.EGSRTDDEVVQREEEAIQLDGLNASQIR.E	10.47	35.07	0.30	3.35
P08113_EN	Hsp90b1	Endoplasm	K.EGVK#FDESEK#.T	124.99	35.78	3.49	0.29
P08113_EN	Hsp90b1	Endoplasm	K.EGVKFDESEKTK.E	61.64	17.02	3.62	0.28
P08113_EN	Hsp90b1	Endoplasm	R.ELISNASDALDK#.I	1142.27	280.81	4.07	0.25
P08113_EN	Hsp90b1	Endoplasm	K.ESDDPM*AYIHFTAEGEVTFK#.S	18.09	4.64	3.89	0.26
P08113_EN	Hsp90b1	Endoplasm	K.ESDDPMAYIHFTAEGEVTFK#.S	21.89	7.13	3.07	0.33
P08113_EN	Hsp90b1	Endoplasm	K.EVEEDEYK#.A	310.86	86.28	3.60	0.28
P08113_EN	Hsp90b1	Endoplasm	K.FAFQAEVNR.M	218.69	245.08	0.89	1.12
P08113_EN	Hsp90b1	Endoplasm	K.FDESEK#TK#.E	18.72	10.56	1.77	0.56
P08113_EN	Hsp90b1	Endoplasm	R.FQNVAK#.E	648.50	168.81	3.84	0.26
P08113_EN	Hsp90b1	Endoplasm	R.FQSSHHSTDITSLDQYVER.M	78.35	87.55	0.89	1.12
P08113_EN	Hsp90b1	Endoplasm	R.GLFDEYGSK#.K	389.58	106.56	3.66	0.27
P08113_EN	Hsp90b1	Endoplasm	R.GLFDEYGSK#K#.S	47.14	14.23	3.31	0.30
P08113_EN	Hsp90b1	Endoplasm	R.GTTITLVLK#.E	65.85	15.81	4.16	0.24
P08113_EN	Hsp90b1	Endoplasm	R.GTTITLVLK#EEASDYLELDTIK#.N	82.69	20.58	4.02	0.25
P08113_EN	Hsp90b1	Endoplasm	K.GVVDSDDLPLNVSR.E	171.83	208.83	0.82	1.22
P08113_EN	Hsp90b1	Endoplasm	K.IADEK#YNDTFWK#.E	311.47	64.33	4.84	0.21
P08113_EN	Hsp90b1	Endoplasm	K.IADEK#YNDTFWK#EFGTNIK#.L	14.63	3.02	4.84	0.21
P08113_EN	Hsp90b1	Endoplasm	K.IYFM*AGSSR.K	67.83	72.71	0.93	1.07
P08113_EN	Hsp90b1	Endoplasm	K.IYFMAGSSR.K	57.77	59.91	0.96	1.04
P08113_EN	Hsp90b1	Endoplasm	R.KEAESSPFVER.L	55.35	59.21	0.93	1.07
P08113_EN	Hsp90b1	Endoplasm	K.K#IADEK#YNDTFWK#.E	57.25	10.85	5.28	0.19
P08113_EN	Hsp90b1	Endoplasm	R.K#TLDMIK#.K	35.61	10.65	3.34	0.30
P08113_EN	Hsp90b1	Endoplasm	R.K#TLDM*IK#.K	32.47	8.08	4.02	0.25
P08113_EN	Hsp90b1	Endoplasm	R.K#YSQFINFPIYVWSSK#.T	177.40	40.57	4.37	0.23
P08113_EN	Hsp90b1	Endoplasm	K.LIINSLYK#.N	820.48	198.35	4.14	0.24
P08113_EN	Hsp90b1	Endoplasm	R.LISLTDENALAGNEELTVK#.I	213.47	55.79	3.83	0.26
P08113_EN	Hsp90b1	Endoplasm	K.NKEIFLR.E	64.85	61.91	1.05	0.95
P08113_EN	Hsp90b1	Endoplasm	K.NLLHVTDTGVGM*TR.E	74.45	82.46	0.90	1.11
P08113_EN	Hsp90b1	Endoplasm	K.NLLHVTDTGVGMTR.E	20.89	28.18	0.74	1.35
P08113_EN	Hsp90b1	Endoplasm	K.NLLHVTDTGVGMTREELVK.N	23.72	29.23	0.81	1.23
P08113_EN	Hsp90b1	Endoplasm	R.RVFITDDFHDMMPK.Y	11.60	12.08	0.96	1.04
P08113_EN	Hsp90b1	Endoplasm	K.SGTSEFLNK#.M	719.59	167.80	4.29	0.23
P08113_EN	Hsp90b1	Endoplasm	R.SGYLLPDTK#.A	601.59	136.68	4.40	0.23
P08113_EN	Hsp90b1	Endoplasm	K.SILFVPTSAPR.G	181.46	225.58	0.80	1.24
P08113_EN	Hsp90b1	Endoplasm	R.TDDEVVQREEEAIQLDGLNASQIR.E	23.04	65.82	0.35	2.86
P08113_EN	Hsp90b1	Endoplasm	K.TETVEEPLEEDEAAK#.E	14.31	3.82	3.74	0.27
P08113_EN	Hsp90b1	Endoplasm	K.TETVEEPLEEDEAAK#EEK#.E	181.02	51.49	3.52	0.28
P08113_EN	Hsp90b1	Endoplasm	K.TETVEEPLEEDEAAKEEKEESDDEAAVEEEEEEK.K	18.63	6.61	2.82	0.35
P08113_EN	Hsp90b1	Endoplasm	K.TFEINPR.H	108.56	121.32	0.89	1.12
P08113_EN	Hsp90b1	Endoplasm	K.TLDMIK#.K	34.50	13.31	2.59	0.39

P08113_E	Hsp90b1	Endoplasm	K.TLDM*IK#K#.I	44.43	7.26	6.12	0.16
P08113_E	Hsp90b1	Endoplasm	R.VFITDDFHDMM*PK#.Y	6.64	3.50	1.90	0.53
P08113_E	Hsp90b1	Endoplasm	K.YNDTFWK#.E	194.03	54.33	3.57	0.28
P08113_E	Hsp90b1	Endoplasm	K.DISTNYYASQK#.K	65.31	19.55	3.34	0.30
P08113_E	Hsp90b1	Endoplasm	K.EEASDYLELDTIK#.N	16.36	3.96	4.13	0.24
P08113_E	Hsp90b1	Endoplasm	K.EFGTNIK#.L	50.61	9.96	5.08	0.20
P08113_E	Hsp90b1	Endoplasm	R.ELISNASDALDK#.I	468.25	115.25	4.06	0.25
P08113_E	Hsp90b1	Endoplasm	K.EVEEDEYK#.A	28.19	10.20	2.76	0.36
P08113_E	Hsp90b1	Endoplasm	K.FAFQAEVNR.M	24.30	26.85	0.91	1.10
P08113_E	Hsp90b1	Endoplasm	K.GVVDSDDLPLNVSR.E	24.20	33.55	0.72	1.39
P08113_E	Hsp90b1	Endoplasm	K.LIINSLYK#.N	89.28	25.27	3.53	0.28
P08113_E	Hsp90b1	Endoplasm	R.LISLTDENALAGNEELTVK#.I	19.62	7.53	2.61	0.38
P08113_E	Hsp90b1	Endoplasm	K.SGTSEFLNK#.M	75.70	19.35	3.91	0.26
P08113_E	Hsp90b1	Endoplasm	R.SGYLLPDTK#.A	70.59	20.51	3.44	0.29
P08113_E	Hsp90b1	Endoplasm	K.SILFVPTSAPR.G	31.24	34.56	0.90	1.11
P08113_E	Hsp90b1	Endoplasm	K.YSQFINFPIYVWSSK#.T	10.92	2.52	4.34	0.23
Q99M31_H	Hspa14	Heat shock	R.ADVVANDAGDR.V	13.48	19.38	0.70	1.44
Q99M31_H	Hspa14	Heat shock	R.DILAVLTMK#.R	11.00	1.32	8.30	0.12
Q99M31_H	Hspa14	Heat shock	K.FAQVVLQDLDK#K#.E	47.80	14.87	3.21	0.31
Q99M31_H	Hspa14	Heat shock	R.FTVLFPSGTPLPAR.R	4.03	6.57	0.61	1.63
Q99M31_H	Hspa14	Heat shock	R.HVSSTVVK#.V	26.03	202.57	0.13	7.78
Q99M31_H	Hspa14	Heat shock	R.VLSTNTSDNIGGAHFTDTLAQYLASEFQR.L	6.81	2.97	2.29	0.44
Q99M31_H	Hspa14	Heat shock	R.VTPAIVAYSER.E	9.63	12.07	0.80	1.25
Q99M31_H	Hspa14	Heat shock	R.YEIDTGEETK#.L	23.12	6.95	3.33	0.30
Q61696_H	Hspa1a	Heat shock	K.NQVALNPQNTVFDAK#.R	5.66	3.52	1.61	0.62
Q61696_H	Hspa1a	Heat shock	R.TTPSYVAFTDTER.L	21.43	84.34	0.25	3.93
Q61696_H	Hspa1a	Heat shock	K.QTQTFTTYSDNQPGVLIQVYEGER.A	16.88	57.55	0.29	3.41
Q61696_H	Hspa1a	Heat shock	R.TTPSYVAFTDTER.L	58.04	205.53	0.28	3.54
Q61696_H	Hspa1a	Heat shock	R.TTPSYVAFTDTER.L	10.59	18.95	0.56	1.79
P48722_H	Hspa4l	Heat shock	R.IGNFTIQNVFPQSDGDSSK#.V	3.55	1.94	1.83	0.55
P20029_G	Hspa5	78 kDa gluc	R.IINEPTAAAIAYGLDK#.R	25.60	23.88	1.07	0.93
P20029_G	Hspa5	78 kDa gluc	R.VEIIANDQGNR.I	24.99	96.80	0.26	3.87
P20029_G	Hspa5	78 kDa gluc	R.AKFEELNM*DLFR.S	21.23	15.17	1.40	0.71
P20029_G	Hspa5	78 kDa gluc	K.DAGTIAGLNVM*R.I	9.47	40.99	0.23	4.33
P20029_G	Hspa5	78 kDa gluc	K.DAGTIAGLNVMR.I	6.02	25.44	0.24	4.22
P20029_G	Hspa5	78 kDa gluc	K.DNHLLGTFDLTGIPPAPR.G	4.69	26.15	0.18	5.58
P20029_G	Hspa5	78 kDa gluc	K.ELEEIVQPIISK.L	27.85	26.76	1.04	0.96
P20029_G	Hspa5	78 kDa gluc	R.IEIESFFEGEDFSETLTR.A	8.21	39.97	0.21	4.87
P20029_G	Hspa5	78 kDa gluc	K.IEWLESHQDADIEDFK#.A	26.13	34.73	0.75	1.33
P20029_G	Hspa5	78 kDa gluc	K.IEWLESHQDADIEDFK#AK#.K	20.42	25.10	0.81	1.23
P20029_G	Hspa5	78 kDa gluc	R.IINEPTAAAIAYGLDK#.R	65.08	53.60	1.21	0.82
P20029_G	Hspa5	78 kDa gluc	K.ITITNDQNR.L	15.78	82.44	0.19	5.22
P20029_G	Hspa5	78 kDa gluc	R.ITPSYVAFTPEGER.L	11.06	79.32	0.14	7.17
P20029_G	Hspa5	78 kDa gluc	K.K#K#ELEEIVQPIISK#.L	52.99	69.14	0.77	1.30
P20029_G	Hspa5	78 kDa gluc	K.KSDIDEIVLVGGSTR.I	3.60	25.99	0.14	7.21
P20029_G	Hspa5	78 kDa gluc	R.LTPEEIER.M	14.40	67.42	0.21	4.68
P20029_G	Hspa5	78 kDa gluc	K.LYGSGGPPPTGEEDTSEK#DEL.-	15.93	19.65	0.81	1.23
P20029_G	Hspa5	78 kDa gluc	R.NELESYAYSLK#.N	87.81	53.84	1.63	0.61
P20029_G	Hspa5	78 kDa gluc	K.NQLTSNPENTVFDAK#.R	57.91	74.41	0.78	1.28
P20029_G	Hspa5	78 kDa gluc	R.NTVVPTK#K#.S	23.45	27.68	0.85	1.18
P20029_G	Hspa5	78 kDa gluc	K.SQIFSTASDNQPTVTIK#.V	40.76	43.42	0.94	1.07
P20029_G	Hspa5	78 kDa gluc	K.TFAPEEISAM*VLTK.M	13.49	13.94	0.97	1.03
P20029_G	Hspa5	78 kDa gluc	K.TFAPEEISAMVLTK#.M	31.86	40.98	0.78	1.29
P20029_G	Hspa5	78 kDa gluc	K.TK#PYIQVDIGGGQTK#.T	40.12	49.12	0.82	1.22
P20029_G	Hspa5	78 kDa gluc	R.TWNDPSVQQDIK#.F	44.04	59.08	0.75	1.34
P20029_G	Hspa5	78 kDa gluc	R.VEIIANDQGNR.I	99.86	382.45	0.26	3.83
P20029_G	Hspa5	78 kDa gluc	K.VTHAVVTVPAYFNDAQR.Q	12.10	55.20	0.22	4.56
P20029_G	Hspa5	78 kDa gluc	K.VYEGERPLTK.D	6.53	27.79	0.24	4.25
P20029_G	Hspa5	78 kDa gluc	K.NQLTSNPENTVFDAK#.R	6.49	7.65	0.85	1.18
P20029_G	Hspa5	78 kDa gluc	K.SQIFSTASDNQPTVTIK#.V	5.13	4.08	1.26	0.80
P63017_H	Hspa8	Heat shock	R.ARFEELNADLFR.G	3.26	39.66	0.08	12.15
P63017_H	Hspa8	Heat shock	K.DAGTIAGLNVLR.I	21.22	83.75	0.25	3.95
P63017_H	Hspa8	Heat shock	R.FDDAVVQSDM*K.H	13.01	10.24	1.27	0.79
P63017_H	Hspa8	Heat shock	R.IINEPTAAAIAYGLDK#K#.G	108.52	92.40	1.17	0.85
P63017_H	Hspa8	Heat shock	K.LDKSQIHDIVLVGGSTR.I	1.99	9.63	0.21	4.84
P63017_H	Hspa8	Heat shock	K.LLQDFFNGK#.E	26.34	20.12	1.31	0.76
P63017_H	Hspa8	Heat shock	K.M*K#EIAEAYLGK#.T	7.12	4.68	1.52	0.66
P63017_H	Hspa8	Heat shock	K.MK#EIAEAYLGK#.T	9.90	8.15	1.21	0.82
P63017_H	Hspa8	Heat shock	R.M*VNHFIAEFK#.R	24.71	19.57	1.26	0.79
P63017_H	Hspa8	Heat shock	K.NQTAEK#EEFEHQQK#.E	21.89	13.68	1.60	0.62
P63017_H	Hspa8	Heat shock	K.NQVAM*NPTNTVFDAK.R	63.54	60.22	1.06	0.95
P63017_H	Hspa8	Heat shock	K.NQVAMNPTNTVFDAK#.R	22.51	21.89	1.03	0.97
P63017_H	Hspa8	Heat shock	K.NSLESYAFNMK#.A	35.22	27.45	1.28	0.78
P63017_H	Hspa8	Heat shock	R.RFDDAVVQSDM*K.H	5.17	15.88	0.33	3.07
P63017_H	Hspa8	Heat shock	K.SFYPEEVSSM*VLTK#.M	18.27	7.89	2.31	0.43
P63017_H	Hspa8	Heat shock	K.SFYPEEVSSMVLTK#.M	27.12	27.52	0.99	1.01
P63017_H	Hspa8	Heat shock	K.SINPDEAVAYGAAVQAAILSGDK#.S	6.25	3.68	1.70	0.59
P63017_H	Hspa8	Heat shock	K.SQIHDIVLVGGSTR.I	4.05	17.53	0.23	4.32
P63017_H	Hspa8	Heat shock	K.STAGDTHLGGEDFDNR.M	27.40	116.47	0.24	4.25
P63017_H	Hspa8	Heat shock	K.TVTNAVVTVPAYFNDSQR.Q	6.41	17.67	0.36	2.76
P63017_H	Hspa8	Heat shock	K.VQVEYK#.G	38.07	40.95	0.93	1.08
P63017_H	Hspa8	Heat shock	R.ARFEELNADLFR.G	12.30	148.06	0.08	12.04
P63017_H	Hspa8	Heat shock	K.DAGTIAGLNVLR.I	81.30	258.31	0.31	3.18
P63017_H	Hspa8	Heat shock	K.DNNLLGK#.F	65.54	56.83	1.15	0.87
P63017_H	Hspa8	Heat shock	K.EIAEAYLGK#.T	60.25	48.19	1.25	0.80
P63017_H	Hspa8	Heat shock	R.FDDAVVQSDM*K#.H	39.50	24.04	1.64	0.61
P63017_H	Hspa8	Heat shock	R.FEELNADLFR.G	19.07	65.35	0.29	3.43
P63017_H	Hspa8	Heat shock	K.FELTGIPPAPR.G	2.00	11.41	0.18	5.71
P63017_H	Hspa8	Heat shock	R.GTLDPVEK#.A	221.87	206.81	1.07	0.93
P63017_H	Hspa8	Heat shock	K.HWPFMVVNDAGRPK.V	11.39	35.34	0.32	3.10
P63017_H	Hspa8	Heat shock	K.LDKSQIHDIVLVGGSTR.I	13.02	40.62	0.32	3.12
P63017_H	Hspa8	Heat shock	K.LLQDFFNGK#.E	101.10	67.91	1.49	0.67
P63017_H	Hspa8	Heat shock	R.LSKEDIER.M	32.56	136.39	0.24	4.19
P63017_H	Hspa8	Heat shock	K.M*K#EIAEAYLGK#.T	84.51	58.16	1.45	0.69
P63017_H	Hspa8	Heat shock	K.MK#EIAEAYLGK#.T	74.36	66.90	1.11	0.90
P63017_H	Hspa8	Heat shock	R.M*VNHFIAEFK#.R	74.00	63.00	1.17	0.85
P63017_H	Hspa8	Heat shock	R.MVNHFIAEFK#.R	31.62	23.97	1.32	0.76
P63017_H	Hspa8	Heat shock	R.M*VNHFIAEFKR.K	2.16	15.15	0.14	7.00
P63017_H	Hspa8	Heat shock	K.NQTAEK#EEFEHQQK#.E	34.29	36.06	0.95	1.05
P63017_H	Hspa8	Heat shock	K.NQVAM*NPTNTVFDAK#.R	155.90	124.36	1.25	0.80
P63017_H	Hspa8	Heat shock	K.NQVAMNPTNTVFDAK#.R	75.21	66.43	1.13	0.88
P63017_H	Hspa8	Heat shock	K.NSLESYAFNM*K#.A	85.04	60.97	1.39	0.72
P63017_H	Hspa8	Heat shock	K.NSLESYAFNMK#.A	110.00	87.76	1.25	0.80

P63017_H	Hspa8	Heat shock	R.RFDDAVVQSDM*K.H	11.21	42.94	0.26	3.83
P63017_H	Hspa8	Heat shock	R.RFDDAVVQSDMK.H	8.48	40.20	0.21	4.74
P63017_H	Hspa8	Heat shock	K.SFYPEEVSSM*VLTK#.M	53.67	38.94	1.38	0.73
P63017_H	Hspa8	Heat shock	K.SFYPEEVSSMVLTK#.M	93.93	75.65	1.24	0.81
P63017_H	Hspa8	Heat shock	K.SFYPEEVSSMVLTK.M	25.21	22.21	1.14	0.88
P63017_H	Hspa8	Heat shock	K.SINPDEAVAYGAAVQAAILSGDK.S	41.79	28.90	1.45	0.69
P63017_H	Hspa8	Heat shock	K.SQIHDIVLVGGSTR.I	35.91	109.36	0.33	3.05
P63017_H	Hspa8	Heat shock	K.TVTNAVVTVPAYFNDSQR.Q	24.65	99.63	0.25	4.04
P63017_H	Hspa8	Heat shock	K.VQVEYKGETK.S	459.64	225.34	2.04	0.49
P63017_H	Hspa8	Heat shock	K.DAGTIAGLNVLR.I	9.33	26.02	0.36	2.79
P63017_H	Hspa8	Heat shock	R.M*VNHFIAEFK#.R	5.50	3.28	1.68	0.60
P63017_H	Hspa8	Heat shock	K.NQVAM*NPTNTVFDAK#.R	24.10	15.64	1.54	0.65
P63017_H	Hspa8	Heat shock	K.NQVAMNPTNTVFDAK#.R	6.97	5.74	1.21	0.82
P38647_G	Hspa9	Stress-70 p	R.AQFEGIVTDLIK#.R	25.27	6.18	4.09	0.24
P38647_G	Hspa9	Stress-70 p	R.QAASSLQQASLK#.L	18.09	4.44	4.08	0.25
P38647_G	Hspa9	Stress-70 p	R.VINEPTAAALAYGLDK#.S	4.12	1.69	2.43	0.41
P38647_G	Hspa9	Stress-70 p	R.AQFEGIVTDLIK#.R	47.94	14.57	3.29	0.30
P38647_G	Hspa9	Stress-70 p	K.LFEMAYK#.K	14.02	4.95	2.83	0.35
P38647_G	Hspa9	Stress-70 p	K.NAVITVPAYFNDSQR.Q	4.25	6.86	0.62	1.62
P38647_G	Hspa9	Stress-70 p	R.QAASSLQQASLK#.L	49.95	9.96	5.02	0.20
P38647_G	Hspa9	Stress-70 p	R.QAVTNPNNTFYATK#.R	34.38	8.39	4.10	0.24
P38647_G	Hspa9	Stress-70 p	K.SQVFSTAADGQTQVEIK#.V	10.98	2.61	4.21	0.24
P38647_G	Hspa9	Stress-70 p	R.TTPSVVAFTADGER.L	14.46	13.56	1.07	0.94
P38647_G	Hspa9	Stress-70 p	R.VINEPTAAALAYGLDK#.S	14.79	4.44	3.33	0.30
P38647_G	Hspa9	Stress-70 p	K.VQQTVQDLFGR.A	12.45	16.38	0.76	1.32
P38647_G	Hspa9	Stress-70 p	R.YDDPEVQK#DTK#.N	3.47	2.92	1.19	0.84
P14602_H	Hspb1	Heat shock	R.AQIGGPEAGK#.S	16.23	13.76	1.18	0.85
P14602_H	Hspb1	Heat shock	R.KYTLPPGVDPTLVSSSLSPEGTLTVEAPLPK.A	3.29	4.07	0.81	1.24
P14602_H	Hspb1	Heat shock	R.LFDQAFGVPR.L	5.36	16.55	0.32	3.09
P14602_H	Hspb1	Heat shock	R.VSLDVNHFAPEELTVK#.T	36.71	28.42	1.29	0.77
P14602_H	Hspb1	Heat shock	R.AQIGGPEAGK#.S	12.51	10.44	1.20	0.83
P14602_H	Hspb1	Heat shock	K.AVTQSAEITIPVTFEAR.A	25.85	98.26	0.26	3.80
P14602_H	Hspb1	Heat shock	K.EGVVEITGK#.H	24.86	22.55	1.10	0.91
P14602_H	Hspb1	Heat shock	R.K#YTLPPGVDPTLVSSSLSPEGTLTVEAPLPK#.A	7.57	11.82	0.64	1.56
P14602_H	Hspb1	Heat shock	R.LFDQAFGVPR.L	17.52	47.21	0.37	2.69
P14602_H	Hspb1	Heat shock	R.QLSSGVSEIR.Q	14.72	66.32	0.22	4.51
P14602_H	Hspb1	Heat shock	R.VSLDVNHFAPEELTVK#.T	187.85	162.55	1.16	0.87
P63038_C	Hspd1	60 kDa hea	K.DDAM*LLK#.G	10.76	2.32	4.64	0.22
P63038_C	Hspd1	60 kDa hea	K.DM*AIATGGAVFGEEGLNLNLEDVQAHDLGK#.V	11.33	3.33	3.40	0.29
P63038_C	Hspd1	60 kDa hea	R.GYISPYFINTSK#.G	68.90	15.44	4.46	0.22
P63038_C	Hspd1	60 kDa hea	K.IGIEIIK#.R	75.10	15.09	4.98	0.20
P63038_C	Hspd1	60 kDa hea	K.ILQSSSEVGYDAM*LGDFVNM*VEK#.G	7.98	3.02	2.65	0.38
P63038_C	Hspd1	60 kDa hea	K.ILQSSSEVGYDAMLGDFVNMVEK#.G	7.18	6.13	1.17	0.85
P63038_C	Hspd1	60 kDa hea	K.IPAM*TIAK#.N	64.72	14.42	4.49	0.22
P63038_C	Hspd1	60 kDa hea	K.IPAMTIAK#.N	51.35	9.62	5.34	0.19
P63038_C	Hspd1	60 kDa hea	R.IQEITEQLDITTSEYEK#.E	17.86	5.11	3.50	0.29
P63038_C	Hspd1	60 kDa hea	R.IQEITEQLDITTSEYEK#EK#.L	47.12	12.14	3.88	0.26
P63038_C	Hspd1	60 kDa hea	R.KPLVIIAEDVDGEALSTLVLNR.L	14.03	12.44	1.13	0.89
P63038_C	Hspd1	60 kDa hea	K.LSDGVAVLK#.V	113.63	24.63	4.61	0.22
P63038_C	Hspd1	60 kDa hea	K.NAGVEGSLIVEK#.I	95.96	21.03	4.56	0.22
P63038_C	Hspd1	60 kDa hea	K.TLNDELEIIEGM*K#.F	25.66	8.73	2.94	0.34
P63038_C	Hspd1	60 kDa hea	K.TLNDELEIIEGMK#.F	41.12	8.57	4.80	0.21
P63038_C	Hspd1	60 kDa hea	R.TVIIEQSWGSPK#.V	110.53	30.05	3.68	0.27
P63038_C	Hspd1	60 kDa hea	K.VGEVIVTK#.D	73.02	14.86	4.92	0.20
P63038_C	Hspd1	60 kDa hea	K.VGGTSDVEVNEK#.K	169.81	47.64	3.56	0.28
P63038_C	Hspd1	60 kDa hea	K.VGGTSDVEVNEK#K#.D	30.91	5.41	5.71	0.18
P63038_C	Hspd1	60 kDa hea	K.VGGTSDVEVNEK#K#.D	7.51	3.13	2.40	0.42
P63038_C	Hspd1	60 kDa hea	K.VGLQVVAVK#.A	165.39	31.52	5.25	0.19
P63038_C	Hspd1	60 kDa hea	R.VTDALNATR.A	43.89	40.40	1.09	0.92
P63038_C	Hspd1	60 kDa hea	R.GYISPYFINTSK#.G	9.80	3.14	3.12	0.32
P63038_C	Hspd1	60 kDa hea	K.LSDGVAVLK#.V	15.86	2.93	5.41	0.18
P63038_C	Hspd1	60 kDa hea	K.NAGVEGSLIVEK#.I	16.30	5.20	3.13	0.32
P63038_C	Hspd1	60 kDa hea	K.VGGTSDVEVNEK#.K	13.85	5.82	2.38	0.42
P63038_C	Hspd1	60 kDa hea	K.VGLQVVAVK#.A	11.76	2.89	4.07	0.25
Q61699_H	Hsph1	Heat shock	R.FVVQNVSAQK#.D	15.17	4.12	3.68	0.27
Q61699_H	Hsph1	Heat shock	K.VLGTAFDPFLGGK#.N	9.24	1.96	4.72	0.21
Q61699_H	Hsph1	Heat shock	R.FVVQNVSAQK#.D	32.93	6.27	5.25	0.19
Q7TMY8_H	Huwe1	E3 ubiquiti	R.IVNQPSSLFGSK#.S	24.74	28.57	0.87	1.15
Q7TMY8_H	Huwe1	E3 ubiquiti	R.LLSLISIALPENK#.V	22.88	5.43	4.22	0.24
Q7TMY8_H	Huwe1	E3 ubiquiti	K.QVVNQVWEAADVLIK#.A	7.56	2.14	3.54	0.28
Q7TMY8_H	Huwe1	E3 ubiquiti	K.TDATTAIIK#.L	12.13	10.93	1.11	0.90
Q9JKR6_H	Hyou1	Hypoxia up	K.AANSLEAFIFETQDK#.L	18.53	3.87	4.79	0.21
Q9JKR6_H	Hyou1	Hypoxia up	R.AEPPLNASAGDQEEK#.V	22.72	3.50	6.48	0.15
Q9JKR6_H	Hyou1	Hypoxia up	R.EVQYLLNK#.A	30.22	4.04	7.48	0.13
Q9JKR6_H	Hyou1	Hypoxia up	R.FLGDSAAGM*AIK#.N	45.85	7.91	5.80	0.17
Q9JKR6_H	Hyou1	Hypoxia up	K.K#YPDYESK#.G	16.01	2.81	5.69	0.18
Q9JKR6_H	Hyou1	Hypoxia up	K.LGNTISSLFGGGTSSDAK#.E	12.19	2.33	5.24	0.19
Q9JKR6_H	Hyou1	Hypoxia up	R.LIPEM*DQVFTEVEM*TTLEK#.V	7.01	2.76	2.54	0.39
Q9JKR6_H	Hyou1	Hypoxia up	R.LIPEM*DQVFTEVEMTTLEK#.V	7.53	2.14	3.51	0.28
Q9JKR6_H	Hyou1	Hypoxia up	K.NINADEAAAM*GAVYQAAALSK#.A	11.52	3.27	3.52	0.28
Q9JKR6_H	Hyou1	Hypoxia up	K.NINADEAAAMGAVYQAAALSK#.A	19.52	2.89	6.75	0.15
Q9JKR6_H	Hyou1	Hypoxia up	R.SLAEDFAEQPIK#.D	10.38	10.69	0.97	1.03
Q9JKR6_H	Hyou1	Hypoxia up	K.TPVTVTLK#.E	35.38	5.52	6.41	0.16
Q9JKR6_H	Hyou1	Hypoxia up	K.TVLSANADHM*AQIEGLM*DDVDFK#.A	9.49	2.05	4.62	0.22
Q9JKR6_H	Hyou1	Hypoxia up	K.TVLSANADHM*AQIEGLMDDVDFK#.A	7.31	2.67	2.74	0.36
Q9JKR6_H	Hyou1	Hypoxia up	K.VAIVK#PGVPM*EIVLNK#.E	75.16	8.77	8.57	0.12
Q9JKR6_H	Hyou1	Hypoxia up	K.VAIVK#PGVPMEIVLNK#.E	37.82	6.76	5.60	0.18
Q9JKR6_H	Hyou1	Hypoxia up	R.VESVFETLVEDSPEEESTLTK#.L	15.23	1.97	7.73	0.13
Q9JKR6_H	Hyou1	Hypoxia up	K.VLQLINDNTATALSYGVFR.R	6.49	5.31	1.22	0.82
Q9JKR6_H	Hyou1	Hypoxia up	K.VQEVLLK#.A	59.79	9.49	6.30	0.16
Q9JKR6_H	Hyou1	Hypoxia up	R.YFQHLLGK#.Q	20.66	3.29	6.29	0.16
Q9JKR6_H	Hyou1	Hypoxia up	K.AANSLEAFIFETQDK#.L	7.22	2.60	2.78	0.36
Q9JKR6_H	Hyou1	Hypoxia up	R.AEPPLNASAGDQEEK#.V	7.99	2.19	3.64	0.27
Q9JKR6_H	Hyou1	Hypoxia up	R.EVQYLLNK#.A	10.37	1.46	7.10	0.14
Q9JKR6_H	Hyou1	Hypoxia up	R.FLGDSAAGM*AIK#.N	11.06	3.06	3.61	0.28
Q9JKR6_H	Hyou1	Hypoxia up	R.VESVFETLVEDSPEEESTLTK#.L	9.25	1.79	5.18	0.19
Q9JKR6_H	Hyou1	Hypoxia up	K.VQEVLLK#.A	17.70	3.55	4.98	0.20
Q9CR41_H	Hypk	Huntingtin	R.EHM*GNVVEALIALTN.-	30.05	30.05	1.00	1.00
Q9CR41_H	Hypk	Huntingtin	R.EHMGNVVEALIALTN.-	30.61	30.61	1.00	1.00
Q8BU30_S	Iars	Isoleucine-	K.APLK#PYPVPTSDNILIQEQTQLK#.G	35.57	7.49	4.75	0.21
Q8BU30_S	Iars	Isoleucine-	K.GDNQLNLVK#.L	21.39	5.71	3.75	0.27
Q8BU30_S	Iars	Isoleucine-	K.GSELEITLTK#.G	28.68	5.79	4.95	0.20
Q8BU30_S	Iars	Isoleucine-	R.LFLNETQTQEITEDIPM*K#.T	9.25	3.61	2.57	0.39

Q8BU30_S	Iars	Isoleucine-	R.LFLNETQTQEITEDIPMK#.T	7.11	1.45	4.90	0.20
Q8BU30_S	Iars	Isoleucine-	K.LLIDPASLR.D	14.95	16.46	0.91	1.10
Q8BU30_S	Iars	Isoleucine-	K.LSVFHGETEIQNQTDLLSLSGR.T	10.59	11.31	0.94	1.07
Q8BU30_S	Iars	Isoleucine-	R.M*QSVIELGR.V	5.78	9.76	0.59	1.69
Q8BU30_S	Iars	Isoleucine-	K.TVVTSVFGVK#.N	44.81	7.02	6.39	0.16
Q8BU30_S	Iars	Isoleucine-	K.YK#PLFDYFIK#.C	11.26	2.83	3.98	0.25
Q8BU30_S	Iars	Isoleucine-	K.APLK#PYPVPTSDNILIQEQTQLK#.G	117.71	22.41	5.25	0.19
Q8BU30_S	Iars	Isoleucine-	R.EFEDAFPADFIAEGIDQTR.G	5.18	6.19	0.84	1.20
Q8BU30_S	Iars	Isoleucine-	K.EIVVIHQDPEALEDIR.S	18.80	17.03	1.10	0.91
Q8BU30_S	Iars	Isoleucine-	R.FFIQNVFR.L	33.30	33.27	1.00	1.00
Q8BU30_S	Iars	Isoleucine-	R.FGNWLK#.E	51.51	9.02	5.71	0.18
Q8BU30_S	Iars	Isoleucine-	R.FPGASLK#.G	56.73	15.25	3.72	0.27
Q8BU30_S	Iars	Isoleucine-	K.GDNQLNLVK#.L	68.42	16.19	4.23	0.24
Q8BU30_S	Iars	Isoleucine-	K.GSELEITLTK#.G	62.06	13.61	4.56	0.22
Q8BU30_S	Iars	Isoleucine-	R.LFLNETQTQEITEDIPM*K#.T	19.02	3.38	5.63	0.18
Q8BU30_S	Iars	Isoleucine-	R.LFLNETQTQEITEDIPM*K#.T	37.40	6.61	5.66	0.18
Q8BU30_S	Iars	Isoleucine-	R.LFLNETQTQEITEDIPMK#.T	14.89	3.35	4.45	0.22
Q8BU30_S	Iars	Isoleucine-	K.LLIDPASLR.D	39.01	34.26	1.14	0.88
Q8BU30_S	Iars	Isoleucine-	R.LM*APYTPFLTELM*YQNLK#.L	5.56	4.20	1.32	0.76
Q8BU30_S	Iars	Isoleucine-	R.LM*APYTPFLTELM*YQNLK#.L	19.66	8.54	2.30	0.43
Q8BU30_S	Iars	Isoleucine-	K.M*GIAEYNK#.Q	39.03	11.54	3.38	0.30
Q8BU30_S	Iars	Isoleucine-	K.TVVTSVFGVK#.N	114.40	22.24	5.14	0.19
Q8BU30_S	Iars	Isoleucine-	K.TVYVSVLPTTADG.-	67.93	67.93	1.00	1.00
Q8BU30_S	Iars	Isoleucine-	K.VTLSTDK#NK#.Y	12.06	35.97	0.34	2.98
Q8BU30_S	Iars	Isoleucine-	R.WIDFDNDYK#.T	43.13	6.80	6.34	0.16
Q8BU30_S	Iars	Isoleucine-	K.YK#PLFDYFIK#.C	33.58	4.28	7.85	0.13
Q8BU30_S	Iars	Isoleucine-	R.YLNNVIESHTDFIFATIK#.A	87.51	10.35	8.45	0.12
Q8BU30_S	Iars	Isoleucine-	R.YSAEWK#.S	54.18	9.76	5.55	0.18
Q9JHR7_ID	Ide	Insulin-deg	K.AIEDM*TEEAFQK#.H	5.93	2.77	2.14	0.47
Q9JHR7_ID	Ide	Insulin-deg	R.ESLDDLTNLVVK#.L	10.18	4.30	2.37	0.42
Q9JHR7_ID	Ide	Insulin-deg	K.NEFIPTNFEILSLEK#.D	14.34	1.76	8.17	0.12
Q9JHR7_ID	Ide	Insulin-deg	K.AIEDM*TEEAFQK#.H	8.13	1.30	6.25	0.16
Q9JHR7_ID	Ide	Insulin-deg	K.GWVNTLVGGQK#.E	8.75	5.38	1.62	0.62
O88844_I	Idh1	Isocitrate d	R.FK#DIFQEIYDK#K#.Y	11.44	4.64	2.46	0.41
O88844_I	Idh1	Isocitrate d	R.IIWELIK#.E	10.89	9.82	1.11	0.90
O88844_I	Idh1	Isocitrate d	K.VEITYTPK#.D	16.61	5.13	3.24	0.31
Q9D6R2_I	Idh3a	Isocitrate d	R.ENTEGEYSGIEHVIVDGVVQSIK#.L	99.36	19.37	5.13	0.19
Q9D6R2_I	Idh3a	Isocitrate d	R.HM*GLFDHAAK#.I	29.11	12.67	2.30	0.44
Q9D6R2_I	Idh3a	Isocitrate d	R.IAEFAFEYAR.N	26.87	28.02	0.96	1.04
Q9D6R2_I	Idh3a	Isocitrate d	R.M*SDGLFLQK#.C	52.81	13.33	3.96	0.25
Q9D6R2_I	Idh3a	Isocitrate d	R.MSDGLFLQK#.C	16.84	3.93	4.28	0.23
Q9D6R2_I	Idh3a	Isocitrate d	R.NVTAIQGPGGK#.W	87.10	21.34	4.08	0.25
Q9D6R2_I	Idh3a	Isocitrate d	K.TPIAAGHPSMNLLLR.K	20.21	16.43	1.23	0.81
Q9D6R2_I	Idh3a	Isocitrate d	K.TPYTDVNIVTIR.E	11.32	13.52	0.84	1.20
Q9D6R2_I	Idh3a	Isocitrate d	R.IAEFAFEYAR.N	2.43	2.31	1.05	0.95
Q91VA7_Q	Idh3b	Isocitrate d	K.AAAVPVEFK#.E	28.89	10.97	2.63	0.38
Q91VA7_Q	Idh3b	Isocitrate d	R.DM*GGYSTTTDFIK#.S	23.97	6.94	3.45	0.29
Q91VA7_Q	Idh3b	Isocitrate d	R.DMGGYSTTTDFIK#.S	11.06	2.60	4.26	0.23
Q91VA7_Q	Idh3b	Isocitrate d	R.K#LDLFANVVHVK#.S	33.02	10.36	3.19	0.31
Q9CR20_IR	Ier3ip1	Immediate	K.NIGWGTDQGIGGFGEEPGIK.S	2.92	2.79	1.05	0.96
P15092_IF	Ifi204	Interferon-	R.SEVTGETSLEK#.N	31.16	12.26	2.54	0.39
P15092_IF	Ifi204	Interferon-	R.GTFVSGEYLVNK#.K	17.13	4.74	3.61	0.28
P15092_IF	Ifi204	Interferon-	K.NFIIISNYFESK#.G	7.39	3.61	2.05	0.49
P15092_IF	Ifi204	Interferon-	R.SEVTGETSLEK#.N	22.23	5.28	4.21	0.24
P15092_IF	Ifi204	Interferon-	K.VFDTALK#.S	19.32	4.52	4.27	0.23
P15092_IF	Ifi204	Interferon-	K.VFNINLK#.E	13.96	5.80	2.41	0.42
P15092_IF	Ifi204	Interferon-	K.DGSGSIEVVGSGK#.W	18.18	6.13	2.97	0.34
P15092_IF	Ifi204	Interferon-	R.SEVTGETSLEK#.N	19.05	3.90	4.89	0.20
P15092_IF	Ifi204	Interferon-	K.VFNINLK#.E	14.03	5.10	2.75	0.36
Q8CGE8_IF	Ifi205a	Interferon-	K.GILEINETSSVLEAAPK#.Q	41.99	12.65	3.32	0.30
Q8CGE8_IF	Ifi205a	Interferon-	K.NNFITISNYFESK#.G	17.58	4.94	3.56	0.28
Q8CGE8_IF	Ifi205a	Interferon-	K.VFNIDLK#.E	30.55	12.65	2.42	0.41
Q9D8C4_I	Ifi35	Interferon-	R.VSPYVSGEIQK.A	13.84	14.13	0.98	1.02
Q8BV66_IF	Ifi44	Interferon-	R.VLLLGPIGAGK#.S	46.81	22.14	2.11	0.47
Q8BV66_IF	Ifi44	Interferon-	R.VLLLGPIGAGK#.S	8.64	3.85	2.24	0.45
Q8BV66_IF	Ifi44	Interferon-	R.VLLLGPIGAGK#.S	29.27	9.18	3.19	0.31
Q8BV66_IF	Ifi44	Interferon-	R.YQFDSMKPITSNHPNYTHDPLLKDR@.I	2.53	3.29	0.77	1.30
Q8BV66_IF	Ifi44	Interferon-	K.EILYTANEFLEDLPLNK#.-	7.12	3.73	1.91	0.52
Q8BV66_IF	Ifi44	Interferon-	K.TNDFSILLDEK#.A	18.20	6.61	2.75	0.36
Q8BV66_IF	Ifi44	Interferon-	R.VLLLGPIGAGK#.S	58.04	25.05	2.32	0.43
Q61635_Q	Ifi47	GTP-bindin	R.FSLNDALLAQK#.I	9.29	5.95	1.56	0.64
Q61635_Q	Ifi47	GTP-bindin	R.TQFLNIVVDDAK#.H	8.09	3.15	2.57	0.39
Q61635_Q	Ifi47	GTP-bindin	K.EFLPQYSALISK#.A	8.41	6.90	1.22	0.82
Q8R5F7_IF	Ifih1	Interferon-	K.AHHLIGAGHSSEVK#PMTQTEQK#.E	14.25	5.80	2.46	0.41
Q8R5F7_IF	Ifih1	Interferon-	K.AHHLIGAGHSSEVK#PM*TQTEQK#.E	5.76	1.98	2.90	0.34
Q8R5F7_IF	Ifih1	Interferon-	R.DSGTM*GSDSDESVIQTK#.R	15.23	6.02	2.53	0.40
Q8R5F7_IF	Ifih1	Interferon-	R.IIGLSGDTQLK#.I	66.04	21.99	3.00	0.33
Q8R5F7_IF	Ifih1	Interferon-	K.ILELQVQSILEK#.K	29.62	9.38	3.16	0.32
Q8R5F7_IF	Ifih1	Interferon-	R.ISAAGNSGNESGVR.E	16.32	23.23	0.70	1.42
Q8R5F7_IF	Ifih1	Interferon-	K.ISFPEVVK#.S	45.69	20.25	2.26	0.44
Q8R5F7_IF	Ifih1	Interferon-	R.K#EFNPYLK#.K	14.81	6.47	2.29	0.44
Q8R5F7_IF	Ifih1	Interferon-	K.K#QNK#PAIPLPQILGLTASPGVGAAK#.K	9.19	3.47	2.65	0.38
Q8R5F7_IF	Ifih1	Interferon-	K.LAENPK#YENEK#.L	7.09	1.96	3.61	0.28
Q8R5F7_IF	Ifih1	Interferon-	K.M*YIQVEPVLDHLIFLSAETK#.E	14.46	3.82	3.79	0.26
Q8R5F7_IF	Ifih1	Interferon-	K.QNK#PAIPLPQILGLTASPGVGAAK#.K	23.84	9.09	2.62	0.38
Q8R5F7_IF	Ifih1	Interferon-	K.VIVLVNK#.V	70.12	26.84	2.61	0.38
Q8R5F7_IF	Ifih1	Interferon-	R.DSGTM*GSDSDESVIQTK#.R	12.48	3.04	4.10	0.24
Q8R5F7_IF	Ifih1	Interferon-	K.ILELQVQSILEK#.K	23.48	7.41	3.17	0.32
Q8R5F7_IF	Ifih1	Interferon-	R.ISAAGNSGNESGVR.E	14.26	22.24	0.64	1.56
Q8R5F7_IF	Ifih1	Interferon-	K.ISFPEVVK#.S	26.76	14.47	1.85	0.54
Q8R5F7_IF	Ifih1	Interferon-	K.LAENPK#YENEK#.L	4.42	1.82	2.42	0.41
Q8R5F7_IF	Ifih1	Interferon-	K.QNK#PAIPLPQILGLTASPGVGAAK#.K	37.59	15.71	2.39	0.42
Q8R5F7_IF	Ifih1	Interferon-	R.QSTYALSQWIMENAK#.F	5.99	1.64	3.65	0.27
Q8R5F7_IF	Ifih1	Interferon-	K.VIVLVNK#.V	37.23	11.76	3.17	0.32
Q64282_IF	Ifit1	Interferon-	K.ALKVEPENPEYNTGYAVVAYR.Q	20.78	65.04	0.32	3.13
Q64282_IF	Ifit1	Interferon-	K.EAEALIQSEQLSK#.R	147.72	93.04	1.59	0.63
Q64282_IF	Ifit1	Interferon-	K.EFSSPFR.Y	7.66	49.64	0.15	6.48
Q64282_IF	Ifit1	Interferon-	K.GQQDEALQSLK#.E	145.06	107.62	1.35	0.74
Q64282_IF	Ifit1	Interferon-	K.GQQDEALQSLK#EAEALIQSEQLSK#.R	12.16	6.03	2.02	0.50
Q64282_IF	Ifit1	Interferon-	R.GSLAEAQIYLDK#.V	41.10	27.64	1.49	0.67
Q64282_IF	Ifit1	Interferon-	R.HLK#GQQDEALQSLK#.E	27.98	14.34	1.95	0.51
Q64282_IF	Ifit1	Interferon-	R.ISEQVQFLDIK#.N	150.10	96.50	1.56	0.64
Q64282_IF	Ifit1	Interferon-	R.K#LLTALEK#.V	82.48	65.54	1.26	0.79

Q64282_IF	Ifit1	Interferon-i	K.LLFENNDIPDLEVR.I	26.78	79.66	0.34	2.97
Q64282_IF	Ifit1	Interferon-i	R.LTGEM*NPAF.-	47.04	47.04	1.00	1.00
Q64282_IF	Ifit1	Interferon-i	K.NALFYYEK#.A	159.68	89.31	1.79	0.56
Q64282_IF	Ifit1	Interferon-i	K.NPLGM*HNLLAYVR.H	4.07	9.85	0.41	2.42
Q64282_IF	Ifit1	Interferon-i	K.NPLGMHNLLAYVR.H	6.80	29.73	0.23	4.37
Q64282_IF	Ifit1	Interferon-i	R.QDLDDNFISLEPLR.K	4.05	13.23	0.31	3.27
Q64282_IF	Ifit1	Interferon-i	R.QDLDDNFISLEPLRK.A	16.85	51.92	0.32	3.08
Q64282_IF	Ifit1	Interferon-i	R.QDNVQELAQQAIHEFQETLK#.L	10.36	5.34	1.94	0.52
Q64282_IF	Ifit1	Interferon-i	R.RQDNVQELAQQAIHEFQETLK.L	31.89	88.68	0.36	2.78
Q64282_IF	Ifit1	Interferon-i	K.TLVAHIEQDIHLR.Y	1.72	6.64	0.26	3.86
Q64282_IF	Ifit1	Interferon-i	K.VEPENPEYNTGYAVVAYR.Q	3.73	15.37	0.24	4.12
Q64282_IF	Ifit1	Interferon-i	K.LLFENNDIPDLEVR.I	1.60	5.54	0.29	3.47
Q64282_IF	Ifit1	Interferon-i	K.AITLYLK#.G	46.64	32.13	1.45	0.69
Q64282_IF	Ifit1	Interferon-i	K.ALKVEPENPEYNTGYAVVAYR.Q	10.80	27.24	0.40	2.52
Q64282_IF	Ifit1	Interferon-i	K.EAEALIQSEQLSK#.R	57.84	39.69	1.46	0.69
Q64282_IF	Ifit1	Interferon-i	K.GQQDEALQSLK#.E	49.45	32.39	1.53	0.66
Q64282_IF	Ifit1	Interferon-i	K.GQQDEALQSLK#EAEALIQSEQLSK#.R	7.70	2.84	2.71	0.37
Q64282_IF	Ifit1	Interferon-i	R.HLK#GQQDEALQSLK#.E	29.03	9.75	2.98	0.34
Q64282_IF	Ifit1	Interferon-i	R.ISEQVQFLDIK#.N	48.60	33.84	1.44	0.70
Q64282_IF	Ifit1	Interferon-i	R.K#LLTALEK#.V	42.91	25.77	1.67	0.60
Q64282_IF	Ifit1	Interferon-i	K.LLFENNDIPDLEVR.I	17.15	38.23	0.45	2.23
Q64282_IF	Ifit1	Interferon-i	K.NALFYYEK#.A	40.65	31.41	1.29	0.77
Q64282_IF	Ifit1	Interferon-i	R.QDLDDNFISLEPLR.K	3.38	6.74	0.50	2.00
Q64282_IF	Ifit1	Interferon-i	R.RQDNVQELAQQAIHEFQETLK.L	17.28	39.78	0.43	2.30
Q64282_IF	Ifit1	Interferon-i	K.VEPENPEYNTGYAVVAYR.Q	2.12	5.39	0.39	2.54
Q64282_IF	Ifit1	Interferon-i	K.ALKVEPENPEYNTGYAVVAYR.Q	16.77	53.90	0.31	3.21
Q64282_IF	Ifit1	Interferon-i	K.EAEALIQSEQLSK#.R	121.61	76.62	1.59	0.63
Q64282_IF	Ifit1	Interferon-i	K.GQQDEALQSLK#.E	108.56	77.18	1.41	0.71
Q64282_IF	Ifit1	Interferon-i	K.GQQDEALQSLK#EAEALIQSEQLSK#.R	22.87	17.36	1.32	0.76
Q64282_IF	Ifit1	Interferon-i	R.HLK#GQQDEALQSLK#.E	61.73	29.51	2.09	0.48
Q64282_IF	Ifit1	Interferon-i	R.ISEQVQFLDIK#.N	133.69	90.82	1.47	0.68
Q64282_IF	Ifit1	Interferon-i	R.K#LLTALEK#.V	66.66	48.05	1.39	0.72
Q64282_IF	Ifit1	Interferon-i	K.LLFENNDIPDLEVR.I	34.09	97.52	0.35	2.86
Q64282_IF	Ifit1	Interferon-i	R.LNPEDPYLK#.V	115.06	70.94	1.62	0.62
Q64282_IF	Ifit1	Interferon-i	R.LTGEM*NPAF.-	47.85	47.85	1.00	1.00
Q64282_IF	Ifit1	Interferon-i	K.NALFYYEK#.A	84.93	51.43	1.65	0.61
Q64282_IF	Ifit1	Interferon-i	K.NPLGMHNLLAYVR.H	4.34	19.41	0.22	4.48
Q64282_IF	Ifit1	Interferon-i	R.QDLDDNFISLEPLRK.A	11.55	39.36	0.29	3.41
Q64282_IF	Ifit1	Interferon-i	R.QDNVQELAQQAIHEFQETLK#.L	34.07	13.94	2.44	0.41
Q64282_IF	Ifit1	Interferon-i	R.RQDNVQELAQQAIHEFQETLK.L	19.79	60.83	0.33	3.07
Q64282_IF	Ifit1	Interferon-i	K.TLVAHIEQDIHLR.Y	17.70	30.07	0.59	1.70
Q64282_IF	Ifit1	Interferon-i	K.VEPENPEYNTGYAVVAYR.Q	5.28	18.18	0.29	3.44
Q9CQW9_I	Ifitm3	Interferon-i	K.M*VGDVTGAQAYASTAK#.C	12.93	9.97	1.30	0.77
Q9D0P8_IF	Ift27	Intraflagell	K.NYTLTTGVDLVVK#.T	6.83	4.80	1.42	0.70
Q9D0P8_IF	Ift27	Intraflagell	R.SQTSGISLPGVLVGTK#.T	21.99	13.63	1.61	0.62
Q61249_IG	Igbp1	Immunoglc	R.AAQQQEDQEQK#DEESEEK#.A	9.31	6.34	1.47	0.68
Q61249_IG	Igbp1	Immunoglc	R.LPELFETSK#.K	15.35	7.51	2.04	0.49
Q61249_IG	Igbp1	Immunoglc	R.WIAVSLEELESIDQEIK#.I	14.99	5.84	2.57	0.39
Q61249_IG	Igbp1	Immunoglc	K.LLEDVEVATEPTGSR.T	2.86	5.03	0.57	1.76
O88477_IF	Igf2bp1	Insulin-like	R.DQTPDENDQVIVK#.I	18.88	8.85	2.13	0.47
O88477_IF	Igf2bp1	Insulin-like	R.LLVPTQYVGAIIGK#.E	66.99	16.95	3.95	0.25
O88477_IF	Igf2bp1	Insulin-like	K.LYIGNLNESVTPADLEK#.V	22.17	3.20	6.92	0.14
O88477_IF	Igf2bp1	Insulin-like	R.MVVITGPPEAQFK#.A	12.88	4.52	2.85	0.35
O88477_IF	Igf2bp1	Insulin-like	K.TADEVPLK#.I	47.24	13.93	3.39	0.29
O88477_IF	Igf2bp1	Insulin-like	K.TVNELQNLTAAEVVVPR.D	2.59	5.83	0.44	2.25
O88477_IF	Igf2bp1	Insulin-like	R.DQTPDENDQVIVK#.I	138.79	59.78	2.32	0.43
O88477_IF	Igf2bp1	Insulin-like	R.FASASIK#.I	61.33	53.21	1.15	0.87
O88477_IF	Igf2bp1	Insulin-like	K.LK#EENFFGPK#.E	15.20	7.01	2.17	0.46
O88477_IF	Igf2bp1	Insulin-like	K.LKEENFFGPK.E	9.72	5.58	1.74	0.57
O88477_IF	Igf2bp1	Insulin-like	R.M*VVITGPPEAQFK#.A	20.91	8.86	2.36	0.42
O88477_IF	Igf2bp1	Insulin-like	R.MVVITGPPEAQFK#.A	9.31	6.39	1.46	0.69
O88477_IF	Igf2bp1	Insulin-like	K.TVNELQNLTAAEVVVPR.D	14.91	28.89	0.52	1.94
Q5SF07_IF	Igf2bp2	Insulin-like	R.DQTPDENEEVIVR.I	6.58	22.27	0.30	3.38
Q5SF07_IF	Igf2bp2	Insulin-like	K.IAPAEGPDVSER.M	35.53	35.12	1.01	0.99
Q5SF07_IF	Igf2bp2	Insulin-like	K.IM*EVDYSVSK#.K	19.65	13.90	1.41	0.71
Q5SF07_IF	Igf2bp2	Insulin-like	K.IMEVDYSVSK#.K	22.75	12.09	1.88	0.53
Q5SF07_IF	Igf2bp2	Insulin-like	K.ITISSLQDLSIYNPER.T	10.45	29.60	0.35	2.83
Q5SF07_IF	Igf2bp2	Insulin-like	R.K#LPLAGQVLLK#.S	26.40	12.49	2.11	0.47
Q5SF07_IF	Igf2bp2	Insulin-like	R.KLPLAGQVLLK.S	20.81	12.45	1.67	0.60
Q5SF07_IF	Igf2bp2	Insulin-like	K.LAEEVPLK#.I	48.09	25.22	1.91	0.52
Q5SF07_IF	Igf2bp2	Insulin-like	K.LSGHQFEDYSFK#.I	30.71	14.26	2.15	0.46
Q5SF07_IF	Igf2bp2	Insulin-like	K.LYIGNLSPAVTADDLR.Q	11.87	41.42	0.29	3.49
Q5SF07_IF	Igf2bp2	Insulin-like	R.MILEIMQK#.E	19.53	9.93	1.97	0.51
Q5SF07_IF	Igf2bp2	Insulin-like	R.M*VIITGPPEAQFK#.A	6.34	5.82	1.09	0.92
Q5SF07_IF	Igf2bp2	Insulin-like	K.SGYAFVDYPDQNWAIR.A	7.05	16.90	0.42	2.40
Q5SF07_IF	Igf2bp2	Insulin-like	K.TVNELQNLTSAEVIVPR.D	1.48	5.25	0.28	3.55
Q5SF07_IF	Igf2bp2	Insulin-like	R.DQTPDENEEVIVR.I	28.90	79.74	0.36	2.76
Q5SF07_IF	Igf2bp2	Insulin-like	K.IAPAEGPDVSER.M	18.12	53.41	0.34	2.95
Q5SF07_IF	Igf2bp2	Insulin-like	R.IIGHFFASQTAQR.K	10.23	30.10	0.34	2.94
Q5SF07_IF	Igf2bp2	Insulin-like	K.LK#EENFFNPK#.E	9.14	8.03	1.14	0.88
Q5SF07_IF	Igf2bp2	Insulin-like	K.LKEENFFNPKEEVK.L	18.70	10.56	1.77	0.56
Q5SF07_IF	Igf2bp2	Insulin-like	R.M*VIITGPPEAQFK#.A	33.34	22.52	1.48	0.68
Q5SF07_IF	Igf2bp2	Insulin-like	R.MVIITGPPEAQFK#.A	50.52	33.39	1.51	0.66
Q5SF07_IF	Igf2bp2	Insulin-like	K.TVNELQNLTSAEVIVPR.D	16.74	37.57	0.45	2.24
A0A0A6YW	Ighg1	Ig gamma-1	K.NTQPIM*DTDGSYFVYSK.L	24.16	227.15	0.11	9.40
Q9QZ85_II	Iigp1	Interferon-i	R.TVFGVDETSLQR.L	2.79	5.97	0.47	2.14
Q9Z1M8_R	Ik	Protein Rec	K.GLDFALLQK#.V	24.70	11.16	2.21	0.45
Q9Z1M8_R	Ik	Protein Rec	K.KPPEADM*NIFEDIGDYVPSTTK.T	7.44	3.88	1.92	0.52
Q9Z1M8_R	Ik	Protein Rec	R.NELFLPGR.M	4.82	17.44	0.28	3.62
Q9Z1M8_R	Ik	Protein Rec	K.AAFQYGIK#.M	37.93	26.59	1.43	0.70
Q9Z1M8_R	Ik	Protein Rec	R.AVGPTAEADKSAAEK.R	15.67	14.25	1.10	0.91
Q9Z1M8_R	Ik	Protein Rec	R.DGVNKDYEETELISTTANYR.A	6.49	19.43	0.33	2.99
Q9Z1M8_R	Ik	Protein Rec	R.EYNEDEDPAAR.R	9.22	26.73	0.35	2.90
Q9Z1M8_R	Ik	Protein Rec	K.FAGSAGWEGTESLK#.K	61.67	12.71	4.85	0.21
Q9Z1M8_R	Ik	Protein Rec	K.GLDFALLQK#.V	61.56	39.92	1.54	0.65
Q9Z1M8_R	Ik	Protein Rec	K.K#DEDPENK#IEFK#.T	53.30	46.74	1.14	0.88
Q9Z1M8_R	Ik	Protein Rec	K.K#PPEADM*NIFEDIGDYVPSTTK#.T	21.35	18.46	1.16	0.86
Q9Z1M8_R	Ik	Protein Rec	K.K#PPEADMNIFEDIGDYVPSTTK#.T	21.52	13.70	1.57	0.64
Q9Z1M8_R	Ik	Protein Rec	R.M*AYVVDLDDEYADTDIPTTLIR.S	3.85	7.98	0.48	2.07
Q9Z1M8_R	Ik	Protein Rec	R.M*EADGVEVK#.R	11.76	6.42	1.83	0.55
Q9Z1M8_R	Ik	Protein Rec	R.WDFDTQEEYSEYMNNK#.E	5.06	2.97	1.70	0.59
Q7TT37_EL	Ikbkap	Elongator c	R.AEQGTVLIGSER.G	4.64	8.08	0.57	1.74
Q7TT37_EL	Ikbkap	Elongator c	K.DFEVIAEEQIHQDDFGEGK#.F	11.69	7.18	1.63	0.61

Q7TT37_EL	Ikbkap	Elongator c	R.EFALQSTSESVPGLGPALAWK#PSGSLIASTQDK#PNQQDVVFFEK#.N	5.15	4.67	1.10	0.91
Q7TT37_EL	Ikbkap	Elongator c	R.IVTVVPQDTK#.L	20.05	16.48	1.22	0.82
Q7TT37_EL	Ikbkap	Elongator c	K.SLAVQLADGQVLK#.Y	14.05	11.20	1.25	0.80
Q7TT37_EL	Ikbkap	Elongator c	R.SSGNSANDLANVAVIDGNR.V	2.48	7.13	0.35	2.87
Q7TT37_EL	Ikbkap	Elongator c	K.VFLENVETFVK#.Q	32.25	22.85	1.41	0.71
Q7TT37_EL	Ikbkap	Elongator c	R.AAM*EAINPR.K	7.02	20.76	0.34	2.96
Q7TT37_EL	Ikbkap	Elongator c	R.AEQGTVLIGSER.G	5.18	18.51	0.28	3.57
Q7TT37_EL	Ikbkap	Elongator c	R.ALVLAQIR.K	6.56	17.70	0.37	2.70
Q7TT37_EL	Ikbkap	Elongator c	K.DFEVIAEEQIHQDDFGEGK#.F	28.45	14.21	2.00	0.50
Q7TT37_EL	Ikbkap	Elongator c	R.EFALQSTSESVPGLGPALAWKPSGSLIASTQDKPNQQDVVFFEK.N	12.45	7.70	1.62	0.62
Q7TT37_EL	Ikbkap	Elongator c	R.IVTVVPQDTK#.L	54.43	37.90	1.44	0.70
Q7TT37_EL	Ikbkap	Elongator c	K.M*LQAALSGSHEASGEILR.K	10.44	7.96	1.31	0.76
Q7TT37_EL	Ikbkap	Elongator c	K.NYM*DFLDSETATFIR.H	1.68	4.77	0.35	2.83
Q7TT37_EL	Ikbkap	Elongator c	K.SLAVQLADGQVLK#.Y	35.41	19.49	1.82	0.55
Q7TT37_EL	Ikbkap	Elongator c	R.SSGNSANDLANVAVIDGNR.V	4.73	14.11	0.34	2.98
Q7TT37_EL	Ikbkap	Elongator c	K.SVQVSTHPDGK#.K	15.84	7.13	2.22	0.45
Q7TT37_EL	Ikbkap	Elongator c	K.TTPELEIVLQK#.V	27.84	14.64	1.90	0.53
Q7TT37_EL	Ikbkap	Elongator c	R.VDIIETSVK#PSILEAQK#.N	44.01	25.21	1.75	0.57
Q7TT37_EL	Ikbkap	Elongator c	K.VFLENVETFVK#.Q	54.49	41.89	1.30	0.77
Q7TT37_EL	Ikbkap	Elongator c	R.VLVTVFR.Q	9.18	23.89	0.38	2.60
Q7TT37_EL	Ikbkap	Elongator c	K.VQELQGNLPFDPESVSVEEALK#.Y	30.90	17.79	1.74	0.58
O88522_N	Ikbkg	NF-kappa-B	K.AQVTSLLGELQESQSR.L	2.09	9.17	0.23	4.39
Q8R459_IL	Il1f10	Interleukin	R.SKVPIFLGM*QGGSCCLACVKTR@.E	11.45	1.78	6.44	0.16
Q9CXY6_IL	Ilf2	Interleukin	R.AQDPSEVLTM*LTNETGFEISSSDATVK#.I	17.89	8.70	2.06	0.49
Q9CXY6_IL	Ilf2	Interleukin	R.AQDPSEVLTMLTNETGFEISSSDATVK#.I	43.89	28.98	1.51	0.66
Q9CXY6_IL	Ilf2	Interleukin	K.GTM*TTGHNVADLVVILK#.I	40.46	13.54	2.99	0.33
Q9CXY6_IL	Ilf2	Interleukin	K.GTM*TTGHNVADLVVILK#.I	15.16	4.77	3.18	0.31
Q9CXY6_IL	Ilf2	Interleukin	K.GTMTTGHNVADLVVILK#.I	48.11	19.60	2.45	0.41
Q9CXY6_IL	Ilf2	Interleukin	K.ILITTVPPNLR.K	12.90	31.74	0.41	2.46
Q9CXY6_IL	Ilf2	Interleukin	K.ILPTLEAVAALGNK#.V	68.69	35.54	1.93	0.52
Q9CXY6_IL	Ilf2	Interleukin	K.ILPTLEAVAALGNK#.V	234.35	118.90	1.97	0.51
Q9CXY6_IL	Ilf2	Interleukin	R.K#LDPELHLDIK#.V	140.01	54.36	2.58	0.39
Q9CXY6_IL	Ilf2	Interleukin	R.NQDLAPNSAEQASILSLVTK#.I	92.33	44.22	2.09	0.48
Q9CXY6_IL	Ilf2	Interleukin	R.QPLALNVAYR.R	28.87	58.56	0.49	2.03
Q9CXY6_IL	Ilf2	Interleukin	R.VK#PAPDETSFSEALLK#.R	133.81	72.27	1.85	0.54
Q9CXY6_IL	Ilf2	Interleukin	K.VLQSALAAIR.H	54.06	120.56	0.45	2.23
Q9CXY6_IL	Ilf2	Interleukin	R.WFEENASQSTVK#.V	98.00	39.05	2.51	0.40
Q9CXY6_IL	Ilf2	Interleukin	K.GTM*TTGHNVADLVVILK#.I	18.79	8.38	2.24	0.45
Q9CXY6_IL	Ilf2	Interleukin	K.GTMTTGHNVADLVVILK#.I	17.83	6.74	2.64	0.38
Q9CXY6_IL	Ilf2	Interleukin	K.ILITTVPPNLR.K	6.66	11.42	0.58	1.71
Q9CXY6_IL	Ilf2	Interleukin	K.ILPTLEAVAALGNK#.V	65.57	27.92	2.35	0.43
Q9CXY6_IL	Ilf2	Interleukin	R.K#LDPELHLDIK#.V	35.43	20.43	1.73	0.58
Q9CXY6_IL	Ilf2	Interleukin	R.NQDLAPNSAEQASILSLVTK#.I	67.61	35.21	1.92	0.52
Q9CXY6_IL	Ilf2	Interleukin	R.QPLALNVAYR.R	5.03	11.89	0.42	2.36
Q9CXY6_IL	Ilf2	Interleukin	R.VKPAPDETSFSEALLK.R	42.35	18.25	2.32	0.43
Q9CXY6_IL	Ilf2	Interleukin	R.VK#PAPDETSFSEALLK#.R	6.25	3.10	2.02	0.50
Q9CXY6_IL	Ilf2	Interleukin	K.VLQSALAAIR.H	15.26	24.43	0.62	1.60
Q9CXY6_IL	Ilf2	Interleukin	R.AQDPSEVLTMLTNETGFEISSSDATVK#.I	24.42	8.06	3.03	0.33
Q9CXY6_IL	Ilf2	Interleukin	K.GTM*TTGHNVADLVVILK#.I	43.68	11.89	3.67	0.27
Q9CXY6_IL	Ilf2	Interleukin	K.GTMTTGHNVADLVVILK#.I	11.78	9.19	1.28	0.78
Q9CXY6_IL	Ilf2	Interleukin	K.ILITTVPPNLR.K	9.10	16.20	0.56	1.78
Q9CXY6_IL	Ilf2	Interleukin	K.ILPTLEAVAALGNK#.V	132.76	59.80	2.22	0.45
Q9CXY6_IL	Ilf2	Interleukin	R.K#LDPELHLDIK#.V	59.06	20.61	2.87	0.35
Q9CXY6_IL	Ilf2	Interleukin	R.NQDLAPNSAEQASILSLVTK#.I	109.41	43.51	2.51	0.40
Q9CXY6_IL	Ilf2	Interleukin	R.NQDLAPNSAEQASILSLVTK#.I	26.82	12.37	2.17	0.46
Q9CXY6_IL	Ilf2	Interleukin	R.VK#PAPDETSFSEALLK#.R	81.07	37.99	2.13	0.47
Q9CXY6_IL	Ilf2	Interleukin	R.VKPAPDETSFSEALLKR.N	12.23	18.75	0.65	1.53
Q9CXY6_IL	Ilf2	Interleukin	K.VLQSALAAIR.H	29.82	48.36	0.62	1.62
Q9CXY6_IL	Ilf2	Interleukin	R.WFEENASQSTVK#.V	52.03	20.46	2.54	0.39
Q9Z1X4_IL	Ilf3	Interleukin	K.AYAALAALEK#.L	12.88	5.36	2.40	0.42
Q9Z1X4_IL	Ilf3	Interleukin	K.LFPDTPLALEANK#.K	6.71	4.18	1.60	0.62
Q9Z1X4_IL	Ilf3	Interleukin	K.ADPPQAM*NALM*R.L	7.57	19.89	0.38	2.63
Q9Z1X4_IL	Ilf3	Interleukin	K.AVSDWIDEQEK#.G	14.48	5.97	2.43	0.41
Q9Z1X4_IL	Ilf3	Interleukin	K.AVSDWIDEQEKGNSELSEAENM*DTPPDDESKEGAGEQK.A	14.45	6.95	2.08	0.48
Q9Z1X4_IL	Ilf3	Interleukin	R.EDITQSAQHALR.L	12.74	32.52	0.39	2.55
Q9Z1X4_IL	Ilf3	Interleukin	K.FNYSGSGGR.S	9.19	23.03	0.40	2.51
Q9Z1X4_IL	Ilf3	Interleukin	R.FVMEVEVDGQK#.F	88.07	42.09	2.09	0.48
Q9Z1X4_IL	Ilf3	Interleukin	K.HGK#NPVM*ELNEK#.R	34.49	14.94	2.31	0.43
Q9Z1X4_IL	Ilf3	Interleukin	K.HSSVYPTQEELEAVQNM*VSHTER.A	2.33	5.68	0.41	2.44
Q9Z1X4_IL	Ilf3	Interleukin	K.HSSVYPTQEELEAVQNMVSHTER.A	5.38	10.20	0.53	1.90
Q9Z1X4_IL	Ilf3	Interleukin	R.LAAFGQLHK#.V	98.24	39.52	2.49	0.40
Q9Z1X4_IL	Ilf3	Interleukin	K.LFPDTPLALEANK#.K	55.16	34.09	1.62	0.62
Q9Z1X4_IL	Ilf3	Interleukin	K.LISQTGPVHAPIFTM*SVEVDGSNFEASGPSK#.K	10.23	4.71	2.17	0.46
Q9Z1X4_IL	Ilf3	Interleukin	K.LISQTGPVHAPIFTMSVEVDGSNFEASGPSK#.K	24.59	8.11	3.03	0.33
Q9Z1X4_IL	Ilf3	Interleukin	K.LISQTGPVHAPIFTMSVEVDGSNFEASGPSK#K#.T	36.08	18.61	1.94	0.52
Q9Z1X4_IL	Ilf3	Interleukin	K.LISQTGPVHAPIFTMSVEVDGSNFEASGPSKK.T	6.34	2.69	2.36	0.42
Q9Z1X4_IL	Ilf3	Interleukin	K.NPVM*ELNEK#.R	25.01	16.34	1.53	0.65
Q9Z1X4_IL	Ilf3	Interleukin	K.NPVMELNEK#.R	45.51	20.65	2.20	0.45
Q9Z1X4_IL	Ilf3	Interleukin	R.NTEHSM*NYQYR.-	2.05	7.48	0.27	3.65
Q9Z1X4_IL	Ilf3	Interleukin	K.NTKEPPLSLTIHLTSPVVR.E	2.72	4.06	0.67	1.50
Q9Z1X4_IL	Ilf3	Interleukin	R.SGGNSYGSSGSSSYNTGSHGGYGTGSGGSSSYQGK#.Q	24.26	12.34	1.97	0.51
Q9Z1X4_IL	Ilf3	Interleukin	K.VLAGETLSVNDPPDVLDR.Q	15.28	35.29	0.43	2.31
Q9Z1X4_IL	Ilf3	Interleukin	K.VLGM*DPLPSK#.M	109.18	58.94	1.85	0.54
Q9Z1X4_IL	Ilf3	Interleukin	K.VLGMDPLPSK#.M	55.19	26.35	2.09	0.48
Q9Z1X4_IL	Ilf3	Interleukin	K.VLQDM*GLPTGAEGR.D	14.26	55.77	0.26	3.91
Q9Z1X4_IL	Ilf3	Interleukin	K.VLQDMGLPTGAEGR.D	14.78	31.83	0.46	2.15
Q9Z1X4_IL	Ilf3	Interleukin	R.VPTWGPLR.G	15.53	37.55	0.41	2.42
Q9Z1X4_IL	Ilf3	Interleukin	K.AVSDWIDEQEK#.G	8.23	3.92	2.10	0.48
Q9Z1X4_IL	Ilf3	Interleukin	K.AYAALAALEK#.L	59.69	24.31	2.46	0.41
Q9Z1X4_IL	Ilf3	Interleukin	K.LFPDTPLALEANK#.K	39.64	19.85	2.00	0.50
Q9Z1X4_IL	Ilf3	Interleukin	K.LISQTGPVHAPIFTM*SVEVDGSNFEASGPSK#.K	3.92	3.52	1.11	0.90
Q9Z1X4_IL	Ilf3	Interleukin	K.LISQTGPVHAPIFTMSVEVDGSNFEASGPSK#.K	4.10	1.82	2.25	0.44
Q9Z1X4_IL	Ilf3	Interleukin	K.NPVMELNEK#.R	11.38	11.13	1.02	0.98
Q9Z1X4_IL	Ilf3	Interleukin	K.VLAGETLSVNDPPDVLDR.Q	6.17	11.99	0.51	1.94
Q9Z1X4_IL	Ilf3	Interleukin	K.VLGM*DPLPSK#.M	49.73	19.12	2.60	0.38
Q9Z1X4_IL	Ilf3	Interleukin	K.VLQDMGLPTGAEGR.D	3.99	7.22	0.55	1.81
Q9Z1X4_IL	Ilf3	Interleukin	R.VPTWGPLR.G	5.92	12.66	0.47	2.14
O55222_IL	Ilk	Integrin-lin	R.EVPFADLSNM*EIGM*K#.V	11.33	10.00	1.13	0.88
O55222_IL	Ilk	Integrin-lin	R.EVPFADLSNM*EIGMK#.V	7.38	6.49	1.14	0.88
O55222_IL	Ilk	Integrin-lin	R.EVPFADLSNMEIGM*K.V	4.41	4.98	0.89	1.13
O55222_IL	Ilk	Integrin-lin	K.FDM*IVPILEK#.M	23.83	23.02	1.04	0.97
O55222_IL	Ilk	Integrin-lin	K.FDMIVPILEK.M	27.64	29.14	0.95	1.05
O55222_IL	Ilk	Integrin-lin	R.GM*AFLHTLEPLIPR.H	6.79	18.93	0.36	2.79

O55222_IL	Ilk	Integrin-lin	R.GMAFLHTLEPLIPR.H	3.69	11.10	0.33	3.01
O55222_IL	Ilk	Integrin-lin	R.M*YAPAWVAPEALQK#.K	13.33	16.11	0.83	1.21
O55222_IL	Ilk	Integrin-lin	R.MYAPAWVAPEALQK#.K	11.00	8.61	1.28	0.78
O55222_IL	Ilk	Integrin-lin	R.SAVVEMLIM*R.G	4.29	10.61	0.40	2.47
O55222_IL	Ilk	Integrin-lin	R.SVM*IDEDM*TAR.I	3.98	14.32	0.28	3.60
O55222_IL	Ilk	Integrin-lin	K.YGEM*PVDK#.A	19.64	18.05	1.09	0.92
O55222_IL	Ilk	Integrin-lin	K.FDM*IVPILEK#.M	10.69	6.71	1.59	0.63
O55222_IL	Ilk	Integrin-lin	K.FDMIVPILEK#.M	15.38	10.55	1.46	0.69
O55222_IL	Ilk	Integrin-lin	K.YGEM*PVDK#.A	6.86	6.89	1.00	1.00
O55222_IL	Ilk	Integrin-lin	R.EVPFADLSNM*EIGM*K#.V	7.49	4.75	1.58	0.63
O55222_IL	Ilk	Integrin-lin	K.FDM*IVPILEK#.M	13.16	15.97	0.82	1.21
O55222_IL	Ilk	Integrin-lin	K.FDMIVPILEK#.M	12.84	9.76	1.32	0.76
Q921Y2_IM	Imp3	U3 small nu	R.HVLEYNEER.D	1.33	7.21	0.18	5.44
Q921Y2_IM	Imp3	U3 small nu	K.LYAM*GLVPTR.G	1.43	5.22	0.27	3.64
Q921Y2_IM	Imp3	U3 small nu	R.SM*EDFVTWVDSSK#.I	2.33	3.68	0.63	1.58
Q921Y2_IM	Imp3	U3 small nu	R.VGPDVVTDPAFLVTR.S	2.42	4.52	0.54	1.86
Q8VHZ7_IM	Imp4	U3 small nu	R.VITFANQDDYISFR.H	1.70	4.18	0.41	2.46
P24547_IM	Impdh2	Inosine-5'-r	K.VAQGVSGAVQDK#.G	31.50	2.86	11.02	0.09
Q9WU62_I	Incenp	Inner centr	R.LAEQQLQEEQAK.K	4.11	19.88	0.21	4.84
Q9WU62_I	Incenp	Inner centr	R.TSSAVWNSPPLK.A	2.50	9.04	0.28	3.62
Q9WU62_I	Incenp	Inner centr	R.LAEQQLQEEQAK.K	5.41	11.35	0.48	2.10
Q9WU62_I	Incenp	Inner centr	R.VLSPILLNNILPTTAK.S	4.21	7.44	0.57	1.77
E9QLA5_E9	Inf2	Inverted fo	K.FDVEVLK#.Q	18.81	10.67	1.76	0.57
E9QLA5_E9	Inf2	Inverted fo	R.LQASIEASQELDK#VFDAIEQK#.K	33.98	16.17	2.10	0.48
E9QLA5_E9	Inf2	Inverted fo	R.NQEEFVPDSDDIK#.A	9.75	4.99	1.96	0.51
E9QLA5_E9	Inf2	Inverted fo	R.TEADSTSEGPEDEAQR.G	3.62	5.36	0.68	1.48
E9QLA5_E9	Inf2	Inverted fo	K.VSASIPEVQK#.Q	14.27	11.73	1.22	0.82
E9QLA5_E9	Inf2	Inverted fo	R.AVM*NSQQGIEYILSNQGYVR.Q	1.22	5.19	0.23	4.26
E9QLA5_E9	Inf2	Inverted fo	K.IGNFLNYGSHTGDADGFK#.I	25.64	9.65	2.66	0.38
E9QLA5_E9	Inf2	Inverted fo	R.LQASIEASQELDK#VFDAIEQK#.K	29.77	13.20	2.25	0.44
E9QLA5_E9	Inf2	Inverted fo	R.NQEEFVPDSDDIK#.A	9.54	5.41	1.76	0.57
E9QLA5_E9	Inf2	Inverted fo	R.TEADSTSEGPEDEAQR.G	3.52	7.20	0.49	2.05
E9QLA5_E9	Inf2	Inverted fo	K.VSASIPEVQK#.Q	24.28	32.07	0.76	1.32
Q9D8Y8_IN	Ing5	Inhibitor o	R.RLDADLAR.F	1.42	22.10	0.06	15.51
Q9D8Y8_IN	Ing5	Inhibitor o	R.RLDADLAR.F	6.53	8.31	0.79	1.27
Q8BHA0_IN	Ino80c	INO80 com	K.LSASGFAQGVSIEAM*NESK#.M	3.48	3.02	1.15	0.87
Q8BHA0_IN	Ino80c	INO80 com	K.MASSELSSGPVEK#.A	4.64	2.12	2.19	0.46
Q8BHA0_IN	Ino80c	INO80 com	K.M*ASSELSSGPVEK#.A	9.36	7.60	1.23	0.81
Q8BHA0_IN	Ino80c	INO80 com	K.YSDISGLLANYTDPQSK#.L	6.76	5.59	1.21	0.83
D3Z3H2_D	Ino80e	Coiled-coil	R.GSGASVGAALTPLPPPK#.M	5.80	4.62	1.26	0.80
Q6P549_SH	Inppl1	Phosphatid	R.LLQQQSLPQTGEQELESLVLK#.L	12.31	6.24	1.97	0.51
Q6P549_SH	Inppl1	Phosphatid	K.SFENDAQSSDNINFLK#.V	5.86	3.70	1.58	0.63
Q6P549_SH	Inppl1	Phosphatid	K.TSDQAYIEFESIEAIVK#.T	7.37	1.20	6.15	0.16
Q6P549_SH	Inppl1	Phosphatid	K.LDVTLGDLTK#.I	13.88	6.94	2.00	0.50
Q6P549_SH	Inppl1	Phosphatid	K.LGVVFEK#.E	13.72	5.04	2.72	0.37
Q6P549_SH	Inppl1	Phosphatid	R.LLLDTLQLSK#.-	23.37	8.97	2.61	0.38
Q6P549_SH	Inppl1	Phosphatid	K.SFENDAQSSDNINFLK#.V	7.27	9.33	0.78	1.28
Q6P549_SH	Inppl1	Phosphatid	K.TGIANTLGNK#.G	13.61	7.65	1.78	0.56
Q6P549_SH	Inppl1	Phosphatid	K.VLSGLEILSK#.V	9.89	4.79	2.06	0.48
Q6P4S8_IN	Ints1	Integrator	R.AVEDVLETLSDIDEM*SR.R	1.24	10.55	0.12	8.52
Q6P4S8_IN	Ints1	Integrator	K.FVIFNELSNAR.N	3.12	13.38	0.23	4.28
Q6P4S8_IN	Ints1	Integrator	R.LQDLLLGPK#.A	13.97	12.90	1.08	0.92
Q6P4S8_IN	Ints1	Integrator	K.VLFTEQPETYYK#.W	11.85	9.37	1.27	0.79
Q8K2A7_IN	Ints10	Integrator	K.ADLSNSIEVLESFK.L	14.20	10.25	1.39	0.72
Q8K2A7_IN	Ints10	Integrator	R.EISIITSALR.N	10.05	12.33	0.82	1.23
Q8K2A7_IN	Ints10	Integrator	K.ILLLQTLT.-	16.76	16.76	1.00	1.00
Q8K2A7_IN	Ints10	Integrator	K.ILNVVGM*R.C	3.56	11.18	0.32	3.14
Q8K2A7_IN	Ints10	Integrator	K.YIIEGLTEK.S	13.30	15.75	0.84	1.18
Q9D168_IN	Ints12	Integrator	K.ALLDESLAR.G	4.67	19.12	0.24	4.10
Q9D168_IN	Ints12	Integrator	K.ATSETSSSTSASLK#.G	19.94	10.69	1.87	0.54
Q9D168_IN	Ints12	Integrator	K.IGSGNSTSPSVPLKPLPPLTLGK.T	11.25	11.63	0.97	1.03
Q9D168_IN	Ints12	Integrator	R.TEVK#PSTVISGNSSSNNVSSSVTSGLTGWAAFAAK#.T	4.36	3.01	1.45	0.69
Q9D168_IN	Ints12	Integrator	K.TQKPPQKPAPTVVSVTPTVKDPLVK.K	5.04	5.01	1.01	0.99
Q7TPD0_IN	Ints3	Integrator	K.FSDLFSLAEEYEDSSTK#PPK#.S	17.41	8.58	2.03	0.49
Q7TPD0_IN	Ints3	Integrator	K.GKGTVAAAASGAAGGGGGGAGAGAPGGGR.L	23.60	18.16	1.30	0.77
Q7TPD0_IN	Ints3	Integrator	R.IPEFELLWK#.D	14.41	6.47	2.23	0.45
Q7TPD0_IN	Ints3	Integrator	R.TQLVWLVR.E	3.94	10.16	0.39	2.58
Q7TPD0_IN	Ints3	Integrator	R.DGM*NIVLNK#.I	13.64	7.25	1.88	0.53
Q7TPD0_IN	Ints3	Integrator	K.FSDLFSLAEEYEDSSTKPPK.S	39.08	21.53	1.82	0.55
Q7TPD0_IN	Ints3	Integrator	K.HDELLAEHIK#.A	17.09	7.73	2.21	0.45
Q7TPD0_IN	Ints3	Integrator	K.INQLLM*EK#.Y	22.21	11.98	1.85	0.54
Q7TPD0_IN	Ints3	Integrator	R.IPEFELLWK#.D	11.79	11.68	1.01	0.99
Q7TPD0_IN	Ints3	Integrator	K.QIAGGDVTAK#.N	23.91	10.25	2.33	0.43
Q7TPD0_IN	Ints3	Integrator	R.VLAHLAPLFDNPK#.L	18.17	11.74	1.55	0.65
Q8CIM8_IN	Ints4	Integrator	K.SPWLEGSEM*SPQVETSIEGTIPFSKPVK.V	2.54	3.13	0.81	1.23
Q8CIM8_IN	Ints4	Integrator	K.ASATIIEPAGESDNPLR.F	2.64	7.94	0.33	3.01
Q8CIM8_IN	Ints4	Integrator	K.IASLLGLLSK#.T	17.80	9.48	1.88	0.53
Q8CIM8_IN	Ints4	Integrator	K.LLSDDYEQVR.S	4.17	10.50	0.40	2.52
Q8CIM8_IN	Ints4	Integrator	K.SPWLEGSEM*SPQVETSIEGTIPFSK#PVK#.V	4.27	2.20	1.94	0.51
Q8CIM8_IN	Ints4	Integrator	K.VVQQQQEEIATK.K	12.11	7.24	1.67	0.60
Q6PCM2_II	Ints6	Integrator	R.ANQINHINSN.-	8.44	8.44	1.00	1.00
Q6PCM2_II	Ints6	Integrator	K.GQDEDQVHSVPIAQM*GNYQEYLK#.Q	5.50	5.16	1.07	0.94
Q6PCM2_II	Ints6	Integrator	K.LTTTSGVQDELHLPLNSPLPGSELTK.E	8.01	8.76	0.91	1.09
Q7TQK1_IN	Ints7	Integrator	K.ILNVDEFVK#.R	14.78	10.43	1.42	0.71
Q7TQK1_IN	Ints7	Integrator	K.IPIDSM*TNEM*EQR.V	5.68	5.38	1.06	0.95
Q7TQK1_IN	Ints7	Integrator	K.SLEDPYSQQIR.L	3.10	9.59	0.32	3.10
Q80V86_IN	Ints8	Integrator	K.AIGQTELNASNPEEVLQLAAQR.R	2.43	6.21	0.39	2.55
Q8K114_IN	Ints9	Integrator	K.VLK#PLLSGSIPVEQFVQTLEK#.H	8.45	7.33	1.15	0.87
Q8K114_IN	Ints9	Integrator	R.LLM*EELVNFIER.V	1.07	3.82	0.28	3.57
Q8K114_IN	Ints9	Integrator	R.LNFIQVSK#.L	19.02	9.19	2.07	0.48
Q8K114_IN	Ints9	Integrator	K.VLK#PLLSGSIPVEQFVQTLEK#.H	18.85	18.45	1.02	0.98
Q8K114_IN	Ints9	Integrator	K.VSYVSGSSLLTTHPQPM*DQASLK#.N	7.22	3.72	1.94	0.51
Q8VI75_IP	Ipo4	Importin-4	K.SLVLTALQK#.E	26.27	6.05	4.34	0.23
Q8VI75_IP	Ipo4	Importin-4	K.SLVLTALQK#.E	41.30	8.69	4.75	0.21
Q8VI75_IP	Ipo4	Importin-4	K.TEPQVLATLLR.A	13.03	10.74	1.21	0.82
Q8VI75_IP	Ipo4	Importin-4	R.VLM*ASPVGK#.T	33.82	3.58	9.46	0.11
Q8BKC5_IP	Ipo5	Importin-5	K.EGFVEYTEQVVK#.L	10.56	2.68	3.94	0.25
Q8BKC5_IP	Ipo5	Importin-5	K.FVPYYDLFMPSLK#.H	8.50	2.72	3.13	0.32
Q8BKC5_IP	Ipo5	Importin-5	K.HIVENAVQK#.E	25.41	11.47	2.21	0.45
Q8BKC5_IP	Ipo5	Importin-5	K.LQELIQK#.G	13.66	2.16	6.31	0.16
Q8BKC5_IP	Ipo5	Importin-5	K.SLLIPYLDNLVK#.H	27.23	4.84	5.62	0.18
Q8BKC5_IP	Ipo5	Importin-5	K.SLVEIADTVPK#.Y	21.45	7.84	2.73	0.37
Q8BKC5_IP	Ipo5	Importin-5	R.VIQAPEAK#.T	25.05	6.99	3.59	0.28

Q8BKC5_IP	Ipo5	Importin-5	K.VSDILHSIFSSYK#.E	18.19	5.02	3.62	0.28
Q8BKC5_IP	Ipo5	Importin-5	K.AIGTEPDSDVLSEIM*HSFAK#.C	32.50	8.38	3.88	0.26
Q8BKC5_IP	Ipo5	Importin-5	K.AIGTEPDSDVLSEIMHSFAK#.C	40.65	10.09	4.03	0.25
Q8BKC5_IP	Ipo5	Importin-5	K.EFQQYLPVVM*GPLM*K#.T	19.10	3.66	5.22	0.19
Q8BKC5_IP	Ipo5	Importin-5	K.EGFVEYTEQVVK#.L	34.02	9.30	3.66	0.27
Q8BKC5_IP	Ipo5	Importin-5	K.FM*QDASDVM*QLLLK#.T	10.00	4.02	2.49	0.40
Q8BKC5_IP	Ipo5	Importin-5	K.FVPYYDLFM*PSLK#.H	28.65	9.64	2.97	0.34
Q8BKC5_IP	Ipo5	Importin-5	K.FVPYYDLFMPSLK#.H	19.29	5.15	3.75	0.27
Q8BKC5_IP	Ipo5	Importin-5	K.HIVENAVQK#.E	93.67	18.49	5.06	0.20
Q8BKC5_IP	Ipo5	Importin-5	R.LLSSAFDEVYPALPSDVQTAIK#.S	52.13	12.66	4.12	0.24
Q8BKC5_IP	Ipo5	Importin-5	K.LM*VPLLK#.F	24.34	6.11	3.98	0.25
Q8BKC5_IP	Ipo5	Importin-5	K.LMVPLLK#.F	20.84	5.47	3.81	0.26
Q8BKC5_IP	Ipo5	Importin-5	K.LQELIQK#.G	58.72	10.39	5.65	0.18
Q8BKC5_IP	Ipo5	Importin-5	R.NLIDEDGNNQWPEGLK#.F	11.38	5.18	2.20	0.46
Q8BKC5_IP	Ipo5	Importin-5	K.RQDEDYDEQVEESLQDEDDNDVYILTK.V	5.64	4.70	1.20	0.83
Q8BKC5_IP	Ipo5	Importin-5	K.SLLIPYLDNLVK#.H	103.52	21.66	4.78	0.21
Q8BKC5_IP	Ipo5	Importin-5	K.SLVEIADTVPK#.Y	97.81	18.82	5.20	0.19
Q8BKC5_IP	Ipo5	Importin-5	R.VIQAPEAK#.T	95.59	25.59	3.74	0.27
Q8BKC5_IP	Ipo5	Importin-5	K.VSDILHSIFSSYK#.E	78.32	12.40	6.32	0.16
Q9EPL8_IP	Ipo7	Importin-7	K.AFAVGVQQVLLK#.V	43.92	7.72	5.69	0.18
Q9EPL8_IP	Ipo7	Importin-7	R.ETENDDLTNVIQK#.M	25.87	5.61	4.61	0.22
Q9EPL8_IP	Ipo7	Importin-7	R.FIQLLSDQSDQSVLIQK#.Q	11.95	3.49	3.42	0.29
Q9EPL8_IP	Ipo7	Importin-7	K.FSAPVVPSSFNFGGPAPGM*N.-	15.93	15.93	1.00	1.00
Q9EPL8_IP	Ipo7	Importin-7	R.QAGVIYLK#.N	13.34	1.71	7.81	0.13
Q9EPL8_IP	Ipo7	Importin-7	R.SPLVAAMQHFLPVLK#.D	16.81	2.41	6.99	0.14
Q91YE6_IP	Ipo9	Importin-9	R.HLQEAEQTK#.A	6.07	4.35	1.39	0.72
Q91YE6_IP	Ipo9	Importin-9	K.YSNDPVVASLAQDIFK#.E	9.34	4.30	2.17	0.46
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.ATFYGEQVDYYK#.S	15.64	7.88	1.98	0.50
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.GVLLEIEDLQANQFK#.N	12.88	8.55	1.51	0.66
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LPYDVTPEQALSHEEVK#.T	14.23	6.65	2.14	0.47
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LQQTYSALNSK#.A	28.38	12.77	2.22	0.45
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LTELGTVDPK#.N	16.35	6.13	2.67	0.37
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.NVIFEIGPTEEVGDFEVK#.A	18.16	9.57	1.90	0.53
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.ALESGDM*TTVWK#.Q	35.27	6.50	5.42	0.18
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.AQETQDESAVLWLDEIQGGIWQSNK#.D	10.95	1.95	5.62	0.18
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.ATFYGEQVDYYK#.S	92.74	32.14	2.89	0.35
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.DHINDIIK#.I	120.55	38.46	3.13	0.32
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.DSLHEK#FPDAGEDELLK#.I	41.17	17.82	2.31	0.43
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.EEIQSSISGVTAAYNR.E	13.46	12.35	1.09	0.92
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.EK#AQETQDESAVLWLDEIQGGIWQSNK#.D	11.79	2.53	4.67	0.21
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.EKLEAYQHLFYLLQTNPTYLAK.L	19.66	4.27	4.61	0.22
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.EQLWLANEGLITK#.L	74.18	19.01	3.90	0.26
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.FALGISAINEAVDSGDVGR.T	10.82	11.08	0.98	1.02
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FDVPGDENAEM*DAR.T	7.28	10.39	0.70	1.43
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FLSAIVSSVDK#.I	43.11	10.55	4.09	0.24
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FM*DSVIFTLYNYASNQR.E	3.38	8.44	0.40	2.50
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FPDAGEDELLK#.I	15.11	8.58	1.76	0.57
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FVHLLDQSDQDFQEELDLM*K#.M	21.42	8.19	2.61	0.38
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FVHLLDQSDQDFQEELDLMK#.M	12.53	6.61	1.90	0.53
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.GLQTQNSDWYM*K#.Q	17.41	5.33	3.27	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.GVLLEIEDLQANQFK#.N	83.10	19.28	4.31	0.23
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.HTDNVIQWLNAM*DEIGLPK#.I	14.26	8.12	1.76	0.57
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.HTDNVIQWLNAMDEIGLPK#.I	31.94	7.06	4.52	0.22
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.IIGNLLYYR.Y	26.37	41.61	0.63	1.58
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.ILAIGLINEALDEGDAQK#.T	74.88	15.80	4.74	0.21
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.ILAIGLINEALDEGDAQK#.T	196.95	56.11	3.51	0.28
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.K#FVHLLDQSDQDFQEELDLM*K#.M	12.44	3.90	3.19	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.K#LTELGTVDPK#.N	20.29	6.67	3.04	0.33
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.LAAVAAINAAIQK#.G	21.28	5.13	4.14	0.24
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.LAYLHSHK#DEVVK#.I	106.81	21.20	5.04	0.20
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LEAYQHLFYLLQTNPTYLAK#.L	21.27	8.16	2.61	0.38
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LEGVLAEVAQHYQDTLIR.A	26.67	37.12	0.72	1.39
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.LFQTALQEEIK#.S	176.83	57.86	3.06	0.33
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LGLAPQIQDLYGK#.V	59.16	12.70	4.66	0.21
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LGNFFSPK#.V	49.22	13.32	3.69	0.27
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LIFQM*PQNK#.S	110.32	40.24	2.74	0.36
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LIFQMPQNK#.S	31.66	12.39	2.55	0.39
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.LIVDVIR.F	21.84	30.96	0.71	1.42
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LPYDVTPEQALSHEEVK#.T	128.22	43.65	2.94	0.34
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LQQTYSALNSK#.A	117.77	39.18	3.01	0.33
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LTELGTVDPK#.N	121.15	35.22	3.44	0.29
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.M*FLGDNAHLSIINEYLSQSYQK#.F	65.50	17.15	3.82	0.26
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.MFLGDNAHLSIINEYLSQSYQK#.F	18.44	4.89	3.77	0.27
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.NPNAM*LVNLEEGLAPTYQDVLYQAK#.Q	9.67	4.02	2.40	0.42
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.NPNAMLVNLEEGLAPTYQDVLYQAK#.Q	8.94	4.60	1.94	0.52
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.NVIFEIGPTEEVGDFEVK#.A	103.12	37.93	2.72	0.37
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.QLQSDLQQK#.R	45.45	13.15	3.46	0.29
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.QSGQTDPLQKEEVQAGVDAANSAAQQYQR.R	3.80	4.48	0.85	1.18
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.SK#VDQIQEIVTGNPTVIK#.M	80.81	20.56	3.93	0.25
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.SNQQLENDLNLM*DIK#.I	55.13	17.27	3.19	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.SNQQLENDLNLMDIK#.I	24.99	8.72	2.87	0.35
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.SWVNQM*ESQTGEASK#.L	20.25	7.56	2.68	0.37
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.SWVNQMESQTGEASK#.L	29.15	6.79	4.29	0.23
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.TEVSLTLTNK#.F	35.14	9.89	3.55	0.28
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.TLINAEDPPM*IVVR.K	3.59	6.82	0.53	1.90
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.TLQALQIPAAK#.L	69.61	15.63	4.45	0.22
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.VAADTFTALK#.N	47.22	12.38	3.82	0.26
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.VDFTEEEINNM*K#.I	2.07	13.73	0.15	6.62
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.VDQIQEIVTGNPTVIK#.M	50.47	13.49	3.74	0.27
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.YGIQM*PAFSK#.I	34.41	7.86	4.38	0.23
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.YGIQMPAFSK#.I	13.69	3.96	3.46	0.29
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.YM*NPAIVAPDAFDIIDLSAGGQLTTDQR.R	8.28	16.24	0.51	1.96
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.YQELINDIAK#.D	114.28	32.15	3.55	0.28
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.ALESGDM*TTVWK#.Q	65.26	20.33	3.21	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.ALESGDMTTVWK#.Q	29.83	9.74	3.06	0.33
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.ALQSLALGLR.G	56.99	46.19	1.23	0.81
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.ATFYGEQVDYYK#.S	198.43	52.46	3.78	0.26
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.DHINDIIK#.I	232.15	67.99	3.41	0.29
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.DSLHEK#FPDAGEDELLK#.I	72.62	23.10	3.14	0.32
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.DVYEELLTQAEIQGNVNK#.V	18.79	5.61	3.35	0.30
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.EDNNLSLQEK#.K	45.13	15.74	2.87	0.35
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.EEIQSSISGVTAAYNR.E	34.29	46.11	0.74	1.34
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.EEVQAGVDAANSAAQQYQR.R	10.18	13.44	0.76	1.32

Q9JKF1_IQ	Iqgap1	Ras GTPase	R.EQLWLANEGLITK#.L	213.89	56.74	3.77	0.27
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.ERDVYEELLTQAEIQGNVNK.V	11.07	27.68	0.40	2.50
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.FALGISAINEAVDSGDVGR.T	43.33	61.28	0.71	1.41
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FDVPGDENAEM*DAR.T	11.24	22.79	0.49	2.03
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FLSAIVSSVDK#.I	63.28	18.02	3.51	0.28
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FPDAGEDELLK#.I	16.57	9.12	1.82	0.55
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FVHLLDQSDQDFQEELDLM*K#.M	51.20	12.49	4.10	0.24
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.FVHLLDQSDQDFQEELDLMK#.M	30.48	7.16	4.26	0.23
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.GLQTQNSDWYM*K#.Q	64.78	17.22	3.76	0.27
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.GVLLEIEDLQANQFK#.N	109.72	38.75	2.83	0.35
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.HTDNVIQWLNAM*DEIGLPK#.I	54.95	24.89	2.21	0.45
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.HTDNVIQWLNAMDEIGLPK#.I	53.52	17.50	3.06	0.33
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.IFYPETTDIYDR.K	11.82	19.27	0.61	1.63
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.IIGNLLYYR.Y	44.25	63.13	0.70	1.43
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.ILAIGLINEALDEGDAQK#.T	639.74	182.34	3.51	0.29
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.ILAIGLINEALDEGDAQK#.T	258.00	79.24	3.26	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.ITLQDVVSHSK#.K	223.40	69.75	3.20	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.K#FVHLLDQSDQDFQEELDLM*K#.M	23.32	27.93	0.84	1.20
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.LAAGDNNSK#.W	8.02	4.64	1.73	0.58
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.LAAVAAINAAIQK#.G	66.95	23.53	2.85	0.35
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LEAYQHLFYLLQTNPTYLAK#.L	46.66	8.81	5.30	0.19
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LEGVLAEVAQHYQDTLIR.A	100.38	129.27	0.78	1.29
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.LFQTALQEEIK#.S	350.97	98.23	3.57	0.28
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LGLAPQIQDLYGK#.V	159.73	47.49	3.36	0.30
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LGLAPQIQDLYGK#VDFTEEEINNMK#.I	11.62	2.16	5.37	0.19
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LGNFFSPK#.V	149.59	40.64	3.68	0.27
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LIFQM*PQNK#.S	254.83	91.88	2.77	0.36
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LIFQMPQNK#.S	62.87	19.44	3.23	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.LIVDVIR.F	50.48	62.06	0.81	1.23
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LPYDVTPEQALSHEEVK#.T	279.76	101.88	2.75	0.36
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LQQTYSALNSK#.A	311.64	95.38	3.27	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.LTAEEM*DER.R	23.87	29.59	0.81	1.24
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.LTELGTVDPK#.N	200.08	48.58	4.12	0.24
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.M*FLGDNAHLSIINEYLSQSYQK#.F	95.59	21.66	4.41	0.23
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.MFLGDNAHLSIINEYLSQSYQK#.F	13.83	3.73	3.71	0.27
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.M*LQHAASNK#.M	4.72	1.78	2.65	0.38
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.M*REEVITLIR.S	5.50	24.69	0.22	4.49
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.NGVYLAK#.L	394.63	14.42	27.36	0.04
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.NPNAM*LVNLEEGLAPTYQDVLYQAK#.Q	22.65	7.77	2.92	0.34
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.NPNAMLVNLEEGLAPTYQDVLYQAK#.Q	48.62	14.91	3.26	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.NVIFEIGPTEEVGDFEVK#.A	243.50	70.84	3.44	0.29
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.QLQSDLQQK#.R	156.03	52.44	2.98	0.34
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.QSGQTDPLQK#.E	23.74	8.37	2.84	0.35
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.QSGQTDPLQKEEVQAGVDAANSAAQQYQR.R	14.96	16.22	0.92	1.08
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.RLIVDVIR.F	3.12	20.32	0.15	6.51
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.SK#VDQIQEIVTGNPTVIK#.M	168.01	46.21	3.64	0.28
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.SNQQLENDLNLM*DIK#.I	75.16	23.49	3.20	0.31
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.SNQQLENDLNLMDIK#.I	52.47	19.10	2.75	0.36
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.SWVNQM*ESQTGEASK#.L	41.44	13.39	3.09	0.32
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.SWVNQMESQTGEASK#.L	33.71	10.86	3.10	0.32
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.SWVNQM*ESQTGEASK#LPYDVTPEQALSHEEVK#.T	28.36	9.33	3.04	0.33
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.TEVSLTLTNK#.F	76.92	22.76	3.38	0.30
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.TEVSLTLTNKFDVPGDENAEM*DAR.T	9.35	13.24	0.71	1.42
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.TILLNTK#.R	195.40	47.85	4.08	0.24
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.TLINAEDPPM*IVVR.K	12.74	17.46	0.73	1.37
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.TLQALQIPAAK#.L	212.11	70.60	3.00	0.33
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.TVLELM*NPEAQLPQVYPFAADLYQK#.E	61.64	15.53	3.97	0.25
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.VAADTFTALK#.N	128.61	38.62	3.33	0.30
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.VAADTFTALK#NPNAM*LVNLEEGLAPTYQDVLYQAK#.Q	14.36	5.35	2.68	0.37
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.VDQIQEIVTGNPTVIK#.M	97.92	27.43	3.57	0.28
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.YGIQM*PAFSK#.I	77.77	25.52	3.05	0.33
Q9JKF1_IQ	Iqgap1	Ras GTPase	K.YGIQMPAFSK#.I	46.69	13.01	3.59	0.28
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.YLDELM*K#.L	94.19	34.93	2.70	0.37
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.YM*NPAIVAPDAFDIIDLSAGGQLTTDQR.R	28.57	41.15	0.69	1.44
Q9JKF1_IQ	Iqgap1	Ras GTPase	R.YQELINDIAK#.D	189.21	48.64	3.89	0.26
F8VQ29_F8	Iqgap3	Protein Iqg	K.FAHLLNQSQEDFSAESELLK.L	6.18	7.38	0.84	1.19
E9Q1P8_I2	Irf2bp2	Interferon	R.AAATLAAVSGTPGLGAQPAELGTHK#.R	13.13	18.82	0.70	1.43
E9Q1P8_I2	Irf2bp2	Interferon	K.RPASVSSAAAEHEAR.E	2.52	23.25	0.11	9.24
E9Q1P8_I2	Irf2bp2	Interferon	R.SPADSLSSAAGASELSAEGAGK.G	9.60	7.91	1.21	0.82
Q8K3X4_I2	Irf2bpl	Interferon	R.QQWM*ANQSEALK.L	2.81	62.94	0.04	22.43
Q8K3X4_I2	Irf2bpl	Interferon	R.QQWMANQSEALK.L	1.91	25.61	0.07	13.41
Q8K3X4_I2	Irf2bpl	Interferon	K.LFIEYPTGSGNVYSSASGVAK#.Q	7.04	2.92	2.41	0.41
Q8K3X4_I2	Irf2bpl	Interferon	R.LLGDLLPEAVR.F	5.14	12.03	0.43	2.34
Q8K3X4_I2	Irf2bpl	Interferon	R.NAEALAELSESLR.N	14.45	7.41	1.95	0.51
Q8K3X4_I2	Irf2bpl	Interferon	R.YGLSAAAAAAAAAAAVEQR.S	3.94	11.62	0.34	2.95
Q64339_IS	Isg15	Ubiquitin-l	R.GHSNIYEVFLTQTVDTLK#.K	81.32	43.71	1.86	0.54
Q64339_IS	Isg15	Ubiquitin-l	R.GHSNIYEVFLTQTVDTLKK.K	38.48	19.29	1.99	0.50
Q64339_IS	Isg15	Ubiquitin-l	R.GHSNIYEVFLTQTVDTLK#K#.K	11.75	9.08	1.29	0.77
Q64339_IS	Isg15	Ubiquitin-l	K.IGVPAFQQR.L	27.70	65.22	0.42	2.35
Q64339_IS	Isg15	Ubiquitin-l	K.M*LGGNDFLVSVTNSMTVSELK#K#.Q	19.72	14.28	1.38	0.72
Q64339_IS	Isg15	Ubiquitin-l	R.GHSNIYEVFLTQTVDTLK#K#.K	38.57	20.14	1.92	0.52
Q64339_IS	Isg15	Ubiquitin-l	K.IGVPAFQQR.L	26.28	71.17	0.37	2.71
Q64339_IS	Isg15	Ubiquitin-l	K.M*LGGNDFLVSVTNSM*TVSELKK.Q	47.54	27.90	1.70	0.59
Q64339_IS	Isg15	Ubiquitin-l	K.M*LGGNDFLVSVTNSMTVSELK#K#.Q	19.60	12.12	1.62	0.62
Q64339_IS	Isg15	Ubiquitin-l	R.GHSNIYEVFLTQTVDTLK#.K	428.08	200.45	2.14	0.47
Q64339_IS	Isg15	Ubiquitin-l	R.GHSNIYEVFLTQTVDTLK#K#.K	143.77	70.78	2.03	0.49
Q64339_IS	Isg15	Ubiquitin-l	K.M*LGGNDFLVSVTNSM*TVSELKK.Q	106.93	42.70	2.50	0.40
Q64339_IS	Isg15	Ubiquitin-l	K.MLGGNDFLVSVTNSM*TVSELKK.Q	53.59	26.58	2.02	0.50
Q64339_IS	Isg15	Ubiquitin-l	K.M*LGGNDFLVSVTNSMTVSELK#K#.Q	79.99	34.39	2.33	0.43
Q64339_IS	Isg15	Ubiquitin-l	K.MLGGNDFLVSVTNSMTVSELK#K#.Q	38.75	23.05	1.68	0.59
Q64339_IS	Isg15	Ubiquitin-l	R.GHSNIYEVFLTQTVDTLK#.K	460.61	187.33	2.46	0.41
Q64339_IS	Isg15	Ubiquitin-l	R.GHSNIYEVFLTQTVDTLK#K#.K	93.81	45.19	2.08	0.48
Q64339_IS	Isg15	Ubiquitin-l	K.IGVPAFQQR.L	133.84	532.74	0.25	3.98
Q64339_IS	Isg15	Ubiquitin-l	K.M*LGGNDFLVSVTNSM*TVSELK#.K	15.61	9.77	1.60	0.63
Q64339_IS	Isg15	Ubiquitin-l	K.M*LGGNDFLVSVTNSM*TVSELKK.Q	200.57	100.41	2.00	0.50
Q64339_IS	Isg15	Ubiquitin-l	K.MLGGNDFLVSVTNSM*TVSELKK.Q	5.42	3.19	1.70	0.59
Q64339_IS	Isg15	Ubiquitin-l	K.M*LGGNDFLVSVTNSMTVSELK#K#.Q	66.25	32.97	2.01	0.50
Q9JL16_IS	Isg20	Interferon-	R.LEILQLLK#.G	34.80	24.33	1.43	0.70
Q9JL16_IS	Isg20	Interferon-	K.YIRPEGEITDYR.T	1.34	20.38	0.07	15.22
Q9JL16_IS	Isg20	Interferon-	K.YTIYDTSTDR.L	7.31	17.53	0.42	2.40
Q3U1G5_I	Isg20l2	Interferon-	K.IDLLGEFQSALPK#.T	24.78	13.10	1.89	0.53
Q3U1G5_I	Isg20l2	Interferon-	K.LVEVEWEQHLAQNPPEN.-	9.36	9.36	1.00	1.00
Q91V64_IS	Isoc1	Isochorism	K.GLGSTVQEIDLTGVK#.L	13.87	2.30	6.02	0.17

Q69ZQ2_IS	Isy1	Pre-mRNA-	K.ELGGPDYGK.V	3.17	6.99	0.45	2.21
Q69ZQ2_IS	Isy1	Pre-mRNA-	K.FIAHVPVPSQQEIEEALVR.R	5.55	24.11	0.23	4.34
Q69ZQ2_IS	Isy1	Pre-mRNA-	K.YASETLQAQSEEAK.R	10.59	6.81	1.56	0.64
Q8C863_IT	Itch	E3 ubiquiti	K.FIDTGFSLPFYK#.R	14.26	5.17	2.76	0.36
Q8C863_IT	Itch	E3 ubiquiti	K.FIDTGFSLPFYK#.R	13.31	8.38	1.59	0.63
Q62470_IT	Itga3	Integrin alp	K.LGLPGLATFGYSLSGK#.M	11.95	9.03	1.32	0.76
P43406_IT	Itgav	Integrin alp	K.IYIGDDNPLTLTVK.A	8.32	6.90	1.21	0.83
P09055_IT	Itgb1	Integrin be	R.GEFFNELVGQQR.I	2.98	8.32	0.36	2.79
P09055_IT	Itgb1	Integrin be	R.IGFGSFVEK#.T	37.95	29.48	1.29	0.78
P09055_IT	Itgb1	Integrin be	K.LRPEDITQIQPQQLLLK.L	9.02	34.74	0.26	3.85
P09055_IT	Itgb1	Integrin be	K.LSENNIQTIFAVTEEFQPVYK#.E	32.93	28.40	1.16	0.86
P09055_IT	Itgb1	Integrin be	K.LSENNIQTIFAVTEEFQPVYK.E	7.28	6.98	1.04	0.96
P09055_IT	Itgb1	Integrin be	K.NVLSLTDRGEFFNELVGQQR.I	1.69	20.90	0.08	12.36
P09055_IT	Itgb1	Integrin be	K.SAVTTVVNPK#.Y	38.59	31.02	1.24	0.80
P09055_IT	Itgb1	Integrin be	K.TVM*PYISTTPAK.L	8.87	13.82	0.64	1.56
P09055_IT	Itgb1	Integrin be	K.WDTGENPIYK#.S	17.18	13.43	1.28	0.78
P09055_IT	Itgb1	Integrin be	K.LRPEDITQIQPQQLLLK.L	1.86	11.37	0.16	6.10
Q9CQ82_C	Itgb3bp	Centromer	K.NLSSIQALEGNR.Q	3.57	10.28	0.35	2.88
Q9Z0R4_IT	Itsn1	Intersectin-	K.GPLTISAQESVK#.V	18.80	6.67	2.82	0.35
Q9Z0R4_IT	Itsn1	Intersectin-	K.IPENEVPTPAK#PVTDLTSAPAPK#.L	6.02	5.36	1.12	0.89
Q9Z0R4_IT	Itsn1	Intersectin-	K.LATQAPWSTTEK#.G	12.66	4.66	2.72	0.37
Q9Z0R4_IT	Itsn1	Intersectin-	R.SHDEITIQPGDIVM*VDESQTGEPGWLGGELK#.G	2.87	1.50	1.92	0.52
Q9Z0R4_IT	Itsn1	Intersectin-	R.SHDEITIQPGDIVMVDESQTGEPGWLGGELK#.G	5.26	3.89	1.35	0.74
Q9Z0R4_IT	Itsn1	Intersectin-	K.TGWFPANYAEKIPENEVPTPAKPVTDLTSAPAPK.L	4.86	5.06	0.96	1.04
Q8C1D8_I	Iws1	Protein IW	K.ILQELPSVSQETLK#.H	9.04	4.27	2.12	0.47
P05627_JU	Jun	Transcripti	K.NVTDEQEGFAEGFVR.A	1.85	8.74	0.21	4.74
P09450_JU	Junb	Transcripti	R.GASAFKEEPQTVPEAR.S	1.37	15.83	0.09	11.54
P15066_JU	Jund	Transcripti	K.SQNTELASTASLLR.E	3.07	10.20	0.30	3.33
P15066_JU	Jund	Transcripti	K.VAASEEQEFAEGFVK.A	9.62	10.09	0.95	1.05
Q99MN1_S	Kars	Lysine--tRN	K.ETAATTETPESTEASPSV.-	3.84	3.84	1.00	1.00
Q99MN1_S	Kars	Lysine--tRN	K.ETAATTETPESTEASPSV.-	23.07	23.07	1.00	1.00
Q99MN1_S	Kars	Lysine--tRN	R.FELFVMK#.K	31.49	5.13	6.14	0.16
Q99MN1_S	Kars	Lysine--tRN	R.ISM*VEELEK#.A	38.86	7.89	4.93	0.20
Q99MN1_S	Kars	Lysine--tRN	R.ISMVEELEK#.A	31.75	4.43	7.17	0.14
Q99MN1_S	Kars	Lysine--tRN	K.ITYHPDGPEGQAYEVDFTPPFR.R	11.68	11.48	1.02	0.98
Q99MN1_S	Kars	Lysine--tRN	K.K#ETAATTETPESTEASPSV.-	12.78	2.38	5.38	0.19
Q99MN1_S	Kars	Lysine--tRN	K.LIFYDLR.G	23.88	15.56	1.53	0.65
Q99MN1_S	Kars	Lysine--tRN	R.LTM*FLTDSNNIK#.E	20.90	9.09	2.30	0.43
Q99MN1_S	Kars	Lysine--tRN	R.NYK#SEEEFVHINNK#.L	34.75	7.28	4.77	0.21
Q99MN1_S	Kars	Lysine--tRN	R.QLFEEQAK#.A	37.40	20.98	1.78	0.56
Q99MN1_S	Kars	Lysine--tRN	K.QLNQTASAPNHTADNGVGAEEETLDPNQYYK#.I	5.01	1.76	2.84	0.35
Q99MN1_S	Kars	Lysine--tRN	R.SQAVQQLK#.V	70.28	9.93	7.08	0.14
Q99MN1_S	Kars	Lysine--tRN	R.YLDLILNDFVR.Q	51.76	21.21	2.44	0.41
Q99MN1_S	Kars	Lysine--tRN	K.ETAATTETPESTEASPSV.-	26.08	26.08	1.00	1.00
Q99MN1_S	Kars	Lysine--tRN	R.FELFVMK#.K	11.33	2.19	5.18	0.19
Q99MN1_S	Kars	Lysine--tRN	R.ISM*VEELEK#.A	41.92	5.03	8.33	0.12
Q99MN1_S	Kars	Lysine--tRN	R.LTM*FLTDSNNIK#.E	18.05	2.59	6.97	0.14
Q99MN1_S	Kars	Lysine--tRN	R.NYK#SEEEFVHINNK#.L	30.65	14.98	2.05	0.49
Q99MN1_S	Kars	Lysine--tRN	R.QLFEEQAK#.A	29.83	4.02	7.41	0.13
Q8BZ21_K	Kat6a	Histone ac	R.AFEGLAETGGSTLK#.S	6.22	6.28	0.99	1.01
Q5SVQ0_K	Kat7	Histone ac	R.LQGQITEGSNM*IK#.T	7.79	5.12	1.52	0.66
Q5SVQ0_K	Kat7	Histone ac	K.VGSPERPLSDLGLISYR.S	1.50	6.43	0.23	4.28
Q5SVQ0_K	Kat7	Histone ac	R.LQGQITEGSNM*IK#.T	20.04	16.52	1.21	0.82
Q5SVQ0_K	Kat7	Histone ac	R.SQQQPTPVTPK.K	15.56	17.27	0.90	1.11
Q5SVQ0_K	Kat7	Histone ac	K.VGSPERPLSDLGLISYR.S	1.50	22.22	0.07	14.84
Q5SVQ0_K	Kat7	Histone ac	R.YELDTWYHSPYPEEYAR.L	1.65	8.55	0.19	5.18
Q5SVQ0_K	Kat7	Histone ac	R.LQGQITEGSNM*IK#.T	24.64	18.70	1.32	0.76
Q5SVQ0_K	Kat7	Histone ac	K.M*LIDFSYLLSK#.V	17.52	14.95	1.17	0.85
Q5SVQ0_K	Kat7	Histone ac	R.SQQQPTPVTPK#.K	15.11	13.48	1.12	0.89
Q9WV86_K	Katna1	Katanin p6	K.TTFFNVSSSTLTSK#.Y	9.67	3.49	2.77	0.36
Q8K0T4_K	Katnal1	Katanin p6	K.SIVSTLESFK#.M	12.87	5.24	2.46	0.41
Q8BG40_K	Katnb1	Katanin p8	K.LQEIVAHASNVSSLVLGK#.A	9.46	3.97	2.39	0.42
Q9CWJ3_K	Katnbl1	KATNB1-lik	K.DVDAYLLQLH.-	12.56	12.56	1.00	1.00
Q6ZQ88_K	Kdm1a	Lysine-spec	R.DITAEFLVK#.S	25.71	13.94	1.84	0.54
Q6ZQ88_K	Kdm1a	Lysine-spec	K.GIFGSSAVPQPK#.E	24.35	17.52	1.39	0.72
Q6ZQ88_K	Kdm1a	Lysine-spec	R.HGLINFGIYK#.R	15.47	10.87	1.42	0.70
Q6ZQ88_K	Kdm1a	Lysine-spec	K.HWDQDDDFEFTGSHLTVR.N	5.67	20.17	0.28	3.56
Q6ZQ88_K	Kdm1a	Lysine-spec	R.IADQFLGAM*YTLPR.Q	2.20	8.89	0.25	4.04
Q6ZQ88_K	Kdm1a	Lysine-spec	K.IQLTFEATLQQLEAPYNSDTVLVHR.V	2.40	6.08	0.39	2.53
Q6ZQ88_K	Kdm1a	Lysine-spec	R.STSQTFIYK#.C	25.49	14.45	1.76	0.57
Q6ZQ88_K	Kdm1a	Lysine-spec	R.TLQLWLDNPK#.I	16.32	22.13	0.74	1.36
Q6ZQ88_K	Kdm1a	Lysine-spec	K.VFLFIR.N	7.01	20.09	0.35	2.86
Q6ZQ88_K	Kdm1a	Lysine-spec	K.VIIIGSGVSGLAAAR.Q	6.55	21.60	0.30	3.30
Q6ZQ88_K	Kdm1a	Lysine-spec	R.DITAEFLVK#.S	18.99	13.98	1.36	0.74
Q6ZQ88_K	Kdm1a	Lysine-spec	K.EYDELAETQGK#.L	11.89	6.56	1.81	0.55
Q6ZQ88_K	Kdm1a	Lysine-spec	R.HGLINFGIYK#.R	11.05	4.95	2.23	0.45
Q6ZQ88_K	Kdm1a	Lysine-spec	K.VIIIGSGVSGLAAAR.Q	8.34	18.19	0.46	2.18
P59997_K	Kdm2a	Lysine-spec	K.AIVPQALSGIIK#.R	17.86	7.11	2.51	0.40
P59997_K	Kdm2a	Lysine-spec	K.LALTGVPIVQWPK#.R	12.45	7.61	1.64	0.61
Q6ZPY7_K	Kdm3b	Lysine-spec	K.LGLGSVVPVEYLVDR.E	3.76	9.19	0.41	2.44
Q6ZPY7_K	Kdm3b	Lysine-spec	K.TIDEGDADEVTK#.Q	7.41	3.32	2.23	0.45
Q6ZPY7_K	Kdm3b	Lysine-spec	K.LGLGSVVPVEYLVDR.E	1.97	9.39	0.21	4.77
Q6ZPY7_K	Kdm3b	Lysine-spec	R.SEEPLK#AEGSASNSNSELK#.A	7.54	6.66	1.13	0.88
Q6ZPY7_K	Kdm3b	Lysine-spec	K.LGLGSVVPVEYLVDR.E	3.69	10.70	0.34	2.90
Q6ZPY7_K	Kdm3b	Lysine-spec	R.SEEPLK#AEGSASNSNSELK#.A	11.99	7.20	1.67	0.60
Q6ZPY7_K	Kdm3b	Lysine-spec	K.TIDEGDADEVTK#.Q	7.78	7.45	1.04	0.96
Q3UXZ9_K	Kdm5a	Lysine-spec	K.NIPAFLPNVLSLK.E	14.30	22.00	0.65	1.54
Q3UXZ9_K	Kdm5a	Lysine-spec	R.SLEPPVLELSPGAK#.A	6.35	10.07	0.63	1.59
Q3UXZ9_K	Kdm5a	Lysine-spec	K.VEAIQSGNNYAYLEQLESLSAK#.G	6.83	11.17	0.61	1.63
Q60749_K	Khdrbs1	KH domain	R.DKAKEEELR.K	2.07	8.91	0.23	4.31
Q60749_K	Khdrbs1	KH domain	K.DSLDPSFTHAMQLLSVEIEK.I	110.89	91.56	1.21	0.83
Q60749_K	Khdrbs1	KH domain	K.FNFVGK#.I	228.64	169.41	1.35	0.74
Q60749_K	Khdrbs1	KH domain	K.GESK#K#DDEENYLDLFSHK#.N	19.60	21.77	0.90	1.11
Q60749_K	Khdrbs1	KH domain	K.ILGPQGNTIK#.R	311.71	255.38	1.22	0.82
Q60749_K	Khdrbs1	KH domain	K.K#DDEENYLDLFSHK#.N	292.51	271.21	1.08	0.93
Q60749_K	Khdrbs1	KH domain	K.RLQEETGAK.I	5.28	17.60	0.30	3.33
Q60749_K	Khdrbs1	KH domain	K.YLPELM*AEKDSLDPSFTHAM*QLLSVEIEK.I	6.83	5.53	1.23	0.81
Q60749_K	Khdrbs1	KH domain	K.DSLDPSFTHAMQLLSVEIEK#.I	41.22	41.46	0.99	1.01
Q60749_K	Khdrbs1	KH domain	K.FNFVGK#.I	149.56	133.54	1.12	0.89
Q60749_K	Khdrbs1	KH domain	K.ILGPQGNTIK#.R	205.39	199.81	1.03	0.97
Q60749_K	Khdrbs1	KH domain	K.K#DDEENYLDLFSHK#.N	7.75	6.93	1.12	0.89
Q60749_K	Khdrbs1	KH domain	K.RLQEETGAK.I	2.31	12.10	0.19	5.25
Q60749_K	Khdrbs1	KH domain	K.FNFVGK#.I	58.39	57.69	1.01	0.99

Q60749_KI	Khdrbs1	KH domain	K.GESKKDDEENYLDLFSHK.N	14.76	15.11	0.98	1.02
Q60749_KI	Khdrbs1	KH domain	K.ILGPQGNTIK#.R	65.39	63.18	1.03	0.97
Q3U0V1_F	Khsrp	Far upstrea	K.AINQQTGAFVEISR.Q	4.19	7.79	0.54	1.86
Q3U0V1_F	Khsrp	Far upstrea	K.IGQQPQQPGAPPQQDYTK#.A	7.02	4.48	1.57	0.64
Q3U0V1_F	Khsrp	Far upstrea	K.AINQQTGAFVEISR.Q	12.43	18.57	0.67	1.49
Q3U0V1_F	Khsrp	Far upstrea	K.DAFADAVQR.A	8.33	13.57	0.61	1.63
Q3U0V1_F	Khsrp	Far upstrea	R.GGGGPGGGGPGGGGASGGPSQPPGGGGPGIRK.D	3.93	4.85	0.81	1.23
Q3U0V1_F	Khsrp	Far upstrea	R.GSPQQIDHAK#.Q	12.09	6.34	1.91	0.52
Q3U0V1_F	Khsrp	Far upstrea	R.HSVGVVIGR.S	26.52	44.68	0.59	1.68
Q3U0V1_F	Khsrp	Far upstrea	K.IGGDAATTVNNNTPDFGFGGQK#.R	9.42	3.29	2.86	0.35
Q3U0V1_F	Khsrp	Far upstrea	K.IGQQPQQPGAPPQQDYTK#.A	23.23	10.84	2.14	0.47
Q3U0V1_F	Khsrp	Far upstrea	R.IINDLLQSLR.S	17.22	24.67	0.70	1.43
Q3U0V1_F	Khsrp	Far upstrea	R.SVSLTGAPESVQK#.A	68.56	30.14	2.27	0.44
Q3U0V1_F	Khsrp	Far upstrea	R.TSMTEEYRVPDGMVGLIIGR.G	1.65	8.21	0.20	4.98
Q3U0V1_F	Khsrp	Far upstrea	R.VGGGIDVPVPR.H	18.49	42.44	0.44	2.29
Q3U0V1_F	Khsrp	Far upstrea	K.VQISPDSGGLPER.S	16.55	37.65	0.44	2.27
Q8BKS9_K	Kiaa0020	Pumilio do	R.DPAHTVPELIELLQK#.G	10.37	7.88	1.32	0.76
Q8C2E7_ST	Kiaa0196	WASH com	R.AQVQQFLK#.E	20.19	8.83	2.29	0.44
Q8C2E7_ST	Kiaa0196	WASH com	R.HLAAALDNLNK#.A	10.67	5.30	2.01	0.50
Q8C2E7_ST	Kiaa0196	WASH com	K.LASALDLPLLR.I	8.14	14.54	0.56	1.79
Q8C2E7_ST	Kiaa0196	WASH com	K.TALNNTLDLANVK#.E	23.85	4.82	4.94	0.20
Q3UMB9_V	Kiaa1033	WASH com	K.LLPYEQSSLLELIK#.T	10.92	3.54	3.09	0.32
Q3UMB9_V	Kiaa1033	WASH com	R.AVFPIYLDDVYENAVDAAR.L	5.95	10.39	0.57	1.75
Q3UMB9_V	Kiaa1033	WASH com	K.LGAAFTDDGFAM*GVAYTLK#.L	8.08	2.95	2.74	0.36
Q3UMB9_V	Kiaa1033	WASH com	K.M*LVDVFAPEFR.R	3.94	10.48	0.38	2.66
Q3UMB9_V	Kiaa1033	WASH com	K.QQNVQSTSQDEK#.L	3.16	2.87	1.10	0.91
Q3UMB9_V	Kiaa1033	WASH com	R.SIFANVEAK#.L	20.64	11.39	1.81	0.55
Q8BWY9_C	Kiaa1524	Protein CIP	K.DNAPALNIEDLIEK.L	8.15	5.68	1.43	0.70
Q8BWY9_C	Kiaa1524	Protein CIP	R.HLEVVSGQK#.L	11.55	9.80	1.18	0.85
Q6P9P6_KI	Kif11	Kinesin-like	R.AIDEHNAEAQESFGK.N	6.94	6.19	1.12	0.89
Q6P9P6_KI	Kif11	Kinesin-like	K.EEYVSSALER.T	17.98	10.64	1.69	0.59
Q6P9P6_KI	Kif11	Kinesin-like	K.GLEEITVHNK#DEVYQILEK#.G	9.72	13.07	0.74	1.34
Q6P9P6_KI	Kif11	Kinesin-like	K.LNLVDLAGSENIGR.S	2.82	20.06	0.14	7.11
Q6P9P6_KI	Kif11	Kinesin-like	K.NLNSLFNNMEELIK#.D	14.93	11.43	1.31	0.77
Q6P9P6_KI	Kif11	Kinesin-like	R.SPNEVYTWEEDPLAGIIPR.T	2.58	6.64	0.39	2.57
Q6P9P6_KI	Kif11	Kinesin-like	K.TIVAPSVVSILNINK.Q	13.35	25.41	0.53	1.90
Q6P9P6_KI	Kif11	Kinesin-like	K.TQELETTQK#.H	12.51	12.54	1.00	1.00
Q6P9P6_KI	Kif11	Kinesin-like	R.TTAATLM*NAYSSR.S	1.20	8.08	0.15	6.74
Q6P9P6_KI	Kif11	Kinesin-like	R.VITALVER.T	4.46	23.36	0.19	5.24
Q6P9P6_KI	Kif11	Kinesin-like	K.GLEEITVHNK#DEVYQILEK#.G	4.08	4.37	0.93	1.07
Q6P9P6_KI	Kif11	Kinesin-like	K.LNLVDLAGSENIGR.S	2.20	8.55	0.26	3.88
Q6P9P6_KI	Kif11	Kinesin-like	K.TIVAPSVVSILNINK#.Q	10.16	39.25	0.26	3.86
E9Q4K7_E	Kif13b	Kinesin-like	R.APLLSEPASAVPTSPFR.I	4.10	8.17	0.50	1.99
E9Q4K7_E	Kif13b	Kinesin-like	R.DSVLTWLLK#.D	23.31	7.73	3.01	0.33
E9Q4K7_E	Kif13b	Kinesin-like	R.EHSVLGPYVDGLSK#.L	10.49	3.41	3.08	0.32
E9Q4K7_E	Kif13b	Kinesin-like	R.GIAPGPPALSVSPQNNQSPDPGLGGVAASYLNPVK#.S	8.67	3.78	2.30	0.44
E9Q4K7_E	Kif13b	Kinesin-like	R.IAGGDDPTEVSSEK#.E	28.08	9.92	2.83	0.35
E9Q4K7_E	Kif13b	Kinesin-like	R.K#NPALWDLGIIQAK#.T	15.88	4.72	3.36	0.30
E9Q4K7_E	Kif13b	Kinesin-like	R.M*AANVENPASADSEAYIEK#.Y	9.00	3.10	2.90	0.34
E9Q4K7_E	Kif13b	Kinesin-like	R.MAANVENPASADSEAYIEK#.Y	5.03	2.40	2.09	0.48
E9Q4K7_E	Kif13b	Kinesin-like	R.QGFAQSLLK#.K	11.10	3.58	3.10	0.32
E9Q4K7_E	Kif13b	Kinesin-like	R.SVLAVENLLTLDR.L	8.94	14.41	0.62	1.61
E9Q4K7_E	Kif13b	Kinesin-like	R.TVAATNM*NEESSR.S	3.18	5.74	0.55	1.81
E9Q4K7_E	Kif13b	Kinesin-like	K.VILNPVNTNLSK#.G	37.94	11.53	3.29	0.30
Q60575_KI	Kif1b	Kinesin-like	K.K#QDPETNLSTEK#.V	2.48	2.43	1.02	0.98
Q80WE4_K	Kif20b	Kinesin-like	R.SQASTVSANIASK.K	2.62	7.57	0.35	2.88
Q9QXL2_KI	Kif21a	Kinesin-like	R.SPYFSASSAFSPTILSSDK#ETIEIIDLAK#.K	5.87	1.56	3.77	0.27
E9Q5G3_KI	Kif23	Kinesin-like	K.LVQAPLDADGDNVLQEK.E	2.15	5.47	0.39	2.54
E9Q5G3_KI	Kif23	Kinesin-like	R.NLQQELESQNQK.L	3.32	6.58	0.50	1.98
E9Q5G3_KI	Kif23	Kinesin-like	K.LLDINDEETLPK.L	1.29	5.68	0.23	4.41
P28740_KI	Kif2a	Kinesin-like	R.AALQEEEQASK#.Q	9.62	6.92	1.39	0.72
P28740_KI	Kif2a	Kinesin-like	K.IDILTELR.D	4.35	8.04	0.54	1.85
P28740_KI	Kif2a	Kinesin-like	R.AALQEEEQASK#.Q	61.95	24.75	2.50	0.40
P28740_KI	Kif2a	Kinesin-like	K.DLDVITIPSK#DVVMVHEPK#.Q	9.67	6.81	1.42	0.70
P28740_KI	Kif2a	Kinesin-like	R.DVFLMLK#.K	9.38	2.12	4.42	0.23
P28740_KI	Kif2a	Kinesin-like	K.FSLIDLAGNER.G	12.16	20.71	0.59	1.70
P28740_KI	Kif2a	Kinesin-like	K.IDILTELR.D	4.33	10.60	0.41	2.45
Q922S8_KI	Kif2c	Kinesin-like	K.DSLPLQENVTVPK#.Q	6.76	8.72	0.77	1.29
P28741_KI	Kif3a	Kinesin-like	R.LLQDSLGGNSK#.T	24.03	9.45	2.54	0.39
P28741_KI	Kif3a	Kinesin-like	R.SAK#PETVIDSLLQ.-	21.73	9.84	2.21	0.45
P28741_KI	Kif3a	Kinesin-like	K.VIVGGVDLLAK#.A	19.81	10.74	1.84	0.54
P28741_KI	Kif3a	Kinesin-like	R.VSYLEIYNEEVR.D	2.51	8.88	0.28	3.54
Q61771_KI	Kif3b	Kinesin-like	K.HLIIENFIPLEEK#.N	17.42	7.76	2.25	0.45
Q61771_KI	Kif3b	Kinesin-like	R.QELEQTQNELTR.E	3.66	5.81	0.63	1.59
Q61771_KI	Kif3b	Kinesin-like	K.TFTFDAVYDWNAK#.Q	8.26	4.82	1.71	0.58
P33174_KI	Kif4	Chromosor	K.GYNATVLAYGQTGSGK.T	8.55	10.24	0.83	1.20
P33174_KI	Kif4	Chromosor	R.IILTEQANEK.M	23.04	33.24	0.69	1.44
P33174_KI	Kif4	Chromosor	K.ILAQDVAQLK#.E	15.63	13.59	1.15	0.87
P33174_KI	Kif4	Chromosor	R.K#ILAQDVAQLK#.E	7.69	8.84	0.87	1.15
P33174_KI	Kif4	Chromosor	K.LTLLQVASK#.Q	16.40	18.94	0.87	1.15
P33174_KI	Kif4	Chromosor	K.NK#PIINIDPQAAELNHLK#.Q	8.97	9.02	0.99	1.01
P33174_KI	Kif4	Chromosor	K.NLESEVLSLQR.E	4.41	16.10	0.27	3.65
P33174_KI	Kif4	Chromosor	R.TVASTAM*NSQSSR.S	3.68	7.97	0.46	2.17
P33174_KI	Kif4	Chromosor	R.VIQLLFK.E	11.02	13.87	0.79	1.26
P33174_KI	Kif4	Chromosor	R.WESIATILEAK.C	7.42	9.22	0.80	1.24
P33174_KI	Kif4	Chromosor	K.YLVGELVSSK#.I	14.77	16.85	0.88	1.14
P33174_KI	Kif4	Chromosor	K.ILAQDVAQLK#.E	7.73	7.26	1.06	0.94
P33174_KI	Kif4	Chromosor	R.TVASTAM*NSQSSR.S	1.41	5.51	0.26	3.90
P33175_KI	Kif5a	Kinesin hea	K.QQMLDQEELLVSTR@.G	38.43	2.37	16.19	0.06
P33175_KI	Kif5a	Kinesin hea	K.ISFLENNLEQLTK#.V	17.32	6.47	2.68	0.37
P33175_KI	Kif5a	Kinesin hea	K.LYLVDLAGSEK#.V	20.46	4.31	4.75	0.21
P33175_KI	Kif5a	Kinesin hea	K.TGAEGAVLDEAK#.N	25.45	11.07	2.30	0.44
P33175_KI	Kif5a	Kinesin hea	K.EVLQALEELAVNYDQK#.S	21.39	7.55	2.83	0.35
P33175_KI	Kif5a	Kinesin hea	K.ISFLENNLEQLTK#.V	109.72	29.51	3.72	0.27
P33175_KI	Kif5a	Kinesin hea	K.LYLVDLAGSEK#.V	100.22	26.26	3.82	0.26
P33175_KI	Kif5a	Kinesin hea	K.TNLSVHEDK#.N	12.31	6.06	2.03	0.49
P33175_KI	Kif5a	Kinesin hea	K.VSYFEIYLDK#.I	18.94	7.15	2.65	0.38
Q61768_KI	Kif5b	Kinesin-1 h	K.LITDLQDQNQK#.M	17.27	6.74	2.56	0.39
Q61768_KI	Kif5b	Kinesin-1 h	R.AAEM*M*ASLLK#.D	35.36	12.24	2.89	0.35
Q61768_KI	Kif5b	Kinesin-1 h	K.ALESALK#.E	55.80	17.73	3.15	0.32
Q61768_KI	Kif5b	Kinesin-1 h	K.ANLEAFTADKDIAITSDKPAAAVGM*AGSFTDAER.R	6.78	7.86	0.86	1.16
Q61768_KI	Kif5b	Kinesin-1 h	K.DLAEIGIAVGNNDVK#.Q	23.07	37.94	0.61	1.64
Q61768_KI	Kif5b	Kinesin-1 h	K.DVLEGYNGTIFAYGQTSSGK#.T	7.54	2.28	3.31	0.30

Q61768_KI	Kif5b	Kinesin-1 h	K.EYELLSDELNQK#.S	28.12	7.87	3.57	0.28
Q61768_KI	Kif5b	Kinesin-1 h	K.LFVQDLATR.V	28.30	24.86	1.14	0.88
Q61768_KI	Kif5b	Kinesin-1 h	K.LITDLQDQNQK#.M	94.20	38.13	2.47	0.40
Q61768_KI	Kif5b	Kinesin-1 h	R.NGETVPIDEQFDK#.E	9.14	2.23	4.09	0.24
Q61768_KI	Kif5b	Kinesin-1 h	R.NGETVPIDEQFDK#EK#.A	48.78	13.44	3.63	0.28
Q61768_KI	Kif5b	Kinesin-1 h	K.QLDDK#DEEINQQSQLVEK#.L	54.18	13.82	3.92	0.26
Q61768_KI	Kif5b	Kinesin-1 h	K.SAEVDSDDTGGSAAQK#.Q	40.88	16.34	2.50	0.40
Q61768_KI	Kif5b	Kinesin-1 h	K.SATLASIDAELQK#.L	85.52	26.15	3.27	0.31
Q61768_KI	Kif5b	Kinesin-1 h	R.SHSIFLINVK#.Q	27.06	7.22	3.75	0.27
Q61768_KI	Kif5b	Kinesin-1 h	K.SLTEYLQNVEQK#.K	61.67	15.60	3.95	0.25
Q61768_KI	Kif5b	Kinesin-1 h	K.TK#EYELLSDELNQK#.S	14.80	3.24	4.57	0.22
Q9QWT9_K	Kifc1	Kinesin-like	R.ASPGSEELTVTNAR.Y	3.02	6.49	0.46	2.15
Q9QWT9_K	Kifc1	Kinesin-like	K.LTYLLQNSLGGSAK#.M	4.84	2.07	2.34	0.43
Q9QWT9_K	Kifc1	Kinesin-like	K.LTYLLQNSLGGSAK#.M	5.05	2.03	2.48	0.40
Q9QWT9_K	Kifc1	Kinesin-like	R.EVQEQATTLGTER.N	8.55	17.48	0.49	2.04
Q9QWT9_K	Kifc1	Kinesin-like	R.GPDQM*EDALEPAK#.K	12.62	3.45	3.65	0.27
Q9QWT9_K	Kifc1	Kinesin-like	R.LLQELQGER.L	62.22	11.85	5.25	0.19
Q9QWT9_K	Kifc1	Kinesin-like	K.LTYLLQNSLGGSAK#.M	22.08	8.68	2.55	0.39
Q9QWT9_K	Kifc1	Kinesin-like	R.NTLEGELASVR.S	7.99	12.07	0.66	1.51
Q9QWT9_K	Kifc1	Kinesin-like	K.LTYLLQNSLGGSAK#.M	16.32	5.62	2.90	0.34
Q8CD76_Q	Klc1	Kinesin ligh	R.ALGIYQTK#.L	13.83	7.14	1.94	0.52
Q8CD76_Q	Klc1	Kinesin ligh	K.DAANLLNDALAIR.E	3.13	6.36	0.49	2.03
Q8CD76_Q	Klc1	Kinesin ligh	K.DGSAFGEYGGWYK#.A	12.04	4.26	2.83	0.35
Q8CD76_Q	Klc1	Kinesin ligh	R.VAEVLNDPESM*EK#.R	26.50	14.78	1.79	0.56
Q8CD76_Q	Klc1	Kinesin ligh	R.VAEVLNDPESMEK#.R	13.16	5.92	2.22	0.45
Q8CD76_Q	Klc1	Kinesin ligh	R.ALGIYQTK#.L	22.41	11.43	1.96	0.51
Q8CD76_Q	Klc1	Kinesin ligh	K.DGSAFGEYGGWYK#.A	11.47	6.89	1.66	0.60
Q8CD76_Q	Klc1	Kinesin ligh	K.LTQDEIISK#.T	50.42	34.60	1.46	0.69
Q8CD76_Q	Klc1	Kinesin ligh	R.VAEVLNDPESM*EK#.R	26.62	14.09	1.89	0.53
Q8CD76_Q	Klc1	Kinesin ligh	R.VAEVLNDPESMEK#.R	10.85	6.37	1.70	0.59
O88448_KI	Klc2	Kinesin ligh	R.DHPAVAATLNNLAVLYGK#.R	20.26	12.29	1.65	0.61
O88448_KI	Klc2	Kinesin ligh	R.LGPDDPNVAK#.T	39.84	16.94	2.35	0.43
O88448_KI	Klc2	Kinesin ligh	K.LSQDEIVLGTK#.A	10.05	3.43	2.93	0.34
O88448_KI	Klc2	Kinesin ligh	R.DHPAVAATLNNLAVLYGK#.R	38.36	20.37	1.88	0.53
O88448_KI	Klc2	Kinesin ligh	R.LGPDDPNVAK#.T	56.89	22.38	2.54	0.39
O88448_KI	Klc2	Kinesin ligh	R.TLHNLVIQYASQGR.Y	5.97	7.58	0.79	1.27
Q91W40_K	Klc3	Kinesin ligh	R.ALSIYEALGGPQDPNVAK#.T	10.22	6.38	1.60	0.62
Q91W40_K	Klc3	Kinesin ligh	R.ASEEAVAQLEEEK#.S	7.40	4.51	1.64	0.61
Q91W40_K	Klc3	Kinesin ligh	R.ASEEAVAQLEEEKSHLQFLGQLR.Q	2.68	5.70	0.47	2.13
Q91W40_K	Klc3	Kinesin ligh	R.DSLASLFPSEEEEK#.K	7.47	6.63	1.13	0.89
Q91W40_K	Klc3	Kinesin ligh	R.EQTLGPEHPAVAATLNNLAVLYGK#.R	28.19	14.44	1.95	0.51
Q91W40_K	Klc3	Kinesin ligh	K.KGPEAAGAAAAQQGGYEIPAR.L	6.26	18.65	0.34	2.98
Q91W40_K	Klc3	Kinesin ligh	R.QVVQGLEALR.A	6.58	14.40	0.46	2.19
Q91W40_K	Klc3	Kinesin ligh	K.YQQAEELYK#.E	10.28	10.08	1.02	0.98
Q9DBS5_KI	Klc4	Kinesin ligh	R.ALAIYESQLGPDNPNVAR.T	3.66	3.37	1.09	0.92
Q9Z2Q2_KI	Knop1	Lysine-rich	K.SEALEFVPIDSPK#.A	7.75	8.31	0.93	1.07
Q9Z2Q2_KI	Knop1	Lysine-rich	K.SEALEFVPIDSPK#.A	6.88	9.30	0.74	1.35
Q60960_IM	Kpna1	Importin su	K.EPNPPIDEVINTPGVVAR.F	2.06	3.45	0.60	1.67
Q60960_IM	Kpna1	Importin su	K.IVQVALNGLENILR.L	2.93	8.58	0.34	2.93
Q60960_IM	Kpna1	Importin su	R.LVELLM*HNDYK#.V	6.04	4.58	1.32	0.76
Q60960_IM	Kpna1	Importin su	K.EAAWAITNATSGGSAEQIK#.Y	7.09	2.37	3.00	0.33
Q60960_IM	Kpna1	Importin su	R.FVEFLK#.R	23.75	10.25	2.32	0.43
P52293_IM	Kpna2	Importin su	R.AIGNIVTGTDEQTQK.V	29.99	36.21	0.83	1.21
P52293_IM	Kpna2	Importin su	K.EATWTM*SNITAGR.Q	2.25	7.50	0.30	3.34
P52293_IM	Kpna2	Importin su	K.GINSNNLESQLQATQAAR.K	2.13	13.26	0.16	6.22
P52293_IM	Kpna2	Importin su	K.LLGATELPIVTPALR.A	6.42	39.49	0.16	6.16
P52293_IM	Kpna2	Importin su	R.NNQGTVNWSVEDIVK.G	11.33	15.15	0.75	1.34
P52293_IM	Kpna2	Importin su	R.NVSSFPDDATSPLQENR.N	5.55	9.03	0.62	1.63
P52293_IM	Kpna2	Importin su	K.VIDAGALAVFPSLLTNPK.T	20.64	29.25	0.71	1.42
P52293_IM	Kpna2	Importin su	R.AIGNIVTGTDEQTQK#.V	16.78	17.29	0.97	1.03
P52293_IM	Kpna2	Importin su	R.NKNPAPPLDAVEQILPTLVR.L	2.71	21.16	0.13	7.82
P52293_IM	Kpna2	Importin su	R.NNQGTVNWSVEDIVK.G	3.69	6.90	0.54	1.87
P52293_IM	Kpna2	Importin su	K.VIDAGALAVFPSLLTNPK.T	15.41	16.85	0.91	1.09
P52293_IM	Kpna2	Importin su	R.AIGNIVTGTDEQTQK#.V	19.47	28.90	0.67	1.48
P52293_IM	Kpna2	Importin su	K.EATWTM*SNITAGR.Q	2.32	7.20	0.32	3.10
P52293_IM	Kpna2	Importin su	K.FVSFLGK#.T	13.48	9.56	1.41	0.71
P52293_IM	Kpna2	Importin su	K.GINSNNLESQLQATQAAR.K	1.96	7.85	0.25	4.00
P52293_IM	Kpna2	Importin su	K.LLGATELPIVTPALR.A	7.24	32.93	0.22	4.54
P52293_IM	Kpna2	Importin su	R.NKNPAPPLDAVEQILPTLVR.L	4.68	33.34	0.14	7.13
P52293_IM	Kpna2	Importin su	K.VIDAGALAVFPSLLTNPK.T	25.96	30.18	0.86	1.16
O35344_IM	Kpna3	Importin su	K.DSQVVQVVLDGLK#.N	66.05	39.68	1.66	0.60
O35344_IM	Kpna3	Importin su	K.IEVLQQHENEDIYK#.L	59.41	34.20	1.74	0.58
O35344_IM	Kpna3	Importin su	R.NVPQEESLEDSDVDADFK#.A	22.95	12.37	1.85	0.54
O35344_IM	Kpna3	Importin su	K.SGILPILVK#.C	42.19	26.87	1.57	0.64
O35344_IM	Kpna3	Importin su	R.NVPQEESLEDSDVDADFK#.A	9.40	4.09	2.30	0.43
O35344_IM	Kpna3	Importin su	K.SGILPILVK#.C	27.45	13.35	2.06	0.49
O35344_IM	Kpna3	Importin su	R.NVPQEESLEDSDVDADFK#.A	10.51	7.18	1.46	0.68
O35344_IM	Kpna3	Importin su	K.SGILPILVK#.C	35.13	16.01	2.19	0.46
O35343_IM	Kpna4	Importin su	K.EAAWAISNLTISGR.K	28.28	69.22	0.41	2.45
O35343_IM	Kpna4	Importin su	R.VQNTSLEAIVQNASSDNQGIQLSAVQAAR.K	9.56	18.60	0.51	1.95
O35343_IM	Kpna4	Importin su	K.EAAWAISNLTISGR.K	25.92	31.16	0.83	1.20
O35343_IM	Kpna4	Importin su	K.IEQLQNHENEDIYK#.L	34.35	23.97	1.43	0.70
O35343_IM	Kpna4	Importin su	R.NPPIDDLIK#.S	20.32	11.42	1.78	0.56
O35343_IM	Kpna4	Importin su	R.VQNTSLEAIVQNASSDNQGIQLSAVQAAR.K	6.32	8.26	0.77	1.31
O35343_IM	Kpna4	Importin su	K.EAAWAISNLTISGR.K	12.19	26.22	0.46	2.15
O35343_IM	Kpna4	Importin su	R.NPPIDDLIK#.S	20.30	19.83	1.02	0.98
O35343_IM	Kpna4	Importin su	R.VQNTSLEAIVQNASSDNQGIQLSAVQAAR.K	4.97	9.34	0.53	1.88
O35345_IM	Kpna6	Importin su	K.EAAWAITNATSGGTPEQIR.Y	4.64	9.49	0.49	2.05
O35345_IM	Kpna6	Importin su	K.EAAWAITNATSGGTPEQIR.Y	5.50	5.22	1.06	0.95
O35345_IM	Kpna6	Importin su	K.LLSKEPSPPIDEVINTPGVVDR.F	2.83	5.65	0.50	2.00
P70168_IM	Kpnb1	Importin su	R.AAVENLPTFLVELSR.V	8.70	9.03	0.96	1.04
P70168_IM	Kpnb1	Importin su	K.LAATNALLNSLEFTK#.A	46.13	16.79	2.75	0.36
P70168_IM	Kpnb1	Importin su	R.SSAYESLMEIVK#.N	6.69	2.32	2.88	0.35
P70168_IM	Kpnb1	Importin su	R.VAAGLQIK#.N	27.71	13.26	2.09	0.48
P70168_IM	Kpnb1	Importin su	R.VAALQNLVK#.I	27.59	10.87	2.54	0.39
P70168_IM	Kpnb1	Importin su	R.VLANPGNSQVAR.V	8.87	20.00	0.44	2.25
P70168_IM	Kpnb1	Importin su	R.AAVENLPTFLVELSR.V	25.22	31.33	0.81	1.24
P70168_IM	Kpnb1	Importin su	K.LAATNALLNSLEFTK#.A	110.90	36.31	3.05	0.33
P70168_IM	Kpnb1	Importin su	R.LQQVLQM*ESHIQSTSDR.I	16.20	16.93	0.96	1.05
P70168_IM	Kpnb1	Importin su	R.SSAYESLM*EIVK#.N	27.58	6.70	4.12	0.24
P70168_IM	Kpnb1	Importin su	R.SSAYESLMEIVK#.N	14.68	4.08	3.60	0.28
P70168_IM	Kpnb1	Importin su	R.VAAGLQIK#.N	73.06	18.90	3.87	0.26
P70168_IM	Kpnb1	Importin su	R.VAALQNLVK#.I	54.18	20.51	2.64	0.38

P70168_IM	Kpnb1	Importin su	R.VLANPGNSQVAR.V	26.65	38.85	0.69	1.46
Q8BGA5_KI	Krr1	KRR1 small	R.GLLEESSFATLFPK#.Y	14.70	4.66	3.15	0.32
Q5RL79_KT	Krtcap2	Keratinocyt	K.ISSTLYQATAPVLTPAK#.I	3.95	1.75	2.26	0.44
Q9D1R2_K	Kti12	Protein KTI	R.QDVVILDSVNYIK#.G	8.06	1.08	7.47	0.13
Q61595_K	Ktn1	Kinectin OS	R.DAVSNTTNQLESK#.Q	11.99	5.83	2.06	0.49
Q61092_LA	Lamc2	Laminin su	K.SEMREMIELAR@K#.E	2.29	2.04	1.12	0.89
P11438_LA	Lamp1	Lysosome-a	K.ALQATVGNSYK#.C	23.04	15.68	1.47	0.68
Q9CQ22_LT	Lamtor1	Ragulator c	R.TDEQALLSSILAK#.T	12.91	7.85	1.65	0.61
Q9JHS3_LT	Lamtor2	Ragulator c	K.AQALVQYLEEPLTQVAAS.-	11.83	11.83	1.00	1.00
Q9JHS3_LT	Lamtor2	Ragulator c	R.NGNQAFNEDSLK#.F	3.76	2.96	1.27	0.79
O89112_LA	Lancl1	LanC-like pr	K.SLAENYFDSTGR.L	4.09	9.12	0.45	2.23
Q9JJK2_LA	Lancl2	LanC-like pr	K.EVVSAIIESGK#.S	20.95	8.73	2.40	0.42
Q9CPY7_AM	Lap3	Cytosol am	K.DK#DDDLPQFTSAGESFNK#.L	41.40	10.45	3.96	0.25
Q9CPY7_AM	Lap3	Cytosol am	R.FAEIIEK#.N	63.21	17.22	3.67	0.27
Q9CPY7_AM	Lap3	Cytosol am	K.GITFDSGGISIK#.A	70.23	16.02	4.38	0.23
Q9CPY7_AM	Lap3	Cytosol am	K.LFEASVETGDR.V	16.38	17.34	0.94	1.06
Q9CPY7_AM	Lap3	Cytosol am	K.LHGSGDLEAWEK#.G	14.92	6.65	2.24	0.45
Q9CPY7_AM	Lap3	Cytosol am	K.SWIEEQEM*GSFLSVAK#.G	8.03	3.03	2.65	0.38
Q9CPY7_AM	Lap3	Cytosol am	K.SWIEEQEMGSFLSVAK#.G	14.17	4.16	3.40	0.29
Q9CPY7_AM	Lap3	Cytosol am	R.TFYGLHQDFPSVVVVGLGK#.R	30.18	7.94	3.80	0.26
Q9CPY7_AM	Lap3	Cytosol am	R.TLIEFLLR.F	15.23	13.37	1.14	0.88
Q9CPY7_AM	Lap3	Cytosol am	K.GITFDSGGISIK#.A	16.33	3.55	4.60	0.22
Q6ZQ58_LA	Larp1	La-related p	R.FQQVPTDALANK.L	5.62	5.91	0.95	1.05
Q6ZQ58_LA	Larp1	La-related p	K.DFQEETVK#DYEAGQLYGLEK#.F	10.83	4.91	2.21	0.45
Q6ZQ58_LA	Larp1	La-related p	R.FQQVPTDALANK#.L	75.50	37.84	2.00	0.50
Q6ZQ58_LA	Larp1	La-related p	R.FSHPTALPQQLPSQQLM*SK#.D	40.38	24.04	1.68	0.60
Q6ZQ58_LA	Larp1	La-related p	K.FWAFLK#.Y	24.35	9.47	2.57	0.39
Q6ZQ58_LA	Larp1	La-related p	K.GLSASLPDLDSESWIEVK#.K	8.38	7.36	1.14	0.88
Q6ZQ58_LA	Larp1	La-related p	K.ILIVTQTPPYM*R.R	5.37	8.44	0.64	1.57
Q6ZQ58_LA	Larp1	La-related p	R.LDIFK#DFQEETVK#DYEAGQLYGLEK#.F	10.63	5.76	1.85	0.54
Q6ZQ58_LA	Larp1	La-related p	K.LFGAPEPSTIAR.S	18.58	35.48	0.52	1.91
Q6ZQ58_LA	Larp1	La-related p	R.LGIGQSQEMNTLFR.F	3.72	9.26	0.40	2.49
Q6ZQ58_LA	Larp1	La-related p	K.LQEYLGK#.F	38.77	23.84	1.63	0.61
Q6ZQ58_LA	Larp1	La-related p	K.NLDIDPK#.L	24.21	9.95	2.43	0.41
Q6ZQ58_LA	Larp1	La-related p	K.VGDFGDAVNWPTPGEIAHK#.S	24.37	12.75	1.91	0.52
Q6ZQ58_LA	Larp1	La-related p	K.VINDGLFYYEQDLWTEK#.F	5.47	3.32	1.65	0.61
Q6ZQ58_LA	Larp1	La-related p	K.VINDGLFYYEQDLWTEK#FEPEYSQIK#.Q	9.21	5.46	1.69	0.59
Q6ZQ58_LA	Larp1	La-related p	K.VVEMVEEK#.V	18.49	7.86	2.35	0.42
Q6ZQ58_LA	Larp1	La-related p	K.VVEM*VEEK#.V	34.69	18.90	1.84	0.54
Q6ZQ58_LA	Larp1	La-related p	R.FQQVPTDALANK#.L	16.28	7.74	2.10	0.48
Q6ZQ58_LA	Larp1	La-related p	K.VGDFGDAVNWPTPGEIAHK#.S	7.34	3.84	1.91	0.52
Q8BWW4_	Larp4	La-related p	K.LTTNTDLILEVLR.S	4.87	13.31	0.37	2.73
Q8BWW4_	Larp4	La-related p	K.AINTFFAK#.N	37.88	22.90	1.65	0.60
Q8BWW4_	Larp4	La-related p	R.AVALQEPR.K	11.98	23.45	0.51	1.96
Q8BWW4_	Larp4	La-related p	K.DLYLISQM*DSDQFVPIWTVANM*EEIKK.L	5.58	7.00	0.80	1.26
Q8BWW4_	Larp4	La-related p	K.DLYLISQM*DSDQFVPIWTVANMEEIK#K#.L	8.02	7.27	1.10	0.91
Q8BWW4_	Larp4	La-related p	K.FDLLATNFPPLPGSSSR.V	3.80	11.29	0.34	2.97
Q8BWW4_	Larp4	La-related p	R.HNPTVTGQQEQTYLPK#.E	31.02	31.31	0.99	1.01
Q8BWW4_	Larp4	La-related p	R.HNPTVTGQQEQTYLPK.E	8.89	11.80	0.75	1.33
Q8BWW4_	Larp4	La-related p	K.LTTNTDLILEVLR.S	15.49	43.74	0.35	2.82
Q8BWW4_	Larp4	La-related p	R.SSSGSEHSTEGSVSLGDGPLSR.S	6.00	21.38	0.28	3.56
Q8BWW4_	Larp4	La-related p	R.VPDELGLENR.M	11.43	39.29	0.29	3.44
Q6A0A2_LA	Larp4b	La-related p	K.AIAINTFLPK#.N	27.78	19.92	1.39	0.72
Q6A0A2_LA	Larp4b	La-related p	R.GPGLLESPSIFNFTADR.L	4.75	13.38	0.36	2.81
Q6A0A2_LA	Larp4b	La-related p	R.LSSLIIGSSK#.E	16.77	9.46	1.77	0.56
Q05CL8_LA	Larp7	La-related p	K.GFAFVEFETK#.E	8.74	5.13	1.70	0.59
Q05CL8_LA	Larp7	La-related p	K.VSAQGPQFVTGVIVK#.I	17.43	8.21	2.12	0.47
Q05CL8_LA	Larp7	La-related p	K.DGVGQAASEVSK#.E	57.90	35.93	1.61	0.62
Q05CL8_LA	Larp7	La-related p	R.DKVEASSLPEAR.A	6.98	23.61	0.30	3.38
Q05CL8_LA	Larp7	La-related p	K.GFAFVEFETK#.E	30.37	21.62	1.40	0.71
Q05CL8_LA	Larp7	La-related p	K.HSWNLEVLSGDHEQR.Y	6.71	15.56	0.43	2.32
Q05CL8_LA	Larp7	La-related p	K.NKPIPSLR.V	3.56	12.59	0.28	3.53
Q05CL8_LA	Larp7	La-related p	K.QVDFWFGDANLHK#.D	10.21	6.51	1.57	0.64
Q05CL8_LA	Larp7	La-related p	K.SSSVVELDLEGTR.I	10.76	17.94	0.60	1.67
Q05CL8_LA	Larp7	La-related p	R.TVYVELLPK#.N	31.12	24.82	1.25	0.80
Q05CL8_LA	Larp7	La-related p	K.VSAQGPQFVTGVIVK#.I	43.49	34.36	1.27	0.79
Q8BMJ2_SY	Lars	Leucine--tR	K.DVWDYVFFK#.D	55.06	8.84	6.23	0.16
Q8BMJ2_SY	Lars	Leucine--tR	K.FSEAEHWLDYFPPLAVQDLK#.T	37.62	9.59	3.92	0.25
Q8BMJ2_SY	Lars	Leucine--tR	R.GFYDGVM*LVDGFK#.G	28.57	7.37	3.88	0.26
Q8BMJ2_SY	Lars	Leucine--tR	K.GTGVVTSVPSDSPDDLAALR.D	8.89	5.13	1.73	0.58
Q8BMJ2_SY	Lars	Leucine--tR	R.LYTWVEWVK#.E	18.49	8.67	2.13	0.47
Q8BMJ2_SY	Lars	Leucine--tR	K.NM*IDAGDALIYM*EPEK#.Q	8.61	3.75	2.29	0.44
Q8BMJ2_SY	Lars	Leucine--tR	R.QTGEGVGPQEYTLVK#.L	19.89	7.09	2.80	0.36
Q8BMJ2_SY	Lars	Leucine--tR	R.TDIGDTM*VYLVH.-	24.90	24.90	1.00	1.00
Q8BMJ2_SY	Lars	Leucine--tR	R.TDIGDTMVYLVH.-	22.84	22.84	1.00	1.00
Q8BMJ2_SY	Lars	Leucine--tR	K.TGFFEFQAAK#.D	59.07	8.44	7.00	0.14
Q8BMJ2_SY	Lars	Leucine--tR	R.VFASEM*NAGIIK#.T	46.38	10.85	4.27	0.23
Q8BMJ2_SY	Lars	Leucine--tR	R.VFASEMNAGIIK#.T	20.52	3.86	5.31	0.19
Q8BMJ2_SY	Lars	Leucine--tR	K.VIASELGSLPELK#.K	43.77	9.36	4.67	0.21
Q8BMJ2_SY	Lars	Leucine--tR	K.VLEPYPSK#.L	44.70	22.03	2.03	0.49
Q8BMJ2_SY	Lars	Leucine--tR	R.WQFLTLR.E	8.45	9.23	0.92	1.09
Q8BMJ2_SY	Lars	Leucine--tR	R.YTIYSPK#.D	35.40	7.73	4.58	0.22
Q8BMJ2_SY	Lars	Leucine--tR	K.DVWDYVFFK#.D	69.93	13.03	5.37	0.19
Q8BMJ2_SY	Lars	Leucine--tR	R.FDDPLLGPR.R	16.46	15.98	1.03	0.97
Q8BMJ2_SY	Lars	Leucine--tR	K.FSEAEHWLDYFPPLAVQDLK#.T	52.24	12.38	4.22	0.24
Q8BMJ2_SY	Lars	Leucine--tR	R.GFYDGVM*LVDGFK#.G	58.44	14.11	4.14	0.24
Q8BMJ2_SY	Lars	Leucine--tR	K.GTGVVTSVPSDSPDDLAALR.D	13.62	12.57	1.08	0.92
Q8BMJ2_SY	Lars	Leucine--tR	K.HNGVVPVVK#.E	32.13	4.80	6.70	0.15
Q8BMJ2_SY	Lars	Leucine--tR	R.LALADAGDTVEDANFVEAM*ADAGILR.L	6.79	11.45	0.59	1.69
Q8BMJ2_SY	Lars	Leucine--tR	K.NM*IDAGDALIYM*EPEK#.Q	11.71	2.75	4.26	0.23
Q8BMJ2_SY	Lars	Leucine--tR	R.NM*SYQGFTK#.H	49.15	9.77	5.03	0.20
Q8BMJ2_SY	Lars	Leucine--tR	R.QTGEGVGPQEYTLVK#.L	33.59	7.83	4.29	0.23
Q8BMJ2_SY	Lars	Leucine--tR	R.SFITTDVNPYYDSFVR.W	16.91	15.13	1.12	0.89
Q8BMJ2_SY	Lars	Leucine--tR	K.SLGLSDDDIVK#.F	78.68	15.65	5.03	0.20
Q8BMJ2_SY	Lars	Leucine--tR	K.STGNFLTLSQAVDK#.F	48.80	8.89	5.49	0.18
Q8BMJ2_SY	Lars	Leucine--tR	R.TDIGDTM*VYLVH.-	35.48	35.48	1.00	1.00
Q8BMJ2_SY	Lars	Leucine--tR	R.TDIGDTMVYLVH.-	25.78	25.78	1.00	1.00
Q8BMJ2_SY	Lars	Leucine--tR	K.TGFFEFQAAK#.D	115.48	15.41	7.49	0.13
Q8BMJ2_SY	Lars	Leucine--tR	K.VDFLK#EIEK#.E	11.86	2.81	4.22	0.24
Q8BMJ2_SY	Lars	Leucine--tR	K.VDFLK#EIEK#EAQQK#.W	18.73	6.49	2.89	0.35
Q8BMJ2_SY	Lars	Leucine--tR	R.VFASEM*NAGIIK#.T	98.51	16.31	6.04	0.17
Q8BMJ2_SY	Lars	Leucine--tR	K.VIASELGSLPELK#.K	83.36	15.47	5.39	0.19
Q8BMJ2_SY	Lars	Leucine--tR	K.VLEPYPSK#.L	97.68	20.57	4.75	0.21

Q8BMJ2_S	Lars	Leucine--tR	K.VVYVLPM*LTIK#.E	21.52	7.98	2.70	0.37
Q8BMJ2_S	Lars	Leucine--tR	K.VVYVLPMLTIK#.E	24.37	3.19	7.64	0.13
Q8BMJ2_S	Lars	Leucine--tR	R.YTIYSPK#.D	71.69	12.14	5.91	0.17
A2BE28_LA	Las1l	Ribosomal	K.LIDAAGTLGTDELR.L	3.89	12.37	0.31	3.18
A2BE28_LA	Las1l	Ribosomal	R.ELLVSYEEEQFK#.V	15.91	13.86	1.15	0.87
A2BE28_LA	Las1l	Ribosomal	R.LGNELPLAVASTADLVR.C	3.32	17.65	0.19	5.31
A2BE28_LA	Las1l	Ribosomal	K.LIDAAGTLGTDELR.L	4.67	19.26	0.24	4.12
Q61792_L	Lasp1	LIM and SH	K.GFSVVADTPELQR.I	18.43	73.38	0.25	3.98
Q61792_L	Lasp1	LIM and SH	R.LKQQSELQSQVR.Y	10.73	48.21	0.22	4.49
Q61792_L	Lasp1	LIM and SH	R.MGPSGGEGVEPERR.E	2.55	8.53	0.30	3.35
Q61792_L	Lasp1	LIM and SH	K.QQSELQSQVR.Y	8.64	47.77	0.18	5.53
Q61792_L	Lasp1	LIM and SH	K.QSFTM*VADTPENLR.L	3.72	11.40	0.33	3.07
Q61792_L	Lasp1	LIM and SH	K.QSFTMVADTPENLR.L	3.48	12.47	0.28	3.58
Q61792_L	Lasp1	LIM and SH	K.TQDQISNIK#.Y	90.26	68.12	1.33	0.75
Q61792_L	Lasp1	LIM and SH	K.YHEEFEK#.S	58.01	42.96	1.35	0.74
Q61792_L	Lasp1	LIM and SH	K.GFSVVADTPELQR.I	1.22	5.00	0.24	4.08
Q8C142_A	Ldlrap1	Low densit	R.ETLLEGM*VFSLK#.Y	7.51	2.35	3.19	0.31
Q8C142_A	Ldlrap1	Low densit	K.GEELSAAAVK#.R	7.38	3.65	2.02	0.49
Q8C142_A	Ldlrap1	Low densit	K.VAQAVTLTVAQAFK#.V	8.62	3.44	2.51	0.40
D3YWS8_D	Leng8	Leukocyte	R.LSLAQLPAF.-	7.09	7.09	1.00	1.00
D3YWS8_D	Leng8	Leukocyte	R.LSLAQLPAF.-	13.97	13.97	1.00	1.00
Q5XJE5_LE	Leo1	RNA polym	R.IEVEIPK#.V	25.28	14.29	1.77	0.57
Q5XJE5_LE	Leo1	RNA polym	R.QGTGLQGQAVFK#.T	27.58	20.62	1.34	0.75
Q5XJE5_LE	Leo1	RNA polym	K.VNTDLGNDLYFVK#.L	26.58	16.03	1.66	0.60
Q3V1T4_P	Lepre1	Prolyl 3-hy	R.LTNAAATSGDGYR.G	4.19	26.95	0.16	6.43
Q3V1T4_P	Lepre1	Prolyl 3-hy	R.SPYNYLQVAYFK.I	24.85	15.65	1.59	0.63
Q3V1T4_P	Lepre1	Prolyl 3-hy	R.TAIEESQAER.K	4.91	11.53	0.43	2.35
Q8CG70_P	Leprel2	Prolyl 3-hy	K.ALNQYQTQLGEPRPDLGPR.E	1.29	7.46	0.17	5.80
Q8CG70_P	Leprel2	Prolyl 3-hy	R.FEGLTVLK#.A	8.81	5.26	1.67	0.60
Q8K2B0_S	Leprel4	Synaptone	R.WGLEDEDFQPR.E	1.53	6.97	0.22	4.56
P16045_LE	Lgals1	Galectin-1	R.LNM*EAINYM*AADGDFK#.I	10.67	14.06	0.76	1.32
P16045_LE	Lgals1	Galectin-1	R.LNM*EAINYMAADGDFK.I	1.70	2.33	0.73	1.37
P16045_LE	Lgals1	Galectin-1	R.LNMEAINYM*AADGDFK#.I	3.65	3.07	1.19	0.84
P16045_LE	Lgals1	Galectin-1	K.SFVLNLGK#.D	26.80	19.34	1.39	0.72
P16045_LE	Lgals1	Galectin-1	K.FPNRLNMEAINYM*AADGDFK#.I	5.24	3.38	1.55	0.64
O08573_LE	Lgals9	Galectin-9	R.NTQINNSWGQEER.S	2.97	9.23	0.32	3.11
P37913_D	Lig1	DNA ligase	K.DTEQIAEFLEQSVK#.D	27.45	6.82	4.03	0.25
P37913_D	Lig1	DNA ligase	R.ENFVETEGEFVFTTSLDTK#.D	8.84	1.05	8.39	0.12
P37913_D	Lig1	DNA ligase	K.GTLDPANYNPSK#.N	36.36	11.86	3.07	0.33
P37913_D	Lig1	DNA ligase	R.IDGAVAPDHWLDPSIVWEVK#.C	44.53	10.52	4.23	0.24
P37913_D	Lig1	DNA ligase	R.LGPPQQGLELGVGDGVLLK#.A	51.76	12.73	4.07	0.25
P37913_D	Lig1	DNA ligase	R.LM*LPPPPLTISGVFTK#.F	15.30	5.12	2.99	0.33
P37913_D	Lig1	DNA ligase	K.TLDVDATYEIAK#.R	25.75	16.20	1.59	0.63
P37913_D	Lig1	DNA ligase	K.TLSSFFTPR.K	12.12	12.36	0.98	1.02
P37913_D	Lig1	DNA ligase	K.VPFLAVAR.T	13.52	18.56	0.73	1.37
P37913_D	Lig1	DNA ligase	R.AQIHVLEGGEVK#.I	10.51	4.26	2.47	0.41
P37913_D	Lig1	DNA ligase	K.DTEQIAEFLEQSVK#.D	11.37	2.82	4.03	0.25
P37913_D	Lig1	DNA ligase	K.EGDQLIVPSEPTK#.S	7.92	3.88	2.04	0.49
P37913_D	Lig1	DNA ligase	R.ENFVETEGEFVFTTSLDTK#.D	3.97	2.91	1.36	0.73
P37913_D	Lig1	DNA ligase	K.GTLDPANYNPSK#.N	21.16	7.90	2.68	0.37
P37913_D	Lig1	DNA ligase	R.IDGAVAPDHWLDPSIVWEVK#.C	27.27	6.98	3.91	0.26
P37913_D	Lig1	DNA ligase	R.LGPPQQGLELGVGDGVLLK#.A	24.23	7.52	3.22	0.31
P37913_D	Lig1	DNA ligase	R.LM*LPPPPLTISGVFTK#.F	9.82	3.85	2.55	0.39
P97386_D	Lig3	DNA ligase	K.AAVWEITGAEFSR.S	2.50	8.94	0.28	3.57
P97386_D	Lig3	DNA ligase	R.DLEQGDVSETIR.I	5.12	22.81	0.22	4.45
P97386_D	Lig3	DNA ligase	K.GASFITSTNPR.K	3.54	12.84	0.28	3.63
P97386_D	Lig3	DNA ligase	K.K#IEDLTELEGWEELEDNEK#EQISQHIADLSSK#.A	8.88	6.96	1.28	0.78
P97386_D	Lig3	DNA ligase	K.LTKEDEQQQALQDIASR.C	5.40	28.50	0.19	5.28
P97386_D	Lig3	DNA ligase	K.LTTTGQVTSPVK#.G	18.97	13.52	1.40	0.71
P97386_D	Lig3	DNA ligase	K.TQIIHDFLQK#.G	12.24	8.58	1.43	0.70
P97386_D	Lig3	DNA ligase	K.VLLDVFTGVR.L	5.25	13.93	0.38	2.65
P97386_D	Lig3	DNA ligase	K.LTTTGQVTSPVK#.G	14.98	8.96	1.67	0.60
Q9ERG0_L	Lima1	LIM domai	K.QSSPASYTNELK#.T	7.09	7.35	0.96	1.04
Q9ERG0_L	Lima1	LIM domai	K.SQDVGFWEGEVVR.E	1.49	6.69	0.22	4.49
Q9ERG0_L	Lima1	LIM domai	R.HEAEK#PETSENTETSGK#.I	19.21	21.09	0.91	1.10
Q9ERG0_L	Lima1	LIM domai	R.IAWPPPAELGGSGSALEEGIK#.V	13.78	13.29	1.04	0.96
Q9ERG0_L	Lima1	LIM domai	R.IAWPPPAELGGSGSALEEGIK#.V	12.10	14.65	0.83	1.21
Q9ERG0_L	Lima1	LIM domai	R.KGWSESEQSEEFGGGIATM*ER.K	2.92	7.19	0.41	2.46
Q9ERG0_L	Lima1	LIM domai	K.QSSPASYTNELK#.T	21.79	22.75	0.96	1.04
Q9ERG0_L	Lima1	LIM domai	K.SDNEETLGRPAQPPNAGESPHSPGVEDAPIAK.V	1.23	15.89	0.08	12.87
Q9ERG0_L	Lima1	LIM domai	K.SQDVGFWEGEVVR.E	5.03	29.90	0.17	5.95
Q9ERG0_L	Lima1	LIM domai	R.TSSLPESSPSK#.T	30.65	30.07	1.02	0.98
Q99JW4_L	Lims1	LIM and se	K.FPLELK#.K	27.20	24.25	1.12	0.89
Q99JW4_L	Lims1	LIM and se	K.LSETLGR.K	118.81	42.83	2.77	0.36
Q99JW4_L	Lims1	LIM and se	R.VIEGDVVSALNK#.A	64.57	58.93	1.10	0.91
Q8CD94_L	Lin52	Protein lin-	K.ELGSLTTANLM*EK.V	4.10	3.17	1.29	0.77
Q571G4_L	Lin54	Protein lin-	R.VLSQSTPGTPSK#.T	12.18	6.93	1.76	0.57
Q571G4_L	Lin54	Protein lin-	K.VTAQAQPGDAK#.L	5.50	3.49	1.58	0.63
O88952_L	Lin7c	Protein lin-	K.TEEGLGFNIM*GGK#.E	12.02	9.43	1.27	0.78
Q8VEE1_L	Lmcd1	LIM and cy	K.SEALGVGEVALPGQGGLPK#.E	6.81	4.30	1.58	0.63
P48678_L	Lmna	Prelamin-A	K.AAYEAELGDAR.K	6.20	19.36	0.32	3.12
P48678_L	Lmna	Prelamin-A	R.AQHEDQVEQYK#K#.E	5.91	4.24	1.39	0.72
P48678_L	Lmna	Prelamin-A	K.EAALSTALSEK#.R	23.06	27.25	0.85	1.18
P48678_L	Lmna	Prelamin-A	R.ITESEEVVSR.E	9.29	32.59	0.29	3.51
P48678_L	Lmna	Prelamin-A	K.LEAALGEAK#.K	175.37	72.48	2.42	0.41
P48678_L	Lmna	Prelamin-A	R.LKDLEALLNSK.E	12.36	11.62	1.06	0.94
P48678_L	Lmna	Prelamin-A	K.LLEGEEER.L	7.23	31.87	0.23	4.41
P48678_L	Lmna	Prelamin-A	R.LQEKEDLQELNDR.L	1.72	5.30	0.32	3.09
P48678_L	Lmna	Prelamin-A	R.LQTLKEELDFQK.N	22.84	18.64	1.23	0.82
P48678_L	Lmna	Prelamin-A	R.M*QQQLDEYQELLDIK#.L	6.85	6.30	1.09	0.92
P48678_L	Lmna	Prelamin-A	R.SLETENAGLR.L	5.11	36.08	0.14	7.06
P48678_L	Lmna	Prelamin-A	K.SNEDQSM*GNWQIR.R	2.51	14.03	0.18	5.59
P48678_L	Lmna	Prelamin-A	R.TALINSTGEEVAM*R.K	2.53	9.13	0.28	3.60
P48678_L	Lmna	Prelamin-A	R.VAVEEVDEEGK.F	14.67	17.02	0.86	1.16
P48678_L	Lmna	Prelamin-A	K.AGQVVTIWASGAGATHSPPTDLVWK#.A	9.63	8.48	1.14	0.88
P48678_L	Lmna	Prelamin-A	K.EAALSTALSEK#.R	18.55	17.15	1.08	0.92
P48678_L	Lmna	Prelamin-A	R.IDSLSAQLSQLQK#.Q	13.48	11.99	1.12	0.89
P48678_L	Lmna	Prelamin-A	R.ITESEEVVSR.E	11.86	46.26	0.26	3.90
P48678_L	Lmna	Prelamin-A	R.LADALQELR.A	9.59	40.84	0.23	4.26
P48678_L	Lmna	Prelamin-A	R.LAVYIDR.V	5.62	22.52	0.25	4.01
P48678_L	Lmna	Prelamin-A	K.LEAALGEAK#.K	46.76	42.11	1.11	0.90
P48678_L	Lmna	Prelamin-A	R.LK#DLEALLNSK#.E	15.18	13.26	1.15	0.87
P48678_L	Lmna	Prelamin-A	K.LLEGEEER.L	6.86	28.66	0.24	4.18

P48678_L	Lmna	Prelamin-A	R.LQEKEDLQELNDR.L	3.74	32.83	0.11	8.79
P48678_L	Lmna	Prelamin-A	R.M*QQQLDEYQELLDIK.L	7.20	7.72	0.93	1.07
P48678_L	Lmna	Prelamin-A	R.NSNLVGAAHEELQQSR.I	3.25	8.59	0.38	2.64
P48678_L	Lmna	Prelamin-A	R.SLETENAGLR.L	3.11	28.28	0.11	9.08
P48678_L	Lmna	Prelamin-A	R.SVGGSGGGSFGDNLVTR.S	4.41	16.49	0.27	3.74
P48678_L	Lmna	Prelamin-A	R.TALINSTGEEVAM*R.K	3.43	10.63	0.32	3.10
P48678_L	Lmna	Prelamin-A	R.TLEGELHDLR.G	4.72	9.59	0.49	2.03
Q9D920_L	Loh12cr1	Loss of hete	R.LNSM*LPEAER.L	2.35	5.24	0.45	2.23
Q8CGK3_L	Lonp1	Lon protea	R.AFLM*EQDPENDFLVTSHIHLHVPEGATPK#.D	7.51	1.51	4.97	0.20
Q8CGK3_L	Lonp1	Lon protea	R.AFLMEQDPENDFLVTSHIHLHVPEGATPK#.D	6.18	3.74	1.65	0.60
Q8CGK3_L	Lonp1	Lon protea	K.AQLSAAVLTLLIK#.Q	16.90	10.36	1.63	0.61
Q8CGK3_L	Lonp1	Lon protea	R.DIIALNPLYR.E	4.62	7.30	0.63	1.58
Q8CGK3_L	Lonp1	Lon protea	K.ELGLEK#DDK#DAIEEK#.F	37.73	9.01	4.19	0.24
Q8CGK3_L	Lonp1	Lon protea	K.EVEDELGPK#PQLEM*VTEAATDTSK#.E	12.15	10.93	1.11	0.90
Q8CGK3_L	Lonp1	Lon protea	K.EVEDELGPK#PQLEMVTEAATDTSK#.E	9.08	2.03	4.47	0.22
Q8CGK3_L	Lonp1	Lon protea	R.FSVGGM*TDVAEIK#.G	38.75	6.64	5.83	0.17
Q8CGK3_L	Lonp1	Lon protea	K.HVM*DVVDEELSK#.L	20.12	5.12	3.93	0.25
Q8CGK3_L	Lonp1	Lon protea	K.IVSGEAQTVQVTPENLQDFVGKPVFTVER.M	11.44	6.65	1.72	0.58
Q8CGK3_L	Lonp1	Lon protea	R.LAQPYVGVFLK#.R	37.50	10.55	3.56	0.28
Q8CGK3_L	Lonp1	Lon protea	R.M*EM*INVSGYVAQEK#.L	11.91	2.98	4.00	0.25
Q8CGK3_L	Lonp1	Lon protea	R.M*IVTGHRR.I	3.28	30.44	0.11	9.30
Q8CGK3_L	Lonp1	Lon protea	R.QLEVEPEGLEPEAEK#.Q	10.55	5.31	1.99	0.50
Q8CGK3_L	Lonp1	Lon protea	K.TENPLVLIDEVDK#.I	12.89	4.44	2.90	0.34
Q8CGK3_L	Lonp1	Lon protea	R.M*IVTGHRR.I	2.76	26.86	0.10	9.74
Q924C6_L	Loxl4	Lysyl oxida	R.EALFGAQLGQGLGPIHLSEVR.C	8.06	15.73	0.51	1.95
Q924C6_L	Loxl4	Lysyl oxida	R.QLGLGFANFALK#.D	11.36	8.14	1.40	0.72
Q924C6_L	Loxl4	Lysyl oxida	K.YGQGEGPIWLDNVR.C	22.41	24.33	0.92	1.09
Q8BFW7_L	Lpp	Lipoma-pre	K.EPIM*PAPGQEETVR.I	2.40	6.89	0.35	2.87
Q8BFW7_L	Lpp	Lipoma-pre	K.SAQPSPHYM*AGPSSGQIYGPGPR.G	3.22	15.76	0.20	4.90
Q8BFW7_L	Lpp	Lipoma-pre	R.SEGDTAYGQQVQPNTWK#.R	9.29	9.21	1.01	0.99
Q8BFW7_L	Lpp	Lipoma-pre	R.YYEPYYAAGPSYGGR.S	4.77	10.04	0.47	2.11
Q9ESE1_LR	Lrba	Lipopolysa	K.ASTSTEAPQPQR.H	2.70	4.29	0.63	1.58
Q9ESE1_LR	Lrba	Lipopolysa	K.YGPDAFFNFPGK#.S	8.52	4.21	2.02	0.49
Q3UMG5_L	Lrch2	Leucine-ric	R.NNLHVLPDELGDLPLVK#.L	8.87	9.01	0.98	1.02
Q3UMG5_L	Lrch2	Leucine-ric	K.YLFDLPLK#.V	13.20	8.74	1.51	0.66
Q91ZX7_L	Lrp1	Prolow-der	K.AVTDEEPFLIFANR.Y	1.62	7.00	0.23	4.32
Q9JI18_LR	Lrp1b	Low-densit	R.NSLASVDER.K	9.72	14.15	0.69	1.46
Q6PB66_L	Lrpprc	Leucine-ric	R.LLAEILK#.T	14.03	3.20	4.38	0.23
Q6PB66_L	Lrpprc	Leucine-ric	K.NVQGIIDILK#.I	14.21	2.87	4.95	0.20
Q6PB66_L	Lrpprc	Leucine-ric	K.TSQVTSSDLESTLEK#.L	13.18	2.39	5.51	0.18
Q6PB66_L	Lrpprc	Leucine-ric	K.AGYPQYVSEILEK#.I	11.54	1.91	6.05	0.17
Q6PB66_L	Lrpprc	Leucine-ric	K.NVQGIIDILK#.I	16.01	3.85	4.16	0.24
Q9CRC8_L	Lrrc40	Leucine-ric	K.ELHLAENQIEK#.L	14.80	6.12	2.42	0.41
Q9CRC8_L	Lrrc40	Leucine-ric	K.GTAAVLEYLR.D	5.48	12.33	0.44	2.25
Q9CRC8_L	Lrrc40	Leucine-ric	R.LLPALTVLDIHDNQLTSLPSAIR.E	8.09	17.07	0.47	2.11
Q9CRC8_L	Lrrc40	Leucine-ric	K.LQSLSDDLR.L	4.58	14.17	0.32	3.10
Q9CRC8_L	Lrrc40	Leucine-ric	K.QATLIPDDLFDATK#.T	14.03	8.55	1.64	0.61
Q9CRC8_L	Lrrc40	Leucine-ric	K.FLALEGNPLR.T	4.57	9.93	0.46	2.17
Q9CRC8_L	Lrrc40	Leucine-ric	K.ILPEEITSLK#.N	23.36	10.48	2.23	0.45
Q9CRC8_L	Lrrc40	Leucine-ric	R.LLPALTVLDIHDNQLTSLPSAIR.E	8.24	15.39	0.54	1.87
Q9CRC8_L	Lrrc40	Leucine-ric	K.LQTINLSFNR.F	7.81	9.96	0.78	1.28
Q9CRC8_L	Lrrc40	Leucine-ric	R.NNFLSSLPEEM*SSLTK#.L	5.20	18.28	0.28	3.52
Q9CRC8_L	Lrrc40	Leucine-ric	K.TTLITSINFSK#.N	11.11	6.20	1.79	0.56
Q505F5_L	Lrrc47	Leucine-ric	R.APGPGLAQGLPQLHSLVLR.R	16.85	27.36	0.62	1.62
Q505F5_L	Lrrc47	Leucine-ric	K.DIMDSLILR.M	4.55	11.99	0.38	2.64
Q505F5_L	Lrrc47	Leucine-ric	R.ELLLTGPGLEER.V	14.73	26.06	0.57	1.77
Q505F5_L	Lrrc47	Leucine-ric	R.ELSPDIAHLASLK#.T	14.20	6.65	2.14	0.47
Q505F5_L	Lrrc47	Leucine-ric	R.ESGEGEEEVADSAR.L	22.64	35.33	0.64	1.56
Q505F5_L	Lrrc47	Leucine-ric	R.FLNSQTK#.L	27.10	15.38	1.76	0.57
Q505F5_L	Lrrc47	Leucine-ric	R.GPLLYAARPPEDLK.I	12.14	25.14	0.48	2.07
Q505F5_L	Lrrc47	Leucine-ric	R.LQSLNLTGNR.L	12.23	34.08	0.36	2.79
Q505F5_L	Lrrc47	Leucine-ric	R.QLQLEAEEQR.K	8.28	13.67	0.61	1.65
Q505F5_L	Lrrc47	Leucine-ric	R.TAATIATHDLQAVR.G	14.07	26.82	0.52	1.91
Q505F5_L	Lrrc47	Leucine-ric	R.VVDLEGSLK#.V	78.28	31.56	2.48	0.40
Q505F5_L	Lrrc47	Leucine-ric	R.APGPGLAQGLPQLHSLVLR.R	6.42	12.21	0.53	1.90
Q505F5_L	Lrrc47	Leucine-ric	R.ELLLTGPGLEER.V	6.38	13.17	0.48	2.06
Q505F5_L	Lrrc47	Leucine-ric	R.ESGEGEEEVADSAR.L	7.00	12.80	0.55	1.83
Q505F5_L	Lrrc47	Leucine-ric	R.NALGPGLSPELGPLPALR.V	6.31	18.63	0.34	2.95
Q505F5_L	Lrrc47	Leucine-ric	R.VVDLEGSLK#.V	34.07	12.33	2.76	0.36
Q9D1G5_L	Lrrc57	Leucine-ric	R.ELPSTFGQLSALK#.T	42.56	19.07	2.23	0.45
Q9D1G5_L	Lrrc57	Leucine-ric	R.GLTEFPSELQK#.L	13.38	5.12	2.61	0.38
Q9D1G5_L	Lrrc57	Leucine-ric	R.SIPDTVGELQAIELNLNQNQISQLSVK#.I	18.60	6.96	2.67	0.37
Q9D1G5_L	Lrrc57	Leucine-ric	K.TGVFQLK#.D	10.24	3.49	2.93	0.34
Q9D1G5_L	Lrrc57	Leucine-ric	R.TIDLSNNK#IDSLPPLIIGK#.F	15.26	7.02	2.17	0.46
Q3UZ39_L	Lrrfip1	Leucine-ric	K.AM*VSNAQLDNEK#.T	11.81	3.80	3.11	0.32
Q3UZ39_L	Lrrfip1	Leucine-ric	K.HAHSILQFQFAEVK#.E	12.69	7.56	1.68	0.60
Q3UZ39_L	Lrrfip1	Leucine-ric	K.AM*VSNAQLDNEK#.T	8.02	1.51	5.33	0.19
Q3UZ39_L	Lrrfip1	Leucine-ric	R.ELTQEVAEPEEAIVQIPQAGGENTITK#.A	9.61	2.68	3.58	0.28
Q3UZ39_L	Lrrfip1	Leucine-ric	K.HAHSILQFQFAEVK#.E	16.22	18.21	0.89	1.12
Q8BUI3_LR	LRWD1	Leucine-ric	R.ELDLSNNLLETLPANLGLSHLR.I	3.93	7.58	0.52	1.93
Q3UM18_L	Lsg1	Large subu	K.LILTPFER.N	4.25	15.03	0.28	3.54
Q3UM18_L	Lsg1	Large subu	K.NAENQQVNNDSYLVSK#.Q	9.03	6.26	1.44	0.69
Q9D0R8_L	Lsm12	Protein LS	R.LQGEVVAFDYQSK#.M	91.08	36.61	2.49	0.40
Q9D0R8_L	Lsm12	Protein LS	R.TETPPPLASLNVSK#.L	24.70	12.89	1.92	0.52
Q8K2F8_LS	Lsm14a	Protein LS	R.YEGILYTIDTENSTVALAK#.V	2.92	1.49	1.95	0.51
Q8CGC4_L	Lsm14b	Protein LS	K.SFFDNISSELK#.T	19.72	10.09	1.96	0.51
P24527_L	Lta4h	Leukotrien	K.GSPMEISLPIALSK#.N	8.58	2.20	3.90	0.26
P24527_L	Lta4h	Leukotrien	K.GSPM*EISLPIALSK#.N	7.57	1.33	5.70	0.18
P24527_L	Lta4h	Leukotrien	K.DLSSHQLNEFLAQVLQK#.A	8.94	2.35	3.81	0.26
P24527_L	Lta4h	Leukotrien	K.DVDPDVAYSSIPYEK#.G	5.08	2.04	2.49	0.40
P24527_L	Lta4h	Leukotrien	K.GSPM*EISLPIALSK#.N	16.75	1.17	14.30	0.07
P24527_L	Lta4h	Leukotrien	K.LTYTAEVSVPK#.E	14.71	5.33	2.76	0.36
Q6A009_L	Ltn1	E3 ubiquiti	K.LPQSITEPK#.L	13.95	7.86	1.78	0.56
Q6A009_L	Ltn1	E3 ubiquiti	K.NFLTSLVTGLSTER.T	4.72	11.91	0.40	2.52
Q6NSQ7_L	Ltv1	Protein LT	K.LPSSVFASEFEEDVGLLNK#.A	9.39	4.51	2.08	0.48
Q6NSQ7_L	Ltv1	Protein LT	R.DPLAADETAPQR@.V	7.71	7.37	1.05	0.95
Q6NSQ7_L	Ltv1	Protein LT	K.HLFWEEETK#.S	17.03	5.98	2.85	0.35
Q6NSQ7_L	Ltv1	Protein LT	K.LPSSVFASEFEEDVGLLNK#.A	27.60	10.16	2.72	0.37
Q6NSQ7_L	Ltv1	Protein LT	R.LQEVLNDYYK#.E	24.87	8.84	2.81	0.36
Q6NSQ7_L	Ltv1	Protein LT	K.NIEGLK#L.-	16.47	5.76	2.86	0.35
Q9CYI4_LU	Luc7l	Putative R	K.AEQLGAEGNVDESQK#.I	108.89	123.90	0.88	1.14
Q9CYI4_LU	Luc7l	Putative R	R.ALLDQLMGTAR.D	5.23	28.96	0.18	5.54
Q9CYI4_LU	Luc7l	Putative R	R.LAETQEEISAEVSAK#.A	27.33	31.47	0.87	1.15

Q9CYI4_LU	Luc7l	Putative RN	K.LHLGFIQIR.E	6.45	26.53	0.24	4.11
Q7TNC4_L	Luc7l2	Putative RN	R.ADYEIASK#.E	260.53	249.35	1.04	0.96
Q7TNC4_L	Luc7l2	Putative RN	R.AM*LDQLM*GTSR.D	8.55	109.70	0.08	12.83
Q7TNC4_L	Luc7l2	Putative RN	R.AMLDQLM*GTSR.D	6.12	26.44	0.23	4.32
Q7TNC4_L	Luc7l2	Putative RN	R.AM*LDQLMGTSR.D	7.59	29.00	0.26	3.82
Q7TNC4_L	Luc7l2	Putative RN	R.AMLDQLMGTSR.D	2.81	11.31	0.25	4.02
Q7TNC4_L	Luc7l2	Putative RN	R.EAEEVYR.N	36.91	145.19	0.25	3.93
Q7TNC4_L	Luc7l2	Putative RN	R.FRDQDLASR.D	2.74	44.56	0.06	16.25
Q7TNC4_L	Luc7l2	Putative RN	R.LADHFGGK#.L	59.82	59.00	1.01	0.99
Q7TNC4_L	Luc7l2	Putative RN	R.LAETQEEISAEVAAK#.A	153.27	145.24	1.06	0.95
Q7TNC4_L	Luc7l2	Putative RN	K.LHLGFIEIR.E	24.13	77.38	0.31	3.21
Q7TNC4_L	Luc7l2	Putative RN	R.NSMPASSFQQQK#.L	112.52	71.94	1.56	0.64
Q7TNC4_L	Luc7l2	Putative RN	R.NSM*PASSFQQQK#.L	105.61	97.53	1.08	0.92
Q7TNC4_L	Luc7l2	Putative RN	K.VEQLGAEGNVEESQK#.V	315.03	282.93	1.11	0.90
Q7TNC4_L	Luc7l2	Putative RN	K.VEQLGAEGNVEESQKVMDEVEK.A	5.74	6.85	0.84	1.19
Q7TNC4_L	Luc7l2	Putative RN	R.VHELNEEIGK#.L	176.90	173.83	1.02	0.98
Q7TNC4_L	Luc7l2	Putative RN	K.VMDEVEK#.A	46.43	39.81	1.17	0.86
Q7TNC4_L	Luc7l2	Putative RN	R.AM*LDQLM*GTSR.D	2.13	4.74	0.45	2.22
Q7TNC4_L	Luc7l2	Putative RN	K.VEQLGAEGNVEESQK#.V	4.72	3.17	1.49	0.67
Q7TNC4_L	Luc7l2	Putative RN	K.VEQLGAEGNVEESQK.V	4.12	7.65	0.54	1.86
Q5SUF2_L	Luc7l3	Luc7-like p	R.EKQSEDTNPESK.E	2.60	3.01	0.86	1.16
Q5SUF2_L	Luc7l3	Luc7-like p	K.IK#ATVEELK#EK#.L	25.04	20.62	1.21	0.82
Q5SUF2_L	Luc7l3	Luc7-like p	R.LALSQNQQSSGAAGPTGK#.N	142.53	106.13	1.34	0.74
Q5SUF2_L	Luc7l3	Luc7-like p	R.STTSTIESFAAQEK#.Q	169.58	119.23	1.42	0.70
Q5SUF2_L	Luc7l3	Luc7-like p	R.YLQSLLAEVER.R	23.07	59.54	0.39	2.58
Q5SUF2_L	Luc7l3	Luc7-like p	R.LALSQNQQSSGAAGPTGK#.N	19.15	14.61	1.31	0.76
Q5SUF2_L	Luc7l3	Luc7-like p	R.STTSTIESFAAQEK.Q	22.20	26.05	0.85	1.17
Q5SUF2_L	Luc7l3	Luc7-like p	R.YLQSLLAEVER.R	6.02	24.98	0.24	4.15
Q5SUF2_L	Luc7l3	Luc7-like p	R.STTSTIESFAAQEK#.Q	25.17	19.71	1.28	0.78
Q5SUF2_L	Luc7l3	Luc7-like p	R.YLQSLLAEVER.R	6.05	19.56	0.31	3.23
Q5SUF2_L	Luc7l3	Luc7-like p	R.LALSQNQQSSGAAGPTGK#.N	18.73	13.58	1.38	0.73
Q5SUF2_L	Luc7l3	Luc7-like p	R.STTSTIESFAAQEK#.Q	20.57	13.16	1.56	0.64
Q8R4U7_L	Luzp1	Leucine zip	K.AIGALSSSQK#.A	12.50	11.42	1.09	0.91
Q8R4U7_L	Luzp1	Leucine zip	K.GAPKPGTESGLK.G	9.89	13.90	0.71	1.41
Q8R4U7_L	Luzp1	Leucine zip	R.IEDGISSTLSSK#.E	25.43	21.55	1.18	0.85
Q8R4U7_L	Luzp1	Leucine zip	K.NNDLQDNYLTELNR.N	1.92	5.11	0.37	2.67
Q8R4U7_L	Luzp1	Leucine zip	R.RLDELEEATK.N	4.93	10.89	0.45	2.21
Q8R4U7_L	Luzp1	Leucine zip	R.SLASQLEEIK#.L	15.08	19.91	0.76	1.32
Q8R4U7_L	Luzp1	Leucine zip	K.SLTLSFVNER.K	3.69	8.33	0.44	2.26
Q8R4U7_L	Luzp1	Leucine zip	R.SQENILQGFSLPNK#.E	7.57	6.22	1.22	0.82
Q08288_L	Lyar	Cell growth	R.ELLQQISAFDNVPR.K	17.70	25.21	0.70	1.42
Q08288_L	Lyar	Cell growth	K.FQNWMK#.N	14.44	7.78	1.86	0.54
Q08288_L	Lyar	Cell growth	R.NGGPGEDAAEGQTK#.T	10.41	6.66	1.56	0.64
Q08288_L	Lyar	Cell growth	K.NQEAGHEAAGEEAAEASGPPEK#.K	51.10	34.97	1.46	0.68
Q08288_L	Lyar	Cell growth	K.NQEAGHEAAGEEAAEASGPPEK#K#.K	23.03	10.87	2.12	0.47
Q08288_L	Lyar	Cell growth	K.QQAWIQK#.I	37.58	22.32	1.68	0.59
P97823_LY	Lypla1	Acyl-protei	K.ALINPANVTFK#.I	10.43	7.95	1.31	0.76
Q3UFF7_LY	Lyplal1	Lysophospl	K.ASVVYQDLQQGGR.M	2.52	4.89	0.52	1.94
Q9JHQ5_L	Lztfl1	Leucine zip	K.LVPINEGGTTELLNK#.E	21.71	6.61	3.28	0.30
P24668_M	M6pr	Cation-dep	K.SFESTVGQGSDTYSYIFR.V	2.89	4.29	0.67	1.48
Q9QXZ0_M	Macf1	Microtubul	K.AFLAELEQNSPK#.I	13.72	3.30	4.15	0.24
Q9QXZ0_M	Macf1	Microtubul	K.AGSELLESSAGDDASSLR.S	6.80	14.30	0.48	2.10
Q9QXZ0_M	Macf1	Microtubul	K.AILEQQVLAEELTTK#.K	6.59	2.52	2.61	0.38
Q9QXZ0_M	Macf1	Microtubul	K.ALNEEIINRK.K	1.17	16.22	0.07	13.92
Q9QXZ0_M	Macf1	Microtubul	R.DQEPIPQNIDR.V	5.98	16.77	0.36	2.80
Q9QXZ0_M	Macf1	Microtubul	R.DQIIELDQTGNQLK#.F	8.97	5.43	1.65	0.61
Q9QXZ0_M	Macf1	Microtubul	R.EAEEELAASGGQSPTGEQIPQFQQR.Q	4.58	12.79	0.36	2.79
Q9QXZ0_M	Macf1	Microtubul	K.ELEEAVTSALQQETEK#.S	6.57	3.43	1.91	0.52
Q9QXZ0_M	Macf1	Microtubul	K.ELNPEEGKM*VEEK.Y	3.95	6.74	0.59	1.71
Q9QXZ0_M	Macf1	Microtubul	K.FLDVLELAEK#.F	38.33	27.78	1.38	0.72
Q9QXZ0_M	Macf1	Microtubul	R.FQQLQLQQQEK#.E	14.02	7.31	1.92	0.52
Q9QXZ0_M	Macf1	Microtubul	R.IAEQEHTQEDLQHLR.S	2.69	9.17	0.29	3.41
Q9QXZ0_M	Macf1	Microtubul	K.LANSEPVGTQTAK#.I	29.14	20.83	1.40	0.71
Q9QXZ0_M	Macf1	Microtubul	R.LEQDQTTAQLQVQK#.A	18.14	12.04	1.51	0.66
Q9QXZ0_M	Macf1	Microtubul	K.LISDTVGQR.V	7.38	17.13	0.43	2.32
Q9QXZ0_M	Macf1	Microtubul	R.LLDAEDVDVPSPDEK#.S	9.43	4.30	2.19	0.46
Q9QXZ0_M	Macf1	Microtubul	R.LQNVQIALDFLK#.Q	11.14	3.63	3.07	0.33
Q9QXZ0_M	Macf1	Microtubul	R.LSGQSAISTQPEAVK#.Q	19.89	7.31	2.72	0.37
Q9QXZ0_M	Macf1	Microtubul	K.LVSDANEQYK#.L	31.91	16.39	1.95	0.51
Q9QXZ0_M	Macf1	Microtubul	R.M*ENQLSASKPTGGLPETAR.E	6.82	20.53	0.33	3.01
Q9QXZ0_M	Macf1	Microtubul	K.NDVLAHQATVATVNK#.A	9.72	6.17	1.58	0.63
Q9QXZ0_M	Macf1	Microtubul	K.QLQEELAEHQVPVEK#.L	17.01	6.17	2.76	0.36
Q9QXZ0_M	Macf1	Microtubul	R.RGEELIGR.S	1.45	22.49	0.06	15.54
Q9QXZ0_M	Macf1	Microtubul	K.SIDEM*NNAWENLNK#.T	9.59	2.83	3.39	0.30
Q9QXZ0_M	Macf1	Microtubul	R.SSQIDQAIVK#.S	58.88	62.93	0.94	1.07
Q9QXZ0_M	Macf1	Microtubul	K.STQYQDLLQDLSEK#.V	7.94	7.61	1.04	0.96
Q9QXZ0_M	Macf1	Microtubul	K.TEQSVALLEQK#.W	17.74	10.07	1.76	0.57
Q9QXZ0_M	Macf1	Microtubul	R.TSLAGDTSNSSSPASTGAK#.A	18.65	10.57	1.76	0.57
Q9QXZ0_M	Macf1	Microtubul	R.YADITLTSSK#.A	23.90	13.89	1.72	0.58
Q9WTX8_M	Mad1l1	Mitotic spi	R.EQEDSLASAR.E	2.64	9.51	0.28	3.60
Q9WTX8_M	Mad1l1	Mitotic spi	R.GGPIPADLEAASSLPSSK.E	7.80	13.02	0.60	1.67
Q9WTX8_M	Mad1l1	Mitotic spi	K.IQELQASQDER.A	1.79	19.20	0.09	10.70
Q9WTX8_M	Mad1l1	Mitotic spi	K.LTLQGDYNQSR.T	3.62	18.04	0.20	4.99
Q9WTX8_M	Mad1l1	Mitotic spi	K.VQQQLQDEVR.Q	2.92	22.26	0.13	7.61
Q9Z1B5_M	Mad2l1	Mitotic spi	K.YGLTLLTTTDPELIK.Y	8.09	10.93	0.74	1.35
Q4VC33_M	Maea	Macrophag	K.AVESIQAEDESAK#.L	17.41	10.74	1.62	0.62
Q4VC33_M	Maea	Macrophag	R.IQEFIELVR.Q	4.75	14.63	0.32	3.08
O54790_M	Mafg	Transcripti	R.GPLAAGLGPLVPGK.V	13.18	14.52	0.91	1.10
O54790_M	Mafg	Transcripti	K.VAATSVITIVK#.S	20.14	17.26	1.17	0.86
Q9QYH6_M	Maged1	Melanoma-	R.IPFTFWAR.Y	2.20	11.85	0.19	5.38
Q9CQL1_M	Magohb	Protein ma	K.IGSLIDVNQSK.D	83.72	91.85	0.91	1.10
Q9CQL1_M	Magohb	Protein ma	R.IIDDSEITKEDDALWPPPDR.V	14.45	67.06	0.22	4.64
Q9CQL1_M	Magohb	Protein ma	R.IIDDSEITKEDDALWPPPDR.V	2.09	5.89	0.35	2.82
Q9CQL1_M	Magohb	Protein ma	R.VFYYLVQDLK#.C	13.67	11.42	1.20	0.83
Q9CQL1_M	Magohb	Protein ma	R.YANNSNYKNDVM*IR.K	5.55	27.33	0.20	4.93
Q8BGS0_M	Mak16	Protein MA	K.ALIAAQLDNAIEK#.E	13.61	9.75	1.40	0.72
Q91W89_M	Man2c1	Alpha-man	R.SLLLVLQSPPN.-	8.96	8.96	1.00	1.00
Q9QYR6_M	Map1a	Microtubul	R.AVLDALLEGK#.A	63.85	27.07	2.36	0.42
Q9QYR6_M	Map1a	Microtubul	R.AVLDALLEGK#.A	70.83	24.36	2.91	0.34
Q9QYR6_M	Map1a	Microtubul	R.EGEGGAGAPDSSSFSSK#.V	13.66	5.75	2.38	0.42
Q9QYR6_M	Map1a	Microtubul	R.ESTFLDEGPNEQEITPLQHTPR.S	3.01	9.15	0.33	3.04
Q9QYR6_M	Map1a	Microtubul	R.FPTSTYDLSGPEGPGPFEASQSAESAVPASSSK#.T	4.06	1.57	2.60	0.39
Q9QYR6_M	Map1a	Microtubul	K.GVEQQDGAVPEK#.T	25.58	14.93	1.71	0.58

Q9QYR6_M	Map1a	Microtubul	K.SSFLEDK#.S	11.64	3.02	3.86	0.26
Q9QYR6_M	Map1a	Microtubul	R.VPSAPGQESPVPDTK#.S	15.61	5.20	3.00	0.33
Q9QYR6_M	Map1a	Microtubul	R.VVSNTIEPLTLFHK#.M	30.04	7.15	4.20	0.24
P14873_M	Map1b	Microtubul	K.ITSFPESESYSYETSTK#.T	8.19	4.06	2.02	0.50
P14873_M	Map1b	Microtubul	R.SSYYVVSGNDPAAEEPSR.A	10.65	12.97	0.82	1.22
P14873_M	Map1b	Microtubul	R.TPEEGGYSYEISEK#.T	12.70	6.11	2.08	0.48
P14873_M	Map1b	Microtubul	R.TPEVSGYTYEK#.T	32.03	18.16	1.76	0.57
P14873_M	Map1b	Microtubul	R.SSYYVVSGNDPAAEEPSR.A	4.79	4.38	1.09	0.92
P14873_M	Map1b	Microtubul	K.DLTGQVPTPPVK#.Q	25.24	3.63	6.95	0.14
P14873_M	Map1b	Microtubul	R.ESSPLYSPGFSDSTSAAK#.E	7.21	2.86	2.52	0.40
P14873_M	Map1b	Microtubul	K.EVSSK#EEQSPVK#AEVAEK#.Q	7.91	1.16	6.82	0.15
P14873_M	Map1b	Microtubul	K.HSPTEDDESAK#AEADVHLK#.E	13.73	2.76	4.97	0.20
P14873_M	Map1b	Microtubul	K.ITSFPESESYSYETSTK#.T	11.09	5.02	2.21	0.45
P14873_M	Map1b	Microtubul	R.SQGSTSNSDWM*K#.N	7.30	2.20	3.32	0.30
P14873_M	Map1b	Microtubul	R.TPEEGGYSYEISEK#.T	22.02	8.21	2.68	0.37
P14873_M	Map1b	Microtubul	R.TPEVSGYTYEK#.T	26.61	12.17	2.19	0.46
P14873_M	Map1b	Microtubul	K.TPQASTYSYETSDR.C	2.59	6.29	0.41	2.42
P14873_M	Map1b	Microtubul	R.VLFPGNSTQYNILEGLEK#.L	16.36	3.91	4.18	0.24
P14873_M	Map1b	Microtubul	R.AIGNIELGIR.S	20.86	31.21	0.67	1.50
P14873_M	Map1b	Microtubul	R.ASLSPM*DEPVPDSESPVEK#.V	6.77	2.15	3.15	0.32
P14873_M	Map1b	Microtubul	R.ASLSPMDEPVPDSESPVEK#.V	5.93	6.38	0.93	1.08
P14873_M	Map1b	Microtubul	K.DIKPQLELIEDEEKLKETQPGEAYVIQK.E	59.32	22.06	2.69	0.37
P14873_M	Map1b	Microtubul	K.DLTGQVPTPPVK#.Q	84.05	34.05	2.47	0.41
P14873_M	Map1b	Microtubul	R.DVM*SDETNNEETESPSQEFVNITK#.Y	13.77	4.88	2.82	0.35
P14873_M	Map1b	Microtubul	R.DVMSDETNNEETESPSQEFVNITK#.Y	7.05	3.55	1.99	0.50
P14873_M	Map1b	Microtubul	R.EEGYEPDK#TEAEDYVM*AVADK#.A	5.58	2.40	2.33	0.43
P14873_M	Map1b	Microtubul	R.EM*SLYASLASEK#.V	16.20	9.40	1.72	0.58
P14873_M	Map1b	Microtubul	K.ESK#EETPEVTK#.T	13.69	4.17	3.28	0.30
P14873_M	Map1b	Microtubul	R.ESSPLYSPGFSDSTSAAK#.E	20.64	9.47	2.18	0.46
P14873_M	Map1b	Microtubul	K.ETQPGEAYVIQK#.E	20.11	11.50	1.75	0.57
P14873_M	Map1b	Microtubul	K.EVSSK#EEQSPVK#AEVAEK#.Q	15.98	5.61	2.85	0.35
P14873_M	Map1b	Microtubul	K.HLDFLK#.Q	26.36	7.88	3.35	0.30
P14873_M	Map1b	Microtubul	R.HNLQDFINIK#.L	43.48	24.81	1.75	0.57
P14873_M	Map1b	Microtubul	K.HSPTEDDESAK#AEADVHLK#.E	112.39	38.74	2.90	0.34
P14873_M	Map1b	Microtubul	K.ITSFPESESYSYETSTK#.T	20.86	9.29	2.25	0.45
P14873_M	Map1b	Microtubul	R.K#ESK#EETPEVTK#.T	31.19	10.17	3.07	0.33
P14873_M	Map1b	Microtubul	K.LEM*YVLNPVK#.S	15.80	10.63	1.49	0.67
P14873_M	Map1b	Microtubul	K.LK#ETQPGEAYVIQK#.E	14.73	13.34	1.10	0.91
P14873_M	Map1b	Microtubul	K.M*SISEGTVSDK#.S	27.07	11.70	2.31	0.43
P14873_M	Map1b	Microtubul	K.NLISPDLGVVFLNVPENLKDPEPNIK.M	88.02	37.85	2.33	0.43
P14873_M	Map1b	Microtubul	R.SPPLLGSESPYEDFLSADSK#.V	18.19	10.13	1.80	0.56
P14873_M	Map1b	Microtubul	R.SQGSTSNSDWM*K#.N	27.28	4.55	5.99	0.17
P14873_M	Map1b	Microtubul	K.STGFIPIK#EDFGPEK#K#.T	42.37	28.35	1.49	0.67
P14873_M	Map1b	Microtubul	R.SVGNTIEPVILFQK#.M	97.02	31.73	3.06	0.33
P14873_M	Map1b	Microtubul	R.SVNFSLTPNEIK#.V	75.70	24.77	3.06	0.33
P14873_M	Map1b	Microtubul	R.THDVGGYYYEK#.T	15.51	9.56	1.62	0.62
P14873_M	Map1b	Microtubul	R.TPEEGGYSYEISEK#.T	42.28	20.13	2.10	0.48
P14873_M	Map1b	Microtubul	R.TPEVSGYTYEK#.T	56.86	36.14	1.57	0.64
P14873_M	Map1b	Microtubul	R.VLFPGNSTQYNILEGLEK#.L	44.39	15.84	2.80	0.36
P14873_M	Map1b	Microtubul	K.YESSLYSQEYSK#PAVASFNGLSEGSK#.T	4.06	4.20	0.97	1.03
Q8C052_M	Map1s	Microtubul	R.AVLDALLAGK#.R	13.34	3.85	3.47	0.29
Q8C052_M	Map1s	Microtubul	R.HSATFSSIVK#.G	10.93	11.70	0.93	1.07
P31938_M	Map2k1	Dual specifi	R.IPEQILGK#.V	89.50	21.76	4.11	0.24
P31938_M	Map2k1	Dual specifi	K.KLEELELDEQQR.K	3.75	14.17	0.26	3.78
P31938_M	Map2k1	Dual specifi	R.LEAFLTQK#.Q	37.08	12.16	3.05	0.33
P31938_M	Map2k1	Dual specifi	K.LPSGVFSLEFQDFVNK#.C	50.15	18.31	2.74	0.37
P31938_M	Map2k1	Dual specifi	K.VGELK#DDDFEK#.I	33.74	14.28	2.36	0.42
P31938_M	Map2k1	Dual specifi	K.VSIAVIK#.G	76.77	27.98	2.74	0.36
P31938_M	Map2k1	Dual specifi	R.YPIPPPDAK#.E	26.11	28.90	0.90	1.11
P31938_M	Map2k1	Dual specifi	K.LPSGVFSLEFQDFVNK#.C	6.05	2.40	2.53	0.40
P31938_M	Map2k1	Dual specifi	K.VSIAVIK#.G	19.17	5.54	3.46	0.29
Q63932_M	Map2k2	Dual specifi	K.LPSGVFSSDFQEFVNK#.C	7.11	1.45	4.91	0.20
Q63932_M	Map2k2	Dual specifi	K.VSIAVLR.G	16.17	16.70	0.97	1.03
P47809_M	Map2k4	Dual specifi	K.WNSVFDQLTQVVK#.G	11.29	3.11	3.63	0.28
P47809_M	Map2k4	Dual specifi	K.WNSVFDQLTQVVK#.G	12.98	2.15	6.05	0.17
P47809_M	Map2k4	Dual specifi	K.YVYSVLDDVIPEEILGK#.I	18.09	4.51	4.01	0.25
P27546_M	Map4	Microtubul	K.TEFIPLLDGDEK#.T	11.49	7.66	1.50	0.67
P27546_M	Map4	Microtubul	K.AAEQM*STLPIDAPSPLENLEQK#.E	13.23	2.48	5.34	0.19
P27546_M	Map4	Microtubul	K.AAEQMSTLPIDAPSPLENLEQK#.E	10.79	3.66	2.95	0.34
P27546_M	Map4	Microtubul	K.ATSPSTLVSTGPSSR.S	9.83	12.55	0.78	1.28
P27546_M	Map4	Microtubul	K.DM*SPLPESEVTLGK#.D	9.22	3.14	2.94	0.34
P27546_M	Map4	Microtubul	K.DMSPLPESEVTLGK#.D	10.45	2.85	3.66	0.27
P27546_M	Map4	Microtubul	K.DM*SPLPESEVTLGK#DVVILPETK#.V	13.71	9.32	1.47	0.68
P27546_M	Map4	Microtubul	K.DMSPSAETEAPLAK#.N	18.52	5.87	3.16	0.32
P27546_M	Map4	Microtubul	K.DVVILPETK#.V	20.15	5.36	3.76	0.27
P27546_M	Map4	Microtubul	K.ETAPPTETNLGM*AK#.D	17.11	6.10	2.81	0.36
P27546_M	Map4	Microtubul	K.ETAPPTETNLGMAK#.D	9.49	55.77	0.17	5.88
P27546_M	Map4	Microtubul	K.ETETTLPIK#.M	32.99	11.51	2.87	0.35
P27546_M	Map4	Microtubul	K.GM*VSLSEIEEALAK#.N	32.31	7.75	4.17	0.24
P27546_M	Map4	Microtubul	K.GMVSLSEIEEALAK#.N	28.60	7.62	3.75	0.27
P27546_M	Map4	Microtubul	K.M*DLAPPEDVLLTK#.E	12.59	3.20	3.93	0.25
P27546_M	Map4	Microtubul	K.MDLAPPEDVLLTK#.E	37.22	11.39	3.27	0.31
P27546_M	Map4	Microtubul	K.NADLHSGTELIVDNSM*APASDLALPLETK#.V	10.64	4.81	2.21	0.45
P27546_M	Map4	Microtubul	K.NADLHSGTELIVDNSMAPASDLALPLETK#.V	17.22	6.25	2.76	0.36
P27546_M	Map4	Microtubul	K.TEFIPLLDGDEK#.T	7.96	5.77	1.38	0.72
P27546_M	Map4	Microtubul	K.TQPTSLPK#.Q	42.24	8.06	5.24	0.19
P27546_M	Map4	Microtubul	K.VAEFNNVTPLSEEEVTSVK#.D	14.46	3.94	3.67	0.27
P27546_M	Map4	Microtubul	K.AAEQM*STLPIDAPSPLENLEQK#.E	59.86	31.94	1.87	0.53
P27546_M	Map4	Microtubul	K.AAEQMSTLPIDAPSPLENLEQK#.E	51.26	21.88	2.34	0.43
P27546_M	Map4	Microtubul	K.AAEVESVK#.E	31.10	13.54	2.30	0.44
P27546_M	Map4	Microtubul	K.AAGSIASAQK#PPAGK#.V	50.69	26.41	1.92	0.52
P27546_M	Map4	Microtubul	K.AAVGVTGNDITTPPNK#.E	14.04	6.13	2.29	0.44
P27546_M	Map4	Microtubul	K.AAVGVTGNDITTPPNK#EPPPSPEK#.K	27.12	11.16	2.43	0.41
P27546_M	Map4	Microtubul	K.AK#PLATTQPAK#.T	102.70	67.03	1.53	0.65
P27546_M	Map4	Microtubul	K.ALETM*AEQTTDVVHSPSTDTTPGPDTEAALAK#.D	31.46	12.71	2.48	0.40
P27546_M	Map4	Microtubul	K.ALETMAEQTTDVVHSPSTDTTPGPDTEAALAK#.D	44.91	22.05	2.04	0.49
P27546_M	Map4	Microtubul	K.ATSPSTLVSTGPSSR.S	26.50	90.36	0.29	3.41
P27546_M	Map4	Microtubul	R.DFMAALEAEPYDDIVGETVEK#.T	8.00	6.32	1.27	0.79
P27546_M	Map4	Microtubul	K.DM*SPLPESEVTLGK#.D	37.66	25.52	1.48	0.68
P27546_M	Map4	Microtubul	K.DMSPLPESEVTLGK#.D	28.42	15.26	1.86	0.54
P27546_M	Map4	Microtubul	K.DM*SPLPESEVTLGK#DVVILPETK#.V	55.97	36.14	1.55	0.65
P27546_M	Map4	Microtubul	K.DM*SPSAETEAPLAK#.N	42.62	25.96	1.64	0.61
P27546_M	Map4	Microtubul	K.DMSPSAETEAPLAK#.N	45.78	20.86	2.19	0.46

P27546_M	Map4	Microtubul	K.DVAPPM*EEEIVPGNDTTSPK#.E	8.89	8.17	1.09	0.92
P27546_M	Map4	Microtubul	K.DVAPPMEEEIVPGNDTTSPK#.E	11.92	8.68	1.37	0.73
P27546_M	Map4	Microtubul	R.DVK#PK#PITEAK#.V	191.73	124.82	1.54	0.65
P27546_M	Map4	Microtubul	K.DVTLPLEAERPLVTDM*TPSLETEM*TLGK.E	11.65	26.90	0.43	2.31
P27546_M	Map4	Microtubul	K.DVTLPLEAERPLVTDMTPSLETEM*TLGK.E	4.88	10.57	0.46	2.16
P27546_M	Map4	Microtubul	K.DVTLPLEAERPLVTDMTPSLETEMTLGK.E	8.28	31.97	0.26	3.86
P27546_M	Map4	Microtubul	K.DVVILPETK#.V	51.44	46.67	1.10	0.91
P27546_M	Map4	Microtubul	K.ETAPPTETNLGM*AK#.D	54.97	27.83	1.98	0.51
P27546_M	Map4	Microtubul	K.ETAPPTETNLGMAK#.D	34.77	17.79	1.95	0.51
P27546_M	Map4	Microtubul	K.ETELAPAK#.G	94.83	51.38	1.85	0.54
P27546_M	Map4	Microtubul	K.ETETTLPIK#.M	65.42	38.32	1.71	0.59
P27546_M	Map4	Microtubul	K.ETETTLPIK#M*DLAPPEDVLLTK#.E	40.69	15.95	2.55	0.39
P27546_M	Map4	Microtubul	K.GM*VSLSEIEEALAK#.N	93.47	44.30	2.11	0.47
P27546_M	Map4	Microtubul	K.GMVSLSEIEEALAK#.N	87.47	39.70	2.20	0.45
P27546_M	Map4	Microtubul	K.HVPGGGNVQIQNK#.K	71.31	31.25	2.28	0.44
P27546_M	Map4	Microtubul	K.K#VSYSHIQSK#.C	60.20	32.64	1.84	0.54
P27546_M	Map4	Microtubul	R.LATTVSAPDLK#.S	219.47	110.93	1.98	0.51
P27546_M	Map4	Microtubul	K.M*DLAPPEDVLLTK#.E	38.17	20.39	1.87	0.53
P27546_M	Map4	Microtubul	K.NADLHSGTELIVDNSM*APASDLALPLETK#.V	65.51	31.83	2.06	0.49
P27546_M	Map4	Microtubul	K.NADLHSGTELIVDNSMAPASDLALPLETK#.V	55.12	25.66	2.15	0.47
P27546_M	Map4	Microtubul	R.NTTPTGAAPPAGM*TSTR.V	22.25	49.79	0.45	2.24
P27546_M	Map4	Microtubul	R.NTTPTGAAPPAGMTSTR.V	8.19	17.62	0.46	2.15
P27546_M	Map4	Microtubul	R.SK#VGSTENIK#.H	19.70	8.25	2.39	0.42
P27546_M	Map4	Microtubul	R.SPATTLPK#.R	196.42	106.01	1.85	0.54
P27546_M	Map4	Microtubul	R.SSGALSVDK#.K	59.98	26.75	2.24	0.45
P27546_M	Map4	Microtubul	R.SSGALSVDKKPTSTKPSSSAPR.V	40.50	63.03	0.64	1.56
P27546_M	Map4	Microtubul	K.TEFIPLLDGDEK.T	38.16	37.64	1.01	0.99
P27546_M	Map4	Microtubul	R.TSPSK#PSSAPALK#PGPK#.T	113.48	41.55	2.73	0.37
P27546_M	Map4	Microtubul	K.VAEFNNVTPLSEEEVTSVK#.D	58.02	27.12	2.14	0.47
P27546_M	Map4	Microtubul	K.VAEFNNVTPLSEEEVTSVKDM*SPSAETEAPLAK.N	8.63	4.87	1.77	0.56
P27546_M	Map4	Microtubul	K.VAEFNNVTPLSEEEVTSVK#DMSPSAETEAPLAK#.N	8.51	5.30	1.61	0.62
P27546_M	Map4	Microtubul	K.VGSTENIK#.H	60.39	27.28	2.21	0.45
P97820_M	Map4k4	Mitogen-ac	K.GQNVLLTENAEVK#.L	8.05	4.69	1.72	0.58
Q8BPM2_N	Map4k5	Mitogen-ac	K.SDEVTQEISDETR.V	3.68	8.44	0.44	2.29
Q8BPM2_N	Map4k5	Mitogen-ac	R.VGSGTYGDVYK#.A	14.28	69.70	0.20	4.88
A2AJI0_MA	Map7d1	MAP7 dom	R.SLQLSAWESSIVDR.L	4.57	14.51	0.32	3.17
P47811_M	Mapk14	Mitogen-ac	K.HENVIGLLDVFTPAR.S	1.72	4.12	0.42	2.39
Q63844_M	Mapk3	Mitogen-ac	R.GTAGVVPVVPGEVEVVK#.G	10.46	1.15	9.07	0.11
Q9ESN9_JI	Mapk8ip3	C-Jun-amin	K.EVGNLLLENSQLLETK#.N	9.01	2.25	4.01	0.25
Q9ESN9_JI	Mapk8ip3	C-Jun-amin	R.VWILTSTLTTSK#.V	8.75	4.24	2.06	0.49
Q9ESN9_JI	Mapk8ip3	C-Jun-amin	K.EVGNLLLENSQLLETK#.N	9.45	5.94	1.59	0.63
Q61166_M	Mapre1	Microtubul	K.FFDANYDGK#.E	25.95	11.31	2.29	0.44
Q61166_M	Mapre1	Microtubul	K.FQDNFEFVQWFK#.K	39.58	10.71	3.70	0.27
Q61166_M	Mapre1	Microtubul	K.GK#FQDNFEFVQWFK#.K	18.79	9.27	2.03	0.49
Q61166_M	Mapre1	Microtubul	K.ILQAGFK#.R	103.22	48.48	2.13	0.47
Q61166_M	Mapre1	Microtubul	R.QGQETAVAPSLVAPALSK#PK#.K	53.45	17.48	3.06	0.33
Q61166_M	Mapre1	Microtubul	R.QGQETAVAPSLVAPALSK#PK#.K	1.71	1.67	1.02	0.98
Q6PER3_M	Mapre3	Microtubul	K.LTVDGLEK#.E	32.57	10.98	2.97	0.34
Q6PER3_M	Mapre3	Microtubul	R.QGQDVAPPPNPGDQIFNK#.S	4.96	1.85	2.68	0.37
Q6PER3_M	Mapre3	Microtubul	K.VLQAAFK#.K	35.43	12.05	2.94	0.34
Q68FL6_SY	Mars	Methionin	R.GIGVFGDM*AK#.D	12.29	5.29	2.32	0.43
Q68FL6_SY	Mars	Methionin	K.GLESLPPLK#.L	15.84	5.09	3.11	0.32
Q68FL6_SY	Mars	Methionin	K.GSPK#PAAVEAVTAAGSQHIQTLTDEVTK#.Q	18.41	5.26	3.50	0.29
Q68FL6_SY	Mars	Methionin	K.GSPK#PAAVEAVTAAGSQHIQTLTDEVTK#.Q	6.80	2.12	3.20	0.31
Q68FL6_SY	Mars	Methionin	K.HIIATEYLNYEDGK#.F	8.46	2.38	3.55	0.28
Q68FL6_SY	Mars	Methionin	R.IGTVSPLFQK#.L	42.16	20.76	2.03	0.49
Q68FL6_SY	Mars	Methionin	K.LINAIELK#.K	27.56	7.02	3.92	0.25
Q68FL6_SY	Mars	Methionin	K.NPEQVDLYQFM*AK#.D	6.91	1.58	4.39	0.23
Q68FL6_SY	Mars	Methionin	R.SSQHLFLDLPK#.L	22.23	5.33	4.17	0.24
Q68FL6_SY	Mars	Methionin	K.ADK#NQVAAEVAK#.L	64.11	11.74	5.46	0.18
Q68FL6_SY	Mars	Methionin	R.GIGVFGDM*AK#.D	43.40	10.21	4.25	0.24
Q68FL6_SY	Mars	Methionin	K.GLESLPPLK#.L	40.56	8.19	4.95	0.20
Q68FL6_SY	Mars	Methionin	K.GSPK#PAAVEAVTAAGSQHIQTLTDEVTK#.Q	8.60	4.71	1.83	0.55
Q68FL6_SY	Mars	Methionin	K.HIIATEYLNYEDGK#FSK#.S	13.09	3.67	3.56	0.28
Q68FL6_SY	Mars	Methionin	R.IGTVSPLFQK#.L	95.95	21.54	4.45	0.22
Q68FL6_SY	Mars	Methionin	K.ITQDIFQR.L	18.45	18.48	1.00	1.00
Q68FL6_SY	Mars	Methionin	R.LFVSEGSPGSLPVLAAAAR.A	11.42	12.93	0.88	1.13
Q68FL6_SY	Mars	Methionin	K.LINAIELK#.K	83.12	17.60	4.72	0.21
Q68FL6_SY	Mars	Methionin	K.NPEQVDLYQFM*AK#.D	23.90	7.11	3.36	0.30
Q68FL6_SY	Mars	Methionin	K.NPEQVDLYQFMAK#.D	8.15	2.24	3.63	0.28
Q68FL6_SY	Mars	Methionin	R.SSQHLFLDLPK#.L	40.80	12.68	3.22	0.31
Q3THS6_M	Mat2a	S-adenosyl	K.TQVTVQYMQDR.G	2.21	7.43	0.30	3.35
Q3THS6_M	Mat2a	S-adenosyl	R.FVIGGPQGDAGLTGR.K	1.25	5.41	0.23	4.34
Q8K310_M	Matr3	Matrin-3 O	R.DLDELSRYPEDK.I	2.48	6.77	0.37	2.73
Q8K310_M	Matr3	Matrin-3 O	R.GDTDQASNILASFGLSAR.D	3.98	18.14	0.22	4.56
Q8K310_M	Matr3	Matrin-3 O	R.IGPYQPNVPVGIDYVIPK.T	3.94	4.13	0.95	1.05
Q8K310_M	Matr3	Matrin-3 O	K.ITPENLPQILLQLK.R	24.25	42.18	0.57	1.74
Q8K310_M	Matr3	Matrin-3 O	K.SFQQSSLGR.D	9.31	44.91	0.21	4.82
Q8K310_M	Matr3	Matrin-3 O	R.TEEGPTLSYGR.D	8.22	32.60	0.25	3.97
Q8K310_M	Matr3	Matrin-3 O	R.IGPYQPNVPVGIDYVIPK#.T	33.94	31.16	1.09	0.92
Q8K310_M	Matr3	Matrin-3 O	K.ALWFQGR.C	24.13	75.18	0.32	3.12
Q8K310_M	Matr3	Matrin-3 O	R.DLDELSRYPEDKITPENLPQILLQLK.R	19.26	109.51	0.18	5.69
Q8K310_M	Matr3	Matrin-3 O	K.FDSEYER.M	11.81	66.91	0.18	5.66
Q8K310_M	Matr3	Matrin-3 O	R.GDTDQASNILASFGLSAR.D	30.78	116.68	0.26	3.79
Q8K310_M	Matr3	Matrin-3 O	R.GNLGAGNGNLQGPR.H	8.29	41.51	0.20	5.01
Q8K310_M	Matr3	Matrin-3 O	R.GPGPLQER.S	17.37	118.37	0.15	6.82
Q8K310_M	Matr3	Matrin-3 O	R.IGPYQPNVPVGIDYVIPK.T	148.54	177.87	0.84	1.20
Q8K310_M	Matr3	Matrin-3 O	K.IKNYILM*R.M	3.35	12.34	0.27	3.68
Q8K310_M	Matr3	Matrin-3 O	K.INEAFIEM*ATTEDAQAAVDYYTTTPALVFGKPVR.V	2.70	13.07	0.21	4.84
Q8K310_M	Matr3	Matrin-3 O	K.INEAFIEMATTEDAQAAVDYYTTTPALVFGKPVR.V	4.59	9.04	0.51	1.97
Q8K310_M	Matr3	Matrin-3 O	K.ITPENLPQILLQLK#.R	202.80	211.38	0.96	1.04
Q8K310_M	Matr3	Matrin-3 O	K.LAEPYGK.I	250.36	228.82	1.09	0.91
Q8K310_M	Matr3	Matrin-3 O	K.NYILMR.M	5.46	16.91	0.32	3.10
Q8K310_M	Matr3	Matrin-3 O	R.RRTEEGPTLSYGR.D	2.09	37.42	0.06	17.88
Q8K310_M	Matr3	Matrin-3 O	K.SFQQSSLGR.D	34.86	186.22	0.19	5.34
Q8K310_M	Matr3	Matrin-3 O	K.SQAFIEM*ETR.E	33.69	126.76	0.27	3.76
Q8K310_M	Matr3	Matrin-3 O	K.SQAFIEMETR.E	18.76	66.36	0.28	3.54
Q8K310_M	Matr3	Matrin-3 O	R.SQESGYYDR.M	8.64	26.59	0.32	3.08
Q8K310_M	Matr3	Matrin-3 O	K.TDAQK#TESPAEGK#EQEEK#.S	5.92	9.16	0.65	1.55
Q8K310_M	Matr3	Matrin-3 O	R.TEEGPTLSYGR.D	35.61	141.25	0.25	3.97
Q8K310_M	Matr3	Matrin-3 O	K.TESPAEGK#EQEEK#.S	18.50	24.61	0.75	1.33
Q8K310_M	Matr3	Matrin-3 O	R.VIHLSNLPHSGYSDSAVLK.L	176.27	161.91	1.09	0.92
Q8K310_M	Matr3	Matrin-3 O	R.VVHIMDFQR.G	21.39	74.97	0.29	3.51

Q8K310_M	Matr3	Matrin-3 O	R.YPEDKITPENLPQILLQLK.R	31.70	29.34	1.08	0.93
Q8K310_M	Matr3	Matrin-3 O	R.DLDELSRYPEDKITPENLPQILLQLK.R	2.57	19.22	0.13	7.47
Q8K310_M	Matr3	Matrin-3 O	R.GDTDQASNILASFGLSAR.D	5.51	17.65	0.31	3.21
Q8K310_M	Matr3	Matrin-3 O	R.IGPYQPNVPVGIDYVIPK.T	24.79	34.37	0.72	1.39
Q8K310_M	Matr3	Matrin-3 O	K.ITPENLPQILLQLK.R	29.44	32.10	0.92	1.09
Q8K310_M	Matr3	Matrin-3 O	K.SQAFIEM*ETR.E	3.56	15.46	0.23	4.34
Q8K310_M	Matr3	Matrin-3 O	R.SQESGYYDR.M	2.86	5.48	0.52	1.92
Q8K310_M	Matr3	Matrin-3 O	R.TEEGPTLSYGR.D	4.78	20.62	0.23	4.31
Q8K310_M	Matr3	Matrin-3 O	K.TESPAEGKEQEEK.S	2.45	1.80	1.36	0.74
Q8K310_M	Matr3	Matrin-3 O	R.VIHLSNLPHSGYSDSAVLK#.L	29.24	32.08	0.91	1.10
P28574_M	Max	Protein ma	R.QNALLEQQVR.A	2.56	15.68	0.16	6.12
P28574_M	Max	Protein ma	R.SSAQLQTNYPSSDNSLYTNAK.G	6.13	11.09	0.55	1.81
Q9Z2E1_M	Mbd2	Methyl-Cp	R.LQGLSASDVTEQIIK#.T	29.36	12.81	2.29	0.44
Q9Z2E1_M	Mbd2	Methyl-Cp	R.LQGLSASDVTEQIIK#.T	7.65	1.21	6.33	0.16
Q9Z2D8_M	Mbd3	Methyl-Cp	K.AFM*VTDDDIR.K	5.59	18.36	0.30	3.29
Q9Z2D8_M	Mbd3	Methyl-Cp	K.AFMVTDDDIR.K	3.19	10.66	0.30	3.34
Q9Z2D8_M	Mbd3	Methyl-Cp	K.KLSGLSAFDIAEELVR.T	9.03	30.66	0.29	3.40
Q9Z2D8_M	Mbd3	Methyl-Cp	R.KQEELVQQVR.K	5.03	19.03	0.26	3.78
Q9Z2D8_M	Mbd3	Methyl-Cp	K.LSGLSAFDIAEELVR.T	10.04	38.85	0.26	3.87
Q9Z2D8_M	Mbd3	Methyl-Cp	R.YLGGSM*DLSTFDFR.T	4.09	16.27	0.25	3.98
Q9Z2D8_M	Mbd3	Methyl-Cp	K.KLSGLSAFDIAEELVR.T	2.80	15.61	0.18	5.58
Q9Z2D8_M	Mbd3	Methyl-Cp	R.YLGGSM*DLSTFDFR.T	3.78	7.60	0.50	2.01
A0A0A6YW	Mbnl1	Muscleblin	K.AAQYQVNQAAAAQAAATAAAMTQSAVK#.S	7.46	8.49	0.88	1.14
A0A0A6YW	Mbnl1	Muscleblin	K.RPLEATFDLGIPQAVLPPLPK.R	8.73	12.48	0.70	1.43
P97310_M	Mcm2	DNA replica	R.ESLVVNYEDLAAR.E	8.52	28.41	0.30	3.34
P97310_M	Mcm2	DNA replica	R.EWTLEAGALVLADR.G	4.81	10.55	0.46	2.19
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#DLM*DK#.A	9.34	6.59	1.42	0.71
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#DLMDK#.A	5.28	5.40	0.98	1.02
P97310_M	Mcm2	DNA replica	R.GLALALFGGEPK#.N	19.01	15.91	1.19	0.84
P97310_M	Mcm2	DNA replica	R.ISHLPLVEELR.S	5.28	17.30	0.31	3.27
P97310_M	Mcm2	DNA replica	R.QINIHNLSAFYDSDLFK#.F	11.77	8.26	1.42	0.70
P97310_M	Mcm2	DNA replica	K.QLVAEQVTYQR.N	6.26	17.05	0.37	2.72
P97310_M	Mcm2	DNA replica	R.TSIHEAM*EQQSISISK#.A	12.10	9.26	1.31	0.77
P97310_M	Mcm2	DNA replica	R.VM*M*ESFIDTQK#.F	9.50	5.38	1.76	0.57
P97310_M	Mcm2	DNA replica	R.VMMESFIDTQK#.F	6.12	4.67	1.31	0.76
P97310_M	Mcm2	DNA replica	R.YDPSLTFSENVDLTEPIISR.F	1.94	7.08	0.27	3.65
P97310_M	Mcm2	DNA replica	K.ESM*ATGSIPITVR.H	6.94	30.27	0.23	4.36
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#DLM*DK#.A	18.70	16.03	1.17	0.86
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#DLMDK#.A	5.63	8.63	0.65	1.53
P97310_M	Mcm2	DNA replica	R.KLILQQF.-	6.88	7.67	0.90	1.12
P97310_M	Mcm2	DNA replica	R.QINIHNLSAFYDSDLFK#.F	24.61	19.59	1.26	0.80
P97310_M	Mcm2	DNA replica	R.VM*M*ESFIDTQK#.F	12.99	11.19	1.16	0.86
P97310_M	Mcm2	DNA replica	K.AGIVTSLQAR.C	65.56	176.33	0.37	2.69
P97310_M	Mcm2	DNA replica	R.AIFTTGQGASAVGLTAYVQR.H	19.41	55.49	0.35	2.86
P97310_M	Mcm2	DNA replica	R.ATEDGEEDEEM*IESIENLEDLK#.G	15.74	9.41	1.67	0.60
P97310_M	Mcm2	DNA replica	R.ATEDGEEDEEM*IESIENLEDLKGHSVR.E	17.16	50.59	0.34	2.95
P97310_M	Mcm2	DNA replica	R.DTVDPVQDEM*LAR.F	17.68	60.31	0.29	3.41
P97310_M	Mcm2	DNA replica	R.DTVDPVQDEMLAR.F	9.73	38.31	0.25	3.94
P97310_M	Mcm2	DNA replica	R.DYRPIPELDVYEAEGLALDDEDVEELTASQR.E	8.60	44.88	0.19	5.22
P97310_M	Mcm2	DNA replica	R.DYVM*EDDVNM*AIR.V	13.34	30.42	0.44	2.28
P97310_M	Mcm2	DNA replica	R.DYVM*EDDVNMAIR.V	4.74	11.80	0.40	2.49
P97310_M	Mcm2	DNA replica	R.DYVMEDDVNM*AIR.V	2.57	5.97	0.43	2.32
P97310_M	Mcm2	DNA replica	R.ESLVVNYEDLAAR.E	48.34	147.67	0.33	3.06
P97310_M	Mcm2	DNA replica	K.ESM*ATGSIPITVR.H	46.29	140.23	0.33	3.03
P97310_M	Mcm2	DNA replica	K.ESMATGSIPITVR.H	14.84	33.57	0.44	2.26
P97310_M	Mcm2	DNA replica	R.EWTLEAGALVLADR.G	25.36	73.11	0.35	2.88
P97310_M	Mcm2	DNA replica	R.EWVSM*AGPR.L	18.37	50.53	0.36	2.75
P97310_M	Mcm2	DNA replica	R.EWVSMAGPR.L	10.82	28.26	0.38	2.61
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#.D	13.85	5.77	2.40	0.42
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#DLM*DK#.A	121.82	66.62	1.83	0.55
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#DLMDK#.A	65.95	38.11	1.73	0.58
P97310_M	Mcm2	DNA replica	R.GLALALFGGEPK#.N	303.28	169.47	1.79	0.56
P97310_M	Mcm2	DNA replica	K.IFASIAPSIYGHEDIKR.G	24.25	59.26	0.41	2.44
P97310_M	Mcm2	DNA replica	R.IQESPGK#.V	55.29	38.46	1.44	0.70
P97310_M	Mcm2	DNA replica	R.ISDPLTSSPGR.S	22.52	32.16	0.70	1.43
P97310_M	Mcm2	DNA replica	R.ISHLPLVEELR.S	43.77	104.59	0.42	2.39
P97310_M	Mcm2	DNA replica	K.K#DEGLTNGGTLEPAM*PNTYGVEPLPQEVLK#.K	7.00	7.10	0.99	1.01
P97310_M	Mcm2	DNA replica	K.K#DEGLTNGGTLEPAMPNTYGVEPLPQEVLK#.K	4.33	4.03	1.07	0.93
P97310_M	Mcm2	DNA replica	R.K#LILQQF.-	91.38	43.25	2.11	0.47
P97310_M	Mcm2	DNA replica	K.K#YIIYAK#.E	32.76	18.71	1.75	0.57
P97310_M	Mcm2	DNA replica	K.LILQQF.-	45.24	45.24	1.00	1.00
P97310_M	Mcm2	DNA replica	K.LNQM*DQDK#.V	8.55	5.56	1.54	0.65
P97310_M	Mcm2	DNA replica	R.QINIHNLSAFYDSDLFK#.F	141.06	66.40	2.12	0.47
P97310_M	Mcm2	DNA replica	K.QLVAEQVTYQR.N	46.76	108.27	0.43	2.32
P97310_M	Mcm2	DNA replica	R.RADALTSSPGR.D	3.60	42.03	0.09	11.67
P97310_M	Mcm2	DNA replica	R.RDNNDLLLFILK.Q	10.02	34.93	0.29	3.49
P97310_M	Mcm2	DNA replica	R.THVDSHGHNVFK#.E	146.14	67.82	2.15	0.46
P97310_M	Mcm2	DNA replica	R.TSIHEAM*EQQSISISK#.A	120.41	69.94	1.72	0.58
P97310_M	Mcm2	DNA replica	R.TSIHEAMEQQSISISK#.A	80.29	65.06	1.23	0.81
P97310_M	Mcm2	DNA replica	R.TSIHEAMEQQSISISK.A	17.19	14.33	1.20	0.83
P97310_M	Mcm2	DNA replica	K.VAVGELTDEDVK#.M	313.74	210.56	1.49	0.67
P97310_M	Mcm2	DNA replica	K.VAVGELTDEDVK#M*ITGLSK#.D	16.97	8.40	2.02	0.49
P97310_M	Mcm2	DNA replica	K.VAVGELTDEDVK#M*ITGLSK#.D	4.13	1.63	2.54	0.39
P97310_M	Mcm2	DNA replica	R.VM*M*ESFIDTQK#.F	102.18	56.45	1.81	0.55
P97310_M	Mcm2	DNA replica	R.VMM*ESFIDTQK#.F	29.44	18.88	1.56	0.64
P97310_M	Mcm2	DNA replica	R.VM*MESFIDTQK#.F	34.58	14.51	2.38	0.42
P97310_M	Mcm2	DNA replica	R.VMMESFIDTQK#.F	45.56	23.65	1.93	0.52
P97310_M	Mcm2	DNA replica	R.YDPSLTFSENVDLTEPIISR.F	15.27	44.60	0.34	2.92
P97310_M	Mcm2	DNA replica	K.AGIVTSLQAR.C	27.98	79.72	0.35	2.85
P97310_M	Mcm2	DNA replica	R.AIFTTGQGASAVGLTAYVQR.H	5.85	20.13	0.29	3.44
P97310_M	Mcm2	DNA replica	R.ATEDGEEDEEM*IESIENLEDLK#.G	14.10	7.59	1.86	0.54
P97310_M	Mcm2	DNA replica	R.ATEDGEEDEEM*IESIENLEDLKGHSVR.E	11.07	22.46	0.49	2.03
P97310_M	Mcm2	DNA replica	R.DTVDPVQDEM*LAR.F	6.11	21.37	0.29	3.50
P97310_M	Mcm2	DNA replica	R.DTVDPVQDEMLAR.F	5.44	9.63	0.57	1.77
P97310_M	Mcm2	DNA replica	R.DYRPIPELDVYEAEGLALDDEDVEELTASQR.E	6.11	19.05	0.32	3.11
P97310_M	Mcm2	DNA replica	R.DYVM*EDDVNM*AIR.V	7.61	20.19	0.38	2.65
P97310_M	Mcm2	DNA replica	R.DYVM*EDDVNMAIR.V	1.46	5.54	0.26	3.79
P97310_M	Mcm2	DNA replica	R.ESLVVNYEDLAAR.E	32.76	81.25	0.40	2.48
P97310_M	Mcm2	DNA replica	K.ESM*ATGSIPITVR.H	24.73	57.20	0.43	2.31
P97310_M	Mcm2	DNA replica	K.ESMATGSIPITVR.H	9.27	16.00	0.58	1.73
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#.D	11.23	6.50	1.73	0.58
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#DLM*DK#.A	76.84	35.88	2.14	0.47
P97310_M	Mcm2	DNA replica	R.FGAQQDTIEIPEK#DLMDK#.A	28.30	23.16	1.22	0.82

P97310_M Mcm2	DNA replica	R.GLALALFGGEPK#.N	166.65	97.10	1.72	0.58
P97310_M Mcm2	DNA replica	K.IFASIAPSIYGHEDIKR.G	21.66	50.05	0.43	2.31
P97310_M Mcm2	DNA replica	R.ISDPLTSSPGR.S	12.68	27.60	0.46	2.18
P97310_M Mcm2	DNA replica	R.ISHLPLVEELR.S	20.11	49.77	0.40	2.47
P97310_M Mcm2	DNA replica	R.K#LILQQF.-	66.40	25.71	2.58	0.39
P97310_M Mcm2	DNA replica	K.LILQQF.-	19.93	19.93	1.00	1.00
P97310_M Mcm2	DNA replica	R.THVDSHGHNVFK#.E	3.91	4.47	0.87	1.14
P97310_M Mcm2	DNA replica	R.TSIHEAM*EQQSISISK#.A	85.17	34.73	2.45	0.41
P97310_M Mcm2	DNA replica	R.TSIHEAMEQQSISISK#.A	40.25	21.45	1.88	0.53
P97310_M Mcm2	DNA replica	K.VAVGELTDEDVK#.M	189.65	119.49	1.59	0.63
P97310_M Mcm2	DNA replica	R.VM*M*ESFIDTQK#.F	62.24	32.44	1.92	0.52
P97310_M Mcm2	DNA replica	R.VMMESFIDTQK#.F	14.64	9.26	1.58	0.63
P97310_M Mcm2	DNA replica	R.YDPSLTFSENVDLTEPIISR.F	6.62	18.82	0.35	2.84
P25206_M Mcm3	DNA replica	K.DIQPAFSADDIAK#.I	21.61	13.39	1.61	0.62
P25206_M Mcm3	DNA replica	R.DYLDFLDDEEDQGIYQNK#.V	7.35	3.56	2.07	0.48
P25206_M Mcm3	DNA replica	R.GDINILLIGDPSVAK#.S	10.92	4.43	2.47	0.41
P25206_M Mcm3	DNA replica	K.IIKPTLTQESAAYIAEEYSR.L	6.55	14.55	0.45	2.22
P25206_M Mcm3	DNA replica	R.LIVSVNDLR.R	7.72	21.98	0.35	2.85
P25206_M Mcm3	DNA replica	R.LLNNAFEELVAFQR.A	3.59	8.61	0.42	2.40
P25206_M Mcm3	DNA replica	R.SVDVILDDDLVDK#.V	9.12	2.58	3.53	0.28
P25206_M Mcm3	DNA replica	K.TPM*ENIGLQDSLLSR.F	3.88	6.79	0.57	1.75
P25206_M Mcm3	DNA replica	R.ALK#DFVASIDATYAK#.Q	202.52	115.92	1.75	0.57
P25206_M Mcm3	DNA replica	K.DFVASIDATYAK#.Q	49.90	31.64	1.58	0.63
P25206_M Mcm3	DNA replica	R.DYLDFLDDEEDQGIYQNK#.V	27.62	14.61	1.89	0.53
P25206_M Mcm3	DNA replica	R.DYLDFLDDEEDQGIYQNK.V	16.65	10.55	1.58	0.63
P25206_M Mcm3	DNA replica	R.EAQRDYLDFLDDEEDQGIYQNK.V	25.18	68.12	0.37	2.70
P25206_M Mcm3	DNA replica	R.LIVSVNDLR.R	106.99	331.20	0.32	3.10
P25206_M Mcm3	DNA replica	R.LLNNAFEELVAFQR.A	32.95	89.15	0.37	2.71
P25206_M Mcm3	DNA replica	K.QYEEFYIGLEGSFGSK.H	7.26	5.53	1.31	0.76
P25206_M Mcm3	DNA replica	K.AALLEVFQEAHEQSVGMLHLTESINR.N	38.15	103.82	0.37	2.72
P25206_M Mcm3	DNA replica	R.ALK#DFVASIDATYAK#.Q	105.46	51.50	2.05	0.49
P25206_M Mcm3	DNA replica	K.APAGQLPR.S	21.41	65.64	0.33	3.07
P25206_M Mcm3	DNA replica	R.APGEQDGDALPLGSSVDILATDDPDFTQDDQQDTR.I	13.78	30.21	0.46	2.19
P25206_M Mcm3	DNA replica	K.ASEDESDLEDEEEK#SQEDTEQK#.R	20.61	15.17	1.36	0.74
P25206_M Mcm3	DNA replica	K.DGESYDPYDFSEAETQM*PQVHTPK#.T	47.99	37.67	1.27	0.79
P25206_M Mcm3	DNA replica	K.DGESYDPYDFSEAETQMPQVHTPK#.T	29.14	17.19	1.69	0.59
P25206_M Mcm3	DNA replica	K.DHQTITIQEM*PEK#.A	12.78	8.57	1.49	0.67
P25206_M Mcm3	DNA replica	K.DHQTITIQEMPEK#.A	5.81	4.95	1.17	0.85
P25206_M Mcm3	DNA replica	K.DHQTITIQEM*PEKAPAGQLPR.S	11.37	13.49	0.84	1.19
P25206_M Mcm3	DNA replica	K.DHQTITIQEMPEKAPAGQLPR.S	8.82	19.25	0.46	2.18
P25206_M Mcm3	DNA replica	K.DIQPAFSADDIAK#.I	254.05	153.56	1.65	0.60
P25206_M Mcm3	DNA replica	R.DYLDFLDDEEDQGIYQNK#.V	40.45	16.70	2.42	0.41
P25206_M Mcm3	DNA replica	R.EAQRDYLDFLDDEEDQGIYQNK.V	9.29	14.36	0.65	1.55
P25206_M Mcm3	DNA replica	R.FDLLFIM*LDQM*DPEQDREISDHVLR.M	2.66	11.83	0.22	4.45
P25206_M Mcm3	DNA replica	R.GDINILLIGDPSVAK#.S	213.06	122.79	1.74	0.58
P25206_M Mcm3	DNA replica	R.GSSGVGLTAAVTTDQETGER.R	28.21	68.24	0.41	2.42
P25206_M Mcm3	DNA replica	K.HDSLLHGTK#.K	21.58	13.04	1.66	0.60
P25206_M Mcm3	DNA replica	K.IIKPTLTQESAAYIAEEYSR.L	71.78	193.85	0.37	2.70
P25206_M Mcm3	DNA replica	K.IIKPTLTQESAAYIAEEYSR.L	4.90	9.26	0.53	1.89
P25206_M Mcm3	DNA replica	R.IQVVGTYR.C	74.18	186.33	0.40	2.51
P25206_M Mcm3	DNA replica	R.LEAGAM*VLADR.G	8.09	25.17	0.32	3.11
P25206_M Mcm3	DNA replica	R.LIVSVNDLR.R	45.84	102.54	0.45	2.24
P25206_M Mcm3	DNA replica	R.LLNNAFEELVAFQR.A	31.75	70.76	0.45	2.23
P25206_M Mcm3	DNA replica	K.M*VSAAFM*K#.K	44.69	24.93	1.79	0.56
P25206_M Mcm3	DNA replica	K.MVSAAFM*K#.K	29.79	15.03	1.98	0.50
P25206_M Mcm3	DNA replica	K.M*VSAAFMK#.K	19.54	12.39	1.58	0.63
P25206_M Mcm3	DNA replica	K.QYEEFYIGLEGSFGSK#.H	6.37	4.60	1.38	0.72
P25206_M Mcm3	DNA replica	R.RLEAGAM*VLADR.G	5.26	53.88	0.10	10.25
P25206_M Mcm3	DNA replica	R.RLEAGAMVLADR.G	3.88	36.88	0.11	9.49
P25206_M Mcm3	DNA replica	R.RYSDLTTLVAFPSSSVYPTKDEENNPLETEYGLSVYK.D	1.27	4.30	0.30	3.38
P25206_M Mcm3	DNA replica	R.SKDVFEQLAR.S	32.76	99.75	0.33	3.04
P25206_M Mcm3	DNA replica	R.SQDSMSSDTAR.T	3.34	5.54	0.60	1.66
P25206_M Mcm3	DNA replica	R.SVDVILDDDLVDK#.V	98.58	59.39	1.66	0.60
P25206_M Mcm3	DNA replica	R.TAIHEVMEQGR.V	24.60	72.45	0.34	2.95
P25206_M Mcm3	DNA replica	R.TAIHEVM*EQGR.V	22.79	69.96	0.33	3.07
P25206_M Mcm3	DNA replica	K.TDDSQEK#TDDSQETQDSQK#.V	3.50	3.38	1.04	0.97
P25206_M Mcm3	DNA replica	K.TDDSQEKTDDSQETQDSQKVELSEPR.L	26.08	55.93	0.47	2.14
P25206_M Mcm3	DNA replica	K.TDDSQETQDSQKVELSEPR.L	5.72	13.93	0.41	2.44
P25206_M Mcm3	DNA replica	R.TLETLIR.L	51.31	148.97	0.34	2.90
P25206_M Mcm3	DNA replica	K.TPM*ENIGLQDSLLSR.F	20.88	55.82	0.37	2.67
P25206_M Mcm3	DNA replica	K.TPMENIGLQDSLLSR.F	52.79	47.73	1.11	0.90
P25206_M Mcm3	DNA replica	K.VELSEPR.L	16.04	43.71	0.37	2.73
P25206_M Mcm3	DNA replica	R.ALK#DFVASIDATYAK#.Q	58.52	17.10	3.42	0.29
P25206_M Mcm3	DNA replica	R.APGEQDGDALPLGSSVDILATDDPDFTQDDQQDTR.I	6.94	9.62	0.72	1.39
P25206_M Mcm3	DNA replica	K.ASEDESDLEDEEEK#.S	12.66	4.49	2.82	0.35
P25206_M Mcm3	DNA replica	K.DEENNPLETEYGLSVYK#.D	9.26	4.21	2.20	0.45
P25206_M Mcm3	DNA replica	K.DIQPAFSADDIAK#.I	116.63	54.22	2.15	0.46
P25206_M Mcm3	DNA replica	R.DYLDFLDDEEDQGIYQNK#.V	24.30	8.58	2.83	0.35
P25206_M Mcm3	DNA replica	R.EAQRDYLDFLDDEEDQGIYQNK.V	7.14	6.23	1.15	0.87
P25206_M Mcm3	DNA replica	R.ELISDNQYR.L	23.59	43.71	0.54	1.85
P25206_M Mcm3	DNA replica	R.GDINILLIGDPSVAK#.S	126.57	47.74	2.65	0.38
P25206_M Mcm3	DNA replica	R.GSSGVGLTAAVTTDQETGER.R	11.59	18.15	0.64	1.57
P25206_M Mcm3	DNA replica	K.IIKPTLTQESAAYIAEEYSR.L	37.54	72.56	0.52	1.93
P25206_M Mcm3	DNA replica	R.IQVVGTYR.C	23.37	48.68	0.48	2.08
P25206_M Mcm3	DNA replica	R.LIVSVNDLR.R	26.92	50.86	0.53	1.89
P25206_M Mcm3	DNA replica	R.LLNNAFEELVAFQR.A	22.69	27.06	0.84	1.19
P25206_M Mcm3	DNA replica	K.M*VSAAFM*K#.K	18.47	12.91	1.43	0.70
P25206_M Mcm3	DNA replica	R.SKDVFEQLAR.S	13.09	27.95	0.47	2.14
P25206_M Mcm3	DNA replica	R.SVDVILDDDLVDK#.V	45.29	23.09	1.96	0.51
P25206_M Mcm3	DNA replica	R.TAIHEVM*EQGR.V	11.57	21.73	0.53	1.88
P25206_M Mcm3	DNA replica	K.TDDSQEKTDDSQETQDSQKVELSEPR.L	10.63	17.98	0.59	1.69
P25206_M Mcm3	DNA replica	K.TPM*ENIGLQDSLLSR.F	6.39	18.63	0.34	2.91
P25206_M Mcm3	DNA replica	K.TVDLQDAEEAVELVQYAYFK#K#.V	26.39	11.19	2.36	0.42
P49717_M Mcm4	DNA replica	R.ALADDDFLTVTGK#.T	10.17	10.03	1.01	0.99
P49717_M Mcm4	DNA replica	R.LASALAPSIYEHEDIK#K#.G	9.29	5.33	1.74	0.57
P49717_M Mcm4	DNA replica	R.ALADDDFLTVTGK#.T	21.41	15.50	1.38	0.72
P49717_M Mcm4	DNA replica	R.LSEEASQALIEAYVNM*R.K	4.59	10.37	0.44	2.26
P49717_M Mcm4	DNA replica	R.TGIVDISILTTGM*SATSR.K	7.28	27.27	0.27	3.75
P49717_M Mcm4	DNA replica	R.TSVLAAANPIESQWNPK#.K	4.32	4.86	0.89	1.13
P49717_M Mcm4	DNA replica	R.ALADDDFLTVTGK#.T	320.32	229.36	1.40	0.72
P49717_M Mcm4	DNA replica	K.DM*FEEALR.A	14.48	49.88	0.29	3.44
P49717_M Mcm4	DNA replica	K.DMFEEALR.A	14.75	42.82	0.34	2.90
P49717_M Mcm4	DNA replica	K.DYIAYAHSTIMPR.L	3.68	13.99	0.26	3.80

P49717_M Mcm4	DNA replica	R.FDLIFLM*LDPQDEAYDRR.L	3.73	19.08	0.20	5.12
P49717_M Mcm4	DNA replica	R.FSNKVEAIDVEEAKR.L	30.51	100.39	0.30	3.29
P49717_M Mcm4	DNA replica	K.GILLQLFGGTR.K	25.38	68.80	0.37	2.71
P49717_M Mcm4	DNA replica	K.GLQVDLQSDGAAAEDIVPSEQSLGQK#.L	31.33	25.59	1.22	0.82
P49717_M Mcm4	DNA replica	R.GM*VSAYPR.Q	24.33	61.02	0.40	2.51
P49717_M Mcm4	DNA replica	R.GQSDTAITK#.D	19.03	11.84	1.61	0.62
P49717_M Mcm4	DNA replica	K.GSSAVGLTAYVMK#.D	8.70	5.08	1.71	0.58
P49717_M Mcm4	DNA replica	R.K#GLQVDLQSDGAAAEDIVPSEQSLGQK#.L	108.81	66.67	1.63	0.61
P49717_M Mcm4	DNA replica	K.LQESPEDM*PAGQTPHTIVLFAHNDLVDK#.V	9.79	5.53	1.77	0.56
P49717_M Mcm4	DNA replica	R.LSEEASQALIEAYVNM*R.K	11.04	39.40	0.28	3.57
P49717_M Mcm4	DNA replica	R.LSEEASQALIEAYVNMR.K	8.49	21.16	0.40	2.49
P49717_M Mcm4	DNA replica	R.NLNPEDIDQLITISGM*VIR.T	19.04	58.08	0.33	3.05
P49717_M Mcm4	DNA replica	R.NLNPEDIDQLITISGM*VIR.T	7.50	20.02	0.37	2.67
P49717_M Mcm4	DNA replica	K.RLHGLDEEAEQK.L	50.84	148.63	0.34	2.92
P49717_M Mcm4	DNA replica	K.SQLLQYVYNLVPR.G	11.36	37.23	0.31	3.28
P49717_M Mcm4	DNA replica	R.SVLHEVM*EQQTLSIAK#.A	94.91	94.24	1.01	0.99
P49717_M Mcm4	DNA replica	R.SVLHEVMEQQTLSIAK#.A	118.94	75.12	1.58	0.63
P49717_M Mcm4	DNA replica	R.SVLHEVMEQQTLSIAK#.A	32.16	19.25	1.67	0.60
P49717_M Mcm4	DNA replica	R.TGIVDISILTTGM*SATSR.K	16.47	43.45	0.38	2.64
P49717_M Mcm4	DNA replica	R.TGIVDISILTTGMSATSR.K	4.57	12.65	0.36	2.77
P49717_M Mcm4	DNA replica	R.TSVLAAANPIESQWNPK#.K	141.03	99.74	1.41	0.71
P49717_M Mcm4	DNA replica	K.TTIENIQLPHTLLSR.F	44.19	150.50	0.29	3.41
P49717_M Mcm4	DNA replica	R.VNVTGIYR.A	54.00	197.27	0.27	3.65
P49717_M Mcm4	DNA replica	K.YQQLFEDIR.G	34.60	116.03	0.30	3.35
P49717_M Mcm4	DNA replica	R.ALADDDFLTVTGK#.T	114.03	65.98	1.73	0.58
P49717_M Mcm4	DNA replica	K.GILLQLFGGTR.K	3.87	21.20	0.18	5.49
P49717_M Mcm4	DNA replica	R.KGLQVDLQSDGAAAEDIVPSEQSLGQK.L	27.30	17.19	1.59	0.63
P49717_M Mcm4	DNA replica	K.LQESPEDM*PAGQTPHTIVLFAHNDLVDK#.V	17.71	14.67	1.21	0.83
P49717_M Mcm4	DNA replica	K.LQESPEDMPAGQTPHTIVLFAHNDLVDKVQPGDR.V	1.86	4.95	0.38	2.65
P49717_M Mcm4	DNA replica	R.LSEEASQALIEAYVNM*R.K	6.93	11.90	0.58	1.72
P49717_M Mcm4	DNA replica	R.NLNPEDIDQLITISGM*VIR.T	8.06	19.82	0.41	2.46
P49717_M Mcm4	DNA replica	K.RLHGLDEEAEQK.L	12.09	35.04	0.35	2.90
P49717_M Mcm4	DNA replica	R.SVLHEVM*EQQTLSIAK#.A	6.08	5.56	1.09	0.92
P49717_M Mcm4	DNA replica	R.SVLHEVMEQQTLSIAK#.A	21.24	40.27	0.53	1.90
P49717_M Mcm4	DNA replica	R.TGIVDISILTTGM*SATSR.K	6.29	22.61	0.28	3.59
P49717_M Mcm4	DNA replica	R.TSVLAAANPIESQWNPK#.K	45.55	29.94	1.52	0.66
P49717_M Mcm4	DNA replica	R.VNVTGIYR.A	14.83	57.21	0.26	3.86
P49717_M Mcm4	DNA replica	K.YQQLFEDIR.G	9.43	18.71	0.50	1.98
P49718_M Mcm5	DNA replica	K.IPGIIISASAVR.A	4.20	27.53	0.15	6.55
P49718_M Mcm5	DNA replica	R.LAALPNIYELISK.S	39.53	65.91	0.60	1.67
P49718_M Mcm5	DNA replica	K.LQPFATEADVEEALR.L	3.43	11.10	0.31	3.23
P49718_M Mcm5	DNA replica	K.SISPSIFGGM*DM*K#.K	6.30	6.13	1.03	0.97
P49718_M Mcm5	DNA replica	R.VAIHEAM*EQQTISIAK.A	13.33	14.45	0.92	1.08
P49718_M Mcm5	DNA replica	R.VLGIQVDTDGSGR.S	8.37	18.32	0.46	2.19
P49718_M Mcm5	DNA replica	R.LFQVSTLDAALSGNLSGVEGFTTQEDQEM*LSR.I	3.14	10.56	0.30	3.37
P49718_M Mcm5	DNA replica	K.LQPFATEADVEEALR.L	10.62	49.31	0.22	4.64
P49718_M Mcm5	DNA replica	K.M*KLQPFATEADVEEALR.L	1.65	11.14	0.15	6.76
P49718_M Mcm5	DNA replica	K.AGITTTLNSR.C	29.58	105.69	0.28	3.57
P49718_M Mcm5	DNA replica	R.FAIGSQVSEHSIVQDFTK#.Q	110.98	87.12	1.27	0.79
P49718_M Mcm5	DNA replica	R.FDMIFIVK#.D	13.22	10.40	1.27	0.79
P49718_M Mcm5	DNA replica	K.FGLNPSK#.G	81.42	67.06	1.21	0.82
P49718_M Mcm5	DNA replica	K.GSSAAGLTASVIR.D	45.19	47.64	0.95	1.05
P49718_M Mcm5	DNA replica	K.HVM*TLHVSALTQTQAVEGEIDLAK#.M	7.52	4.41	1.70	0.59
P49718_M Mcm5	DNA replica	K.HVM*TLHVSALTQTQAVEGEIDLAK#.M	11.93	6.80	1.75	0.57
P49718_M Mcm5	DNA replica	R.IAEALSK#.M	164.98	120.76	1.37	0.73
P49718_M Mcm5	DNA replica	K.IPGIIISASAVR.A	38.25	161.34	0.24	4.22
P49718_M Mcm5	DNA replica	R.LAALPNIYELISK#.S	297.11	234.67	1.27	0.79
P49718_M Mcm5	DNA replica	R.LFQVSTLDAALSGNLSGVEGFTTQEDQEM*LSR.I	9.49	22.07	0.43	2.32
P49718_M Mcm5	DNA replica	R.LFQVSTLDAALSGNLSGVEGFTTQEDQEMLSR.I	11.99	23.20	0.52	1.94
P49718_M Mcm5	DNA replica	K.LQELPDAVPHGEMPR.H	12.95	54.97	0.24	4.24
P49718_M Mcm5	DNA replica	K.LQPFATEADVEEALR.L	25.79	93.45	0.28	3.62
P49718_M Mcm5	DNA replica	R.LSAEAAEK#.L	85.43	69.83	1.22	0.82
P49718_M Mcm5	DNA replica	K.QPAEHLQLLEEAAK.E	49.02	43.54	1.13	0.89
P49718_M Mcm5	DNA replica	R.RFAIGSQVSEHSIVQDFTK.Q	2.26	8.18	0.28	3.62
P49718_M Mcm5	DNA replica	R.RGDINLLM*LGDPGTAK.S	12.65	47.19	0.27	3.73
P49718_M Mcm5	DNA replica	R.RGDINLLMLGDPGTAK.S	5.54	27.52	0.20	4.97
P49718_M Mcm5	DNA replica	K.SISPSIFGGM*DM*K#.K	23.87	20.04	1.19	0.84
P49718_M Mcm5	DNA replica	K.SISPSIFGGMDM*K#.K	10.28	11.18	0.92	1.09
P49718_M Mcm5	DNA replica	K.SISPSIFGGM*DM*KK.A	15.40	10.72	1.44	0.70
P49718_M Mcm5	DNA replica	R.VAIHEAM*EQQTISIAK#.A	86.25	68.05	1.27	0.79
P49718_M Mcm5	DNA replica	R.VAIHEAM*EQQTISIAK#.A	15.23	15.38	0.99	1.01
P49718_M Mcm5	DNA replica	R.VAIHEAMEQQTISIAK#.A	39.30	32.73	1.20	0.83
P49718_M Mcm5	DNA replica	R.VAIHEAMEQQTISIAK#.A	10.12	5.77	1.75	0.57
P49718_M Mcm5	DNA replica	R.VLGIQVDTDGSGR.S	24.92	85.30	0.29	3.42
P49718_M Mcm5	DNA replica	K.VLQLM*LR.R	5.57	24.44	0.23	4.39
P49718_M Mcm5	DNA replica	K.VLQLMLR.R	6.65	18.93	0.35	2.85
P49718_M Mcm5	DNA replica	R.VTIM*GIYSIK#.K	16.48	11.38	1.45	0.69
P49718_M Mcm5	DNA replica	R.VTIMGIYSIK#.K	43.41	27.17	1.60	0.63
P49718_M Mcm5	DNA replica	R.WDETKGEDNIDFMPTILSR.F	14.65	28.65	0.51	1.96
P49718_M Mcm5	DNA replica	K.AGITTTLNSR.C	35.55	86.09	0.41	2.42
P49718_M Mcm5	DNA replica	R.EDDRVAIHEAMEQQTISIAK.A	4.88	7.52	0.65	1.54
P49718_M Mcm5	DNA replica	K.EVADEVTRPRPAGDELLQDIQVM*LK.S	4.45	14.54	0.31	3.26
P49718_M Mcm5	DNA replica	R.FAIGSQVSEHSIVQDFTK.Q	20.24	10.00	2.02	0.49
P49718_M Mcm5	DNA replica	R.FAIGSQVSEHSIVQDFTK#.Q	199.78	140.30	1.42	0.70
P49718_M Mcm5	DNA replica	K.FGLNPSK#.G	141.90	96.83	1.47	0.68
P49718_M Mcm5	DNA replica	R.GDINLLM*LGDPGTAK#.S	15.57	11.69	1.33	0.75
P49718_M Mcm5	DNA replica	K.GSSAAGLTASVIR.D	11.79	36.56	0.32	3.10
P49718_M Mcm5	DNA replica	K.HVM*TLHVSALTQTQAVEGEIDLAK#.M	7.92	5.23	1.51	0.66
P49718_M Mcm5	DNA replica	R.IAEALSK#.M	177.27	110.00	1.61	0.62
P49718_M Mcm5	DNA replica	K.IPGIIISASAVR.A	31.94	111.88	0.29	3.50
P49718_M Mcm5	DNA replica	R.LAALPNIYELISK#.S	522.97	371.55	1.41	0.71
P49718_M Mcm5	DNA replica	R.LFQVSTLDAALSGNLSGVEGFTTQEDQEM*LSR.I	15.66	39.81	0.39	2.54
P49718_M Mcm5	DNA replica	R.LFQVSTLDAALSGNLSGVEGFTTQEDQEMLSR.I	8.30	19.82	0.42	2.39
P49718_M Mcm5	DNA replica	K.LQELPDAVPHGEMPR.H	13.68	32.85	0.42	2.40
P49718_M Mcm5	DNA replica	K.LQPFATEADVEEALR.L	30.33	106.55	0.28	3.51
P49718_M Mcm5	DNA replica	R.LSAEAAEK#.L	101.72	69.04	1.47	0.68
P49718_M Mcm5	DNA replica	K.QPAEHLQLLEEAAK.E	47.61	39.51	1.21	0.83
P49718_M Mcm5	DNA replica	R.RGDINLLM*LGDPGTAK.S	17.45	46.85	0.37	2.68
P49718_M Mcm5	DNA replica	K.RLPDGLTR.R	4.12	52.24	0.08	12.67
P49718_M Mcm5	DNA replica	K.SDM*M*SHLVK#.I	21.40	12.16	1.76	0.57
P49718_M Mcm5	DNA replica	R.SFAGSVSPQEEEEFR.R	4.17	17.07	0.24	4.09
P49718_M Mcm5	DNA replica	K.SISPSIFGGM*DM*K#.K	33.07	30.56	1.08	0.92
P49718_M Mcm5	DNA replica	R.VAIHEAM*EQQTISIAK#.A	117.89	70.66	1.67	0.60

P49718_M	Mcm5	DNA replica	R.VAIHEAMEQQTISIAK#.A	26.32	17.02	1.55	0.65
P49718_M	Mcm5	DNA replica	R.VAIHEAMEQQTISIAK#.A	6.80	5.14	1.32	0.76
P49718_M	Mcm5	DNA replica	R.VLGIQVDTDGSGR.S	35.53	122.44	0.29	3.45
P49718_M	Mcm5	DNA replica	K.VLQLM*LR.R	8.81	32.44	0.27	3.68
P49718_M	Mcm5	DNA replica	R.VTIM*GIYSIK#.K	19.04	13.55	1.41	0.71
P49718_M	Mcm5	DNA replica	R.VTIMGIYSIK#.K	26.41	15.05	1.75	0.57
P49718_M	Mcm5	DNA replica	R.WDETKGEDNIDFM*PTILSR.F	8.33	25.78	0.32	3.10
P49718_M	Mcm5	DNA replica	R.WDETKGEDNIDFMPTILSR.F	6.78	19.37	0.35	2.86
P97311_M	Mcm6	DNA replica	K.DFYVAFQDLPTR.H	6.23	15.80	0.39	2.54
P97311_M	Mcm6	DNA replica	K.HVDEFSPR.A	2.52	9.40	0.27	3.72
P97311_M	Mcm6	DNA replica	R.LTHYDHVLIELTQAGLK#.G	12.61	12.94	0.97	1.03
P97311_M	Mcm6	DNA replica	R.AEAVESAQAGDR.C	15.90	40.06	0.40	2.52
P97311_M	Mcm6	DNA replica	K.ASSAAGLTAAVVR.D	10.22	37.33	0.27	3.65
P97311_M	Mcm6	DNA replica	K.DFYVAFQDLPTR.H	35.98	117.02	0.31	3.25
P97311_M	Mcm6	DNA replica	R.DQVAIHEAM*EQQTISITK#.A	62.34	36.93	1.69	0.59
P97311_M	Mcm6	DNA replica	R.DQVAIHEAM*EQQTISITK.A	12.84	7.31	1.76	0.57
P97311_M	Mcm6	DNA replica	R.DQVAIHEAMEQQTISITK#.A	52.97	31.69	1.67	0.60
P97311_M	Mcm6	DNA replica	K.DVEQQFK#.Y	47.34	46.04	1.03	0.97
P97311_M	Mcm6	DNA replica	K.EIESEIDSEEELINK#.K	7.96	4.13	1.92	0.52
P97311_M	Mcm6	DNA replica	K.ELRDEEQTAESIKNQM*TVK.E	11.78	37.54	0.31	3.19
P97311_M	Mcm6	DNA replica	K.ELRDEEQTAESIKNQMTVK.E	4.03	15.59	0.26	3.87
P97311_M	Mcm6	DNA replica	R.FLLDTNK#.S	166.25	103.96	1.60	0.63
P97311_M	Mcm6	DNA replica	R.FVDFQK#.V	290.44	175.63	1.65	0.60
P97311_M	Mcm6	DNA replica	R.GVLLM*LFGGVPK#.T	84.16	58.25	1.44	0.69
P97311_M	Mcm6	DNA replica	R.GVLLMLFGGVPK#.T	85.28	51.09	1.67	0.60
P97311_M	Mcm6	DNA replica	K.HVDEFSPR.A	55.60	157.77	0.35	2.84
P97311_M	Mcm6	DNA replica	R.IQETQAELPR.G	78.24	222.94	0.35	2.85
P97311_M	Mcm6	DNA replica	R.ISGQVVR.T	37.47	100.24	0.37	2.67
P97311_M	Mcm6	DNA replica	K.ISKESEDFIVEQYKR.L	8.34	18.78	0.44	2.25
P97311_M	Mcm6	DNA replica	R.ISNLIVLHLR.K	22.83	55.68	0.41	2.44
P97311_M	Mcm6	DNA replica	R.IVDLHSR.I	6.05	20.20	0.30	3.34
P97311_M	Mcm6	DNA replica	R.K#M*EEEEDESALK#.R	9.46	6.16	1.54	0.65
P97311_M	Mcm6	DNA replica	R.KM*EEEEDESALKR.S	37.36	132.55	0.28	3.55
P97311_M	Mcm6	DNA replica	R.KMEEEEDESALKR.S	25.76	63.06	0.41	2.45
P97311_M	Mcm6	DNA replica	R.LTHYDHVLIELTQAGLK#.G	153.71	91.16	1.69	0.59
P97311_M	Mcm6	DNA replica	K.QNINLSAPIM*SR.F	18.57	58.51	0.32	3.15
P97311_M	Mcm6	DNA replica	K.QNINLSAPIMSR.F	14.96	32.19	0.46	2.15
P97311_M	Mcm6	DNA replica	R.SELVNWYLK#.E	148.82	83.78	1.78	0.56
P97311_M	Mcm6	DNA replica	R.TSILAAANPVSGHYDR.S	8.07	26.93	0.30	3.34
P97311_M	Mcm6	DNA replica	K.TTGEGTSLR.G	20.24	66.37	0.30	3.28
P97311_M	Mcm6	DNA replica	R.VETPDVNLDQEEEIQM*ETDEGQGGVNGHADSPAPVNR.F	2.03	2.17	0.94	1.07
P97311_M	Mcm6	DNA replica	K.VFEM*SQDK#.N	59.50	40.52	1.47	0.68
P97311_M	Mcm6	DNA replica	R.VSGADGYETEGIR.G	62.23	177.76	0.35	2.86
P97311_M	Mcm6	DNA replica	R.VYSLDDIR.R	12.68	25.56	0.50	2.02
P97311_M	Mcm6	DNA replica	R.AEAVESAQAGDR.C	7.51	22.05	0.34	2.94
P97311_M	Mcm6	DNA replica	K.ASSAAGLTAAVVR.D	8.70	25.84	0.34	2.97
P97311_M	Mcm6	DNA replica	R.DEEQTAESIK#.N	18.21	8.71	2.09	0.48
P97311_M	Mcm6	DNA replica	K.DFYVAFQDLPTR.H	22.36	41.98	0.53	1.88
P97311_M	Mcm6	DNA replica	R.DQVAIHEAM*EQQTISITK#.A	34.56	22.59	1.53	0.65
P97311_M	Mcm6	DNA replica	R.DQVAIHEAMEQQTISITK#.A	25.35	21.74	1.17	0.86
P97311_M	Mcm6	DNA replica	K.DVEQQFK#.Y	32.02	38.57	0.83	1.20
P97311_M	Mcm6	DNA replica	K.EIESEIDSEEELINK#.K	9.53	5.30	1.80	0.56
P97311_M	Mcm6	DNA replica	K.EIESEIDSEEELINKK.T	15.87	11.59	1.37	0.73
P97311_M	Mcm6	DNA replica	K.ELRDEEQTAESIKNQMTVK.E	2.49	7.80	0.32	3.14
P97311_M	Mcm6	DNA replica	R.FLLDTNK#.S	79.08	56.90	1.39	0.72
P97311_M	Mcm6	DNA replica	R.FNGSSEDASQETVSKPSLR.L	11.56	34.55	0.33	2.99
P97311_M	Mcm6	DNA replica	R.FVDFQK#.V	142.31	97.70	1.46	0.69
P97311_M	Mcm6	DNA replica	R.GVLLM*LFGGVPK#.T	59.71	28.84	2.07	0.48
P97311_M	Mcm6	DNA replica	R.GVLLMLFGGVPK#.T	30.43	21.05	1.45	0.69
P97311_M	Mcm6	DNA replica	K.HVDEFSPR.A	19.99	70.46	0.28	3.52
P97311_M	Mcm6	DNA replica	R.IQETQAELPR.G	40.17	114.04	0.35	2.84
P97311_M	Mcm6	DNA replica	R.ISGQVVR.T	30.05	64.01	0.47	2.13
P97311_M	Mcm6	DNA replica	R.ISNLIVLHLR.K	6.83	28.30	0.24	4.14
P97311_M	Mcm6	DNA replica	R.KM*EEEEDESALKR.S	19.49	70.66	0.28	3.62
P97311_M	Mcm6	DNA replica	R.KMEEEEDESALKR.S	8.57	19.53	0.44	2.28
P97311_M	Mcm6	DNA replica	R.LTHYDHVLIELTQAGLK#.G	36.92	19.38	1.91	0.52
P97311_M	Mcm6	DNA replica	K.VFEM*SQDK#.N	25.32	15.42	1.64	0.61
P97311_M	Mcm6	DNA replica	R.VSGADGYETEGIR.G	36.48	100.51	0.36	2.76
P97311_M	Mcm6	DNA replica	R.VYSLDDIRR.Y	1.27	13.99	0.09	11.05
P97311_M	Mcm6	DNA replica	K.YLQFAEELIRPER.N	8.61	50.49	0.17	5.86
Q61881_M	Mcm7	DNA replica	K.AGILTTLNAR.C	4.85	13.28	0.37	2.74
Q61881_M	Mcm7	DNA replica	K.ALLLLLVGGVDQSPQGM*K#.I	11.23	8.71	1.29	0.78
Q61881_M	Mcm7	DNA replica	K.FLQEFYYENELGK#.K	8.70	5.86	1.49	0.67
Q61881_M	Mcm7	DNA replica	R.GSSGVGLTAAVLR.D	11.24	21.19	0.53	1.88
Q61881_M	Mcm7	DNA replica	R.IAQPGDHVSVTGIFLPVLR.T	3.41	22.18	0.15	6.51
Q61881_M	Mcm7	DNA replica	R.LFGDVVQELLPEYK#.E	17.68	15.24	1.16	0.86
Q61881_M	Mcm7	DNA replica	K.QIAEEDFYEK.L	8.26	8.61	0.96	1.04
Q61881_M	Mcm7	DNA replica	K.SDDDVSGAGELSSEELK#.Q	13.42	12.99	1.03	0.97
Q61881_M	Mcm7	DNA replica	R.TGFQQM*AQGLLSETYLEAHWIVK#.M	8.81	7.95	1.11	0.90
Q61881_M	Mcm7	DNA replica	K.FLQEFYYENELGK.K	7.90	5.53	1.43	0.70
Q61881_M	Mcm7	DNA replica	R.LFGDVVQELLPEYK.E	11.05	9.92	1.11	0.90
Q61881_M	Mcm7	DNA replica	R.SLEQNVQLPAALLSR.F	1.12	3.81	0.29	3.42
Q61881_M	Mcm7	DNA replica	K.AGILTTLNAR.C	52.16	190.75	0.27	3.66
Q61881_M	Mcm7	DNA replica	K.ALLLLLVGGVDQSPQGM*K#.I	157.05	113.82	1.38	0.72
Q61881_M	Mcm7	DNA replica	K.ALLLLLVGGVDQSPQGMK#.I	39.70	33.88	1.17	0.85
Q61881_M	Mcm7	DNA replica	K.DSLLGEK#.G	127.08	93.69	1.36	0.74
Q61881_M	Mcm7	DNA replica	K.EVVNKDVLDVYIEHR.L	16.60	53.36	0.31	3.21
Q61881_M	Mcm7	DNA replica	R.FELYFR.G	8.65	32.20	0.27	3.72
Q61881_M	Mcm7	DNA replica	K.FLQEFYYENELGK#.K	89.34	72.15	1.24	0.81
Q61881_M	Mcm7	DNA replica	R.GFTPAQFQAALDEYEELNVWQVNTSR.T	63.35	67.55	0.94	1.07
Q61881_M	Mcm7	DNA replica	R.GSSGVGLTAAVLR.D	43.79	141.95	0.31	3.24
Q61881_M	Mcm7	DNA replica	R.IAQPGDHVSVTGIFLPVLR.T	82.31	272.49	0.30	3.31
Q61881_M	Mcm7	DNA replica	K.IQEHSDQVPVGNIPR.S	45.38	159.94	0.28	3.52
Q61881_M	Mcm7	DNA replica	K.K#FLQEFYYENELGK#.K	12.00	5.13	2.34	0.43
Q61881_M	Mcm7	DNA replica	R.LAQHITYVHQHSR.Q	18.48	58.15	0.32	3.15
Q61881_M	Mcm7	DNA replica	R.LAQHITYVHQHSR.Q	5.00	15.22	0.33	3.04
Q61881_M	Mcm7	DNA replica	R.LFGDVVQELLPEYK#.E	207.92	160.01	1.30	0.77
Q61881_M	Mcm7	DNA replica	R.LSTALAR.L	51.46	148.55	0.35	2.89
Q61881_M	Mcm7	DNA replica	R.LYLQTR.G	42.44	146.73	0.29	3.46
Q61881_M	Mcm7	DNA replica	R.M*VDIVEKEDVNEAIR.L	29.26	100.19	0.29	3.42
Q61881_M	Mcm7	DNA replica	R.MVDIVEKEDVNEAIR.L	9.63	30.81	0.31	3.20
Q61881_M	Mcm7	DNA replica	R.MVDIVEKEDVNEAIR.L	6.51	6.72	0.97	1.03
Q61881_M	Mcm7	DNA replica	R.NPQNQYPSELM*R.R	36.36	140.35	0.26	3.86

Q61881_M	Mcm7	DNA replica	R.NPQNQYPSELMR.R	19.76	39.07	0.51	1.98
Q61881_M	Mcm7	DNA replica	K.QIAEEDFYEK#.L	107.91	91.04	1.19	0.84
Q61881_M	Mcm7	DNA replica	R.QPPAQFEPLDM*K#.L	30.56	22.73	1.34	0.74
Q61881_M	Mcm7	DNA replica	R.QPTVPESLADYITAAYVEM*R.R	9.69	27.69	0.35	2.86
Q61881_M	Mcm7	DNA replica	R.RFELYFR.G	2.88	38.86	0.07	13.48
Q61881_M	Mcm7	DNA replica	K.SDDDVSGAGELSSEELK#.Q	160.71	121.26	1.33	0.75
Q61881_M	Mcm7	DNA replica	K.SDDDVSGAGELSSEELK#QIAEEDFYEK#.L	18.02	11.69	1.54	0.65
Q61881_M	Mcm7	DNA replica	R.SITVVLEGENTR.I	38.95	119.56	0.33	3.07
Q61881_M	Mcm7	DNA replica	R.SLEQNVQLPAALLSR.F	28.31	98.59	0.29	3.48
Q61881_M	Mcm7	DNA replica	K.SQLLSYIDR.L	59.11	164.17	0.36	2.78
Q61881_M	Mcm7	DNA replica	R.SVHFSEAEQR.C	41.11	183.15	0.22	4.46
Q61881_M	Mcm7	DNA replica	R.TAIHEVM*EQQTISIAK#.A	83.45	63.83	1.31	0.76
Q61881_M	Mcm7	DNA replica	R.TAIHEVMEQQTISIAK#.A	76.81	51.62	1.49	0.67
Q61881_M	Mcm7	DNA replica	R.TGFQQM*AQGLLSETYLEAHWIVK#.M	133.73	72.79	1.84	0.54
Q61881_M	Mcm7	DNA replica	R.TLLAILR.L	37.77	100.58	0.38	2.66
Q61881_M	Mcm7	DNA replica	R.TQRPADVIFATIR.E	5.10	97.76	0.05	19.16
Q61881_M	Mcm7	DNA replica	R.VSEVKPR.M	8.44	27.87	0.30	3.30
Q61881_M	Mcm7	DNA replica	K.AGILTTLNAR.C	29.46	81.37	0.36	2.76
Q61881_M	Mcm7	DNA replica	K.ALLLLLVGGVDQSPQGM*K#.I	60.69	38.74	1.57	0.64
Q61881_M	Mcm7	DNA replica	K.DSLLGEK#.G	62.41	40.95	1.52	0.66
Q61881_M	Mcm7	DNA replica	K.EVVNKDVLDVYIEHR.L	5.12	13.78	0.37	2.69
Q61881_M	Mcm7	DNA replica	K.FLQEFYYENELGK#.K	51.47	32.70	1.57	0.64
Q61881_M	Mcm7	DNA replica	R.GFTPAQFQAALDEYEELNVWQVNTSR.T	166.12	40.54	4.10	0.24
Q61881_M	Mcm7	DNA replica	R.GSSGVGLTAAVLR.D	29.01	75.29	0.39	2.60
Q61881_M	Mcm7	DNA replica	R.IAQPGDHVSVTGIFLPVLR.T	69.09	212.66	0.32	3.08
Q61881_M	Mcm7	DNA replica	K.IQEHSDQVPVGNIPR.S	30.78	106.96	0.29	3.47
Q61881_M	Mcm7	DNA replica	R.LAQHITYVHQHSR.Q	5.83	24.53	0.24	4.21
Q61881_M	Mcm7	DNA replica	R.LFGDVVQELLPEYK#.E	148.34	88.79	1.67	0.60
Q61881_M	Mcm7	DNA replica	R.LYLQTR.G	21.91	68.67	0.32	3.13
Q61881_M	Mcm7	DNA replica	R.M*VDIVEKEDVNEAIR.L	25.79	65.74	0.39	2.55
Q61881_M	Mcm7	DNA replica	R.NPQNQYPSELM*R.R	20.14	59.90	0.34	2.97
Q61881_M	Mcm7	DNA replica	R.NPQNQYPSELMR.R	4.23	13.47	0.31	3.18
Q61881_M	Mcm7	DNA replica	K.QIAEEDFYEK#.L	75.14	52.39	1.43	0.70
Q61881_M	Mcm7	DNA replica	R.QPPAQFEPLDM*K#.L	15.60	14.93	1.04	0.96
Q61881_M	Mcm7	DNA replica	R.QPTVPESLADYITAAYVEM*R.R	9.20	23.36	0.39	2.54
Q61881_M	Mcm7	DNA replica	K.SDDDVSGAGELSSEELK#.Q	102.89	62.07	1.66	0.60
Q61881_M	Mcm7	DNA replica	K.SDDDVSGAGELSSEELK#QIAEEDFYEK#.L	12.01	8.10	1.48	0.67
Q61881_M	Mcm7	DNA replica	R.SITVVLEGENTR.I	23.77	66.27	0.36	2.79
Q61881_M	Mcm7	DNA replica	R.SLEQNVQLPAALLSR.F	17.33	57.18	0.30	3.30
Q61881_M	Mcm7	DNA replica	K.SQLLSYIDR.L	27.13	81.13	0.33	2.99
Q61881_M	Mcm7	DNA replica	R.TAIHEVM*EQQTISIAK#.A	60.73	34.72	1.75	0.57
Q61881_M	Mcm7	DNA replica	R.TAIHEVMEQQTISIAK#.A	32.61	20.49	1.59	0.63
Q61881_M	Mcm7	DNA replica	R.TGFQQM*AQGLLSETYLEAHWIVK#.M	36.08	22.61	1.60	0.63
Q61881_M	Mcm7	DNA replica	R.TLLAILR.L	19.32	63.23	0.31	3.27
Q61881_M	Mcm7	DNA replica	R.TQRPADVIFATIR.E	3.86	46.08	0.08	11.92
Q8R3C0_M	Mcmbp	Mini-chron	R.FLDYNLSDDITK#.A	13.90	9.28	1.50	0.67
Q5PSV9_M	Mdc1	Mediator o	K.TPEASVPTTPELQPFTSK#.K	8.81	4.96	1.78	0.56
Q5PSV9_M	Mdc1	Mediator o	R.TPESVVSTGPELQPLTSIEQPVIPEPR.A	5.40	6.46	0.84	1.20
P08249_M	Mdh2	Malate deh	K.VAVLGASGGIGQPLSLLLK#.N	9.66	4.27	2.26	0.44
Q9D967_M	Mdp1	Magnesium	R.DGM*SLQTLTQGLETFAK#.A	12.86	6.50	1.98	0.51
Q9D967_M	Mdp1	Magnesium	R.LQSLGVPVAAASR.T	9.73	23.58	0.41	2.42
Q2VPQ9_E	Meaf6	Chromatin	K.SSVTSAAAVSALAGVQDQLIEK#.R	17.71	14.66	1.21	0.83
Q2VPQ9_E	Meaf6	Chromatin	K.SSVTSAAAVSALAGVQDQLIEK#.R	16.69	9.96	1.68	0.60
Q2VPQ9_E	Meaf6	Chromatin	K.SSVTSAAAVSALAGVQDQLIEK#.R	34.58	36.06	0.96	1.04
Q2VPQ9_E	Meaf6	Chromatin	K.SSVTSAAAVSALAGVQDQLIEKR.E	4.37	17.42	0.25	3.99
P14404_EV	Mecom	MDS1 and E	R.AAAESSAIQSISHV.-	19.09	19.09	1.00	1.00
P14404_EV	Mecom	MDS1 and E	R.APPNTLPENLLR.K	1.91	23.31	0.08	12.22
P14404_EV	Mecom	MDS1 and E	R.KLTDPLEALKEK.Y	2.96	9.54	0.31	3.22
P14404_EV	Mecom	MDS1 and E	K.NHFAAGGFFGQGISLPGTPAM*DK.T	3.62	7.65	0.47	2.11
Q9Z2D6_M	Mecp2	Methyl-CpG	K.AAASEGVQVK#.R	26.28	29.41	0.89	1.12
Q9Z2D6_M	Mecp2	Methyl-CpG	K.AETSESSGSAPAVPEASASPK#.Q	7.21	5.45	1.32	0.76
Q9Z2D6_M	Mecp2	Methyl-CpG	K.EVVK#PLLVSTLGEK#.S	9.27	13.34	0.69	1.44
Q9Z2D6_M	Mecp2	Methyl-CpG	K.GEGGGATTSAQVMVIK#.R	8.09	6.18	1.31	0.76
Q9Z2D6_M	Mecp2	Methyl-CpG	R.K#AEADPQAIPK#.K	13.61	29.27	0.47	2.15
Q9Z2D6_M	Mecp2	Methyl-CpG	K.SEDQDLQGLR.D	4.02	21.83	0.18	5.43
Q9Z2D6_M	Mecp2	Methyl-CpG	K.TQPM*VATTTTVAEK#.Y	13.20	10.43	1.27	0.79
Q9Z2D6_M	Mecp2	Methyl-CpG	K.TQPMVATTTTVAEK#.Y	16.38	14.75	1.11	0.90
Q9Z2D6_M	Mecp2	Methyl-CpG	K.VGDTSLDPNDFDFTVTGR.G	4.78	17.57	0.27	3.68
Q925J9_M	Med1	Mediator o	R.VPLILNM*IR.H	2.91	10.73	0.27	3.68
Q9CXU0_M	Med10	Mediator o	K.LNFIVTGLQDIDK#.C	7.00	8.73	0.80	1.25
Q9CXU0_M	Med10	Mediator o	R.QLGIIVSDFQPSSQAGLSQK#.L	12.19	9.25	1.32	0.76
Q9CXU0_M	Med10	Mediator o	R.QLGIIVSDFQPSSQAGLSQK.L	7.10	6.54	1.09	0.92
Q9CXU0_M	Med10	Mediator o	K.SLLIQELSK#.V	22.64	17.02	1.33	0.75
Q9D8C6_M	Med11	Mediator o	R.QAAAFTTSVQHVEAELSAQIR.Y	4.38	14.16	0.31	3.23
A2AGH6_M	Med12	Mediator o	R.IVDGAVFAVLK.A	8.60	11.77	0.73	1.37
A2AGH6_M	Med12	Mediator o	R.SGVWLVAPLIAK#.L	14.10	16.99	0.83	1.21
A2AGH6_M	Med12	Mediator o	K.TGSPLDHLPIAPSNLPM*PEGNSAFTQQVR.A	1.48	3.47	0.43	2.35
Q5SWW4_	Med13	Mediator o	R.GAGGPASAQGSVK.Y	10.29	9.47	1.09	0.92
Q5SWW4_	Med13	Mediator o	K.LDLLPSGPSM*PFIK#.E	7.01	9.06	0.77	1.29
Q5SWW4_	Med13	Mediator o	K.NQYLSAIASDTEQEPK#.I	7.06	4.58	1.54	0.65
Q5SWW4_	Med13	Mediator o	K.TLTGFGPGLAM*ETALK#.S	5.70	4.63	1.23	0.81
A2ABV5_M	Med14	Mediator o	R.DGAYSLFDNSK#.L	9.30	6.07	1.53	0.65
A2ABV5_M	Med14	Mediator o	R.IIQQETLQLINSNEPGVIM*FK#.T	11.75	6.27	1.87	0.53
A2ABV5_M	Med14	Mediator o	K.LVEGFYPAPGLK.T	13.38	15.31	0.87	1.14
Q6PGF3_M	Med16	Mediator o	K.LPISLTNTDLK#.V	14.71	13.48	1.09	0.92
Q8VCD5_M	Med17	Mediator o	R.IEDPQIQAHWSNINDVYESSVK#.V	7.00	4.76	1.47	0.68
Q8VCD5_M	Med17	Mediator o	R.LSGPQAFDK#NEINSIQSTEGLLEK#.I	11.41	9.01	1.27	0.79
Q8C1S0_M	Med19	Mediator o	R.SLIEKPPILGGSFNPITGTM*LSGFR.L	3.63	15.09	0.24	4.15
Q8C1S0_M	Med19	Mediator o	K.STAGSGPFYLM*R.E	10.32	12.40	0.83	1.20
Q9R0X0_M	Med20	Mediator o	K.SLQQTVELLTK.K	17.27	22.53	0.77	1.30
Q9R0X0_M	Med20	Mediator o	K.VGTVTM*GPSAR.G	3.43	11.50	0.30	3.35
Q9CQ39_M	Med21	Mediator o	K.IQSALADIAQSQLK#.T	9.56	8.16	1.17	0.85
Q62276_M	Med22	Mediator o	K.ETLLQSYNKR.L	2.28	7.27	0.31	3.19
Q62276_M	Med22	Mediator o	K.QFLILNDFPSVNEAIDQR.N	2.65	6.73	0.39	2.54
Q62276_M	Med22	Mediator o	K.SIMDNFTEIIK#.T	24.08	15.19	1.59	0.63
Q80YQ2_M	Med23	Mediator o	K.DVGNALLNVVLK#.S	14.35	14.18	1.01	0.99
Q80YQ2_M	Med23	Mediator o	R.FLELLPVSK.S	14.90	15.39	0.97	1.03
Q80YQ2_M	Med23	Mediator o	K.FLTEALLPVVK#.T	14.98	13.53	1.11	0.90
Q80YQ2_M	Med23	Mediator o	R.LITALGSSEVQPQFTR.F	2.84	13.05	0.22	4.59
Q80YQ2_M	Med23	Mediator o	R.TFADFLVYEFSTSAGGQQLNK#.C	5.63	6.10	0.92	1.08
Q80YQ2_M	Med23	Mediator o	K.TVLSAESEELNR.A	4.70	15.80	0.30	3.36
Q99K74_M	Med24	Mediator o	K.SLDLLLAAAAATGK#.L	9.27	4.64	2.00	0.50
Q99K74_M	Med24	Mediator o	K.VVLAITDLSLPLGR.Q	4.27	8.94	0.48	2.10

Q99K74_M	Med24	Mediator o	K.LGEILANLSNPQLR.S	2.74	9.26	0.30	3.38
Q99K74_M	Med24	Mediator o	R.LQEGLEAGTPAPGEK#.Q	19.35	14.85	1.30	0.77
Q99K74_M	Med24	Mediator o	K.SLDLLLAAAAATGK#.L	13.15	10.12	1.30	0.77
Q99K74_M	Med24	Mediator o	K.SSENANIQPNPGLILR.A	1.85	5.71	0.32	3.09
Q99K74_M	Med24	Mediator o	K.VVLAITDLSLPLGR.Q	4.78	15.10	0.32	3.16
Q8VCB2_M	Med25	Mediator o	R.GLVLPVGGSSTSGSLQTK#.Q	13.41	4.56	2.94	0.34
Q8VCB2_M	Med25	Mediator o	R.GLVLPVGGSSTSGSLQTK#.Q	4.60	1.87	2.47	0.41
Q9DB40_M	Med27	Mediator o	K.AQPTTLVLPPQYVDDVISR.I	1.67	3.55	0.47	2.12
Q920D3_M	Med28	Mediator o	R.HWQQVLEDINVQHK.K	3.45	4.29	0.80	1.24
Q920D3_M	Med28	Mediator o	K.K#PADM*PQGSLAFLEQASANIPAPLK#QT.-	7.16	2.82	2.54	0.39
Q9CQI9_M	Med30	Mediator o	R.EIVEVNKK.L	22.02	21.89	1.01	0.99
Q9CXU1_M	Med31	Mediator o	R.LQQALAEQQQQNNTAGK#.-	10.52	9.46	1.11	0.90
Q9CQA5_M	Med4	Mediator o	R.LLSALEDLEVLSR.E	4.56	12.73	0.36	2.79
Q9D7W5_	Med8	Mediator o	K.QTFNPGDTNALVAAVAFGK#.G	6.05	5.67	1.07	0.94
Q8BP48_M	Metap1	Methionin	R.EVLDIAAGM*IK#.A	8.94	8.73	1.02	0.98
Q8BP48_M	Metap1	Methionin	K.LLSSEDIEGM*R.L	5.04	15.09	0.33	2.99
O08663_M	Metap2	Methionin	R.M*EEGEVYAIETFGSTGK#.G	4.82	2.07	2.33	0.43
O08663_M	Metap2	Methionin	K.YDILLTAVK#.D	17.38	8.24	2.11	0.47
Q8C3P7_M	Mettl3	N6-adenosi	K.FAAQELIEVK#.R	10.80	6.91	1.56	0.64
Q8C3P7_M	Mettl3	N6-adenosi	K.GLGEVAGTIAGQK#.R	9.69	6.70	1.45	0.69
Q8C3P7_M	Mettl3	N6-adenosi	R.VDEIIWVK#.T	12.18	12.28	0.99	1.01
Q9CQU1_M	Mfap1	Microfibril	R.DFSAPTLEDHFNK.T	11.04	7.56	1.46	0.69
Q9CQU1_M	Mfap1	Microfibril	K.QPPIQSTAGAVPVR.N	1.93	9.81	0.20	5.09
Q9CQU1_M	Mfap1	Microfibril	K.YTHLVDQDTTSFDSAWGQESAQNTK#.F	8.01	6.15	1.30	0.77
P21956_M	Mfge8	Lactadheri	R.DFGHIQYVASYK#.V	10.96	8.47	1.29	0.77
P21956_M	Mfge8	Lactadheri	K.INAWTAQSNSAK#.E	18.90	9.81	1.93	0.52
P21956_M	Mfge8	Lactadheri	R.K#FEFIQDESGGDK#EFLGNLDNNSLK#.V	8.43	5.37	1.57	0.64
P21956_M	Mfge8	Lactadheri	R.KFEFIQDESGGDKEFLGNLDNNSLK.V	14.30	14.09	1.01	0.99
P21956_M	Mfge8	Lactadheri	R.QVTGIITQGAR.D	7.15	22.76	0.31	3.18
P21956_M	Mfge8	Lactadheri	K.VFQGNLDNNSHK#K#.N	2.53	11.17	0.23	4.40
P21956_M	Mfge8	Lactadheri	K.VNM*FNPTLEAQYIK#.L	10.13	5.99	1.69	0.59
P21956_M	Mfge8	Lactadheri	K.VNMFNPTLEAQYIK.L	8.69	8.24	1.06	0.95
P26187_M	Mgmt	Methylated	K.FGETVSYQQLAALAGNPK#.A	7.80	5.42	1.44	0.70
P26187_M	Mgmt	Methylated	K.YSVLDSPLGK#.M	4.31	2.67	1.61	0.62
Q8VDP3_M	Mical1	Protein-me	K.NTSHSSGLVSQPSGTPSAILFLGK#.L	7.77	3.38	2.30	0.44
Q8VDP3_M	Mical1	Protein-me	R.NVAQYGLDPATR.Y	7.72	9.29	0.83	1.20
Q8VDP3_M	Mical1	Protein-me	R.AKEEEM*K#.R	5.83	4.43	1.32	0.76
Q8VDP3_M	Mical1	Protein-me	K.NTSHSSGLVSQPSGTPSAILFLGK#.L	13.96	7.92	1.76	0.57
Q8VDP3_M	Mical1	Protein-me	R.QDLSETDQLLGK#.A	10.35	6.10	1.70	0.59
Q8VDP3_M	Mical1	Protein-me	R.TVEETQVPEISGVAR.I	4.10	6.46	0.63	1.58
Q8CD10_M	Micu2	Calcium up	K.VATGQELSDNLLDTVFK#.I	5.88	1.46	4.04	0.25
Q3UBZ5_M	Mif4gd	MIF4G dom	R.DGFLLPTDLSSLAR.L	1.97	6.69	0.29	3.40
Q3UBZ5_M	Mif4gd	MIF4G dom	K.IQSFDAETQQLLK#.T	6.29	2.72	2.31	0.43
E9PVX6_E9	Mki67	Protein Mk	R.APGTPAPVQEENDSTAFM*ETPKQK#LDFAENSSGSK.R	3.65	1.68	2.18	0.46
E9PVX6_E9	Mki67	Protein Mk	K.MSLESSQAEPVK.T	3.56	4.47	0.80	1.26
E9PVX6_E9	Mki67	Protein Mk	K.SPQVTTENITTNTKPQTSTSGK.K	2.45	9.61	0.26	3.92
E9PVX6_E9	Mki67	Protein Mk	R.AQPLEDLDGFQELFQTPAGANDSVTVEESAK.M	5.48	4.02	1.36	0.73
E9PVX6_E9	Mki67	Protein Mk	R.EQKVDQQVQDNENAPQR.C	3.05	10.72	0.28	3.52
E9PVX6_E9	Mki67	Protein Mk	K.ETLQTAADGTR.L	2.97	17.79	0.17	5.99
E9PVX6_E9	Mki67	Protein Mk	R.GGM*VPVQTSTETAK.M	5.46	14.55	0.38	2.66
E9PVX6_E9	Mki67	Protein Mk	K.GLSADSPASDGSK#.N	7.48	9.41	0.80	1.26
E9PVX6_E9	Mki67	Protein Mk	R.HSVNLDEGESAQAVHK.T	23.20	36.12	0.64	1.56
E9PVX6_E9	Mki67	Protein Mk	R.KVDFSEDLSGLTEM*FK.T	4.01	6.80	0.59	1.70
E9PVX6_E9	Mki67	Protein Mk	R.SGASEANLIVAK.S	18.21	29.59	0.62	1.62
E9PVX6_E9	Mki67	Protein Mk	K.SPQVTTENITTNTKPQTSTSGK.K	15.90	27.87	0.57	1.75
E9PVX6_E9	Mki67	Protein Mk	K.SSGSTPVTAASSPK.V	15.98	30.60	0.52	1.92
E9PVX6_E9	Mki67	Protein Mk	K.TPVSETEPLK.T	3.81	9.66	0.39	2.54
E9PVX6_E9	Mki67	Protein Mk	K.VDQQVQDNENAPQR.C	1.66	11.48	0.14	6.90
E9PVX6_E9	Mki67	Protein Mk	R.YSASPTLR.R	27.40	20.24	1.35	0.74
E9PVX6_E9	Mki67	Protein Mk	K.TPVSETEPLK.T	3.37	16.91	0.20	5.02
Q9JK91_M	Mlh1	DNA misma	K.HFTEDGNVLQLANLPDLYK#.V	7.32	3.71	1.97	0.51
Q9JK91_M	Mlh1	DNA misma	R.SIFGNAVSR.E	2.81	25.52	0.11	9.09
Q8VDG6_M	Mlk4	Mitogen-ac	K.SVMCQPSIYALEK#DFLT.-	3.39	4.02	0.84	1.19
Q9QZQ1_A	Mllt4	Afadin OS=	R.VSSTATTQDVIETLAEK#.F	4.12	33.78	0.12	8.21
Q9QZQ1_A	Mllt4	Afadin OS=	R.ESSEDSFLSAIINYTNSSTVHFK#.L	29.09	17.83	1.63	0.61
Q9QZQ1_A	Mllt4	Afadin OS=	R.EYFTFPASK#.S	20.79	7.07	2.94	0.34
Q9QZQ1_A	Mllt4	Afadin OS=	K.GILVFQLK#.R	19.04	8.24	2.31	0.43
Q9QZQ1_A	Mllt4	Afadin OS=	R.HKPGAVQETTFELGGDVHSGTALPASR.S	8.17	10.52	0.78	1.29
Q9QZQ1_A	Mllt4	Afadin OS=	R.IVQATTLLTM*DK#.Y	16.80	11.44	1.47	0.68
Q9QZQ1_A	Mllt4	Afadin OS=	R.LDQEQEYR.R	5.16	7.55	0.68	1.46
Q9QZQ1_A	Mllt4	Afadin OS=	R.SM*DAETYVDGQR.I	7.09	10.74	0.66	1.51
Q9QZQ1_A	Mllt4	Afadin OS=	R.SQDADLPGSSGAPENLTFK#.E	4.57	4.18	1.09	0.91
Q9QZQ1_A	Mllt4	Afadin OS=	K.TILLSTTDTADFAVAESLEK#.Y	29.79	4.98	5.98	0.17
Q9QZQ1_A	Mllt4	Afadin OS=	R.TSSVVTLEVAK#.Q	32.46	12.84	2.53	0.40
Q9QZQ1_A	Mllt4	Afadin OS=	R.VSSTATTQDVIETLAEK#.F	29.03	8.56	3.39	0.29
Q9D071_M	Mms19	MMS19 nu	R.LPTSVLLPYK#.S	26.64	7.10	3.75	0.27
Q9D071_M	Mms19	MMS19 nu	K.LLQAAAGASAR.A	8.96	9.57	0.94	1.07
Q9D071_M	Mms19	MMS19 nu	R.LPTSVLLPYK#.S	47.49	14.04	3.38	0.30
Q9D071_M	Mms19	MMS19 nu	K.VDSEILSAK#.L	24.62	5.02	4.90	0.20
Q99LX5_M	Mmtag2	Multiple m	R.VDSEGPSTAPTAPR.K	3.09	7.37	0.42	2.39
P51949_M	Mnat1	CDK-activa	R.LFIQKEEELQQALK.R	3.20	3.32	0.97	1.04
Q921Y0_M	Mob1a	MOB kinas	R.ELAPLQELIEK#.L	228.85	167.63	1.37	0.73
Q921Y0_M	Mob1a	MOB kinas	K.HAEATLGSGNLR.Q	11.05	31.14	0.35	2.82
Q921Y0_M	Mob1a	MOB kinas	K.HFIFFVQEFNLIDRR.E	2.03	4.50	0.45	2.22
Q921Y0_M	Mob1a	MOB kinas	K.IGVPFPK#.N	128.28	99.30	1.29	0.77
Q921Y0_M	Mob1a	MOB kinas	K.K#NIPEGSHQYELLK#.H	5.34	2.05	2.60	0.38
Q921Y0_M	Mob1a	MOB kinas	K.NIPEGSHQYELLK#.H	10.57	5.26	2.01	0.50
Q921Y0_M	Mob1a	MOB kinas	R.YEYHWADGTNIK#.K	42.82	28.30	1.51	0.66
Q921Y0_M	Mob1a	MOB kinas	R.ELAPLQELIEK#.L	21.61	13.42	1.61	0.62
Q921Y0_M	Mob1a	MOB kinas	K.IGVPFPK#.N	16.63	16.11	1.03	0.97
Q6PEB6_P	Mob4	MOB-like p	K.DNLIVPILEEEVQNSVSGESEA.-	49.55	49.55	1.00	1.00
Q6PEB6_P	Mob4	MOB-like p	K.ILEPPEGQDEGVWK#.Y	9.55	6.09	1.57	0.64
Q69ZX6_M	Morc2a	MORC fami	R.TNIVALLQK#.V	23.73	13.37	1.78	0.56
P60762_M	Morf4l1	Mortality f	R.GNTDNK#EYAVNEVVAGIK#.E	2.43	2.07	1.17	0.85
P23249_M	Mov10	Putative he	K.AQLETTLK#.S	30.28	16.41	1.84	0.54
P23249_M	Mov10	Putative he	R.EGEGGLPLQVEPEWR.N	4.38	14.20	0.31	3.24
P23249_M	Mov10	Putative he	R.EGNSPSFFNPEEAATVTSYLK#.Q	16.30	8.73	1.87	0.54
P23249_M	Mov10	Putative he	K.ETGNPGGQLVLAGDPR.Q	7.32	12.96	0.56	1.77
P23249_M	Mov10	Putative he	R.FESFLAER.G	29.99	15.20	1.97	0.51
P23249_M	Mov10	Putative he	R.GDHLFALLSSETQQDDPVTYK#.G	27.06	16.00	1.69	0.59
P23249_M	Mov10	Putative he	R.GVSLLPSDVK#.F	28.60	13.65	2.09	0.48
P23249_M	Mov10	Putative he	K.IANLAFVTK#.T	43.43	20.69	2.10	0.48
P23249_M	Mov10	Putative he	K.LDLQQGQDLLQGLSK#.L	32.36	13.52	2.39	0.42

P23249_M	Mov10	Putative he	R.LLAYNSLYK#.K	28.31	15.38	1.84	0.54
P23249_M	Mov10	Putative he	R.QLLPTLLQGPSIFTAPK#.E	18.38	9.01	2.04	0.49
P23249_M	Mov10	Putative he	K.RFNVAVTR.A	3.03	15.69	0.19	5.17
P23249_M	Mov10	Putative he	R.SLESNPEQLQAM*K#.H	28.52	18.91	1.51	0.66
P23249_M	Mov10	Putative he	K.VGSVEEFQGQER.S	11.57	33.98	0.34	2.94
P23249_M	Mov10	Putative he	R.WEGLPQQGFPIIFHGVM*GK#.D	11.87	4.35	2.73	0.37
P23249_M	Mov10	Putative he	K.AQLETTLK#.S	38.40	15.37	2.50	0.40
P23249_M	Mov10	Putative he	R.EGEGGLPLQVEPEWR.N	5.63	13.56	0.42	2.41
P23249_M	Mov10	Putative he	R.EGNSPSFFNPEEAATVTSYLK#.Q	16.68	7.67	2.17	0.46
P23249_M	Mov10	Putative he	K.ETGNPGGQLVLAGDPR.Q	5.40	10.69	0.51	1.98
P23249_M	Mov10	Putative he	R.FESFLAER.G	9.72	20.27	0.48	2.09
P23249_M	Mov10	Putative he	R.FLAAVAHSPLAAQLKPTTPFK.R	9.70	3.06	3.17	0.32
P23249_M	Mov10	Putative he	R.FVDGLTFK#.V	15.32	9.15	1.67	0.60
P23249_M	Mov10	Putative he	R.GDHLFALLSSETQQDDPVTYK#.G	26.55	10.70	2.48	0.40
P23249_M	Mov10	Putative he	R.GVSLLPSDVK#.F	27.79	14.31	1.94	0.52
P23249_M	Mov10	Putative he	K.HGVDVEVQGPHEAR.D	17.25	26.93	0.64	1.56
P23249_M	Mov10	Putative he	K.IANLAFVTK#.T	53.98	23.03	2.34	0.43
P23249_M	Mov10	Putative he	K.LDLQQGQDLLQGLSK#.L	33.27	15.84	2.10	0.48
P23249_M	Mov10	Putative he	R.LLAYNSLYK#.K	38.63	59.38	0.65	1.54
P23249_M	Mov10	Putative he	R.SLESNPEQLQAM*K#.H	21.60	16.49	1.31	0.76
P23249_M	Mov10	Putative he	R.VLITTLITASR.L	7.66	20.14	0.38	2.63
P23249_M	Mov10	Putative he	R.WADVQLPEK#.R	13.59	13.16	1.03	0.97
Q9D1Q1_M	Mphosph6	M-phase ph	R.ANYEEDENGTIK#.A	15.84	7.73	2.05	0.49
Q9D1Q1_M	Mphosph6	M-phase ph	K.M*ISDEHWYLDLPELK#.E	26.60	15.57	1.71	0.59
Q9D1Q1_M	Mphosph6	M-phase ph	R.RYETLVGTIGKK.F	7.92	23.65	0.34	2.98
Q3TYA6_M	Mphosph8	M-phase ph	K.TAQETVQEGIFEK.H	6.65	5.45	1.22	0.82
P70290_E	Mpp1	55 kDa eryt	K.FVTGDIIQIINK#.D	15.94	10.54	1.51	0.66
P70290_E	Mpp1	55 kDa eryt	K.IAILDIEPQTLK#.T	35.69	14.77	2.42	0.41
P70290_E	Mpp1	55 kDa eryt	K.ITEEPM*GITLK#.L	13.66	8.00	1.71	0.59
Q9JLB0_M	Mpp6	MAGUK p5	K.EGGSAGLIPSQFLEEK#.R	13.54	9.12	1.48	0.67
Q9JLB0_M	Mpp6	MAGUK p5	R.FIVLNPAR.F	2.97	8.08	0.37	2.72
Q9JLB0_M	Mpp6	MAGUK p5	K.IDSILEVVQTGR.T	5.67	15.51	0.37	2.73
Q9JLB0_M	Mpp6	MAGUK p5	K.LQTAIEK#.L	25.78	7.22	3.57	0.28
Q9JLB0_M	Mpp6	MAGUK p5	R.VENNDLVIAR.I	4.28	9.26	0.46	2.16
Q9JLB0_M	Mpp6	MAGUK p5	K.YLEHGEYEGNLYGTK#.I	16.74	9.00	1.86	0.54
Q9JLB0_M	Mpp6	MAGUK p5	K.YLEHGEYEGNLYGTK#.I	5.64	2.66	2.12	0.47
G5E8S8_G	Mpp7	MAGUK p5	K.HLFETDVQNNK#.F	12.72	2.99	4.25	0.24
G5E8S8_G	Mpp7	MAGUK p5	R.LIVLVGPVGVGLNELK#.R	9.35	2.34	3.99	0.25
G5E8S8_G	Mpp7	MAGUK p5	K.IIINDDLTVAFNELK#.T	7.87	1.98	3.98	0.25
P97434_M	Mprip	Myosin pho	R.LLAEETAATISAIEAM*K.N	7.67	11.91	0.64	1.55
P97434_M	Mprip	Myosin pho	K.SPEGTTVSGYDIM*K.S	4.05	6.75	0.60	1.67
P97434_M	Mprip	Myosin pho	K.TFDWAEFRPIQQALAQER.A	2.10	6.86	0.31	3.27
P97434_M	Mprip	Myosin pho	R.TLLTGDGGGESTGLPLTQGK.D	6.47	8.83	0.73	1.37
Q61216_M	Mre11a	Double-stra	R.FFIEDVVLANHPNLFNPDNPK#.V	24.51	15.42	1.59	0.63
Q61216_M	Mre11a	Double-stra	R.GMGEAVQEFVDK#EEK#DAIEELVK#.Y	10.89	7.42	1.47	0.68
Q61216_M	Mre11a	Double-stra	R.GNDTFVTFDEILR.L	5.07	23.62	0.21	4.66
Q61216_M	Mre11a	Double-stra	K.IGPIK#NEQQLFYVSQPGSSVVTSLSPGEAVK#.K	13.50	9.88	1.37	0.73
Q61216_M	Mre11a	Double-stra	K.LALYGLGSIPDER.L	7.18	15.01	0.48	2.09
Q61216_M	Mre11a	Double-stra	K.NVQLSLLTER.G	8.75	18.92	0.46	2.16
Q61216_M	Mre11a	Double-stra	K.TGEEINFGMLITKPASEGATLR.V	4.26	7.33	0.58	1.72
Q61216_M	Mre11a	Double-stra	K.VDISPVLLQK#.G	40.85	24.11	1.69	0.59
Q61216_M	Mre11a	Double-stra	R.VDYSGGFEPFNVLR.F	4.68	11.05	0.42	2.36
Q61216_M	Mre11a	Double-stra	R.VEDLVK#.Q	26.62	10.65	2.50	0.40
Q9CQL7_M	Mrfap1	MORF4 fam	K.M*AEM*LVQLVR.R	2.13	7.85	0.27	3.68
Q9CQL7_M	Mrfap1	MORF4 fam	K.TQVEASEESALNHLQGAGGAEPR.G	5.18	30.98	0.17	5.98
Q9DAT2_M	Mrgbp	MRG/MORI	K.VLTANSNPSSPSAAK#.R	6.87	2.78	2.47	0.41
Q9CQT1_M	Mri1	Methylthio	R.DLGQVAAQEAER.E	5.10	17.08	0.30	3.35
Q9CQT1_M	Mri1	Methylthio	K.IGTYQLAIVAK#.H	14.85	6.61	2.25	0.45
G3XA21_G	Mroh1	MCG13444	R.LVSTNLFYFK#.S	13.07	4.03	3.24	0.31
E9PYI4_E9	Mroh8	Protein Mr	R.SGKWLQERAGGDAR.D	1.83	12.94	0.14	7.07
Q99N96_R	Mrpl1	39S ribosor	K.IAEENGAAFAGGTDLVKK.I	3.06	50.89	0.06	16.64
Q9D1I6_R	Mrpl14	39S ribosor	K.VLAIAQNFV.-	8.24	8.24	1.00	1.00
Q8VE22_R	Mrps23	28S ribosor	K.YTELQNLGETDEEK#LFVETGK#.A	6.45	2.66	2.43	0.41
Q80ZS3_RT	Mrps26	28S ribosor	R.LQLEAQAQEVQK#.A	23.92	5.45	4.39	0.23
Q80ZS3_RT	Mrps26	28S ribosor	R.VQTPPAVDPAEFFVLTER.Y	3.35	4.05	0.83	1.21
Q9D2R8_R	Mrps33	28S ribosor	K.VVSLFSEQPLAK#.K	17.19	4.95	3.47	0.29
Q80X85_R	Mrps7	28S ribosor	K.AAAATETSSVFADPVISK#.F	8.07	2.69	3.00	0.33
Q9D0I8_M	Mrto4	mRNA turn	K.ATLTVSLDPGPLK#.Q	19.01	9.73	1.95	0.51
Q9D0I8_M	Mrto4	mRNA turn	K.EGDVLTPEQAR.I	4.98	11.35	0.44	2.28
Q9D0I8_M	Mrto4	mRNA turn	R.GEVGLLFTNR.T	10.09	17.19	0.59	1.70
Q9D0I8_M	Mrto4	mRNA turn	K.LFGYEM*AEFK#.V	12.91	7.12	1.81	0.55
Q9D0I8_M	Mrto4	mRNA turn	K.LFGYEMAEFK#.V	15.03	7.06	2.13	0.47
Q9D0I8_M	Mrto4	mRNA turn	R.SPSDEYK#DNLHQVSK#.K	43.35	25.56	1.70	0.59
Q9D0I8_M	Mrto4	mRNA turn	R.TK#EEVNEWFTK#.Y	28.97	14.69	1.97	0.51
Q9D0I8_M	Mrto4	mRNA turn	R.TKEEVNEWFTK.Y	21.76	10.41	2.09	0.48
Q9D0I8_M	Mrto4	mRNA turn	R.GEVGLLFTNR.T	5.79	11.47	0.50	1.98
Q9D0I8_M	Mrto4	mRNA turn	K.LFGYEM*AEFK#.V	8.75	5.54	1.58	0.63
Q9D0I8_M	Mrto4	mRNA turn	K.LFGYEMAEFK#.V	6.55	5.49	1.19	0.84
Q9D0I8_M	Mrto4	mRNA turn	R.TK#EEVNEWFTK#.Y	7.80	3.68	2.12	0.47
Q9D0I8_M	Mrto4	mRNA turn	R.TKEEVNEWFTK.Y	12.79	5.37	2.38	0.42
Q9D0I8_M	Mrto4	mRNA turn	K.YTEM*DFAR.A	1.61	4.13	0.39	2.56
P43247_M	Msh2	DNA misma	R.ALNLFQGSVEDTTGSQSLAALLNK#.C	48.20	21.26	2.27	0.44
P43247_M	Msh2	DNA misma	K.ASK#ENEWYLAFK#.A	8.69	3.64	2.39	0.42
P43247_M	Msh2	DNA misma	K.ASPGNLSQFEDILFGNNDM*SASVGVM*GIK#.M	14.22	3.61	3.93	0.25
P43247_M	Msh2	DNA misma	K.ASPGNLSQFEDILFGNNDM*SASVGVMGIK#.M	14.59	7.51	1.94	0.51
P43247_M	Msh2	DNA misma	K.DSLIIIDELGR.G	9.25	20.68	0.45	2.23
P43247_M	Msh2	DNA misma	K.ENEWYLAFK#.A	18.67	8.37	2.23	0.45
P43247_M	Msh2	DNA misma	K.ETLQLEGAAEAGFVR.F	11.53	27.93	0.41	2.42
P43247_M	Msh2	DNA misma	K.FTNSELSSLNEEYTK#.N	29.69	15.94	1.86	0.54
P43247_M	Msh2	DNA misma	R.GLGLDPGK#.Q	21.02	7.22	2.91	0.34
P43247_M	Msh2	DNA misma	K.IILEFLSK#.V	49.38	20.80	2.37	0.42
P43247_M	Msh2	DNA misma	K.K#GEQINSAALPEM*ENQVAVSSLSAVIK#.F	17.64	8.17	2.16	0.46
P43247_M	Msh2	DNA misma	K.K#GEQINSAALPEMENQVAVSSLSAVIK#.F	8.26	5.03	1.64	0.61
P43247_M	Msh2	DNA misma	K.LDSSAQFGYYFR.V	7.32	11.68	0.63	1.60
P43247_M	Msh2	DNA misma	R.LNLVEAFVEDSELR.Q	10.55	20.70	0.51	1.96
P43247_M	Msh2	DNA misma	R.LYQGINQLPSVIQALEK#.Y	12.15	7.22	1.68	0.59
P43247_M	Msh2	DNA misma	K.MNFESFVK#.D	16.15	5.93	2.72	0.37
P43247_M	Msh2	DNA misma	K.NK#GEYEEAQDAIVK#.E	30.67	10.74	2.85	0.35
P43247_M	Msh2	DNA misma	K.NKGEYEEAQDAIVK.E	16.30	8.97	1.82	0.55
P43247_M	Msh2	DNA misma	K.QVPFTAMSEESISAK#.L	7.57	2.87	2.64	0.38
P43247_M	Msh2	DNA misma	K.TLQSVVLSK#.M	55.72	24.69	2.26	0.44
P43247_M	Msh2	DNA misma	R.VGAGDSQLK#.G	49.24	49.67	0.99	1.01
P43247_M	Msh2	DNA misma	R.ALNLFQGSVEDTTGSQSLAALLNK#.C	94.14	33.75	2.79	0.36

P43247_M	Msh2	DNA misma	R.ALNLFQGSVEDTTGSQSLAALLNK#.C	9.46	2.51	3.77	0.27
P43247_M	Msh2	DNA misma	K.ASPGNLSQFEDILFGNNDM*SASVGVM*GIK#.M	28.84	9.54	3.02	0.33
P43247_M	Msh2	DNA misma	K.DSLIIIDELGR.G	14.83	29.30	0.51	1.98
P43247_M	Msh2	DNA misma	K.ENEWYLAFK#.A	17.37	10.68	1.63	0.61
P43247_M	Msh2	DNA misma	K.FTNSELSSLNEEYTK#.N	34.43	13.12	2.63	0.38
P43247_M	Msh2	DNA misma	R.GLGLDPGK#.Q	37.43	14.94	2.50	0.40
P43247_M	Msh2	DNA misma	R.HVGVGYVDSTQR.K	10.58	23.81	0.44	2.25
P43247_M	Msh2	DNA misma	K.IILEFLSK#.V	52.82	24.88	2.12	0.47
P43247_M	Msh2	DNA misma	K.K#GEQINSAALPEM*ENQVAVSSLSAVIK#.F	22.00	11.39	1.93	0.52
P43247_M	Msh2	DNA misma	K.K#GEQINSAALPEMENQVAVSSLSAVIK#.F	13.91	3.32	4.19	0.24
P43247_M	Msh2	DNA misma	K.LDSSAQFGYYFR.V	6.82	12.49	0.55	1.83
P43247_M	Msh2	DNA misma	R.LNLVEAFVEDSELR.Q	12.23	18.36	0.67	1.50
P43247_M	Msh2	DNA misma	R.LYQGINQLPSVIQALEK#.Y	33.45	14.89	2.25	0.45
P43247_M	Msh2	DNA misma	R.LYQGINQLPSVIQALEK#.Y	18.67	6.73	2.77	0.36
P43247_M	Msh2	DNA misma	K.MNFESFVK#.D	10.42	4.07	2.56	0.39
P43247_M	Msh2	DNA misma	K.NFSTVDIQK#.N	47.98	20.16	2.38	0.42
P43247_M	Msh2	DNA misma	K.NK#GEYEEAQDAIVK#.E	18.58	7.94	2.34	0.43
P43247_M	Msh2	DNA misma	K.QVPFTAM*SEESISAK#.L	17.21	10.10	1.70	0.59
P43247_M	Msh2	DNA misma	K.QVPFTAMSEESISAK#.L	5.56	2.76	2.01	0.50
P43247_M	Msh2	DNA misma	K.TLQSVVLSK#.M	58.75	22.33	2.63	0.38
P43247_M	Msh2	DNA misma	R.VGAGDSQLK#.G	35.11	18.86	1.86	0.54
P54276_M	Msh6	DNA misma	R.AIM*YEETTYSK#.K	14.26	5.56	2.56	0.39
P54276_M	Msh6	DNA misma	R.LANLPEEVIQK#.G	30.70	15.79	1.94	0.51
P54276_M	Msh6	DNA misma	R.SAAVSASSPEAK#.D	13.07	5.14	2.54	0.39
P54276_M	Msh6	DNA misma	R.TLVAHYPPVQILFEK#.G	14.40	5.99	2.41	0.42
P54276_M	Msh6	DNA misma	R.VEQTETPEM*M*EAR.C	3.31	4.74	0.70	1.43
P54276_M	Msh6	DNA misma	K.VSGLLEEVAGGFTSK#.T	16.80	8.30	2.02	0.49
P54276_M	Msh6	DNA misma	R.AIM*YEETTYSK#.K	44.30	16.33	2.71	0.37
P54276_M	Msh6	DNA misma	R.AIMYEETTYSK#.K	13.27	6.17	2.15	0.46
P54276_M	Msh6	DNA misma	R.FSDSLVQK#.G	68.58	64.24	1.07	0.94
P54276_M	Msh6	DNA misma	K.GRFPDLTAELQR.W	1.94	10.63	0.18	5.48
P54276_M	Msh6	DNA misma	R.GTATFDGTAIANAVVK#.E	56.09	18.17	3.09	0.32
P54276_M	Msh6	DNA misma	K.GTQTYSVLDGDPSENYSR.Y	6.41	11.01	0.58	1.72
P54276_M	Msh6	DNA misma	K.IHNVGSPLK#.S	25.60	10.72	2.39	0.42
P54276_M	Msh6	DNA misma	R.LANLPEEVIQK#.G	91.37	36.95	2.47	0.40
P54276_M	Msh6	DNA misma	R.LDAVEDLM*AVPDK#VTEVADLLK#.K	15.27	9.08	1.68	0.59
P54276_M	Msh6	DNA misma	R.QSTLYSFFPK#.S	16.35	11.36	1.44	0.69
P54276_M	Msh6	DNA misma	R.SAAVSASSPEAK#.D	41.70	15.01	2.78	0.36
P54276_M	Msh6	DNA misma	K.SPALGDTK#K#.A	11.61	6.31	1.84	0.54
P54276_M	Msh6	DNA misma	K.SQNFDLVIFYK#.V	21.11	11.54	1.83	0.55
P54276_M	Msh6	DNA misma	R.TLVAHYPPVQILFEK#.G	40.99	17.24	2.38	0.42
P54276_M	Msh6	DNA misma	R.VEQTETPEM*M*EAR.C	5.97	8.37	0.71	1.40
P54276_M	Msh6	DNA misma	K.VSGLLEEVAGGFTSK#.T	83.02	27.65	3.00	0.33
Q61474_M	Msi1	RNA-bindin	R.GFGFVTFM*DQAGVDK#.V	5.03	3.33	1.51	0.66
Q61474_M	Msi1	RNA-bindin	R.GFGFVTFMDQAGVDK#.V	7.24	4.35	1.66	0.60
Q61474_M	Msi1	RNA-bindin	K.HYFEQFGK#.V	12.18	7.49	1.63	0.61
Q920Q6_	Msi2	RNA-bindin	K.IFVGGLSANTVVEDVK#.Q	32.29	25.77	1.25	0.80
Q920Q6_	Msi2	RNA-bindin	K.VEDAM*LM*FDK#.T	6.24	5.99	1.04	0.96
Q920Q6_	Msi2	RNA-bindin	K.VLGQPHHELDSK.T	7.78	10.24	0.76	1.32
Q69ZF8_M	Msl2	E3 ubiquiti	K.K#SHEHGSK#.K	9.57	3.42	2.80	0.36
Q2YDW2_	Msto1	Protein mis	K.GAAVQSIPVFGALR.S	9.13	17.05	0.54	1.87
Q2YDW2_	Msto1	Protein mis	K.GLAM*DSTPK#.G	6.82	5.16	1.32	0.76
Q2YDW2_	Msto1	Protein mis	R.GVLTWGLLPGPYSLGEPQK#.N	8.81	8.81	1.00	1.00
Q2YDW2_	Msto1	Protein mis	K.NPNLQGLLSAEGVR.S	3.86	11.88	0.32	3.08
Q2YDW2_	Msto1	Protein mis	K.TAELLQDEYAGR.G	4.29	11.79	0.36	2.74
Q2YDW2_	Msto1	Protein mis	R.TLGDLAEELSR.L	5.10	9.36	0.55	1.83
F8WHY8_F	Mta1	Metastasis-	R.DISSSLIALADK#.H	9.78	5.29	1.85	0.54
F8WHY8_F	Mta1	Metastasis-	R.DISSSLIALADK#.H	41.09	23.97	1.71	0.58
F8WHY8_F	Mta1	Metastasis-	R.EVEEEVENPEM*VDLPEK#.L	5.75	5.20	1.10	0.91
F8WHY8_F	Mta1	Metastasis-	R.LPEASQSPLVLK#.Q	34.04	23.60	1.44	0.69
F8WHY8_F	Mta1	Metastasis-	K.QVYIPNYNK#PNPNQISASSVK#.A	17.18	9.77	1.76	0.57
F8WHY8_F	Mta1	Metastasis-	K.SSSSVLSSLTPAK#.S	29.96	18.89	1.59	0.63
F8WHY8_F	Mta1	Metastasis-	K.YGK#DFTDIQQDFLPWK#.S	16.96	15.11	1.12	0.89
F8WHY8_F	Mta1	Metastasis-	R.DISSSLIALADK#.H	13.47	5.68	2.37	0.42
Q9R190_M	Mta2	Metastasis-	R.DISSSLNSLADSNAR.E	5.31	12.71	0.42	2.40
Q9R190_M	Mta2	Metastasis-	K.DLVAQAPLK#PK#.T	13.82	11.00	1.26	0.80
Q9R190_M	Mta2	Metastasis-	R.EFEEESKQPGVSEQQR.H	6.00	16.99	0.35	2.83
Q9R190_M	Mta2	Metastasis-	K.LNPADAPNPVVFVATK#.D	10.18	8.75	1.16	0.86
Q9R190_M	Mta2	Metastasis-	R.LPLATIVK#.D	34.08	22.29	1.53	0.65
Q9R190_M	Mta2	Metastasis-	K.TPTQLEGAAR.G	13.44	23.31	0.58	1.73
Q9R190_M	Mta2	Metastasis-	R.VGDYVYFENSSSNPYLVR.R	3.59	11.92	0.30	3.32
Q9R190_M	Mta2	Metastasis-	R.VGDYVYFENSSSNPYLVR.R	1.86	3.19	0.59	1.71
Q9R190_M	Mta2	Metastasis-	R.DISSSLNSLADSNAR.E	8.11	19.75	0.41	2.44
Q9R190_M	Mta2	Metastasis-	K.DLVAQAPLK#PK#.T	41.52	24.53	1.69	0.59
Q9R190_M	Mta2	Metastasis-	R.EFEEESKQPGVSEQQR.H	15.40	35.36	0.44	2.30
Q9R190_M	Mta2	Metastasis-	R.GLGGIM*VK#.R	27.14	13.74	1.98	0.51
Q9R190_M	Mta2	Metastasis-	K.LNPADAPNPVVFVATK#.D	33.60	22.10	1.52	0.66
Q9R190_M	Mta2	Metastasis-	R.QK#LNPADAPNPVVFVATK#.D	16.38	8.66	1.89	0.53
Q9R190_M	Mta2	Metastasis-	K.TLLADQGEIR.V	14.28	33.21	0.43	2.33
Q9R190_M	Mta2	Metastasis-	K.TPTQLEGAAR.G	22.50	62.60	0.36	2.78
Q9R190_M	Mta2	Metastasis-	R.VGDYVYFENSSSNPYLVR.R	6.75	15.43	0.44	2.29
Q924K8_M	Mta3	Metastasis-	R.DISNTLIM*LADK#.H	7.16	5.58	1.28	0.78
Q924K8_M	Mta3	Metastasis-	K.QIDQFLVVAR.S	6.48	15.81	0.41	2.44
Q924K8_M	Mta3	Metastasis-	R.VGDYVYFENSSSNPYLIR.R	2.38	7.05	0.34	2.96
Q924K8_M	Mta3	Metastasis-	K.ETEEESETPVEADLTEK#.Q	7.68	5.00	1.54	0.65
Q924K8_M	Mta3	Metastasis-	R.VGDYVYFENSSSNPYLIR.R	3.18	9.59	0.33	3.01
Q924K8_M	Mta3	Metastasis-	K.ETEEESETPVEADLTEK#.Q	12.45	7.81	1.59	0.63
Q924K8_M	Mta3	Metastasis-	R.VGDYVYFENSSSNPYLIR.R	1.93	7.09	0.27	3.67
Q9CQ65_	Mtap	S-methyl-5'	K.IGIIGGTGLDDPEILEGR.T	1.77	7.46	0.24	4.22
Q922D8_C	Mthfd1	C-1-tetrahy	R.ASQAPSSFQLLYDLK#.L	18.90	5.61	3.37	0.30
Q922D8_C	Mthfd1	C-1-tetrahy	K.AYTEEDLDLVEK#.G	9.63	3.86	2.50	0.40
Q922D8_C	Mthfd1	C-1-tetrahy	K.TDPTTLTDDEINR.F	3.16	6.98	0.45	2.20
Q922D8_C	Mthfd1	C-1-tetrahy	K.AAEEIGIK#.A	101.23	45.97	2.20	0.45
Q922D8_C	Mthfd1	C-1-tetrahy	R.ASQAPSSFQLLYDLK#.L	135.57	49.72	2.73	0.37
Q922D8_C	Mthfd1	C-1-tetrahy	K.AYTEEDLDLVEK#.G	129.79	51.32	2.53	0.40
Q922D8_C	Mthfd1	C-1-tetrahy	K.DAIKPNLM*QTLEGTPVFVHAGPFANIAHGNSSIIADR.I	3.42	3.14	1.09	0.92
Q922D8_C	Mthfd1	C-1-tetrahy	K.DVDGLTSVSAGK#.L	12.35	5.24	2.36	0.42
Q922D8_C	Mthfd1	C-1-tetrahy	R.EIGLLTEEVELYGETK#.A	99.51	36.39	2.73	0.37
Q922D8_C	Mthfd1	C-1-tetrahy	K.FSDIQIR.R	15.50	25.00	0.62	1.61
Q922D8_C	Mthfd1	C-1-tetrahy	R.IFHELTQTDK#.A	128.59	58.82	2.19	0.46
Q922D8_C	Mthfd1	C-1-tetrahy	K.ITIGQSPTEK#.G	56.75	24.04	2.36	0.42
Q922D8_C	Mthfd1	C-1-tetrahy	R.IYGADDIELLPEAQNK#.A	74.29	32.09	2.31	0.43
Q922D8_C	Mthfd1	C-1-tetrahy	R.IYGADDIELLPEAQNK#AEIYTK#.Q	20.63	6.47	3.19	0.31

Q922D8_C	Mthfd1	C-1-tetrahy	R.K#ITIGQSPTEK#.G	70.33	27.62	2.55	0.39
Q922D8_C	Mthfd1	C-1-tetrahy	R.K#VVGDVAYDEAK#.E	37.33	15.40	2.42	0.41
Q922D8_C	Mthfd1	C-1-tetrahy	R.LDIDPETITWQR.V	25.98	47.27	0.55	1.82
Q922D8_C	Mthfd1	C-1-tetrahy	K.LK#AAEEIGIK#.A	23.11	9.91	2.33	0.43
Q922D8_C	Mthfd1	C-1-tetrahy	K.LVGPEGFVVTEAGFGADIGM*EK#.F	86.40	37.85	2.28	0.44
Q922D8_C	Mthfd1	C-1-tetrahy	K.LVGPEGFVVTEAGFGADIGMEK#.F	20.67	8.49	2.44	0.41
Q922D8_C	Mthfd1	C-1-tetrahy	R.M*FGVPVVVAVNVFK#.T	99.92	40.02	2.50	0.40
Q922D8_C	Mthfd1	C-1-tetrahy	K.TDPTTLTDDEINR.F	37.95	62.32	0.61	1.64
Q922D8_C	Mthfd1	C-1-tetrahy	K.TDTDAELDLVSR.L	10.94	55.98	0.20	5.11
Q922D8_C	Mthfd1	C-1-tetrahy	K.THLSLSHNPEQK#.G	156.17	63.93	2.44	0.41
Q922D8_C	Mthfd1	C-1-tetrahy	K.TPVPSDIAISR.S	43.88	74.05	0.59	1.69
Q922D8_C	Mthfd1	C-1-tetrahy	K.VLLSALDR.L	33.34	64.07	0.52	1.92
Q922D8_C	Mthfd1	C-1-tetrahy	K.VVGDVAYDEAK#.E	71.65	26.07	2.75	0.36
Q922D8_C	Mthfd1	C-1-tetrahy	K.WTIQYNK#.L	73.36	28.85	2.54	0.39
Q922D8_C	Mthfd1	C-1-tetrahy	R.YSGLQPHVVVLVATVR.A	9.55	18.74	0.51	1.96
Q922D8_C	Mthfd1	C-1-tetrahy	K.YVVVTGITPTPLGEGK#.S	126.44	58.06	2.18	0.46
Q922D8_C	Mthfd1	C-1-tetrahy	R.ASQAPSSFQLLYDLK#.L	43.95	14.41	3.05	0.33
Q922D8_C	Mthfd1	C-1-tetrahy	K.AYTEEDLDLVEK#.G	35.38	16.86	2.10	0.48
Q922D8_C	Mthfd1	C-1-tetrahy	R.EIGLLTEEVELYGETK#.A	26.15	8.71	3.00	0.33
Q922D8_C	Mthfd1	C-1-tetrahy	K.GVPTGFVLPIR.D	9.97	24.06	0.41	2.41
Q922D8_C	Mthfd1	C-1-tetrahy	K.ITIGQSPTEK#.G	20.95	7.48	2.80	0.36
Q922D8_C	Mthfd1	C-1-tetrahy	R.IYGADDIELLPEAQNK#.A	26.66	12.24	2.18	0.46
Q922D8_C	Mthfd1	C-1-tetrahy	R.K#VVGDVAYDEAK#.E	8.45	1.46	5.78	0.17
Q922D8_C	Mthfd1	C-1-tetrahy	R.LDIDPETITWQR.V	5.99	11.24	0.53	1.88
Q922D8_C	Mthfd1	C-1-tetrahy	K.LVGPEGFVVTEAGFGADIGM*EK#.F	37.04	14.52	2.55	0.39
Q922D8_C	Mthfd1	C-1-tetrahy	R.M*FGVPVVVAVNVFK#.T	28.22	12.88	2.19	0.46
Q922D8_C	Mthfd1	C-1-tetrahy	K.TDTDAELDLVSR.L	7.61	16.98	0.45	2.23
Q922D8_C	Mthfd1	C-1-tetrahy	K.VLLSALDR.L	8.97	33.46	0.27	3.73
Q922D8_C	Mthfd1	C-1-tetrahy	K.VVGDVAYDEAK#.E	16.56	7.19	2.30	0.43
Q922D8_C	Mthfd1	C-1-tetrahy	K.YVVVTGITPTPLGEGK#.S	38.38	14.91	2.57	0.39
Q3V3R1_C	Mthfd1l	Monofunct	K.DIELSPEAQSK#.I	18.52	6.06	3.06	0.33
Q3V3R1_C	Mthfd1l	Monofunct	K.EIGLLADEIEIYGK#.S	20.17	6.20	3.25	0.31
Q3V3R1_C	Mthfd1l	Monofunct	K.EVLSLLQEK#.N	15.73	4.43	3.55	0.28
Q3V3R1_C	Mthfd1l	Monofunct	R.FQFLYDVQLPIVEK#.I	19.84	4.96	4.00	0.25
Q3V3R1_C	Mthfd1l	Monofunct	K.LIAEESVSLLAAALR.I	10.12	8.92	1.13	0.88
Q3V3R1_C	Mthfd1l	Monofunct	R.LNIDPATITWQR.V	3.52	8.09	0.43	2.30
Q3V3R1_C	Mthfd1l	Monofunct	K.LQPLSPVPSDIEISR.G	6.05	7.57	0.80	1.25
Q3V3R1_C	Mthfd1l	Monofunct	K.LSGGSPGVPVDK#.L	34.34	18.92	1.82	0.55
Q3V3R1_C	Mthfd1l	Monofunct	R.VHGLTLQISEDSLSNK#.V	15.28	6.83	2.24	0.45
Q3V3R1_C	Mthfd1l	Monofunct	R.VIAQTVYGAK#.D	42.43	13.55	3.13	0.32
Q3V3R1_C	Mthfd1l	Monofunct	K.YVLVAGITPTPLGEGK#.S	22.67	9.68	2.34	0.43
Q3V3R1_C	Mthfd1l	Monofunct	K.EIGLLADEIEIYGK#.S	8.04	2.43	3.30	0.30
Q3V3R1_C	Mthfd1l	Monofunct	K.YVLVAGITPTPLGEGK#.S	9.69	4.63	2.09	0.48
P18155_M	Mthfd2	Bifunction	K.LVGDVDFEGVK#.K	14.48	6.61	2.19	0.46
Q9JLN9_M	Mtor	Serine/thre	K.GPTPAILESLISINNK#.L	9.78	4.86	2.01	0.50
Q5HZI1_M	Mtus1	Microtubul	K.GEPTNM*PK#PNLGK#.S	36.23	1.19	30.42	0.03
Q5HZI1_M	Mtus1	Microtubul	K.HMAISR@QLSTEQAALQESLEK.E	1.84	5.01	0.37	2.73
Q6DID5_M	Mum1	PWWP do	R.LDGGQNPPTR.Q	2.08	9.43	0.22	4.54
A2AMM0_	Murc	Muscle-rel	K.GGYSPQEGGDPPTPEPLK.V	5.25	6.77	0.78	1.29
A2AMM0_	Murc	Muscle-rel	K.LSQSHSNTGYVVNK#.L	7.85	14.03	0.56	1.79
A2AMM0_	Murc	Muscle-rel	R.LSSVTEDEDQDAALTIVTVLDR.V	1.95	11.87	0.16	6.07
A2AMM0_	Murc	Muscle-rel	R.VASVVDSVQASQK.R	20.07	28.81	0.70	1.44
A2AMM0_	Murc	Muscle-rel	R.VEDDESLLLELK.Q	9.09	10.73	0.85	1.18
Q9EQK5_M	Mvp	Major vault	K.ALQPLEEGEGEEK#.V	15.91	3.86	4.12	0.24
Q9EQK5_M	Mvp	Major vault	K.AQQLADVEAK#.K	22.80	12.53	1.82	0.55
Q9EQK5_M	Mvp	Major vault	R.AVIGSTYM*LTQDEVLWEK#.E	2.40	1.80	1.33	0.75
Q9EQK5_M	Mvp	Major vault	K.DITPLQVVLPNTALHLK#.A	18.49	6.72	2.75	0.36
Q9EQK5_M	Mvp	Major vault	K.EVEVVEIIQATVIK#.Q	9.30	2.76	3.37	0.30
Q9EQK5_M	Mvp	Major vault	R.GAVASVTFDDFHK#.N	28.96	16.06	1.80	0.55
Q9EQK5_M	Mvp	Major vault	R.GIQDVYVLSEQQGLLLK#.A	11.13	2.19	5.09	0.20
Q9EQK5_M	Mvp	Major vault	R.IEGEGSVLQAK#.L	23.45	7.55	3.11	0.32
Q9EQK5_M	Mvp	Major vault	R.LAQDPFPLYPGELLEK.D	16.88	11.59	1.46	0.69
Q9EQK5_M	Mvp	Major vault	R.QAIPLDQNEGIYVQDVK#.T	5.29	3.17	1.67	0.60
O35682_M	Myadm	Myeloid-as	R.ALTQPLGLLR.L	9.20	36.54	0.25	3.97
O35682_M	Myadm	Myeloid-as	R.TTITTTTSSSTTVGSAR.A	8.51	34.05	0.25	4.00
Q7TPV4_M	Mybbp1a	Myb-bindi	K.AEPATPAEAAQSDR.H	3.06	9.63	0.32	3.15
Q7TPV4_M	Mybbp1a	Myb-bindi	R.ALDLIEVLVTK#.Q	12.81	2.80	4.58	0.22
Q7TPV4_M	Mybbp1a	Myb-bindi	K.ATQTLQTLGEAQSK#.G	13.74	3.95	3.48	0.29
Q7TPV4_M	Mybbp1a	Myb-bindi	K.LPNVALDLLR.L	4.51	11.43	0.39	2.53
Q7TPV4_M	Mybbp1a	Myb-bindi	K.LSVDLTAPLGVLQSK#.Q	12.84	7.71	1.67	0.60
Q7TPV4_M	Mybbp1a	Myb-bindi	K.NAASQQDAVTEGAMPAATGK#.D	6.99	3.64	1.92	0.52
Q7TPV4_M	Mybbp1a	Myb-bindi	R.NVTSVTSLTTQQR.Q	5.95	4.60	1.29	0.77
Q7TPV4_M	Mybbp1a	Myb-bindi	K.SPAPSNPTLSPSTPAK.T	9.41	9.35	1.01	0.99
Q7TPV4_M	Mybbp1a	Myb-bindi	K.YLELFLLAK#.Q	13.22	5.56	2.38	0.42
Q7TPV4_M	Mybbp1a	Myb-bindi	K.AEPATPAEAAQSDR.H	11.82	33.77	0.35	2.86
Q7TPV4_M	Mybbp1a	Myb-bindi	R.ALDLIEVLVTK#.Q	95.55	51.18	1.87	0.54
Q7TPV4_M	Mybbp1a	Myb-bindi	R.AQDASLNVPER.A	17.03	52.91	0.32	3.11
Q7TPV4_M	Mybbp1a	Myb-bindi	K.ATQTLQTLGEAQSK#.G	70.71	36.50	1.94	0.52
Q7TPV4_M	Mybbp1a	Myb-bindi	R.EFLDFFWDIAKPDQETR.L	7.87	20.16	0.39	2.56
Q7TPV4_M	Mybbp1a	Myb-bindi	R.FELFWK#.K	28.85	12.46	2.31	0.43
Q7TPV4_M	Mybbp1a	Myb-bindi	R.FLNAEALQSYVAWLR.D	3.49	11.29	0.31	3.23
Q7TPV4_M	Mybbp1a	Myb-bindi	R.HFGENM*VISK#PQNLFK#.I	20.02	10.32	1.94	0.52
Q7TPV4_M	Mybbp1a	Myb-bindi	R.HFGENMVISKPQNLFK.I	15.40	6.54	2.35	0.42
Q7TPV4_M	Mybbp1a	Myb-bindi	K.ILSQHPNHLQGQPIK#.A	39.55	24.29	1.63	0.61
Q7TPV4_M	Mybbp1a	Myb-bindi	R.K#SPHPQSALPK#.K	3.90	1.47	2.65	0.38
Q7TPV4_M	Mybbp1a	Myb-bindi	R.LITGLGVGR.E	15.84	41.33	0.38	2.61
Q7TPV4_M	Mybbp1a	Myb-bindi	R.LLGASLPLLSEEQLQLVM*R.G	13.05	25.14	0.52	1.93
Q7TPV4_M	Mybbp1a	Myb-bindi	K.LPNVALDLLR.L	13.14	37.02	0.35	2.82
Q7TPV4_M	Mybbp1a	Myb-bindi	K.LSVDLTAPLGVLQSK#.Q	89.18	50.10	1.78	0.56
Q7TPV4_M	Mybbp1a	Myb-bindi	R.LVQLADMLLNHNR.N	7.11	16.98	0.42	2.39
Q7TPV4_M	Mybbp1a	Myb-bindi	K.NAASQQDAVTEGAM*PAATGK#.D	12.43	8.39	1.48	0.67
Q7TPV4_M	Mybbp1a	Myb-bindi	K.NAASQQDAVTEGAMPAATGK#.D	14.49	8.09	1.79	0.56
Q7TPV4_M	Mybbp1a	Myb-bindi	R.NVTSVTSLTTQQR.Q	25.62	54.02	0.47	2.11
Q7TPV4_M	Mybbp1a	Myb-bindi	K.SPAPSNPTLSPSTPAK#.T	43.37	34.92	1.24	0.81
Q7TPV4_M	Mybbp1a	Myb-bindi	K.VLEEGLLK#.N	45.91	23.89	1.92	0.52
Q7TPV4_M	Mybbp1a	Myb-bindi	K.YLELFLLAK#.Q	24.98	10.05	2.49	0.40
Q7TPV4_M	Mybbp1a	Myb-bindi	K.YSLQAM*NK#.A	20.68	10.81	1.91	0.52
Q7TPV4_M	Mybbp1a	Myb-bindi	K.AEPATPAEAAQSDR.H	42.28	117.16	0.36	2.77
Q7TPV4_M	Mybbp1a	Myb-bindi	R.ALDLIEVLVTK#.Q	250.04	119.83	2.09	0.48
Q7TPV4_M	Mybbp1a	Myb-bindi	R.AQDASLNVPER.A	58.52	144.41	0.41	2.47
Q7TPV4_M	Mybbp1a	Myb-bindi	K.ATPQIPETK#.Q	172.80	105.18	1.64	0.61
Q7TPV4_M	Mybbp1a	Myb-bindi	K.ATQTLQTLGEAQSK#.G	232.53	113.46	2.05	0.49
Q7TPV4_M	Mybbp1a	Myb-bindi	K.DIPSDTQSPVSTK#.R	133.00	65.05	2.04	0.49

Q7TPV4_M	Mybbp1a	Myb-bindir	R.DM*FLQPDLNSLVDFSTANQK#.R	110.84	53.32	2.08	0.48
Q7TPV4_M	Mybbp1a	Myb-bindir	R.DMFLQPDLNSLVDFSTANQK#.R	23.56	20.86	1.13	0.89
Q7TPV4_M	Mybbp1a	Myb-bindir	R.FELFWK#.K	45.87	25.81	1.78	0.56
Q7TPV4_M	Mybbp1a	Myb-bindir	R.FLNAEALQSYVAWLR.D	11.40	30.78	0.37	2.70
Q7TPV4_M	Mybbp1a	Myb-bindir	K.GSTK#QEQDLLHK#.T	11.42	16.40	0.70	1.44
Q7TPV4_M	Mybbp1a	Myb-bindir	R.HFGENM*VISK#PQNLFK#.I	58.05	35.06	1.66	0.60
Q7TPV4_M	Mybbp1a	Myb-bindir	K.ILSQHPNHLQGQPIK#.A	136.45	70.06	1.95	0.51
Q7TPV4_M	Mybbp1a	Myb-bindir	K.K#ATPQIPETK#.Q	55.92	26.17	2.14	0.47
Q7TPV4_M	Mybbp1a	Myb-bindir	K.K#GFLPETK#.K	45.79	16.42	2.79	0.36
Q7TPV4_M	Mybbp1a	Myb-bindir	K.K#VLEEGLLK#.N	48.31	23.58	2.05	0.49
Q7TPV4_M	Mybbp1a	Myb-bindir	R.LITGLGVGR.E	59.28	144.41	0.41	2.44
Q7TPV4_M	Mybbp1a	Myb-bindir	K.LK#SEGTTPEK#.N	23.68	15.04	1.57	0.64
Q7TPV4_M	Mybbp1a	Myb-bindir	K.LLEYLR.T	35.73	74.26	0.48	2.08
Q7TPV4_M	Mybbp1a	Myb-bindir	R.LLGASLPLLSEEQLQLVM*R.G	46.73	108.46	0.43	2.32
Q7TPV4_M	Mybbp1a	Myb-bindir	K.LPNVALDLLR.L	66.05	140.55	0.47	2.13
Q7TPV4_M	Mybbp1a	Myb-bindir	K.LSQVNGATPVSPIEPESK#.K	14.80	6.70	2.21	0.45
Q7TPV4_M	Mybbp1a	Myb-bindir	K.LSVDLTAPLGVLQSK#.Q	325.85	181.38	1.80	0.56
Q7TPV4_M	Mybbp1a	Myb-bindir	K.LSVDLTAPLGVLQSK#.Q	35.84	21.29	1.68	0.59
Q7TPV4_M	Mybbp1a	Myb-bindir	R.LVQLADMLLNHNR.N	14.06	34.12	0.41	2.43
Q7TPV4_M	Mybbp1a	Myb-bindir	R.LYDLYWQAMR.M	5.96	13.77	0.43	2.31
Q7TPV4_M	Mybbp1a	Myb-bindir	R.M*LGVQRPK.S	6.52	19.68	0.33	3.02
Q7TPV4_M	Mybbp1a	Myb-bindir	K.NAASQQDAVTEGAM*PAATGK#.D	28.91	15.17	1.91	0.52
Q7TPV4_M	Mybbp1a	Myb-bindir	K.NAASQQDAVTEGAMPAATGK#.D	37.51	22.29	1.68	0.59
Q7TPV4_M	Mybbp1a	Myb-bindir	K.NAASQQDAVTEGAM*PAATGK#DQPPSTGK#.K	14.89	10.77	1.38	0.72
Q7TPV4_M	Mybbp1a	Myb-bindir	R.NVTSVTSLTTQQR.Q	62.70	142.09	0.44	2.27
Q7TPV4_M	Mybbp1a	Myb-bindir	R.QAWDQM*M*STLK#.E	39.38	16.23	2.43	0.41
Q7TPV4_M	Mybbp1a	Myb-bindir	K.SPAPSNPTLSPSTPAK#.T	240.18	133.23	1.80	0.55
Q7TPV4_M	Mybbp1a	Myb-bindir	R.SPSLLQSGVK#.K	184.90	87.81	2.11	0.47
Q7TPV4_M	Mybbp1a	Myb-bindir	K.SPTKAEPATPAEAAQSDR.H	11.22	27.79	0.40	2.48
Q7TPV4_M	Mybbp1a	Myb-bindir	K.VLEEGLLK#.N	123.32	60.88	2.03	0.49
Q7TPV4_M	Mybbp1a	Myb-bindir	R.VYSASLESLLTK#.R	229.86	105.74	2.17	0.46
Q7TPV4_M	Mybbp1a	Myb-bindir	K.YSLQAM*NK#.A	82.02	42.63	1.92	0.52
Q7TPV4_M	Mybbp1a	Myb-bindir	K.YSLQAMNK#.A	39.28	5.62	6.99	0.14
Q9EQS3_M	Mycbp	C-Myc-bind	K.HHLGAATPENPEIELLR.L	3.37	10.22	0.33	3.04
Q9EQS3_M	Mycbp	C-Myc-bind	K.LVQYEPPQEEK#.R	70.78	54.43	1.30	0.77
Q9EQS3_M	Mycbp	C-Myc-bind	K.SGVLDTLTK#.V	59.16	35.75	1.65	0.60
Q9EQS3_M	Mycbp	C-Myc-bind	K.VLVALYEEPEK#PTSALDFLK#.H	75.91	50.61	1.50	0.67
Q9EQS3_M	Mycbp	C-Myc-bind	K.VLVALYEEPEKPTSALDFLK.H	4.94	1.94	2.55	0.39
Q8C854_M	Myef2	Myelin expi	R.EK#VGEVTYVELFK#.D	23.31	21.67	1.08	0.93
Q8C854_M	Myef2	Myelin expi	R.EKVGEVTYVELFK.D	10.04	9.01	1.11	0.90
Q8C854_M	Myef2	Myelin expi	R.EK#VGEVTYVELFK#DAEGK#.S	8.82	6.49	1.36	0.74
Q8C854_M	Myef2	Myelin expi	K.EVFSIAGTVK#.R	47.37	48.98	0.97	1.03
Q8C854_M	Myef2	Myelin expi	R.FESAESAEK#.A	55.60	56.99	0.98	1.02
Q8C854_M	Myef2	Myelin expi	R.GFLSGPM*GSGM*R.D	13.50	55.29	0.24	4.10
Q8C854_M	Myef2	Myelin expi	K.GNQIFVR.N	30.82	138.88	0.22	4.51
Q8C854_M	Myef2	Myelin expi	R.IGGGVGFGGLEAMNSM*AGFGGVGR.M	1.66	3.61	0.46	2.17
Q8C854_M	Myef2	Myelin expi	R.IGGGVGFGGLEAMNSMAGFGGVGR.M	2.16	5.91	0.37	2.74
Q8C854_M	Myef2	Myelin expi	R.IMNGIK#ISGR.E	4.75	14.78	0.32	3.12
Q8C854_M	Myef2	Myelin expi	R.LGSAM*IGGFAGR.I	8.05	41.63	0.19	5.17
Q8C854_M	Myef2	Myelin expi	R.LGSAMIGGFAGR.I	4.51	21.03	0.21	4.67
Q8C854_M	Myef2	Myelin expi	R.LGSTIFVANLDFK#.V	119.70	100.62	1.19	0.84
Q8C854_M	Myef2	Myelin expi	K.LK#EVFSIAGTVK#.R	26.30	27.36	0.96	1.04
Q8C854_M	Myef2	Myelin expi	K.M*ENDESVKEEK.S	5.35	6.83	0.78	1.28
Q8C854_M	Myef2	Myelin expi	K.MENDESVK#EEK#.S	14.46	10.71	1.35	0.74
Q8C854_M	Myef2	Myelin expi	R.M*GPGIGAILER.S	27.69	137.47	0.20	4.96
Q8C854_M	Myef2	Myelin expi	R.MGPGIGAILER.S	11.50	64.42	0.18	5.60
Q8C854_M	Myef2	Myelin expi	R.NLPFDLTWQK#.L	101.23	99.35	1.02	0.98
Q8C854_M	Myef2	Myelin expi	K.SEAAAGDDGSQQQPAEPR.R	3.57	12.32	0.29	3.45
Q8C854_M	Myef2	Myelin expi	R.TGTSFQGSHASDVGSGLVNLPPSILNNPNIPPEVISNLQAGR.L	2.21	2.87	0.77	1.30
Q8C854_M	Myef2	Myelin expi	R.VFISNIPYDM*K#.W	68.27	67.32	1.01	0.99
Q8C854_M	Myef2	Myelin expi	R.VFISNIPYDMK#.W	59.34	56.62	1.05	0.95
Q8C854_M	Myef2	Myelin expi	K.VGEVTYVELFK#.D	87.90	93.45	0.94	1.06
Q8C854_M	Myef2	Myelin expi	K.VGEVTYVELFK#DAEGK#.S	20.39	19.86	1.03	0.97
Q8C854_M	Myef2	Myelin expi	R.FESAESAEK.A	17.96	18.44	0.97	1.03
Q8C854_M	Myef2	Myelin expi	R.GFGDSFGR.L	5.31	29.51	0.18	5.56
Q8C854_M	Myef2	Myelin expi	R.LGSAM*IGGFAGR.I	3.78	13.94	0.27	3.68
Q8C854_M	Myef2	Myelin expi	R.LGSTIFVANLDFK#.V	30.41	30.60	0.99	1.01
Q8C854_M	Myef2	Myelin expi	R.M*GPGIGAILER.S	6.32	28.83	0.22	4.56
Q8C854_M	Myef2	Myelin expi	R.MGPGIGAILER.S	3.97	12.68	0.31	3.20
Q8C854_M	Myef2	Myelin expi	R.VFISNIPYDMK.W	14.36	15.73	0.91	1.10
Q8C854_M	Myef2	Myelin expi	K.VGEVTYVELFK.D	19.29	20.54	0.94	1.07
Q3U898_M	Myeov2	Myeloma-o	K.AVHADFFNDFEDLFDDDDVQ.-	22.38	22.38	1.00	1.00
Q61879_M	Myh10	Myosin-10	K.ADEWLM*K#.N	137.58	80.26	1.71	0.58
Q61879_M	Myh10	Myosin-10	K.ADEWLMK#.N	41.39	22.17	1.87	0.54
Q61879_M	Myh10	Myosin-10	R.ADM*EDLM*SSK#.D	20.94	16.47	1.27	0.79
Q61879_M	Myh10	Myosin-10	R.AGVLAHLEEERDLK.I	135.80	344.84	0.39	2.54
Q61879_M	Myh10	Myosin-10	K.AK#LQELEGAVK#.S	33.71	21.34	1.58	0.63
Q61879_M	Myh10	Myosin-10	K.ALEDETKNHEAQIQDM*R.Q	14.12	60.60	0.23	4.29
Q61879_M	Myh10	Myosin-10	K.ALEDETKNHEAQIQDMR.Q	10.48	44.68	0.23	4.27
Q61879_M	Myh10	Myosin-10	R.ALEEALEAK#.E	48.91	43.77	1.12	0.89
Q61879_M	Myh10	Myosin-10	R.ALELDPNLYR.I	41.53	154.70	0.27	3.72
Q61879_M	Myh10	Myosin-10	R.ALEQQVEEM*R.T	46.31	69.09	0.67	1.49
Q61879_M	Myh10	Myosin-10	R.ALEQQVEEMR.T	18.06	60.54	0.30	3.35
Q61879_M	Myh10	Myosin-10	K.ATDK#TFVEK#.L	21.55	22.62	0.95	1.05
Q61879_M	Myh10	Myosin-10	K.ATISALEAK#.I	183.05	145.75	1.26	0.80
Q61879_M	Myh10	Myosin-10	R.AVIYNPATQADWTAK#.K	122.32	97.70	1.25	0.80
Q61879_M	Myh10	Myosin-10	K.DAAGLESQLQDTQELLQEETR.Q	49.69	163.86	0.30	3.30
Q61879_M	Myh10	Myosin-10	K.DDVGK#NVHELEK#.S	61.57	50.09	1.23	0.81
Q61879_M	Myh10	Myosin-10	R.DEIFAQSK#.E	35.96	28.69	1.25	0.80
Q61879_M	Myh10	Myosin-10	R.DELADEIANSASGK#.S	26.79	23.68	1.13	0.88
Q61879_M	Myh10	Myosin-10	K.DHNIPGELER.Q	18.07	59.30	0.30	3.28
Q61879_M	Myh10	Myosin-10	K.DLEAQIEAANK#.A	58.35	54.18	1.08	0.93
Q61879_M	Myh10	Myosin-10	R.DLQTRDEQNEEK.K	1.53	8.21	0.19	5.36
Q61879_M	Myh10	Myosin-10	R.DLSEELEALK#.T	21.41	16.28	1.32	0.76
Q61879_M	Myh10	Myosin-10	K.DVEALSQR.L	19.36	64.01	0.30	3.31
Q61879_M	Myh10	Myosin-10	R.ELDDATEANEGLSR.E	66.62	220.69	0.30	3.31
Q61879_M	Myh10	Myosin-10	R.ELEAELEDER.K	18.04	66.63	0.27	3.69
Q61879_M	Myh10	Myosin-10	R.ELEAELEDERK.Q	8.23	28.43	0.29	3.46
Q61879_M	Myh10	Myosin-10	R.ELQAQIAELQEDFESEK#.A	61.32	45.60	1.34	0.74
Q61879_M	Myh10	Myosin-10	R.ELQAQIAELQEDFESEK#.A	161.56	118.51	1.36	0.73
Q61879_M	Myh10	Myosin-10	K.EQADFAVEALAK#.A	160.82	148.30	1.08	0.92
Q61879_M	Myh10	Myosin-10	K.FDQLLAEEK#.G	281.59	155.06	1.82	0.55
Q61879_M	Myh10	Myosin-10	K.FK#ATISALEAK#.I	11.40	13.11	0.87	1.15

Q61879_M	Myh10	Myosin-10	R.FVAELWK#.D	93.91	77.85	1.21	0.83
Q61879_M	Myh10	Myosin-10	R.GGPISFSSSR.S	20.27	69.29	0.29	3.42
Q61879_M	Myh10	Myosin-10	R.HAEQERDELADEIANSASGK.S	27.97	81.96	0.34	2.93
Q61879_M	Myh10	Myosin-10	R.HATALEELSEQLEQAK#.R	88.89	66.45	1.34	0.75
Q61879_M	Myh10	Myosin-10	R.HATALEELSEQLEQAKR.F	26.41	86.08	0.31	3.26
Q61879_M	Myh10	Myosin-10	R.HEM*PPHIYAISESAYR.C	8.35	20.36	0.41	2.44
Q61879_M	Myh10	Myosin-10	R.HGFEAASIK#.E	34.20	35.54	0.96	1.04
Q61879_M	Myh10	Myosin-10	R.HGFEAASIKEER.G	23.31	86.66	0.27	3.72
Q61879_M	Myh10	Myosin-10	K.HQQLLEEK#.N	91.82	64.72	1.42	0.70
Q61879_M	Myh10	Myosin-10	R.IAQLEEELEEEQSNM*ELLNDR.F	16.67	49.47	0.34	2.97
Q61879_M	Myh10	Myosin-10	R.IAQLEEELEEEQSNMELLNDR.F	9.19	35.16	0.26	3.83
Q61879_M	Myh10	Myosin-10	R.IAQLEEELEEEQSNM*ELLNDRFR.K	1.59	6.49	0.25	4.07
Q61879_M	Myh10	Myosin-10	K.IGQLEEQLEQEAK#.E	222.16	174.04	1.28	0.78
Q61879_M	Myh10	Myosin-10	R.IVFQEFR.Q	43.14	130.47	0.33	3.02
Q61879_M	Myh10	Myosin-10	R.IVGLDQVTGM*TETAFGSAYK#.T	103.78	75.93	1.37	0.73
Q61879_M	Myh10	Myosin-10	R.IVGLDQVTGM*TETAFGSAYK.T	78.89	57.31	1.38	0.73
Q61879_M	Myh10	Myosin-10	R.IVGLDQVTGMTETAFGSAYK#.T	24.72	16.35	1.51	0.66
Q61879_M	Myh10	Myosin-10	K.KEEELQGALAR.G	23.04	111.41	0.21	4.84
Q61879_M	Myh10	Myosin-10	K.K#FDQLLAEEK#.G	469.94	250.39	1.88	0.53
Q61879_M	Myh10	Myosin-10	R.K#HQQLLEEK#.N	124.24	117.43	1.06	0.95
Q61879_M	Myh10	Myosin-10	R.KKLDAQVQELHAK.V	174.02	104.49	1.67	0.60
Q61879_M	Myh10	Myosin-10	K.K#K#VDDDLGTIESLEEAK#.K	106.27	85.20	1.25	0.80
Q61879_M	Myh10	Myosin-10	K.K#LDAQVQELHAK#.V	133.09	121.78	1.09	0.92
Q61879_M	Myh10	Myosin-10	R.K#LDGETTDLQDQIAELQAQVDELK#.V	175.34	104.95	1.67	0.60
Q61879_M	Myh10	Myosin-10	R.K#LQAQM*K#.D	14.91	10.98	1.36	0.74
Q61879_M	Myh10	Myosin-10	K.K#M*EEEVLLLEDQNSK#.F	47.20	20.95	2.25	0.44
Q61879_M	Myh10	Myosin-10	K.KMQAHIQDLEEQLDEEEGAR.Q	3.11	4.65	0.67	1.49
Q61879_M	Myh10	Myosin-10	K.KQELEEILHDLESR.V	36.51	104.50	0.35	2.86
Q61879_M	Myh10	Myosin-10	K.K#QQQLSALK#.V	94.07	71.42	1.32	0.76
Q61879_M	Myh10	Myosin-10	R.KTTLQVDTLNTELAAER.S	18.83	61.55	0.31	3.27
Q61879_M	Myh10	Myosin-10	K.K#VDDDLGTIESLEEAK#.K	70.95	63.10	1.12	0.89
Q61879_M	Myh10	Myosin-10	K.KVDDDLGTIESLEEAKK.K	106.27	85.20	1.25	0.80
Q61879_M	Myh10	Myosin-10	K.KVIQYLAHVASSHK.G	67.86	33.43	2.03	0.49
Q61879_M	Myh10	Myosin-10	K.LDPHLVLDQLR.C	189.20	480.73	0.39	2.54
Q61879_M	Myh10	Myosin-10	R.LEVNMQAM*K#.A	15.58	15.36	1.01	0.99
Q61879_M	Myh10	Myosin-10	R.LEVNMQAMK#.A	10.53	9.31	1.13	0.88
Q61879_M	Myh10	Myosin-10	R.LEVNM*QAM*K#.A	49.00	47.93	1.02	0.98
Q61879_M	Myh10	Myosin-10	K.LLKDVEALSQR.L	10.67	34.20	0.31	3.21
Q61879_M	Myh10	Myosin-10	K.LQELEGAVK#.S	233.99	161.94	1.44	0.69
Q61879_M	Myh10	Myosin-10	K.LQNELDNVSTLLEEAEK#.K	55.59	47.06	1.18	0.85
Q61879_M	Myh10	Myosin-10	K.LQNELDNVSTLLEEAEK#K#.G	283.88	215.29	1.32	0.76
Q61879_M	Myh10	Myosin-10	R.LQQELDDLTVDLDHQR.Q	72.59	240.99	0.30	3.32
Q61879_M	Myh10	Myosin-10	K.LQQLFNHTM*FILEQEEYQR.E	34.56	80.42	0.43	2.33
Q61879_M	Myh10	Myosin-10	K.LQQLFNHTM*FILEQEEYQR.E	1.62	3.07	0.53	1.90
Q61879_M	Myh10	Myosin-10	K.LQQLFNHTMFILEQEEYQR.E	16.03	30.14	0.53	1.88
Q61879_M	Myh10	Myosin-10	R.LRVELAEK.A	11.77	34.62	0.34	2.94
Q61879_M	Myh10	Myosin-10	K.LVQEQGSHSK#.F	18.77	16.92	1.11	0.90
Q61879_M	Myh10	Myosin-10	K.LVWIPSER.H	29.78	90.03	0.33	3.02
Q61879_M	Myh10	Myosin-10	K.M*EEEVLLLEDQNSK#.F	33.47	26.84	1.25	0.80
Q61879_M	Myh10	Myosin-10	K.MEEEVLLLEDQNSK#.F	11.52	11.46	1.01	0.99
Q61879_M	Myh10	Myosin-10	K.M*EIDLK#DLEAQIEAANK#.A	15.59	12.89	1.21	0.83
Q61879_M	Myh10	Myosin-10	K.M*QAHIQDLEEQLDEEEGAR.Q	16.31	54.22	0.30	3.32
Q61879_M	Myh10	Myosin-10	K.MQAHIQDLEEQLDEEEGAR.Q	12.02	43.91	0.27	3.65
Q61879_M	Myh10	Myosin-10	K.NHEAQIQDM*R.Q	3.51	8.10	0.43	2.30
Q61879_M	Myh10	Myosin-10	K.NILAEQLQAETELFAEAEEM*R.A	24.36	82.65	0.29	3.39
Q61879_M	Myh10	Myosin-10	K.NILAEQLQAETELFAEAEEMR.A	14.18	40.30	0.35	2.84
Q61879_M	Myh10	Myosin-10	R.NKQEVM*ISDLEER.L	18.21	47.44	0.38	2.60
Q61879_M	Myh10	Myosin-10	R.NKQEVMISDLEER.L	7.49	18.08	0.41	2.42
Q61879_M	Myh10	Myosin-10	K.NLPIYSENIIEM*YR.G	16.55	56.62	0.29	3.42
Q61879_M	Myh10	Myosin-10	K.NLPIYSENIIEMYR.G	9.08	38.46	0.24	4.24
Q61879_M	Myh10	Myosin-10	K.NM*DPLNDNVATLLHQSSDR.F	26.70	94.13	0.28	3.53
Q61879_M	Myh10	Myosin-10	R.NQILQNEK#.K	49.89	41.47	1.20	0.83
Q61879_M	Myh10	Myosin-10	K.NSLQEQQEEEEEAR.K	125.19	35.88	3.49	0.29
Q61879_M	Myh10	Myosin-10	R.NTDQASMPENTVAQK#.L	28.03	23.22	1.21	0.83
Q61879_M	Myh10	Myosin-10	R.NTDQASM*PENTVAQK#.L	116.03	77.61	1.49	0.67
Q61879_M	Myh10	Myosin-10	R.NTNPNFVR.C	194.27	455.76	0.43	2.35
Q61879_M	Myh10	Myosin-10	R.QEEELQAKDEELLK.V	117.46	98.04	1.20	0.83
Q61879_M	Myh10	Myosin-10	R.QGFPNR.I	52.58	124.71	0.42	2.37
Q61879_M	Myh10	Myosin-10	R.QIVSNLEK#.K	114.30	84.14	1.36	0.74
Q61879_M	Myh10	Myosin-10	R.QLEEAEEEATR.A	30.15	103.76	0.29	3.44
Q61879_M	Myh10	Myosin-10	R.QLEEEKNSLQEQQEEEEEAR.K	4.91	17.22	0.28	3.51
Q61879_M	Myh10	Myosin-10	R.QLHIEGASLELSDDDTESK#.T	16.42	14.00	1.17	0.85
Q61879_M	Myh10	Myosin-10	R.QLLQANPILESFGNAK#.T	134.07	102.24	1.31	0.76
Q61879_M	Myh10	Myosin-10	R.QRYEILTPNAIPK.G	9.53	28.77	0.33	3.02
Q61879_M	Myh10	Myosin-10	K.QVLALQSQLADTK#.K	114.73	93.04	1.23	0.81
Q61879_M	Myh10	Myosin-10	R.RGGPISFSSSR.S	9.37	37.83	0.25	4.04
Q61879_M	Myh10	Myosin-10	K.SALLDEK#.R	105.35	65.58	1.61	0.62
Q61879_M	Myh10	Myosin-10	K.SALLDEKR.R	19.03	44.25	0.43	2.33
Q61879_M	Myh10	Myosin-10	K.SDLLLEGFNNYR.F	37.98	130.05	0.29	3.42
Q61879_M	Myh10	Myosin-10	K.SLEAEILQLQEELASSER.A	83.15	323.56	0.26	3.89
Q61879_M	Myh10	Myosin-10	K.TELEDTLDTTAAQQELR.T	2.59	11.47	0.23	4.43
Q61879_M	Myh10	Myosin-10	R.TGLEDPER.Y	31.70	113.71	0.28	3.59
Q61879_M	Myh10	Myosin-10	R.TQLEELEDELQATEDAK#.L	260.08	161.48	1.61	0.62
Q61879_M	Myh10	Myosin-10	K.TSDVNDTQPPQSE.-	59.70	59.70	1.00	1.00
Q61879_M	Myh10	Myosin-10	K.TTLQVDTLNTELAAER.S	14.43	54.62	0.26	3.79
Q61879_M	Myh10	Myosin-10	R.TVGQLYK#.E	827.31	466.88	1.77	0.56
Q61879_M	Myh10	Myosin-10	K.VDDDLGTIESLEEAK#.K	31.64	22.44	1.41	0.71
Q61879_M	Myh10	Myosin-10	K.VDYK#ADEWLM*K#.N	152.03	87.26	1.74	0.57
Q61879_M	Myh10	Myosin-10	K.VDYK#ADEWLMK#.N	51.46	21.96	2.34	0.43
Q61879_M	Myh10	Myosin-10	R.VEEEEER.N	5.02	10.93	0.46	2.18
Q61879_M	Myh10	Myosin-10	R.VEEEEERNQILQNEK.K	24.85	103.91	0.24	4.18
Q61879_M	Myh10	Myosin-10	K.VEGELEEM*ER.K	24.55	107.16	0.23	4.36
Q61879_M	Myh10	Myosin-10	K.VIQYLAHVASSHK#.G	652.52	348.56	1.87	0.53
Q61879_M	Myh10	Myosin-10	R.YLFVDR.A	34.16	124.04	0.28	3.63
Q6URW6_	Myh14	Myosin-14	R.DEM*AEEVASGNLSK#AATLEEK.R	7.95	1.70	4.69	0.21
Q6URW6_	Myh14	Myosin-14	K.ATDK#SFVEK#.L	34.13	15.91	2.15	0.47
Q6URW6_	Myh14	Myosin-14	K.EQADFAIEALAK#.A	826.50	367.04	2.25	0.44
Q6URW6_	Myh14	Myosin-14	R.NWQWWR.L	9.30	18.21	0.51	1.96
Q6URW6_	Myh14	Myosin-14	K.QLLQANPILEAFGNAK#.T	962.58	497.21	1.94	0.52
Q02566_M	Myh6	Myosin-6 O	K.EDQVM*QQNPPK.F	5.48	17.66	0.31	3.22
Q8VDD5_	Myh9	Myosin-9 O	R.ALEEAM*EQK#.A	6.85	2.69	2.55	0.39
Q8VDD5_	Myh9	Myosin-9 O	R.ALEQQVEEMK#TQLEELEDELQATEDAK#.L	5.29	1.37	3.86	0.26
Q8VDD5_	Myh9	Myosin-9 O	R.ELEDATETADAM*NR.E	6.00	9.89	0.61	1.65

Q8VDD5_M	Myh9	Myosin-9 O	K.GALALEEK#.R	23.44	7.91	2.96	0.34
Q8VDD5_M	Myh9	Myosin-9 O	R.IAQLEEELEEEQGNTELINDR.L	4.40	5.59	0.79	1.27
Q8VDD5_M	Myh9	Myosin-9 O	K.IAQLEEQLDNETK#.E	17.92	8.81	2.03	0.49
Q8VDD5_M	Myh9	Myosin-9 O	R.IIGLDQVAGM*SETALPGAFK#.T	5.49	3.86	1.42	0.70
Q8VDD5_M	Myh9	Myosin-9 O	K.LQEM*ESAVK#.S	19.43	7.04	2.76	0.36
Q8VDD5_M	Myh9	Myosin-9 O	R.NTDQASM*PDNTAAQK#.V	3.02	2.73	1.11	0.90
Q8VDD5_M	Myh9	Myosin-9 O	K.AK#LQEMESAVK#.S	74.06	35.72	2.07	0.48
Q8VDD5_M	Myh9	Myosin-9 O	K.AK#LQEM*ESAVK#.S	96.94	49.25	1.97	0.51
Q8VDD5_M	Myh9	Myosin-9 O	K.AKLQEM*ESAVK.S	130.21	87.15	1.49	0.67
Q8VDD5_M	Myh9	Myosin-9 O	K.AKQTLENERGELANEVK.A	78.20	130.60	0.60	1.67
Q8VDD5_M	Myh9	Myosin-9 O	R.ALEEAMEQK#.A	264.41	138.81	1.90	0.52
Q8VDD5_M	Myh9	Myosin-9 O	R.ALEEAM*EQK#.A	356.29	179.63	1.98	0.50
Q8VDD5_M	Myh9	Myosin-9 O	R.ALEEAMEQKAELER.L	25.29	54.79	0.46	2.17
Q8VDD5_M	Myh9	Myosin-9 O	K.ALELDSNLYR.I	200.13	471.55	0.42	2.36
Q8VDD5_M	Myh9	Myosin-9 O	R.ALEQQVEEM*K#.T	210.27	93.64	2.25	0.45
Q8VDD5_M	Myh9	Myosin-9 O	R.ALEQQVEEMK#.T	255.27	125.78	2.03	0.49
Q8VDD5_M	Myh9	Myosin-9 O	R.ALEQQVEEM*K#TQLEELEDELQATEDAK#.L	143.19	107.87	1.33	0.75
Q8VDD5_M	Myh9	Myosin-9 O	K.ANLQIDQINTDLNLER.S	49.28	118.29	0.42	2.40
Q8VDD5_M	Myh9	Myosin-9 O	K.ASIAALEAK#.I	877.72	436.08	2.01	0.50
Q8VDD5_M	Myh9	Myosin-9 O	R.ASREEILAQAK.E	139.48	352.43	0.40	2.53
Q8VDD5_M	Myh9	Myosin-9 O	R.ASREEILAQAKENEK.K	13.72	42.57	0.32	3.10
Q8VDD5_M	Myh9	Myosin-9 O	R.DELADEIANSSGK#.G	222.11	130.57	1.70	0.59
Q8VDD5_M	Myh9	Myosin-9 O	K.DFSALESQLQDTQELLQEENR.Q	207.64	392.71	0.53	1.89
Q8VDD5_M	Myh9	Myosin-9 O	K.DFSALESQLQDTQELLQEENRQK.L	27.23	43.88	0.62	1.61
Q8VDD5_M	Myh9	Myosin-9 O	K.DLEAHIDTANK#.N	230.03	108.19	2.13	0.47
Q8VDD5_M	Myh9	Myosin-9 O	K.DLEGLSQR.L	183.26	392.34	0.47	2.14
Q8VDD5_M	Myh9	Myosin-9 O	R.DLGEELEALK#.T	77.33	41.92	1.84	0.54
Q8VDD5_M	Myh9	Myosin-9 O	R.DLQGRDEQSEEK.K	21.38	52.96	0.40	2.48
Q8VDD5_M	Myh9	Myosin-9 O	K.DM*FQETM*EAM*R.I	6.09	13.58	0.45	2.23
Q8VDD5_M	Myh9	Myosin-9 O	R.EEILAQAK#.E	315.77	167.19	1.89	0.53
Q8VDD5_M	Myh9	Myosin-9 O	K.EEVGEEAIVELVENGK#.K	38.16	19.32	1.98	0.51
Q8VDD5_M	Myh9	Myosin-9 O	R.ELEDATETADAM*NR.E	136.91	318.03	0.43	2.32
Q8VDD5_M	Myh9	Myosin-9 O	R.ELEDATETADAMNR.E	77.66	186.96	0.42	2.41
Q8VDD5_M	Myh9	Myosin-9 O	R.ELETQISELQEDLESER.A	48.03	107.47	0.45	2.24
Q8VDD5_M	Myh9	Myosin-9 O	R.EM*EAELEDER.K	66.27	159.04	0.42	2.40
Q8VDD5_M	Myh9	Myosin-9 O	R.EMEAELEDER.K	27.42	76.07	0.36	2.77
Q8VDD5_M	Myh9	Myosin-9 O	R.FLSNGHVTIPGQQDK#.D	11.61	4.03	2.88	0.35
Q8VDD5_M	Myh9	Myosin-9 O	R.FLSNGHVTIPGQQDKDM*FQETM*EAMR.I	4.16	11.94	0.35	2.87
Q8VDD5_M	Myh9	Myosin-9 O	K.FVSELWK#.D	201.32	94.74	2.13	0.47
Q8VDD5_M	Myh9	Myosin-9 O	K.GALALEEK#.R	613.82	297.71	2.06	0.49
Q8VDD5_M	Myh9	Myosin-9 O	K.GALALEEKR.R	40.85	102.18	0.40	2.50
Q8VDD5_M	Myh9	Myosin-9 O	R.GDLPFVVTR.R	46.24	117.94	0.39	2.55
Q8VDD5_M	Myh9	Myosin-9 O	R.GELANEVK#.A	221.47	129.55	1.71	0.58
Q8VDD5_M	Myh9	Myosin-9 O	K.HEAM*ITDLEER.L	16.19	33.11	0.49	2.05
Q8VDD5_M	Myh9	Myosin-9 O	R.HEDELLAK#.E	768.94	370.65	2.07	0.48
Q8VDD5_M	Myh9	Myosin-9 O	R.HEM*PPHIYAITDTAYR.S	30.92	62.36	0.50	2.02
Q8VDD5_M	Myh9	Myosin-9 O	K.HLAAENR.L	17.86	47.37	0.38	2.65
Q8VDD5_M	Myh9	Myosin-9 O	K.HSQAVEELADQLEQTK#.R	244.67	110.51	2.21	0.45
Q8VDD5_M	Myh9	Myosin-9 O	K.HSQAVEELADQLEQTKR.V	170.21	312.40	0.54	1.84
Q8VDD5_M	Myh9	Myosin-9 O	R.IAQLEEELEEEQGNTELINDR.L	108.38	230.23	0.47	2.12
Q8VDD5_M	Myh9	Myosin-9 O	K.IAQLEEQLDNETK#.E	527.16	242.01	2.18	0.46
Q8VDD5_M	Myh9	Myosin-9 O	K.IAQLEEQLDNETKER.Q	165.61	366.47	0.45	2.21
Q8VDD5_M	Myh9	Myosin-9 O	R.IIGLDQVAGM*SETALPGAFK#.T	464.55	201.90	2.30	0.43
Q8VDD5_M	Myh9	Myosin-9 O	R.IIGLDQVAGMSETALPGAFK#.T	122.04	55.91	2.18	0.46
Q8VDD5_M	Myh9	Myosin-9 O	R.IM*GIPEDEQM*GLLR.V	85.83	191.92	0.45	2.24
Q8VDD5_M	Myh9	Myosin-9 O	R.IM*GIPEDEQMGLLR.V	24.14	55.09	0.44	2.28
Q8VDD5_M	Myh9	Myosin-9 O	R.IMGIPEDEQM*GLLR.V	24.14	55.09	0.44	2.28
Q8VDD5_M	Myh9	Myosin-9 O	R.IMGIPEDEQMGLLR.V	22.59	29.02	0.78	1.28
Q8VDD5_M	Myh9	Myosin-9 O	K.IRELETQISELQEDLESER.A	19.84	150.14	0.13	7.57
Q8VDD5_M	Myh9	Myosin-9 O	K.KANLQIDQINTDLNLER.S	81.85	166.73	0.49	2.04
Q8VDD5_M	Myh9	Myosin-9 O	K.KEEELQAALAR.L	88.47	202.39	0.44	2.29
Q8VDD5_M	Myh9	Myosin-9 O	R.K#K#VEAQLQELQVK#.F	65.82	33.19	1.98	0.50
Q8VDD5_M	Myh9	Myosin-9 O	R.KKVEAQLQELQVK.F	630.62	276.73	2.28	0.44
Q8VDD5_M	Myh9	Myosin-9 O	R.K#LEGDSTDLSDQIAELQAQIAELK#.M	477.18	229.52	2.08	0.48
Q8VDD5_M	Myh9	Myosin-9 O	K.K#LEMDLK#.D	46.05	21.97	2.10	0.48
Q8VDD5_M	Myh9	Myosin-9 O	K.K#LEM*DLK#.D	56.64	30.93	1.83	0.55
Q8VDD5_M	Myh9	Myosin-9 O	K.K#LVWVPSSK#.N	402.05	160.79	2.50	0.40
Q8VDD5_M	Myh9	Myosin-9 O	K.KM*QQNIQELEEQLEEEESAR.Q	24.97	45.29	0.55	1.81
Q8VDD5_M	Myh9	Myosin-9 O	K.KMQQNIQELEEQLEEEESAR.Q	16.01	32.36	0.49	2.02
Q8VDD5_M	Myh9	Myosin-9 O	K.K#TLEDEAK#.T	38.37	21.24	1.81	0.55
Q8VDD5_M	Myh9	Myosin-9 O	K.K#VEAQLQELQVK#.F	118.04	57.05	2.07	0.48
Q8VDD5_M	Myh9	Myosin-9 O	K.LEGDSTDLSDQIAELQAQIAELK#.M	147.62	69.38	2.13	0.47
Q8VDD5_M	Myh9	Myosin-9 O	R.LEVNLQAM*K#.A	270.52	124.92	2.17	0.46
Q8VDD5_M	Myh9	Myosin-9 O	R.LEVNLQAMK#.A	170.67	79.01	2.16	0.46
Q8VDD5_M	Myh9	Myosin-9 O	K.LKDVLLQVEDER.R	12.51	26.97	0.46	2.16
Q8VDD5_M	Myh9	Myosin-9 O	K.LKDVLLQVEDERR.N	21.94	148.99	0.15	6.79
Q8VDD5_M	Myh9	Myosin-9 O	K.LKNKHEAM*ITDLEER.L	5.01	11.83	0.42	2.36
Q8VDD5_M	Myh9	Myosin-9 O	K.LKSM*EAEM*IQLQEELAAAER.A	10.61	24.83	0.43	2.34
Q8VDD5_M	Myh9	Myosin-9 O	K.LQEMESAVK#.S	411.80	176.42	2.33	0.43
Q8VDD5_M	Myh9	Myosin-9 O	K.LQEM*ESAVK#.S	599.88	298.22	2.01	0.50
Q8VDD5_M	Myh9	Myosin-9 O	R.LQQELDDLLVDLDHQR.Q	347.18	734.48	0.47	2.12
Q8VDD5_M	Myh9	Myosin-9 O	K.LQVELDSVTGLLSQSDSK#.S	280.37	129.89	2.16	0.46
Q8VDD5_M	Myh9	Myosin-9 O	R.LTEM*ETM*QSQLMAEK#.L	100.66	51.62	1.95	0.51
Q8VDD5_M	Myh9	Myosin-9 O	R.LTEMETM*QSQLM*AEK#.L	100.66	51.62	1.95	0.51
Q8VDD5_M	Myh9	Myosin-9 O	R.LTEM*ETMQSQLM*AEK#.L	13.49	8.03	1.68	0.59
Q8VDD5_M	Myh9	Myosin-9 O	R.LTEMETM*QSQLMAEK#.L	29.86	14.49	2.06	0.49
Q8VDD5_M	Myh9	Myosin-9 O	R.LTEM*ETMQSQLMAEK#.L	11.81	6.33	1.87	0.54
Q8VDD5_M	Myh9	Myosin-9 O	R.LTEMETMQSQLM*AEK#.L	17.23	9.06	1.90	0.53
Q8VDD5_M	Myh9	Myosin-9 O	R.LTEMETMQSQLMAEK#.L	30.44	14.90	2.04	0.49
Q8VDD5_M	Myh9	Myosin-9 O	K.LVWVPSSK#.N	327.88	178.87	1.83	0.55
Q8VDD5_M	Myh9	Myosin-9 O	K.M*QQNIQELEEQLEEEESAR.Q	65.05	122.60	0.53	1.88
Q8VDD5_M	Myh9	Myosin-9 O	K.MQQNIQELEEQLEEEESAR.Q	8.50	18.93	0.45	2.23
Q8VDD5_M	Myh9	Myosin-9 O	R.NAEQFKDQADK.A	274.07	134.75	2.03	0.49
Q8VDD5_M	Myh9	Myosin-9 O	R.NAEQFKDQADKASTR.L	32.04	76.20	0.42	2.38
Q8VDD5_M	Myh9	Myosin-9 O	K.NFINNPLAQADWAAK#.K	430.13	214.11	2.01	0.50
Q8VDD5_M	Myh9	Myosin-9 O	K.NGFEPASLK#.E	23.91	8.49	2.82	0.35
Q8VDD5_M	Myh9	Myosin-9 O	K.NGFEPASLK#EEVGEEAIVELVENGK#.K	11.94	7.27	1.64	0.61
Q8VDD5_M	Myh9	Myosin-9 O	K.NGFEPASLK#EEVGEEAIVELVENGK#K#.V	13.40	4.80	2.79	0.36
Q8VDD5_M	Myh9	Myosin-9 O	K.NKHEAM*ITDLEER.L	36.45	100.09	0.36	2.75
Q8VDD5_M	Myh9	Myosin-9 O	K.NKHEAMITDLEER.L	29.41	69.83	0.42	2.37
Q8VDD5_M	Myh9	Myosin-9 O	K.NLPIYSEEIVEM*YK#.G	288.40	150.90	1.91	0.52
Q8VDD5_M	Myh9	Myosin-9 O	K.NLPIYSEEIVEMYK#.G	218.65	109.60	2.00	0.50
Q8VDD5_M	Myh9	Myosin-9 O	K.NM*DPLNDNIATLLHQSSDK#.F	221.93	121.34	1.83	0.55

Q8VDD5_M	Myh9	Myosin-9 O	R.NTDQASM*PDNTAAQK#.V	295.61	179.32	1.65	0.61
Q8VDD5_M	Myh9	Myosin-9 O	R.NTDQASMPDNTAAQK#.V	242.12	114.31	2.12	0.47
Q8VDD5_M	Myh9	Myosin-9 O	R.QAQQERDELADEIANSSGK.G	154.58	338.85	0.46	2.19
Q8VDD5_M	Myh9	Myosin-9 O	K.QIATLHAQVTDM*K#K#.K	131.68	63.76	2.07	0.48
Q8VDD5_M	Myh9	Myosin-9 O	K.QIATLHAQVTDM*KK.K	18.75	5.16	3.63	0.28
Q8VDD5_M	Myh9	Myosin-9 O	R.QK#HSQAVEELADQLEQTK#.R	14.27	9.54	1.50	0.67
Q8VDD5_M	Myh9	Myosin-9 O	R.QLEEAEEEAQR.A	172.08	289.61	0.59	1.68
Q8VDD5_M	Myh9	Myosin-9 O	R.QQQLTAM*K#.V	196.29	92.45	2.12	0.47
Q8VDD5_M	Myh9	Myosin-9 O	R.QRYEILTPNSIPK.G	40.88	101.29	0.40	2.48
Q8VDD5_M	Myh9	Myosin-9 O	K.REQEVSILK.K	4.17	14.80	0.28	3.55
Q8VDD5_M	Myh9	Myosin-9 O	R.RGDLPFVVTR.R	30.71	226.75	0.14	7.38
Q8VDD5_M	Myh9	Myosin-9 O	R.RKLEGDSTDLSDQIAELQAQIAELK.M	49.78	88.72	0.56	1.78
Q8VDD5_M	Myh9	Myosin-9 O	K.RQAQQERDELADEIANSSGK.G	6.63	37.43	0.18	5.65
Q8VDD5_M	Myh9	Myosin-9 O	K.RQLEEAEEEAQR.A	12.97	102.79	0.13	7.93
Q8VDD5_M	Myh9	Myosin-9 O	K.SM*EAEM*IQLQEELAAAER.A	19.46	36.61	0.53	1.88
Q8VDD5_M	Myh9	Myosin-9 O	K.SMEAEM*IQLQEELAAAER.A	3.64	6.34	0.57	1.74
Q8VDD5_M	Myh9	Myosin-9 O	K.SM*EAEMIQLQEELAAAER.A	20.65	49.07	0.42	2.38
Q8VDD5_M	Myh9	Myosin-9 O	K.SMEAEMIQLQEELAAAER.A	47.47	104.62	0.45	2.20
Q8VDD5_M	Myh9	Myosin-9 O	K.SVHELEK#.S	211.06	108.41	1.95	0.51
Q8VDD5_M	Myh9	Myosin-9 O	K.TDLLLEPYNK#.Y	583.08	276.12	2.11	0.47
Q8VDD5_M	Myh9	Myosin-9 O	R.TELADK#VTK#.L	184.04	106.13	1.73	0.58
Q8VDD5_M	Myh9	Myosin-9 O	K.TELEDTLDSTAAQQELR.S	20.64	46.13	0.45	2.23
Q8VDD5_M	Myh9	Myosin-9 O	R.TEMEDLM*SSK#.D	25.72	13.26	1.94	0.52
Q8VDD5_M	Myh9	Myosin-9 O	R.TEMEDLMSSK#.D	38.42	15.64	2.46	0.41
Q8VDD5_M	Myh9	Myosin-9 O	R.TEM*EDLM*SSK#.D	106.50	57.81	1.84	0.54
Q8VDD5_M	Myh9	Myosin-9 O	R.TEMEDLM*SSKDDVGK.S	27.52	14.61	1.88	0.53
Q8VDD5_M	Myh9	Myosin-9 O	R.TEM*EDLM*SSKDDVGK.S	794.69	419.40	1.89	0.53
Q8VDD5_M	Myh9	Myosin-9 O	K.THEAQIQEMR.Q	41.58	109.41	0.38	2.63
Q8VDD5_M	Myh9	Myosin-9 O	K.THEAQIQEM*R.Q	33.23	87.63	0.38	2.64
Q8VDD5_M	Myh9	Myosin-9 O	K.TLEDEAK#.T	224.36	126.61	1.77	0.56
Q8VDD5_M	Myh9	Myosin-9 O	K.TLEDEAKTHEAQIQEM*R.Q	34.69	65.65	0.53	1.89
Q8VDD5_M	Myh9	Myosin-9 O	K.TLEDEAKTHEAQIQEMR.Q	36.61	63.57	0.58	1.74
Q8VDD5_M	Myh9	Myosin-9 O	R.TVGQLYK#EQLAK#.L	26.58	8.38	3.17	0.32
Q8VDD5_M	Myh9	Myosin-9 O	K.VAAYDK#LEK#.T	427.65	212.27	2.01	0.50
Q8VDD5_M	Myh9	Myosin-9 O	R.VAEFTTNLM*EEEEK#.S	178.91	102.14	1.75	0.57
Q8VDD5_M	Myh9	Myosin-9 O	R.VAEFTTNLMEEEEK#.S	116.33	57.50	2.02	0.49
Q8VDD5_M	Myh9	Myosin-9 O	K.VEAQLQELQVK#.F	307.13	136.79	2.25	0.45
Q8VDD5_M	Myh9	Myosin-9 O	R.VEEEAAQK#.N	53.76	26.51	2.03	0.49
Q8VDD5_M	Myh9	Myosin-9 O	R.VISGVLQLGNIAFK#.K	657.34	316.13	2.08	0.48
Q8VDD5_M	Myh9	Myosin-9 O	K.VK#VNK#DDIQK#.M	53.20	24.90	2.14	0.47
Q8VDD5_M	Myh9	Myosin-9 O	K.VNK#DDIQK#.M	112.42	64.77	1.74	0.58
Q8VDD5_M	Myh9	Myosin-9 O	R.VRTELADKVTK.L	52.25	135.69	0.39	2.60
Q8VDD5_M	Myh9	Myosin-9 O	K.VSHLLGINVTDFTR.G	186.25	405.10	0.46	2.18
Q8VDD5_M	Myh9	Myosin-9 O	R.VVFQEFR.Q	246.66	537.03	0.46	2.18
Q8VDD5_M	Myh9	Myosin-9 O	K.VVQEQGTHPK#.F	218.61	111.19	1.97	0.51
Q8VDD5_M	Myh9	Myosin-9 O	R.YEILTPNSIPK#.G	284.50	136.56	2.08	0.48
Q8VDD5_M	Myh9	Myosin-9 O	K.YK#ASIAALEAK#.I	59.65	32.24	1.85	0.54
Q8VDD5_M	Myh9	Myosin-9 O	K.YLYVDK#.N	266.72	147.60	1.81	0.55
Q8VDD5_M	Myh9	Myosin-9 O	K.YLYVDK#NFINNPLAQADWAAK#.K	124.30	65.27	1.90	0.53
Q6ZWQ9_C	Myl12a	MCG5400 (	R.DGFIDKEDLHDM*LASM*GK.N	215.28	131.60	1.64	0.61
Q6ZWQ9_C	Myl12a	MCG5400 (	R.DGFIDKEDLHDM*LASM*GK.N	18.66	11.15	1.67	0.60
Q6ZWQ9_C	Myl12a	MCG5400 (	R.DGFIDK#EDLHDM*LASMGK#.N	27.45	16.97	1.62	0.62
Q6ZWQ9_C	Myl12a	MCG5400 (	R.DGFIDKEDLHDMLASM*GK.N	85.47	48.39	1.77	0.57
Q6ZWQ9_C	Myl12a	MCG5400 (	R.DGFIDK#EDLHDMLASMGK#.N	111.48	60.24	1.85	0.54
Q6ZWQ9_C	Myl12a	MCG5400 (	R.ELLTTM*GDRFTDEEVDELYR.E	29.39	211.30	0.14	7.19
Q6ZWQ9_C	Myl12a	MCG5400 (	R.ELLTTMGDRFTDEEVDELYR.E	40.43	270.35	0.15	6.69
Q6ZWQ9_C	Myl12a	MCG5400 (	R.FTDEEVDELYR.E	236.31	706.12	0.33	2.99
Q6ZWQ9_C	Myl12a	MCG5400 (	R.FTDEEVDELYREAPIDKK.G	3.12	8.16	0.38	2.61
Q6ZWQ9_C	Myl12a	MCG5400 (	K.GNFNYIEFTR.I	373.60	962.58	0.39	2.58
Q6ZWQ9_C	Myl12a	MCG5400 (	K.KGNFNYIEFTR.I	11.81	30.29	0.39	2.56
Q6ZWQ9_C	Myl12a	MCG5400 (	K.GNFNYIEFTR.I	5.05	18.71	0.27	3.71
Q60605_M	Myl6	Myosin ligh	K.EAFQLFDR.T	9.35	28.20	0.33	3.02
Q60605_M	Myl6	Myosin ligh	R.HVLVTLGEK#.M	69.55	43.49	1.60	0.63
Q60605_M	Myl6	Myosin ligh	K.NKDQGTYEDYVEGLR.V	3.59	9.16	0.39	2.55
Q60605_M	Myl6	Myosin ligh	K.VLDFEHFLPM*LQTVAK#.N	29.63	95.45	0.31	3.22
Q60605_M	Myl6	Myosin ligh	K.DQGTYEDYVEGLR.V	116.92	335.40	0.35	2.87
Q60605_M	Myl6	Myosin ligh	K.EAFQLFDR.T	260.81	683.85	0.38	2.62
Q60605_M	Myl6	Myosin ligh	R.HVLVTLGEK#.M	964.50	475.83	2.03	0.49
Q60605_M	Myl6	Myosin ligh	K.NKDQGTYEDYVEGLR.V	227.71	600.79	0.38	2.64
Q60605_M	Myl6	Myosin ligh	K.SDEMNVK#.V	44.60	22.02	2.03	0.49
Q60605_M	Myl6	Myosin ligh	K.VLDFEHFLPM*LQTVAK#.N	1724.18	997.07	1.73	0.58
Q60605_M	Myl6	Myosin ligh	K.VLDFEHFLPMLQTVAK#.N	392.19	252.88	1.55	0.64
Q60605_M	Myl6	Myosin ligh	K.VLGNPK#SDEM*NVK#.V	3.62	14.81	0.24	4.09
Q60605_M	Myl6	Myosin ligh	R.HVLVTLGEK#.M	34.02	23.76	1.43	0.70
Q60605_M	Myl6	Myosin ligh	K.VLDFEHFLPM*LQTVAK#.N	18.62	71.82	0.26	3.86
Q8CI43_M	Myl6b	Myosin ligh	R.ALGQNPTNAEVLK#.V	116.28	63.46	1.83	0.55
Q8CI43_M	Myl6b	Myosin ligh	R.ALGQNPTNAEVLK#.V	2105.55	1318.02	1.60	0.63
Q8CI43_M	Myl6b	Myosin ligh	R.HVLTTLGEK#.M	7.92	8.81	0.90	1.11
Q8CI43_M	Myl6b	Myosin ligh	K.ILYSQCGDLM*R.A	3.67	9.57	0.38	2.61
Q8CI43_M	Myl6b	Myosin ligh	R.ALGQNPTNAEVLK#.V	49.23	24.52	2.01	0.50
Q9CQ19_M	Myl9	Myosin reg	R.ATSNVFAMFDQSQIQEFK#.E	10.82	4.10	2.64	0.38
Q9CQ19_M	Myl9	Myosin reg	K.EAFNM*IDQNR.D	5.34	15.42	0.35	2.89
Q9CQ19_M	Myl9	Myosin reg	R.ATSNVFAM*FDQSQIQEFK#.E	714.59	370.25	1.93	0.52
Q9CQ19_M	Myl9	Myosin reg	R.ATSNVFAM*FDQSQIQEFK.E	490.39	248.80	1.97	0.51
Q9CQ19_M	Myl9	Myosin reg	R.ATSNVFAMFDQSQIQEFK#.E	162.89	106.96	1.52	0.66
Q9CQ19_M	Myl9	Myosin reg	R.ATSNVFAMFDQSQIQEFK#.E	113.85	71.66	1.59	0.63
Q9CQ19_M	Myl9	Myosin reg	R.ATSNVFAM*FDQSQIQEFKEAFNM*IDQNR.D	12.21	23.61	0.52	1.93
Q9CQ19_M	Myl9	Myosin reg	R.ATSNVFAM*FDQSQIQEFKEAFNMIDQNR.D	9.89	21.82	0.45	2.21
Q9CQ19_M	Myl9	Myosin reg	R.ATSNVFAMFDQSQIQEFKEAFNM*IDQNR.D	9.89	21.82	0.45	2.21
Q9CQ19_M	Myl9	Myosin reg	R.DGFIDK#EDLHDM*LASLGK#.N	43.30	23.58	1.84	0.54
Q9CQ19_M	Myl9	Myosin reg	R.DGFIDK#EDLHDMLASLGK#.N	36.92	23.53	1.57	0.64
Q9CQ19_M	Myl9	Myosin reg	K.EAFNM*IDQNR.D	183.95	545.26	0.34	2.96
Q9CQ19_M	Myl9	Myosin reg	K.EAFNMIDQNR.D	50.08	149.66	0.33	2.99
Q9CQ19_M	Myl9	Myosin reg	R.EAPIDKK.G	33.57	24.14	1.39	0.72
Q9CQ19_M	Myl9	Myosin reg	R.ELLTTM*GDR.F	132.24	323.93	0.41	2.45
Q9CQ19_M	Myl9	Myosin reg	R.ELLTTMGDR.F	45.13	127.89	0.35	2.83
Q9CQ19_M	Myl9	Myosin reg	K.GNFNYVEFTR.I	2.21	10.36	0.21	4.69
Q9CQ19_M	Myl9	Myosin reg	K.LNGTDPEDVIR.N	139.84	424.36	0.33	3.03
Q9CQ19_M	Myl9	Myosin reg	R.ATSNVFAM*FDQSQIQEFK#.E	5.71	6.47	0.88	1.13
Q6PDN3_M	Mylk	Myosin ligh	R.K#QIQESEHIK.V	4.20	30.71	0.14	7.30
Q9JMH9_M	Myo18a	Unconvent	R.AVEELLESLDLEK.S	10.95	10.89	1.01	0.99
Q9JMH9_M	Myo18a	Unconvent	K.IISNLFLGR.A	3.78	18.38	0.21	4.86
Q9JMH9_M	Myo18a	Unconvent	K.LK#QM*EVQLEEEYEDK.Q	14.17	10.92	1.30	0.77

Q9JMH9_M	Myo18a	Unconvent	R.LPALVPPPPPALR.E	3.90	32.55	0.12	8.35
Q9JMH9_M	Myo18a	Unconvent	K.LSTLSDQVNQR.D	4.70	29.84	0.16	6.35
Q9JMH9_M	Myo18a	Unconvent	R.NTGESASQLLDAETAER.L	1.60	6.28	0.26	3.92
Q9JMH9_M	Myo18a	Unconvent	R.QDQSIVLLGSSGSGK#.T	10.63	9.36	1.14	0.88
Q9JMH9_M	Myo18a	Unconvent	R.QGPEESGLGEGTK.L	14.50	16.19	0.90	1.12
Q9JMH9_M	Myo18a	Unconvent	K.SEELSLPEGK.A	14.25	16.97	0.84	1.19
Q9JMH9_M	Myo18a	Unconvent	K.TALEEQLSR.L	5.16	25.02	0.21	4.85
Q9JMH9_M	Myo18a	Unconvent	K.VKDQEEELDEQAGSIQM*LEQAK.L	4.73	9.10	0.52	1.92
Q9JMH9_M	Myo18a	Unconvent	K.VKDQEEELDEQAGSIQMLEQAK.L	6.43	7.66	0.84	1.19
Q9JMH9_M	Myo18a	Unconvent	K.VLAISPEEQK#.T	10.48	14.95	0.70	1.43
Q9JMH9_M	Myo18a	Unconvent	R.YGASLLHTYAGPSLLVLSTR.G	2.58	14.69	0.18	5.70
P46735_M	Myo1b	Unconvent	K.EQLLQSNPVLEAFGNAK#.T	14.68	7.41	1.98	0.50
P46735_M	Myo1b	Unconvent	R.IFLLTNNNLLLADQK#.S	15.50	8.92	1.74	0.58
P46735_M	Myo1b	Unconvent	K.IIIAEVVNK#.I	42.67	15.64	2.73	0.37
P46735_M	Myo1b	Unconvent	K.LEASELFK#.D	16.01	6.36	2.52	0.40
P46735_M	Myo1b	Unconvent	K.SEVPLVDVTK#.V	18.25	10.13	1.80	0.56
P46735_M	Myo1b	Unconvent	R.SGVEVLFNELEIPVEEHSFGR.S	3.46	19.14	0.18	5.53
Q9WTI7_M	Myo1c	Unconvent	R.ASFLLNLR.R	7.72	10.15	0.76	1.32
Q9WTI7_M	Myo1c	Unconvent	R.DGIIDFTSGSELLITK#.A	31.92	10.34	3.09	0.32
Q9WTI7_M	Myo1c	Unconvent	R.DQAVM*ISGESGAGK#.T	18.01	38.29	0.47	2.13
Q9WTI7_M	Myo1c	Unconvent	R.DQAVMISGESGAGK#.T	17.28	2.03	8.51	0.12
Q9WTI7_M	Myo1c	Unconvent	R.LGTEEISPR.V	14.28	19.18	0.74	1.34
Q9WTI7_M	Myo1c	Unconvent	R.NPQSYLYLVK#.G	40.05	12.02	3.33	0.30
Q9WTI7_M	Myo1c	Unconvent	R.NVLDTSWPTPPPALR.E	6.08	7.00	0.87	1.15
Q9WTI7_M	Myo1c	Unconvent	R.QLLLTPSAVVIVEDAK#.V	26.90	10.11	2.66	0.38
Q9WTI7_M	Myo1c	Unconvent	R.VLQSLGSEPIQYAVPVVK#.Y	35.86	9.85	3.64	0.27
Q9WTI7_M	Myo1c	Unconvent	R.ASFLLNLR.R	18.82	25.87	0.73	1.37
Q9WTI7_M	Myo1c	Unconvent	K.AVASEIFK#.G	150.76	41.95	3.59	0.28
Q9WTI7_M	Myo1c	Unconvent	R.DGIIDFTSGSELLITK#.A	150.52	42.71	3.52	0.28
Q9WTI7_M	Myo1c	Unconvent	R.DQAVM*ISGESGAGK#.T	71.82	111.29	0.65	1.55
Q9WTI7_M	Myo1c	Unconvent	R.DQAVMISGESGAGK#.T	21.59	7.46	2.89	0.35
Q9WTI7_M	Myo1c	Unconvent	R.EDNK#QK#GDVVLQSDHVIETLTK#.T	15.55	3.58	4.34	0.23
Q9WTI7_M	Myo1c	Unconvent	R.FDEVLIR.H	13.38	15.81	0.85	1.18
Q9WTI7_M	Myo1c	Unconvent	K.GDVVLQSDHVIETLTK#.T	109.90	31.03	3.54	0.28
Q9WTI7_M	Myo1c	Unconvent	K.GEELLSPLNLEQAAYAR.D	28.08	36.17	0.78	1.29
Q9WTI7_M	Myo1c	Unconvent	R.HLGYK#PEEYK#.M	114.79	24.19	4.75	0.21
Q9WTI7_M	Myo1c	Unconvent	R.LGTEEISPR.V	53.56	74.59	0.72	1.39
Q9WTI7_M	Myo1c	Unconvent	R.LLGVEGTTLR.E	67.29	72.39	0.93	1.08
Q9WTI7_M	Myo1c	Unconvent	R.LLHYAGEVTYSVTGFLDK#.N	19.05	5.24	3.63	0.28
Q9WTI7_M	Myo1c	Unconvent	R.LLQSNPVLEAFGNAK#.T	160.20	44.15	3.63	0.28
Q9WTI7_M	Myo1c	Unconvent	R.NPQSYLYLVK#.G	172.09	41.60	4.14	0.24
Q9WTI7_M	Myo1c	Unconvent	R.NVLDTSWPTPPPALR.E	24.70	37.55	0.66	1.52
Q9WTI7_M	Myo1c	Unconvent	K.QK#GDVVLQSDHVIETLTK#.T	28.90	8.71	3.32	0.30
Q9WTI7_M	Myo1c	Unconvent	R.QLLLTPSAVVIVEDAK#.V	124.10	26.81	4.63	0.22
Q9WTI7_M	Myo1c	Unconvent	K.RPETVATQFK.M	5.81	9.25	0.63	1.59
Q9WTI7_M	Myo1c	Unconvent	R.TFTWLVR.K	14.52	17.18	0.85	1.18
Q9WTI7_M	Myo1c	Unconvent	K.TLFATEDSLEVR.R	22.68	25.63	0.88	1.13
Q9WTI7_M	Myo1c	Unconvent	R.VLQSLGSEPIQYAVPVVK#.Y	150.93	38.18	3.95	0.25
Q9WTI7_M	Myo1c	Unconvent	R.VNNININQGSITFAGGPGR.D	9.45	12.06	0.78	1.28
Q9WTI7_M	Myo1c	Unconvent	K.YM*DVQFDFK#.G	80.56	21.48	3.75	0.27
Q5SYD0_M	Myo1d	Unconvent	R.AWEGNYLASK#PDTPQTSGTFVPVANELK#.R	2.78	2.60	1.07	0.94
Q5SYD0_M	Myo1d	Unconvent	R.IGELVGVLVNHFK#.S	10.82	6.50	1.66	0.60
Q5SYD0_M	Myo1d	Unconvent	K.VVSVIAELLSTK#.A	13.74	8.59	1.60	0.63
E9Q634_M	Myo1e	Unconvent	K.FSNTLELK#.L	8.53	5.76	1.48	0.67
E9Q634_M	Myo1e	Unconvent	R.SFHIFYQLIEGASPEQK#.Q	5.43	6.19	0.88	1.14
E9Q634_M	Myo1e	Unconvent	K.DIILQSNPLLEAFGNAK#.T	33.77	20.37	1.66	0.60
E9Q634_M	Myo1e	Unconvent	K.FSNTLELK#.L	13.10	12.22	1.07	0.93
E9Q634_M	Myo1e	Unconvent	K.TEFLSLLAK#.R	20.01	9.04	2.21	0.45
E9Q634_M	Myo1e	Unconvent	K.VLQVSIGPGLPK#.N	19.56	11.94	1.64	0.61
E9Q634_M	Myo1e	Unconvent	K.YFEIQFSPGGEPDGGK#.I	9.42	4.39	2.14	0.47
Q99104_M	Myo5a	Unconvent	R.NPDILVGENDLTALSYLHEPAVLHNLR.V	2.92	9.49	0.31	3.25
Q99104_M	Myo5a	Unconvent	K.SAPEVTAPGAPAYR.V	1.61	6.53	0.25	4.05
Q99104_M	Myo5a	Unconvent	K.VLNLYTPVNEFEER.V	2.61	7.25	0.36	2.78
P97479_M	Myo7a	Unconvent	K.YVVALQDNPNPAGEESGFLSFAK#.G	4.71	3.69	1.28	0.78
Q9QY06_M	Myo9b	Unconvent	K.FLDEFLLNK#.V	11.88	8.58	1.39	0.72
Q9QY06_M	Myo9b	Unconvent	K.LILPYSLSEAITAR.D	1.23	8.18	0.15	6.67
Q9QY06_M	Myo9b	Unconvent	R.TILGAGPVLEAFGNAK#.T	15.10	10.44	1.45	0.69
Q9QY06_M	Myo9b	Unconvent	K.TPIESLFIEATER.F	3.52	8.88	0.40	2.52
Q9CQ25_M	Mzt2	Mitotic-spi	R.LASDPQDSVPISLSTSTSETR.G	2.02	4.30	0.47	2.13
G3X8Y3_G	Naa15	N-alpha-ace	K.FGEALK#K#.C	27.42	13.58	2.02	0.50
G3X8Y3_G	Naa15	N-alpha-ace	K.IYEEAWTK#.Y	41.41	13.84	2.99	0.33
G3X8Y3_G	Naa15	N-alpha-ace	R.LEDAADVYR.G	14.38	24.50	0.59	1.70
G3X8Y3_G	Naa15	N-alpha-ace	K.M*VYYLDSSSQK#.R	25.15	5.86	4.29	0.23
G3X8Y3_G	Naa15	N-alpha-ace	R.NPENWAYYK#.G	31.33	9.41	3.33	0.30
G3X8Y3_G	Naa15	N-alpha-ace	K.TQQTSPDKVDYEYSELLLYQNQVLR.E	6.12	8.89	0.69	1.45
G3X8Y3_G	Naa15	N-alpha-ace	K.VAIVEELVVGYETSLK#.S	11.17	2.92	3.82	0.26
G3X8Y3_G	Naa15	N-alpha-ace	K.VAIVEELVVGYETSLK#.S	22.83	7.28	3.14	0.32
G3X8Y3_G	Naa15	N-alpha-ace	K.VETPLEEAIK#.F	57.57	20.73	2.78	0.36
G3X8Y3_G	Naa15	N-alpha-ace	R.AIELATTLDGSLTNR.N	12.12	16.28	0.74	1.34
G3X8Y3_G	Naa15	N-alpha-ace	K.ITVNGDSSAETEELANEI.-	9.15	9.15	1.00	1.00
G3X8Y3_G	Naa15	N-alpha-ace	K.IYEEAWTK#.Y	63.44	21.53	2.95	0.34
G3X8Y3_G	Naa15	N-alpha-ace	K.K#K#DDDDEEIGGPK#.E	2.76	2.82	0.98	1.02
G3X8Y3_G	Naa15	N-alpha-ace	R.LFGATNPK#.N	123.02	31.77	3.87	0.26
G3X8Y3_G	Naa15	N-alpha-ace	K.LHDNPLTDENK#EHEADTANM*SDK#.E	33.76	8.75	3.86	0.26
G3X8Y3_G	Naa15	N-alpha-ace	K.M*VYYLDSSSQK#.R	44.08	12.44	3.54	0.28
G3X8Y3_G	Naa15	N-alpha-ace	K.MVYYLDSSSQK#.R	12.93	4.44	2.91	0.34
G3X8Y3_G	Naa15	N-alpha-ace	K.NFNETFLK#.R	74.31	16.33	4.55	0.22
G3X8Y3_G	Naa15	N-alpha-ace	R.NPENWAYYK#.G	69.96	18.78	3.73	0.27
G3X8Y3_G	Naa15	N-alpha-ace	R.SYVDLLK#.L	59.38	11.79	5.04	0.20
G3X8Y3_G	Naa15	N-alpha-ace	K.TQQTSPDKVDYEYSELLLYQNQVLR.E	10.45	10.94	0.96	1.05
G3X8Y3_G	Naa15	N-alpha-ace	K.VAIVEELVVGYETSLK#.S	23.24	4.80	4.84	0.21
G3X8Y3_G	Naa15	N-alpha-ace	K.VETPLEEAIK#.F	124.11	37.17	3.34	0.30
G3X8Y3_G	Naa15	N-alpha-ace	R.WM*DEAQALDTADR.F	8.21	9.15	0.90	1.11
Q9DBB4_N	Naa16	N-alpha-ace	K.FAEHGETLAM*K#.G	29.78	11.65	2.56	0.39
Q9DBB4_N	Naa16	N-alpha-ace	K.FLLM*LQSVK#.R	14.37	5.44	2.64	0.38
Q9DBB4_N	Naa16	N-alpha-ace	K.FLLMLQSVK#.R	10.78	4.45	2.42	0.41
Q9DBB4_N	Naa16	N-alpha-ace	K.FAEHGETLAM*K#.G	65.94	18.01	3.66	0.27
Q9DBB4_N	Naa16	N-alpha-ace	K.FLLM*LQSVK#.R	24.86	8.37	2.97	0.34
Q9DBB4_N	Naa16	N-alpha-ace	K.FLLMLQSVK#.R	14.54	5.35	2.72	0.37
Q9DBB4_N	Naa16	N-alpha-ace	R.VDNPLEEAIK#.F	8.82	3.57	2.47	0.40
Q6PHQ8_N	Naa35	N-alpha-ace	K.VLNFEQAIK#.D	16.48	6.59	2.50	0.40
Q8VE10_N	Naa40	N-alpha-ace	R.VSGLEPATVDWAFDLTK.T	3.62	4.72	0.77	1.30
Q8VE10_N	Naa40	N-alpha-ace	K.FLIQILQLM*ANSTQM*K.K	1.54	4.44	0.35	2.88

Q8VE10_N/	Naa40	N-alpha-ace	R.LGDPLEAFPVFK.K	11.08	21.80	0.51	1.97
Q8VE10_N/	Naa40	N-alpha-ace	R.VSGLEPATVDWAFDLTK.T	9.33	9.59	0.97	1.03
Q8VE10_N/	Naa40	N-alpha-ace	R.VSGLEPATVDWAFDLTK.T	2.89	4.53	0.64	1.57
Q6PGB6_N	Naa50	N-alpha-ace	K.FGFEIIETK#.K	5.01	4.61	1.09	0.92
Q61127_N	Nab2	NGFI-A-bin	R.GDTGEIASLLK#.L	38.58	28.83	1.34	0.75
Q61127_N	Nab2	NGFI-A-bin	R.HILQQTLM*DEGLR.L	2.26	5.28	0.43	2.33
Q61127_N	Nab2	NGFI-A-bin	R.M*VVESVER.I	8.69	22.98	0.38	2.64
Q61127_N	Nab2	NGFI-A-bin	K.SPLELGEK#.L	21.15	20.37	1.04	0.96
Q61127_N	Nab2	NGFI-A-bin	K.YSVIYGR.L	6.67	20.26	0.33	3.04
P70670_N/	Naca	Nascent po	K.IEDLSQQAQLAAAEK#.F	90.22	33.53	2.69	0.37
P70670_N/	Naca	Nascent po	K.IEDLSQQAQLAAAEK#.F	25.28	9.35	2.70	0.37
P70670_N/	Naca	Nascent po	K.KAPK#TVDPK.Q	3.53	2.47	1.43	0.70
P70670_N/	Naca	Nascent po	K.NILFVITKPDVYK.S	26.13	11.59	2.25	0.44
P70670_N/	Naca	Nascent po	K.NNSNDIVNAIM*ELTM*.-	16.92	16.92	1.00	1.00
P70670_N/	Naca	Nascent po	K.SPASDTYIVFGEAK#.I	96.95	41.71	2.32	0.43
P70670_N/	Naca	Nascent po	R.LLAVDSGAAPSDDK#.G	20.31	2.76	7.36	0.14
Q7TSZ8_NA	Nacc1	Nucleus acc	R.AVLAASSSYFR.D	1.92	5.57	0.34	2.91
Q99KQ4_N	Nampt	Nicotinami	K.AVPEGSVIPR.G	24.04	36.52	0.66	1.52
Q99KQ4_N	Nampt	Nicotinami	R.EHFQDDVFNER.G	7.13	16.72	0.43	2.35
Q99KQ4_N	Nampt	Nicotinami	K.GTDTVAGIALIK#.K	158.24	60.38	2.62	0.38
Q99KQ4_N	Nampt	Nicotinami	R.GWNYILEK#.Y	73.89	27.22	2.71	0.37
Q99KQ4_N	Nampt	Nicotinami	K.K#WSIENVSFGSGGALLQK#.L	19.28	8.21	2.35	0.43
Q99KQ4_N	Nampt	Nicotinami	K.NAQLNIEQDVAPH.-	113.08	113.08	1.00	1.00
Q99KQ4_N	Nampt	Nicotinami	K.SYSFDEVRK.N	7.95	9.38	0.85	1.18
Q99KQ4_N	Nampt	Nicotinami	R.VIQGDGVDINTLQEIVEGM*K#.Q	41.81	10.21	4.09	0.24
Q99KQ4_N	Nampt	Nicotinami	R.VIQGDGVDINTLQEIVEGMK#.Q	20.79	6.37	3.27	0.31
Q99KQ4_N	Nampt	Nicotinami	K.VK#YEETVFYGLQYILNK#.Y	37.67	17.42	2.16	0.46
Q99KQ4_N	Nampt	Nicotinami	K.VLDILGK#.K	71.54	25.87	2.77	0.36
Q99KQ4_N	Nampt	Nicotinami	K.WSIENVSFGSGGALLQK#.L	36.64	11.63	3.15	0.32
Q99KQ4_N	Nampt	Nicotinami	K.YDGHLPIEVK#.A	111.28	49.29	2.26	0.44
Q99KQ4_N	Nampt	Nicotinami	K.YEETVFYGLQYILNK#.Y	39.39	13.63	2.89	0.35
Q99KQ4_N	Nampt	Nicotinami	K.YLLETSGNLDGLEYK#.L	98.06	33.08	2.96	0.34
Q99KQ4_N	Nampt	Nicotinami	K.K#WSIENVSFGSGGALLQK#.L	32.16	15.22	2.11	0.47
Q99KQ4_N	Nampt	Nicotinami	K.NAQLNIEQDVAPH.-	119.61	119.61	1.00	1.00
Q99KQ4_N	Nampt	Nicotinami	R.STEAPLIIRPDSGNPLDTVLK.V	74.64	182.86	0.41	2.45
Q99KQ4_N	Nampt	Nicotinami	K.SYSFDEVRK.N	6.28	11.40	0.55	1.82
Q99KQ4_N	Nampt	Nicotinami	R.TPAGNFVTLEEGK#GDLEEYGHDLLHTVFK#.N	43.08	17.05	2.53	0.40
Q99KQ4_N	Nampt	Nicotinami	R.VIQGDGVDINTLQEIVEGM*K#.Q	24.81	12.78	1.94	0.51
Q99KQ4_N	Nampt	Nicotinami	R.VIQGDGVDINTLQEIVEGMK#.Q	19.56	7.42	2.64	0.38
Q99KQ4_N	Nampt	Nicotinami	K.VLDILGK#.K	47.64	17.37	2.74	0.36
Q99KQ4_N	Nampt	Nicotinami	K.WSIENVSFGSGGALLQK#.L	57.78	24.85	2.33	0.43
Q99KQ4_N	Nampt	Nicotinami	K.YLLETSGNLDGLEYK#.L	5.60	4.48	1.25	0.80
Q99KQ4_N	Nampt	Nicotinami	R.GWNYILEK#.Y	18.04	6.18	2.92	0.34
Q99KQ4_N	Nampt	Nicotinami	K.NAQLNIEQDVAPH.-	25.13	25.13	1.00	1.00
Q99KQ4_N	Nampt	Nicotinami	R.STEAPLIIRPDSGNPLDTVLK.V	9.65	14.31	0.67	1.48
Q99KQ4_N	Nampt	Nicotinami	R.TPAGNFVTLEEGK#GDLEEYGHDLLHTVFK#.N	19.56	10.93	1.79	0.56
Q99KQ4_N	Nampt	Nicotinami	R.VIQGDGVDINTLQEIVEGM*K#.Q	13.24	5.00	2.65	0.38
Q99KQ4_N	Nampt	Nicotinami	K.VK#YEETVFYGLQYILNK#.Y	10.21	9.15	1.12	0.90
Q99KQ4_N	Nampt	Nicotinami	K.VLDILGK#.K	16.69	5.83	2.86	0.35
Q99KQ4_N	Nampt	Nicotinami	K.WSIENVSFGSGGALLQK#.L	9.52	3.57	2.67	0.37
Q99KQ4_N	Nampt	Nicotinami	K.YDGHLPIEVK#.A	17.01	6.35	2.68	0.37
Q99KQ4_N	Nampt	Nicotinami	K.YLLETSGNLDGLEYK#.L	20.45	4.74	4.32	0.23
Q99KQ4_N	Nampt	Nicotinami	R.GWNYILEK#.Y	16.42	4.71	3.48	0.29
Q99KQ4_N	Nampt	Nicotinami	K.NAQLNIEQDVAPH.-	29.86	29.86	1.00	1.00
Q99KQ4_N	Nampt	Nicotinami	R.STEAPLIIRPDSGNPLDTVLK.V	15.00	21.14	0.71	1.41
Q99KQ4_N	Nampt	Nicotinami	R.VIQGDGVDINTLQEIVEGM*K#.Q	12.93	7.18	1.80	0.56
Q99KQ4_N	Nampt	Nicotinami	R.VIQGDGVDINTLQEIVEGMK#.Q	4.07	4.01	1.02	0.98
Q99KQ4_N	Nampt	Nicotinami	K.VLDILGK#.K	29.80	9.69	3.08	0.33
Q99KQ4_N	Nampt	Nicotinami	K.WSIENVSFGSGGALLQK#.L	13.19	3.98	3.32	0.30
Q99KQ4_N	Nampt	Nicotinami	K.YDGHLPIEVK#.A	30.39	12.10	2.51	0.40
Q99J77_Q9	Nans	N-acetylne	K.VGSGDTNNFPYLEK#.T	13.06	2.35	5.57	0.18
Q99J77_Q9	Nans	N-acetylne	K.VK#IPAGTTLTLDM*LTVK#.V	8.21	2.86	2.87	0.35
P28656_NI	Nap1l1	Nucleosom	K.FSDAGQPM*SFVLEFHFEPNDYFTNEVLTK#.T	13.27	3.59	3.69	0.27
P28656_NI	Nap1l1	Nucleosom	K.FYEEVHDLER.K	7.60	11.08	0.69	1.46
P28656_NI	Nap1l1	Nucleosom	R.LDGLVDTPTGYIESLPK#.V	132.67	31.84	4.17	0.24
P28656_NI	Nap1l1	Nucleosom	K.NVDLLSDM*VQEHDEPILK#.H	60.56	14.09	4.30	0.23
P28656_NI	Nap1l1	Nucleosom	K.NVDLLSDMVQEHDEPILK#.H	43.81	10.97	3.99	0.25
P28656_NI	Nap1l1	Nucleosom	K.YAVLYQPLFDK#.R	18.53	5.07	3.65	0.27
P28656_NI	Nap1l1	Nucleosom	R.LDGLVDTPTGYIESLPK#.V	13.35	5.88	2.27	0.44
Q78ZA7_NI	Nap1l4	Nucleosom	R.LDNVSHTPSSYIETLPK#.A	15.00	3.53	4.26	0.24
Q78ZA7_NI	Nap1l4	Nucleosom	K.QVPNESFFNFFSPLK#.A	13.10	4.96	2.64	0.38
Q78ZA7_NI	Nap1l4	Nucleosom	K.YAALYQPLFDK#.R	7.92	2.34	3.38	0.30
Q9DB05_SI	Napa	Alpha-solul	K.AIAHYEQSADYYK#GEESNSSANK#.C	18.18	2.58	7.06	0.14
Q9DB05_SI	Napa	Alpha-solul	K.AIDIYEQVGTSAM*DSPLLK#.Y	13.82	5.18	2.67	0.37
Q9DB05_SI	Napa	Alpha-solul	K.AIDIYEQVGTSAMDSPLLK#.Y	10.39	2.54	4.09	0.24
Q9DB05_SI	Napa	Alpha-solul	K.HHISIAEIYETELVDVEK#.A	11.89	5.70	2.09	0.48
Q9DB05_SI	Napa	Alpha-solul	K.LLEAHEEQNVDSYTEAVK#.E	23.18	9.76	2.37	0.42
Q9DB05_SI	Napa	Alpha-solul	K.NSQSFFSGLFGGSSK#.I	53.24	14.31	3.72	0.27
Q9DB05_SI	Napa	Alpha-solul	K.VAGYAAQLEQYQK#.A	52.66	15.03	3.50	0.29
Q9DB05_SI	Napa	Alpha-solul	K.VAGYAAQLEQYQK#.A	12.61	6.02	2.09	0.48
Q9DB05_SI	Napa	Alpha-solul	K.NSQSFFSGLFGGSSK#.I	11.55	4.32	2.67	0.37
Q9DB05_SI	Napa	Alpha-solul	K.VAGYAAQLEQYQK#.A	14.18	4.77	2.97	0.34
Q9CWZ7_S	Napg	Gamma-sol	K.LGLSLVVPGGGIK#.K	7.34	3.49	2.11	0.47
Q8BP47_SY	Nars	Asparagine-	K.SPVASIVYELNPNFK#PPK#.R	17.22	4.35	3.96	0.25
Q8BP47_SY	Nars	Asparagine-	R.MNYSDAIEWLK#.E	19.64	6.50	3.02	0.33
Q8BP47_SY	Nars	Asparagine-	K.SPVASIVYELNPNFK#PPK#.R	52.69	7.97	6.62	0.15
Q8BP47_SY	Nars	Asparagine-	R.SWDSEEILEGYK#.R	8.16	2.52	3.23	0.31
Q99MD9_N	Nasp	Nuclear aut	R.SGNVAELALK#.A	27.38	6.27	4.37	0.23
Q99MD9_N	Nasp	Nuclear aut	R.SGNVAELALK#.A	18.92	3.66	5.17	0.19
Q8K224_N	Nat10	N-acetyltra	R.QQSAQSQVSTTAENK#.T	10.76	4.92	2.18	0.46
Q8K224_N	Nat10	N-acetyltra	K.AGQNASIVSLK#.S	27.06	15.43	1.75	0.57
Q8K224_N	Nat10	N-acetyltra	K.FIEGISEK#.T	23.06	10.18	2.26	0.44
Q8K224_N	Nat10	N-acetyltra	R.K#DLPPLLLK#.L	9.35	6.49	1.44	0.69
Q8K224_N	Nat10	N-acetyltra	R.LDYLGVSYGLTPR.L	7.86	8.83	0.89	1.12
Q8K224_N	Nat10	N-acetyltra	K.SGTLNLKQDDPFELFVAATNIR.Y	3.98	5.00	0.80	1.26
Q8BVG8_N	Nat14	N-acetyltra	R.AWAGSMGEPRAR.L	1.77	10.85	0.16	6.14
Q8K2Z4_CI	Ncapd2	Condensin	K.GFAAFLTELAER.I	3.58	6.96	0.52	1.94
Q8K2Z4_CI	Ncapd2	Condensin	K.GNAIYNLLPDIISR.L	3.11	11.08	0.28	3.56
Q8K2Z4_CI	Ncapd2	Condensin	K.ITEAIGIISK#.M	22.02	15.05	1.46	0.68
Q8K2Z4_CI	Ncapd2	Condensin	K.LPQEEGDHQIADAETAEEVK#.G	14.08	7.35	1.91	0.52
Q8K2Z4_CI	Ncapd2	Condensin	K.LSDIDLAGPLQK#.E	11.22	7.10	1.58	0.63
Q8K2Z4_CI	Ncapd2	Condensin	K.STLQQLLK#.L	15.00	8.29	1.81	0.55
Q8K2Z4_CI	Ncapd2	Condensin	K.AIIDEFEQK#.L	87.01	43.96	1.98	0.51

Q8K2Z4_CI	Ncapd2	Condensin	K.DK#QTESLVEK#.L	28.31	15.66	1.81	0.55
Q8K2Z4_CI	Ncapd2	Condensin	R.DQFLDILQAHGHDVNSFVR.S	7.07	19.52	0.36	2.76
Q8K2Z4_CI	Ncapd2	Condensin	K.DSPSVPEPEGSQSNDELVK#.Q	14.78	9.70	1.52	0.66
Q8K2Z4_CI	Ncapd2	Condensin	R.EAVLNAYR.Q	17.90	35.06	0.51	1.96
Q8K2Z4_CI	Ncapd2	Condensin	R.FPNLVDPWTPHLYAR.L	8.50	24.17	0.35	2.85
Q8K2Z4_CI	Ncapd2	Condensin	K.GFAAFLTELAER.I	12.27	34.20	0.36	2.79
Q8K2Z4_CI	Ncapd2	Condensin	K.GFAHPDPLWIPFK#.E	30.68	22.73	1.35	0.74
Q8K2Z4_CI	Ncapd2	Condensin	R.GM*DGIEEFETGQGGSQR.A	5.61	12.21	0.46	2.18
Q8K2Z4_CI	Ncapd2	Condensin	K.GNAIYNLLPDIISR.L	13.66	49.67	0.27	3.64
Q8K2Z4_CI	Ncapd2	Condensin	K.ITEAIGIISK#.M	88.28	55.09	1.60	0.62
Q8K2Z4_CI	Ncapd2	Condensin	R.LLESFENMTSQTSLIDLDIGGK#.G	4.28	1.84	2.32	0.43
Q8K2Z4_CI	Ncapd2	Condensin	R.LLFTM*LEK#.S	27.90	16.83	1.66	0.60
Q8K2Z4_CI	Ncapd2	Condensin	R.LLFTMLEK#.S	11.56	11.40	1.01	0.99
Q8K2Z4_CI	Ncapd2	Condensin	K.LPQEEGDHQIADAETAEEVK#.G	58.76	38.89	1.51	0.66
Q8K2Z4_CI	Ncapd2	Condensin	K.LPQEEGDHQIADAETAEEVKGR.I	3.23	11.74	0.28	3.63
Q8K2Z4_CI	Ncapd2	Condensin	K.LSDIDLAGPLQK#.E	44.23	28.44	1.56	0.64
Q8K2Z4_CI	Ncapd2	Condensin	R.LSDPEGGVEEEPFHTIM*K#.Q	56.49	31.32	1.80	0.55
Q8K2Z4_CI	Ncapd2	Condensin	R.LSDPEGGVEEEPFHTIMK#.Q	27.37	18.19	1.50	0.66
Q8K2Z4_CI	Ncapd2	Condensin	R.M*LPLIWSK#.E	21.13	13.47	1.57	0.64
Q8K2Z4_CI	Ncapd2	Condensin	K.NFFNELSHK#.G	19.07	6.93	2.75	0.36
Q8K2Z4_CI	Ncapd2	Condensin	K.QLLSYITK#.D	39.79	24.01	1.66	0.60
Q8K2Z4_CI	Ncapd2	Condensin	R.SAAATAALDPEEEWDAM*LPELK#.S	5.11	2.00	2.55	0.39
Q8K2Z4_CI	Ncapd2	Condensin	K.SGGVNQYVVR.E	15.15	39.93	0.38	2.64
Q8K2Z4_CI	Ncapd2	Condensin	K.STLQQLLK#.L	61.48	31.97	1.92	0.52
Q8K2Z4_CI	Ncapd2	Condensin	K.TASSETTM*EEELGLVGGATADDTEAELIR.S	5.35	11.53	0.46	2.15
Q8K2Z4_CI	Ncapd2	Condensin	K.VK#GQVSEM*AVLLIDPVPQIAALAK#.N	21.15	10.11	2.09	0.48
Q8K2Z4_CI	Ncapd2	Condensin	R.VLQLFAR.I	8.70	23.69	0.37	2.72
Q6ZQK0_CI	Ncapd3	Condensin-	R.SNFTPTLPPISENGPLK#.I	4.36	1.95	2.24	0.45
Q6ZQK0_CI	Ncapd3	Condensin-	K.TVLEEQGLLK#.Q	19.82	15.64	1.27	0.79
Q6ZQK0_CI	Ncapd3	Condensin-	R.TYAAQSLVQLLTK#.L	18.76	9.23	2.03	0.49
Q6ZQK0_CI	Ncapd3	Condensin-	K.YNEQLAQEQALTEHANATK#.G	12.11	5.94	2.04	0.49
E9PWG6_E	Ncapg	Protein Nca	K.ALSLVELSSNVTK#.D	20.11	9.84	2.04	0.49
E9PWG6_E	Ncapg	Protein Nca	R.EFIGQQLILIM*K#.S	9.16	5.77	1.59	0.63
E9PWG6_E	Ncapg	Protein Nca	R.EFIGQQLILIMK#.S	13.88	8.82	1.57	0.64
E9PWG6_E	Ncapg	Protein Nca	R.IQAVLALSR.L	3.97	13.02	0.30	3.28
E9PWG6_E	Ncapg	Protein Nca	R.IQIVTEIISEIR.A	4.87	7.76	0.63	1.59
E9PWG6_E	Ncapg	Protein Nca	R.K#LAYQVLAEK#.V	16.80	7.69	2.19	0.46
E9PWG6_E	Ncapg	Protein Nca	K.LAYQVLAEK#.V	14.78	10.31	1.43	0.70
E9PWG6_E	Ncapg	Protein Nca	K.LLGNM*PENAQIDDDLFDKINEAM*LIR.L	8.53	4.69	1.82	0.55
E9PWG6_E	Ncapg	Protein Nca	K.LLSDFLDSEVSELR.T	16.74	36.36	0.46	2.17
E9PWG6_E	Ncapg	Protein Nca	K.LNLAEFLNEDTS.-	11.96	11.96	1.00	1.00
E9PWG6_E	Ncapg	Protein Nca	K.SK#LNLAEFLNEDTS.-	19.99	10.84	1.84	0.54
E9PWG6_E	Ncapg	Protein Nca	R.VLLLQQGLNDR.S	12.01	32.55	0.37	2.71
E9PWG6_E	Ncapg	Protein Nca	K.AIIDQLM*M*FGIEPFK#.T	18.13	7.77	2.33	0.43
E9PWG6_E	Ncapg	Protein Nca	K.ALSLVELSSNVTK#.D	25.85	12.95	2.00	0.50
E9PWG6_E	Ncapg	Protein Nca	K.EAFQLAQQPHQNQAK#.L	6.73	4.14	1.63	0.61
E9PWG6_E	Ncapg	Protein Nca	R.EFIGQQLILIM*K#.S	19.78	9.78	2.02	0.49
E9PWG6_E	Ncapg	Protein Nca	R.EFIGQQLILIMK#.S	12.63	5.61	2.25	0.44
E9PWG6_E	Ncapg	Protein Nca	K.ESDPGVVTQDVNTTTAVLQNENEYM*TPVR.D	2.68	5.07	0.53	1.89
E9PWG6_E	Ncapg	Protein Nca	R.FTEGNILEFLHR.L	12.31	32.56	0.38	2.65
E9PWG6_E	Ncapg	Protein Nca	K.GDFTFIGDLM*K#.R	9.92	6.42	1.54	0.65
E9PWG6_E	Ncapg	Protein Nca	R.IQAVLALSR.L	9.17	16.49	0.56	1.80
E9PWG6_E	Ncapg	Protein Nca	R.K#LAYQVLAEK#.V	18.48	12.09	1.53	0.65
E9PWG6_E	Ncapg	Protein Nca	K.LAYQVLAEK#.V	29.80	12.55	2.37	0.42
E9PWG6_E	Ncapg	Protein Nca	K.LLSDFLDSEVSELR.T	20.04	39.74	0.50	1.98
E9PWG6_E	Ncapg	Protein Nca	K.LNLAEFLNEDTS.-	19.24	19.24	1.00	1.00
E9PWG6_E	Ncapg	Protein Nca	K.NSQDYQALTVHDNLAIK#.I	36.62	15.59	2.35	0.43
E9PWG6_E	Ncapg	Protein Nca	K.SK#LNLAEFLNEDTS.-	30.21	12.09	2.50	0.40
E9PWG6_E	Ncapg	Protein Nca	K.SLDTSEEGGR.K	6.91	9.67	0.71	1.40
E9PWG6_E	Ncapg	Protein Nca	R.VLLLQQGLNDR.S	21.17	42.08	0.50	1.99
Q6DFV1_CI	Ncapg2	Condensin-	K.FAAVLPEYLK.V	7.87	6.88	1.14	0.87
Q6DFV1_CI	Ncapg2	Condensin-	R.LKDLLTETLLESPVDR.W	2.75	10.94	0.25	3.97
Q6DFV1_CI	Ncapg2	Condensin-	R.VAFVDLLLK#.I	18.63	17.67	1.05	0.95
Q6DFV1_CI	Ncapg2	Condensin-	K.VLPLLEDQEEEYLK#.L	7.99	8.09	0.99	1.01
Q6DFV1_CI	Ncapg2	Condensin-	K.FAAVLPEYLK#.V	15.10	15.72	0.96	1.04
Q6DFV1_CI	Ncapg2	Condensin-	R.LKDLLTETLLESPVDR.W	2.56	14.89	0.17	5.82
Q6DFV1_CI	Ncapg2	Condensin-	R.VAFVDLLLK#.I	29.15	23.39	1.25	0.80
Q6DFV1_CI	Ncapg2	Condensin-	K.VLPLLEDQEEEYLK#.L	14.81	12.96	1.14	0.87
Q8C156_CI	Ncaph	Condensin	K.VAAGTLDASTK#.I	32.50	35.40	0.92	1.09
Q8C156_CI	Ncaph	Condensin	K.AATILTK#.S	57.36	41.19	1.39	0.72
Q8C156_CI	Ncaph	Condensin	K.EADTEANHTESGQEGAPEEVADEK.K	10.81	14.40	0.75	1.33
Q8C156_CI	Ncaph	Condensin	K.EADTEANHTESGQEGAPEEVADEKK.L	17.73	7.66	2.32	0.43
Q8C156_CI	Ncaph	Condensin	R.GQQDVLSSPLER.V	15.33	42.03	0.36	2.74
Q8C156_CI	Ncaph	Condensin	R.NIDVSTTISK#.F	80.25	50.19	1.60	0.63
Q8C156_CI	Ncaph	Condensin	R.SETM*NSSFLK#.A	28.73	40.01	0.72	1.39
Q8C156_CI	Ncaph	Condensin	K.TTQENGHISPENQGVDITTYQELNLVAEPQK#.V	3.01	1.92	1.57	0.64
Q8C156_CI	Ncaph	Condensin	K.VAAGTLDASTK#.I	111.27	67.48	1.65	0.61
Q8C156_CI	Ncaph	Condensin	R.VFDLQFSTDSIHLASPNR.N	10.94	31.15	0.35	2.85
Q8C156_CI	Ncaph	Condensin	K.WDSETHNESVSALVDK#.F	36.32	22.86	1.59	0.63
Q8C156_CI	Ncaph	Condensin	K.VAAGTLDASTK#.I	18.91	11.31	1.67	0.60
Q8BSP2_CI	Ncaph2	Condensin-	K.FIQETELSQR.I	5.81	18.87	0.31	3.25
Q8BSP2_CI	Ncaph2	Condensin-	R.LQETPDPWQSLDPFDSLESK.V	6.42	6.01	1.07	0.94
Q8BSP2_CI	Ncaph2	Condensin-	R.SQKDPEDAEEQPM*EVSR.N	3.00	12.84	0.23	4.28
Q8BSP2_CI	Ncaph2	Condensin-	R.TSQQSAILPR.R	6.66	20.94	0.32	3.14
Q3UYV9_N	Ncbp1	Nuclear cap	K.ANNYNEAVYLVR.F	7.39	17.10	0.43	2.31
Q3UYV9_N	Ncbp1	Nuclear cap	K.ATNDEIFSILK#.D	60.42	36.51	1.65	0.60
Q3UYV9_N	Ncbp1	Nuclear cap	R.IFSTTESYLK#.R	68.36	27.06	2.53	0.40
Q3UYV9_N	Ncbp1	Nuclear cap	K.ANNYNEAVYLVR.F	9.73	20.50	0.47	2.11
Q3UYV9_N	Ncbp1	Nuclear cap	K.ATNDEIFSILK#.D	105.02	41.25	2.55	0.39
Q3UYV9_N	Ncbp1	Nuclear cap	K.DGALEEQIER.L	23.29	23.48	0.99	1.01
Q3UYV9_N	Ncbp1	Nuclear cap	K.DVPNPNQVDDDDEGFR.F	5.68	8.35	0.68	1.47
Q3UYV9_N	Ncbp1	Nuclear cap	K.FHEVFK#.T	26.03	8.18	3.18	0.31
Q3UYV9_N	Ncbp1	Nuclear cap	R.IFSTTESYLK#.R	78.78	31.34	2.51	0.40
Q3UYV9_N	Ncbp1	Nuclear cap	R.M*FDYTDDPEGPVM*PGSHSVER.F	3.64	9.33	0.39	2.56
Q3UYV9_N	Ncbp1	Nuclear cap	R.NHPQMIAVLVDK#.M	9.45	3.10	3.05	0.33
Q9CQ49_N	Ncbp2	Nuclear cap	K.IIM*GLDK#.M	29.19	22.58	1.29	0.77
Q9CQ49_N	Ncbp2	Nuclear cap	R.SDSYVELSEYR.D	14.43	54.39	0.27	3.77
Q9CQ49_N	Ncbp2	Nuclear cap	R.TDWDAGFK#.E	26.32	22.63	1.16	0.86
Q9CQ49_N	Ncbp2	Nuclear cap	R.TDWDAGFKEGR.Q	2.15	7.39	0.29	3.43
P28660_N	Nckap1	Nck-associa	K.ELATVLSDQPGLLGPK#.A	10.15	2.05	4.96	0.20
P28660_N	Nckap1	Nck-associa	R.NNNQQLAQLQK#.E	13.37	4.48	2.98	0.34
P28660_N	Nckap1	Nck-associa	R.SVLQPSQQK#.L	12.59	2.40	5.25	0.19
P28660_N	Nckap1	Nck-associa	K.AINQIAAALFTIHK#.G	28.58	4.50	6.35	0.16

P28660_N	Nckap1	Nck-associa	K.ELATVLSDQPGLLGPK#.A	22.59	6.82	3.31	0.30
P28660_N	Nckap1	Nck-associa	R.NNNQQLAQLQK#.E	39.07	7.48	5.22	0.19
P28660_N	Nckap1	Nck-associa	R.SVLQPSQQK#.L	32.93	10.07	3.27	0.31
P09405_N	Ncl	Nucleolin	K.FAISELFAK#.N	18.21	4.87	3.74	0.27
P09405_N	Ncl	Nucleolin	K.GFGFVDFNSEEDAK#.A	9.21	1.66	5.56	0.18
P09405_N	Ncl	Nucleolin	K.GYAFIEFASFEDAK#.E	7.82	2.19	3.56	0.28
P09405_N	Ncl	Nucleolin	K.SEADAEK#NLEEK#.Q	4.70	2.01	2.34	0.43
P09405_N	Ncl	Nucleolin	K.ALELTGLK#.V	126.73	70.16	1.81	0.55
P09405_N	Ncl	Nucleolin	K.EAM*EDGEIDGNKVTLDWAKPK.G	20.57	7.27	2.83	0.35
P09405_N	Ncl	Nucleolin	K.ETLEEVFEK#.A	112.72	55.44	2.03	0.49
P09405_N	Ncl	Nucleolin	K.FAISELFAK#.N	235.63	120.77	1.95	0.51
P09405_N	Ncl	Nucleolin	K.FGYVDFESAEDLEK#.A	75.59	41.61	1.82	0.55
P09405_N	Ncl	Nucleolin	K.GFGFVDFNSEEDAK#.A	127.65	69.98	1.82	0.55
P09405_N	Ncl	Nucleolin	K.GLSEDTTEETLKESFEGSVR.A	30.43	64.12	0.47	2.11
P09405_N	Ncl	Nucleolin	K.GYAFIEFASFEDAK#.E	71.27	33.29	2.14	0.47
P09405_N	Ncl	Nucleolin	R.IVTDRETGSSK.G	4.41	10.32	0.43	2.34
P09405_N	Ncl	Nucleolin	R.K#FGYVDFESAEDLEK#.A	50.80	20.76	2.45	0.41
P09405_N	Ncl	Nucleolin	R.LELQGSNSR.S	33.63	59.69	0.56	1.77
P09405_N	Ncl	Nucleolin	K.NLSFNITEDELK#.E	17.87	8.48	2.11	0.47
P09405_N	Ncl	Nucleolin	K.NLSFNITEDELKEVFEDAM*EIR.L	9.34	16.52	0.57	1.77
P09405_N	Ncl	Nucleolin	K.QK#VEGSEPTTPFNLFIGNLNPNK#.S	20.74	13.75	1.51	0.66
P09405_N	Ncl	Nucleolin	K.SEADAEK#NLEEK#.Q	77.41	37.35	2.07	0.48
P09405_N	Ncl	Nucleolin	R.SVSLYYTGEK#.G	178.78	83.94	2.13	0.47
P09405_N	Ncl	Nucleolin	K.TLVLSNLSYSATK#.E	148.44	67.14	2.21	0.45
P09405_N	Ncl	Nucleolin	K.TLVLSNLSYSATK#ETLEEVFEK#.A	18.63	6.75	2.76	0.36
P09405_N	Ncl	Nucleolin	K.VEGSEPTTPFNLFIGNLNPNK#.S	72.92	36.70	1.99	0.50
P09405_N	Ncl	Nucleolin	K.FAISELFAK#.N	17.75	7.42	2.39	0.42
P09405_N	Ncl	Nucleolin	K.FGYVDFESAEDLEK#.A	5.05	2.56	1.97	0.51
P09405_N	Ncl	Nucleolin	K.GFGFVDFNSEEDAK#.A	13.73	2.58	5.32	0.19
O09000_N	Ncoa3	Nuclear rec	K.ELQPQADSGDSK.L	2.18	3.03	0.72	1.39
Q91W39_	Ncoa5	Nuclear rec	R.GGHPPAIQSLINLLADNR.Y	2.96	22.60	0.13	7.63
Q91W39_	Ncoa5	Nuclear rec	R.GPPGPESQSR.A	4.20	20.53	0.20	4.89
Q91W39_	Ncoa5	Nuclear rec	R.YFEEIQR.R	2.89	14.13	0.20	4.89
Q60974_N	Ncor1	Nuclear rec	R.GTAGAVQEGSITR.G	2.93	11.11	0.26	3.79
Q60974_N	Ncor1	Nuclear rec	K.ISVETISSLR.G	2.50	12.02	0.21	4.80
Q60974_N	Ncor1	Nuclear rec	R.SAAVSEQQQLEQK#.N	10.78	10.11	1.07	0.94
F8VQL9_F8	Ncor2	Nuclear rec	K.EAEKPAFFPAFPTEGPK.L	21.87	36.90	0.59	1.69
F8VQL9_F8	Ncor2	Nuclear rec	K.EGSITQGTPLK#.Y	21.03	28.34	0.74	1.35
F8VQL9_F8	Ncor2	Nuclear rec	R.ESSLALNYAAGPR.G	2.13	12.61	0.17	5.93
F8VQL9_F8	Ncor2	Nuclear rec	R.GHIPLAFDPTSIPR.G	4.53	33.33	0.14	7.37
F8VQL9_F8	Ncor2	Nuclear rec	R.GIIDLSQVPHLPVLVPPTPGTPATAIDR.L	2.32	15.09	0.15	6.51
F8VQL9_F8	Ncor2	Nuclear rec	R.GQAGPPESLGVPTAQETSVLR.G	5.66	6.91	0.82	1.22
F8VQL9_F8	Ncor2	Nuclear rec	R.GTALGSATSGSITK#.G	41.34	47.55	0.87	1.15
F8VQL9_F8	Ncor2	Nuclear rec	K.GTEAIETVSEAPLK#VEEAGSK#.A	36.12	44.84	0.81	1.24
F8VQL9_F8	Ncor2	Nuclear rec	R.GVTGVDLYR.G	4.59	21.78	0.21	4.74
F8VQL9_F8	Ncor2	Nuclear rec	K.GVVTSVEPGTPTVLR.W	2.85	15.24	0.19	5.34
F8VQL9_F8	Ncor2	Nuclear rec	R.GYPDTAALENR.Q	5.71	24.23	0.24	4.25
F8VQL9_F8	Ncor2	Nuclear rec	R.ILEGLGPQVELPLYNQPSDTR.Q	8.18	20.39	0.40	2.49
F8VQL9_F8	Ncor2	Nuclear rec	K.LILYFK#.R	17.36	3.77	4.60	0.22
F8VQL9_F8	Ncor2	Nuclear rec	K.NFGLIASFLER.K	0.88	14.77	0.06	16.87
F8VQL9_F8	Ncor2	Nuclear rec	K.SEAEEIDVGKPEEPEASEEPPESVK.S	5.48	8.42	0.65	1.54
F8VQL9_F8	Ncor2	Nuclear rec	R.SGTSSGAGGSITR.G	4.93	17.72	0.28	3.59
F8VQL9_F8	Ncor2	Nuclear rec	K.SPGNTSQPPAFFSK.L	8.69	11.15	0.78	1.28
F8VQL9_F8	Ncor2	Nuclear rec	K.TQSKPFSIQELELR.S	1.39	11.18	0.12	8.02
F8VQL9_F8	Ncor2	Nuclear rec	R.VVTLAQHISEVITQDYTR.H	2.71	15.64	0.17	5.76
F8VQL9_F8	Ncor2	Nuclear rec	K.YDSGAPSTGTK.K	6.98	8.62	0.81	1.23
Q8BNY6_N	Ncs1	Neuronal c	K.LYDLDNDGYITR.N	6.25	10.77	0.58	1.72
Q9D0F1_N	Ndc80	Kinetochor	K.ASLQADVQNYK.A	5.25	13.08	0.40	2.49
Q9D0F1_N	Ndc80	Kinetochor	K.SASELESLEK.H	6.75	12.37	0.55	1.83
Q9CPR8_M	Ndnl2	Melanoma-	R.DVYPNLLK#.L	8.60	5.64	1.53	0.66
Q9CPR8_M	Ndnl2	Melanoma-	K.VAELVQFLLIK#.D	33.76	19.45	1.74	0.58
Q62433_N	Ndrg1	Protein ND	R.LNITPNSGATGNNAGPK#.S	13.41	8.18	1.64	0.61
P33215_N	Nedd1	Protein NE	K.AASSVTAGVASSLSEK#.I	20.68	11.86	1.74	0.57
P46935_N	Nedd4	E3 ubiquiti	R.DDFLGQVDVPLYPLPTENPR.M	2.10	8.66	0.24	4.13
P46935_N	Nedd4	E3 ubiquiti	K.DILGASDPYVR.V	3.45	10.19	0.34	2.96
P46935_N	Nedd4	E3 ubiquiti	R.QISEDVDGPDNR.E	2.09	8.14	0.26	3.90
P46935_N	Nedd4	E3 ubiquiti	R.DDFLGQVDVPLYPLPTENPR.M	4.27	18.26	0.23	4.28
P46935_N	Nedd4	E3 ubiquiti	K.EGFFELIPQDLIK#.I	23.20	13.55	1.71	0.58
P46935_N	Nedd4	E3 ubiquiti	R.EWFFLLSK#.E	16.75	7.07	2.37	0.42
P46935_N	Nedd4	E3 ubiquiti	K.GLDYGGVAR.E	6.95	19.49	0.36	2.80
P46935_N	Nedd4	E3 ubiquiti	R.LLFEVFDENR.L	10.53	24.62	0.43	2.34
P46935_N	Nedd4	E3 ubiquiti	R.LQNVAITGPAVPYSR.D	3.81	17.04	0.22	4.47
P46935_N	Nedd4	E3 ubiquiti	R.LWIEFDGEK#.G	23.87	12.83	1.86	0.54
P46935_N	Nedd4	E3 ubiquiti	K.RPSPDDDLTDEDNDDM*QLQAQR.A	3.75	12.46	0.30	3.33
P46935_N	Nedd4	E3 ubiquiti	K.TGGSEIVVTNK#.N	38.63	25.37	1.52	0.66
P46935_N	Nedd4	E3 ubiquiti	K.VIAGIGLAK#.K	22.38	12.73	1.76	0.57
P46935_N	Nedd4	E3 ubiquiti	R.VTLYDPM*SGILTSVQTK#.T	7.41	5.66	1.31	0.76
P46935_N	Nedd4	E3 ubiquiti	R.VTLYDPMSGILTSVQTK#.T	7.28	3.98	1.83	0.55
P46935_N	Nedd4	E3 ubiquiti	K.WNEEILFR.V	6.03	13.50	0.45	2.24
P46935_N	Nedd4	E3 ubiquiti	R.DDFLGQVDVPLYPLPTENPR.M	1.70	5.71	0.30	3.36
Q9ES74_N	Nek7	Serine/thre	R.DIK#PANVFITATGVVK#.L	9.86	2.76	3.57	0.28
Q8K1R7_N	Nek9	Serine/thre	R.LGLDSEEDYYTPQR.V	4.32	6.85	0.63	1.59
Q8K1R7_N	Nek9	Serine/thre	R.TSEVYVWGGGK#.S	12.87	4.59	2.80	0.36
Q8K1R7_N	Nek9	Serine/thre	K.VTLLNAPTK#.R	13.75	7.78	1.77	0.57
Q8BG30_N	Nelfa	Negative el	R.EASRPPEEPSAPSPTLPTQFK.Q	3.59	5.88	0.61	1.64
Q8BG30_N	Nelfa	Negative el	K.LLDISELNTVGAGR.E	4.53	10.38	0.44	2.29
Q8BG30_N	Nelfa	Negative el	R.EASRPPEEPSAPSPTLPTQFK.Q	4.60	11.07	0.42	2.41
Q8BG30_N	Nelfa	Negative el	K.LLDISELNTVGAGR.E	7.03	15.19	0.46	2.16
Q8BG30_N	Nelfa	Negative el	K.NALTTLAGPLTPPVK#.H	11.08	5.34	2.08	0.48
Q8BG30_N	Nelfa	Negative el	R.SPTTPSVFSPSGNR.T	4.18	12.22	0.34	2.92
Q8BG30_N	Nelfa	Negative el	K.TLDTEVVEK#PTK#EETVVENATPDYAAGLVSTQK#.L	13.18	4.88	2.70	0.37
Q8C4Y3_N	Nelfb	Negative el	K.ALEPTGQSGEAVK#.E	35.55	15.27	2.33	0.43
Q8C4Y3_N	Nelfb	Negative el	K.ASVTYPNTLPESFTK#.F	16.55	7.04	2.35	0.43
Q8C4Y3_N	Nelfb	Negative el	R.DSPDLLLLLR.L	6.22	13.87	0.45	2.23
Q8C4Y3_N	Nelfb	Negative el	R.VSAIASEGK#.A	17.42	8.05	2.16	0.46
Q8C4Y3_N	Nelfb	Negative el	K.ALEPTGQSGEAVK#.E	19.33	7.04	2.75	0.36
Q8C4Y3_N	Nelfb	Negative el	K.ASVTYPNTLPESFTK#.F	16.99	4.96	3.43	0.29
Q8C4Y3_N	Nelfb	Negative el	R.LLALGQGAWDLIDSQVFK#EPK#.M	27.90	11.50	2.43	0.41
Q8C4Y3_N	Nelfb	Negative el	K.ALEPTGQSGEAVK#.E	53.33	22.51	2.37	0.42
Q8C4Y3_N	Nelfb	Negative el	K.ASVTYPNTLPESFTK#.F	28.20	12.64	2.23	0.45
Q8C4Y3_N	Nelfb	Negative el	R.DSPDLLLLLR.L	15.05	23.29	0.65	1.55
Q8C4Y3_N	Nelfb	Negative el	R.ELQGFLDGVK#.K	13.91	6.90	2.02	0.50
Q922L6_N	Nelfcd	Negative el	R.GALNPADITVLFK#.M	17.45	7.86	2.22	0.45

Q922L6_NI	Nelfcd	Negative el	R.GALNPADITVLFK#.M	21.13	10.52	2.01	0.50
Q922L6_NI	Nelfcd	Negative el	R.TSLATILDGGEENLEK#.N	12.72	82.60	0.15	6.49
Q922L6_NI	Nelfcd	Negative el	R.DYIM*EPSIFNTLK#.R	13.36	8.17	1.64	0.61
Q922L6_NI	Nelfcd	Negative el	R.FPVVAMGVLK#.W	8.37	3.39	2.47	0.40
Q922L6_NI	Nelfcd	Negative el	R.GALNPADITVLFK#.M	52.69	24.12	2.18	0.46
Q922L6_NI	Nelfcd	Negative el	R.TSLATILDGGEENLEK#.N	7.24	94.28	0.08	13.03
Q922L6_NI	Nelfcd	Negative el	R.VSIGK#DELK#.S	18.92	7.86	2.41	0.42
P19426_NI	Nelfe	Negative el	R.SLSEQPVVDTATATEQAK#.Q	22.23	9.17	2.43	0.41
P19426_NI	Nelfe	Negative el	K.SLYESFVSSSDR.L	4.59	6.82	0.67	1.49
P19426_NI	Nelfe	Negative el	R.SM*SADEDLQEPSR.R	4.98	7.48	0.67	1.50
P19426_NI	Nelfe	Negative el	K.SVWGSLAVQNSPK#.G	20.70	7.19	2.88	0.35
Q8CCP0_NI	Nemf	Nuclear exp	R.LTEVIAAAPK#.G	9.21	2.69	3.43	0.29
Q6P5H2_N	Nes	Nestin OS=I	K.AVEEGELLQDAVGEAWSLGSSEPK#.E	29.65	28.36	1.05	0.96
Q6P5H2_N	Nes	Nestin OS=I	K.EAGALDSGIPELPK#.T	20.44	5.88	3.48	0.29
Q6P5H2_N	Nes	Nestin OS=I	R.SLDENQETIVLLESK#.N	11.83	5.32	2.22	0.45
Q6P5H2_N	Nes	Nestin OS=I	R.SLDK#ENQESLVSLNEGGM*ETVK#.S	13.33	5.40	2.47	0.41
Q04690_NI	Nf1	Neurofibro	R.FINPAIVSPYEAGILDK#.K	4.55	4.38	1.04	0.96
Q04690_NI	Nf1	Neurofibro	K.ILQQGTEFDTLAETVLADRFER.L	2.12	6.53	0.32	3.08
Q9WV30_N	Nfat5	Nuclear fac	R.SHDVQPFTYTPDPAAGALNVNVK#.K	7.41	6.00	1.24	0.81
Q9WV30_N	Nfat5	Nuclear fac	K.VIFQENVSDENSWK#.S	7.69	4.18	1.84	0.54
Q80TR0_Q	Nfat5	MKIAA082	R.SHDVQPFTYTPDPAGALNVNVK#.K	6.52	3.11	2.10	0.48
Q9WV30_N	Nfat5	Nuclear fac	R.SHDVQPFTYTPDPAAGALNVNVK#.K	5.91	6.38	0.93	1.08
O09130_NI	Nfatc2ip	NFATC2-int	R.ILLLFGESELSPTATPSTLK#.L	8.18	5.00	1.63	0.61
O09130_NI	Nfatc2ip	NFATC2-int	R.LLDPGEAPVVPVYSGK#.V	8.05	4.25	1.89	0.53
O09130_NI	Nfatc2ip	NFATC2-int	K.VQSSLNLIPDNSSLLK#.L	8.99	3.27	2.75	0.36
P97863_NI	Nfib	Nuclear fac	K.NPPGYLEDSFVK#.S	7.48	9.43	0.79	1.26
P97863_NI	Nfib	Nuclear fac	K.SGVFNVSELVR.V	2.86	12.23	0.23	4.28
P70255_NI	Nfic	Nuclear fac	R.NWTEDIEGGISSPVK#.K	8.58	6.00	1.43	0.70
P70255_NI	Nfic	Nuclear fac	R.TPVVTGTGPNFSLGELQGHLAYDLNPASAGM*R.R	3.13	6.49	0.48	2.08
P70255_NI	Nfic	Nuclear fac	R.TPVVTGTGPNFSLGELQGHLAYDLNPASAGMR.R	2.15	2.20	0.98	1.02
P70255_NI	Nfic	Nuclear fac	R.TPVVTGTGPNFSLGELQGHLAYDLNPASAGM*R.R	3.09	5.46	0.57	1.77
O08750_NI	Nfil3	Nuclear fac	R.FIATQPISASDSR.-	4.22	9.44	0.45	2.24
P70257_NI	Nfix	Nuclear fac	R.AFSYTWFNLQAR.K	2.16	6.30	0.34	2.92
P70257_NI	Nfix	Nuclear fac	R.SITSPPSTSSTK.R	11.22	17.68	0.63	1.58
P70257_NI	Nfix	Nuclear fac	R.VSQTPVATASGPNFSLADLESPSYYNINQVTLGR.R	2.61	6.06	0.43	2.32
P70257_NI	Nfix	Nuclear fac	R.AVK#DELLGEK#PEIK#.Q	14.10	20.29	0.69	1.44
P70257_NI	Nfix	Nuclear fac	R.AVKDELLGEKPEIK.Q	15.86	22.97	0.69	1.45
P70257_NI	Nfix	Nuclear fac	R.SITSPPSTSSTK.R	9.16	10.15	0.90	1.11
P70257_NI	Nfix	Nuclear fac	R.SPAAGSSQSSGWPNDVDAGPASLKK.S	2.54	6.51	0.39	2.57
P70257_NI	Nfix	Nuclear fac	R.VSQTPVATASGPNFSLADLESPSYYNINQVTLGR.R	3.04	12.26	0.25	4.03
P70257_NI	Nfix	Nuclear fac	R.SITSPPSTSSTK.R	15.00	15.97	0.94	1.06
P70257_NI	Nfix	Nuclear fac	R.SPAAGSSQSSGWPNDVDAGPASLKK.S	2.78	8.03	0.35	2.89
P70257_NI	Nfix	Nuclear fac	R.VSQTPVATASGPNFSLADLESPSYYNINQVTLGR.R	3.35	12.54	0.27	3.75
P25799_NI	Nfkb1	Nuclear fac	R.GYNPGLLVHSDLAYLQAEGGGDR.Q	4.59	16.35	0.28	3.56
P25799_NI	Nfkb1	Nuclear fac	R.K#SDLETSEPK#PFLYYPEIK#.D	3.68	5.60	0.66	1.52
P25799_NI	Nfkb1	Nuclear fac	R.RLEPVVSDAIYDSK.A	4.44	10.53	0.42	2.37
P25799_NI	Nfkb1	Nuclear fac	K.VFETLEAR.M	8.05	17.83	0.45	2.22
P25799_NI	Nfkb1	Nuclear fac	R.GYNPGLLVHSDLAYLQAEGGGDR.Q	2.66	6.55	0.41	2.46
P25799_NI	Nfkb1	Nuclear fac	K.LGLGILNNAFR.L	4.31	11.13	0.39	2.58
P25799_NI	Nfkb1	Nuclear fac	K.TLM*DNYEVSGGTIK#.E	4.53	3.57	1.27	0.79
P25799_NI	Nfkb1	Nuclear fac	R.VGADLSLLDR.W	2.25	11.03	0.20	4.90
Q9WTK5_N	Nfkb2	Nuclear fac	K.DPAPETADGPYLVIVEQPK.Q	7.51	7.21	1.04	0.96
Q9WTK5_N	Nfkb2	Nuclear fac	K.DPAPETADGPYLVIVEQPK#.Q	7.01	8.64	0.81	1.23
Q9WTK5_N	Nfkb2	Nuclear fac	R.LFGLAQR.S	5.87	13.32	0.44	2.27
Q9WTK5_N	Nfkb2	Nuclear fac	R.TALHLATEMEELGLVTHLVTK#.L	8.24	8.37	0.98	1.02
Q9WTK5_N	Nfkb2	Nuclear fac	R.TFAGNTPLHLAAGLGSPTLTR.L	4.76	16.17	0.29	3.40
Q9WTK5_N	Nfkb2	Nuclear fac	R.ALLDYGVTADAR.A	2.58	11.42	0.23	4.42
Q6PIJ4_NF	Nfrkb	Nuclear fac	K.APSASVPSSAPAGTTVVK#.V	7.09	5.73	1.24	0.81
Q6PIJ4_NF	Nfrkb	Nuclear fac	R.AVPSSFSPFVEFK#.E	12.44	9.27	1.34	0.75
P70353_NI	Nfyc	Nuclear tra	K.AAQIFITELTLR.A	5.92	14.67	0.40	2.48
P70353_NI	Nfyc	Nuclear tra	K.M*ISAEAPVLFAK#.A	9.02	3.64	2.48	0.40
Q9DB96_N	Ngdn	Neuroguidi	K.NLQEQVM*AVTAQIQALTTK#.V	8.34	5.38	1.55	0.64
Q9D0T1_NI	Nhp2l1	NHP2-like p	K.AYPLADAHLTK#K#.L	5.57	3.86	1.44	0.69
Q9D0T1_NI	Nhp2l1	NHP2-like p	K.QQIQSIQQSIER.L	17.77	50.89	0.35	2.86
O88322_NI	Nid2	Nidogen-2 (	R.ITQTAEGLDPENYLSIK#.T	2.11	4.12	0.51	1.95
Q9CXK8_NI	Nip7	60S ribosor	K.LAANISGDK#.L	32.99	9.15	3.61	0.28
Q9CXK8_NI	Nip7	60S ribosor	R.LHVTALDYLAPYAK#.Y	25.11	24.42	1.03	0.97
Q9CXK8_NI	Nip7	60S ribosor	R.LHVTALDYLAPYAK.Y	5.66	6.25	0.90	1.11
Q9CXK8_NI	Nip7	60S ribosor	R.VYYVSEM*M*LK#.L	3.99	4.86	0.82	1.22
Q6KCD5_N	Nipbl	Nipped-B-li	K.AVYIEDVIER.V	3.38	14.05	0.24	4.16
Q6KCD5_N	Nipbl	Nipped-B-li	K.HQLNELGSESAK#.I	23.58	15.82	1.49	0.67
Q6KCD5_N	Nipbl	Nipped-B-li	K.LLM*EHLDPDEEEEEGEVSASTNAR.N	2.09	5.43	0.38	2.60
Q6KCD5_N	Nipbl	Nipped-B-li	K.LVNETFQK#.L	16.61	15.26	1.09	0.92
Q6KCD5_N	Nipbl	Nipped-B-li	R.NK#ADQQLVEIDK#K#.Y	18.14	10.78	1.68	0.59
Q6KCD5_N	Nipbl	Nipped-B-li	K.QVSGGEDEIQQLQK#.A	10.59	6.18	1.71	0.58
Q6KCD5_N	Nipbl	Nipped-B-li	R.TAQNFLSIFLK#.K	22.40	13.54	1.65	0.60
Q6KCD5_N	Nipbl	Nipped-B-li	R.VLGENAIAVR.T	6.17	18.98	0.32	3.08
Q80TM9_N	Nisch	Nischarin C	R.EVQWQVFVPSAESR.E	2.11	6.91	0.31	3.28
Q80TM9_N	Nisch	Nischarin C	R.GPAPAGGPAPAEALAQAEVPAQYPSER.L	4.34	14.68	0.30	3.38
Q80TM9_N	Nisch	Nischarin C	R.VPLSTVLLDPTR.S	4.14	19.76	0.21	4.77
Q9D0F4_NI	Nkap	NF-kappa-B	R.ALASFNQEER.R	5.84	25.62	0.23	4.39
Q9D0F4_NI	Nkap	NF-kappa-B	R.SKAEEPSDLIGPEAPK.T	20.48	20.19	1.01	0.99
Q9D0F4_NI	Nkap	NF-kappa-B	K.TLASQDDK#PLNYGHALLPGEGAAM*AEYVK#.A	8.60	7.43	1.16	0.86
Q9D0F4_NI	Nkap	NF-kappa-B	K.TLASQDDK#PLNYGHALLPGEGAAM*AEYVK#.A	2.00	3.12	0.64	1.56
Q8BY02_NI	Nkrf	NF-kappa-B	K.YEAAGEAVK#.T	51.50	25.87	1.99	0.50
P30415_NI	Nktr	NK-tumor r	R.DMPAITVEPEQNIPDVAPVVSDQKPSVSK.S	3.47	5.02	0.69	1.45
P30415_NI	Nktr	NK-tumor r	K.TTHLLPVQSTYSLTNIK.A	10.57	12.39	0.85	1.17
Q8VEJ4_NL	Nle1	Notchless p	K.TLESQSVETEK#.I	12.94	7.36	1.76	0.57
Q2LKV8_Q	Nlrp1b	NACHT-, LR	R.TLEENNLK#.L	18.77	4.26	4.40	0.23
Q99L48_NI	Nmd3	60S ribosor	R.DATIPVESDTDDEGAPR.I	2.22	7.96	0.28	3.59
Q99L48_NI	Nmd3	60S ribosor	R.DATIPVESDTDDEGAPR.I	3.12	14.62	0.21	4.69
O35309_NI	Nmi	N-myc-inte	R.SAVITFVETGVVDK#.I	9.07	6.77	1.34	0.75
Q8K2T1_NI	Nmral1	NmrA-like f	R.HTAEEYAALLSK#.H	10.91	7.03	1.55	0.64
Q9WV70_N	Noc2l	Nucleolar c	R.LEDLNFPEIK#.R	19.05	12.18	1.56	0.64
Q8R5K4_N	Nol6	Nucleolar p	R.EAVVWEAESLFEK.R	5.67	8.31	0.68	1.47
Q8R5K4_N	Nol6	Nucleolar p	R.LQVEELLK#.E	19.01	13.66	1.39	0.72
Q8R5K4_N	Nol6	Nucleolar p	R.TEPPAEGLLQPVNLSR.E	1.71	7.00	0.24	4.09
Q8R5K4_N	Nol6	Nucleolar p	K.VPPVPEAELTDQSWLPAGVR.V	3.78	12.18	0.31	3.22
Q9D7Z3_N	Nol7	Nucleolar p	K.AAAQFLTSTWGAQK#.Q	7.75	3.15	2.46	0.41
Q9D7Z3_N	Nol7	Nucleolar p	K.LLPDAVLEQLTTASEADIK#.K	3.69	3.76	0.98	1.02
Q3TZX8_N	Nol9	Polynucleo	K.FTPTLTSEYVELTDGLYTK#.S	5.35	5.48	0.98	1.02
Q3TZX8_N	Nol9	Polynucleo	R.LLVDLIR.V	3.18	10.18	0.31	3.20
Q3TZX8_N	Nol9	Polynucleo	K.FTPTLTSEYVELTDGLYTK#.S	5.87	4.75	1.24	0.81

Q99K48_N	Nono	Non-POU d	K.AFNLEK#.Q	124.71	72.30	1.72	0.58
Q99K48_N	Nono	Non-POU d	K.AGEVFIHK#.D	160.22	91.84	1.74	0.57
Q99K48_N	Nono	Non-POU d	K.AGEVFIHK#DK#.G	6.71	3.83	1.75	0.57
Q99K48_N	Nono	Non-POU d	K.ALIEMEK#.Q	46.16	24.45	1.89	0.53
Q99K48_N	Nono	Non-POU d	R.AVVIVDDR.G	30.38	80.96	0.38	2.66
Q99K48_N	Nono	Non-POU d	K.DKGFGFIR.L	22.11	54.12	0.41	2.45
Q99K48_N	Nono	Non-POU d	R.EKLEMEM*EAAR.H	4.38	10.88	0.40	2.48
Q99K48_N	Nono	Non-POU d	R.EKLEMEMEAAR.H	3.51	15.13	0.23	4.31
Q99K48_N	Nono	Non-POU d	R.EKLEM*EM*EAAR.H	6.42	18.01	0.36	2.80
Q99K48_N	Nono	Non-POU d	R.FAQPGSFEYEYAM*R.W	13.51	31.07	0.43	2.30
Q99K48_N	Nono	Non-POU d	R.FAQPGSFEYEYAMR.W	19.46	48.30	0.40	2.48
Q99K48_N	Nono	Non-POU d	R.FGQAATM*EGIGAIGGTPPAFNRPAPGAEFAPNK.R	3.19	3.80	0.84	1.19
Q99K48_N	Nono	Non-POU d	R.LFVGNLPPDITEEEM*R.K	5.15	16.42	0.31	3.19
Q99K48_N	Nono	Non-POU d	R.MEELHNQEVQK#.R	22.13	10.76	2.06	0.49
Q99K48_N	Nono	Non-POU d	R.RMEELHNQEVQK.R	22.19	65.50	0.34	2.95
Q99K48_N	Nono	Non-POU d	K.VELDNM*PLR.G	37.44	103.25	0.36	2.76
Q99K48_N	Nono	Non-POU d	R.AVVIVDDR.G	32.47	82.87	0.39	2.55
Q9CQS2_N	Nop10	H/ACA ribo	-.M*FLQYYLNEQGDR.V	1.96	3.66	0.53	1.87
Q9CQS2_N	Nop10	H/ACA ribo	K.VLM*TQQPRPVL.-	3.60	10.74	0.34	2.98
Q8R3N1_N	Nop14	Nucleolar p	K.AVAAELPYVFAAPESFEELK#.F	9.27	5.46	1.70	0.59
Q8R3N1_N	Nop14	Nucleolar p	K.AVAAELPYVFAAPESFEELK#.F	14.57	12.79	1.14	0.88
Q8R3N1_N	Nop14	Nucleolar p	K.AVAAELPYVFAAPESFEELK.F	20.04	17.17	1.17	0.86
Q9CPT5_N	Nop16	Nucleolar p	R.DEK#NYYQDTPK#.Q	4.92	1.41	3.49	0.29
Q9CPT5_N	Nop16	Nucleolar p	R.K#PYVVNDLEAEASLPEK#K#.G	27.83	17.58	1.58	0.63
Q9CPT5_N	Nop16	Nucleolar p	R.QNLAEM*GLAM*DPNK#.A	6.85	4.06	1.69	0.59
E9QN31_E	Nop2	Probable 2	K.AQDATAGVLWNEEDTDEDEDDDGVSPESHPR.K	2.16	6.20	0.35	2.87
E9QN31_E	Nop2	Probable 2	R.DLAQALINR.G	11.80	46.53	0.25	3.94
E9QN31_E	Nop2	Probable 2	K.DLATYYSYGDFLLSK#.L	26.55	21.11	1.26	0.79
E9QN31_E	Nop2	Probable 2	K.ELLLSAIDSVNAASK#.T	24.35	20.01	1.22	0.82
E9QN31_E	Nop2	Probable 2	K.ELLLSAIDSVNAASK.T	52.55	36.94	1.42	0.70
E9QN31_E	Nop2	Probable 2	K.FSNSIPQPHAGNSAAATPTEPDLKDQVTPK.S	4.65	4.36	1.07	0.94
E9QN31_E	Nop2	Probable 2	R.LVPTGLDFGQEGFTR.F	7.47	39.26	0.19	5.25
E9QN31_E	Nop2	Probable 2	K.NTGVILANDANADR.L	6.82	30.41	0.22	4.46
E9QN31_E	Nop2	Probable 2	R.TPPVPTPSEIR.A	3.58	54.58	0.07	15.26
E9QN31_E	Nop2	Probable 2	K.TSYIAQLMK#.N	11.24	7.11	1.58	0.63
E9QN31_E	Nop2	Probable 2	K.ELLLSAIDSVNAASK#.T	16.53	9.77	1.69	0.59
E9QN31_E	Nop2	Probable 2	R.LVPTGLDFGQEGFTR.F	8.70	12.69	0.69	1.46
Q9D6Z1_N	Nop56	Nucleolar p	K.EAVVQAEEAAAEITR.K	1.69	10.87	0.16	6.41
Q9D6Z1_N	Nop56	Nucleolar p	K.M*SQVAPSLSALIGEAVGAR.L	1.72	11.05	0.16	6.42
Q9D6Z1_N	Nop56	Nucleolar p	K.YPASTVQILGAEK#.A	9.23	9.05	1.02	0.98
Q9D6Z1_N	Nop56	Nucleolar p	K.EAVVQAEEAAAEITR.K	3.12	9.54	0.33	3.06
Q9D6Z1_N	Nop56	Nucleolar p	K.FSEEPEVAANFTK#.S	9.69	8.13	1.19	0.84
Q9D6Z1_N	Nop56	Nucleolar p	R.LLLETYLPSK.K	9.14	10.54	0.87	1.15
Q9D6Z1_N	Nop56	Nucleolar p	R.VVSLSEYR.Q	2.93	16.18	0.18	5.52
Q9D6Z1_N	Nop56	Nucleolar p	K.YPASTVQILGAEK#.A	15.08	16.30	0.92	1.08
Q9D6Z1_N	Nop56	Nucleolar p	K.EAVVQAEEAAAEITR.K	4.87	22.04	0.22	4.53
Q9D6Z1_N	Nop56	Nucleolar p	K.FSEEPEVAANFTK#.S	15.92	9.79	1.63	0.62
Q9D6Z1_N	Nop56	Nucleolar p	R.LAQFIGNR.R	7.36	23.71	0.31	3.22
Q9D6Z1_N	Nop56	Nucleolar p	K.LEEITM*DGAK#.A	13.94	17.02	0.82	1.22
Q9D6Z1_N	Nop56	Nucleolar p	R.LIAHAGSLTNLAK#.Y	44.28	36.60	1.21	0.83
Q9D6Z1_N	Nop56	Nucleolar p	R.LLLETYLPSK#.K	18.31	16.22	1.13	0.89
Q9D6Z1_N	Nop56	Nucleolar p	R.LLLETYLPSK#K#.K	25.46	13.84	1.84	0.54
Q9D6Z1_N	Nop56	Nucleolar p	R.LSFYETGEIPR.K	2.81	17.66	0.16	6.28
Q9D6Z1_N	Nop56	Nucleolar p	K.M*SQVAPSLSALIGEAVGAR.L	6.17	37.96	0.16	6.15
Q9D6Z1_N	Nop56	Nucleolar p	K.M*SQVAPSLSALIGEAVGAR.L	6.02	33.87	0.18	5.62
Q9D6Z1_N	Nop56	Nucleolar p	R.SSM*GM*DISAIDLINIESFSSR.V	4.22	10.01	0.42	2.37
Q9D6Z1_N	Nop56	Nucleolar p	K.SSPK#EEVASEPEEAASPTTPK#.K	19.34	10.78	1.79	0.56
Q9D6Z1_N	Nop56	Nucleolar p	K.VLLGVGDPK#.I	80.99	14.93	5.42	0.18
Q9D6Z1_N	Nop56	Nucleolar p	R.VVSLSEYR.Q	9.62	25.78	0.37	2.68
Q9D6Z1_N	Nop56	Nucleolar p	K.YPASTVQILGAEK#.A	43.95	32.49	1.35	0.74
Q6DFW4_N	Nop58	Nucleolar p	K.FQDTAEALAAFTALM*EGK#.I	7.80	5.36	1.45	0.69
Q6DFW4_N	Nop58	Nucleolar p	K.IKAEVEEEM*EEEEAEEEQVVEEEPTVK.K	3.61	2.78	1.30	0.77
Q6DFW4_N	Nop58	Nucleolar p	K.IK#AEVEEEMEEEEAEEEQVVEEEPTVK#.K	3.52	2.79	1.26	0.79
Q6DFW4_N	Nop58	Nucleolar p	R.K#IEEVDK#EDEITEK#.K	28.09	30.26	0.93	1.08
Q6DFW4_N	Nop58	Nucleolar p	K.K#LQEVDSLWK#.E	14.24	12.25	1.16	0.86
Q6DFW4_N	Nop58	Nucleolar p	R.LIAHAGSLLNLAK#.H	17.19	10.12	1.70	0.59
Q6DFW4_N	Nop58	Nucleolar p	K.NYASASLSEFLSEEVEAEVK#.A	11.07	5.53	2.00	0.50
Q6DFW4_N	Nop58	Nucleolar p	R.SQM*DGLIPGVEPR.E	2.44	13.03	0.19	5.34
Q6DFW4_N	Nop58	Nucleolar p	R.SQMDGLIPGVEPR.E	2.67	9.29	0.29	3.48
Q6DFW4_N	Nop58	Nucleolar p	R.TQLYEYLQNR.M	8.47	20.45	0.41	2.41
Q6DFW4_N	Nop58	Nucleolar p	R.YDAFGEDSSSAMGIENR.A	2.14	6.32	0.34	2.95
Q6DFW4_N	Nop58	Nucleolar p	K.YGLIYHASLVGQSSPK#.H	5.30	3.95	1.34	0.75
Q6DFW4_N	Nop58	Nucleolar p	K.NYASASLSEFLSEEVEAEVK#.A	9.03	4.36	2.07	0.48
Q6DFW4_N	Nop58	Nucleolar p	R.YDAFGEDSSSAM*GIENR.A	2.09	5.12	0.41	2.45
Q6DFW4_N	Nop58	Nucleolar p	K.FQDTAEALAAFTALM*EGK.I	7.14	3.98	1.79	0.56
Q6DFW4_N	Nop58	Nucleolar p	K.HAASTVQILGAEK#.A	14.38	10.48	1.37	0.73
Q6DFW4_N	Nop58	Nucleolar p	R.K#IEEVDK#EDEITEK#.K	20.64	18.41	1.12	0.89
Q6DFW4_N	Nop58	Nucleolar p	K.NYASASLSEFLSEEVEAEVK#.A	10.10	7.24	1.39	0.72
Q6DFW4_N	Nop58	Nucleolar p	K.YGLIYHASLVGQSSPK#.H	19.88	8.58	2.32	0.43
Q8BMC4_N	Nop9	Nucleolar p	R.TLLQVLGGTLLESER.G	2.88	7.35	0.39	2.55
Q8BMC4_N	Nop9	Nucleolar p	R.AEQAPEALPHLSPEALGYFR.R	8.39	23.56	0.36	2.81
Q8BMC4_N	Nop9	Nucleolar p	R.NVALTTFLK#.R	21.59	10.54	2.05	0.49
Q8BMC4_N	Nop9	Nucleolar p	R.VLDAIWSGAALGAR.K	3.87	10.68	0.36	2.76
Q9D6T0_N	Nosip	Nitric oxid	K.AATLPNTEGEQPGPSVGPVGK.D	8.35	15.23	0.55	1.82
Q9D6T0_N	Nosip	Nitric oxid	K.ALPSFWIPSLTPEAK.A	12.53	18.26	0.69	1.46
P60670_N	Nploc4	Nuclear pr	K.ESSSEQYVPDVFYK#.D	25.76	8.40	3.07	0.33
P60670_N	Nploc4	Nuclear pr	K.HGDLLFLFPSSLAGPSSEM*ETSTSVGLK#.A	11.67	5.91	1.97	0.51
P60670_N	Nploc4	Nuclear pr	K.AFGAPNVVEDEIDQYLSK#.Q	39.50	15.05	2.62	0.38
P60670_N	Nploc4	Nuclear pr	K.ESSSEQYVPDVFYK#.D	26.92	7.35	3.66	0.27
P60670_N	Nploc4	Nuclear pr	K.HGDLLFLFPSSLAGPSSEM*ETSTSVGLK#.A	13.41	3.74	3.59	0.28
P60670_N	Nploc4	Nuclear pr	K.HGDLLFLFPSSLAGPSSEMETSTSVGLK#.A	7.32	5.34	1.37	0.73
P60670_N	Nploc4	Nuclear pr	K.SLHLLK#.I	12.32	5.51	2.23	0.45
Q61937_N	Npm1	Nucleopho	K.DELHIVEAEAM*NYEGSPIK#.V	14.12	8.01	1.76	0.57
Q61937_N	Npm1	Nucleopho	K.FINYVK#.N	145.36	82.90	1.75	0.57
Q61937_N	Npm1	Nucleopho	K.GPSSVEDIK#.A	195.44	141.68	1.38	0.72
Q61937_N	Npm1	Nucleopho	K.M*QASIEK#.G	42.65	26.58	1.60	0.62
Q61937_N	Npm1	Nucleopho	K.MQASIEK#.G	77.98	44.52	1.75	0.57
Q61937_N	Npm1	Nucleopho	K.M*SVQPTVSLGGFEITPPVVLR.L	28.57	77.42	0.37	2.71
Q61937_N	Npm1	Nucleopho	K.MSVQPTVSLGGFEITPPVVLR.L	18.65	51.30	0.36	2.75
Q61937_N	Npm1	Nucleopho	R.M*TDQEAIQDLWQWR.K	8.58	15.95	0.54	1.86
Q61937_N	Npm1	Nucleopho	R.MTDQEAIQDLWQWR.K	6.55	17.33	0.38	2.65
Q61937_N	Npm1	Nucleopho	R.SAPGGGNK#VPQK#.K	35.32	29.07	1.21	0.82
Q61937_N	Npm1	Nucleopho	R.SAPGGGNK#VPQK#K#.V	9.72	8.46	1.15	0.87

Q61937_N	Npm1	Nucleopho	R.TVSLGAGAK#DELHIVEAEAM*NYEGSPIK#.V	15.00	7.48	2.01	0.50
Q61937_N	Npm1	Nucleopho	R.TVSLGAGAK#DELHIVEAEAMNYEGSPIK#.V	35.81	22.74	1.57	0.64
Q61937_N	Npm1	Nucleopho	K.VDNDENEHQLSLR.T	11.33	30.80	0.37	2.72
Q61937_N	Npm1	Nucleopho	K.VTLATLK#.M	170.10	127.07	1.34	0.75
Q61937_N	Npm1	Nucleopho	K.DELHIVEAEAM*NYEGSPIK#.V	9.87	11.12	0.89	1.13
Q61937_N	Npm1	Nucleopho	K.DELHIVEAEAMNYEGSPIK#.V	7.01	5.46	1.28	0.78
Q61937_N	Npm1	Nucleopho	K.M*SVQPTVSLGGFEITPPVVLR.L	1.78	8.03	0.22	4.51
Q61937_N	Npm1	Nucleopho	K.MSVQPTVSLGGFEITPPVVLR.L	5.13	18.61	0.28	3.62
Q61937_N	Npm1	Nucleopho	R.TVSLGAGAK#DELHIVEAEAM*NYEGSPIK#.V	28.09	24.45	1.15	0.87
Q61937_N	Npm1	Nucleopho	R.TVSLGAGAKDELHIVEAEAM*NYEGSPIK.V	8.07	5.62	1.43	0.70
Q61937_N	Npm1	Nucleopho	R.TVSLGAGAK#DELHIVEAEAMNYEGSPIK#.V	7.32	4.66	1.57	0.64
P49117_N	Nr2c2	Nuclear rec	R.IQIVTDQQTGQK#.I	6.27	2.33	2.69	0.37
Q60632_C	Nr2f1	COUP trans	R.TVSSSVIEQLFFVR.L	3.27	17.61	0.19	5.38
Q60632_C	Nr2f1	COUP trans	R.IFQEQVEK#.L	31.97	25.16	1.27	0.79
Q60632_C	Nr2f1	COUP trans	K.TPIETLIR.D	7.27	20.57	0.35	2.83
Q99J45_N	Nrbp1	Nuclear rec	R.ELLFHPALFEVPSLK#.L	21.18	5.64	3.76	0.27
Q9WU00_	Nrf1	Nuclear res	K.VFGAAPLENVVR.K	3.95	8.20	0.48	2.08
Q9WU00_	Nrf1	Nuclear res	K.VFGAAPLENVVR.K	3.81	15.86	0.24	4.16
Q9WU00_	Nrf1	Nuclear res	R.VSWTQALR.T	3.59	12.74	0.28	3.55
P46460_N	Nsf	Vesicle-fusi	R.GSMAGSTGVHDTVVNQLLSK#.I	5.28	5.97	0.89	1.13
P46460_N	Nsf	Vesicle-fusi	K.IAEESNFPFIK#.I	30.57	22.17	1.38	0.73
P46460_N	Nsf	Vesicle-fusi	K.LFGLLVK#.D	10.72	11.71	0.91	1.09
P46460_N	Nsf	Vesicle-fusi	R.LLDYVPIGPR.F	9.95	54.60	0.18	5.49
P46460_N	Nsf	Vesicle-fusi	K.M*GIGGLDKEFSDIFR.R	4.66	13.46	0.35	2.89
P46460_N	Nsf	Vesicle-fusi	K.NFSGAELEGLVR.A	9.82	42.78	0.23	4.36
P46460_N	Nsf	Vesicle-fusi	R.QSIINPDWNFEK.M	11.74	16.09	0.73	1.37
P46460_N	Nsf	Vesicle-fusi	R.TPLVSVLLEGPPHSGK#.T	23.15	25.98	0.89	1.12
P46460_N	Nsf	Vesicle-fusi	R.VLDDGELLVQQTK#.N	17.35	6.08	2.85	0.35
P46460_N	Nsf	Vesicle-fusi	R.VLDDGELLVQQTK#.N	111.68	58.42	1.91	0.52
P46460_N	Nsf	Vesicle-fusi	K.VVNGPEILNK#.Y	17.60	15.86	1.11	0.90
P46460_N	Nsf	Vesicle-fusi	K.YVGESEANIR.K	15.65	32.72	0.48	2.09
P46460_N	Nsf	Vesicle-fusi	K.IAEESNFPFIK.I	9.13	8.01	1.14	0.88
P46460_N	Nsf	Vesicle-fusi	K.NFSGAELEGLVR.A	15.92	8.45	1.88	0.53
Q9CZ44_N	Nsfl1c	NSFL1 cofa	R.HSGQDVHVVLK#.L	16.97	2.20	7.73	0.13
Q9CZ44_N	Nsfl1c	NSFL1 cofa	R.LGAAPEEESAYVAGER.R	9.82	7.68	1.28	0.78
Q9CZ44_N	Nsfl1c	NSFL1 cofa	K.LGSTAPQVLNTSSPAQQAENEAK#.A	24.55	3.95	6.21	0.16
Q9CZ44_N	Nsfl1c	NSFL1 cofa	K.SPNELVDDLFK#.G	26.27	3.11	8.46	0.12
Q9D720_N	Nsmce1	Non-struct	R.AILEM*EQFIR.E	3.10	11.45	0.27	3.69
Q9D720_N	Nsmce1	Non-struct	R.AILEMEQFIR.E	4.86	12.17	0.40	2.50
Q91VT1_N	Nsmce2	E3 SUMO-p	R.M*SDLIPDEALR.R	2.30	14.77	0.16	6.41
G3XA30_G	Nsmce4a	MCG1618,	R.ALINSVQQNR.E	5.29	18.17	0.29	3.43
G3XA30_G	Nsmce4a	MCG1618,	R.EAVLDAQFLVLASDLGK#.E	15.13	12.66	1.19	0.84
G3XA30_G	Nsmce4a	MCG1618,	R.ILGLLQTYFR.E	2.85	12.21	0.23	4.28
Q1HFZ0_N	Nsun2	tRNA (cytos	K.SEGALELADVSAELPGLK#.W	5.31	2.46	2.16	0.46
Q1HFZ0_N	Nsun2	tRNA (cytos	K.EILFYDR.I	7.82	18.42	0.42	2.36
Q1HFZ0_N	Nsun2	tRNA (cytos	K.FHQFLVSETESGNISR.Q	8.17	29.14	0.28	3.57
Q1HFZ0_N	Nsun2	tRNA (cytos	R.FQQPPQPEGEEDASDGGR.K	6.24	15.86	0.39	2.54
Q1HFZ0_N	Nsun2	tRNA (cytos	K.FYALDPSFPR.M	9.89	27.39	0.36	2.77
Q1HFZ0_N	Nsun2	tRNA (cytos	R.GAEQLAEGGR.M	23.93	38.89	0.62	1.62
Q1HFZ0_N	Nsun2	tRNA (cytos	R.GQAGWEGGYPEIVK#.E	25.56	16.75	1.53	0.66
Q1HFZ0_N	Nsun2	tRNA (cytos	R.IITVSM*EDVK#.T	64.44	40.10	1.61	0.62
Q1HFZ0_N	Nsun2	tRNA (cytos	R.IITVSMEDVK#.T	37.31	22.61	1.65	0.61
Q1HFZ0_N	Nsun2	tRNA (cytos	R.K#LSSEAYSQVK#.D	44.93	30.76	1.46	0.68
Q1HFZ0_N	Nsun2	tRNA (cytos	R.LAQEGIYTLYPFINSR.I	6.16	15.27	0.40	2.48
Q1HFZ0_N	Nsun2	tRNA (cytos	K.LFEHYYQELK#.I	20.49	9.36	2.19	0.46
Q1HFZ0_N	Nsun2	tRNA (cytos	R.LTVDVDGR.K	9.06	17.66	0.51	1.95
Q1HFZ0_N	Nsun2	tRNA (cytos	R.M*M*GLEVLGEK#.K	28.28	15.29	1.85	0.54
Q1HFZ0_N	Nsun2	tRNA (cytos	K.NIDVWK#.K	25.87	12.28	2.11	0.47
Q1HFZ0_N	Nsun2	tRNA (cytos	R.NVLLNNSEK#.M	64.92	45.31	1.43	0.70
Q1HFZ0_N	Nsun2	tRNA (cytos	K.SEGALELADVSAELPGLK#.W	63.65	34.94	1.82	0.55
Q1HFZ0_N	Nsun2	tRNA (cytos	K.TLLTQENPFFR.K	22.35	51.13	0.44	2.29
Q1HFZ0_N	Nsun2	tRNA (cytos	K.SEGALELADVSAELPGLK#.W	9.11	5.07	1.80	0.56
Q8R2U4_N	Ntmt1	N-terminal	R.LLLPLFR.V	3.94	8.06	0.49	2.04
Q8R2U4_N	Ntmt1	N-terminal	R.TAGLSLLAEER.Q	6.22	18.76	0.33	3.02
Q8R2U4_N	Ntmt1	N-terminal	R.VVDM*VDVTEDFLAK#.A	24.30	9.42	2.58	0.39
P54729_N	Nub1	NEDD8 ulti	K.SLEEQGVTHNVK#.A	5.27	3.69	1.43	0.70
P54729_N	Nub1	NEDD8 ulti	K.AM*VLELK#.Q	12.12	7.39	1.64	0.61
P54729_N	Nub1	NEDD8 ulti	K.SLEEQGVTHNVK#.A	30.25	16.35	1.85	0.54
P54729_N	Nub1	NEDD8 ulti	K.VHNLLQLGFTAQEAR.L	4.17	14.24	0.29	3.41
P54729_N	Nub1	NEDD8 ulti	K.VLLSNPHMWWLQDADPENNSR.Q	6.95	4.13	1.68	0.59
P54729_N	Nub1	NEDD8 ulti	K.AMVLELK#QSEEDVR@.K	100.76	2.68	37.61	0.03
P54729_N	Nub1	NEDD8 ulti	R.GNLDDALK#.V	16.41	13.63	1.20	0.83
P54729_N	Nub1	NEDD8 ulti	K.NLQLEEEEQNEAELK#.E	6.20	3.03	2.04	0.49
Q9R061_N	Nubp2	Cytosolic F	R.LAGVPFLGSVPLDSQLTR.S	2.58	8.47	0.30	3.28
O35685_N	Nudc	Nuclear mi	K.DAEDQEAQLK#.N	15.38	3.59	4.29	0.23
O35685_N	Nudc	Nuclear mi	K.GQPPVVDGELYNEVK#.V	27.02	6.75	4.00	0.25
O35685_N	Nudc	Nuclear mi	K.GQPPVVDGELYNEVK#VEESSWLIEDGK#.V	3.20	1.93	1.65	0.60
O35685_N	Nudc	Nuclear mi	R.K#TDFFIGGEEGM*AEK#.L	7.29	2.42	3.01	0.33
O35685_N	Nudc	Nuclear mi	R.LQLEIDQK#.K	20.57	5.82	3.53	0.28
O35685_N	Nudc	Nuclear mi	R.LVTSDPEINTK#.K	85.97	22.01	3.91	0.26
O35685_N	Nudc	Nuclear mi	K.SM*GLPTSDEQK#.K	22.64	5.52	4.10	0.24
O35685_N	Nudc	Nuclear mi	K.TDFFIGGEEGM*AEK#.L	14.25	3.15	4.52	0.22
O35685_N	Nudc	Nuclear mi	K.VEESSWLIEDGK#.V	12.26	3.86	3.17	0.32
O35685_N	Nudc	Nuclear mi	R.WTQTLAELDLAVPFR.V	5.61	5.90	0.95	1.05
Q6PIP5_N	Nudcd1	NudC dom	K.EDIQIQFLPDNINIK#.L	11.33	5.19	2.18	0.46
Q6PIP5_N	Nudcd1	NudC dom	K.ENDSLEISLIK#.K	16.79	6.07	2.77	0.36
Q6PIP5_N	Nudcd1	NudC dom	R.FDGNTLQTTHVVNLGSNQYLFSVIVDPK#.E	6.11	1.44	4.23	0.24
Q6PIP5_N	Nudcd1	NudC dom	R.LFVLTTK#.N	28.51	7.68	3.71	0.27
Q6PIP5_N	Nudcd1	NudC dom	R.LPESSTK#EDIQIQFLPDNINIK#.L	14.50	3.74	3.87	0.26
Q8VHN8_S	Nudt16l1	Protein syn	K.YQLLFALK#.V	24.30	7.72	3.15	0.32
Q9CQF3_C	Nudt21	Cleavage an	K.LFLVQLQEK#.A	9.80	4.48	2.19	0.46
Q9CQF3_C	Nudt21	Cleavage an	K.LPGGELNPGEDEVEGLKR.L	5.78	7.50	0.77	1.30
Q9CQF3_C	Nudt21	Cleavage an	R.FNFIYN.-	11.92	11.92	1.00	1.00
Q9CQF3_C	Nudt21	Cleavage an	R.GVNQFGNK#.Y	68.02	27.42	2.48	0.40
Q9CQF3_C	Nudt21	Cleavage an	K.K#LFLVQLQEK#.A	31.16	13.61	2.29	0.44
Q9CQF3_C	Nudt21	Cleavage an	K.LFLVQLQEK#.A	235.27	105.54	2.23	0.45
Q9CQF3_C	Nudt21	Cleavage an	R.LM*TEILGR.Q	15.08	24.95	0.60	1.65
Q9CQF3_C	Nudt21	Cleavage an	K.LPGGELNPGEDEVEGLK#.R	14.77	8.77	1.68	0.59
Q9CQF3_C	Nudt21	Cleavage an	K.LPGGELNPGEDEVEGLKR.L	65.14	166.07	0.39	2.55
Q9CQF3_C	Nudt21	Cleavage an	R.TINLYPLTNYTFGTK#.E	148.96	75.08	1.98	0.50
Q9CQF3_C	Nudt21	Cleavage an	K.YIQQTKPLTLER.T	8.29	16.05	0.52	1.94
Q9JKX6_N	Nudt5	ADP-sugar	K.VYAYGLALK#.H	12.39	5.56	2.23	0.45
Q5F2E7_N	Nufip2	Nuclear fra	K.GADNDGSGSESGYTTPK#.K	5.53	4.59	1.21	0.83

Q5F2E7_NU	Nufip2	Nuclear fra	K.IMQETSVPALK#.Q	6.45	7.45	0.87	1.16
Q5F2E7_NU	Nufip2	Nuclear fra	R.LSQVPM*SALK#.S	9.41	7.97	1.18	0.85
Q5F2E7_NU	Nufip2	Nuclear fra	R.LSQVPMSALK#.S	6.68	7.25	0.92	1.09
Q5F2E7_NU	Nufip2	Nuclear fra	K.SLSSDEATNPISR.V	3.82	15.30	0.25	4.00
Q5F2E7_NU	Nufip2	Nuclear fra	K.ADTSSQGALVFLSK#.D	3.75	3.05	1.23	0.81
Q5F2E7_NU	Nufip2	Nuclear fra	K.DYEIENQNPLASPTNTLLGSAK#.E	10.76	5.21	2.06	0.48
Q5F2E7_NU	Nufip2	Nuclear fra	R.IITYNEAM*DSPDQ.-	11.09	11.09	1.00	1.00
Q5F2E7_NU	Nufip2	Nuclear fra	K.DYEIENQNPLASPTNTLLGSAK#.E	3.08	4.12	0.75	1.34
Q5F2E7_NU	Nufip2	Nuclear fra	R.IITYNEAM*DSPDQ.-	9.26	9.26	1.00	1.00
Q5F2E7_NU	Nufip2	Nuclear fra	K.SLSSDEATNPISR.V	3.63	12.07	0.30	3.32
E9Q7G0_E9	Numa1	Protein Nu	R.IATTTTGTATVATTPR.A	1.37	7.30	0.19	5.32
E9Q7G0_E9	Numa1	Protein Nu	R.VSSETHQGPGTPESK.K	2.58	3.26	0.79	1.26
E9Q7G0_E9	Numa1	Protein Nu	R.AEELGQELK#.A	22.40	16.71	1.34	0.75
E9Q7G0_E9	Numa1	Protein Nu	K.AGEQQETASLELLKEPPR.A	3.63	11.99	0.30	3.30
E9Q7G0_E9	Numa1	Protein Nu	K.AIQQVQEK.E	16.26	18.27	0.89	1.12
E9Q7G0_E9	Numa1	Protein Nu	K.ALETLQGQLEEK#.A	40.82	28.28	1.44	0.69
E9Q7G0_E9	Numa1	Protein Nu	K.AQLQEQLR.A	13.86	28.03	0.49	2.02
E9Q7G0_E9	Numa1	Protein Nu	R.DNAQTSVTQAQQEK#.A	45.71	37.18	1.23	0.81
E9Q7G0_E9	Numa1	Protein Nu	R.EAEQMGGELER.L	2.14	9.87	0.22	4.61
E9Q7G0_E9	Numa1	Protein Nu	R.EAEQM*GGELER.L	5.52	18.41	0.30	3.34
E9Q7G0_E9	Numa1	Protein Nu	R.ELGELGSLR.Q	5.84	19.64	0.30	3.36
E9Q7G0_E9	Numa1	Protein Nu	R.ELGHNQAASASAQR.E	1.48	13.03	0.11	8.78
E9Q7G0_E9	Numa1	Protein Nu	R.ELQQAGLK#.T	38.92	30.50	1.28	0.78
E9Q7G0_E9	Numa1	Protein Nu	K.FM*LDHEESLNLTEDLESFLEK#.V	16.70	8.62	1.94	0.52
E9Q7G0_E9	Numa1	Protein Nu	K.FQVATDALK#.S	45.80	33.38	1.37	0.73
E9Q7G0_E9	Numa1	Protein Nu	R.GQAQADLAQEK#.A	43.38	31.81	1.36	0.73
E9Q7G0_E9	Numa1	Protein Nu	R.IATTTTGTATVATTPR.A	4.90	20.03	0.24	4.09
E9Q7G0_E9	Numa1	Protein Nu	R.IDHLALLNEK#.Q	48.05	21.57	2.23	0.45
E9Q7G0_E9	Numa1	Protein Nu	K.KLELEEPDSANSSFYSTQSAPASQANLR.A	4.03	12.71	0.32	3.15
E9Q7G0_E9	Numa1	Protein Nu	R.KSSLISSLEEEVSILNR.Q	3.43	9.77	0.35	2.85
E9Q7G0_E9	Numa1	Protein Nu	K.LATDNTQLQTR.V	13.61	33.90	0.40	2.49
E9Q7G0_E9	Numa1	Protein Nu	K.LKEQQLEEAAKEQEATR.Q	7.20	20.34	0.35	2.82
E9Q7G0_E9	Numa1	Protein Nu	R.LLQVETASNSAR.A	15.46	44.13	0.35	2.85
E9Q7G0_E9	Numa1	Protein Nu	R.LPPKVESLESLYFTPTPAR.G	4.14	11.23	0.37	2.71
E9Q7G0_E9	Numa1	Protein Nu	K.LQEQLQDLEELQK#.E	13.03	9.68	1.35	0.74
E9Q7G0_E9	Numa1	Protein Nu	R.LQESPAPEK#GEVLGDALQLDTLK#.Q	8.43	6.84	1.23	0.81
E9Q7G0_E9	Numa1	Protein Nu	R.LQESPAPEK#GEVLGDALQLDTLK#QEAAK#.L	22.79	12.59	1.81	0.55
E9Q7G0_E9	Numa1	Protein Nu	R.LQNTLNEQR.V	12.43	40.46	0.31	3.26
E9Q7G0_E9	Numa1	Protein Nu	K.LSQLEDQATR.L	9.68	27.17	0.36	2.81
E9Q7G0_E9	Numa1	Protein Nu	R.QFLEVELDQAR.E	20.74	11.97	1.73	0.58
E9Q7G0_E9	Numa1	Protein Nu	R.QQVEQLSSSLK#.L	20.99	16.50	1.27	0.79
E9Q7G0_E9	Numa1	Protein Nu	K.SSLISSLEEEVSILNR.Q	4.72	16.16	0.29	3.42
E9Q7G0_E9	Numa1	Protein Nu	R.TELK#ELQQTLEQLK#.I	11.27	9.07	1.24	0.80
E9Q7G0_E9	Numa1	Protein Nu	K.TGQEVQEEAVEIHSEGQPGQQQSQLAQLHASLAK#.A	27.82	12.67	2.20	0.46
E9Q7G0_E9	Numa1	Protein Nu	R.TQPDGTSVPGEPASPISQR.L	3.06	10.47	0.29	3.42
E9Q7G0_E9	Numa1	Protein Nu	K.VIEGSEM*ELAK#.M	42.48	32.25	1.32	0.76
E9Q7G0_E9	Numa1	Protein Nu	R.VSSETHQGPGTPESK#.K	7.37	4.72	1.56	0.64
E9Q7G0_E9	Numa1	Protein Nu	R.AEELGQELK#.A	72.61	64.24	1.13	0.88
E9Q7G0_E9	Numa1	Protein Nu	R.AEQDKALETLQGQLEEK.A	20.40	17.56	1.16	0.86
E9Q7G0_E9	Numa1	Protein Nu	K.AGEQQETASLELLK#.E	17.05	15.80	1.08	0.93
E9Q7G0_E9	Numa1	Protein Nu	K.AGEQQETASLELLKEPPR.A	13.56	86.60	0.16	6.39
E9Q7G0_E9	Numa1	Protein Nu	K.AIQQVQEK.E	60.61	71.21	0.85	1.17
E9Q7G0_E9	Numa1	Protein Nu	R.ALEESLK#.I	84.58	83.82	1.01	0.99
E9Q7G0_E9	Numa1	Protein Nu	K.ALETLQGQLEEK#.A	86.52	99.40	0.87	1.15
E9Q7G0_E9	Numa1	Protein Nu	K.AQLQEQLR.A	32.73	143.91	0.23	4.40
E9Q7G0_E9	Numa1	Protein Nu	R.ASM*QPAQIAEGVGITTR.Q	17.74	18.38	0.97	1.04
E9Q7G0_E9	Numa1	Protein Nu	R.ASMQPAQIAEGVGITTR.Q	2.92	11.51	0.25	3.94
E9Q7G0_E9	Numa1	Protein Nu	K.ASQEWAEK#.Q	20.17	22.60	0.89	1.12
E9Q7G0_E9	Numa1	Protein Nu	R.ATSSTQSLAR.L	10.10	48.64	0.21	4.81
E9Q7G0_E9	Numa1	Protein Nu	K.DAKLESLQQQLQAANDAR.D	1.10	21.20	0.05	19.33
E9Q7G0_E9	Numa1	Protein Nu	K.DAQIAMMQQR.I	1.84	8.29	0.22	4.50
E9Q7G0_E9	Numa1	Protein Nu	K.DAQIAM*M*QQR.I	7.52	26.87	0.28	3.57
E9Q7G0_E9	Numa1	Protein Nu	R.DNAQTSVTQAQQEK#.A	158.15	142.61	1.11	0.90
E9Q7G0_E9	Numa1	Protein Nu	R.DQELASLKEQAK.K	22.33	27.62	0.81	1.24
E9Q7G0_E9	Numa1	Protein Nu	R.EAEQMGGELER.L	6.22	34.17	0.18	5.49
E9Q7G0_E9	Numa1	Protein Nu	R.EAEQM*GGELER.L	10.92	59.28	0.18	5.43
E9Q7G0_E9	Numa1	Protein Nu	R.EFANHLQQLQGAFNDLIEEHSK#.A	22.81	19.33	1.18	0.85
E9Q7G0_E9	Numa1	Protein Nu	K.EGQQILQQPLPER.L	8.15	34.55	0.24	4.24
E9Q7G0_E9	Numa1	Protein Nu	K.EGTDQELAK.L	21.32	23.16	0.92	1.09
E9Q7G0_E9	Numa1	Protein Nu	K.EHPAGGASGEDASGPGTQSETAGK#.T	29.54	38.48	0.77	1.30
E9Q7G0_E9	Numa1	Protein Nu	K.EK#EHPAGGASGEDASGPGTQSETAGK#.T	20.16	21.47	0.94	1.06
E9Q7G0_E9	Numa1	Protein Nu	R.EKYVQELAAVR.T	4.54	12.32	0.37	2.71
E9Q7G0_E9	Numa1	Protein Nu	R.ELGELGSLR.Q	14.83	72.54	0.20	4.89
E9Q7G0_E9	Numa1	Protein Nu	R.ELGHNQAASASAQR.E	33.50	118.32	0.28	3.53
E9Q7G0_E9	Numa1	Protein Nu	R.ELQQAGLK.T	101.06	122.06	0.83	1.21
E9Q7G0_E9	Numa1	Protein Nu	K.ELQQTLEQLK#.I	67.06	56.05	1.20	0.84
E9Q7G0_E9	Numa1	Protein Nu	K.EQALSALQLEHTSTQALVSELLPAK#.H	115.03	102.21	1.13	0.89
E9Q7G0_E9	Numa1	Protein Nu	K.EQAQMLQTMQEQEQAAQGLR.Q	3.52	8.92	0.39	2.54
E9Q7G0_E9	Numa1	Protein Nu	R.FLEIQR.I	22.62	101.90	0.22	4.50
E9Q7G0_E9	Numa1	Protein Nu	K.FM*LDHEESLNLTEDLESFLEK#.V	15.34	20.22	0.76	1.32
E9Q7G0_E9	Numa1	Protein Nu	K.FQVATDALK#.S	108.58	89.49	1.21	0.82
E9Q7G0_E9	Numa1	Protein Nu	R.GESQQEVQR.L	3.16	14.15	0.22	4.48
E9Q7G0_E9	Numa1	Protein Nu	R.GKQEAQLLAER.S	13.03	60.20	0.22	4.62
E9Q7G0_E9	Numa1	Protein Nu	R.GQAPLETSLDSLGDAFPDSGR.K	2.71	15.72	0.17	5.79
E9Q7G0_E9	Numa1	Protein Nu	R.GQAPLETSLDSLGDAFPDSGR.K	2.04	13.70	0.15	6.73
E9Q7G0_E9	Numa1	Protein Nu	R.GQAQADLAQEK#.A	125.80	136.70	0.92	1.09
E9Q7G0_E9	Numa1	Protein Nu	R.HLTAQVR.S	20.44	91.25	0.22	4.46
E9Q7G0_E9	Numa1	Protein Nu	R.IASSSSENNFLSGSPSSPM*GDILQTPQFQM*R.R	2.53	8.44	0.30	3.33
E9Q7G0_E9	Numa1	Protein Nu	R.IASSSSENNFLSGSPSSPM*GDILQTPQFQMR.R	2.56	2.48	1.03	0.97
E9Q7G0_E9	Numa1	Protein Nu	R.IASSSSENNFLSGSPSSPMGDILQTPQFQM*R.R	1.51	3.84	0.39	2.54
E9Q7G0_E9	Numa1	Protein Nu	R.IATTTTGTATVATTPR.A	10.87	57.87	0.19	5.33
E9Q7G0_E9	Numa1	Protein Nu	R.IDHLALLNEK#.Q	93.15	107.21	0.87	1.15
E9Q7G0_E9	Numa1	Protein Nu	K.ISQLSEENGDLSFK#.V	21.36	26.98	0.79	1.26
E9Q7G0_E9	Numa1	Protein Nu	K.KEQAQM*LQTM*QEQEQAAQGLR.Q	3.65	17.03	0.21	4.67
E9Q7G0_E9	Numa1	Protein Nu	K.KEQAQMLQTMQEQEQAAQGLR.Q	3.37	13.35	0.25	3.96
E9Q7G0_E9	Numa1	Protein Nu	K.KLELEEPDSANSSFYSTQSAPASQANLR.A	7.88	46.16	0.17	5.86
E9Q7G0_E9	Numa1	Protein Nu	R.KSSLISSLEEEVSILNR.Q	9.83	39.48	0.25	4.02
E9Q7G0_E9	Numa1	Protein Nu	K.LATDNTQLQTR.V	43.98	193.53	0.23	4.40
E9Q7G0_E9	Numa1	Protein Nu	R.LENELSTALQDK.K	19.47	26.33	0.74	1.35
E9Q7G0_E9	Numa1	Protein Nu	R.LENELSTALQDK#K#.C	119.16	101.40	1.18	0.85
E9Q7G0_E9	Numa1	Protein Nu	K.LESLQQQLQAANDAR.D	11.84	48.24	0.25	4.08
E9Q7G0_E9	Numa1	Protein Nu	K.LK#EQQLEEAAK#.E	15.64	24.95	0.63	1.60
E9Q7G0_E9	Numa1	Protein Nu	K.LKEQQLEEAAKEQEATR.Q	17.05	69.17	0.25	4.06

E9Q7G0_E	Numa1	Protein Nu	R.LLQVETASNSAR.A	31.13	143.77	0.22	4.62
E9Q7G0_E	Numa1	Protein Nu	K.LLTEKDAQIAM*M*QQR.I	10.28	37.86	0.27	3.68
E9Q7G0_E	Numa1	Protein Nu	R.LPPKVESLESLYFTPTPAR.G	7.71	41.15	0.19	5.34
E9Q7G0_E	Numa1	Protein Nu	K.LQEQLQDLEELQK#ENK#.E	81.70	111.28	0.73	1.36
E9Q7G0_E	Numa1	Protein Nu	R.LQESPAPEK#GEVLGDALQLDTLK#.Q	26.13	32.33	0.81	1.24
E9Q7G0_E	Numa1	Protein Nu	R.LQESPAPEK#GEVLGDALQLDTLK#QEAAK#.L	14.08	13.08	1.08	0.93
E9Q7G0_E	Numa1	Protein Nu	R.LQNTLNEQR.V	19.82	103.43	0.19	5.22
E9Q7G0_E	Numa1	Protein Nu	R.LQTQLNELQAQLSQK#.E	38.75	41.17	0.94	1.06
E9Q7G0_E	Numa1	Protein Nu	K.LSQLEDQATR.L	39.50	173.82	0.23	4.40
E9Q7G0_E	Numa1	Protein Nu	K.LVDDLSALQEK#.M	122.82	161.57	0.76	1.32
E9Q7G0_E	Numa1	Protein Nu	R.LVVAESEK.S	90.61	94.76	0.96	1.05
E9Q7G0_E	Numa1	Protein Nu	K.QAAGGLQAELM*R.A	5.79	23.27	0.25	4.02
E9Q7G0_E	Numa1	Protein Nu	K.QAASSQEPSELEELR.G	10.38	31.76	0.33	3.06
E9Q7G0_E	Numa1	Protein Nu	K.QAASSQEPSELEELRGK.N	10.25	50.75	0.20	4.95
E9Q7G0_E	Numa1	Protein Nu	R.QDHAQQLAIVAEAR.E	9.01	55.98	0.16	6.21
E9Q7G0_E	Numa1	Protein Nu	R.QDHAQQLAIVAEAR.E	3.68	16.25	0.23	4.41
E9Q7G0_E	Numa1	Protein Nu	R.QFLEVELDQAR.E	13.91	35.13	0.40	2.53
E9Q7G0_E	Numa1	Protein Nu	R.QQVEQLSSSLK#.L	98.57	75.90	1.30	0.77
E9Q7G0_E	Numa1	Protein Nu	R.QSM*AFSILNTPK#.K	11.36	17.03	0.67	1.50
E9Q7G0_E	Numa1	Protein Nu	R.QSMAFSILNTPK.K	5.45	8.78	0.62	1.61
E9Q7G0_E	Numa1	Protein Nu	R.SLEAQVAHADQQLR.D	7.92	46.25	0.17	5.84
E9Q7G0_E	Numa1	Protein Nu	R.SNRDDLELELSESLK.L	11.52	49.95	0.23	4.34
E9Q7G0_E	Numa1	Protein Nu	K.SSLISSLEEEVSILNR.Q	9.83	41.10	0.24	4.18
E9Q7G0_E	Numa1	Protein Nu	R.TDAETHLAEM*R.Q	14.33	25.40	0.56	1.77
E9Q7G0_E	Numa1	Protein Nu	K.TDAPGPELQALR.A	15.00	100.85	0.15	6.73
E9Q7G0_E	Numa1	Protein Nu	R.TELKELQQTLEQLK.I	30.49	31.14	0.98	1.02
E9Q7G0_E	Numa1	Protein Nu	K.TGQEVQEEAVEIHSEGQPGQQQSQLAQLHASLAK#.A	8.19	5.55	1.47	0.68
E9Q7G0_E	Numa1	Protein Nu	R.TQPDGTSVPGEPASPISQR.L	6.14	30.37	0.20	4.95
E9Q7G0_E	Numa1	Protein Nu	R.TTQIINITM*TK.K	26.60	24.31	1.09	0.91
E9Q7G0_E	Numa1	Protein Nu	R.VEFAALQEALAHALTEKEGTDQELAK.L	16.24	17.66	0.92	1.09
E9Q7G0_E	Numa1	Protein Nu	K.VESLESLYFTPTPAR.G	3.30	22.53	0.15	6.83
E9Q7G0_E	Numa1	Protein Nu	K.VIEGSEMELAK#.M	35.16	32.77	1.07	0.93
E9Q7G0_E	Numa1	Protein Nu	R.VTELEAQLK#.A	65.44	80.47	0.81	1.23
E9Q7G0_E	Numa1	Protein Nu	R.YGAMFQEQLMALK#.G	7.28	6.64	1.10	0.91
E9Q7G0_E	Numa1	Protein Nu	K.YVQELAAVR.T	23.36	98.22	0.24	4.20
F6ZQA3_F6	Numa1	Protein Nu	K.LTAQVEQLEVFQR.E	9.02	44.19	0.20	4.90
F6ZQA3_F6	Numa1	Protein Nu	R.QKLTAQVEQLEVFQR.E	3.90	17.06	0.23	4.38
E9Q3G8_E	Nup153	Protein Nu	K.FGIPSSSSGLSQTLTSTGNFK#.F	6.35	4.42	1.44	0.70
E9Q3G8_E	Nup153	Protein Nu	K.GFGTSSSLNPAPSAFK#.F	13.01	12.16	1.07	0.93
E9Q3G8_E	Nup153	Protein Nu	K.SGFNFGTLDTK#.S	12.17	5.52	2.20	0.45
E9Q3G8_E	Nup153	Protein Nu	R.SGIDNTVFQAK#.K	17.47	15.21	1.15	0.87
E9Q3G8_E	Nup153	Protein Nu	K.TEFSGSNSSSETVLSSSAQDITAVNSSSYK#.K	3.94	2.60	1.52	0.66
Q6ZQH8_N	Nup188	Nucleopori	R.SDGPEGQGQGQLLIK#.T	5.60	2.98	1.88	0.53
B9EJ54_B9	Nup205	MCG21756	K.ASSEGVAIQGQQGTR.L	6.06	21.78	0.28	3.59
B9EJ54_B9	Nup205	MCG21756	R.DPPVFIPTPVDR.Y	5.11	9.45	0.54	1.85
B9EJ54_B9	Nup205	MCG21756	K.LLDIEGLYSK#.V	12.03	6.82	1.76	0.57
B9EJ54_B9	Nup205	MCG21756	R.SGLSQVNQHDIDQLQSDAVNAFGESLQK#.K	10.71	5.71	1.88	0.53
B9EJ54_B9	Nup205	MCG21756	K.VLTLLSQIDVNNEFEK#.L	6.61	4.15	1.59	0.63
Q80U93_N	Nup214	Nuclear po	R.AAPGSGTSTFSFAPPSK#.G	9.66	6.69	1.44	0.69
Q80U93_N	Nup214	Nuclear po	R.LNQLVDSLQQLR.L	2.12	10.60	0.20	4.99
Q80U93_N	Nup214	Nuclear po	R.STQTAPSSAPSTGQK#.S	11.83	8.68	1.36	0.73
Q9JIH2_N	Nup50	Nuclear po	K.AASSLFSAK#.A	32.81	16.37	2.00	0.50
Q9JIH2_N	Nup50	Nuclear po	K.AEDTSEKVEFTAEK.K	11.47	7.75	1.48	0.68
Q9JIH2_N	Nup50	Nuclear po	R.ATAGM*EPPSLFGSTK#.L	14.85	8.70	1.71	0.59
Q9JIH2_N	Nup50	Nuclear po	R.ATAGMEPPSLFGSTK#.L	43.15	9.19	4.70	0.21
Q9JIH2_N	Nup50	Nuclear po	K.LQQESPFSFHGNK#.A	15.78	5.35	2.95	0.34
Q9JIH2_N	Nup50	Nuclear po	R.NVGFESDSGGAFK#.G	38.60	22.76	1.70	0.59
Q9JIH2_N	Nup50	Nuclear po	K.SDAAQGATSASFSFGK#.K	10.52	7.02	1.50	0.67
Q9JIH2_N	Nup50	Nuclear po	K.TSEDADELHK#.I	6.46	2.73	2.36	0.42
Q8BTS4_N	Nup54	Nuclear po	R.LDIISEDISELQK#.N	26.55	11.29	2.35	0.43
Q8BTS4_N	Nup54	Nuclear po	K.QLLQNPPAGVDPIIWEQAK#.V	6.45	3.30	1.96	0.51
Q8BTS4_N	Nup54	Nuclear po	K.VLGGNQTLTVNVEGIK#.T	14.69	5.11	2.87	0.35
Q8BTS4_N	Nup54	Nuclear po	R.VQLDTIQGELNAPTQFK#.G	12.53	4.26	2.94	0.34
Q8CEC0_N	Nup88	Nuclear po	K.FLGSDEEDK#DSLQELTAEQK#.C	6.05	3.25	1.86	0.54
Q8CEC0_N	Nup88	Nuclear po	R.ILAETPDSFEK#.H	14.94	7.36	2.03	0.49
Q8BJ71_N	Nup93	Nuclear po	K.ASVLLGSR.G	6.65	16.29	0.41	2.45
Q8BJ71_N	Nup93	Nuclear po	R.EALQYFYFLR.D	5.21	10.85	0.48	2.08
Q8BJ71_N	Nup93	Nuclear po	R.LESLSAATTFEPLEPVK#DTDIQGFLK#.N	34.59	21.81	1.59	0.63
Q8BJ71_N	Nup93	Nuclear po	K.LLSPVVPQISAPQSNK#.E	17.83	10.28	1.73	0.58
Q8BJ71_N	Nup93	Nuclear po	K.LVPLNQESVEER.V	12.44	31.92	0.39	2.57
Q8BJ71_N	Nup93	Nuclear po	K.QM*TDVVLTPATDALK#.S	10.93	5.44	2.01	0.50
Q8BJ71_N	Nup93	Nuclear po	R.LESLSAATTFEPLEPVK#DTDIQGFLK#.N	27.12	16.65	1.63	0.61
Q8BJ71_N	Nup93	Nuclear po	K.LLSPVVPQISAPQSNK#.E	9.88	2.91	3.40	0.29
Q8BJ71_N	Nup93	Nuclear po	K.LVPLNQESVEER.V	10.71	22.95	0.47	2.14
Q8BJ71_N	Nup93	Nuclear po	K.QM*TDVVLTPATDALK#.S	6.85	6.80	1.01	0.99
Q6PFD9_N	Nup98	Nuclear po	R.FSFLSKPVDENNQQDGEDDSLVSR.F	2.33	7.83	0.30	3.36
Q6PFD9_N	Nup98	Nuclear po	R.LADINYEGR.L	4.13	12.74	0.32	3.09
Q9ERH4_N	Nusap1	Nucleolar a	K.LM*TEATQTPSSSK#.K	6.52	2.58	2.52	0.40
Q9DBY8_N	Nvl	Nuclear val	K.AVANESGLNFISVK.G	9.83	18.67	0.53	1.90
Q9DBY8_N	Nvl	Nuclear val	R.EATTSTPLLTSK.T	19.30	23.95	0.81	1.24
Q9DBY8_N	Nvl	Nuclear val	R.ESEGGWFIDK.T	2.29	7.79	0.29	3.40
Q9DBY8_N	Nvl	Nuclear val	K.GPELLNM*YVGESER.A	2.33	13.87	0.17	5.95
Q9DBY8_N	Nvl	Nuclear val	K.KKPEIEGLPSEGDQEER.L	1.94	22.05	0.09	11.34
Q9DBY8_N	Nvl	Nuclear val	R.LGAEPTSETQDELQR.L	3.44	37.73	0.09	10.97
Q9DBY8_N	Nvl	Nuclear val	R.STELQISNVK.F	14.70	27.41	0.54	1.87
Q9DBY8_N	Nvl	Nuclear val	K.TLLAHAIAGELDLPILK.V	14.24	18.24	0.78	1.28
Q9DBY8_N	Nvl	Nuclear val	K.VAAPEIVSGVSGESEQK.L	10.74	21.68	0.50	2.02
Q80SZ6_Q	Nxf7	Nuclear RN	K.EEMEQLKLAMR@K.R	33.32	5.12	6.51	0.15
P11928_O	Oas1a	2'-5'-oligoa	K.FIEDYLLPDTTFGADVK#.S	7.46	9.65	0.77	1.29
Q8VI93_O	Oas3	2'-5'-oligoa	R.AGILDLGHPIYQGPNQALEDNK#GHLAVQSK#.E	15.95	2.25	7.09	0.14
Q8VI93_O	Oas3	2'-5'-oligoa	R.HFLTQVK#.R	13.71	10.44	1.31	0.76
Q8VI93_O	Oas3	2'-5'-oligoa	K.IPAM*PNPSANK#.T	11.75	6.72	1.75	0.57
Q8VI93_O	Oas3	2'-5'-oligoa	R.VDLSVLPAFDAVGPLK#.S	28.52	7.20	3.96	0.25
Q8VI93_O	Oas3	2'-5'-oligoa	R.HFLTQVK#.R	73.22	15.42	4.75	0.21
Q8VI93_O	Oas3	2'-5'-oligoa	K.IPAM*PNPSANK#.T	66.41	16.67	3.98	0.25
Q8VI93_O	Oas3	2'-5'-oligoa	R.M*LLESWGGHPGPGLTFEFSQSK#.A	14.38	4.45	3.23	0.31
Q8VI93_O	Oas3	2'-5'-oligoa	K.QASGVLVQPWEGPGLPR.A	7.92	7.33	1.08	0.93
Q8VI93_O	Oas3	2'-5'-oligoa	R.SQK#PSNSAPGFPEAATK#.I	75.70	18.03	4.20	0.24
Q8VI93_O	Oas3	2'-5'-oligoa	R.TVLALIQHSK#.Y	27.14	5.39	5.03	0.20
Q8VI93_O	Oas3	2'-5'-oligoa	R.VDLSVLPAFDAVGPLK#.S	91.55	21.36	4.29	0.23
Q8VI94_O	Oasl1	2'-5'-oligoa	R.GQRPIILDPADPTNNVAEGYR.W	2.42	9.53	0.25	3.94
Q8VI94_O	Oasl1	2'-5'-oligoa	K.HWYQQYVR.D	6.07	7.50	0.81	1.23
Q8VI94_O	Oasl1	2'-5'-oligoa	K.LDSFVAQWLQPTR.E	11.96	12.30	0.97	1.03

Q8VI94_OA	Oasl1	2'-5'-oligoa	R.LEFQGHILEDWFDFK#.S	37.10	13.40	2.77	0.36
Q8VI94_OA	Oasl1	2'-5'-oligoa	R.SHAYAIHPLDYVLNLK#.Q	15.76	5.22	3.02	0.33
Q8VI94_OA	Oasl1	2'-5'-oligoa	K.SYGIQDSVTVILSK#.T	26.17	3.53	7.41	0.14
Q8VI94_OA	Oasl1	2'-5'-oligoa	R.VPSSLIFTIQTR.E	6.60	10.76	0.61	1.63
Q8VI94_OA	Oasl1	2'-5'-oligoa	R.GQRPIILDPADPTNNVAEGYR.W	2.67	7.12	0.37	2.67
Q8VI94_OA	Oasl1	2'-5'-oligoa	K.LDSFVAQWLQPTR.E	9.22	8.98	1.03	0.97
Q8VI94_OA	Oasl1	2'-5'-oligoa	R.LEFQGHILEDWFDFK#.S	23.07	4.71	4.89	0.20
Q8VI94_OA	Oasl1	2'-5'-oligoa	R.LSFQEPGGER.Q	14.12	15.54	0.91	1.10
Q8VI94_OA	Oasl1	2'-5'-oligoa	R.SHAYAIHPLDYVLNLK#.Q	18.50	6.84	2.70	0.37
Q8VI94_OA	Oasl1	2'-5'-oligoa	K.SYGIQDSVTVILSK#.T	31.37	5.15	6.10	0.16
Q8VI94_OA	Oasl1	2'-5'-oligoa	R.GQRPIILDPADPTNNVAEGYR.W	5.67	20.21	0.28	3.56
Q8VI94_OA	Oasl1	2'-5'-oligoa	K.IQLSQGYLGLQR.L	16.35	24.92	0.66	1.52
Q8VI94_OA	Oasl1	2'-5'-oligoa	K.LDSFVAQWLQPTR.E	21.61	22.44	0.96	1.04
Q8VI94_OA	Oasl1	2'-5'-oligoa	R.LSFQEPGGER.Q	12.93	28.97	0.45	2.24
Q8VI94_OA	Oasl1	2'-5'-oligoa	R.SHAYAIHPLDYVLNLK#.Q	30.05	10.29	2.92	0.34
Q8VI94_OA	Oasl1	2'-5'-oligoa	K.SYGIQDSVTVILSK#.T	60.28	11.56	5.22	0.19
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	R.DSKPAPAIYETLIR.S	12.16	28.52	0.43	2.35
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	R.DWKEEGQDAWER.I	5.18	16.46	0.31	3.18
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	R.EVVISFIK#.K	46.57	27.05	1.72	0.58
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	K.GYPGDFSPSFTELQR.H	5.99	19.59	0.31	3.27
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	R.K#TLADYGIFSK#.V	17.52	9.78	1.79	0.56
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	K.QTGTVDWTLWTNPYSPIR.K	1.88	4.07	0.46	2.17
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	K.YPGGQSK#PFTIDPDDTILDLK#.E	39.89	27.41	1.46	0.69
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	K.YYNFQNEVVR.N	14.65	33.43	0.44	2.28
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	K.GYPGDFSPSFTELQR.H	4.16	10.57	0.39	2.54
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	R.K#TLADYGIFSK#.V	11.68	5.94	1.97	0.51
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	K.YPGGQSK#PFTIDPDDTILDLK#.E	15.32	12.06	1.27	0.79
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	K.YYNFQNEVVR.N	8.64	21.85	0.40	2.53
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	R.EVVISFIK#.K	38.02	14.30	2.66	0.38
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	R.K#TLADYGIFSK#.V	14.61	5.04	2.90	0.34
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	K.YPGGQSK#PFTIDPDDTILDLK#.E	30.05	16.54	1.82	0.55
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	K.YYNFQNEVVR.N	12.01	15.80	0.76	1.31
Q8K2X3_ST	Obfc1	CST comple	K.K#LQETIEQK#.T	3.84	2.19	1.75	0.57
Q8K2X3_ST	Obfc1	CST comple	R.NPALQEEEALNNK#DNLDLAGLTSLLSEK#.I	11.42	2.49	4.58	0.22
Q8K2X3_ST	Obfc1	CST comple	R.VLELLEDQSDIVSTADHYYAAF.-	4.25	4.25	1.00	1.00
Q60597_OI	Ogdh	2-oxogluta	K.YAELLVSQGVVNQPEYEEEISK#YDK#.I	3.15	1.97	1.60	0.63
Q60597_OI	Ogdh	2-oxogluta	R.GHHVAQLDPLGILDADLDSSVPADIISSTDK#.L	17.63	2.93	6.02	0.17
Q60597_OI	Ogdh	2-oxogluta	K.LEAADEGSGDM*K#.Y	6.40	1.64	3.92	0.26
Q99PG2_O	Ogfr	Opioid gro	K.SQVGPEDPK#.S	14.47	6.08	2.38	0.42
Q8CGY8_O	Ogt	UDP-N-acet	K.AFLDSLPDVK#.I	29.10	29.54	0.98	1.02
Q8CGY8_O	Ogt	UDP-N-acet	R.EQGNIEEAVR.L	12.51	28.40	0.44	2.27
Q8CGY8_O	Ogt	UDP-N-acet	R.EYQAGDFEAAER.H	3.69	17.87	0.21	4.84
Q8CGY8_O	Ogt	UDP-N-acet	R.FPAVGEPNIQQYAQNM*GLPQNR.I	2.54	6.62	0.38	2.61
Q8CGY8_O	Ogt	UDP-N-acet	K.IDPSTLQMWANILK#.R	8.01	6.55	1.22	0.82
Q8CGY8_O	Ogt	UDP-N-acet	R.IIFSPVAPK#.E	22.15	15.91	1.39	0.72
Q8CGY8_O	Ogt	UDP-N-acet	R.ISPTFADAYSNM*GNTLK.E	10.69	7.80	1.37	0.73
Q8CGY8_O	Ogt	UDP-N-acet	R.ISPTFADAYSNMGNTLK.E	6.88	3.62	1.90	0.53
Q8CGY8_O	Ogt	UDP-N-acet	K.LVSIVAEQLEK#.N	36.89	26.16	1.41	0.71
Q8CGY8_O	Ogt	UDP-N-acet	K.QNPLLAEAYSNLGNVYK#.E	5.73	2.52	2.27	0.44
Q8CGY8_O	Ogt	UDP-N-acet	K.AFLDSLPDVK#.I	17.55	9.77	1.80	0.56
Q8CGY8_O	Ogt	UDP-N-acet	K.ALEVFPEFAAAHSNLASVLQQQGK#.L	10.50	7.24	1.45	0.69
Q8CGY8_O	Ogt	UDP-N-acet	R.IIFSPVAPK#.E	9.58	10.76	0.89	1.12
Q8CGY8_O	Ogt	UDP-N-acet	R.ISPTFADAYSNM*GNTLK#.E	4.14	5.30	0.78	1.28
Q9CZ30_OI	Ola1	Obg-like AT	K.IGIVGLPNVGK#.S	22.67	3.94	5.75	0.17
Q9CZ30_OI	Ola1	Obg-like AT	R.NYIVEDGDIIFFK#.F	8.88	1.66	5.34	0.19
Q9CZ30_OI	Ola1	Obg-like AT	K.YLEANM*TQSALPK#.I	6.27	2.70	2.32	0.43
Q8CI95_OS	Osbpl11	Oxysterol-b	K.GALPSGTTIEWLEPK#.I	11.13	3.75	2.97	0.34
Q8CI95_OS	Osbpl11	Oxysterol-b	R.SILTVPWVELGGK#.V	27.08	8.22	3.29	0.30
Q8CI95_OS	Osbpl11	Oxysterol-b	R.SVILHLLSQLK#.L	13.47	5.32	2.53	0.40
Q8CI95_OS	Osbpl11	Oxysterol-b	K.VSVNCAK#.T	35.65	3.59	9.92	0.10
Q8CI95_OS	Osbpl11	Oxysterol-b	R.VVLPTFILEK#.R	53.79	17.94	3.00	0.33
Q8CI95_OS	Osbpl11	Oxysterol-b	K.GALPSGTTIEWLEPK#.I	12.52	1.12	11.22	0.09
Q8CI95_OS	Osbpl11	Oxysterol-b	R.GTLQLAGAVISPSDEDSHTFTVNAASGEQYK#.L	6.14	3.08	1.99	0.50
Q8CI95_OS	Osbpl11	Oxysterol-b	R.SILTVPWVELGGK#.V	26.45	8.46	3.13	0.32
Q8CI95_OS	Osbpl11	Oxysterol-b	R.VVLPTFILEK#.R	53.97	18.30	2.95	0.34
Q9DBS9_O	Osbpl3	Oxysterol-b	R.LLEEGNIEEAEVQK#.Q	12.76	8.91	1.43	0.70
Q9DBS9_O	Osbpl3	Oxysterol-b	K.NLGVSQK#.L	71.91	28.44	2.53	0.40
Q9DBS9_O	Osbpl3	Oxysterol-b	K.SYSDGSEASSEFSK#.M	11.00	4.56	2.41	0.41
A2A8Z1_OS	Osbpl9	Oxysterol-b	K.YATGENTVFVDTK#.K	8.41	1.21	6.98	0.14
Q62422_O	Ostf1	Osteoclast-	K.GYADIVQLLLAK#.G	10.58	22.67	0.47	2.14
Q7TQI3_OT	Otub1	Ubiquitin t	R.AFGFSHLEALLDDSKELQR.F	5.72	8.37	0.68	1.46
Q7TQI3_OT	Otub1	Ubiquitin t	R.IQQEIAVQNPLVSER.L	3.25	7.43	0.44	2.29
Q7TQI3_OT	Otub1	Ubiquitin t	R.LELSVLYK#.E	14.66	7.76	1.89	0.53
B2RRE7_OT	Otud4	OTU domai	K.TAADVVSPGANSVDR.L	4.28	13.45	0.32	3.14
B2RRE7_OT	Otud4	OTU domai	R.VEGAHSLSAASVSSK#.H	25.76	16.09	1.60	0.62
B2RUR8_O	Otud7b	OTU domai	K.KPEPDGGEDQPSDSPAEPK.A	3.13	3.36	0.93	1.07
B2RUR8_O	Otud7b	OTU domai	K.GPK#PGGLGSGSGISSGTETLEK#.K	33.01	12.52	2.64	0.38
B2RUR8_O	Otud7b	OTU domai	K.K#PEPDGGEDQPSDSPAEPK#.A	12.33	4.85	2.55	0.39
B2RUR8_O	Otud7b	OTU domai	R.SPLVLAYDQAHFSALVSM*EQK#.E	7.73	2.40	3.23	0.31
B2RUR8_O	Otud7b	OTU domai	K.YIFVGTLK#.M	19.12	5.78	3.31	0.30
B2RUR8_O	Otud7b	OTU domai	K.GPK#PGGLGSGSGISSGTETLEK#.K	22.14	6.28	3.53	0.28
B2RUR8_O	Otud7b	OTU domai	R.SPLVLAYDQAHFSALVSM*EQK#.E	5.53	2.07	2.66	0.38
Q9D0K2_S	Oxct1	Succinyl-Co	R.AGGAGVPAFYTSTGYGTLVQEGGSPIK#.Y	16.24	6.33	2.56	0.39
Q9D0K2_S	Oxct1	Succinyl-Co	K.GM*GGAM*DLVSSSK#.T	10.37	3.32	3.13	0.32
Q9D0K2_S	Oxct1	Succinyl-Co	K.YGDLANWM*IPGK#.M	7.71	1.80	4.28	0.23
Q6P9R2_O	Oxsr1	Serine/thre	K.IPISLVLR.L	9.52	20.07	0.47	2.11
Q6P9R2_O	Oxsr1	Serine/thre	K.LLSGGSVLDIIK#.H	56.34	18.95	2.97	0.34
Q6P9R2_O	Oxsr1	Serine/thre	R.DLVIVAANLQK#.I	12.09	2.26	5.36	0.19
Q6P9R2_O	Oxsr1	Serine/thre	K.IPISLVLR.L	12.57	11.95	1.05	0.95
Q6P9R2_O	Oxsr1	Serine/thre	K.LLSGGSVLDIIK#.H	27.76	6.12	4.53	0.22
Q6P9R2_O	Oxsr1	Serine/thre	R.EVLEGLEYLHK#.N	11.18	3.59	3.11	0.32
Q6P9R2_O	Oxsr1	Serine/thre	K.LLSGGSVLDIIK#.H	52.34	10.84	4.83	0.21
Q6P9R2_O	Oxsr1	Serine/thre	K.SGVLDEPTIATILR.E	13.72	21.47	0.64	1.57
Q60715_P	P4ha1	Prolyl 4-hy	K.AEEDK#LEQIK#K#.W	89.97	68.56	1.31	0.76
Q60715_P	P4ha1	Prolyl 4-hy	K.AEEDKLEQIKK.W	20.84	13.65	1.53	0.66
Q60715_P	P4ha1	Prolyl 4-hy	K.DPEGFVGHPVNAFK#.L	52.91	42.10	1.26	0.80
Q60715_P	P4ha1	Prolyl 4-hy	K.DPEGFVGHPVNAFK#.L	21.12	14.40	1.47	0.68
Q60715_P	P4ha1	Prolyl 4-hy	R.FHDIISDAEIEIVK#.D	16.07	9.30	1.73	0.58
Q60715_P	P4ha1	Prolyl 4-hy	K.FILAPAK#.Q	17.76	8.27	2.15	0.47
Q60715_P	P4ha1	Prolyl 4-hy	K.GIAVDYLPER.Q	18.51	66.64	0.28	3.60
Q60715_P	P4ha1	Prolyl 4-hy	R.KDEPDAFR.E	11.58	29.72	0.39	2.57
Q60715_P	P4ha1	Prolyl 4-hy	K.KLLELDPEHQR.A	10.25	18.12	0.57	1.77
Q60715_P	P4ha1	Prolyl 4-hy	R.LNTEWSELENLILK#.D	83.18	54.42	1.53	0.65

Q60715_P4	P4ha1	Prolyl 4-hy	R.LQDTYNLDTNTISK#.G	89.85	51.78	1.74	0.58
Q60715_P4	P4ha1	Prolyl 4-hy	R.LTSTATKDPEGFVGHPVNAFK.L	23.18	10.94	2.12	0.47
Q60715_P4	P4ha1	Prolyl 4-hy	R.QYFPNDEDQVGAAK#.A	19.71	12.32	1.60	0.62
Q60715_P4	P4ha1	Prolyl 4-hy	K.RLNTEWSELENLILK.D	5.89	13.41	0.44	2.28
Q60715_P4	P4ha1	Prolyl 4-hy	K.VSVLDYLSYAVYQQGDLDK#.A	33.90	24.97	1.36	0.74
Q60715_P4	P4ha1	Prolyl 4-hy	R.FHDIISDAEIEIVK.D	3.98	4.75	0.84	1.19
Q60715_P4	P4ha1	Prolyl 4-hy	R.LNTEWSELENLILK#.D	15.90	8.90	1.79	0.56
Q60715_P4	P4ha1	Prolyl 4-hy	R.LQDTYNLDTNTISK#.G	19.11	11.46	1.67	0.60
Q60715_P4	P4ha1	Prolyl 4-hy	R.LQDTYNLDTNTISK#.G	7.03	3.47	2.03	0.49
Q60716_P4	P4ha2	Prolyl 4-hy	K.QLDAGEEATVTK#.S	18.77	12.78	1.47	0.68
Q60716_P4	P4ha2	Prolyl 4-hy	K.SSWLEEDDDPVVAR.V	4.50	6.99	0.64	1.55
P09103_P	P4hb	Protein dis	R.EADDIVNWLK#.K	104.36	55.14	1.89	0.53
P09103_P	P4hb	Protein dis	K.HNQLPLVIEFTEQTAPK#.I	12.02	7.76	1.55	0.65
P09103_P	P4hb	Protein dis	K.IK#PHLMSQEVPEDWDK#QPVK#.V	39.51	27.54	1.43	0.70
P09103_P	P4hb	Protein dis	R.ILEFFGLK#.K	157.68	77.63	2.03	0.49
P09103_P	P4hb	Protein dis	K.K#SNFEEALAAHK#.Y	42.57	25.71	1.66	0.60
P09103_P	P4hb	Protein dis	K.LGETYKDHENIIIAK.M	82.36	39.34	2.09	0.48
P09103_P	P4hb	Protein dis	R.LITLEEEM*TK#.Y	95.78	48.56	1.97	0.51
P09103_P	P4hb	Protein dis	K.M*DSTANEVEAVK#.V	67.38	38.78	1.74	0.58
P09103_P	P4hb	Protein dis	K.MDSTANEVEAVK#.V	47.58	22.99	2.07	0.48
P09103_P	P4hb	Protein dis	K.QLAPIWDK#.L	76.19	46.85	1.63	0.61
P09103_P	P4hb	Protein dis	K.SNFEEALAAHK#.Y	86.03	44.79	1.92	0.52
P09103_P	P4hb	Protein dis	K.THILLFLPK#.S	55.77	33.34	1.67	0.60
P09103_P	P4hb	Protein dis	K.VDATEESDLAQQYGVR.G	21.79	48.45	0.45	2.22
P09103_P	P4hb	Protein dis	K.VLVGANFEEVAFDEK#.K	58.37	35.89	1.63	0.61
P09103_P	P4hb	Protein dis	K.YK#PESDELTAEK#.I	74.02	55.62	1.33	0.75
P09103_P	P4hb	Protein dis	K.YKPESDELTAEK.I	61.57	42.53	1.45	0.69
P09103_P	P4hb	Protein dis	K.YQLDK#DGVVLFK#.K	35.05	18.57	1.89	0.53
P09103_P	P4hb	Protein dis	R.EADDIVNWLK#.K	11.46	7.52	1.52	0.66
P09103_P	P4hb	Protein dis	K.HNQLPLVIEFTEQTAPK#.I	7.48	5.10	1.46	0.68
P09103_P	P4hb	Protein dis	R.ILEFFGLK#.K	13.88	7.85	1.77	0.57
P09103_P	P4hb	Protein dis	K.M*DSTANEVEAVK#.V	7.44	5.51	1.35	0.74
P29341_P	Pabpc1	Polyadenyl	R.AK#EFTNVYIK#.N	43.89	28.71	1.53	0.65
P29341_P	Pabpc1	Polyadenyl	R.ALDTM*NFDVIK#.G	81.67	55.88	1.46	0.68
P29341_P	Pabpc1	Polyadenyl	R.ALDTMNFDVIK#.G	37.21	23.81	1.56	0.64
P29341_P	Pabpc1	Polyadenyl	K.EFSPFGTITSAK#.V	51.37	30.90	1.66	0.60
P29341_P	Pabpc1	Polyadenyl	K.FGPALSVK#.V	105.76	67.54	1.57	0.64
P29341_P	Pabpc1	Polyadenyl	K.FSPAGPILSIR.V	39.03	100.40	0.39	2.57
P29341_P	Pabpc1	Polyadenyl	K.GFGFVSFER.H	35.39	53.91	0.66	1.52
P29341_P	Pabpc1	Polyadenyl	K.GYGFVHFETQEAAER.A	20.67	55.81	0.37	2.70
P29341_P	Pabpc1	Polyadenyl	R.IVATKPLYVALAQR.K	34.96	94.73	0.37	2.71
P29341_P	Pabpc1	Polyadenyl	R.K#SGVGNIFIK#.N	11.43	8.70	1.31	0.76
P29341_P	Pabpc1	Polyadenyl	K.NFGEDM*DDER.L	8.11	18.03	0.45	2.22
P29341_P	Pabpc1	Polyadenyl	K.NLDDGIDDER.L	16.98	41.63	0.41	2.45
P29341_P	Pabpc1	Polyadenyl	K.SGVGNIFIK#.N	66.44	35.20	1.89	0.53
P29341_P	Pabpc1	Polyadenyl	R.SK#VDEAVAVLQAHQAK#.E	85.13	60.25	1.41	0.71
P29341_P	Pabpc1	Polyadenyl	R.YQGVNLYVK#.N	131.42	63.35	2.07	0.48
P29341_P	Pabpc1	Polyadenyl	R.AK#EFTNVYIK#.N	127.79	77.41	1.65	0.61
P29341_P	Pabpc1	Polyadenyl	R.AK#EFTNVYIK#.N	100.50	56.85	1.77	0.57
P29341_P	Pabpc1	Polyadenyl	R.ALDTM*NFDVIK#.G	179.36	111.53	1.61	0.62
P29341_P	Pabpc1	Polyadenyl	R.ALDTMNFDVIK#.G	78.35	43.20	1.81	0.55
P29341_P	Pabpc1	Polyadenyl	K.AVNSATGVPTV.-	123.22	123.22	1.00	1.00
P29341_P	Pabpc1	Polyadenyl	R.AVPNPVINPYQPAPPSGYFMAAIPQTQNR.A	1.86	3.74	0.50	2.01
P29341_P	Pabpc1	Polyadenyl	K.EFSPFGTITSAK#.V	125.92	83.95	1.50	0.67
P29341_P	Pabpc1	Polyadenyl	K.FGPALSVK#.V	223.60	137.94	1.62	0.62
P29341_P	Pabpc1	Polyadenyl	K.FSPAGPILSIR.V	53.83	153.72	0.35	2.86
P29341_P	Pabpc1	Polyadenyl	K.GFGFVSFER.H	41.07	124.39	0.33	3.03
P29341_P	Pabpc1	Polyadenyl	K.GYGFVHFETQEAAER.A	47.43	139.55	0.34	2.94
P29341_P	Pabpc1	Polyadenyl	K.ITGMLLEIDNSELLHM*LESPESLR.S	11.36	27.34	0.42	2.41
P29341_P	Pabpc1	Polyadenyl	R.IVATKPLYVALAQR.K	54.47	139.28	0.39	2.56
P29341_P	Pabpc1	Polyadenyl	R.K#EFSPFGTITSAK#.V	90.78	75.41	1.20	0.83
P29341_P	Pabpc1	Polyadenyl	R.K#SGVGNIFIK#.N	40.00	22.80	1.75	0.57
P29341_P	Pabpc1	Polyadenyl	K.NLDDGIDDER.L	27.30	79.08	0.35	2.90
P29341_P	Pabpc1	Polyadenyl	R.QAHLTNQYM*QR.M	22.29	53.68	0.42	2.41
P29341_P	Pabpc1	Polyadenyl	R.RSLGYAYVNFQQPADAER.A	3.20	20.57	0.16	6.44
P29341_P	Pabpc1	Polyadenyl	K.SGVGNIFIK#.N	187.63	102.99	1.82	0.55
P29341_P	Pabpc1	Polyadenyl	R.SK#VDEAVAVLQAHQAK#.E	325.85	177.95	1.83	0.55
P29341_P	Pabpc1	Polyadenyl	R.SLGYAYVNFQQPADAER.A	28.99	84.95	0.34	2.93
P29341_P	Pabpc1	Polyadenyl	K.VDEAVAVLQAHQAK#.E	32.15	18.90	1.70	0.59
P29341_P	Pabpc1	Polyadenyl	R.YQGVNLYVK#.N	251.32	151.96	1.65	0.60
Q6PHQ9_Q	Pabpc4	MCG5546,	R.ALDTM*NFDVM*K#.G	36.07	17.06	2.11	0.47
Q6PHQ9_Q	Pabpc4	MCG5546,	R.EFSPFGSITSAK#.V	57.75	38.60	1.50	0.67
Q6PHQ9_Q	Pabpc4	MCG5546,	R.IVGSKPLYVALAQR.K	9.41	36.20	0.26	3.85
Q6PHQ9_Q	Pabpc4	MCG5546,	K.NFGEEVDDGNLK#ELFSQFGK#.T	89.30	46.32	1.93	0.52
Q6PHQ9_Q	Pabpc4	MCG5546,	K.NFGEEVDDGNLK#ELFSQFGK#.T	9.09	5.69	1.60	0.63
Q6PHQ9_Q	Pabpc4	MCG5546,	K.SGVGNVFIK#.N	56.10	32.80	1.71	0.58
Q6PHQ9_Q	Pabpc4	MCG5546,	R.YQGVNLYIK#.N	71.22	31.44	2.27	0.44
Q8CCS6_P	Pabpn1	Polyadenyl	K.ELQNEVEK#.Q	61.42	58.68	1.05	0.96
Q8CCS6_P	Pabpn1	Polyadenyl	K.GFAYIEFSDK.E	18.99	27.42	0.69	1.44
Q8CCS6_P	Pabpn1	Polyadenyl	R.TSLALDESLFR.G	24.01	95.46	0.25	3.98
Q8CCS6_P	Pabpn1	Polyadenyl	R.TSLALDESLFR.G	9.07	39.05	0.23	4.31
Q8K212_P	Pacs1	Phosphofu	K.FIPFIGVVK#.V	12.57	7.80	1.61	0.62
Q8K212_P	Pacs1	Phosphofu	K.VAAVGSQSYLSSILR.F	2.40	6.03	0.40	2.51
Q9WVE8_P	Pacsin2	Protein kin	K.ADPSLNPEQLK#.K	73.55	26.08	2.82	0.35
Q9WVE8_P	Pacsin2	Protein kin	R.ANHGPGM*AM*NWPQFEEWSADLNR.T	2.73	5.70	0.48	2.09
Q9WVE8_P	Pacsin2	Protein kin	K.ASLM*NEDFEK#.I	99.56	43.13	2.31	0.43
Q9WVE8_P	Pacsin2	Protein kin	K.ASLMNEDFEK#.I	57.79	14.24	4.06	0.25
Q9WVE8_P	Pacsin2	Protein kin	K.AWIAVM*SEAER.V	10.30	10.57	0.97	1.03
Q9WVE8_P	Pacsin2	Protein kin	K.AWIAVMSEAER.V	13.34	19.42	0.69	1.46
Q9WVE8_P	Pacsin2	Protein kin	R.EVLLEVQK#.H	111.31	27.22	4.09	0.24
Q9WVE8_P	Pacsin2	Protein kin	K.GPQYGTVEK#.A	233.25	59.49	3.92	0.26
Q9WVE8_P	Pacsin2	Protein kin	K.GRLDSGQVGLYPANYVEAIQ.-	3.44	10.31	0.33	3.00
Q9WVE8_P	Pacsin2	Protein kin	K.HLDLSNVASYK#.T	206.33	43.45	4.75	0.21
Q9WVE8_P	Pacsin2	Protein kin	R.VSELHLEVK#.A	107.22	29.33	3.66	0.27
Q9WVE8_P	Pacsin2	Protein kin	K.AADAVEDLR.W	8.32	10.22	0.81	1.23
Q9WVE8_P	Pacsin2	Protein kin	K.ADPSLNPEQLK#.K	15.15	10.39	1.46	0.69
Q9WVE8_P	Pacsin2	Protein kin	K.ASLM*NEDFEK#.I	22.07	4.57	4.83	0.21
Q9WVE8_P	Pacsin2	Protein kin	R.EVLLEVQK#.H	35.38	9.60	3.69	0.27
Q9WVE8_P	Pacsin2	Protein kin	K.GPQYGTVEK#.A	46.44	12.28	3.78	0.26
Q9WVE8_P	Pacsin2	Protein kin	K.HLDLSNVASYK#.T	57.79	15.76	3.67	0.27
Q8K2T8_P	Paf1	RNA polym	K.AGVQSGTNALLVVK#.H	42.55	28.71	1.48	0.67
Q8K2T8_P	Paf1	RNA polym	R.EGDGVYYNELETR.V	11.28	23.31	0.48	2.07
Q8K2T8_P	Paf1	RNA polym	R.IDPNVLLDPADEK#LLEEEIQAPTSSK#.R	18.58	20.72	0.90	1.12

Q8K2T8_P	Paf1	RNA polym	K.LLEEEIQAPTSSK#.R	9.96	13.47	0.74	1.35
Q8K2T8_P	Paf1	RNA polym	K.TEYISTEFNR.Y	5.63	14.29	0.39	2.54
P63005_LI	Pafah1b1	Platelet-act	K.EEFTSGGPLGQK#.R	13.01	5.28	2.46	0.41
P63005_LI	Pafah1b1	Platelet-act	K.GHTDSVQDISFDHSGK#.L	66.14	16.51	4.00	0.25
P63005_LI	Pafah1b1	Platelet-act	K.LNEAK#EEFTSGGPLGQK#.R	65.34	15.23	4.29	0.23
P63005_LI	Pafah1b1	Platelet-act	K.TAPYVVTGSVDQTVK#.V	39.73	9.69	4.10	0.24
P63005_LI	Pafah1b1	Platelet-act	R.VIFHPVFSVMVSASEDATIK#.V	6.45	3.01	2.15	0.47
P63005_LI	Pafah1b1	Platelet-act	K.VWDYETGDFER.T	11.40	11.51	0.99	1.01
P63005_LI	Pafah1b1	Platelet-act	R.VWVVATK#.E	59.27	11.55	5.13	0.19
P63005_LI	Pafah1b1	Platelet-act	K.YAGLLEK#.K	50.41	14.05	3.59	0.28
P63005_LI	Pafah1b1	Platelet-act	K.GHTDSVQDISFDHSGK#.L	47.81	6.66	7.18	0.14
P63005_LI	Pafah1b1	Platelet-act	K.K#VM*ELESK#.L	8.10	5.44	1.49	0.67
P63005_LI	Pafah1b1	Platelet-act	K.LNEAK#EEFTSGGPLGQK#.R	57.94	7.13	8.13	0.12
P63005_LI	Pafah1b1	Platelet-act	K.TAPYVVTGSVDQTVK#.V	42.01	8.06	5.21	0.19
P63005_LI	Pafah1b1	Platelet-act	R.VWVVATK#.E	29.17	3.64	8.02	0.12
P63005_LI	Pafah1b1	Platelet-act	K.YAGLLEK#.K	27.47	5.01	5.49	0.18
P63005_LI	Pafah1b1	Platelet-act	K.GHTDSVQDISFDHSGK#.L	65.92	4.03	16.35	0.06
P63005_LI	Pafah1b1	Platelet-act	K.K#VM*ELESK#.L	14.50	22.74	0.64	1.57
P63005_LI	Pafah1b1	Platelet-act	K.LNEAK#EEFTSGGPLGQK#.R	59.49	10.58	5.62	0.18
P63005_LI	Pafah1b1	Platelet-act	K.TAPYVVTGSVDQTVK#.V	75.20	18.38	4.09	0.24
P63005_LI	Pafah1b1	Platelet-act	K.YAGLLEK#.K	42.87	7.19	5.96	0.17
Q9DCL9_P	Paics	Multifuncti	K.DDANNDPQWSEEQLIAAK#.F	3.21	2.68	1.20	0.84
Q9DCL9_P	Paics	Multifuncti	R.IATGSFLK#.R	40.44	13.55	2.98	0.34
Q9DCL9_P	Paics	Multifuncti	K.IEFGVDVTTK#.E	25.86	8.21	3.15	0.32
Q9DCL9_P	Paics	Multifuncti	R.NPGVQEGYK#.F	48.18	17.39	2.77	0.36
Q9DCL9_P	Paics	Multifuncti	K.VEMFFK#DDANNDPQWSEEQLIAAK#.F	5.93	9.10	0.65	1.53
Q9DCL9_P	Paics	Multifuncti	R.ASILNTWISLK#.Q	16.32	4.24	3.85	0.26
Q9DCL9_P	Paics	Multifuncti	K.IEFGVDVTTK#.E	21.69	3.08	7.03	0.14
Q9DCL9_P	Paics	Multifuncti	R.NPGVQEGYK#.F	24.96	7.70	3.24	0.31
Q9DCL9_P	Paics	Multifuncti	R.ASILNTWISLK#.Q	24.31	4.52	5.38	0.19
Q9DCL9_P	Paics	Multifuncti	K.EIVLADVIDNDSWR.L	8.10	9.31	0.87	1.15
Q9DCL9_P	Paics	Multifuncti	K.EVTPEGLQM*VK#.K	37.03	8.70	4.26	0.24
Q9DCL9_P	Paics	Multifuncti	K.EVYELLDTPGR.V	3.69	6.07	0.61	1.64
Q9DCL9_P	Paics	Multifuncti	K.IEFGVDVTTK#.E	28.80	6.97	4.13	0.24
Q9DCL9_P	Paics	Multifuncti	R.IKAEYEGDGIPTVFVSVAGR.S	7.47	9.90	0.75	1.32
Q9DCL9_P	Paics	Multifuncti	R.NPGVQEGYK#.F	35.66	6.99	5.10	0.20
Q9D6V8_P	Paip2	Polyadenyl	R.DLPQTM*DQIQDQFNDLVISDGSSLEDLVVK#.S	16.81	10.39	1.62	0.62
Q8CIN4_P	Pak2	Serine/thre	K.IISIFSGTEK#.G	16.63	6.95	2.39	0.42
Q8CIN4_P	Pak2	Serine/thre	R.LLQTSNITK#.S	43.40	16.89	2.57	0.39
Q8CIN4_P	Pak2	Serine/thre	K.SDNVLLGM*EGSVK#.L	12.89	1.96	6.58	0.15
Q8CIN4_P	Pak2	Serine/thre	R.SVIDPIPAPVGDSNVDSGAK#.S	8.16	32.52	0.25	3.99
Q9ET54_P	Palld	Palladin OS	K.AAFQPEASPSHLTLNSGLVESEDL.-	8.85	8.85	1.00	1.00
Q9ET54_P	Palld	Palladin OS	K.AAFQPEASPSHLTLNSGLVESEDL.-	2.77	2.77	1.00	1.00
Q9ET54_P	Palld	Palladin OS	R.IASDEEIQGTK#.D	22.85	15.08	1.52	0.66
Q9ET54_P	Palld	Palladin OS	R.LISEIEYR.L	4.86	13.95	0.35	2.87
Q9ET54_P	Palld	Palladin OS	K.LQNTGVADGYPVR.L	4.35	11.07	0.39	2.55
Q9ET54_P	Palld	Palladin OS	R.YAALSDQGLDIK#.A	10.67	8.52	1.25	0.80
Q61183_P	Papola	Poly(A) pol	K.LFEAPNFFQK#.Y	18.40	3.32	5.55	0.18
Q60967_P	Papss1	Bifunctiona	K.TDAEALPALK#.I	12.15	2.44	4.98	0.20
Q99LX0_P	Park7	Protein deg	R.ALVILAK#.G	15.56	4.79	3.25	0.31
Q8VDG3_P	Parn	Poly(A)-spe	K.LM*ASTQPFK#DIINNTSLAELEK#.R	4.96	3.34	1.48	0.67
Q8VDG3_P	Parn	Poly(A)-spe	R.VM*DIPYLNLEGPDLQPK#.R	6.08	4.34	1.40	0.71
Q921K2_Q	Parp1	Poly (ADP-r	R.K#GDEVDGTDEVAK#.K	8.54	5.45	1.57	0.64
Q921K2_Q	Parp1	Poly (ADP-r	K.TLGDFLAEYAK#.S	35.11	22.52	1.56	0.64
Q921K2_Q	Parp1	Poly (ADP-r	K.TLGDFLAEYAK#.S	63.78	29.77	2.14	0.47
Q921K2_Q	Parp1	Poly (ADP-r	K.AEPGEVVAPK#.G	78.34	77.43	1.01	0.99
Q921K2_Q	Parp1	Poly (ADP-r	K.ALVEYEIDLQK#.M	85.62	71.76	1.19	0.84
Q921K2_Q	Parp1	Poly (ADP-r	K.AQNELIWNIK#DELK#K#.A	61.33	51.30	1.20	0.84
Q921K2_Q	Parp1	Poly (ADP-r	K.ELLIFNQQQVPSGESAILDR.V	9.29	37.30	0.25	4.01
Q921K2_Q	Parp1	Poly (ADP-r	K.GAVK#EEGVNK#SEK#.R	1.44	2.86	0.50	1.99
Q921K2_Q	Parp1	Poly (ADP-r	R.GGSDDSSK#DPIDVNYEK#.L	81.08	70.92	1.14	0.87
Q921K2_Q	Parp1	Poly (ADP-r	K.GIYFADM*VSK#.S	24.38	19.31	1.26	0.79
Q921K2_Q	Parp1	Poly (ADP-r	K.K#FYPLEIDYGQDEEAVK#.K	29.10	25.82	1.13	0.89
Q921K2_Q	Parp1	Poly (ADP-r	K.K#FYPLEIDYGQDEEAVK#K#.L	42.10	30.39	1.39	0.72
Q921K2_Q	Parp1	Poly (ADP-r	R.K#GDEVDGTDEVAK#.K	31.06	23.65	1.31	0.76
Q921K2_Q	Parp1	Poly (ADP-r	K.K#PPLLNNADSVQAK#.V	64.92	67.13	0.97	1.03
Q921K2_Q	Parp1	Poly (ADP-r	K.LQLLEDDKESR.Y	7.02	20.21	0.35	2.88
Q921K2_Q	Parp1	Poly (ADP-r	K.NTHATTHNAYDLEVIDIFK#.I	42.84	23.88	1.79	0.56
Q921K2_Q	Parp1	Poly (ADP-r	K.RKGDEVDGTDEVAK.K	12.02	59.54	0.20	4.95
Q921K2_Q	Parp1	Poly (ADP-r	R.RQIQAAYSILSEVQQAVSQGSSESQILDLSNR.F	2.59	17.27	0.15	6.67
Q921K2_Q	Parp1	Poly (ADP-r	K.SLQELLSAHSLSSWGAEVK#.A	5.91	5.43	1.09	0.92
Q921K2_Q	Parp1	Poly (ADP-r	K.TLGDFLAEYAK#.S	115.61	89.22	1.30	0.77
Q921K2_Q	Parp1	Poly (ADP-r	R.TTNFAGILSQGLR.I	24.13	84.43	0.29	3.50
Q921K2_Q	Parp1	Poly (ADP-r	K.VFSATLGLVDIVK#.G	131.44	100.36	1.31	0.76
Q921K2_Q	Parp1	Poly (ADP-r	R.VGTVIGSNK#.L	36.78	24.55	1.50	0.67
Q921K2_Q	Parp1	Poly (ADP-r	K.VVDRDSEEAEVIR.K	10.17	62.59	0.16	6.16
Q921K2_Q	Parp1	Poly (ADP-r	K.VVDRDSEEAEVIRK.Y	1.22	69.81	0.02	57.10
Q921K2_Q	Parp1	Poly (ADP-r	K.FYPLEIDYGQDEEAVK#.K	3.67	2.01	1.82	0.55
Q921K2_Q	Parp1	Poly (ADP-r	K.GGAAVDPDSGLEHSAHVLEK#.G	22.27	17.52	1.27	0.79
Q921K2_Q	Parp1	Poly (ADP-r	R.GGSDDSSK#DPIDVNYEK#.L	37.16	25.90	1.44	0.70
Q921K2_Q	Parp1	Poly (ADP-r	K.K#FYPLEIDYGQDEEAVK#.K	7.81	8.00	0.98	1.02
Q921K2_Q	Parp1	Poly (ADP-r	K.K#FYPLEIDYGQDEEAVK#K#.L	8.00	11.27	0.71	1.41
Q921K2_Q	Parp1	Poly (ADP-r	K.K#PPLLNNADSVQAK#.V	31.69	26.05	1.22	0.82
Q921K2_Q	Parp1	Poly (ADP-r	K.RKGDEVDGTDEVAK.K	5.32	22.71	0.23	4.27
Q921K2_Q	Parp1	Poly (ADP-r	K.SLQELLSAHSLSSWGAEVK#.A	20.07	17.95	1.12	0.89
Q921K2_Q	Parp1	Poly (ADP-r	K.TLGDFLAEYAK#.S	37.30	26.75	1.39	0.72
Q921K2_Q	Parp1	Poly (ADP-r	R.TTNFAGILSQGLR.I	9.80	22.11	0.44	2.26
Q921K2_Q	Parp1	Poly (ADP-r	K.VFSATLGLVDIVK#.G	42.06	29.67	1.42	0.71
Q8CIE4_Q8	Parp10	Plec1 prote	K.EKPGGPGETVVEQQEEIPTLEAEEEPVALSTGAR.G	1.75	1.88	0.93	1.08
Q8BZ20_P	Parp12	Poly [ADP-r	R.LGLSSDLVSR.L	3.99	14.44	0.28	3.62
Q2EMV9_P	Parp14	Poly [ADP-r	K.AIIDAIEEFVQK#.K	32.02	14.16	2.26	0.44
Q2EMV9_P	Parp14	Poly [ADP-r	R.DASAVLSGIK#.S	24.55	21.67	1.13	0.88
Q2EMV9_P	Parp14	Poly [ADP-r	K.DHENIQAFSDEFDKR.N	8.07	22.24	0.36	2.76
Q2EMV9_P	Parp14	Poly [ADP-r	K.DVQVSSEVFEFLQQVDSQR.L	18.81	43.73	0.43	2.32
Q2EMV9_P	Parp14	Poly [ADP-r	K.EGGVVLPGNAVISK#.A	42.86	26.67	1.61	0.62
Q2EMV9_P	Parp14	Poly [ADP-r	R.FPVDVVVNAANENLK#.H	13.61	8.89	1.53	0.65
Q2EMV9_P	Parp14	Poly [ADP-r	K.GTALFLVGSSFK#.D	42.75	22.31	1.92	0.52
Q2EMV9_P	Parp14	Poly [ADP-r	K.HISGLAQALSK#.A	32.58	19.38	1.68	0.59
Q2EMV9_P	Parp14	Poly [ADP-r	K.IASFLGFPK#.Q	26.20	13.94	1.88	0.53
Q2EMV9_P	Parp14	Poly [ADP-r	K.IKPSLIVDYLR.T	8.71	30.35	0.29	3.48
Q2EMV9_P	Parp14	Poly [ADP-r	K.IYLVGLPAK#.V	35.59	17.19	2.07	0.48
Q2EMV9_P	Parp14	Poly [ADP-r	K.K#NTLVLEK#.K	19.31	13.53	1.43	0.70
Q2EMV9_P	Parp14	Poly [ADP-r	K.LPASFQESLDLPLWK#.F	31.66	16.79	1.89	0.53

Q2EMV9_P	Parp14	Poly [ADP-r	K.LTVLM*PTDPEEASASK#K#.S	10.92	9.46	1.15	0.87
Q2EMV9_P	Parp14	Poly [ADP-r	K.M*PLSVFPYYPSLGTALYGEEK#PLIK#.L	20.33	16.86	1.21	0.83
Q2EMV9_P	Parp14	Poly [ADP-r	K.QGSLLVSPEGLR.I	5.17	11.52	0.45	2.23
Q2EMV9_P	Parp14	Poly [ADP-r	K.SLFEAQNILAIYELK#.G	29.67	17.94	1.65	0.60
Q2EMV9_P	Parp14	Poly [ADP-r	K.SNNSAWSLK#.I	13.22	7.27	1.82	0.55
Q2EMV9_P	Parp14	Poly [ADP-r	R.SNQQLQLAPR.L	7.79	28.23	0.28	3.63
Q2EMV9_P	Parp14	Poly [ADP-r	K.TLQEVQFLLHPK#.D	20.31	14.23	1.43	0.70
Q2EMV9_P	Parp14	Poly [ADP-r	K.TTENLSLQSIAFPAIGTGNLR.F	6.36	25.10	0.25	3.95
Q2EMV9_P	Parp14	Poly [ADP-r	R.VLFSPEDVR.Q	62.11	25.95	2.39	0.42
Q2EMV9_P	Parp14	Poly [ADP-r	R.VLVEFEK#.E	14.46	13.39	1.08	0.93
Q3ULW8_C	Parp3	Protein Par	K.ALSPQVYSGPVR.T	1.82	11.91	0.15	6.53
Q3ULW8_C	Parp3	Protein Par	K.GIYFASENSK#.S	22.44	16.60	1.35	0.74
Q3ULW8_C	Parp3	Protein Par	K.NAM*TLM*NLDVK.K	10.72	16.32	0.66	1.52
Q3ULW8_C	Parp3	Protein Par	R.QGTEEEDSFR.S	5.48	17.61	0.31	3.21
Q3ULW8_C	Parp3	Protein Par	K.SPPSGFDSVIAR.G	12.94	48.28	0.27	3.73
Q3ULW8_C	Parp3	Protein Par	R.SRPPPINSPDVLQAK.K	8.79	41.15	0.21	4.68
Q3ULW8_C	Parp3	Protein Par	K.SSSFSQSEYLIYK#.E	37.13	26.78	1.39	0.72
Q3ULW8_C	Parp3	Protein Par	R.YLLEIHL.-	14.20	14.20	1.00	1.00
Q3ULW8_C	Parp3	Protein Par	K.YTLIEVQGEAESQEAVVK#.A	17.39	18.56	0.94	1.07
Q3ULW8_C	Parp3	Protein Par	K.SSSFSQSEYLIYK#.E	9.19	8.13	1.13	0.88
Q3ULW8_C	Parp3	Protein Par	K.AIQTYLK#.Q	17.66	16.57	1.07	0.94
Q3ULW8_C	Parp3	Protein Par	R.FVAQPNK#.Y	15.66	17.29	0.91	1.10
Q3ULW8_C	Parp3	Protein Par	K.FYIIQLLEEGSR.F	4.00	12.31	0.33	3.08
Q3ULW8_C	Parp3	Protein Par	K.GIYFASENSK#.S	16.63	5.92	2.81	0.36
Q3ULW8_C	Parp3	Protein Par	K.YTLIEVQGEAESQEAVVK#.A	4.84	3.84	1.26	0.79
Q8CAS9_P	Parp9	Poly [ADP-r	R.DLSSWGGPETDPASTM*TLR.I	4.97	7.29	0.68	1.47
Q8CAS9_P	Parp9	Poly [ADP-r	R.EIHLVSNEDPTVASFK#.S	37.69	26.43	1.43	0.70
Q8CAS9_P	Parp9	Poly [ADP-r	R.EIHLVSNEDPTVASFK.S	8.10	4.76	1.70	0.59
Q8CAS9_P	Parp9	Poly [ADP-r	R.GGLEAGSPAINLM*GVK#.V	12.37	7.70	1.61	0.62
Q8CAS9_P	Parp9	Poly [ADP-r	K.GPQADLIDAVMR.I	3.88	10.46	0.37	2.70
Q8CAS9_P	Parp9	Poly [ADP-r	K.HNVFEILK#.S	35.20	22.26	1.58	0.63
Q8CAS9_P	Parp9	Poly [ADP-r	K.ISVGGIAITGAGR.L	36.64	21.99	1.67	0.60
Q8CAS9_P	Parp9	Poly [ADP-r	K.IVIFPVDVETYK#.I	58.05	44.02	1.32	0.76
Q8CAS9_P	Parp9	Poly [ADP-r	R.M*YSTSYNPVYGAGIYFTK#.S	7.51	3.30	2.27	0.44
Q8CAS9_P	Parp9	Poly [ADP-r	R.MYSTSYNPVYGAGIYFTK#.S	4.56	3.17	1.44	0.70
Q8CAS9_P	Parp9	Poly [ADP-r	K.SASESILGR.D	11.86	27.77	0.43	2.34
Q8CAS9_P	Parp9	Poly [ADP-r	R.SNELNLSGNSGALALQWSSGEQR.R	2.54	5.19	0.49	2.04
Q8CAS9_P	Parp9	Poly [ADP-r	R.VAQSILR.Q	14.17	30.21	0.47	2.13
Q8CAS9_P	Parp9	Poly [ADP-r	K.VLLAAFQEK#.K	44.31	26.97	1.64	0.61
Q8CAS9_P	Parp9	Poly [ADP-r	R.VSISETVSPR.T	10.93	38.67	0.28	3.54
Q8CAS9_P	Parp9	Poly [ADP-r	R.WTVTNSQTAIELLK#.F	24.59	21.43	1.15	0.87
Q8CAS9_P	Parp9	Poly [ADP-r	R.YPASLTQELQDR.K	7.42	40.44	0.18	5.45
Q8CAS9_P	Parp9	Poly [ADP-r	R.EIHLVSNEDPTVASFK#.S	23.84	19.55	1.22	0.82
Q8CAS9_P	Parp9	Poly [ADP-r	K.HNVFEILK#.S	18.17	19.70	0.92	1.08
Q8CAS9_P	Parp9	Poly [ADP-r	K.IVIFPVDVETYK#.I	46.42	26.13	1.78	0.56
Q8CAS9_P	Parp9	Poly [ADP-r	K.VLLAAFQEK#.K	26.65	15.92	1.67	0.60
Q8CAS9_P	Parp9	Poly [ADP-r	R.WTVTNSQTAIELLK#.F	14.90	8.63	1.73	0.58
Q9EPC1_P	Parva	Alpha-parvi	R.DAFDTLFDHAPDK#LNVVK#.K	58.66	21.25	2.76	0.36
Q9EPC1_P	Parva	Alpha-parvi	K.DLAEDLYDGQVLQK#.L	79.01	45.88	1.72	0.58
Q9EPC1_P	Parva	Alpha-parvi	R.IIVK#DLAEDLYDGQVLQK#.L	9.14	6.32	1.45	0.69
Q9EPC1_P	Parva	Alpha-parvi	K.K#TLITFVNK#.H	14.48	5.91	2.45	0.41
Q9EPC1_P	Parva	Alpha-parvi	K.LESEK#LNVAEVTQSEIAQK#.Q	31.63	14.98	2.11	0.47
Q9EPC1_P	Parva	Alpha-parvi	K.LNVAEVTQSEIAQK#.Q	76.42	33.42	2.29	0.44
Q9EPC1_P	Parva	Alpha-parvi	R.QIQEEITGNTEALSGR.H	12.73	28.85	0.44	2.27
Q9EPC1_P	Parva	Alpha-parvi	K.TLITFVNK#.H	52.05	21.81	2.39	0.42
Q9EPC1_P	Parva	Alpha-parvi	R.VLYNLFTK#.Y	61.47	31.25	1.97	0.51
Q9ES46_P	Parvb	Beta-parvin	K.LNVAEVTQSEIGQK#.Q	13.52	2.94	4.59	0.22
Q925B0_P	Pawr	PRKC apop	R.DANAPASFSSSSTLEK#.R	19.65	13.62	1.44	0.69
Q925B0_P	Pawr	PRKC apop	R.KREDAITQQNTIQNEAATLPDPGTSYLPQDPSR.T	3.22	5.44	0.59	1.69
Q925B0_P	Pawr	PRKC apop	R.SGGSTTTDFLEEWK#.A	18.01	11.01	1.63	0.61
Q00288_P	Pax8	Paired box	K.ATLTSSNTPLGR.N	3.18	11.19	0.28	3.51
Q00288_P	Pax8	Paired box	R.LSIDSQSSSSGPR.K	2.38	19.33	0.12	8.13
P58501_P	Paxbp1	PAX3- and	R.ASLLSFQDEEEENEEVFK#.V	4.67	3.88	1.20	0.83
P58501_P	Paxbp1	PAX3- and	R.LQLLTWTPLEAK#.C	19.53	13.55	1.44	0.69
P58501_P	Paxbp1	PAX3- and	K.TDNTVPFK#.T	14.64	11.31	1.29	0.77
Q9D0B6_P	Pbdc1	Protein PB	K.AVSVSIQDK#EGEEGAGNK#EEAAEK#.G	8.01	2.27	3.54	0.28
Q9D0B6_P	Pbdc1	Protein PB	R.AM*QHAEVYYK#.L	10.02	3.30	3.04	0.33
Q9D0B6_P	Pbdc1	Protein PB	R.IQFFAIEIAR.N	14.87	27.62	0.54	1.86
Q9D0B6_P	Pbdc1	Protein PB	K.LISSVDPQFLK#.L	62.77	28.54	2.20	0.45
Q9D0B6_P	Pbdc1	Protein PB	K.VDDQIYSEFR.E	10.11	18.77	0.54	1.86
Q8BSQ9_P	Pbrm1	Protein pol	K.LNEVYEAVK#.N	19.92	15.60	1.28	0.78
Q8BSQ9_P	Pbrm1	Protein pol	K.AQHPDYSFGELSR.L	5.90	25.17	0.23	4.27
Q8BSQ9_P	Pbrm1	Protein pol	R.DGAAYFYGPIFIHPEETEHEPTK.M	5.20	6.08	0.85	1.17
Q8BSQ9_P	Pbrm1	Protein pol	R.EAEKSEDSSGTTGLSGLHR.T	3.93	28.06	0.14	7.14
Q8BSQ9_P	Pbrm1	Protein pol	K.ELGPLPDDDDM*ASPK.L	27.95	20.82	1.34	0.75
Q8BSQ9_P	Pbrm1	Protein pol	K.IILEPM*DLK#.I	19.39	13.74	1.41	0.71
Q8BSQ9_P	Pbrm1	Protein pol	R.K#PIIPQK#EPSPLLEK#.K	21.90	24.35	0.90	1.11
Q8BSQ9_P	Pbrm1	Protein pol	R.LLHSEAYLK#.Y	18.27	21.17	0.86	1.16
Q8BSQ9_P	Pbrm1	Protein pol	K.LNEVYEAVK#.N	59.85	37.55	1.59	0.63
Q8BSQ9_P	Pbrm1	Protein pol	R.LSAIFLR.L	6.16	23.23	0.27	3.77
Q8BSQ9_P	Pbrm1	Protein pol	K.MPISLQQIR.T	1.29	8.84	0.15	6.86
Q8BSQ9_P	Pbrm1	Protein pol	K.NGEILLSPALSYTTK#.H	7.05	5.31	1.33	0.75
Q8BSQ9_P	Pbrm1	Protein pol	R.NHQGQLIAEPFFHLPSK.K	9.77	12.54	0.78	1.28
Q8BSQ9_P	Pbrm1	Protein pol	R.NQPDYYEVVSQPIDLM*K#.I	7.76	8.27	0.94	1.07
Q8BSQ9_P	Pbrm1	Protein pol	R.RDDIEDGDSM*ISSATSDTGSAK.R	2.78	18.05	0.15	6.50
Q8BSQ9_P	Pbrm1	Protein pol	K.TYNEPGSQVFK#.D	31.90	30.86	1.03	0.97
Q8BSQ9_P	Pbrm1	Protein pol	K.VLLETR.R	7.34	32.75	0.22	4.46
Q8BSQ9_P	Pbrm1	Protein pol	K.VQYPDYYAIIK#.E	6.27	7.86	0.80	1.25
Q8BSQ9_P	Pbrm1	Protein pol	K.VVDDEIYYFR.K	7.36	31.80	0.23	4.32
Q8BSQ9_P	Pbrm1	Protein pol	R.YEEGESEAESITSFM*DVSNPFHQLYDTVR.S	2.90	4.93	0.59	1.70
Q8BSQ9_P	Pbrm1	Protein pol	K.YIEGLSAESNSISK#.W	27.36	24.85	1.10	0.91
O35984_P	Pbx2	Pre-B-cell l	R.LDNM*LLAEGVAGPEK#.G	7.05	4.17	1.69	0.59
Q05920_P	Pc	Pyruvate c	R.GANAVGYTNYPDNVVFK#.F	7.04	1.89	3.72	0.27
Q05920_P	Pc	Pyruvate c	R.LDNASAFQGAVISPHYDSLLVK#.V	16.48	4.40	3.75	0.27
P60335_P	Pcbp1	Poly(rC)-bi	K.AFAM*IIDKLEEDINSSM*TNSTAASRPPVTLR.L	4.60	29.53	0.16	6.43
P60335_P	Pcbp1	Poly(rC)-bi	K.AFAMIIDKLEEDINSSM*TNSTAASRPPVTLR.L	9.45	42.33	0.22	4.48
P60335_P	Pcbp1	Poly(rC)-bi	K.AFAM*IIDKLEEDINSSMTNSTAASRPPVTLR.L	4.38	22.03	0.20	5.03
P60335_P	Pcbp1	Poly(rC)-bi	K.AFAMIIDKLEEDINSSMTNSTAASRPPVTLR.L	92.77	42.36	2.19	0.46
P60335_P	Pcbp1	Poly(rC)-bi	R.ESTGAQVQVAGDM*LPNSTER.A	40.81	103.99	0.39	2.55
P60335_P	Pcbp1	Poly(rC)-bi	R.ESTGAQVQVAGDMLPNSTER.A	20.06	49.96	0.40	2.49
P60335_P	Pcbp1	Poly(rC)-bi	K.IANPVEGSSGR.Q	113.99	343.53	0.33	3.01
P60335_P	Pcbp1	Poly(rC)-bi	R.IITLTGPTNAIFK#.A	746.25	452.63	1.65	0.61
P60335_P	Pcbp1	Poly(rC)-bi	R.LVVPATQCGSLIGK#.G	32.53	18.51	1.76	0.57

P60335_P(	Pcbp1	Poly(rC)-bir	R.QGANINEIR.Q	85.98	221.27	0.39	2.57
P60335_P(	Pcbp1	Poly(rC)-bir	R.QM*SGAQIK#.I	51.53	35.49	1.45	0.69
P60335_P(	Pcbp1	Poly(rC)-bir	R.QMSGAQIK#.I	135.79	76.74	1.77	0.57
P60335_P(	Pcbp1	Poly(rC)-bir	R.QVTITGSAASISLAQYLINAR.L	22.64	57.02	0.40	2.52
P60335_P(	Pcbp1	Poly(rC)-bir	R.ESTGAQVQVAGDM*LPNSTER.A	2.81	9.73	0.29	3.47
P60335_P(	Pcbp1	Poly(rC)-bir	R.ESTGAQVQVAGDMLPNSTER.A	2.54	5.69	0.45	2.24
P60335_P(	Pcbp1	Poly(rC)-bir	K.IANPVEGSSGR.Q	4.76	14.20	0.34	2.98
P60335_P(	Pcbp1	Poly(rC)-bir	R.IITLTGPTNAIFK#.A	159.23	101.26	1.57	0.64
P60335_P(	Pcbp1	Poly(rC)-bir	R.QVTITGSAASISLAQYLINAR.L	3.70	5.37	0.69	1.45
P60335_P(	Pcbp1	Poly(rC)-bir	R.ESTGAQVQVAGDM*LPNSTER.A	11.24	22.63	0.50	2.01
P60335_P(	Pcbp1	Poly(rC)-bir	K.IANPVEGSSGR.Q	19.62	53.30	0.37	2.72
P60335_P(	Pcbp1	Poly(rC)-bir	R.IITLTGPTNAIFK#.A	128.81	68.25	1.89	0.53
P60335_P(	Pcbp1	Poly(rC)-bir	R.QQSHFAM*M*HGGTGFAGIDSSSPEVK#.G	7.83	4.36	1.80	0.56
P60335_P(	Pcbp1	Poly(rC)-bir	R.QVTITGSAASISLAQYLINAR.L	5.34	12.22	0.44	2.29
P60335_P(	Pcbp1	Poly(rC)-bir	R.ESTGAQVQVAGDM*LPNSTER.A	9.73	31.82	0.31	3.27
P60335_P(	Pcbp1	Poly(rC)-bir	R.ESTGAQVQVAGDMLPNSTER.A	2.76	6.42	0.43	2.33
P60335_P(	Pcbp1	Poly(rC)-bir	K.IANPVEGSSGR.Q	21.62	32.09	0.67	1.48
P60335_P(	Pcbp1	Poly(rC)-bir	R.IITLTGPTNAIFK#.A	128.09	83.46	1.53	0.65
P60335_P(	Pcbp1	Poly(rC)-bir	R.QGANINEIR.Q	11.64	27.52	0.42	2.36
Q61990_P(	Pcbp2	Poly(rC)-bir	K.AFAM*IIDKLEEDISSSM*TNSTAASRPPVTLR.L	5.76	19.40	0.30	3.37
Q61990_P(	Pcbp2	Poly(rC)-bir	K.AFAMIIDKLEEDISSSM*TNSTAASRPPVTLR.L	2.16	7.34	0.29	3.41
Q61990_P(	Pcbp2	Poly(rC)-bir	K.AFAM*IIDKLEEDISSSMTNSTAASRPPVTLR.L	6.60	21.93	0.30	3.32
Q61990_P(	Pcbp2	Poly(rC)-bir	K.IANPVEGSTDR.Q	120.93	330.47	0.37	2.73
Q61990_P(	Pcbp2	Poly(rC)-bir	R.IITLAGPTNAIFK#.A	785.85	398.48	1.97	0.51
Q61990_P(	Pcbp2	Poly(rC)-bir	K.LEEDISSSM*TNSTAASRPPVTLR.L	1.30	8.81	0.15	6.80
Q61990_P(	Pcbp2	Poly(rC)-bir	K.LHQLAM*QQSHFPM*THGNTGFSGIESSSPEVK#.G	8.32	3.54	2.35	0.43
Q61990_P(	Pcbp2	Poly(rC)-bir	K.LHQLAMQQSHFPMTHGNTGFSGIESSSPEVK#.G	6.79	2.89	2.35	0.43
Q61990_P(	Pcbp2	Poly(rC)-bir	R.QVTITGSAASISLAQYLINVR.L	9.61	20.86	0.46	2.17
Q61990_P(	Pcbp2	Poly(rC)-bir	R.IITLAGPTNAIFK#.A	33.58	21.25	1.58	0.63
Q61990_P(	Pcbp2	Poly(rC)-bir	K.IANPVEGSTDR.Q	21.45	48.73	0.44	2.27
Q61990_P(	Pcbp2	Poly(rC)-bir	R.IITLAGPTNAIFK#.A	132.50	72.76	1.82	0.55
Q61990_P(	Pcbp2	Poly(rC)-bir	K.LHQLAM*QQSHFPM*THGNTGFSGIESSSPEVK#.G	6.28	4.14	1.52	0.66
Q61990_P(	Pcbp2	Poly(rC)-bir	K.IANPVEGSTDR.Q	30.22	82.28	0.37	2.72
Q61990_P(	Pcbp2	Poly(rC)-bir	R.IITLAGPTNAIFK#.A	194.63	108.47	1.79	0.56
Q61990_P(	Pcbp2	Poly(rC)-bir	K.LHQLAM*QQSHFPM*THGNTGFSGIESSSPEVK#.G	12.54	5.43	2.31	0.43
P57722_P(	Pcbp3	Poly(rC)-bir	K.LHQLAM*QQTPFPPLGQTNPAFPGEK#.L	2.48	3.68	0.67	1.48
P57722_P(	Pcbp3	Poly(rC)-bir	K.LHQLAMQQTPFPPLGQTNPAFPGEK#.L	5.12	2.47	2.08	0.48
Q3UK78_P(	Pcgf5	Polycomb g	R.LDNTLEEIIFK.L	3.67	2.93	1.25	0.80
Q8BH04_P(	Pck2	Phosphoen	R.DEGWLAEHM*LILGITNPAGK#.K	7.40	3.27	2.26	0.44
Q8BH04_P(	Pck2	Phosphoen	K.EGALDLSGLSAVDTSQLFSIPK#.D	12.09	2.86	4.23	0.24
Q8BH04_P(	Pck2	Phosphoen	R.EIVSFGSGYGGNSLLGK#.K	33.55	9.86	3.40	0.29
Q8BH04_P(	Pck2	Phosphoen	R.GYLTEQVNQDLPK#.E	16.73	6.00	2.79	0.36
Q8BH04_P(	Pck2	Phosphoen	R.LGTPVLQALGDGDFIK#.C	42.81	14.94	2.87	0.35
Q8BH04_P(	Pck2	Phosphoen	R.RLEGEDSAQETPIGLVPK.E	5.49	11.97	0.46	2.18
Q8BH04_P(	Pck2	Phosphoen	R.GYLTEQVNQDLPK#.E	7.61	2.80	2.72	0.37
Q8BH04_P(	Pck2	Phosphoen	K.EGALDLSGLSAVDTSQLFSIPK#.D	11.65	2.99	3.89	0.26
Q8BH04_P(	Pck2	Phosphoen	R.EIVSFGSGYGGNSLLGK#.K	12.61	5.35	2.36	0.42
Q8BH04_P(	Pck2	Phosphoen	R.GYLTEQVNQDLPK#.E	13.62	5.23	2.61	0.38
Q8BH04_P(	Pck2	Phosphoen	R.LGTPVLQALGDGDFIK#.C	23.13	7.34	3.15	0.32
Q8BH04_P(	Pck2	Phosphoen	K.EGALDLSGLSAVDTSQLFSIPK#.D	12.31	2.00	6.17	0.16
Q8BH04_P(	Pck2	Phosphoen	R.EIVSFGSGYGGNSLLGK#.K	10.39	2.10	4.95	0.20
Q8BH04_P(	Pck2	Phosphoen	R.GYLTEQVNQDLPK#.E	11.29	3.54	3.19	0.31
Q8BH04_P(	Pck2	Phosphoen	R.LGTPVLQALGDGDFIK#.C	20.05	8.50	2.36	0.42
P23506_PI	Pcmt1	Protein-L-is	K.ELVDDSITNVK#.K	27.76	6.00	4.63	0.22
P17918_P(	Pcna	Proliferatin	R.AEDNADTLALVFEAPNQEK.V	12.40	23.22	0.53	1.87
P17918_P(	Pcna	Proliferatin	K.ATPLSPTVTLSM*SADVPLVVEYK.I	7.58	29.00	0.26	3.82
P17918_P(	Pcna	Proliferatin	K.FSASGELGNGNIK.L	8.66	28.34	0.31	3.27
P17918_P(	Pcna	Proliferatin	K.MPSGEFAR.I	3.22	33.88	0.10	10.52
P17918_P(	Pcna	Proliferatin	R.NLAMGVNLTSM*SK.I	3.28	9.46	0.35	2.88
P17918_P(	Pcna	Proliferatin	R.SEGFDTYR.C	3.39	36.25	0.09	10.69
P17918_P(	Pcna	Proliferatin	R.YLNFFTK.A	29.54	81.64	0.36	2.76
P17918_P(	Pcna	Proliferatin	R.AEDNADTLALVFEAPNQEK.V	2.72	3.44	0.79	1.26
P17918_P(	Pcna	Proliferatin	R.AEDNADTLALVFEAPNQEK.V	3.13	6.34	0.49	2.03
P49586_P(	Pcyt1a	Choline-ph	K.ELNVSFINEK#.K	38.41	20.76	1.85	0.54
P49586_P(	Pcyt1a	Choline-ph	R.IDFVAHDDIPYSSAGSDDVYK#.H	29.64	13.89	2.13	0.47
P49586_P(	Pcyt1a	Choline-ph	R.TEGISTSDIITR.I	8.12	18.73	0.43	2.31
Q8VE70_PI	Pdcd10	Programme	R.VNLSAAQTLR.A	5.78	8.01	0.72	1.39
Q8VE70_PI	Pdcd10	Programme	K.AEK#ENPGLTQDIIM*K#.I	3.41	1.70	2.01	0.50
Q8VE70_PI	Pdcd10	Programme	R.LIHQTNLILQTFK#.T	27.31	11.91	2.29	0.44
Q8VE70_PI	Pdcd10	Programme	R.M*AADDVEEYMIERPEPEFQDLNEK.A	2.00	3.98	0.50	1.99
Q6NS46_RI	Pdcd11	Protein RRI	K.AIFENTLSTYPK#.R	42.89	21.83	1.96	0.51
Q6NS46_RI	Pdcd11	Protein RRI	R.AVQYNEPLK#.V	26.13	29.03	0.90	1.11
Q6NS46_RI	Pdcd11	Protein RRI	R.EGEDEVGEPK#.L	15.21	14.78	1.03	0.97
Q6NS46_RI	Pdcd11	Protein RRI	K.EYGVFVQFPSGLSGLSPK.T	5.29	7.09	0.75	1.34
Q6NS46_RI	Pdcd11	Protein RRI	K.FAQLEFQLGDVER.A	5.67	15.02	0.38	2.65
Q6NS46_RI	Pdcd11	Protein RRI	K.FQVGQAIEATVVDPDVPR.A	3.98	18.78	0.21	4.72
Q6NS46_RI	Pdcd11	Protein RRI	R.GLTVSFPFGK#.I	32.46	32.71	0.99	1.01
Q6NS46_RI	Pdcd11	Protein RRI	K.GTVLAIK#PFGILVK#.V	13.38	11.83	1.13	0.88
Q6NS46_RI	Pdcd11	Protein RRI	K.HELSTQHIPDPETVFYTGQVVK#.V	11.73	4.90	2.39	0.42
Q6NS46_RI	Pdcd11	Protein RRI	R.IGQLVDVK.V	28.57	30.25	0.94	1.06
Q6NS46_RI	Pdcd11	Protein RRI	R.ILDDVPVGTSPTTTLK#.A	41.06	36.40	1.13	0.89
Q6NS46_RI	Pdcd11	Protein RRI	R.IPLLLTSLSFK#.V	20.27	17.47	1.16	0.86
Q6NS46_RI	Pdcd11	Protein RRI	R.LEEGEVAM*GR.V	3.96	16.96	0.23	4.29
Q6NS46_RI	Pdcd11	Protein RRI	R.LKDGVLAYAR.V	2.09	17.63	0.12	8.45
Q6NS46_RI	Pdcd11	Protein RRI	K.LNEQVAQEEPLEDLLR.L	2.98	9.52	0.31	3.19
Q6NS46_RI	Pdcd11	Protein RRI	K.M*GSYSSNQTVK.A	6.95	4.75	1.46	0.68
Q6NS46_RI	Pdcd11	Protein RRI	K.SIIAAPFLR.Y	13.38	28.72	0.47	2.15
Q6NS46_RI	Pdcd11	Protein RRI	K.SSQQVVEQDNLFDVSTEEGPIK#.R	5.75	3.74	1.54	0.65
Q6NS46_RI	Pdcd11	Protein RRI	K.SSQQVVEQDNLFDVSTEEGPIKR.K	11.03	16.96	0.65	1.54
Q6NS46_RI	Pdcd11	Protein RRI	K.TTEPGVTGLILAVEGPASK.R	21.66	24.32	0.89	1.12
Q6NS46_RI	Pdcd11	Protein RRI	K.VFLHLADIYTK#.S	17.44	16.50	1.06	0.95
Q6NS46_RI	Pdcd11	Protein RRI	K.YGAFVLGR.S	4.79	15.70	0.31	3.27
Q61823_PI	Pdcd4	Programme	R.IYNEIPDINLDVPHSYSVLER.F	4.29	30.84	0.14	7.19
Q61823_PI	Pdcd4	Programme	K.SGVPVLAVSLALEGK#.A	13.49	7.84	1.72	0.58
P12815_PI	Pdcd6	Programme	K.AGVNFSEFTGVWK#.Y	18.46	7.29	2.53	0.40
P12815_PI	Pdcd6	Programme	K.YITDWQNVFR.T	6.78	15.10	0.45	2.23
Q9WU78_F	Pdcd6ip	Programme	K.ATLVK#PTPVNVPVSQK#.F	38.48	22.77	1.69	0.59
Q9WU78_F	Pdcd6ip	Programme	K.EVFPTLAAK#.Q	29.72	17.56	1.69	0.59
Q9WU78_F	Pdcd6ip	Programme	K.FLTALAQDGVINEEALSVTELDR.I	5.13	7.88	0.65	1.54
Q9WU78_F	Pdcd6ip	Programme	K.FYNELTEILVR.F	9.31	16.35	0.57	1.76
Q9WU78_F	Pdcd6ip	Programme	K.LALASLGYEK#.S	41.97	15.66	2.68	0.37
Q9WU78_F	Pdcd6ip	Programme	K.LANQAADYFGDAFK#.Q	20.15	6.44	3.13	0.32
Q9WU78_F	Pdcd6ip	Programme	R.LLDEEEATDNDLR.A	9.53	20.90	0.46	2.19

Q9WU78_F	Pdcd6ip	Programme	K.NIQVSHQEFSK#.M	25.25	10.83	2.33	0.43
Q9WU78_F	Pdcd6ip	Programme	K.STSVVEQGGIQTVDQLIK#.E	14.27	7.80	1.83	0.55
Q9WU78_F	Pdcd6ip	Programme	K.STSVVEQGGIQTVDQLIK#.E	22.87	9.62	2.38	0.42
Q9WU78_F	Pdcd6ip	Programme	K.TM*QGSEVVSVLK#.S	19.46	11.11	1.75	0.57
Q9WU78_F	Pdcd6ip	Programme	K.TMQGSEVVSVLK#.S	10.44	8.96	1.17	0.86
Q9WU78_F	Pdcd6ip	Programme	K.ATLVK#PTPVNVPVSQK#.F	28.50	12.98	2.19	0.46
Q9WU78_F	Pdcd6ip	Programme	K.FLTALAQDGVINEEALSVTELDR.I	2.92	8.75	0.33	2.99
Q9WU78_F	Pdcd6ip	Programme	K.FYNELTEILVR.F	4.29	8.36	0.51	1.95
Q9WU78_F	Pdcd6ip	Programme	R.LLDEEEATDNDLR.A	4.56	6.90	0.66	1.51
Q9WU78_F	Pdcd6ip	Programme	K.STSVVEQGGIQTVDQLIK#.E	8.86	2.82	3.14	0.32
Q9WU78_F	Pdcd6ip	Programme	K.TM*QGSEVVSVLK#.S	8.58	7.09	1.21	0.83
Q8BVF2_PI	Pdcl3	Phosducin-	K.ELEEEEAEK#EEQLLQQSVVK#.T	10.71	8.60	1.24	0.80
Q8BVF2_PI	Pdcl3	Phosducin-	K.ESLKELEEEEAEKEEQLLQQSVVK.T	13.43	8.99	1.49	0.67
Q8BFQ8_PI	Pddc1	Parkinson c	K.DSGAGFSASEPDAVHVVLDR.H	8.50	21.90	0.39	2.58
Q8BFQ8_PI	Pddc1	Parkinson c	R.LPLIVEDFVK#.D	38.37	16.04	2.39	0.42
Q8BFQ8_PI	Pddc1	Parkinson c	R.SWVFQGYSLTGPSVYELIR.A	3.91	4.60	0.85	1.18
O55057_PI	Pde6d	Retinal rod	R.ELNFSSAEQM*EK#.F	6.51	4.16	1.56	0.64
Q9D051_O	Pdhb	Pyruvate de	K.DIIFAVK#.K	31.41	6.93	4.54	0.22
Q9D051_O	Pdhb	Pyruvate de	K.VFLLGEEVAQYDGAYK#.V	12.35	5.70	2.17	0.46
Q9D051_O	Pdhb	Pyruvate de	K.VLEDNSVPQVK#.D	55.44	9.67	5.73	0.17
Q9D051_O	Pdhb	Pyruvate de	R.VTGADVPM*PYAK#.V	10.86	1.44	7.52	0.13
Q9D051_O	Pdhb	Pyruvate de	R.VTGADVPMPYAK#.V	12.19	6.56	1.86	0.54
Q9D051_O	Pdhb	Pyruvate de	K.VVSPWNSEDAK#.G	42.28	12.40	3.41	0.29
P27773_PI	Pdia3	Protein dis	K.ALEQFLQEYFDGNLK#.R	11.80	8.57	1.38	0.73
P27773_PI	Pdia3	Protein dis	R.DGEEAGAYDGPR.T	4.18	10.81	0.39	2.59
P27773_PI	Pdia3	Protein dis	R.EATNPPIIQEEKPK.K	6.85	6.67	1.03	0.97
P27773_PI	Pdia3	Protein dis	R.ELNDFISYLQR.E	9.52	25.55	0.37	2.68
P27773_PI	Pdia3	Protein dis	R.FAHTNIESLVK#.E	12.65	13.11	0.97	1.04
P27773_PI	Pdia3	Protein dis	K.FVM*QEEFSR.D	22.35	18.79	1.19	0.84
P27773_PI	Pdia3	Protein dis	K.FVMQEEFSR.D	7.39	17.13	0.43	2.32
P27773_PI	Pdia3	Protein dis	K.GFPTIYFSPANK#.K	16.09	14.72	1.09	0.91
P27773_PI	Pdia3	Protein dis	R.LAPEYEAAATR.L	18.50	69.36	0.27	3.75
P27773_PI	Pdia3	Protein dis	K.M*DATANDVPSPYEVK#.G	13.14	12.92	1.02	0.98
P27773_PI	Pdia3	Protein dis	K.MDATANDVPSPYEVK.G	12.44	8.28	1.50	0.67
P27773_PI	Pdia3	Protein dis	K.SEPIPESNEGPVK#.V	49.57	44.25	1.12	0.89
Q3TML0_Q	Pdia6	Protein dis	K.AATALK#DVVK#.V	124.12	41.68	2.98	0.34
Q3TML0_Q	Pdia6	Protein dis	K.DGELPVEDDIDLSDVELDDLEK#.D	20.51	9.19	2.23	0.45
Q3TML0_Q	Pdia6	Protein dis	K.DVVELTDDTFDK#.N	24.25	9.00	2.69	0.37
Q3TML0_Q	Pdia6	Protein dis	R.EPWDGK#DGELPVEDDIDLSDVELDDLEK#.D	63.28	18.45	3.43	0.29
Q3TML0_Q	Pdia6	Protein dis	K.GESPVDYDGGR.T	86.64	146.15	0.59	1.69
Q3TML0_Q	Pdia6	Protein dis	K.GSFSEQGINEFLR.E	66.99	94.60	0.71	1.41
Q3TML0_Q	Pdia6	Protein dis	K.HQSLGGQYGVQGFPTIK#.I	29.91	10.31	2.90	0.34
Q3TML0_Q	Pdia6	Protein dis	K.K#DVVELTDDTFDK#.N	5.67	2.62	2.16	0.46
Q3TML0_Q	Pdia6	Protein dis	K.LAAVDATM*NQVLASR.Y	34.96	51.05	0.68	1.46
Q3TML0_Q	Pdia6	Protein dis	K.LAAVDATMNQVLASR.Y	39.85	49.89	0.80	1.25
Q3TML0_Q	Pdia6	Protein dis	K.NLEPEWAAAATEVK#.E	260.39	75.81	3.43	0.29
Q3TML0_Q	Pdia6	Protein dis	R.NSYLEVLLK#.L	251.45	65.92	3.81	0.26
Q3TML0_Q	Pdia6	Protein dis	R.TGEAIVDAALSALR.Q	62.32	95.78	0.65	1.54
Q3TML0_Q	Pdia6	Protein dis	K.VGAVNADK#.H	71.64	21.64	3.31	0.30
Q3TML0_Q	Pdia6	Protein dis	K.VGAVNADK#HQSLGGQYGVQGFPTIK#.I	56.04	16.60	3.38	0.30
Q3TML0_Q	Pdia6	Protein dis	R.GSTAPVGGGSFPTITPR.E	7.16	6.35	1.13	0.89
Q3TML0_Q	Pdia6	Protein dis	K.NLEPEWAAAATEVK#.E	10.40	3.69	2.82	0.35
Q3TML0_Q	Pdia6	Protein dis	R.NSYLEVLLK#.L	13.49	3.93	3.43	0.29
Q3TML0_Q	Pdia6	Protein dis	K.VGAVNADK#HQSLGGQYGVQGFPTIK#.I	3.82	1.82	2.10	0.48
O70400_PI	Pdlim1	PDZ and LIN	K.DFEQPLAISR.V	14.48	35.08	0.41	2.42
O70400_PI	Pdlim1	PDZ and LIN	R.LVGGKDFEQPLAISR.V	11.09	23.13	0.48	2.09
O70400_PI	Pdlim1	PDZ and LIN	K.QSTSFLVLQEILESDGKGDPNKPSGFR.S	7.80	23.60	0.33	3.03
O70400_PI	Pdlim1	PDZ and LIN	R.SAM*PFTASPAPSTR.V	10.66	21.31	0.50	2.00
O70400_PI	Pdlim1	PDZ and LIN	R.SAMPFTASPAPSTR.V	5.80	12.17	0.48	2.10
O70400_PI	Pdlim1	PDZ and LIN	K.VAASVGNAQK#.L	41.06	32.29	1.27	0.79
O70400_PI	Pdlim1	PDZ and LIN	R.VITNQYNSPTGLYSSENISNFNNAVESK#.T	25.73	14.53	1.77	0.56
P70271_PI	Pdlim4	PDZ and LIN	R.DFSAPLTISR.V	7.36	34.34	0.21	4.66
P70271_PI	Pdlim4	PDZ and LIN	R.GYFFLDER.L	4.73	17.02	0.28	3.60
P70271_PI	Pdlim4	PDZ and LIN	R.MLREPAEPTASEPK.Q	1.30	12.28	0.11	9.44
P70271_PI	Pdlim4	PDZ and LIN	R.SGLGSPYGQPPR.L	6.55	43.28	0.15	6.61
P70271_PI	Pdlim4	PDZ and LIN	R.SSVSGISLEDNR.S	3.15	17.81	0.18	5.65
P70271_PI	Pdlim4	PDZ and LIN	R.VDLGSEVYR.M	9.92	42.08	0.24	4.24
P70271_PI	Pdlim4	PDZ and LIN	R.VKPPEGYDVVAVYPNAK.V	15.83	16.69	0.95	1.05
Q8CI51_PD	Pdlim5	PDZ and LIN	R.GPFLVALGK#.S	22.89	23.85	0.96	1.04
Q8CI51_PD	Pdlim5	PDZ and LIN	K.ILGEVINALK#.Q	15.47	12.16	1.27	0.79
Q8CI51_PD	Pdlim5	PDZ and LIN	K.NTM*AYIGFVEEK#.G	8.11	10.64	0.76	1.31
Q8CI51_PD	Pdlim5	PDZ and LIN	R.SAAAFK#PVGSTSVK#.S	30.56	27.53	1.11	0.90
Q8CI51_PD	Pdlim5	PDZ and LIN	R.GPFLVALGK#.S	9.74	12.88	0.76	1.32
Q8CI51_PD	Pdlim5	PDZ and LIN	K.DFNMPLTISSLK#.D	7.25	6.63	1.09	0.92
Q8CI51_PD	Pdlim5	PDZ and LIN	K.EVVK#PVPITSPAVSK#.V	17.68	17.32	1.02	0.98
Q8CI51_PD	Pdlim5	PDZ and LIN	R.GPFLVALGK#.S	36.73	35.36	1.04	0.96
Q8CI51_PD	Pdlim5	PDZ and LIN	R.IGDVVLSIDGISAQGM*THLEAQNK#.I	9.04	6.12	1.48	0.68
Q8CI51_PD	Pdlim5	PDZ and LIN	K.ILGEVINALK#.Q	15.75	15.94	0.99	1.01
Q8CI51_PD	Pdlim5	PDZ and LIN	K.KANSTQEPSQQPASSGASPLSASEGPESPGSSRPSVAGLR.S	3.11	12.18	0.26	3.92
Q8CI51_PD	Pdlim5	PDZ and LIN	R.NTEFYHIPTHSDASK#.K	25.43	15.15	1.68	0.60
Q8CI51_PD	Pdlim5	PDZ and LIN	K.NTMAYIGFVEEK.G	9.24	10.47	0.88	1.13
Q8CI51_PD	Pdlim5	PDZ and LIN	R.SAAAFKPVGSTSVK.S	32.28	31.37	1.03	0.97
Q8CI51_PD	Pdlim5	PDZ and LIN	K.SPSWQRPNQAAPSTGR.I	1.52	37.49	0.04	24.69
Q8CI51_PD	Pdlim5	PDZ and LIN	R.SSGTGASVGPPQPSDQDTLVQR.A	2.15	10.74	0.20	4.99
Q8CI51_PD	Pdlim5	PDZ and LIN	K.VTSTTNMAYNK#.A	13.15	11.45	1.15	0.87
Q8CI51_PD	Pdlim5	PDZ and LIN	R.GPFLVALGK.S	19.73	21.87	0.90	1.11
Q8CI51_PD	Pdlim5	PDZ and LIN	R.ILAQITGTEHLTESENDNTK#.K	5.90	17.40	0.34	2.95
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.AAQAGVAVGDWVLNIDGENAGSLTHIEAQNK#.I	16.99	10.51	1.62	0.62
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.ALTPPADPPR.Y	1.53	10.05	0.15	6.57
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.DFNVPLSISR.L	7.45	24.46	0.30	3.28
Q3TJD7_PD	Pdlim7	PDZ and LIN	R.HSQPATPTPLQNR.T	4.06	19.15	0.21	4.72
Q3TJD7_PD	Pdlim7	PDZ and LIN	R.ILAHLTGTEFMQDPDEEFMK#K#.S	6.10	8.85	0.69	1.45
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.VLEEGGFFEEK#.G	49.62	40.32	1.23	0.81
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.VVLEGPAPWGFR.L	10.85	44.10	0.25	4.06
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.VLEEGGFFEEK#.G	2.76	3.13	0.88	1.13
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.VLEEGGFFEEK#.G	16.30	13.32	1.22	0.82
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.VVLEGPAPWGFR.L	4.80	15.28	0.31	3.18
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.AAQAGVAVGDWVLNIDGENAGSLTHIEAQNK#.I	8.22	3.06	2.68	0.37
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.VLEEGGFFEEK#.G	15.41	14.15	1.09	0.92
Q3TJD7_PD	Pdlim7	PDZ and LIN	K.VVLEGPAPWGFR.L	4.39	10.02	0.44	2.28
Q9Z2A0_PI	Pdpk1	3-phosphoi	R.FYTAEIVSALEYLHGK#.G	19.14	4.13	4.63	0.22
Q9Z2A0_PI	Pdpk1	3-phosphoi	K.ILGEGSFSTVVLAR.E	5.01	7.31	0.69	1.46
P59048_PI	Pdrg1	p53 and DN	K.GFNLNPLSPDEVK#.A	13.46	8.93	1.51	0.66

Q6A026_P	Pds5a	Sister chro	R.AAGSQESLEAGNAK#.A	4.57	1.52	3.01	0.33
Q6A026_P	Pds5a	Sister chro	R.AAGSQESLEAGNAK#.A	13.27	4.70	2.82	0.35
Q6A026_P	Pds5a	Sister chro	R.DLALVNDQLLGFVR.E	6.55	17.29	0.38	2.64
Q6A026_P	Pds5a	Sister chro	R.IAPVHIDSEAISALVK#.L	54.92	17.19	3.19	0.31
Q6A026_P	Pds5a	Sister chro	K.IFAQYLVPHNLETEER.M	4.71	5.64	0.83	1.20
Q6A026_P	Pds5a	Sister chro	K.LWSPDEEVSPEVLAK#.V	12.09	4.68	2.58	0.39
Q6A026_P	Pds5a	Sister chro	K.SIEGTADDEEEGVSPDSAIR.S	3.12	8.47	0.37	2.71
Q6A026_P	Pds5a	Sister chro	K.SVVANFIVK#.D	20.87	7.60	2.75	0.36
Q6A026_P	Pds5a	Sister chro	R.AAGSQESLEAGNAK#.A	24.16	13.86	1.74	0.57
Q6A026_P	Pds5a	Sister chro	K.ALNEM*WK#.C	17.24	72.03	0.24	4.18
Q6A026_P	Pds5a	Sister chro	R.DLALVNDQLLGFVR.E	17.98	47.97	0.37	2.67
Q6A026_P	Pds5a	Sister chro	K.DLTEYLK.V	79.49	35.51	2.24	0.45
Q6A026_P	Pds5a	Sister chro	K.EINSDQSTQGNISSDR.G	4.13	9.43	0.44	2.28
Q6A026_P	Pds5a	Sister chro	R.IAPVHIDSEAISALVK#.L	107.68	50.43	2.14	0.47
Q6A026_P	Pds5a	Sister chro	K.IAYPPGVK#.E	17.55	7.47	2.35	0.43
Q6A026_P	Pds5a	Sister chro	K.LLHIYYQNSIDDK#.L	14.59	5.45	2.68	0.37
Q6A026_P	Pds5a	Sister chro	K.NDDLNK#PVSK#.G	10.48	6.60	1.59	0.63
Q6A026_P	Pds5a	Sister chro	K.NKEINSDQSTQGNISSDR.G	6.19	20.22	0.31	3.26
Q6A026_P	Pds5a	Sister chro	K.SIEGTADDEEEGVSPDSAIR.S	11.03	27.40	0.40	2.48
Q6A026_P	Pds5a	Sister chro	K.SVVANFIVK#.D	36.84	16.52	2.23	0.45
Q6A026_P	Pds5a	Sister chro	R.TLFSVINNSHNTK#.V	11.83	7.66	1.54	0.65
Q4VA53_P	Pds5b	Sister chro	K.FTQVLEDDEK#.I	12.16	9.05	1.34	0.74
Q4VA53_P	Pds5b	Sister chro	R.IAPVHIDTESISALIK#.Q	45.18	28.03	1.61	0.62
Q4VA53_P	Pds5b	Sister chro	R.IYAPEAPYTSPDK#.L	8.26	8.23	1.00	1.00
Q4VA53_P	Pds5b	Sister chro	R.LAAGSAIVK#.L	38.24	21.35	1.79	0.56
Q4VA53_P	Pds5b	Sister chro	R.LLTTILHSDGDLTEQGK#.I	11.74	5.63	2.08	0.48
Q4VA53_P	Pds5b	Sister chro	K.LWVPDEEVSPETM*VK#.I	6.09	3.46	1.76	0.57
Q4VA53_P	Pds5b	Sister chro	K.QPTNPFLEMIK#.F	7.23	6.52	1.11	0.90
Q4VA53_P	Pds5b	Sister chro	K.SIDGTADDEDEGVPTDQAIR.A	4.84	15.96	0.30	3.30
Q4VA53_P	Pds5b	Sister chro	K.SLVATFIVK#.D	15.69	7.26	2.16	0.46
Q4VA53_P	Pds5b	Sister chro	K.YSLQSAAGK#.D	25.57	19.44	1.32	0.76
Q4VA53_P	Pds5b	Sister chro	R.AGLELLK#.V	59.88	45.31	1.32	0.76
Q4VA53_P	Pds5b	Sister chro	K.APVTDPEEK#.L	20.46	16.71	1.22	0.82
Q4VA53_P	Pds5b	Sister chro	K.DIFM*FITR.Q	4.24	13.03	0.33	3.07
Q4VA53_P	Pds5b	Sister chro	R.FFTQPDK#.N	20.04	13.35	1.50	0.67
Q4VA53_P	Pds5b	Sister chro	R.FFTQPDKNFSNTK.N	38.18	30.93	1.23	0.81
Q4VA53_P	Pds5b	Sister chro	K.FTQVLEDDEK#.I	51.57	34.80	1.48	0.67
Q4VA53_P	Pds5b	Sister chro	R.HK#EELLENEDEQNSPPK#.K	9.68	4.57	2.12	0.47
Q4VA53_P	Pds5b	Sister chro	R.IAPVHIDTESISALIK#.Q	212.16	136.25	1.56	0.64
Q4VA53_P	Pds5b	Sister chro	K.IEEDFPHIR.S	22.69	77.18	0.29	3.40
Q4VA53_P	Pds5b	Sister chro	R.IYAPEAPYTSPDK#.L	31.65	27.52	1.15	0.87
Q4VA53_P	Pds5b	Sister chro	K.K#APVTDPEEK#.L	11.60	10.88	1.07	0.94
Q4VA53_P	Pds5b	Sister chro	K.KDILLVNDHLLNFVR.E	5.42	18.64	0.29	3.44
Q4VA53_P	Pds5b	Sister chro	R.K#K#APVTDPEEK#.L	26.12	18.63	1.40	0.71
Q4VA53_P	Pds5b	Sister chro	R.KKAPVTDPEEK.L	3.89	5.05	0.77	1.30
Q4VA53_P	Pds5b	Sister chro	R.LAAGSAIVK#.L	108.35	75.81	1.43	0.70
Q4VA53_P	Pds5b	Sister chro	K.LGM*DDLTK#.L	31.06	23.06	1.35	0.74
Q4VA53_P	Pds5b	Sister chro	R.LLTTILHSDGDLTEQGK#.I	146.32	99.81	1.47	0.68
Q4VA53_P	Pds5b	Sister chro	R.LLTTILHSDGDLTEQGK.I	18.58	11.82	1.57	0.64
Q4VA53_P	Pds5b	Sister chro	K.LWVPDEEVSPETM*VK#.I	12.14	9.78	1.24	0.81
Q4VA53_P	Pds5b	Sister chro	K.LWVPDEEVSPETMVK.I	15.41	10.72	1.44	0.70
Q4VA53_P	Pds5b	Sister chro	K.M*DDEK#VAEAALQIFK#.N	12.09	7.07	1.71	0.58
Q4VA53_P	Pds5b	Sister chro	K.SIDGTADDEDEGVPTDQAIR.A	12.69	51.88	0.24	4.09
Q4VA53_P	Pds5b	Sister chro	K.SLVATFIVK#.D	41.00	22.31	1.84	0.54
Q4VA53_P	Pds5b	Sister chro	K.VAEAALQIFK#.N	24.03	18.83	1.28	0.78
Q4VA53_P	Pds5b	Sister chro	K.YSLQSAAGK#.D	65.49	50.79	1.29	0.78
Q99K01_P	Pdxdc1	Pyridoxal-d	K.AVPVSNIAPAAVGR.E	4.99	12.44	0.40	2.49
Q99K01_P	Pdxdc1	Pyridoxal-d	K.GIQEAQVQLQK#.A	14.32	7.98	1.79	0.56
Q99K01_P	Pdxdc1	Pyridoxal-d	K.ILVEDELSSPVVVFR.F	4.40	8.03	0.55	1.82
Q99K01_P	Pdxdc1	Pyridoxal-d	R.YEDFVVDGFNVLYNK.K	11.08	5.81	1.91	0.52
Q99K01_P	Pdxdc1	Pyridoxal-d	K.HDDPALTLVAGLTSNK#PADK#.L	11.18	3.41	3.28	0.30
Q99K01_P	Pdxdc1	Pyridoxal-d	K.ILVEDELSSPVVVFR.F	1.94	6.84	0.28	3.53
Q99K01_P	Pdxdc1	Pyridoxal-d	R.YEDFVVDGFNVLYNK.K	7.00	4.60	1.52	0.66
Q9CZG9_P	Pdzd11	PDZ domai	R.AGLQEGDQVLAVNDVDFQDIEHSK#.A	8.26	5.20	1.59	0.63
Q9CZG9_P	Pdzd11	PDZ domai	R.VYHPDYNNELTQFLPR.I	1.89	6.94	0.27	3.67
Q80X73_P	Pelo	Protein pel	K.GTNIQENEYVK#.M	15.73	13.51	1.16	0.86
Q80X73_P	Pelo	Protein pel	R.HINFEVVK#.C	11.58	15.81	0.73	1.36
Q9DBD5_P	Pelp1	Proline-, gl	R.GSSDGGLQSGK#PSAPK#.K	6.63	6.68	0.99	1.01
Q9DBD5_P	Pelp1	Proline-, gl	R.LPSLGAGFSQGLK#.H	14.02	10.95	1.28	0.78
Q9DBD5_P	Pelp1	Proline-, gl	R.FGALISR.L	9.29	23.11	0.40	2.49
Q9DBD5_P	Pelp1	Proline-, gl	K.LASFFLSR.L	9.45	24.81	0.38	2.63
Q9DBD5_P	Pelp1	Proline-, gl	K.LDM*GEALAPPSQR.K	8.93	31.73	0.28	3.55
Q9DBD5_P	Pelp1	Proline-, gl	R.LLPQVLNAWSTGR.D	5.74	24.93	0.23	4.34
Q9DBD5_P	Pelp1	Proline-, gl	R.LPSLGAGFSQGLK#.H	44.37	35.62	1.25	0.80
Q9DBD5_P	Pelp1	Proline-, gl	K.NINLLGDGPLR.L	9.49	34.56	0.27	3.64
Q9CWM4_	Pfdn1	Prefoldin s	K.LADIQIEQLNR.T	24.91	8.61	2.89	0.35
O70591_P	Pfdn2	Prefoldin s	K.GAVSAEQVIAGFNR.L	2.66	5.32	0.50	2.00
O70591_P	Pfdn2	Prefoldin s	K.IIETLSQQLQAK#.G	40.54	15.00	2.70	0.37
Q3UWL8_	Pfdn4	Protein Pfd	K.AAAEDVNVTFEDQQK#.I	25.23	8.47	2.98	0.34
Q3UWL8_	Pfdn4	Protein Pfd	K.TLQEEIDALESR.V	4.86	6.42	0.76	1.32
Q9WU28_	Pfdn5	Prefoldin s	K.ELLVPLTSSM*YVPGK#.L	12.02	7.57	1.59	0.63
Q9WU28_	Pfdn5	Prefoldin s	K.ELLVPLTSSMYVPGK#.L	10.26	2.96	3.47	0.29
Q9WU28_	Pfdn5	Prefoldin s	K.IQQLTALGAAQATVK#.A	32.27	12.25	2.63	0.38
Q9WU28_	Pfdn5	Prefoldin s	K.IQQLTALGAAQATVK#A.-	20.75	6.71	3.09	0.32
Q9WU28_	Pfdn5	Prefoldin s	R.K#IDFLTK#.Q	16.19	4.87	3.33	0.30
Q9WU28_	Pfdn5	Prefoldin s	K.LHDVEHVLIDVGTGYYVEK#.T	17.68	6.99	2.53	0.40
Q9WU28_	Pfdn5	Prefoldin s	K.NQLDQEVEFLSTSIAQLK#.V	67.30	21.83	3.08	0.32
P12382_P	Pfkl	ATP-depen	K.AIGVLTSGGDAQGM*NAAVR.A	12.31	10.92	1.13	0.89
P12382_P	Pfkl	ATP-depen	K.AM*LWVSEK#.L	21.21	7.17	2.96	0.34
P12382_P	Pfkl	ATP-depen	K.AMLWVSEK#.L	14.12	1.17	12.05	0.08
P12382_P	Pfkl	ATP-depen	R.EQWWLNLR.L	10.10	9.15	1.10	0.91
P12382_P	Pfkl	ATP-depen	K.GQVQEVGWHDVAGWLGR.G	16.04	16.78	0.96	1.05
P12382_P	Pfkl	ATP-depen	R.NEWGSLLEELVK#.E	75.78	15.19	4.99	0.20
P12382_P	Pfkl	ATP-depen	R.TGISEGHTVYIVHDGFEGLAK#.G	28.02	2.45	11.45	0.09
P12382_P	Pfkl	ATP-depen	R.TNVLGHLQQGGAPTPFDR.N	12.17	13.94	0.87	1.15
P12382_P	Pfkl	ATP-depen	K.AIGVLTSGGDAQGM*NAAVR.A	15.36	15.71	0.98	1.02
P12382_P	Pfkl	ATP-depen	K.AM*LWVSEK#.L	36.29	8.18	4.44	0.23
P12382_P	Pfkl	ATP-depen	K.K#VVAFSPVTELK#K#.E	21.26	3.44	6.18	0.16
P12382_P	Pfkl	ATP-depen	R.NEWGSLLEELVK#.E	99.93	26.30	3.80	0.26
Q9WUA3_	Pfkp	ATP-depen	R.DLLFQPVAELK#.K	29.78	9.04	3.29	0.30
Q9WUA3_	Pfkp	ATP-depen	K.EIGWADVGGWTGQGGSILGTK#.R	17.44	4.95	3.52	0.28
Q9WUA3_	Pfkp	ATP-depen	R.LNIIIVSEGAIDM*QNK#PITSEK#.I	22.69	6.16	3.68	0.27
Q9WUA3_	Pfkp	ATP-depen	R.NGDIDNDTVQK#.Y	19.23	4.23	4.54	0.22

Q9WUA3_	Pfkp	ATP-depen	K.VYFIYEGYQGLVDGGSNIVEAK#.W	19.88	2.86	6.96	0.14
Q9WUA3_	Pfkp	ATP-depen	K.YEASYDM*SDSGK#LESLQHHEEL.-	6.58	2.05	3.21	0.31
Q9WUA3_	Pfkp	ATP-depen	K.AM*EWISAK#.L	13.32	3.88	3.44	0.29
Q9WUA3_	Pfkp	ATP-depen	R.DLLFQPVAELK#.K	37.73	9.72	3.88	0.26
Q9WUA3_	Pfkp	ATP-depen	R.LNIIIVSEGAIDM*QNK#PITSEK#.I	16.97	3.31	5.13	0.19
Q9WUA3_	Pfkp	ATP-depen	R.NGDIDNDTVQK#.Y	17.69	4.38	4.04	0.25
Q9WUA3_	Pfkp	ATP-depen	K.VYFIYEGYQGLVDGGSNIVEAK#.W	21.43	5.74	3.74	0.27
Q8BX10_P	Pgam5	Serine/thre	R.NVESGEDELTSR.L	7.54	16.88	0.45	2.24
Q8BX10_P	Pgam5	Serine/thre	R.TLGDTGFM*PPDK#.I	10.17	5.75	1.77	0.57
O55022_P	Pgrmc1	Membrane	K.EALK#DEYDDLSDLTPAQQETLSDWDSQFTFK#.Y	2.59	2.90	0.89	1.12
O55022_P	Pgrmc1	Membrane	K.EGEEPTVYSDDEEPK#.D	3.39	2.83	1.19	0.84
O55022_P	Pgrmc1	Membrane	R.KFYGPEGPYGVFAGR.D	4.47	20.87	0.21	4.67
Q80UU9_P	Pgrmc2	Membrane	R.DFSLEQLR.Q	3.34	9.59	0.35	2.87
Q80UU9_P	Pgrmc2	Membrane	K.FYGPAGPYGIFAGR.D	4.47	13.15	0.34	2.94
Q9JJT9_PH	Phax	Phosphoryl	R.TPGGVFLNLLK#.N	18.07	13.10	1.38	0.72
Q9QWH1_	Phc2	Polyhome	R.AQEIDGQALLLLK#.E	8.94	10.62	0.84	1.19
Q9QWH1_	Phc2	Polyhome	R.DLVGVGHHFLPSEPTK#.W	25.90	20.24	1.28	0.78
Q9QWH1_	Phc2	Polyhome	R.SSLLVGNLK#.K	18.74	16.81	1.11	0.90
Q9QWH1_	Phc2	Polyhome	K.WNVEDVYEFIR.S	5.44	19.44	0.28	3.57
Q8CHP6_P	Phc3	Polyhome	R.GEDLTSEHPLLEQVELPAVASVSASVIK.S	12.84	9.09	1.41	0.71
Q9D8M7_	Phf10	PHD finger	K.VSSYPVALIPGQFQEYYK#.R	10.17	6.34	1.60	0.62
A6H5X4_P	Phf11	PHD finger	R.GDSPIIEK.M	63.60	71.90	0.88	1.13
A6H5X4_P	Phf11	PHD finger	R.HMTEEPHGHTDAAVK#.S	4.39	2.67	1.64	0.61
A6H5X4_P	Phf11	PHD finger	K.K#DQAILQVDGNHGTYK#.L	59.01	72.75	0.81	1.23
A6H5X4_P	Phf11	PHD finger	R.KFQEVIK.S	109.82	89.59	1.23	0.82
A6H5X4_P	Phf11	PHD finger	R.LSSGPPAQPK#.T	199.89	233.94	0.85	1.17
A6H5X4_P	Phf11	PHD finger	R.SQESPEVQAGSGDSL.-	10.25	10.25	1.00	1.00
Q9D4H9_P	Phf14	PHD finger	R.KAELM*GISTDIFPVDNSDTSSSVDGR.R	2.52	6.59	0.38	2.62
Q9D4H9_P	Phf14	PHD finger	K.LNVPAILR.A	3.02	16.56	0.18	5.48
Q9D4H9_P	Phf14	PHD finger	R.NSADDEELTNDSLTLSQSK.S	3.77	5.66	0.67	1.50
Q9D4H9_P	Phf14	PHD finger	K.NSTEEIM*PSDK.Q	4.71	8.47	0.56	1.80
Q9D4H9_P	Phf14	PHD finger	R.SEGQGIWALLGR.I	3.19	20.82	0.15	6.53
Q9D4H9_P	Phf14	PHD finger	K.SNEDSLILEK#.S	9.88	14.99	0.66	1.52
Q9WTU0_	Phf2	Lysine-spec	R.VASIETGLAAAAAK#.L	13.42	8.25	1.63	0.61
Q9WTU0_	Phf2	Lysine-spec	R.VLNVTNLEFSDTR.M	254.96	9.31	27.39	0.04
Q9WTU0_	Phf2	Lysine-spec	R.VPGSQLTVGYM*EEHGFTEPILVPK#.K	5.26	3.28	1.60	0.62
Q9WTU0_	Phf2	Lysine-spec	R.VPGSQLTVGYMEEHGFTEPILVPK#.K	6.69	6.78	0.99	1.01
Q9WTU0_	Phf2	Lysine-spec	R.VASIETGLAAAAAK#.L	13.00	11.10	1.17	0.85
Q9WTU0_	Phf2	Lysine-spec	R.VPGSQLTVGYMEEHGFTEPILVPK#.K	6.32	2.76	2.29	0.44
Q8BSN5_P	Phf23	PHD finger	K.LGPGGGAGFGVLR.R	2.18	13.19	0.17	6.04
Q8BSN5_P	Phf23	PHD finger	R.AVQSGPTQPGPPR.S	3.72	10.86	0.34	2.92
B2RQG2_B	Phf3	PHD finger	K.EGSDQTTSIESK#.Y	4.15	2.93	1.42	0.71
B2RQG2_B	Phf3	PHD finger	K.EGSDQTTSIESK#.Y	8.92	10.29	0.87	1.15
B2RQG2_B	Phf3	PHD finger	R.SFSLDEPPLFIPDNIATVK#.K	9.92	10.19	0.97	1.03
P83870_P	Phf5a	PHD finger-	K.IVNLGSSK#.T	84.03	67.86	1.24	0.81
P83870_P	Phf5a	PHD finger-	K.TDLFYER.K	20.58	74.08	0.28	3.60
Q9D4J7_P	Phf6	PHD finger	R.AEFGDFDIK#.T	35.27	40.28	0.88	1.14
Q9D4J7_P	Phf6	PHD finger	K.TAHNSEADLEESFNEHELEPSSPK.T	5.78	5.63	1.03	0.97
Q61753_S	Phgdh	D-3-phosp	R.AGTGVDNVDLEAATR.K	102.22	149.69	0.68	1.46
Q61753_S	Phgdh	D-3-phosp	R.GGIVDEGALLR.A	112.28	141.49	0.79	1.26
Q61753_S	Phgdh	D-3-phosp	R.GQPLLVFR.A	70.80	95.06	0.74	1.34
Q61753_S	Phgdh	D-3-phosp	K.GTIQVVTQGTSLK#.N	402.01	125.45	3.20	0.31
Q61753_S	Phgdh	D-3-phosp	K.ILQDGGLQVVEK#.Q	293.98	91.98	3.20	0.31
Q61753_S	Phgdh	D-3-phosp	R.K#ILQDGGLQVVEK#.Q	22.56	7.69	2.93	0.34
Q61753_S	Phgdh	D-3-phosp	R.MQSFGMK#.T	25.02	7.99	3.13	0.32
Q61753_S	Phgdh	D-3-phosp	K.QADVNLVNAK#.L	269.23	94.03	2.86	0.35
Q61753_S	Phgdh	D-3-phosp	R.QIPQATASM*K#.D	138.82	47.80	2.90	0.34
Q61753_S	Phgdh	D-3-phosp	R.RGQPLLVFR.A	2.14	11.11	0.19	5.18
Q61753_S	Phgdh	D-3-phosp	K.TLGILGLGR.I	67.97	90.06	0.75	1.33
Q61753_S	Phgdh	D-3-phosp	K.VTADVINAAEK#.L	589.41	212.32	2.78	0.36
Q61753_S	Phgdh	D-3-phosp	R.GGIVDEGALLR.A	10.66	14.74	0.72	1.38
Q61753_S	Phgdh	D-3-phosp	K.GTIQVVTQGTSLK#.N	64.85	17.01	3.81	0.26
Q61753_S	Phgdh	D-3-phosp	K.ILQDGGLQVVEK#.Q	47.53	16.19	2.94	0.34
Q61753_S	Phgdh	D-3-phosp	R.QIPQATASM*K#.D	15.08	6.76	2.23	0.45
Q61753_S	Phgdh	D-3-phosp	K.TLGILGLGR.I	13.78	13.60	1.01	0.99
Q61753_S	Phgdh	D-3-phosp	K.VTADVINAAEK#.L	96.59	34.18	2.83	0.35
Q61753_S	Phgdh	D-3-phosp	R.AGTGVDNVDLEAATR.K	11.35	19.35	0.59	1.70
Q61753_S	Phgdh	D-3-phosp	R.GQPLLVFR.A	7.00	14.54	0.48	2.08
Q61753_S	Phgdh	D-3-phosp	K.GTIQVVTQGTSLK#.N	91.03	31.54	2.89	0.35
Q61753_S	Phgdh	D-3-phosp	K.ILQDGGLQVVEK#.Q	59.12	15.49	3.82	0.26
Q61753_S	Phgdh	D-3-phosp	R.QIPQATASM*K#.D	63.03	4.76	13.23	0.08
Q61753_S	Phgdh	D-3-phosp	K.VTADVINAAEK#.L	136.44	47.53	2.87	0.35
Q8VDD9_P	Phip	PH-interact	R.DANNFVLDEQTQQAPHLM*PPPFLVDVDGNPHPSR.Y	2.53	5.18	0.49	2.05
Q8VDD9_P	Phip	PH-interact	R.SLIYKPLDGEWGANPR.D	1.32	8.48	0.16	6.42
Q8VDD9_P	Phip	PH-interact	R.TFNEPGSPIVK#.S	16.31	22.13	0.74	1.36
Q8VDD9_P	Phip	PH-interact	R.VAVDPVVTEQPSTSSATK.A	16.87	17.52	0.96	1.04
Q8VDD9_P	Phip	PH-interact	R.VLFSAGHDGNVIVWDLAR.G	8.02	11.92	0.67	1.49
Q8VDD9_P	Phip	PH-interact	R.VYFFGSGQPEK.I	17.60	14.48	1.22	0.82
Q9WV95_	Phlda3	Pleckstrin	R.SGGLLQLWK#.R	45.43	19.68	2.31	0.43
Q6PDH0_P	Phldb1	Pleckstrin	R.ADGGPETGELPSIGEATAALALAGR.R	4.25	5.83	0.73	1.37
Q8K1N2_P	Phldb2	Pleckstrin	K.DLPHSLVDSDNYLNFSSLSSGASPYK#.T	5.74	5.37	1.07	0.94
Q8K1N2_P	Phldb2	Pleckstrin	K.EGLYLSDTLPR.K	4.21	12.48	0.34	2.96
Q8K1N2_P	Phldb2	Pleckstrin	R.LQELYSEQK#.T	11.27	12.61	0.89	1.12
Q8K1N2_P	Phldb2	Pleckstrin	R.M*VILNNLEELEQK#.I	4.80	4.86	0.99	1.01
Q8K1N2_P	Phldb2	Pleckstrin	K.SPNPLLTFSVK.T	10.36	11.05	0.94	1.07
Q8K1N2_P	Phldb2	Pleckstrin	K.TPEDIGEEQR.T	2.97	13.92	0.21	4.69
Q8K1N2_P	Phldb2	Pleckstrin	K.DLPHSLVDSDNYLNFSSLSSGASPYK.T	6.49	6.84	0.95	1.05
Q8K1N2_P	Phldb2	Pleckstrin	R.LQELYSEQK#.T	10.74	7.92	1.36	0.74
Q8K1N2_P	Phldb2	Pleckstrin	K.SPNPLLTFSVK.T	11.34	8.49	1.34	0.75
Q8C5D8_P	Pias2	E3 SUMO-p	K.LTADPDSEIATTSLR.V	3.54	4.31	0.82	1.22
Q9JM05_P	Pias4	E3 SUMO-p	R.TPLSGPTVDYPVLYGK#.Y	3.50	4.38	0.80	1.25
Q7M6Y3_P	Picalm	Phosphatid	R.ATTLSNAVSSLASTGLSLTK#.V	51.34	28.53	1.80	0.56
Q7M6Y3_P	Picalm	Phosphatid	R.FIQYLASR.N	7.58	15.51	0.49	2.05
Q7M6Y3_P	Picalm	Phosphatid	R.LFAAYNEGIINLLEK#.Y	51.45	25.82	1.99	0.50
Q7M6Y3_P	Picalm	Phosphatid	R.NTLFNLSNFLDK#.S	95.28	36.53	2.61	0.38
Q7M6Y3_P	Picalm	Phosphatid	K.QAALEEEQAR.L	5.55	10.76	0.52	1.94
Q7M6Y3_P	Picalm	Phosphatid	K.SGLQGYDM*STFIR.R	8.87	22.21	0.40	2.50
Q7M6Y3_P	Picalm	Phosphatid	K.SGLQGYDMSTFIR.R	7.43	14.08	0.53	1.89
Q7M6Y3_P	Picalm	Phosphatid	K.STNVAVDSGGFDELGGLLK#PTVASQNQSLPVAK#.L	7.35	3.29	2.23	0.45
Q7M6Y3_P	Picalm	Phosphatid	R.TTNSSWVVVFK#.S	42.88	16.36	2.62	0.38
Q7M6Y3_P	Picalm	Phosphatid	K.VAEQVGIDR.G	10.64	25.86	0.41	2.43
Q7M6Y3_P	Picalm	Phosphatid	R.ATTLSNAVSSLASTGLSLTK#.V	24.45	50.77	0.48	2.08
Q7M6Y3_P	Picalm	Phosphatid	R.FIQYLASR.N	6.14	11.00	0.56	1.79

Q7M6Y3_P	Picalm	Phosphatid	R.LFAAYNEGIINLLEK#.Y	32.48	18.04	1.80	0.56
Q7M6Y3_P	Picalm	Phosphatid	K.NDVSWSQPGEK#.K	11.93	8.12	1.47	0.68
Q7M6Y3_P	Picalm	Phosphatid	R.NTLFNLSNFLDK#.S	54.89	30.89	1.78	0.56
Q7M6Y3_P	Picalm	Phosphatid	K.QAALEEEQAR.L	3.36	15.28	0.22	4.55
Q7M6Y3_P	Picalm	Phosphatid	K.SGLQGYDM*STFIR.R	3.73	8.88	0.42	2.38
Q7M6Y3_P	Picalm	Phosphatid	K.STNVAVDSGGFDELGGLLK#PTVASQNQSLPVAK#.L	5.97	1.80	3.32	0.30
Q7M6Y3_P	Picalm	Phosphatid	R.TTNSSWVVVFK#.S	24.80	15.50	1.60	0.62
Q7M6Y3_P	Picalm	Phosphatid	R.ATTLSNAVSSLASTGLSLTK#.V	23.07	33.78	0.68	1.46
Q7M6Y3_P	Picalm	Phosphatid	R.LFAAYNEGIINLLEK#.Y	18.00	6.86	2.63	0.38
Q7M6Y3_P	Picalm	Phosphatid	R.NTLFNLSNFLDK#.S	43.64	22.89	1.91	0.52
Q9CQJ2_PI	Pih1d1	PIH1 doma	R.FQELLLK#.A	31.47	19.57	1.61	0.62
Q9CQJ2_PI	Pih1d1	PIH1 doma	R.LVIGGPQQLYHLDATVPLR.I	10.35	26.84	0.39	2.59
Q9CQJ2_PI	Pih1d1	PIH1 doma	R.SFLGSISQQNIR.S	5.37	18.69	0.29	3.48
Q61194_P3	Pik3c2a	Phosphatid	-.MAQISNNSEFK#.Q	26.31	1.44	18.26	0.05
Q61194_P3	Pik3c2a	Phosphatid	R.LIESSLGSIATK#.F	9.45	7.18	1.32	0.76
Q61194_P3	Pik3c2a	Phosphatid	R.TAEDDEAPVDLNK#.Y	11.50	6.22	1.85	0.54
P26450_P8	Pik3r1	Phosphatid	R.TAIEAFNETIK#.I	21.38	8.97	2.38	0.42
P26450_P8	Pik3r1	Phosphatid	K.TATGYGFAEPYNLYSSLK#.E	5.67	3.57	1.59	0.63
Q8VD65_PI	Pik3r4	Phosphoin	R.FLELVQLK#.T	13.38	7.77	1.72	0.58
Q8VD65_PI	Pik3r4	Phosphoin	K.VVTLLSDPENIVK#.Q	28.11	10.94	2.57	0.39
Q9QUR7_P	Pin1	Peptidyl-pr	R.GQM*QKPFEDASFALR.T	32.76	90.57	0.36	2.76
Q9QUR7_P	Pin1	Peptidyl-pr	R.GQMQKPFEDASFALR.T	10.50	23.02	0.46	2.19
Q9QUR7_P	Pin1	Peptidyl-pr	R.SKEEALELINGYIQK.I	100.56	57.08	1.76	0.57
Q9QUR7_P	Pin1	Peptidyl-pr	R.TGEMSGPVFTDSGIHIILR.T	18.77	10.67	1.76	0.57
Q9QUR7_P	Pin1	Peptidyl-pr	R.VYYFNHITNASQWERPSGGSTVGGSSK.N	9.01	15.90	0.57	1.77
Q9CZX5_PI	Pinx1	PIN2/TERF1	K.NKPQASAPGSDLSETPVER.K	2.37	10.69	0.22	4.51
Q80XI4_PI4	Pip4k2b	Phosphatid	R.FGIDDQDYQNSVTR.S	2.77	3.84	0.72	1.38
Q91XU3_PI	Pip4k2c	Phosphatid	K.HGAGAEISTVHPEQYAK#.R	37.29	12.17	3.06	0.33
E9PX91_E9	Pisd	Phosphatid	R.ALGPLSQVGWR@PMSR.V	1.65	5.05	0.33	3.07
P52480_KF	Pkm	Pyruvate ki	R.APIIAVTR.N	8.10	16.34	0.50	2.02
P52480_KF	Pkm	Pyruvate ki	K.GADFLVTEVENGGSLGSK#.K	7.82	2.06	3.80	0.26
P52480_KF	Pkm	Pyruvate ki	R.GDLGIEIPAEK#.V	21.91	18.04	1.21	0.82
P52480_KF	Pkm	Pyruvate ki	R.LAPITSDPTEAAAVGAVEASFK#.C	10.73	4.39	2.44	0.41
P52480_KF	Pkm	Pyruvate ki	R.LDIDSAPITAR.N	9.05	14.25	0.63	1.57
P70268_Pk	Pkn1	Serine/thre	K.LNLGADSDSSSQK#.S	8.43	2.51	3.36	0.30
P70268_Pk	Pkn1	Serine/thre	K.LNLGADSDSSSQK#.S	9.15	4.23	2.16	0.46
Q8BWW9_	Pkn2	Serine/thre	R.DLK#LDNLLLDTEGFVK#.I	13.75	4.59	2.99	0.33
Q8BWW9_	Pkn2	Serine/thre	R.IPDLAPPASDSTVTKLDFDLEPEPPPAPPR.A	1.88	3.54	0.53	1.89
Q8BWW9_	Pkn2	Serine/thre	K.LDNTVVGQTSWK#PISNQSWDQK#.F	6.50	4.21	1.55	0.65
P47713_PA	Pla2g4a	Cytosolic p	K.YGTFM*APDLFGSK#.F	6.29	2.96	2.13	0.47
P27612_PL	Plaa	Phospholip	K.EALTFDQANPTQILGK#.L	7.78	2.77	2.81	0.36
P27612_PL	Plaa	Phospholip	K.FGTLLSGSWDTTAK#.V	14.47	2.74	5.27	0.19
P27612_PL	Plaa	Phospholip	K.IGDVVGSSGANQQTSGK#.V	20.27	3.55	5.72	0.17
P27612_PL	Plaa	Phospholip	K.IGDVVGSSGANQQTSGK#.V	22.81	4.00	5.71	0.18
P27612_PL	Plaa	Phospholip	K.TVNIYFPK#.K	13.05	1.84	7.09	0.14
Q62077_PI	Plcg1	1-phosphat	R.FVVYEEDM*FSDQNFLAQATFPVK#.G	3.97	2.01	1.97	0.51
Q4KWH5_F	Plch1	1-phosphat	K.ILIDSIYK#.V	43.13	9.38	4.60	0.22
Q9QXS1_PI	Plec	Plectin OS=	R.FLEEEAEKM*K#.Q	2.54	51.50	0.05	20.25
Q9QXS1_PI	Plec	Plectin OS=	K.LAAISEATR.L	2.19	7.13	0.31	3.26
Q9QXS1_PI	Plec	Plectin OS=	K.ALLEEIER.H	1.88	9.27	0.20	4.93
Q9QXS1_PI	Plec	Plectin OS=	K.AQLEPVASPAK#.K	12.70	8.10	1.57	0.64
Q9QXS1_PI	Plec	Plectin OS=	K.AQVEQELTTLR.L	3.67	8.17	0.45	2.23
Q9QXS1_PI	Plec	Plectin OS=	R.ESADPLSAWLQDAK#.R	6.47	7.58	0.85	1.17
Q9QXS1_PI	Plec	Plectin OS=	R.IISLETYNLFR.E	3.31	7.72	0.43	2.33
Q9QXS1_PI	Plec	Plectin OS=	R.LEDLLQDAQDEK#EQLNEYK#.G	8.72	5.21	1.67	0.60
Q9QXS1_PI	Plec	Plectin OS=	R.LLDPEDVDVPQPDEK#.S	9.65	7.54	1.28	0.78
Q9QXS1_PI	Plec	Plectin OS=	R.LQAEEVAQQK#.S	16.62	12.06	1.38	0.73
Q9QXS1_PI	Plec	Plectin OS=	R.SDQLTGLSLLPLSEK#.A	6.05	6.53	0.93	1.08
Q9QXS1_PI	Plec	Plectin OS=	R.VLADPSDDTK#.G	21.49	7.82	2.75	0.36
Q9QXS1_PI	Plec	Plectin OS=	K.VLALPEPSPAAPTLR.S	2.79	11.29	0.25	4.04
Q9QXS1_PI	Plec	Plectin OS=	R.VYHDPSTQEPVTYSQLQQR.C	1.99	7.47	0.27	3.75
E9Q6H8_E9	Plekha5	Protein Ple	R.LGEVQSESAGIQR.A	5.40	13.24	0.41	2.45
Q91WB4_F	Plekhf2	Pleckstrin h	K.SFAVYAATATEK.S	5.26	3.65	1.44	0.69
Q66T02_Pk	Plekhg5	Pleckstrin h	K.SLGEVLLPVFER.K	3.00	6.58	0.46	2.19
Q66T02_Pk	Plekhg5	Pleckstrin h	K.SLGEVLLPVFER.K	3.81	21.65	0.18	5.68
Q8K124_PI	Plekho2	Pleckstrin h	R.DLGELNQETPGLVQK#.R	10.29	6.56	1.57	0.64
Q9DBG5_P	Plin3	Perilipin-3	K.TLTTAAVSTAQPILSK#.L	7.29	4.74	1.54	0.65
Q9DBG5_P	Plin3	Perilipin-3	R.LQESLPILQQPTEK#.V	7.50	3.21	2.34	0.43
Q9DBG5_P	Plin3	Perilipin-3	K.TLTTAAVSTAQPILSK#.L	12.67	4.20	3.01	0.33
Q9R1Q7_PI	Plp2	Proteolipid	R.HTAAPTDPTDGP.-	183.08	183.08	1.00	1.00
Q922V4_PI	Plrg1	Pleiotropic	R.AVVLHPLLYTFASGSPDNIK.Q	29.71	31.74	0.94	1.07
Q922V4_PI	Plrg1	Pleiotropic	K.QYPANQGQDVEYLVTGTHPYPAGPGVALTADTK#.I	9.89	11.08	0.89	1.12
Q922V4_PI	Plrg1	Pleiotropic	R.SQPTAMNSIM*ETGNTK.N	3.34	4.13	0.81	1.24
Q922V4_PI	Plrg1	Pleiotropic	R.TGYNFQR.V	2.91	21.54	0.14	7.40
Q9CPV5_PI	Pmf1	Polyamine-	R.DSEAAERGPEGSSPEAVPGDATIPR.V	1.67	5.21	0.32	3.12
Q9CPV5_PI	Pmf1	Polyamine-	R.ELLSVLR.A	6.17	16.84	0.37	2.73
Q60953_PI	Pml	Protein PM	R.ELLEAVNDR.Y	2.62	15.00	0.17	5.72
Q60953_PI	Pml	Protein PM	K.EVQSVQAQALELSK.T	5.94	9.58	0.62	1.61
Q60953_PI	Pml	Protein PM	R.TLVFFDLK#.I	8.99	9.36	0.96	1.04
Q60953_PI	Pml	Protein PM	R.VLIQPEAFSVYSK#.A	9.61	12.53	0.77	1.30
Q60953_PI	Pml	Protein PM	K.APGQADANGEALDNVFFESLQR.R	2.86	12.43	0.23	4.34
Q60953_PI	Pml	Protein PM	K.EVQSVQAQALELSK.T	9.00	9.78	0.92	1.09
Q60953_PI	Pml	Protein PM	K.ISQLAAVNR.E	4.02	19.10	0.21	4.75
Q60953_PI	Pml	Protein PM	R.QVVDYVQAQER.E	1.73	12.66	0.14	7.32
Q60953_PI	Pml	Protein PM	R.TLVFFDLK#.I	15.02	12.39	1.21	0.82
Q60953_PI	Pml	Protein PM	R.VLIQPEAFSVYSK#.A	19.67	23.64	0.83	1.20
A2AJT4_PN	Pnisr	Arginine/se	R.TPNEAPSVLEPK#.R	22.75	21.45	1.06	0.94
O35691_PI	Pnn	Pinin OS=M	R.ALQEQLEK#.A	27.12	14.32	1.89	0.53
O35691_PI	Pnn	Pinin OS=M	R.DLIQDQNM*DEK#.G	18.56	7.34	2.53	0.40
O35691_PI	Pnn	Pinin OS=M	K.FKQESTVATER.Q	5.89	12.61	0.47	2.14
O35691_PI	Pnn	Pinin OS=M	R.GFSDSGGGPPAK#.Q	26.41	13.38	1.97	0.51
O35691_PI	Pnn	Pinin OS=M	R.IFGLLM*GTLQK#.F	14.39	8.40	1.71	0.58
O35691_PI	Pnn	Pinin OS=M	R.IFGLLMGTLQK#.F	10.35	5.57	1.86	0.54
O35691_PI	Pnn	Pinin OS=M	K.LEVQAEEER.K	9.73	29.23	0.33	3.00
O35691_PI	Pnn	Pinin OS=M	R.RIEFAEQINK.M	4.53	11.38	0.40	2.51
O35691_PI	Pnn	Pinin OS=M	R.ALQEQLEK.A	103.61	106.72	0.97	1.03
O35691_PI	Pnn	Pinin OS=M	R.DLEGAVSR.L	20.15	76.54	0.26	3.80
O35691_PI	Pnn	Pinin OS=M	R.DLIQDQNM*DEK#.G	32.94	36.51	0.90	1.11
O35691_PI	Pnn	Pinin OS=M	K.FKQESTVATER.Q	13.66	77.31	0.18	5.66
O35691_PI	Pnn	Pinin OS=M	R.GFSDSGGGPPAK.Q	32.87	48.08	0.68	1.46
O35691_PI	Pnn	Pinin OS=M	R.IFGLLM*GTLQK#.F	62.30	66.54	0.94	1.07
O35691_PI	Pnn	Pinin OS=M	R.IFGLLMGTLQK#.F	23.63	25.39	0.93	1.07
O35691_PI	Pnn	Pinin OS=M	R.KM*NALFEGR.R	1.97	14.27	0.14	7.23

O35691_PI	Pnn	Pinin OS=N	K.LEVQAEEER.K	21.84	134.50	0.16	6.16
O35691_PI	Pnn	Pinin OS=N	R.NEEQKAEQEEGK.V	4.69	6.15	0.76	1.31
O35691_PI	Pnn	Pinin OS=N	R.RGFSDSGGGPPAK.Q	3.86	15.73	0.25	4.07
O35691_PI	Pnn	Pinin OS=N	R.RIEFAEQINK.M	12.60	34.49	0.37	2.74
O35691_PI	Pnn	Pinin OS=N	K.TKPHLFYIPGR.M	12.93	62.31	0.21	4.82
O35691_PI	Pnn	Pinin OS=N	K.VELAQLQEEWNEHNAK#.I	10.87	8.25	1.32	0.76
O35691_PI	Pnn	Pinin OS=N	K.DFPLESIK#LPEVSVEPVLTVHSENK#.S	23.09	16.43	1.41	0.71
O35691_PI	Pnn	Pinin OS=N	R.DLIQDQNM*DEK.G	7.65	11.80	0.65	1.54
O35691_PI	Pnn	Pinin OS=N	K.FKQESTVATER.Q	3.13	18.27	0.17	5.84
O35691_PI	Pnn	Pinin OS=N	R.GFSDSGGGPPAK#.Q	13.47	21.74	0.62	1.61
O35691_PI	Pnn	Pinin OS=N	R.IFGLLM*GTLQK.F	16.88	19.68	0.86	1.17
O35691_PI	Pnn	Pinin OS=N	K.LEVQAEEER@.K	16.28	35.07	0.46	2.15
Q8BZH4_P(	Pogz	Pogo trans	R.FANVPDSILLEAK#.D	18.91	18.36	1.03	0.97
Q8BZH4_P(	Pogz	Pogo trans	R.FQASQGENLEGK.Y	12.37	13.53	0.91	1.09
Q8BZH4_P(	Pogz	Pogo trans	K.RPGVTGENSNEVAK.L	1.50	6.62	0.23	4.43
Q8BZH4_P(	Pogz	Pogo trans	R.SFLVASVLPGPDGNVNSPTR.N	1.46	7.62	0.19	5.21
Q8BZH4_P(	Pogz	Pogo trans	K.VPEPNENAGDAVQTK.L	5.54	8.11	0.68	1.46
Q8BZH4_P(	Pogz	Pogo trans	R.EQQLPVNEETLFQK.A	18.02	18.14	0.99	1.01
Q8BZH4_P(	Pogz	Pogo trans	R.FANVPDSILLEAK.D	35.31	44.32	0.80	1.26
Q8BZH4_P(	Pogz	Pogo trans	R.FQASQGENLEGK#.Y	23.79	28.06	0.85	1.18
Q8BZH4_P(	Pogz	Pogo trans	K.ISYEWAVR.F	1.06	16.78	0.06	15.85
Q8BZH4_P(	Pogz	Pogo trans	K.LAEWVLIQR.E	2.99	21.62	0.14	7.24
Q8BZH4_P(	Pogz	Pogo trans	R.LQFLFAK#.D	18.49	20.59	0.90	1.11
Q8BZH4_P(	Pogz	Pogo trans	R.SFLVASVLPGPDGNVNSPTR.N	2.72	13.25	0.21	4.87
Q8BZH4_P(	Pogz	Pogo trans	K.VPEPNENAGDAVQTK#.L	13.46	15.55	0.87	1.16
Q8BZH4_P(	Pogz	Pogo trans	K.VTSSIPVFDLQDGGR.K	4.36	23.25	0.19	5.33
Q8BZH4_P(	Pogz	Pogo trans	K.YLSFEAEEK.L	13.62	20.99	0.65	1.54
P33609_DI	Pola1	DNA polym	K.DTGNFVIGQILSDQSR.D	9.01	22.07	0.41	2.45
P33609_DI	Pola1	DNA polym	R.DTIVENIQK#.R	36.09	19.86	1.82	0.55
P33609_DI	Pola1	DNA polym	K.DVYEEFDSK#.I	13.96	6.95	2.01	0.50
P33609_DI	Pola1	DNA polym	R.FYAK#PLAALVTYK#.G	18.14	12.32	1.47	0.68
P33609_DI	Pola1	DNA polym	K.LDNLAIDTQYYLAQQIHPVVAR.I	14.54	34.28	0.42	2.36
P33609_DI	Pola1	DNA polym	K.LGDEDEEIDGDTNK#.Y	33.73	22.89	1.47	0.68
P33609_DI	Pola1	DNA polym	R.LIEIGENVLNGSVPVSQFEINK#.A	9.15	6.67	1.37	0.73
P33609_DI	Pola1	DNA polym	R.NEPLLTPIPLK#.R	12.35	7.89	1.57	0.64
P33609_DI	Pola1	DNA polym	K.NIAEQFLSWSGYSEVNLSK#.L	4.69	5.52	0.85	1.18
P33609_DI	Pola1	DNA polym	K.NYAFEIPDVPEKSEYLEVR.Y	5.64	21.21	0.27	3.76
P33609_DI	Pola1	DNA polym	K.QQDLNPDLVLQYDIR.Q	1.59	5.12	0.31	3.21
P33609_DI	Pola1	DNA polym	R.TLIGFFLAK#.V	52.01	24.81	2.10	0.48
P33609_DI	Pola1	DNA polym	K.TWDQETEPVER.V	5.28	19.72	0.27	3.74
P33609_DI	Pola1	DNA polym	K.VEIAATER.T	10.28	29.31	0.35	2.85
P33609_DI	Pola1	DNA polym	K.YAALVVEPTSDGNYITK#.Q	29.63	15.75	1.88	0.53
P33609_DI	Pola1	DNA polym	R.YSAEVPQLPQNLK#.G	33.92	20.13	1.69	0.59
P33611_DI	Pola2	DNA polym	R.QLLSPSSFSPSATPSQK#.Y	6.52	4.92	1.32	0.76
P33611_DI	Pola2	DNA polym	K.SVILEGDQEHSYGAQIPVDLSELK#.E	13.62	6.37	2.14	0.47
P33611_DI	Pola2	DNA polym	K.VVGDPEPLTGSYK#.A	51.62	340.48	0.15	6.60
P33611_DI	Pola2	DNA polym	R.QLLSPSSFSPSATPSQK#.Y	6.78	3.73	1.82	0.55
P33611_DI	Pola2	DNA polym	K.SVILEGDQEHSYGAQIPVDLSELK#.E	10.28	5.53	1.86	0.54
P33611_DI	Pola2	DNA polym	K.VVGDPEPLTGSYK#.A	26.44	26.78	0.99	1.01
P52431_DI	Pold1	DNA polym	R.ALDPSTEPLIFQQLEIDHYVGSAPPLPEGPLPSR.N	2.30	3.72	0.62	1.62
P52431_DI	Pold1	DNA polym	K.VYFPYLLISK#.K	10.51	6.54	1.61	0.62
P52431_DI	Pold1	DNA polym	R.ALDPSTEPLIFQQLEIDHYVGSAPPLPEGPLPSR.N	3.31	4.01	0.83	1.21
P52431_DI	Pold1	DNA polym	K.TEGSEDYTGATVIEPLK#.G	9.40	6.25	1.50	0.66
P52431_DI	Pold1	DNA polym	K.VSANSVYGFTGAQVGK#.L	7.13	5.72	1.25	0.80
P52431_DI	Pold1	DNA polym	K.VYFPYLLISK#.K	21.31	15.86	1.34	0.74
O35654_DI	Pold2	DNA polym	R.FLGTSGQNVSDIFR.Y	3.83	8.15	0.47	2.13
O35654_DI	Pold2	DNA polym	K.K#TQAASVEAVK#.M	8.41	3.41	2.46	0.41
O35654_DI	Pold2	DNA polym	K.LVTGTVLAVLGSAK#.D	15.83	7.78	2.03	0.49
O35654_DI	Pold2	DNA polym	R.VPVATYTNSSQPFR.L	5.29	6.47	0.82	1.22
Q9EQ28_DI	Pold3	DNA polym	K.DSGPLFNTDYDILK#.S	5.43	3.42	1.59	0.63
Q9EQ28_DI	Pold3	DNA polym	K.TVEQPPVSVTEPK#.L	9.16	7.15	1.28	0.78
Q8BG81_PI	Poldip3	Polymerase	K.IGLSDAR.L	9.67	25.14	0.38	2.60
Q8BG81_PI	Poldip3	Polymerase	R.INVVNNHQAK#.Q	9.94	8.32	1.19	0.84
Q8BG81_PI	Poldip3	Polymerase	R.LVHPGVAEVVFVK#.K	36.95	24.38	1.52	0.66
Q8BG81_PI	Poldip3	Polymerase	R.RGNPASSNPPAEVDPDTVLR.A	2.79	19.03	0.15	6.83
Q8BG81_PI	Poldip3	Polymerase	R.SPAAFTSPPIGTVTPALK.L	8.73	8.87	0.98	1.02
Q8BG81_PI	Poldip3	Polymerase	K.SSGASVTTQPTEFK#.I	30.67	23.75	1.29	0.77
Q8BG81_PI	Poldip3	Polymerase	K.TIQVPQQK#.A	20.71	14.01	1.48	0.68
Q8BG81_PI	Poldip3	Polymerase	K.VVQNDAYTAPVLPSSVR.T	3.51	10.25	0.34	2.92
Q9WVF7_D	Pole	DNA polym	K.IFQSSVFEAFLK.G	17.30	6.82	2.54	0.39
Q9WVF7_D	Pole	DNA polym	K.IITIPAALQQVK#.N	12.57	7.77	1.62	0.62
O54956_DI	Pole2	DNA polym	K.TIETLLGSTSK#.V	7.78	10.31	0.75	1.33
Q9JKP7_DF	Pole3	DNA polym	K.EALPDGVNISK#.E	25.19	15.29	1.65	0.61
Q9JKP7_DF	Pole3	DNA polym	R.LDEDDQNEEEEIDN.-	19.74	19.74	1.00	1.00
Q9CQ36_D	Pole4	DNA polym	R.AAELFVETIAK#.D	40.73	20.58	1.98	0.51
O35134_RI	Polr1a	DNA-direct	R.DSDGSVVQFLYGEDGLDIPK#.T	3.88	4.75	0.82	1.22
O35134_RI	Polr1a	DNA-direct	K.TPM*M*SVPVFDTK#.K	3.45	1.88	1.84	0.54
P52432_RI	Polr1c	DNA-direct	K.DSSDPNELYVNHK#.V	7.26	5.09	1.43	0.70
P52432_RI	Polr1c	DNA-direct	R.ILLAEVPTM*AVEK#.V	23.73	16.60	1.43	0.70
P52432_RI	Polr1c	DNA-direct	R.ILLAEVPTMAVEK#.V	13.55	6.32	2.14	0.47
P52432_RI	Polr1c	DNA-direct	R.LGLIPILADPR.L	7.89	24.43	0.32	3.09
P52432_RI	Polr1c	DNA-direct	R.NQGEEEGTEIDTLQFR.L	5.09	11.22	0.45	2.20
P08775_RI	Polr2a	DNA-direct	R.AEIQELAM*VPR.M	3.75	33.61	0.11	8.96
P08775_RI	Polr2a	DNA-direct	K.AHNNELEPTPGNTLR.Q	3.27	11.88	0.28	3.63
P08775_RI	Polr2a	DNA-direct	K.AK#QDVIEVIEK#.A	28.59	30.19	0.95	1.06
P08775_RI	Polr2a	DNA-direct	K.AKQDVIEVIEK.A	12.14	10.63	1.14	0.88
P08775_RI	Polr2a	DNA-direct	K.ALQEWILETDGVSLM*R.V	4.94	11.34	0.44	2.29
P08775_RI	Polr2a	DNA-direct	K.ALQEWILETDGVSLMR.V	1.77	7.50	0.24	4.23
P08775_RI	Polr2a	DNA-direct	R.DVFLER.G	6.87	29.78	0.23	4.34
P08775_RI	Polr2a	DNA-direct	R.EGLIDTAVK#.T	33.23	34.30	0.97	1.03
P08775_RI	Polr2a	DNA-direct	K.FGVEQPEGDEDLTK.E	20.99	30.24	0.69	1.44
P08775_RI	Polr2a	DNA-direct	R.GFVENSYLAGLTPTEFFFHAM*GGR.E	4.32	14.34	0.30	3.32
P08775_RI	Polr2a	DNA-direct	K.IIITEDGEFK#.A	45.14	50.84	0.89	1.13
P08775_RI	Polr2a	DNA-direct	K.INISQVIAVVGQQNVEGK.R	21.12	20.44	1.03	0.97
P08775_RI	Polr2a	DNA-direct	K.INISQVIAVVGQQNVEGK#.R	85.40	90.72	0.94	1.06
P08775_RI	Polr2a	DNA-direct	R.KLTM*EQIAEK.I	18.39	19.37	0.95	1.05
P08775_RI	Polr2a	DNA-direct	R.LK#ELINISK#.K	45.27	38.68	1.17	0.85
P08775_RI	Polr2a	DNA-direct	K.LLQFHVATM*VDNELPGLPR.A	3.92	10.67	0.37	2.72
P08775_RI	Polr2a	DNA-direct	K.LLVDSNNPK#.I	55.60	56.87	0.98	1.02
P08775_RI	Polr2a	DNA-direct	R.LPSDLHPIK.V	20.64	18.99	1.09	0.92
P08775_RI	Polr2a	DNA-direct	K.LTM*EQIAEK#.I	14.18	15.30	0.93	1.08
P08775_RI	Polr2a	DNA-direct	R.NSINQVVQLR.Y	11.58	47.94	0.24	4.14
P08775_RI	Polr2a	DNA-direct	R.SIAANM*TFAEIVTPFNIDR.L	2.50	11.63	0.21	4.65

P08775_RI	Polr2a	DNA-direct	K.SLSEYNNFK#.S	38.23	34.47	1.11	0.90
P08775_RI	Polr2a	DNA-direct	K.TAETGYIQR.R	13.88	68.58	0.20	4.94
P08775_RI	Polr2a	DNA-direct	R.TLQEDLVK#.D	19.32	18.17	1.06	0.94
P08775_RI	Polr2a	DNA-direct	K.TPSLTVFLLGQSAR.D	5.14	29.25	0.18	5.69
P08775_RI	Polr2a	DNA-direct	R.TVITPDPNLSIDQVGVPR.S	4.93	38.50	0.13	7.82
P08775_RI	Polr2a	DNA-direct	K.TYQDIQNTIK#.K	35.71	32.24	1.11	0.90
P08775_RI	Polr2a	DNA-direct	R.VLSEKDVDPVR.T	3.15	11.22	0.28	3.56
P08775_RI	Polr2a	DNA-direct	R.VQFGVLSPDELK#.R	12.06	11.47	1.05	0.95
P08775_RI	Polr2a	DNA-direct	R.VQFGVLSPDELKR.M	5.93	29.16	0.20	4.91
P08775_RI	Polr2a	DNA-direct	R.YGEDGLAGESVEFQNLATLKPSNK.A	40.31	46.80	0.86	1.16
P08775_RI	Polr2a	DNA-direct	K.YSPTSPTYSPTSPK.Y	53.00	54.54	0.97	1.03
P08775_RI	Polr2a	DNA-direct	K.YSPTSPTYSPTSPVYTPTSPK#.Y	9.67	7.89	1.22	0.82
P08775_RI	Polr2a	DNA-direct	K.YSPTSPTYSPTTPK#.Y	25.11	30.03	0.84	1.20
P08775_RI	Polr2a	DNA-direct	R.YTPQSPTYTPSSPSYSPSSPSYSPTSPK.Y	5.06	4.47	1.13	0.88
P08775_RI	Polr2a	DNA-direct	K.YTPTSPSYSPSSPEYTPASPK.Y	7.96	8.82	0.90	1.11
Q8CFI7_RP	Polr2b	DNA-direct	R.AGVSQVLNR.L	6.68	32.80	0.20	4.91
Q8CFI7_RP	Polr2b	DNA-direct	R.GPIQILNR.Q	6.03	20.45	0.29	3.39
Q8CFI7_RP	Polr2b	DNA-direct	K.ISNLLSDYGYHLR.G	3.68	24.29	0.15	6.59
Q8CFI7_RP	Polr2b	DNA-direct	R.IVATLPYIK.Q	16.78	19.95	0.84	1.19
Q8CFI7_RP	Polr2b	DNA-direct	K.KGFDQEEVFEKPTR.E	3.40	22.06	0.15	6.49
Q8CFI7_RP	Polr2b	DNA-direct	K.M*ATNTVYVFAK.K	13.96	12.73	1.10	0.91
Q8CFI7_RP	Polr2b	DNA-direct	R.NLTYSAPLYVDITK#.T	13.20	19.87	0.66	1.50
Q8CFI7_RP	Polr2b	DNA-direct	K.QEVPIIIVFR.A	4.19	19.44	0.22	4.64
Q8CFI7_RP	Polr2b	DNA-direct	K.TVIKEGEEQLQTQHQK.T	22.58	24.05	0.94	1.06
Q8CFI7_RP	Polr2b	DNA-direct	K.TVTLPENEDELESTNR.R	2.27	6.50	0.35	2.87
Q8CFI7_RP	Polr2b	DNA-direct	K.VSANK#GEIGDATPFNDAVNVQK#.I	12.26	10.75	1.14	0.88
Q8CFI7_RP	Polr2b	DNA-direct	R.VSGDDVIIGK#.T	20.82	23.47	0.89	1.13
Q8CFI7_RP	Polr2b	DNA-direct	K.YSLATGNWGDQK#.K	10.60	9.02	1.17	0.85
Q8CFI7_RP	Polr2b	DNA-direct	R.AGVSQVLNR.L	9.17	39.82	0.23	4.34
Q8CFI7_RP	Polr2b	DNA-direct	K.GEIGDATPFNDAVNVQK#.I	14.82	10.87	1.36	0.73
Q8CFI7_RP	Polr2b	DNA-direct	R.GPIQILNR.Q	4.14	20.41	0.20	4.94
Q8CFI7_RP	Polr2b	DNA-direct	R.IPQIGDK#.F	43.79	36.99	1.18	0.84
Q8CFI7_RP	Polr2b	DNA-direct	K.ISNLLSDYGYHLR.G	11.69	45.15	0.26	3.86
Q8CFI7_RP	Polr2b	DNA-direct	R.IVATLPYIK#.Q	29.72	23.01	1.29	0.77
Q8CFI7_RP	Polr2b	DNA-direct	K.KGFDQEEVFEKPTR.E	8.40	27.74	0.30	3.30
Q8CFI7_RP	Polr2b	DNA-direct	K.LDDDGLIAPGVR.V	6.23	19.19	0.32	3.08
Q8CFI7_RP	Polr2b	DNA-direct	R.LLLAALGR.R	5.80	30.64	0.19	5.29
Q8CFI7_RP	Polr2b	DNA-direct	R.NLTYSAPLYVDITK.T	30.34	24.85	1.22	0.82
Q8CFI7_RP	Polr2b	DNA-direct	K.QEVPIIIVFR.A	3.67	19.71	0.19	5.37
Q8CFI7_RP	Polr2b	DNA-direct	K.TVIK#EGEEQLQTQHQK#.T	39.62	31.44	1.26	0.79
Q8CFI7_RP	Polr2b	DNA-direct	K.TVTLPENEDELESTNR.R	2.20	13.31	0.17	6.04
Q8CFI7_RP	Polr2b	DNA-direct	K.VLIAQEK#.M	33.94	28.11	1.21	0.83
Q8CFI7_RP	Polr2b	DNA-direct	K.VSANK#GEIGDATPFNDAVNVQK#.I	24.54	20.59	1.19	0.84
Q8CFI7_RP	Polr2b	DNA-direct	R.VSGDDVIIGK#.T	43.83	42.21	1.04	0.96
Q99M46_C	Polr2c	DNA-direct	K.FIIENTDLAVANSIR.R	13.45	50.95	0.26	3.79
Q99M46_C	Polr2c	DNA-direct	R.ITELTEENVK#.F	79.50	61.19	1.30	0.77
Q99M46_C	Polr2c	DNA-direct	R.LGLIPLTSDDIVDK#.L	28.48	32.43	0.88	1.14
Q99M46_C	Polr2c	DNA-direct	R.NRDNDPNDYVEQDDILIVK.L	4.71	18.67	0.25	3.96
Q99M46_C	Polr2c	DNA-direct	K.SEYSELDEDESQAPYDPNGKPER.F	3.37	8.20	0.41	2.43
Q99M46_C	Polr2c	DNA-direct	K.WNPTAGVAFEYDPDNALR.H	5.50	20.15	0.27	3.67
Q9D7M8_F	Polr2d	DNA-direct	R.AGDVEEDASQLIFPK#.E	83.62	84.38	0.99	1.01
Q9D7M8_F	Polr2d	DNA-direct	R.FEDEELQQILDDIQTK.R	27.58	35.02	0.79	1.27
Q9D7M8_F	Polr2d	DNA-direct	R.K#QQNESAEDEQELSEVFM*K#.T	14.15	18.68	0.76	1.32
Q9D7M8_F	Polr2d	DNA-direct	R.KQQNESAEDEQELSEVFMK.T	16.61	7.15	2.32	0.43
Q80UW8_F	Polr2e	DNA-direct	R.ALIVVQQGM*TPSAK#.Q	53.05	62.18	0.85	1.17
Q80UW8_F	Polr2e	DNA-direct	R.ALIVVQQGMTPSAK#.Q	7.46	8.31	0.90	1.11
Q80UW8_F	Polr2e	DNA-direct	R.GYLVTQDELDQTLEEFK#.A	31.26	38.16	0.82	1.22
Q80UW8_F	Polr2e	DNA-direct	R.IQAGDPVAR.Y	17.43	107.99	0.16	6.19
P62488_RI	Polr2g	DNA-direct	K.AIVFRPFKGEVVDAVVTQVNK.V	5.64	28.77	0.20	5.10
P62488_RI	Polr2g	DNA-direct	R.GFVLYPVK#.Y	32.93	21.76	1.51	0.66
P62488_RI	Polr2g	DNA-direct	K.TM*DEDIVIQQDDEIR.L	2.88	11.77	0.24	4.09
P62488_RI	Polr2g	DNA-direct	R.VDK#NDIFAIGSLM*DDYLGLVS.-	11.06	10.26	1.08	0.93
P62488_RI	Polr2g	DNA-direct	R.YFGPNLLNTVK#.Q	87.26	82.45	1.06	0.94
P62488_RI	Polr2g	DNA-direct	K.YGFVIAVTTIDNIGAGVIQPGR.G	2.09	14.77	0.14	7.07
Q923G2_RI	Polr2h	DNA-direct	R.IEGDETSTEAATR.L	6.09	24.34	0.25	4.00
Q923G2_RI	Polr2h	DNA-direct	R.LSAYVSYGGLLM*R.L	7.48	32.05	0.23	4.29
Q923G2_RI	Polr2h	DNA-direct	R.LVIASTLYEDGTLDDGEYNPTDDRPSR.A	2.46	27.85	0.09	11.32
Q923G2_RI	Polr2h	DNA-direct	R.VYLLMK#.K	14.08	8.44	1.67	0.60
Q923G2_RI	Polr2h	DNA-direct	K.VYRIEGDETSTEAATR.L	4.63	63.93	0.07	13.81
P60898_RI	Polr2i	DNA-direct	K.EAVFFQSHSAR.A	4.15	7.94	0.52	1.91
P60898_RI	Polr2i	DNA-direct	K.ITHEVDELTQIIADVSQDPTLPR.T	11.14	79.66	0.14	7.15
Q6PI63_Q6	Polr2j	DNA-direct	K.DPQVLFAGYK#.V	14.87	15.63	0.95	1.05
Q6PI63_Q6	Polr2j	DNA-direct	K.SQLLK#DPQVLFAGYK#.V	38.47	39.64	0.97	1.03
Q6PI63_Q6	Polr2j	DNA-direct	K.SQLLKDPQVLFAGYK.V	4.32	4.91	0.88	1.14
Q6PI63_Q6	Polr2j	DNA-direct	R.VAIK#DK#QEGIE.-	14.51	18.36	0.79	1.26
Q63871_RI	Polr2k	DNA-direct	R.LVVFDAR.-	12.32	45.47	0.27	3.69
P62876_RI	Polr2l	DNA-direct	K.LLNYAPLEK#.-	35.27	36.27	0.97	1.03
B2RXC6_B2	Polr3a	Polymerase	R.GFSIGIGDVTPGQGLLK#.A	12.03	6.36	1.89	0.53
Q8K205_Q	Pop1	Blood vesse	R.LGWGSGWDVLIPK#.G	7.20	4.20	1.71	0.58
P37040_N	Por	NADPH--cyt	K.DVQNTFYDIVAEFGPM*EHTQAVDYVK#.K	7.53	4.32	1.74	0.57
P37040_N	Por	NADPH--cyt	R.TNVLYELAQYASEPSEQEHLHK#.M	8.90	6.64	1.34	0.75
Q91YU8_SS	Ppan	Suppressor	R.LPGGPTLTFQISK#.Y	14.34	6.30	2.28	0.44
Q91YU8_SS	Ppan	Suppressor	R.NLESYAAQPHSFVFTR.G	6.05	9.93	0.61	1.64
Q91YU8_SS	Ppan	Suppressor	R.QAVGEEPDEDLFPTAAK#.R	9.87	3.01	3.28	0.31
Q8C8U0_LI	Ppfibp1	Liprin-beta	R.LENDK#ESLVLQVSVLTDQVEAQGEK#.I	4.42	6.09	0.73	1.38
Q8C8U0_LI	Ppfibp1	Liprin-beta	R.SPSASITDEDSNV.-	10.58	10.58	1.00	1.00
Q8C8U0_LI	Ppfibp1	Liprin-beta	R.WLDDIGLPQYK#.T	14.23	13.95	1.02	0.98
G3X959_G	Pphln1	Periphilin 1	R.FITEYDNSAQDFGDPF.-	20.18	20.18	1.00	1.00
G3X959_G	Pphln1	Periphilin 1	K.WANETLEK.S	16.21	20.98	0.77	1.29
P17742_PI	Ppia	Peptidyl-pr	K.FEDENFILK.H	7.45	11.25	0.66	1.51
P24369_PI	Ppib	Peptidyl-pr	K.TVDNFVALATGEK#.G	8.07	9.27	0.87	1.15
P24369_PI	Ppib	Peptidyl-pr	R.VVFGLFGK#.T	19.30	16.39	1.18	0.85
P30412_PI	Ppic	Peptidyl-pr	R.DGTGGM*SIYGETFPDENFK#.L	3.05	2.01	1.52	0.66
Q9QZH3_PI	Ppie	Peptidyl-pr	K.HVVFGEVTEGLDVLR.Q	2.01	11.30	0.18	5.61
Q9QZH3_PI	Ppie	Peptidyl-pr	K.KFDDENFILK.H	20.46	14.72	1.39	0.72
Q9QZH3_PI	Ppie	Peptidyl-pr	K.TLEENKEEEGPEPPKAEAQEGEPTAK.K	21.42	27.83	0.77	1.30
Q9QZH3_PI	Ppie	Peptidyl-pr	K.TLEENK#EEEGPEPPK#AEAQEGEPTAK#.K	8.38	9.75	0.86	1.16
Q9QZH3_PI	Ppie	Peptidyl-pr	R.VLYVGGLAEEVDDK#.V	11.04	13.40	0.82	1.21
A2AR02_PI	Ppig	Peptidyl-pr	R.GGESIYGGFFEDESFAVK#.H	5.83	2.03	2.87	0.35
A2AR02_PI	Ppig	Peptidyl-pr	R.GGESIYGGFFEDESFAVK#.H	24.34	16.91	1.44	0.69
A2BGI8_A2	Ppih	Peptidyl-pr	R.GPFADENFK#.L	88.70	49.99	1.77	0.56
A2BGI8_A2	Ppih	Peptidyl-pr	K.IELFADVVPK#.T	67.10	41.44	1.62	0.62
A2BGI8_A2	Ppih	Peptidyl-pr	K.IENVPTGPNNKPK.L	13.66	11.60	1.18	0.85

A2BGI8_A2	Ppih	Peptidyl-pr	K.IIDGLLVM*R.K	21.30	41.21	0.52	1.93
A2BGI8_A2	Ppih	Peptidyl-pr	K.IIDGLLVMR.K	6.02	18.67	0.32	3.10
A2BGI8_A2	Ppih	Peptidyl-pr	R.K#IENVPTGPNNK#PK#.L	93.99	72.94	1.29	0.78
A2BGI8_A2	Ppih	Peptidyl-pr	R.K#IENVPTGPNNK#PK#.L	2.62	3.12	0.84	1.19
A2BGI8_A2	Ppih	Peptidyl-pr	R.M*K#IELFADVVPK#.T	34.55	18.13	1.91	0.52
A2BGI8_A2	Ppih	Peptidyl-pr	R.MK#IELFADVVPK#.T	21.50	10.37	2.07	0.48
Q9D0W5_F	Ppil1	Peptidyl-pr	K.DFM*IQGGDPTGTGR.G	2.40	13.52	0.18	5.64
Q9D0W5_F	Ppil1	Peptidyl-pr	R.IIKDFM*IQGGDPTGTGR.G	7.56	23.40	0.32	3.09
Q9D787_PI	Ppil2	Peptidyl-pr	R.GVLSM*ANSGPNTNK.S	7.11	10.22	0.70	1.44
Q9D787_PI	Ppil2	Peptidyl-pr	R.GVLSMANSGPNTNK.S	2.77	4.87	0.57	1.76
Q9D787_PI	Ppil2	Peptidyl-pr	R.IIDPDEEK#.A	14.62	25.19	0.58	1.72
Q9D787_PI	Ppil2	Peptidyl-pr	R.NFVIQGGDPTGTGTGGESFWGKPFK.D	5.38	6.20	0.87	1.15
Q9D787_PI	Ppil2	Peptidyl-pr	R.SAEEEPSTSTATPTAK.K	15.06	20.41	0.74	1.36
Q9D787_PI	Ppil2	Peptidyl-pr	K.SQFFITFR.S	6.79	12.55	0.54	1.85
Q9D787_PI	Ppil2	Peptidyl-pr	R.TTGNVYTYEAVEQLNIK.A	4.13	7.96	0.52	1.93
Q9D6L8_PI	Ppil3	Peptidyl-pr	K.DITIHANPFAQ.-	28.46	28.46	1.00	1.00
Q9D6L8_PI	Ppil3	Peptidyl-pr	K.GFM*VQTGDPTGTGR.G	2.36	10.69	0.22	4.52
Q9D6L8_PI	Ppil3	Peptidyl-pr	K.K#FEDEYSEYLK#.H	6.36	4.34	1.47	0.68
Q9D6L8_PI	Ppil3	Peptidyl-pr	K.VIDGLETLDELEK#LPVNEK#.T	31.56	26.96	1.17	0.85
Q9CXG3_PI	Ppil4	Peptidyl-pr	K.LNPVTTDEDLEIIFSR.F	2.44	9.02	0.27	3.69
Q9CXG3_PI	Ppil4	Peptidyl-pr	R.SAEEVEEIK#AEK#.E	9.30	6.17	1.51	0.66
Q9CXG3_PI	Ppil4	Peptidyl-pr	K.YDLILDEQGEDSK#.S	7.58	7.13	1.06	0.94
Q6ZQB6_VI	Ppip5k2	Inositol he›	K.ALADIVIPQEYGITK#.A	6.83	1.76	3.88	0.26
P63087_PF	Ppp1cc	Serine/thre	R.AHQVVEDGYEFFAK#.R	10.13	8.43	1.20	0.83
P63087_PF	Ppp1cc	Serine/thre	R.AHQVVEDGYEFFAK.R	13.96	16.06	0.87	1.15
P63087_PF	Ppp1cc	Serine/thre	K.NVQLQENEIR.G	2.36	13.05	0.18	5.52
P63087_PF	Ppp1cc	Serine/thre	R.YPENFFLLR.G	2.30	8.08	0.28	3.51
P63087_PF	Ppp1cc	Serine/thre	R.AHQVVEDGYEFFAK#.R	7.59	5.64	1.35	0.74
P63087_PF	Ppp1cc	Serine/thre	R.AHQVVEDGYEFFAK#.R	3.84	3.83	1.00	1.00
P63087_PF	Ppp1cc	Serine/thre	R.AHQVVEDGYEFFAK#.R	15.84	7.74	2.05	0.49
P63087_PF	Ppp1cc	Serine/thre	K.NVQLQENEIR.G	2.57	11.19	0.23	4.35
Q80W00_F	Ppp1r10	Serine/thre	R.APEVLVK#.F	28.00	25.72	1.09	0.92
Q80W00_F	Ppp1r10	Serine/thre	R.EYFYFELDETER.V	1.76	6.54	0.27	3.71
Q80W00_F	Ppp1r10	Serine/thre	K.FIDVGGYK.L	25.26	26.05	0.97	1.03
Q80W00_F	Ppp1r10	Serine/thre	K.GILQELFLNK#.E	32.22	37.60	0.86	1.17
Q80W00_F	Ppp1r10	Serine/thre	K.IIPPQPM*EGLGFLDALNSAPVPGIK#.I	20.53	16.77	1.22	0.82
Q80W00_F	Ppp1r10	Serine/thre	K.LPPVLANLM*GSM*GAGK.S	4.26	5.38	0.79	1.26
Q80W00_F	Ppp1r10	Serine/thre	R.QSATAAPGDAAPPAEK.K	12.08	15.93	0.76	1.32
Q80W00_F	Ppp1r10	Serine/thre	R.QSATAAPGDAAPPAEKK.Y	15.29	24.48	0.62	1.60
Q80W00_F	Ppp1r10	Serine/thre	R.STGLELDTPSLVPVKK.N	43.20	36.31	1.19	0.84
Q9DBR7_M	Ppp1r12a	Protein pho	K.AQLHDTNM*ELTDLK#.L	34.19	13.59	2.52	0.40
Q9DBR7_M	Ppp1r12a	Protein pho	R.LAYVTPTIPR.R	13.25	36.79	0.36	2.78
Q9DBR7_M	Ppp1r12a	Protein pho	K.NK#ETLIIEPEK#.N	6.46	3.92	1.65	0.61
Q9DBR7_M	Ppp1r12a	Protein pho	R.SASYSYLEDR.K	7.12	21.09	0.34	2.96
Q9DBR7_M	Ppp1r12a	Protein pho	K.SGGTALHVAAAK#.G	38.29	15.39	2.49	0.40
Q9DBR7_M	Ppp1r12a	Protein pho	K.SPLIESTANM*ENNQPQK#.A	9.67	6.26	1.54	0.65
Q9DBR7_M	Ppp1r12a	Protein pho	K.TGSYGALAEISASK#.E	27.91	16.27	1.72	0.58
Q9DBR7_M	Ppp1r12a	Protein pho	R.TYDETYTR.Y	6.85	14.25	0.48	2.08
Q8BQ30_PI	Ppp1r18	Phostensin	K.EVLESILSPGEPGDQK#.A	14.58	5.12	2.85	0.35
Q8BQ30_PI	Ppp1r18	Phostensin	R.LSPGETPEESLR.L	17.42	19.58	0.89	1.12
Q3TDD9_PI	Ppp1r21	Protein pho	R.IQIFPVDSAIDTISPLNQK#.F	5.96	2.85	2.09	0.48
P63330_PF	Ppp2ca	Serine/thre	K.SPDTNYLFM*GDYVDR.G	2.78	8.34	0.33	3.00
P63330_PF	Ppp2ca	Serine/thre	K.SPDTNYLFM*GDYVDR.G	5.89	5.91	1.00	1.00
P63330_PF	Ppp2ca	Serine/thre	K.YGNANVWK#.Y	31.20	7.27	4.29	0.23
P63330_PF	Ppp2ca	Serine/thre	K.YSFLQFDPAPR.R	12.72	13.60	0.94	1.07
Q76MZ3_2	Ppp2r1a	Serine/thre	R.AISHEHSPSDLEAHFVPLVK#.R	21.19	9.03	2.35	0.43
Q76MZ3_2	Ppp2r1a	Serine/thre	K.IGPILDNSTLQSEVK#PILEK#.L	143.51	50.27	2.85	0.35
Q76MZ3_2	Ppp2r1a	Serine/thre	R.LAGGDWFTSR.T	22.40	34.77	0.64	1.55
Q76MZ3_2	Ppp2r1a	Serine/thre	K.LSTIALALGVER.T	14.29	19.40	0.74	1.36
Q76MZ3_2	Ppp2r1a	Serine/thre	K.LTQDQDVDVK#.Y	215.34	77.51	2.78	0.36
Q76MZ3_2	Ppp2r1a	Serine/thre	R.MAGDPVANVR.F	7.42	14.33	0.52	1.93
Q76MZ3_2	Ppp2r1a	Serine/thre	R.NEDVQLR.L	34.14	37.63	0.91	1.10
Q76MZ3_2	Ppp2r1a	Serine/thre	K.SALASVIM*GLSPILGK#.D	47.10	16.37	2.88	0.35
Q76MZ3_2	Ppp2r1a	Serine/thre	K.SEIIPM*FSNLASDEQDSVR.L	4.55	7.02	0.65	1.54
Q76MZ3_2	Ppp2r1a	Serine/thre	K.SEIIPMFSNLASDEQDSVR.L	4.41	6.20	0.71	1.40
Q76MZ3_2	Ppp2r1a	Serine/thre	K.TDLVPAFQNLM*K#.D	24.04	9.56	2.52	0.40
Q76MZ3_2	Ppp2r1a	Serine/thre	K.VLELDNVK#.S	129.57	36.32	3.57	0.28
Q76MZ3_2	Ppp2r1a	Serine/thre	K.IGPILDNSTLQSEVKPILEK.L	9.78	5.43	1.80	0.55
Q76MZ3_2	Ppp2r1a	Serine/thre	K.LSTIALALGVER.T	5.75	14.75	0.39	2.57
Q76MZ3_2	Ppp2r1a	Serine/thre	R.AISHEHSPSDLEAHFVPLVK#.R	52.22	15.36	3.40	0.29
Q76MZ3_2	Ppp2r1a	Serine/thre	K.AVGPEITK#.T	56.68	12.27	4.62	0.22
Q76MZ3_2	Ppp2r1a	Serine/thre	K.ELVSDANQHVK#.S	24.62	2.69	9.14	0.11
Q76MZ3_2	Ppp2r1a	Serine/thre	K.IGPILDNSTLQSEVKPILEK.L	76.84	24.06	3.19	0.31
Q76MZ3_2	Ppp2r1a	Serine/thre	K.IGPILDNSTLQSEVK#PILEK#.L	4.63	2.01	2.30	0.43
Q76MZ3_2	Ppp2r1a	Serine/thre	K.LSTIALALGVER.T	6.43	7.86	0.82	1.22
Q76MZ3_2	Ppp2r1a	Serine/thre	K.LTQDQDVDVK#.Y	107.83	24.87	4.34	0.23
Q76MZ3_2	Ppp2r1a	Serine/thre	K.SALASVIM*GLSPILGK#.D	36.52	5.78	6.32	0.16
Q76MZ3_2	Ppp2r1a	Serine/thre	K.SEIIPM*FSNLASDEQDSVR.L	3.18	3.63	0.88	1.14
Q76MZ3_2	Ppp2r1a	Serine/thre	K.VLELDNVK#.S	71.71	19.68	3.64	0.27
Q76MZ3_2	Ppp2r1a	Serine/thre	R.AISHEHSPSDLEAHFVPLVK#.R	72.51	25.32	2.86	0.35
Q76MZ3_2	Ppp2r1a	Serine/thre	K.AVGPEITK#.T	90.97	28.42	3.20	0.31
Q76MZ3_2	Ppp2r1a	Serine/thre	K.FGK#EWAHATIIPK#.V	12.12	6.79	1.78	0.56
Q76MZ3_2	Ppp2r1a	Serine/thre	K.IGPILDNSTLQSEVK#PILEK#.L	173.01	47.20	3.67	0.27
Q76MZ3_2	Ppp2r1a	Serine/thre	R.LAGGDWFTSR.T	16.88	18.10	0.93	1.07
Q76MZ3_2	Ppp2r1a	Serine/thre	K.LSTIALALGVER.T	8.77	13.27	0.66	1.51
Q76MZ3_2	Ppp2r1a	Serine/thre	K.LTQDQDVDVK#.Y	264.00	68.35	3.86	0.26
Q76MZ3_2	Ppp2r1a	Serine/thre	R.M*AGDPVANVR.F	20.48	37.69	0.54	1.84
Q76MZ3_2	Ppp2r1a	Serine/thre	K.SALASVIM*GLSPILGK#.D	98.51	24.90	3.96	0.25
Q76MZ3_2	Ppp2r1a	Serine/thre	K.SEIIPM*FSNLASDEQDSVR.L	3.28	6.00	0.55	1.83
Q76MZ3_2	Ppp2r1a	Serine/thre	K.TDLVPAFQNLM*K#.D	29.33	7.80	3.76	0.27
Q76MZ3_2	Ppp2r1a	Serine/thre	K.VLELDNVK#.S	107.83	31.84	3.39	0.30
Q7TNP2_2/	Ppp2r1b	Serine/thre	R.ETVIM*NQILPYIK#.E	16.73	2.59	6.46	0.15
Q7TNP2_2/	Ppp2r1b	Serine/thre	K.IGPILDTNALQGEVK#PVLQK#.L	17.51	8.75	2.00	0.50
Q6P1F6_2/	Ppp2r2a	Serine/thre	R.DYLSVK#.I	25.46	5.08	5.01	0.20
Q6P1F6_2/	Ppp2r2a	Serine/thre	K.ENIIAVATTNNLYIFQDK#.V	6.79	2.45	2.77	0.36
Q6P1F6_2/	Ppp2r2a	Serine/thre	K.GAVDDDVAEADIISTVEFNHSGELLATGDK#.G	13.32	4.89	2.72	0.37
Q6P1F6_2/	Ppp2r2a	Serine/thre	K.NAAQFLLSTNDK#.T	32.61	16.81	1.94	0.52
Q6P1F6_2/	Ppp2r2a	Serine/thre	R.VVIFQQEQENK#.I	51.62	340.48	0.15	6.60
Q6P1F6_2/	Ppp2r2a	Serine/thre	K.GAVDDDVAEADIISTVEFNHSGELLATGDK#.G	6.47	1.78	3.63	0.28
Q6P1F6_2/	Ppp2r2a	Serine/thre	R.VVIFQQEQENK#.I	10.34	2.43	4.26	0.23
Q6P1F6_2/	Ppp2r2a	Serine/thre	K.NAAQFLLSTNDK#.T	2.45	11.21	0.22	4.57
P58389_P1	Ppp2r4	Serine/thre	K.FGSLLPIHPVTSG.-	20.85	20.85	1.00	1.00
P58389_P1	Ppp2r4	Serine/thre	K.TGPFAEHSNQLWNISAVPSWSK#.V	3.83	3.03	1.26	0.79

P58389_P	Ppp2r4	Serine/thre	R.VDDQVAIVFK#.V	38.98	4.27	9.13	0.11
P58389_P	Ppp2r4	Serine/thre	K.FGSLLPIHPVTSG.-	11.25	11.25	1.00	1.00
P58389_P	Ppp2r4	Serine/thre	K.FGSLLPIHPVTSG.-	10.85	10.85	1.00	1.00
Q91V89_Q	Ppp2r5d	Protein Pp	K.ESSLTEPVIVGLLK#.F	15.76	5.57	2.83	0.35
Q91V89_Q	Ppp2r5d	Protein Pp	R.FLESPDFQPNIAK#.K	32.33	11.63	2.78	0.36
Q91V89_Q	Ppp2r5d	Protein Pp	R.TVETEAVQMLK#.D	11.28	4.87	2.32	0.43
Q91V89_Q	Ppp2r5d	Protein Pp	R.AEEFLTASQEAL.-	12.73	12.73	1.00	1.00
Q91V89_Q	Ppp2r5d	Protein Pp	K.ESSLTEPVIVGLLK#.F	26.32	12.91	2.04	0.49
Q91V89_Q	Ppp2r5d	Protein Pp	R.FLESPDFQPNIAK#.K	37.77	16.04	2.36	0.42
Q91V89_Q	Ppp2r5d	Protein Pp	R.TVETEAVQM*LK#.D	17.66	6.43	2.75	0.36
Q91V89_Q	Ppp2r5d	Protein Pp	R.TVETEAVQMLK#.D	17.07	6.69	2.55	0.39
Q91V89_Q	Ppp2r5d	Protein Pp	K.YSGGPQIVK#.K	20.61	9.54	2.16	0.46
Q91V89_Q	Ppp2r5d	Protein Pp	K.DGGGENTDEAQPQPQSQSPSSNK#.R	10.81	3.61	2.99	0.33
Q91V89_Q	Ppp2r5d	Protein Pp	K.ESSLTEPVIVGLLK#.F	44.04	17.20	2.56	0.39
Q91V89_Q	Ppp2r5d	Protein Pp	R.FLESPDFQPNIAK#.K	30.03	16.13	1.86	0.54
Q91V89_Q	Ppp2r5d	Protein Pp	R.ILPIM*FPALYR.N	7.37	14.94	0.49	2.03
Q91V89_Q	Ppp2r5d	Protein Pp	R.K#SELPQDVYTIK#.A	10.21	117.26	0.09	11.49
Q91V89_Q	Ppp2r5d	Protein Pp	K.TIHGLIYNALK#.L	12.91	4.50	2.87	0.35
Q91V89_Q	Ppp2r5d	Protein Pp	R.TVETEAVQM*LK#.D	19.58	12.89	1.52	0.66
Q91V89_Q	Ppp2r5d	Protein Pp	R.TVETEAVQMLK#.D	12.59	6.36	1.98	0.51
Q61151_2	Ppp2r5e	Serine/thre	R.FLESQEFQPSIAK#.K	8.36	1.98	4.23	0.24
P63328_P	Ppp3ca	Serine/thre	K.LFEVGGSPANTR.Y	4.97	10.70	0.46	2.15
Q63810_C	Ppp3r1	Calcineuri	K.DGYISNGELFQVLK#.M	8.97	82.19	0.11	9.16
Q63810_C	Ppp3r1	Calcineuri	K.DTQLQQIVDK#.T	12.95	8.98	1.44	0.69
Q63810_C	Ppp3r1	Calcineuri	K.LDLDNSGSLSVEEFM*SLPELQQNPLVQR.V	2.60	3.03	0.86	1.17
Q922D4_P	Ppp6r3	Serine/thre	K.ETGWASFSEFTSSLSTK#.E	6.49	3.13	2.07	0.48
Q91VJ5_P	Pqbp1	Polyglutam	K.HLEPEPEEEIIAEDYDDDPVDYEATR.I	1.52	2.89	0.52	1.91
Q9JIG8_PR	Praf2	PRA1 famil	R.ALDDFVLGSAR.L	1.99	7.79	0.26	3.92
Q9JIG8_PR	Praf2	PRA1 famil	R.TPM*GLLLEALGQEQEAGS.-	7.47	7.47	1.00	1.00
Q99K43_P	Prc1	Protein reg	K.LLQEQEQELR.D	4.00	8.36	0.48	2.09
Q9EQC8_Q	Prcc	Papillary re	K.TK#PASLAPVLGTTTTTPSPSAIK#.A	12.91	8.56	1.51	0.66
Q9EQC8_Q	Prcc	Papillary re	K.VVLQGSGEGTGLSALLPQPK#.N	4.73	2.65	1.78	0.56
P35700_P	Prdx1	Peroxiredo	K.ATAVM*PDGQFK#.D	9.89	7.20	1.37	0.73
P35700_P	Prdx1	Peroxiredo	K.ADEGISFR.G	18.69	22.88	0.82	1.22
P35700_P	Prdx1	Peroxiredo	K.ATAVM*PDGQFK#.D	101.67	31.35	3.24	0.31
P35700_P	Prdx1	Peroxiredo	K.ATAVMPDGQFK#.D	22.60	8.65	2.61	0.38
P35700_P	Prdx1	Peroxiredo	R.GLFIIDDK#.G	73.93	19.80	3.73	0.27
P35700_P	Prdx1	Peroxiredo	K.IGYPAPNFK#.A	39.59	14.75	2.68	0.37
P35700_P	Prdx1	Peroxiredo	R.QITINDLPVGR.S	21.23	37.28	0.57	1.76
P35700_P	Prdx1	Peroxiredo	R.TIAQDYGVLK#.A	82.16	24.47	3.36	0.30
P35700_P	Prdx1	Peroxiredo	K.ATAVM*PDGQFK#.D	14.98	4.86	3.08	0.32
Q61171_P	Prdx2	Peroxiredo	R.K#EGGLGPLNIPLLADVTK#.S	37.04	7.65	4.84	0.21
Q61171_P	Prdx2	Peroxiredo	R.QITVNDLPVGR.S	1.37	2.83	0.49	2.06
Q61171_P	Prdx2	Peroxiredo	K.SAPDFTATAVVDGAFK#.E	28.51	7.17	3.97	0.25
P20108_P	Prdx3	Thioredoxi	R.DYGVLLESAGIALR.G	6.49	8.08	0.80	1.24
P20108_P	Prdx3	Thioredoxi	K.ELSLDDFK#.G	12.25	4.31	2.84	0.35
P20108_P	Prdx3	Thioredoxi	R.GLFIIDPNGVVK#.H	18.74	8.32	2.25	0.44
P99029_P	Prdx5	Peroxiredo	K.K#VNLAELFK#.G	5.90	1.71	3.45	0.29
P99029_P	Prdx5	Peroxiredo	R.LLADPTGAFGK#.A	24.45	7.96	3.07	0.33
P99029_P	Prdx5	Peroxiredo	K.VGDAIPSVEVFEGEPGK#.K	18.33	6.19	2.96	0.34
P99029_P	Prdx5	Peroxiredo	K.VNLAELFK#.G	8.13	5.63	1.44	0.69
P20664_P	Prim1	DNA prima	K.LGAFQAQEK#.E	19.45	19.32	1.01	0.99
P20664_P	Prim1	DNA prima	R.SGIVEYLSLVK#.G	22.00	14.32	1.54	0.65
P20664_P	Prim1	DNA prima	K.TSLAPYVK#.V	14.90	3.75	3.97	0.25
P20664_P	Prim1	DNA prima	R.SGIVEYLSLVK#.G	14.05	9.06	1.55	0.64
P20664_P	Prim1	DNA prima	K.LGAFQAQEK#.E	16.24	14.72	1.10	0.91
P20664_P	Prim1	DNA prima	K.VFEQFLENLDK#.S	17.44	10.89	1.60	0.62
P33610_P	Prim2	DNA prima	R.EQDIM*ASSPSLSGIK#.L	15.83	12.47	1.27	0.79
P33610_P	Prim2	DNA prima	R.EQDIMASSPSLSGIK#.L	5.15	3.11	1.66	0.60
P33610_P	Prim2	DNA prima	K.IPASGISQILDLVK#.G	58.52	39.78	1.47	0.68
P33610_P	Prim2	DNA prima	K.VPFADALDLFR.G	7.96	28.35	0.28	3.56
P33610_P	Prim2	DNA prima	R.EQDIM*ASSPSLSGIK#.L	4.92	4.44	1.11	0.90
P33610_P	Prim2	DNA prima	K.VPFADALDLFR.G	2.88	11.16	0.26	3.87
P33610_P	Prim2	DNA prima	K.AIENLGVSYVK#.G	18.19	11.39	1.60	0.63
P33610_P	Prim2	DNA prima	K.DSHLHFEAISDEEK#.T	15.21	8.25	1.84	0.54
P33610_P	Prim2	DNA prima	R.HSDAELLK#.Q	11.87	8.42	1.41	0.71
P33610_P	Prim2	DNA prima	K.IPASGISQILDLVK#.G	41.97	28.91	1.45	0.69
P33610_P	Prim2	DNA prima	K.VPFADALDLFR.G	6.29	15.18	0.41	2.41
Q5EG47_A	Prkaa1	5'-AMP-acti	R.HTLDELNPQK#.S	19.27	14.98	1.29	0.78
Q5EG47_A	Prkaa1	5'-AMP-acti	K.IADFGLSNM*M*SDGEFLR.T	3.21	5.22	0.62	1.62
Q5EG47_A	Prkaa1	5'-AMP-acti	K.IGHYILGDTLGVGTFGK#.V	23.74	14.85	1.60	0.63
Q5EG47_A	Prkaa1	5'-AMP-acti	R.VPFLVAETPR.A	10.97	29.88	0.37	2.72
Q5EG47_A	Prkaa1	5'-AMP-acti	R.HTLDELNPQK#.S	11.88	7.00	1.70	0.59
Q5EG47_A	Prkaa1	5'-AMP-acti	K.IGHYILGDTLGVGTFGK#.V	12.43	9.72	1.28	0.78
Q5EG47_A	Prkaa1	5'-AMP-acti	R.SIDDEITEAK#.S	13.35	9.25	1.44	0.69
Q5EG47_A	Prkaa1	5'-AMP-acti	R.HTLDELNPQK#.S	13.69	8.44	1.62	0.62
Q5EG47_A	Prkaa1	5'-AMP-acti	K.IGHYILGDTLGVGTFGK#.V	25.75	9.80	2.63	0.38
Q9R078_A	Prkab1	5'-AMP-acti	K.K#TDFEVFDALM*VDSQK#.C	13.87	8.31	1.67	0.60
Q9R078_A	Prkab1	5'-AMP-acti	R.SQNNFVAILDLPEGEHQYK#.F	17.06	12.10	1.41	0.71
Q9R078_A	Prkab1	5'-AMP-acti	K.YVTTLLYK#PI.-	17.49	11.35	1.54	0.65
P05132_K	Prkaca	cAMP-depe	R.DLK#PENLLIDQQGYIQVTDFGFAK#.R	22.05	5.74	3.84	0.26
P05132_K	Prkaca	cAMP-depe	R.ILQAVNFPFLVK#.L	28.81	8.28	3.48	0.29
P05132_K	Prkaca	cAMP-depe	R.NLLQVDLTK#.R	25.41	6.69	3.80	0.26
P68181_K	Prkacb	cAMP-depe	K.ATEQYYAM*K#.I	10.43	3.14	3.32	0.30
P68181_K	Prkacb	cAMP-depe	R.ILQAVEFPFLVR.L	10.19	7.92	1.29	0.78
P68181_K	Prkacb	cAMP-depe	R.LEYSFK#.D	21.32	3.94	5.42	0.18
O54950_A	Prkag1	5'-AMP-acti	K.FDVINLAAEK#.T	62.02	46.00	1.35	0.74
O54950_A	Prkag1	5'-AMP-acti	R.LPVIDPESGNTLYILTHK#.R	33.80	25.39	1.33	0.75
O54950_A	Prkag1	5'-AMP-acti	K.LVVFDTSLQVK#.K	22.69	13.30	1.71	0.59
O54950_A	Prkag1	5'-AMP-acti	K.TYNNLDVSVTK#.A	45.69	33.41	1.37	0.73
O54950_A	Prkag1	5'-AMP-acti	R.VSALPVVDEK#.G	30.06	22.92	1.31	0.76
O54950_A	Prkag1	5'-AMP-acti	R.VVDIYSK#.F	38.51	26.21	1.47	0.68
O54950_A	Prkag1	5'-AMP-acti	R.LPVIDPESGNTLYILTHK#.R	12.45	5.46	2.28	0.44
O54950_A	Prkag1	5'-AMP-acti	K.LVVFDTSLQVK#.K	8.46	4.28	1.98	0.51
O54950_A	Prkag1	5'-AMP-acti	K.FDVINLAAEK#.T	11.66	6.50	1.79	0.56
O54950_A	Prkag1	5'-AMP-acti	R.LPVIDPESGNTLYILTHK#.R	14.54	6.05	2.40	0.42
Q9DBC7_K	Prkar1a	cAMP-depe	K.HNIQALLK#.D	20.41	7.08	2.88	0.35
Q9DBC7_K	Prkar1a	cAMP-depe	R.LTVADALEPVQFEDGQK#.I	43.74	12.04	3.63	0.28
P12849_K	Prkar1b	cAMP-depe	R.LTVADALEPVQFEDGEK#.I	4.97	1.80	2.76	0.36
P12367_K	Prkar2a	cAMP-depe	K.NLDQEQLSQVLDAMFEK#.I	9.68	4.44	2.18	0.46
P31324_K	Prkar2b	cAMP-depe	R.AASAHAIGTVK#.C	15.22	5.73	2.66	0.38
P31324_K	Prkar2b	cAMP-depe	R.GTFDIYVK#.C	9.69	4.13	2.35	0.43
P31324_K	Prkar2b	cAMP-depe	R.TWGDAGAAAGGGIPSK#.G	21.23	8.74	2.43	0.41

P20444_K	Prkca	Protein kin	K.LTDFNFLM*VLGK#.G	13.45	18.21	0.74	1.35
P20444_K	Prkca	Protein kin	K.LTDFNFLM*VLGK#.G	18.03	11.22	1.61	0.62
P28867_K	Prkcd	Protein kin	K.AEFWLDLQPQAK#.V	11.27	4.36	2.58	0.39
P28867_K	Prkcd	Protein kin	K.FEQFLDI.-	9.27	9.27	1.00	1.00
P28867_K	Prkcd	Protein kin	K.AEFWLDLQPQAK#.V	11.39	2.57	4.44	0.23
P28867_K	Prkcd	Protein kin	K.FEQFLDI.-	9.82	9.82	1.00	1.00
P28867_K	Prkcd	Protein kin	R.K#LDTTESVGIYQGFEK#.K	18.92	2.06	9.20	0.11
Q62074_K	Prkci	Protein kin	K.ASSSLGLQDFDLLR.V	2.96	9.40	0.31	3.18
Q62074_K	Prkci	Protein kin	K.ASSSLGLQDFDLLR.V	9.23	17.04	0.54	1.84
Q62074_K	Prkci	Protein kin	R.DLK#LDNVLLDSEGHIK#.L	25.47	12.27	2.08	0.48
Q62074_K	Prkci	Protein kin	K.ELVNDDEDIDWVQTEK#.H	9.95	5.29	1.88	0.53
Q62074_K	Prkci	Protein kin	K.ASSSLGLQDFDLLR.V	5.79	19.17	0.30	3.31
Q62074_K	Prkci	Protein kin	R.DLK#LDNVLLDSEGHIK#.L	28.28	21.20	1.33	0.75
Q62074_K	Prkci	Protein kin	K.ELVNDDEDIDWVQTEK#.H	8.85	6.89	1.28	0.78
Q62101_K	Prkd1	Serine/thre	R.SVVGTPAYLAPEVLR.N	4.10	8.89	0.46	2.17
Q9WTX2_P	Prkra	Interferon-i	R.AAEAAINILK#.A	17.14	10.06	1.70	0.59
Q9WTX2_P	Prkra	Interferon-i	K.NQLNPIGSLQELAIHHGWR.L	6.27	10.37	0.61	1.65
Q9JIF0_AN	Prmt1	Protein arg	K.ANK#LDHVVTIIK#.G	98.89	29.20	3.39	0.30
Q9JIF0_AN	Prmt1	Protein arg	R.ATLYVTAIEDR.Q	36.45	49.13	0.74	1.35
Q9JIF0_AN	Prmt1	Protein arg	R.DKWLAPDGLIFPDR.A	15.96	20.85	0.77	1.31
Q9JIF0_AN	Prmt1	Protein arg	K.DVAIK#EPLVDVVDPK#.Q	48.77	10.92	4.47	0.22
Q9JIF0_AN	Prmt1	Protein arg	K.GK#VEEVELPVEK#.V	66.55	11.27	5.91	0.17
Q9JIF0_AN	Prmt1	Protein arg	K.LDHVVTIIK#.G	25.10	4.29	5.85	0.17
Q9JIF0_AN	Prmt1	Protein arg	K.QTVFYM*EDYLTVK#.T	21.05	5.26	4.00	0.25
Q9JIF0_AN	Prmt1	Protein arg	K.QTVFYMEDYLTVK#.T	42.66	7.41	5.76	0.17
Q9JIF0_AN	Prmt1	Protein arg	R.TGFSTSPESPYTHWK#.Q	160.47	40.30	3.98	0.25
Q9JIF0_AN	Prmt1	Protein arg	K.VEEVELPVEK#.V	30.51	14.20	2.15	0.47
Q9JIF0_AN	Prmt1	Protein arg	K.WLAPDGLIFPDR.A	15.66	18.40	0.85	1.17
Q9JIF0_AN	Prmt1	Protein arg	K.ANK#LDHVVTIIK#.G	125.23	21.21	5.90	0.17
Q9JIF0_AN	Prmt1	Protein arg	R.ATLYVTAIEDR.Q	37.93	39.35	0.96	1.04
Q9JIF0_AN	Prmt1	Protein arg	R.DKWLAPDGLIFPDR.A	18.74	23.65	0.79	1.26
Q9JIF0_AN	Prmt1	Protein arg	K.DVAIK#EPLVDVVDPK#.Q	44.58	11.69	3.81	0.26
Q9JIF0_AN	Prmt1	Protein arg	K.EVDIYTVK#.V	106.57	23.73	4.49	0.22
Q9JIF0_AN	Prmt1	Protein arg	K.GK#VEEVELPVEK#.V	35.82	12.14	2.95	0.34
Q9JIF0_AN	Prmt1	Protein arg	R.TGFSTSPESPYTHWK#.Q	23.60	5.73	4.12	0.24
Q9JIF0_AN	Prmt1	Protein arg	K.ANK#LDHVVTIIK#.G	213.61	46.23	4.62	0.22
Q9JIF0_AN	Prmt1	Protein arg	R.ATLYVTAIEDR.Q	70.35	73.94	0.95	1.05
Q9JIF0_AN	Prmt1	Protein arg	R.DKWLAPDGLIFPDR.A	23.80	27.12	0.88	1.14
Q9JIF0_AN	Prmt1	Protein arg	K.DVAIK#EPLVDVVDPK#.Q	85.77	21.83	3.93	0.25
Q9JIF0_AN	Prmt1	Protein arg	K.EVDIYTVK#.V	119.89	33.76	3.55	0.28
Q9JIF0_AN	Prmt1	Protein arg	K.GK#VEEVELPVEK#.V	51.30	12.87	3.99	0.25
Q9JIF0_AN	Prmt1	Protein arg	K.GKVEEVELPVEK.V	119.32	27.79	4.29	0.23
Q9JIF0_AN	Prmt1	Protein arg	K.LDHVVTIIK#.G	19.54	4.52	4.32	0.23
Q9JIF0_AN	Prmt1	Protein arg	K.QTVFYM*EDYLTVK#.T	34.32	8.12	4.22	0.24
Q8CIG8_A	Prmt5	Protein arg	K.AAILPTSIFLTNK#.K	19.81	6.70	2.96	0.34
Q8CIG8_A	Prmt5	Protein arg	R.DWNTLIVGK#.L	17.44	8.63	2.02	0.49
Q8CIG8_A	Prmt5	Protein arg	K.DDGVSIPGEYTSFLAPISSSK#.L	8.03	4.04	1.99	0.50
Q8CIG8_A	Prmt5	Protein arg	R.DWNTLIVGK#.L	30.57	7.88	3.88	0.26
Q8CIG8_A	Prmt5	Protein arg	R.GPLVNASLR.A	7.70	10.91	0.71	1.42
Q8CIG8_A	Prmt5	Protein arg	K.YSQYQQAIYK#.C	26.74	8.76	3.05	0.33
Q9Z2Y8_P	Prosc	Proline syn	R.TFGENYVQELLEK#.A	9.34	4.00	2.33	0.43
Q99KP6_P	Prpf19	Pre-mRNA-	R.AHESAVTGLSLHATGDYLLSSSDDQYWAFSDIQTGR.V	3.22	2.75	1.17	0.85
Q99KP6_P	Prpf19	Pre-mRNA-	K.ALQDEWDAVMLHSFTLR.Q	35.32	84.88	0.42	2.40
Q99KP6_P	Prpf19	Pre-mRNA-	K.ALQDEWDAVMLHSFTLR.Q	2.94	8.98	0.33	3.06
Q99KP6_P	Prpf19	Pre-mRNA-	K.ATVLTTER.K	54.21	126.48	0.43	2.33
Q99KP6_P	Prpf19	Pre-mRNA-	R.EALATLKPQAGLIVPQAVPSSQPSVVGAGEPM*DLGELVGM*TPEIIQK.L	9.72	6.73	1.44	0.69
Q99KP6_P	Prpf19	Pre-mRNA-	K.FIASTGM*DR.S	31.08	78.81	0.39	2.54
Q99KP6_P	Prpf19	Pre-mRNA-	K.ILTGGADK#NVVVFDK#.S	69.12	54.03	1.28	0.78
Q99KP6_P	Prpf19	Pre-mRNA-	K.KVTSVVFHPSQELVFSASPDATIR.I	12.15	39.93	0.30	3.29
Q99KP6_P	Prpf19	Pre-mRNA-	K.NVVVFDK#.S	111.87	60.28	1.86	0.54
Q99KP6_P	Prpf19	Pre-mRNA-	K.STEQILATLK#.G	277.93	166.00	1.67	0.60
Q99KP6_P	Prpf19	Pre-mRNA-	K.TLQLDNNFEVK#.S	201.71	124.29	1.62	0.62
Q99KP6_P	Prpf19	Pre-mRNA-	R.TNVANFPGHSGPITSIAFSENGYYLATAADDSSVK#.L	50.33	10.28	4.90	0.20
Q99KP6_P	Prpf19	Pre-mRNA-	K.YIAENGTDPINNQPLSEEQLIDIK#.V	38.40	25.15	1.53	0.66
Q99KP6_P	Prpf19	Pre-mRNA-	K.YIAENGTDPINNQPLSEEQLIDIK#.V	9.98	4.64	2.15	0.47
Q99KP6_P	Prpf19	Pre-mRNA-	R.TNVANFPGHSGPITSIAFSENGYYLATAADDSSVK#.L	4.40	3.51	1.25	0.80
Q922U1_P	Prpf3	U4/U6 sma	K.DVNVVVVEGGPK#.A	20.31	10.80	1.88	0.53
Q922U1_P	Prpf3	U4/U6 sma	R.LALIAPK#.K	32.03	18.03	1.78	0.56
Q922U1_P	Prpf3	U4/U6 sma	R.LGLTPPPEPK#.V	52.16	36.69	1.42	0.70
Q922U1_P	Prpf3	U4/U6 sma	R.VLGTEAVQDPTK#.V	22.87	9.02	2.54	0.39
Q922U1_P	Prpf3	U4/U6 sma	R.VLGTEAVQDPTKVEAHVR.A	2.60	7.45	0.35	2.86
Q922U1_P	Prpf3	U4/U6 sma	K.LQAEISQAAR.K	4.25	12.26	0.35	2.88
Q922U1_P	Prpf3	U4/U6 sma	K.DVNVVVVEGGPK#.A	14.22	9.49	1.50	0.67
Q922U1_P	Prpf3	U4/U6 sma	R.LGLTPPPEPK#.V	30.18	20.00	1.51	0.66
Q922U1_P	Prpf3	U4/U6 sma	K.LQAEISQAAR.K	5.35	19.67	0.27	3.67
Q922U1_P	Prpf3	U4/U6 sma	R.VLGTEAVQDPTK#.V	13.96	5.46	2.56	0.39
Q8CCF0_P	Prpf31	U4/U6 sma	K.IEEYISK#.Q	79.50	48.34	1.64	0.61
Q8CCF0_P	Prpf31	U4/U6 sma	K.IM*GVAGGLTNLSK#.M	42.21	29.05	1.45	0.69
Q8CCF0_P	Prpf31	U4/U6 sma	R.IYEYVESR.M	15.76	36.87	0.43	2.34
Q8CCF0_P	Prpf31	U4/U6 sma	R.LGLTEIR.K	12.80	32.04	0.40	2.50
Q8CCF0_P	Prpf31	U4/U6 sma	R.M*SFGEIEEDAYQEDLGFSLGHLGK#.S	43.59	21.95	1.99	0.50
Q8CCF0_P	Prpf31	U4/U6 sma	R.M*SFIAPNLSIIIGASTAAK#.I	9.14	9.39	0.97	1.03
Q8CCF0_P	Prpf31	U4/U6 sma	K.QANVSEVM*GPVEAAPEYR.V	5.18	11.98	0.43	2.31
Q8CCF0_P	Prpf31	U4/U6 sma	K.RFPELESLVPNALDYIR.T	8.82	52.99	0.17	6.01
Q8CCF0_P	Prpf31	U4/U6 sma	R.SSGTASSVAFTPLQGLEIVNPQAAEK#.K	43.92	25.82	1.70	0.59
Q8CCF0_P	Prpf31	U4/U6 sma	R.SSGTASSVAFTPLQGLEIVNPQAAEK#K#.V	13.08	7.96	1.64	0.61
Q8CCF0_P	Prpf31	U4/U6 sma	K.TLSGFSSTSVLPHTGYIYHSDIVQSLPPDLR.R	2.34	2.69	0.87	1.15
Q8CCF0_P	Prpf31	U4/U6 sma	K.VGYELKDEIER.K	4.89	16.26	0.30	3.32
Q8CCF0_P	Prpf31	U4/U6 sma	R.VIVDANNLTVEIENELNIIHK#.F	83.24	42.90	1.94	0.52
Q8CCF0_P	Prpf31	U4/U6 sma	K.YFSSMAEFLK#.V	27.79	21.38	1.30	0.77
Q8CCF0_P	Prpf31	U4/U6 sma	R.M*SFGEIEEDAYQEDLGFSLGHLGK#.S	9.51	5.45	1.75	0.57
Q8CCF0_P	Prpf31	U4/U6 sma	R.VIVDANNLTVEIENELNIIHK#.F	15.34	8.64	1.78	0.56
Q8CCF0_P	Prpf31	U4/U6 sma	R.M*SFGEIEEDAYQEDLGFSLGHLGK#.S	10.12	5.71	1.77	0.56
Q4FK66_P	Prpf38a	Pre-mRNA-	K.DAHSIHGTNPQYLVEK#.I	20.33	16.38	1.24	0.81
Q4FK66_P	Prpf38a	Pre-mRNA-	K.YLEPLYNDYR.K	3.05	12.34	0.25	4.05
Q4FK66_P	Prpf38a	Pre-mRNA-	R.YVLEEAEQLEPR.V	11.50	14.65	0.79	1.27
Q4FK66_P	Prpf38a	Pre-mRNA-	K.DAHSIHGTNPQYLVEK.I	15.86	10.69	1.48	0.67
Q4FK66_P	Prpf38a	Pre-mRNA-	K.DAHSIHGTNPQYLVEK#.I	21.53	17.36	1.24	0.81
Q4FK66_P	Prpf38a	Pre-mRNA-	R.YVLEEAEQLEPR.V	3.71	11.26	0.33	3.03
Q80SY5_P	Prpf38b	Pre-mRNA-	R.IPVPVQK#.N	33.09	18.91	1.75	0.57
Q80SY5_P	Prpf38b	Pre-mRNA-	K.LEWFSTLFPR.I	4.11	12.08	0.34	2.94
Q80SY5_P	Prpf38b	Pre-mRNA-	K.QGNVLPLWGNEK#.T	12.11	4.57	2.65	0.38
Q80SY5_P	Prpf38b	Pre-mRNA-	K.VQLYELK#.T	22.69	14.02	1.62	0.62

Q80SY5_P	Prpf38b	Pre-mRNA-	K.LEWFSTLFPR.I	2.92	9.25	0.32	3.17
Q80SY5_P	Prpf38b	Pre-mRNA-	K.VQLYELK#.T	16.26	11.52	1.41	0.71
Q8K2Z2_P	Prpf39	Pre-mRNA-	K.SNNESSFYAIK#.L	10.22	3.54	2.88	0.35
Q9DAW6_	Prpf4	U4/U6 sma	K.AGIEAGNINITSGEVFEIEEHISER.Q	8.60	13.83	0.62	1.61
Q9DAW6_	Prpf4	U4/U6 sma	R.ALGEPITLFGEGPAER.R	23.57	50.87	0.46	2.16
Q9DAW6_	Prpf4	U4/U6 sma	K.FEPIHGDFLLTGAYDNTAK#.I	89.71	40.45	2.22	0.45
Q9DAW6_	Prpf4	U4/U6 sma	R.GHNTNVGAIVFHPK#.S	6.07	4.44	1.37	0.73
Q9DAW6_	Prpf4	U4/U6 sma	K.K#PHIYYGSLEEK#.E	83.84	49.35	1.70	0.59
Q9DAW6_	Prpf4	U4/U6 sma	R.NILSVVGTDALK#.K	42.64	21.85	1.95	0.51
Q9DAW6_	Prpf4	U4/U6 sma	R.QINVSTDDSEVK#.A	67.04	33.56	2.00	0.50
Q9DAW6_	Prpf4	U4/U6 sma	K.SKEEYQQTWYHEGPNSLK.V	30.84	15.30	2.02	0.50
Q9DAW6_	Prpf4	U4/U6 sma	K.STVSLDQK#.D	71.24	18.20	3.91	0.26
Q9DAW6_	Prpf4	U4/U6 sma	K.TK#APDDLVAPVVK#.K	31.97	16.83	1.90	0.53
Q9DAW6_	Prpf4	U4/U6 sma	K.TKAPDDLVAPVVK.K	17.87	7.73	2.31	0.43
Q9DAW6_	Prpf4	U4/U6 sma	R.GHNTNVGAIVFHPK#.S	15.10	8.06	1.87	0.53
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.AEQMFGEMEVWNAISER.D	2.46	7.28	0.34	2.96
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.ALEK#EEEEEK#QK#.T	21.14	21.60	0.98	1.02
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.ELEDLEGYQNTIVAGGLITK#.S	43.23	29.79	1.45	0.69
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.ELEDLEGYQNTIVAGGLITK#.S	29.36	24.29	1.21	0.83
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.FLENHEK#.M	33.24	24.71	1.35	0.74
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.FTNM*LGQPGSTALDLFK#.F	49.69	32.27	1.54	0.65
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.FTNMLGQPGSTALDLFK#.F	25.51	19.81	1.29	0.78
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.FVKEPAFEDITLESER.K	32.66	104.79	0.31	3.21
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.FYVEDLK#.A	98.05	62.02	1.58	0.63
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.IIK#DILK#.D	17.29	14.05	1.23	0.81
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.KAEQMFGEMEVWNAISER.D	4.38	6.97	0.63	1.59
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.K#QAFNAYK#.V	19.88	21.05	0.94	1.06
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.LAFNSLLEK#.A	163.05	103.04	1.58	0.63
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.M*IINDPR.Y	7.64	29.89	0.26	3.91
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.QATPPIELDAVWEDIR.E	4.46	11.04	0.40	2.48
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.QSTWEKPDDLKTPAEQLLSK.C	13.53	13.61	0.99	1.01
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.RTLLEQLDDDQ.-	5.02	13.98	0.36	2.78
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.RVPSNASWEQAM*K.M	2.63	10.19	0.26	3.87
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.SDSGKPYYYNSQTK.E	44.68	34.74	1.29	0.78
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.SNLHAM*IK#.A	22.54	11.37	1.98	0.50
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.STTLDAGNIK#.L	164.88	121.10	1.36	0.73
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.TLLEQLDDDQ.-	82.06	82.06	1.00	1.00
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.TPAEQLLSK#.C	20.71	15.89	1.30	0.77
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.TYYYNTETK#.Q	70.94	38.76	1.83	0.55
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.VPSNASWEQAM*K#.M	20.37	12.37	1.65	0.61
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.VPSNASWEQAMK#.M	14.74	10.52	1.40	0.71
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.VQTEKEEKEEAR.S	1.18	1.62	0.73	1.37
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.ALEK#EEEEEK#QK#.T	3.70	3.37	1.10	0.91
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.ELEDLEGYQNTIVAGGLITK#.S	9.13	5.42	1.69	0.59
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.FTNM*LGQPGSTALDLFK#.F	14.20	9.36	1.52	0.66
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.FVKEPAFEDITLESER.K	9.05	22.36	0.40	2.47
Q9R1C7_P	Prpf40a	Pre-mRNA-	K.LAFNSLLEK#.A	41.91	29.31	1.43	0.70
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.STTLDAGNIK#.L	34.11	24.48	1.39	0.72
Q9R1C7_P	Prpf40a	Pre-mRNA-	R.TLLEQLDDDQ.-	14.85	14.85	1.00	1.00
Q61136_P	Prpf4b	Serine/thre	R.DNWTDAEGYYR.V	3.86	8.53	0.45	2.21
Q61136_P	Prpf4b	Serine/thre	R.ENVDTFEASVK#.A	12.74	8.26	1.54	0.65
Q61136_P	Prpf4b	Serine/thre	K.MPNK#M*IR@.K	10.03	1.46	6.89	0.15
Q61136_P	Prpf4b	Serine/thre	R.YNVYGYTGQGVFSNVVR.A	3.04	7.86	0.39	2.59
Q61136_P	Prpf4b	Serine/thre	K.AELDNELM*EGK.V	9.78	10.62	0.92	1.09
Q61136_P	Prpf4b	Serine/thre	R.ANQEVAVK#.I	19.06	7.80	2.44	0.41
Q61136_P	Prpf4b	Serine/thre	R.ENVDTFEASVK#.A	12.23	9.07	1.35	0.74
Q61136_P	Prpf4b	Serine/thre	R.YNVYGYTGQGVFSNVVR.A	5.46	9.06	0.60	1.66
Q91YR7_P	Prpf6	Pre-mRNA-	R.AAELETDIR.A	11.84	35.31	0.34	2.98
Q91YR7_P	Prpf6	Pre-mRNA-	K.AAVELEEPEDAR.I	15.13	34.74	0.44	2.30
Q91YR7_P	Prpf6	Pre-mRNA-	K.AEVLWLM*GAK#.S	10.45	3.33	3.13	0.32
Q91YR7_P	Prpf6	Pre-mRNA-	K.AEVLWLMGAK#.S	20.34	6.46	3.15	0.32
Q91YR7_P	Prpf6	Pre-mRNA-	K.FELQHGTEEQQEEVR.K	12.92	28.28	0.46	2.19
Q91YR7_P	Prpf6	Pre-mRNA-	K.GQIEEQGELM*EK#.A	25.40	15.11	1.68	0.59
Q91YR7_P	Prpf6	Pre-mRNA-	R.HIWITAAK#.L	36.12	22.20	1.63	0.61
Q91YR7_P	Prpf6	Pre-mRNA-	R.HYEDFPK#.L	22.78	11.72	1.94	0.51
Q91YR7_P	Prpf6	Pre-mRNA-	K.IDSDLGDAWAFFYK#.F	31.67	19.76	1.60	0.62
Q91YR7_P	Prpf6	Pre-mRNA-	K.LEEANGNTQM*VEK#.I	8.56	2.93	2.92	0.34
Q91YR7_P	Prpf6	Pre-mRNA-	K.LESENNEYER.A	9.46	21.27	0.44	2.25
Q91YR7_P	Prpf6	Pre-mRNA-	R.LSQVSDSVSGQTVVDPK#.G	21.96	8.40	2.61	0.38
Q91YR7_P	Prpf6	Pre-mRNA-	K.NPGLWLESVR.L	8.24	21.56	0.38	2.62
Q91YR7_P	Prpf6	Pre-mRNA-	K.WLAGDVPAAR.S	8.42	30.78	0.27	3.66
Q91YR7_P	Prpf6	Pre-mRNA-	K.AEVLWLMGAK#.S	13.57	6.80	2.00	0.50
Q91YR7_P	Prpf6	Pre-mRNA-	K.GQIEEQGELM*EK#.A	31.37	17.26	1.82	0.55
Q91YR7_P	Prpf6	Pre-mRNA-	K.GQIEEQGELMEK#.A	12.59	4.24	2.97	0.34
Q91YR7_P	Prpf6	Pre-mRNA-	R.HIWITAAK#.L	30.21	11.32	2.67	0.37
Q91YR7_P	Prpf6	Pre-mRNA-	K.IDSDLGDAWAFFYK#.F	29.24	14.30	2.04	0.49
Q91YR7_P	Prpf6	Pre-mRNA-	K.IQQQFSDLK#.R	16.73	8.86	1.89	0.53
Q91YR7_P	Prpf6	Pre-mRNA-	K.LEEANGNTQM*VEK#.I	11.13	5.56	2.00	0.50
Q91YR7_P	Prpf6	Pre-mRNA-	K.LESENNEYER.A	7.93	19.06	0.42	2.40
Q91YR7_P	Prpf6	Pre-mRNA-	R.LSQVSDSVSGQTVVDPK#.G	33.09	16.06	2.06	0.49
Q99PV0_P	Prpf8	Pre-mRNA-	R.ALDIPLVK#.N	73.91	47.17	1.57	0.64
Q99PV0_P	Prpf8	Pre-mRNA-	K.ALNM*AIPGGPK.F	66.05	41.20	1.60	0.62
Q99PV0_P	Prpf8	Pre-mRNA-	K.ANIPWK#.V	54.96	28.40	1.94	0.52
Q99PV0_P	Prpf8	Pre-mRNA-	K.ANPALYVLR.E	26.65	53.97	0.49	2.03
Q99PV0_P	Prpf8	Pre-mRNA-	R.AQIAGYLYGVSPPDNPQVK#.E	26.69	15.65	1.71	0.59
Q99PV0_P	Prpf8	Pre-mRNA-	R.AQIAGYLYGVSPPDNPQVK#.E	35.93	18.86	1.91	0.52
Q99PV0_P	Prpf8	Pre-mRNA-	R.ASEM*AGPPQM*PNDFLSFQDIATEAAHPIR.L	12.52	33.86	0.37	2.70
Q99PV0_P	Prpf8	Pre-mRNA-	K.ASGFEESM*K#.W	26.09	16.94	1.54	0.65
Q99PV0_P	Prpf8	Pre-mRNA-	R.AVFWDIK#.N	67.26	33.59	2.00	0.50
Q99PV0_P	Prpf8	Pre-mRNA-	R.DIILGM*EISAPSQQR.Q	4.66	14.55	0.32	3.12
Q99PV0_P	Prpf8	Pre-mRNA-	R.DINLQDEDWNEFNDINK#.I	30.99	21.92	1.41	0.71
Q99PV0_P	Prpf8	Pre-mRNA-	R.DINLQDEDWNEFNDINK#.I	14.97	9.53	1.57	0.64
Q99PV0_P	Prpf8	Pre-mRNA-	K.DM*NHTNSYGIIR.G	9.15	18.91	0.48	2.07
Q99PV0_P	Prpf8	Pre-mRNA-	K.DVM*DSTTTQK#.Y	12.05	8.78	1.37	0.73
Q99PV0_P	Prpf8	Pre-mRNA-	K.ELGGLGM*LSM*GHVLIPQSDLR.W	13.96	33.69	0.41	2.41
Q99PV0_P	Prpf8	Pre-mRNA-	K.EQSQLTATQTR.T	27.64	74.60	0.37	2.70
Q99PV0_P	Prpf8	Pre-mRNA-	K.ETGYTYILPK#.N	55.18	32.71	1.69	0.59
Q99PV0_P	Prpf8	Pre-mRNA-	K.EVGIEFM*DLYSHLVPVYDVEPLEK#.I	67.17	44.06	1.52	0.66
Q99PV0_P	Prpf8	Pre-mRNA-	K.FGDLILK#.A	102.96	57.94	1.78	0.56
Q99PV0_P	Prpf8	Pre-mRNA-	K.FGFVDAQK#.E	15.63	7.43	2.10	0.48
Q99PV0_P	Prpf8	Pre-mRNA-	R.FNTGPVGK#.G	134.63	81.16	1.66	0.60
Q99PV0_P	Prpf8	Pre-mRNA-	R.FPPVVFYTPK#.E	37.86	24.02	1.58	0.63
Q99PV0_P	Prpf8	Pre-mRNA-	R.FSPIPFPPLSYK#.H	63.61	44.03	1.44	0.69

Q99PV0_P	Prpf8	Pre-mRNA-	R.FTLWWSPTINR.A	6.42	15.12	0.42	2.35
Q99PV0_P	Prpf8	Pre-mRNA-	R.GPGNPVPGPLAPLPDYM*SEEK.L	7.09	5.42	1.31	0.76
Q99PV0_P	Prpf8	Pre-mRNA-	R.GPGNPVPGPLAPLPDYMSEEK#.L	4.41	3.62	1.22	0.82
Q99PV0_P	Prpf8	Pre-mRNA-	R.GPGNPVPGPLAPLPDYM*SEEK#LQEK#.A	28.54	20.20	1.41	0.71
Q99PV0_P	Prpf8	Pre-mRNA-	R.GPGNPVPGPLAPLPDYMSEEK#LQEK#.A	15.67	20.15	0.78	1.29
Q99PV0_P	Prpf8	Pre-mRNA-	K.GTYFPTWEGLFWEK#.A	32.20	18.92	1.70	0.59
Q99PV0_P	Prpf8	Pre-mRNA-	R.HDPNM*KYELQLANPK.E	44.83	32.57	1.38	0.73
Q99PV0_P	Prpf8	Pre-mRNA-	K.HGDEIITSTTSNYETQTFSSK#.T	96.13	53.10	1.81	0.55
Q99PV0_P	Prpf8	Pre-mRNA-	K.IDLTLLNR.L	29.75	79.08	0.38	2.66
Q99PV0_P	Prpf8	Pre-mRNA-	K.IIHTSVWAGQK#.R	51.23	32.53	1.57	0.63
Q99PV0_P	Prpf8	Pre-mRNA-	K.IM*ADNPSWDGEK#.T	24.18	19.88	1.22	0.82
Q99PV0_P	Prpf8	Pre-mRNA-	K.IMADNPSWDGEK#.T	9.79	4.68	2.09	0.48
Q99PV0_P	Prpf8	Pre-mRNA-	K.ISLIQIFR.A	19.82	50.83	0.39	2.56
Q99PV0_P	Prpf8	Pre-mRNA-	K.ITDAYLDQYLWYEADK#.R	7.95	5.35	1.49	0.67
Q99PV0_P	Prpf8	Pre-mRNA-	R.K#GM*LDPLEVHLLDFPNIVIK#.G	26.06	12.75	2.04	0.49
Q99PV0_P	Prpf8	Pre-mRNA-	R.K#WQQLQAK#.R	43.77	27.09	1.62	0.62
Q99PV0_P	Prpf8	Pre-mRNA-	R.LIVDHNIADYM*TAK#.N	105.45	71.89	1.47	0.68
Q99PV0_P	Prpf8	Pre-mRNA-	R.LIVDHNIADYMTAK.N	8.20	5.96	1.37	0.73
Q99PV0_P	Prpf8	Pre-mRNA-	R.LKEAYSVK.S	39.55	18.72	2.11	0.47
Q99PV0_P	Prpf8	Pre-mRNA-	K.LLENM*PM*PWEQIR.D	3.58	8.98	0.40	2.51
Q99PV0_P	Prpf8	Pre-mRNA-	K.LLILALER.L	21.00	61.66	0.34	2.94
Q99PV0_P	Prpf8	Pre-mRNA-	R.LNQSQREELGLIEQAYDNPHEALSR.I	4.62	15.32	0.30	3.32
Q99PV0_P	Prpf8	Pre-mRNA-	R.LTLEDLEDSWDR.G	10.00	24.03	0.42	2.40
Q99PV0_P	Prpf8	Pre-mRNA-	K.LTPSGYEWGR.Q	18.22	48.09	0.38	2.64
Q99PV0_P	Prpf8	Pre-mRNA-	K.LWNLNNYR.T	10.03	29.85	0.34	2.98
Q99PV0_P	Prpf8	Pre-mRNA-	K.NNVNVASLTQSEIR.D	8.91	24.72	0.36	2.77
Q99PV0_P	Prpf8	Pre-mRNA-	K.NNVVINYK#.D	79.08	44.97	1.76	0.57
Q99PV0_P	Prpf8	Pre-mRNA-	R.QILM*ASGSTTFTK#.I	34.18	25.45	1.34	0.74
Q99PV0_P	Prpf8	Pre-mRNA-	R.QQIAEIEK#.Q	71.05	38.52	1.84	0.54
Q99PV0_P	Prpf8	Pre-mRNA-	R.RALDIPLVK.N	3.97	14.31	0.28	3.60
Q99PV0_P	Prpf8	Pre-mRNA-	R.RLTLEDLEDSWDR.G	1.78	11.75	0.15	6.61
Q99PV0_P	Prpf8	Pre-mRNA-	R.SGM*SHEEDQLIPNLYR.Y	13.47	39.94	0.34	2.97
Q99PV0_P	Prpf8	Pre-mRNA-	R.SLPVEEQPK#.Q	84.29	57.19	1.47	0.68
Q99PV0_P	Prpf8	Pre-mRNA-	R.SVTTVQWENSFVSVYSK#.D	33.44	20.17	1.66	0.60
Q99PV0_P	Prpf8	Pre-mRNA-	K.TAEEVAALIR.S	27.81	73.66	0.38	2.65
Q99PV0_P	Prpf8	Pre-mRNA-	R.TGQLFLK#.I	60.15	35.59	1.69	0.59
Q99PV0_P	Prpf8	Pre-mRNA-	K.TISSYTAFSR.L	16.82	53.26	0.32	3.17
Q99PV0_P	Prpf8	Pre-mRNA-	R.TNHIYVSSDDIK#.E	55.14	42.20	1.31	0.77
Q99PV0_P	Prpf8	Pre-mRNA-	R.TNHIYVSSDDIK#ETGYTYILPK#.N	20.08	7.28	2.76	0.36
Q99PV0_P	Prpf8	Pre-mRNA-	R.TNHIYVSSDDIKETGYTYILPK.N	5.36	2.26	2.37	0.42
Q99PV0_P	Prpf8	Pre-mRNA-	R.TSYEEFTHK#.D	47.24	21.50	2.20	0.46
Q99PV0_P	Prpf8	Pre-mRNA-	R.TVNK#HGDEIITSTTSNYETQTFSSK#.T	15.32	10.06	1.52	0.66
Q99PV0_P	Prpf8	Pre-mRNA-	R.TVNK#HGDEIITSTTSNYETQTFSSK#.T	7.02	3.67	1.91	0.52
Q99PV0_P	Prpf8	Pre-mRNA-	K.VPGLPTPIENM*ILR.Y	8.99	26.95	0.33	3.00
Q99PV0_P	Prpf8	Pre-mRNA-	K.VPGLPTPIENMILR.Y	8.36	28.75	0.29	3.44
Q99PV0_P	Prpf8	Pre-mRNA-	R.VQM*LLSDR.F	17.27	19.22	0.90	1.11
Q99PV0_P	Prpf8	Pre-mRNA-	R.VWAEYALK#.R	55.61	42.84	1.30	0.77
Q99PV0_P	Prpf8	Pre-mRNA-	R.VYLGALK#.Y	91.72	48.60	1.89	0.53
Q99PV0_P	Prpf8	Pre-mRNA-	R.WLGNLLAR.Q	9.42	28.22	0.33	3.00
Q99PV0_P	Prpf8	Pre-mRNA-	R.WQFTLPM*M*STLYR.L	6.91	13.01	0.53	1.88
Q99PV0_P	Prpf8	Pre-mRNA-	R.YIQPWESEFIDSQR.V	10.41	30.06	0.35	2.89
Q99PV0_P	Prpf8	Pre-mRNA-	R.YLTEHPDPNNENIVGYNNK#.K	38.19	22.75	1.68	0.60
Q99PV0_P	Prpf8	Pre-mRNA-	R.YLTEHPDPNNENIVGYNNKK.C	16.69	8.67	1.92	0.52
E9PYL2_E9	Prr12	Protein Prr	K.GLGGSGGAGGAPGTPYELAK.E	14.97	8.73	1.72	0.58
E9PYL2_E9	Prr12	Protein Prr	R.IRPLEGPAM*AGPASITTDGAK.K	1.74	8.65	0.20	4.97
E9PYL2_E9	Prr12	Protein Prr	R.LDEELK#.R	19.97	6.64	3.01	0.33
E9Q7C4_E9	Prr14l	Protein Prr	R.IDTEIYK#.H	23.76	13.78	1.72	0.58
Q3UPH1_P	Prrc1	Protein PR	R.GQDDAPAGGIWGFIK#.G	13.10	3.99	3.28	0.30
Q3UPH1_P	Prrc1	Protein PR	K.GVAGNPMVK#.S	6.46	5.18	1.25	0.80
Q7TPM1_P	Prrc2b	Protein PR	R.LLSFSPEEFPTLK.A	5.27	9.56	0.55	1.81
Q3TLH4_P	Prrc2c	Protein PR	K.AQSGLAFQQTSNPQPIPILYDHQLGQASGLGSSQLIDTHLLQAR.A	4.09	4.68	0.88	1.14
Q3TLH4_P	Prrc2c	Protein PR	K.LPDLSLVENK#.E	26.02	16.68	1.56	0.64
Q3TLH4_P	Prrc2c	Protein PR	K.M*EDTLVNNVPLPNTLPLPK#.R	4.64	3.41	1.36	0.73
Q3TLH4_P	Prrc2c	Protein PR	K.SSSQIPAQPPVTK#.S	11.81	4.30	2.75	0.36
Q3TLH4_P	Prrc2c	Protein PR	K.LPDLSLVENK#.E	20.49	11.86	1.73	0.58
Q3TLH4_P	Prrc2c	Protein PR	R.LPSAQTSNGTDFVAAGK#.S	8.45	4.68	1.81	0.55
Q3TLH4_P	Prrc2c	Protein PR	R.SQPAFM*QSSLSQPSVVLSGTAIHNFPAVQHQELAK#.A	9.98	5.64	1.77	0.57
Q3TLH4_P	Prrc2c	Protein PR	K.VAAPAVLNDISK#.K	16.04	15.98	1.00	1.00
Q99K85_S	Psat1	Phosphose	R.ASLYNAVTTEDVEK#.L	173.46	27.43	6.32	0.16
Q99K85_S	Psat1	Phosphose	K.AVELNM*ISLK#.G	57.68	12.70	4.54	0.22
Q99K85_S	Psat1	Phosphose	K.AVELNMISLK#.G	92.19	13.28	6.94	0.14
Q99K85_S	Psat1	Phosphose	R.DDLLGFSLR.E	17.03	8.73	1.95	0.51
Q99K85_S	Psat1	Phosphose	K.FGTVNIVHPK#.L	88.23	65.91	1.34	0.75
Q99K85_S	Psat1	Phosphose	K.FGVIFAGAQK#.N	357.96	51.36	6.97	0.14
Q99K85_S	Psat1	Phosphose	K.IIGNTENLVR.E	80.88	56.10	1.44	0.69
Q99K85_S	Psat1	Phosphose	K.LPHSVLLEIQK#.Q	113.67	23.37	4.86	0.21
Q99K85_S	Psat1	Phosphose	K.NFLEMHQL.-	50.38	50.38	1.00	1.00
Q99K85_S	Psat1	Phosphose	K.NVGSAGVTVVIVR.D	16.33	11.85	1.38	0.73
Q99K85_S	Psat1	Phosphose	K.QVVNFGPGPAK#.L	82.73	14.57	5.68	0.18
Q99K85_S	Psat1	Phosphose	R.SADYVVTGAWSAK#.A	127.22	29.12	4.37	0.23
Q99K85_S	Psat1	Phosphose	R.ASLYNAVTTEDVEK#.L	19.97	8.68	2.30	0.43
Q99K85_S	Psat1	Phosphose	R.ASLYNAVTTEDVEK#.L	57.27	8.95	6.40	0.16
Q99K85_S	Psat1	Phosphose	K.AVELNMISLK#.G	29.51	3.34	8.83	0.11
Q99K85_S	Psat1	Phosphose	R.ELLAVPNNYK#.V	38.65	30.53	1.27	0.79
Q99K85_S	Psat1	Phosphose	K.FGTVNIVHPK#.L	73.63	22.95	3.21	0.31
Q99K85_S	Psat1	Phosphose	K.FGVIFAGAQK#.N	80.06	9.51	8.42	0.12
Q99K85_S	Psat1	Phosphose	K.LPHSVLLEIQK#.Q	79.86	13.59	5.88	0.17
Q99K85_S	Psat1	Phosphose	K.QVVNFGPGPAK#.L	55.45	57.25	0.97	1.03
Q99K85_S	Psat1	Phosphose	R.SADYVVTGAWSAK#.A	30.17	5.06	5.96	0.17
Q99K85_S	Psat1	Phosphose	R.ASLYNAVTTEDVEK#.L	82.84	10.55	7.86	0.13
Q99K85_S	Psat1	Phosphose	K.AVELNM*ISLK#.G	28.99	4.28	6.77	0.15
Q99K85_S	Psat1	Phosphose	K.AVELNMISLK#.G	24.31	3.43	7.09	0.14
Q99K85_S	Psat1	Phosphose	R.ELLAVPNNYK#.V	51.02	27.12	1.88	0.53
Q99K85_S	Psat1	Phosphose	K.FGTVNIVHPK#.L	58.90	26.78	2.20	0.45
Q99K85_S	Psat1	Phosphose	K.FGVIFAGAQK#.N	110.33	14.58	7.57	0.13
Q99K85_S	Psat1	Phosphose	K.K#FGTVNIVHPK#.L	14.24	5.86	2.43	0.41
Q99K85_S	Psat1	Phosphose	K.LPHSVLLEIQK#.Q	65.62	11.35	5.78	0.17
Q99K85_S	Psat1	Phosphose	K.QVVNFGPGPAK#.L	63.77	10.52	6.06	0.16
Q99K85_S	Psat1	Phosphose	R.SADYVVTGAWSAK#.A	44.69	6.52	6.85	0.15
Q99JF8_PS	Psip1	PC4 and SF	K.GFNEGLWEIDNNPK#.V	5.67	1.05	5.42	0.18
Q9R1P4_P	Psma1	Proteasom	R.ETLPAEQDLTTK#.N	13.04	6.73	1.94	0.52
P49722_P	Psma2	Proteasom	R.GYSFSLTTFSPSGK#.L	16.39	11.53	1.42	0.70
P49722_P	Psma2	Proteasom	R.KLAQQYYLVYQEPIPTAQLVQR.V	2.66	6.73	0.40	2.52

P49722_PS	Psma2	Proteasom	K.LAQQYYLVYQEPIPTAQLVQR.V	1.54	3.05	0.50	1.98
P49722_PS	Psma2	Proteasom	K.LVQIEYALAAVAGGAPSVGIK#.A	3.31	3.67	0.90	1.11
P49722_PS	Psma2	Proteasom	R.YNEDLELEDAIHTAILTLK#.E	17.28	13.27	1.30	0.77
Q9R1P0_PS	Psma4	Proteasom	K.LLDEVFFSEK#.I	20.95	6.95	3.01	0.33
Q9R1P0_PS	Psma4	Proteasom	K.SALALAVK#.V	11.70	3.73	3.14	0.32
Q9Z2U1_PS	Psma5	Proteasom	R.AIGSASEGAQSSLQEVYHK#.S	26.85	15.02	1.79	0.56
Q9Z2U1_PS	Psma5	Proteasom	R.ITSPLM*EPSSIEK#.I	26.05	14.58	1.79	0.56
Q9Z2U1_PS	Psma5	Proteasom	R.LFQVEYAIEAIK#.L	58.70	26.83	2.19	0.46
Q9Z2U1_PS	Psma5	Proteasom	K.SSLIILK#.Q	18.93	11.04	1.71	0.58
Q9QUM9_P	Psma6	Proteasom	R.LYQVEYAFK#.A	27.65	9.85	2.81	0.36
Q9Z2U0_PS	Psma7	Proteasom	K.ALLEVVQSGGK#.N	13.64	2.09	6.53	0.15
Q9Z2U0_PS	Psma7	Proteasom	R.AITVFSPDGHLFQVEYAQEAVK#.K	15.47	3.87	4.00	0.25
Q9Z2U0_PS	Psma7	Proteasom	K.ALLEVVQSGGK#.N	31.51	10.88	2.90	0.35
Q9Z2U0_PS	Psma7	Proteasom	R.GK#DIVVLGVEK#.K	7.64	3.47	2.20	0.45
Q9Z2U0_PS	Psma7	Proteasom	K.LTVEDPVTVEYITR.F	7.51	6.74	1.11	0.90
Q9Z2U0_PS	Psma7	Proteasom	K.NYTDDAIETDDLTIK#.L	27.01	11.70	2.31	0.43
Q9R1P3_PS	Psmb2	Proteasom	R.FILNLPTFSVR.V	2.76	9.19	0.30	3.33
Q9R1P1_PS	Psmb3	Proteasom	R.FGIQAQM*VTTDFQK#.I	4.92	1.09	4.49	0.22
Q9R1P1_PS	Psmb3	Proteasom	R.LYIGLAGLATDVQTVAQR.L	3.67	7.04	0.52	1.92
P28063_PS	Psmb8	Proteasom	K.VESSDVSDLLYK#.Y	4.21	3.05	1.38	0.73
P62192_P	Psmc1	26S protea	K.APQETYADIGGLDNQIQEIK#.E	33.06	5.01	6.60	0.15
P62192_P	Psmc1	26S protea	K.AVANQTSATFLR.V	46.05	62.56	0.74	1.36
P62192_P	Psmc1	26S protea	K.DDLSGADIK#.A	63.87	14.73	4.34	0.23
P62192_P	Psmc1	26S protea	K.ESVELPLTHPEYYEEMGIK#PPK#.G	9.07	1.91	4.76	0.21
P62192_P	Psmc1	26S protea	K.IEFPLPDEK#.T	28.26	11.26	2.51	0.40
P62192_P	Psmc1	26S protea	R.IKDYLLMEEEFIR.N	14.17	7.48	1.89	0.53
P62192_P	Psmc1	26S protea	K.K#QEGTPEGLYL.-	78.85	14.54	5.42	0.18
P62192_P	Psmc1	26S protea	R.M*TLADDVTLDDLIM*AK#.D	33.09	4.72	7.02	0.14
P62192_P	Psmc1	26S protea	R.MTLADDVTLDDLIM*AK#.D	16.85	3.53	4.77	0.21
P62192_P	Psmc1	26S protea	R.NQEQM*K#PLEEK#.Q	14.13	2.26	6.27	0.16
P62192_P	Psmc1	26S protea	K.SK#ENVLYK#.K	98.25	10.34	9.51	0.11
P62192_P	Psmc1	26S protea	R.TM*LELLNQLDGFDSR.G	10.61	6.95	1.53	0.66
P62192_P	Psmc1	26S protea	R.TMLELLNQLDGFDSR.G	19.22	15.96	1.20	0.83
P62192_P	Psmc1	26S protea	R.VAEEHAPSIVFIDEIDAIGTK#.R	134.60	24.73	5.44	0.18
P62192_P	Psmc1	26S protea	K.VHAVIGVLM*DDTDPLVTVM*K#.V	21.36	2.72	7.85	0.13
P62192_P	Psmc1	26S protea	K.VHAVIGVLM*DDTDPLVTVMK#.V	27.30	6.82	4.00	0.25
P62192_P	Psmc1	26S protea	K.VHAVIGVLMDDTDPLVTVMK#.V	45.60	6.07	7.51	0.13
P62192_P	Psmc1	26S protea	K.VTNEDFK#K#.S	42.02	5.28	7.96	0.13
P62192_P	Psmc1	26S protea	R.VVGSELIQK#.Y	441.32	64.17	6.88	0.15
P62192_P	Psmc1	26S protea	K.APQETYADIGGLDNQIQEIK#.E	11.46	3.48	3.29	0.30
P62192_P	Psmc1	26S protea	K.GVILYGPPGTGK#.T	22.12	5.43	4.07	0.25
P62192_P	Psmc1	26S protea	R.VAEEHAPSIVFIDEIDAIGTK#.R	28.07	7.09	3.96	0.25
P46471_P	Psmc2	26S protea	R.ALDEGDIALLK#.T	204.51	32.91	6.21	0.16
P46471_P	Psmc2	26S protea	K.DFLEAVNK#.V	54.12	3.05	17.72	0.06
P46471_P	Psmc2	26S protea	K.ESDTGLAPPALWDLAADK#.Q	102.76	22.64	4.54	0.22
P46471_P	Psmc2	26S protea	R.FDDGAGGDNEVQR.T	46.88	25.76	1.82	0.55
P46471_P	Psmc2	26S protea	R.FVNLGIEPPK#.G	95.88	15.23	6.30	0.16
P46471_P	Psmc2	26S protea	R.FVNLGIEPPK#GVLLFGPPGTGK#.T	20.73	2.36	8.78	0.11
P46471_P	Psmc2	26S protea	K.FVVDLSDQVAPTDIEEGMR.V	3.68	5.13	0.72	1.40
P46471_P	Psmc2	26S protea	K.GVLLFGPPGTGK#.T	138.97	18.93	7.34	0.14
P46471_P	Psmc2	26S protea	K.IATEK#DFLEAVNK#.V	41.21	4.86	8.48	0.12
P46471_P	Psmc2	26S protea	K.IINADSEDPK#YIINVK#.Q	9.04	2.47	3.66	0.27
P46471_P	Psmc2	26S protea	K.INELTGIK#.E	23.43	5.18	4.52	0.22
P46471_P	Psmc2	26S protea	R.K#IATEK#DFLEAVNK#.V	57.07	8.74	6.53	0.15
P46471_P	Psmc2	26S protea	K.K#INELTGIK#.E	92.40	13.34	6.93	0.14
P46471_P	Psmc2	26S protea	K.YQIHIPLPPK#.I	21.46	5.80	3.70	0.27
P46471_P	Psmc2	26S protea	R.ALDEGDIALLK#.T	14.05	4.33	3.25	0.31
P46471_P	Psmc2	26S protea	R.FVNLGIEPPK#GVLLFGPPGTGK#.T	7.68	2.42	3.18	0.31
P46471_P	Psmc2	26S protea	R.TM*LELINQLDGFDPR.G	2.20	5.82	0.38	2.65
P46471_P	Psmc2	26S protea	R.ALDEGDIALLK#.T	18.99	3.67	5.17	0.19
P46471_P	Psmc2	26S protea	K.GVLLFGPPGTGK#.T	20.00	3.83	5.22	0.19
O88685_P	Psmc3	26S protea	K.AM*EVDERPTEQYSDIGGLDK.Q	34.73	21.77	1.60	0.63
O88685_P	Psmc3	26S protea	K.APSIIFIDELDAIGTK#.R	61.92	9.72	6.37	0.16
O88685_P	Psmc3	26S protea	K.EK#APSIIFIDELDAIGTK#.R	191.93	27.56	6.96	0.14
O88685_P	Psmc3	26S protea	K.EK#FENLGIQPPK#.G	24.58	3.95	6.22	0.16
O88685_P	Psmc3	26S protea	R.GATELTHEDYM*EGILEVQAK#.K	48.86	6.24	7.82	0.13
O88685_P	Psmc3	26S protea	R.GATELTHEDYMEGILEVQAK#.K	4.99	2.40	2.08	0.48
O88685_P	Psmc3	26S protea	K.GVLM*YGPPGTGK#.T	78.40	14.73	5.32	0.19
O88685_P	Psmc3	26S protea	K.GVLMYGPPGTGK#.T	64.02	11.11	5.76	0.17
O88685_P	Psmc3	26S protea	R.KM*NVSPDVNYEELAR.C	22.30	18.49	1.21	0.83
O88685_P	Psmc3	26S protea	K.LAGPQLVQM*FIGDGAK#.L	42.56	8.68	4.90	0.20
O88685_P	Psmc3	26S protea	K.LAGPQLVQMFIGDGAK#.L	63.80	10.42	6.13	0.16
O88685_P	Psmc3	26S protea	R.LLDSEIK#.I	236.52	32.01	7.39	0.14
O88685_P	Psmc3	26S protea	K.M*ATVWDEAEQDGIGEEVLK#.M	26.53	3.27	8.11	0.12
O88685_P	Psmc3	26S protea	K.MATVWDEAEQDGIGEEVLK#.M	12.18	2.34	5.21	0.19
O88685_P	Psmc3	26S protea	K.M*STEEIVQR.T	22.57	12.29	1.84	0.54
O88685_P	Psmc3	26S protea	K.MSTEEIVQR.T	20.57	12.69	1.62	0.62
O88685_P	Psmc3	26S protea	K.QIQELVEAIVLPM*NHK#.E	27.77	5.56	5.00	0.20
O88685_P	Psmc3	26S protea	K.QIQELVEAIVLPMNHK#.E	12.98	2.64	4.92	0.20
O88685_P	Psmc3	26S protea	R.QTYFLPVIGLVDAEK#.L	132.50	18.42	7.19	0.14
O88685_P	Psmc3	26S protea	R.TM*LELLNQLDGFQPNTQVK#.V	50.05	8.06	6.21	0.16
O88685_P	Psmc3	26S protea	R.TMLELLNQLDGFQPNTQVK#.V	61.56	5.95	10.35	0.10
O88685_P	Psmc3	26S protea	R.VDILDPALLR.S	49.95	41.94	1.19	0.84
O88685_P	Psmc3	26S protea	R.VTHELQAM*K#.D	19.27	2.89	6.68	0.15
O88685_P	Psmc3	26S protea	R.VTHELQAMK#.D	18.19	2.86	6.36	0.16
O88685_P	Psmc3	26S protea	R.VTHELQAMK#DK#.I	28.60	6.03	4.74	0.21
O88685_P	Psmc3	26S protea	R.VTHELQAMK#DK#.I	5.30	1.37	3.87	0.26
O88685_P	Psmc3	26S protea	K.EK#APSIIFIDELDAIGTK#.R	16.81	2.80	6.00	0.17
P54775_P	Psmc4	26S protea	K.DEQEHEFYK#.-	28.04	6.10	4.60	0.22
P54775_P	Psmc4	26S protea	K.EFLHAQEEVK#.R	13.29	4.29	3.10	0.32
P54775_P	Psmc4	26S protea	R.ILLELLNQM*DGFDQNVNVK#.V	70.16	10.38	6.76	0.15
P54775_P	Psmc4	26S protea	R.ILLELLNQM*DGFDQNVNVK#.V	17.42	5.25	3.32	0.30
P54775_P	Psmc4	26S protea	R.ILLELLNQMDGFDQNVNVK#.V	65.33	6.19	10.56	0.09
P54775_P	Psmc4	26S protea	K.K#DEQEHEFYK#.-	177.17	34.68	5.11	0.20
P54775_P	Psmc4	26S protea	R.LIFSTITSK#.M	248.88	54.64	4.55	0.22
P54775_P	Psmc4	26S protea	K.M*NLSEEVDLEDYVARPDK.I	3.22	5.58	0.58	1.73
P54775_P	Psmc4	26S protea	R.VVGSEFVQK#.Y	137.78	29.26	4.71	0.21
P54775_P	Psmc4	26S protea	R.YIVLAK#.D	257.58	34.19	7.53	0.13
P54775_P	Psmc4	26S protea	K.LQQELEFLEVQEEYIK#DEQK#.N	15.09	3.94	3.83	0.26
P62196_P	Psmc5	26S protea	R.EHAPSIIFM*DEIDSIGSSR.L	12.36	11.36	1.09	0.92
P62196_P	Psmc5	26S protea	K.EVIELPVK#.H	16.69	1.77	9.41	0.11
P62196_P	Psmc5	26S protea	K.EVIELPVK#HPELFEALGIAQPK#.G	56.38	10.78	5.23	0.19
P62196_P	Psmc5	26S protea	K.FVVDVDK#.N	30.44	5.29	5.76	0.17

P62196_P	Psmc5	26S protea	K.HPELFEALGIAQPK#.G	20.70	4.78	4.33	0.23
P62196_P	Psmc5	26S protea	K.IAELM*PGASGAEVK#.G	68.01	13.99	4.86	0.21
P62196_P	Psmc5	26S protea	K.IAELMPGASGAEVK#.G	61.35	14.22	4.31	0.23
P62196_P	Psmc5	26S protea	K.IEELQLIVNDK#.S	112.31	30.02	3.74	0.27
P62196_P	Psmc5	26S protea	K.ILPNK#VDPLVSLMMVEK#.V	37.32	38.02	0.98	1.02
P62196_P	Psmc5	26S protea	R.LEGGSGGDSEVQR.T	37.34	36.34	1.03	0.97
P62196_P	Psmc5	26S protea	R.LLREELQLLQEQGSYVGEVVR.A	4.86	6.16	0.79	1.27
P62196_P	Psmc5	26S protea	R.TM*LELLNQLDGFEATK#.N	64.94	9.11	7.13	0.14
P62196_P	Psmc5	26S protea	R.TM*LELLNQLDGFEATK#.N	17.64	2.04	8.64	0.12
P62196_P	Psmc5	26S protea	R.TMLELLNQLDGFEATK#.N	85.24	17.75	4.80	0.21
P62196_P	Psmc5	26S protea	R.VHVTQEDFEM*AVAK#.V	27.04	5.97	4.53	0.22
P62196_P	Psmc5	26S protea	R.VHVTQEDFEMAVAK#.V	22.35	3.32	6.74	0.15
P62196_P	Psmc5	26S protea	K.VPDSTYEM*IGGLDK#.Q	98.12	16.95	5.79	0.17
P62196_P	Psmc5	26S protea	R.VSGSELVQK#.F	244.18	42.04	5.81	0.17
P62196_P	Psmc5	26S protea	K.EVIELPVK#HPELFEALGIAQPK#.G	5.47	1.30	4.21	0.24
P62196_P	Psmc5	26S protea	K.VPDSTYEM*IGGLDK#.Q	5.12	1.42	3.59	0.28
P62334_P	Psmc6	26S protea	R.ADHDFVVQEDFM*K#.A	76.34	15.72	4.86	0.21
P62334_P	Psmc6	26S protea	K.ALQSVGQIVGEVLK#.Q	174.07	35.39	4.92	0.20
P62334_P	Psmc6	26S protea	R.EVDPLVYNM*SHEDPGNVSYSEIGGLSEQIR.E	12.06	9.24	1.31	0.77
P62334_P	Psmc6	26S protea	R.EVDPLVYNMSHEDPGNVSYSEIGGLSEQIR.E	7.48	6.64	1.13	0.89
P62334_P	Psmc6	26S protea	K.HGEIDYEAIVK#.L	147.73	51.54	2.87	0.35
P62334_P	Psmc6	26S protea	K.IHAGPITK#.H	124.47	29.64	4.20	0.24
P62334_P	Psmc6	26S protea	K.LSDGFNGADLR.N	20.49	21.06	0.97	1.03
P62334_P	Psmc6	26S protea	R.VALDMTTLTIMR.Y	12.46	14.74	0.84	1.18
P62334_P	Psmc6	26S protea	R.VGIIPPK#.G	32.70	11.89	2.75	0.36
P62334_P	Psmc6	26S protea	K.VVSSSIVDK#.Y	207.90	39.39	5.28	0.19
P62334_P	Psmc6	26S protea	K.ALQSVGQIVGEVLK#.Q	24.59	2.64	9.31	0.11
P62334_P	Psmc6	26S protea	K.HGEIDYEAIVK#.L	25.28	12.02	2.10	0.48
P62334_P	Psmc6	26S protea	K.ALQSVGQIVGEVLK#.Q	11.95	10.06	1.19	0.84
Q3TXS7_PS	Psmd1	26S protea	K.DTSEDVEELVEPVAAHGPK#.I	115.00	20.44	5.63	0.18
Q3TXS7_PS	Psmd1	26S protea	K.EALQLM*ATYLPK#.D	49.13	13.02	3.77	0.26
Q3TXS7_PS	Psmd1	26S protea	K.EALQLMATYLPK#.D	37.87	5.40	7.01	0.14
Q3TXS7_PS	Psmd1	26S protea	K.IEEEEQEPEPPEPFEYIDD.-	30.54	30.54	1.00	1.00
Q3TXS7_PS	Psmd1	26S protea	R.LEGIVNK#.M	158.51	16.43	9.65	0.10
Q3TXS7_PS	Psmd1	26S protea	-.M*ITSAAGIISLLDEEEPQLK#.E	16.05	2.35	6.83	0.15
Q3TXS7_PS	Psmd1	26S protea	R.NNNTDLMILK#.N	19.63	21.48	0.91	1.09
Q3TXS7_PS	Psmd1	26S protea	R.QDVYDLLK#.T	61.45	11.98	5.13	0.19
Q3TXS7_PS	Psmd1	26S protea	K.TILESNDVPGM*LAYSLK#.L	13.40	2.27	5.91	0.17
Q3TXS7_PS	Psmd1	26S protea	K.TILESNDVPGMLAYSLK#.L	9.75	2.68	3.63	0.28
Q3TXS7_PS	Psmd1	26S protea	K.TNLYQDDAVTGEAAGLALGLVM*LGSK#.N	43.20	7.34	5.89	0.17
Q3TXS7_PS	Psmd1	26S protea	K.TPDASPEPK#.D	65.17	12.14	5.37	0.19
Q3TXS7_PS	Psmd1	26S protea	R.TVGTPIASVPGSTNTGTVPGSEK#DSDPM*ETEEK#.T	29.69	5.72	5.19	0.19
Q3TXS7_PS	Psmd1	26S protea	K.VINDK#HDDVM*AK#.F	15.21	4.06	3.74	0.27
Q3TXS7_PS	Psmd1	26S protea	K.VSTAVLSITAK#.A	130.53	20.99	6.22	0.16
Q3TXS7_PS	Psmd1	26S protea	R.AAVESLGFILFR.T	17.83	12.17	1.47	0.68
Q3TXS7_PS	Psmd1	26S protea	K.DTSEDVEELVEPVAAHGPK#.I	113.46	15.78	7.19	0.14
Q3TXS7_PS	Psmd1	26S protea	K.EALQLM*ATYLPK#.D	28.01	5.87	4.77	0.21
Q3TXS7_PS	Psmd1	26S protea	K.IEEEEQEPEPPEPFEYIDD.-	23.01	23.01	1.00	1.00
Q3TXS7_PS	Psmd1	26S protea	-.M*ITSAAGIISLLDEEEPQLK#.E	18.81	2.65	7.11	0.14
Q3TXS7_PS	Psmd1	26S protea	K.NAQAIEDM*VGYAQETQHEK#.I	67.98	7.02	9.68	0.10
Q3TXS7_PS	Psmd1	26S protea	K.NAQAIEDMVGYAQETQHEK#.I	33.49	4.27	7.85	0.13
Q3TXS7_PS	Psmd1	26S protea	R.NNNTDLM*ILK#.N	23.11	15.38	1.50	0.67
Q3TXS7_PS	Psmd1	26S protea	R.NNNTDLMILK#.N	9.96	3.16	3.15	0.32
Q3TXS7_PS	Psmd1	26S protea	R.QDVYDLLK#.T	30.08	6.52	4.62	0.22
Q3TXS7_PS	Psmd1	26S protea	K.TILESNDVPGM*LAYSLK#.L	12.34	1.67	7.40	0.14
Q3TXS7_PS	Psmd1	26S protea	K.TNLYQDDAVTGEAAGLALGLVM*LGSK#.N	38.29	6.01	6.38	0.16
Q3TXS7_PS	Psmd1	26S protea	K.TPDASPEPK#.D	75.19	13.52	5.56	0.18
Q3TXS7_PS	Psmd1	26S protea	K.VINDK#HDDVM*AK#.F	8.51	1.27	6.72	0.15
Q3TXS7_PS	Psmd1	26S protea	K.VSTAVLSITAK#.A	68.05	8.44	8.07	0.12
Q9Z2X2_PS	Psmd10	26S protea	K.FLVTQGASIYIENK#.E	9.67	2.95	3.28	0.30
Q9Z2X2_PS	Psmd10	26S protea	K.FLVTQGASIYIENK#EEK#.T	3.08	2.03	1.52	0.66
Q9Z2X2_PS	Psmd10	26S protea	K.GGLGLILK#.R	12.96	4.61	2.81	0.36
Q8BG32_P	Psmd11	26S protea	R.AELRDDPIISTHLAK.L	19.28	14.47	1.33	0.75
Q8BG32_P	Psmd11	26S protea	K.ALLVEVQLLESK#.T	21.52	4.16	5.17	0.19
Q8BG32_P	Psmd11	26S protea	R.DIQENDEEAVQVK#.E	122.30	12.86	9.51	0.11
Q8BG32_P	Psmd11	26S protea	K.EQSILELGSLLAK#.T	231.95	32.03	7.24	0.14
Q8BG32_P	Psmd11	26S protea	K.FHGILDQGEGVLIIFDEPPVDK#.T	37.86	10.35	3.66	0.27
Q8BG32_P	Psmd11	26S protea	K.IM*LNTPEDVQALVSGK#.L	60.34	9.63	6.27	0.16
Q8BG32_P	Psmd11	26S protea	R.K#LSQMILDK#K#.F	56.70	6.66	8.52	0.12
Q8BG32_P	Psmd11	26S protea	K.LQATLDM*QSGIIHAAEEK#.D	33.49	6.88	4.87	0.21
Q8BG32_P	Psmd11	26S protea	K.LQATLDMQSGIIHAAEEK#DWK#.T	24.13	3.48	6.94	0.14
Q8BG32_P	Psmd11	26S protea	R.LVSLYFDTK#.R	99.39	15.33	6.48	0.15
Q8BG32_P	Psmd11	26S protea	K.LYDNLLEQNLIR.V	33.25	26.36	1.26	0.79
Q8BG32_P	Psmd11	26S protea	R.SLADFEK#.A	80.02	19.27	4.15	0.24
Q8BG32_P	Psmd11	26S protea	K.TAYSYFYEAFEGYDSIDSPK#.A	21.51	4.08	5.27	0.19
Q8BG32_P	Psmd11	26S protea	K.TYEAALETIQNM*SK#.V	14.59	1.63	8.94	0.11
Q8BG32_P	Psmd11	26S protea	K.TYEAALETIQNMSK#.V	11.81	2.89	4.08	0.24
Q8BG32_P	Psmd11	26S protea	K.TYHALSNLPK#.A	91.82	13.68	6.71	0.15
Q8BG32_P	Psmd11	26S protea	K.VVDSLYSK#.A	115.07	14.31	8.04	0.12
Q8BG32_P	Psmd11	26S protea	K.YVRPFLNSISK.A	28.87	17.86	1.62	0.62
Q8BG32_P	Psmd11	26S protea	R.DIQENDEEAVQVK#.E	23.22	5.99	3.87	0.26
Q8BG32_P	Psmd11	26S protea	K.EQSILELGSLLAK#.T	42.56	5.00	8.52	0.12
Q8BG32_P	Psmd11	26S protea	K.FHGILDQGEGVLIIFDEPPVDK#.T	3.49	1.24	2.82	0.35
Q8BG32_P	Psmd11	26S protea	K.TAYSYFYEAFEGYDSIDSPK#.A	4.32	1.67	2.58	0.39
Q8BG32_P	Psmd11	26S protea	R.DIQENDEEAVQVK#.E	30.37	5.44	5.58	0.18
Q8BG32_P	Psmd11	26S protea	K.EQSILELGSLLAK#.T	54.09	11.19	4.83	0.21
Q8BG32_P	Psmd11	26S protea	K.IM*LNTPEDVQALVSGK#.L	15.64	2.16	7.25	0.14
Q8BG32_P	Psmd11	26S protea	K.LYDNLLEQNLIR.V	6.56	5.75	1.14	0.88
Q8BG32_P	Psmd11	26S protea	R.SLADFEK#.A	25.51	5.02	5.09	0.20
Q8BG32_P	Psmd11	26S protea	K.TAYSYFYEAFEGYDSIDSPK#.A	4.32	1.38	3.13	0.32
Q8BG32_P	Psmd11	26S protea	K.VVDSLYSK#.A	28.39	10.74	2.64	0.38
Q9D8W5_P	Psmd12	26S protea	K.DPNNLLNDWSQK#.L	57.63	1.51	38.20	0.03
Q9D8W5_P	Psmd12	26S protea	K.EAASILQELQVETYGSM*EK#.K	14.95	2.13	7.01	0.14
Q9D8W5_P	Psmd12	26S protea	K.EAASILQELQVETYGSMEK#.K	12.45	2.77	4.49	0.22
Q9D8W5_P	Psmd12	26S protea	K.EWDLLNENIM*LLSK#.R	24.42	4.61	5.30	0.19
Q9D8W5_P	Psmd12	26S protea	K.EWDLLNENIMLLSK#.R	10.45	2.69	3.88	0.26
Q9D8W5_P	Psmd12	26S protea	K.FFQEENTENLK#.L	83.77	12.43	6.74	0.15
Q9D8W5_P	Psmd12	26S protea	R.ILVAVVK#.M	59.11	76.48	0.77	1.29
Q9D8W5_P	Psmd12	26S protea	K.IYVEIER.A	25.76	16.18	1.59	0.63
Q9D8W5_P	Psmd12	26S protea	K.LNSLM*SLVNK#.T	48.06	7.32	6.56	0.15
Q9D8W5_P	Psmd12	26S protea	K.LNSLMSLVNK#.T	8.44	3.33	2.54	0.39
Q9D8W5_P	Psmd12	26S protea	R.LQEVIETLLSLEK#.Q	116.04	16.82	6.90	0.14
Q9D8W5_P	Psmd12	26S protea	R.WSTLVEDYGVELR.K	14.44	8.67	1.66	0.60

Q9D8W5_	Psmd12	26S protea	K.EAASILQELQVETYGSM*EK#.K	12.04	2.08	5.80	0.17
Q9D8W5_	Psmd12	26S protea	K.EWDLLNENIM*LLSK#.R	9.58	3.35	2.86	0.35
Q9D8W5_	Psmd12	26S protea	K.FFQEENTENLK#.L	63.39	8.11	7.82	0.13
Q9D8W5_	Psmd12	26S protea	R.ILVAVVK#.M	35.23	41.76	0.84	1.19
Q9D8W5_	Psmd12	26S protea	K.LNSLM*SLVNK#.T	18.42	3.22	5.72	0.17
Q9D8W5_	Psmd12	26S protea	R.LQEVIETLLSLEK#.Q	72.38	10.74	6.74	0.15
Q9D8W5_	Psmd12	26S protea	K.DPNNLLNDWSQK#.L	28.33	6.27	4.52	0.22
Q9D8W5_	Psmd12	26S protea	K.EAASILQELQVETYGSM*EK#.K	22.70	4.01	5.66	0.18
Q9D8W5_	Psmd12	26S protea	K.EWDLLNENIM*LLSK#.R	15.55	3.66	4.25	0.24
Q9D8W5_	Psmd12	26S protea	K.FFQEENTENLK#.L	83.23	12.73	6.54	0.15
Q9D8W5_	Psmd12	26S protea	R.ILVAVVK#.M	69.17	35.89	1.93	0.52
Q9D8W5_	Psmd12	26S protea	K.K#LEEIPK#.Y	59.71	7.47	8.00	0.13
Q9D8W5_	Psmd12	26S protea	K.LNSLM*SLVNK#.T	22.98	3.37	6.82	0.15
Q9D8W5_	Psmd12	26S protea	K.LNSLMSLVNK#.T	14.24	1.55	9.21	0.11
Q9D8W5_	Psmd12	26S protea	R.LQEVIETLLSLEK#.Q	63.63	6.26	10.16	0.10
Q9WVJ2_P	Psmd13	26S protea	K.ALSVGLVR.G	20.89	15.73	1.33	0.75
Q9WVJ2_P	Psmd13	26S protea	K.DLPVSEQQER.A	30.74	20.85	1.47	0.68
Q9WVJ2_P	Psmd13	26S protea	K.ITVNK#VELLVM*K#.A	30.75	3.77	8.16	0.12
Q9WVJ2_P	Psmd13	26S protea	K.ITVNK#VELLVMK#.A	24.17	6.86	3.52	0.28
Q9WVJ2_P	Psmd13	26S protea	K.LNIGDLQATK#.E	123.80	18.84	6.57	0.15
Q9WVJ2_P	Psmd13	26S protea	R.QM*TDPNVALTFLEK#.T	58.82	4.12	14.28	0.07
Q9WVJ2_P	Psmd13	26S protea	R.QMTDPNVALTFLEK#.T	11.67	8.67	1.35	0.74
Q9WVJ2_P	Psmd13	26S protea	K.SM*EM*LVEHQAQDILT.-	9.72	9.72	1.00	1.00
Q9WVJ2_P	Psmd13	26S protea	K.SM*EMLVEHQAQDILT.-	5.97	5.97	1.00	1.00
Q9WVJ2_P	Psmd13	26S protea	K.SMEMLVEHQAQDILT.-	19.29	19.29	1.00	1.00
Q9WVJ2_P	Psmd13	26S protea	R.VLDLQQIK#.G	156.66	22.98	6.82	0.15
Q9WVJ2_P	Psmd13	26S protea	R.LEELYTK#.K	22.14	1.73	12.78	0.08
Q9WVJ2_P	Psmd13	26S protea	K.LNIGDLQATK#.E	56.90	4.96	11.48	0.09
Q9WVJ2_P	Psmd13	26S protea	R.QM*TDPNVALTFLEK#.T	9.58	3.39	2.83	0.35
Q9WVJ2_P	Psmd13	26S protea	R.QMTDPNVALTFLEK#.T	6.04	4.15	1.45	0.69
Q9WVJ2_P	Psmd13	26S protea	R.VLDLQQIK#.G	57.97	9.61	6.03	0.17
Q9WVJ2_P	Psmd13	26S protea	K.YYQTIGNHASYYK#.D	12.08	1.40	8.62	0.12
Q9WVJ2_P	Psmd13	26S protea	K.DLPVSEQQER.A	17.17	13.00	1.32	0.76
Q9WVJ2_P	Psmd13	26S protea	K.ITVNK#VELLVM*K#.A	25.21	3.02	8.34	0.12
Q9WVJ2_P	Psmd13	26S protea	K.ITVNK#VELLVMK#.A	14.28	1.66	8.61	0.12
Q9WVJ2_P	Psmd13	26S protea	K.LNIGDLQATK#.E	74.37	14.26	5.21	0.19
Q9WVJ2_P	Psmd13	26S protea	R.QM*TDPNVALTFLEK#.T	19.54	3.44	5.67	0.18
Q9WVJ2_P	Psmd13	26S protea	R.QMTDPNVALTFLEK#.T	6.69	7.63	0.88	1.14
Q9WVJ2_P	Psmd13	26S protea	R.VLDLQQIK#.G	95.38	13.10	7.28	0.14
O35593_P	Psmd14	26S protea	R.AVAVVVDPIQSVK#.G	158.22	31.54	5.02	0.20
O35593_P	Psmd14	26S protea	K.AVEEEDK#M*TPEQLAIK#.N	48.80	9.14	5.34	0.19
O35593_P	Psmd14	26S protea	K.AVEEEDK#MTPEQLAIK#.N	13.30	4.70	2.83	0.35
O35593_P	Psmd14	26S protea	K.MLDMLK#.Q	10.34	2.31	4.48	0.22
O35593_P	Psmd14	26S protea	R.VIDVFAMPQSGTGVSVEAVDPVFQAK#.M	78.08	13.20	5.92	0.17
O35593_P	Psmd14	26S protea	R.VIDVFAMPQSGTGVSVEAVDPVFQAK#.M	11.36	2.06	5.51	0.18
Q8VDM4_	Psmd2	26S protea	R.AVPLALALISVSNPR.L	14.63	12.87	1.14	0.88
Q8VDM4_	Psmd2	26S protea	R.DK#TPVQSQQPSATTPSGADEK#.S	68.65	14.49	4.74	0.21
Q8VDM4_	Psmd2	26S protea	K.DPNNLFMVR.L	9.34	7.42	1.26	0.79
Q8VDM4_	Psmd2	26S protea	R.EDVLTLLLPVM*GDSK#.S	28.99	40.07	0.72	1.38
Q8VDM4_	Psmd2	26S protea	R.ELDIM*EPK#.V	58.07	10.81	5.37	0.19
Q8VDM4_	Psmd2	26S protea	R.EPLLTLVK#.E	49.68	6.87	7.23	0.14
Q8VDM4_	Psmd2	26S protea	K.EWQELDDAEK#.A	78.35	12.63	6.20	0.16
Q8VDM4_	Psmd2	26S protea	R.FGGSGSQVDSAR.M	58.73	45.33	1.30	0.77
Q8VDM4_	Psmd2	26S protea	R.HLAGEVAK#.E	73.16	13.12	5.58	0.18
Q8VDM4_	Psmd2	26S protea	R.LAQGLTHLGK#.G	106.47	12.14	8.77	0.11
Q8VDM4_	Psmd2	26S protea	K.LK#EIYENM*APGENK#.C	12.15	1.84	6.60	0.15
Q8VDM4_	Psmd2	26S protea	K.LLTDDGNK#.W	19.76	2.94	6.73	0.15
Q8VDM4_	Psmd2	26S protea	R.LNILDTLSK#.F	218.16	39.05	5.59	0.18
Q8VDM4_	Psmd2	26S protea	R.M*NLASSFVNGFVNAAFGQDK#.L	18.23	2.16	8.44	0.12
Q8VDM4_	Psmd2	26S protea	R.SSTTSM*TSVPK#PLK#.F	40.29	5.86	6.87	0.15
Q8VDM4_	Psmd2	26S protea	K.TPVQSQQPSATTPSGADEK#.S	61.05	11.00	5.55	0.18
Q8VDM4_	Psmd2	26S protea	R.VGQAVDVVGQAGK#PK#.T	278.52	38.22	7.29	0.14
Q8VDM4_	Psmd2	26S protea	K.VPDDIYK#.T	115.25	86.21	1.34	0.75
Q8VDM4_	Psmd2	26S protea	K.YLYSSEDYIK#.S	99.54	16.93	5.88	0.17
Q8VDM4_	Psmd2	26S protea	R.DK#TPVQSQQPSATTPSGADEK#.S	32.29	3.90	8.29	0.12
Q8VDM4_	Psmd2	26S protea	R.ELDIM*EPK#.V	14.84	2.92	5.09	0.20
Q8VDM4_	Psmd2	26S protea	K.EWQELDDAEK#.A	19.03	3.17	6.00	0.17
Q8VDM4_	Psmd2	26S protea	R.HLAGEVAK#.E	29.54	3.63	8.14	0.12
Q8VDM4_	Psmd2	26S protea	R.LAQGLTHLGK#.G	36.01	7.06	5.10	0.20
Q8VDM4_	Psmd2	26S protea	R.LNILDTLSK#.F	78.10	10.19	7.67	0.13
Q8VDM4_	Psmd2	26S protea	K.TPVQSQQPSATTPSGADEK#.S	19.93	3.39	5.89	0.17
Q8VDM4_	Psmd2	26S protea	R.VGQAVDVVGQAGK#PK#.T	104.73	14.72	7.11	0.14
Q8VDM4_	Psmd2	26S protea	K.YLYSSEDYIK#.S	34.19	6.36	5.37	0.19
P14685_P	Psmd3	26S protea	K.AIQLEYSEAR.R	122.07	13.37	9.13	0.11
P14685_P	Psmd3	26S protea	K.AK#PPPGGEQEPPPPAPQDVEMK#.E	6.83	2.71	2.52	0.40
P14685_P	Psmd3	26S protea	R.ALDLVAAK#.C	71.35	13.01	5.48	0.18
P14685_P	Psmd3	26S protea	R.DGVIEASINHEK#.G	60.10	21.19	2.84	0.35
P14685_P	Psmd3	26S protea	R.ELDTVTLEDIK#.E	26.35	8.41	3.13	0.32
P14685_P	Psmd3	26S protea	K.FNQVLDQFGEK#.F	94.40	15.53	6.08	0.16
P14685_P	Psmd3	26S protea	K.FQTDGTYTLIIR.L	22.97	48.49	0.47	2.11
P14685_P	Psmd3	26S protea	K.ISDDLMQK#.I	40.76	5.83	6.99	0.14
P14685_P	Psmd3	26S protea	K.ISDDLM*QK#.I	61.41	9.18	6.69	0.15
P14685_P	Psmd3	26S protea	R.ISLADIAQK#.L	119.63	16.27	7.35	0.14
P14685_P	Psmd3	26S protea	R.LNHYVLYK#.A	65.12	13.35	4.88	0.21
P14685_P	Psmd3	26S protea	K.LQLDSPEDAEFIVAK#.A	126.37	18.35	6.89	0.15
P14685_P	Psmd3	26S protea	R.VYEFLDK#.L	20.05	3.50	5.73	0.17
P14685_P	Psmd3	26S protea	R.VYEFLDKLDVVR.S	19.36	13.21	1.47	0.68
P14685_P	Psmd3	26S protea	R.YLYYTGR.I	17.11	16.57	1.03	0.97
P14685_P	Psmd3	26S protea	R.DGVIEASINHEK#.G	14.38	2.95	4.88	0.21
P14685_P	Psmd3	26S protea	R.ISLADIAQK#.L	35.33	6.07	5.82	0.17
P14685_P	Psmd3	26S protea	K.LQLDSPEDAEFIVAK#.A	46.23	41.44	1.12	0.90
P14685_P	Psmd3	26S protea	R.ALDLVAAK#.C	23.60	6.04	3.91	0.26
P14685_P	Psmd3	26S protea	R.ELDTVTLEDIK#.E	9.78	1.75	5.61	0.18
P14685_P	Psmd3	26S protea	K.FNQVLDQFGEK#.F	44.43	9.69	4.58	0.22
P14685_P	Psmd3	26S protea	K.ISDDLM*QK#.I	26.14	8.31	3.14	0.32
P14685_P	Psmd3	26S protea	R.ISLADIAQK#.L	53.69	11.30	4.75	0.21
P14685_P	Psmd3	26S protea	K.LQLDSPEDAEFIVAK#.A	65.95	25.92	2.54	0.39
P14685_P	Psmd3	26S protea	R.NYLHYSLYDQAEK#.L	6.96	2.49	2.80	0.36
F7AI87_F7	Psmd4	26S protea	R.AAAASAAEAGIATPGTEGER.D	4.32	6.66	0.65	1.54
F7AI87_F7	Psmd4	26S protea	R.DSDDALLK#.M	16.69	4.38	3.81	0.26
O35226_P	Psmd4	26S protea	K.EK#VNVDIINFGEEEVNTEK#.L	56.50	15.55	3.63	0.28
O35226_P	Psmd4	26S protea	R.IIAFVGSPVEDNEK#.D	19.28	7.85	2.46	0.41
O35226_P	Psmd4	26S protea	K.LTAFVNTLNGK#.D	12.13	26.09	0.47	2.15

O35226_P	Psmd4	26S protea	R.SVM*GALASQATK#.D	67.54	24.29	2.78	0.36
O35226_P	Psmd4	26S protea	R.SVMGALASQATK#.D	63.99	14.73	4.34	0.23
O35226_P	Psmd4	26S protea	K.VNVDIINFGEEEVNTEK#.L	54.33	13.20	4.11	0.24
O35226_P	Psmd4	26S protea	K.EK#VNVDIINFGEEEVNTEK#.L	19.46	3.45	5.65	0.18
O35226_P	Psmd4	26S protea	R.IIAFVGSPVEDNEK#.D	12.38	2.07	6.00	0.17
O35226_P	Psmd4	26S protea	K.VNVDIINFGEEEVNTEK#.L	28.72	4.48	6.42	0.16
Q8BJY1_PS	Psmd5	26S protea	R.AYLSEGPYYVK#PVATTAVEGAD.-	10.79	1.77	6.11	0.16
Q8BJY1_PS	Psmd5	26S protea	R.IVENSEAVTEILNNAELLK#.Q	21.71	2.11	10.28	0.10
Q8BJY1_PS	Psmd5	26S protea	R.GLTHPDDSVK#.T	18.24	2.85	6.40	0.16
Q8BJY1_PS	Psmd5	26S protea	R.IVENSEAVTEILNNAELLK#.Q	35.10	5.09	6.89	0.15
Q8BJY1_PS	Psmd5	26S protea	K.VFEM*ADSQDPTM*IGVAVDTVGILGSSVEGK#.Q	7.97	2.26	3.52	0.28
Q99JI4_PSI	Psmd6	26S protea	K.SLDWQM*DVDLLSK#.M	16.37	2.76	5.93	0.17
Q99JI4_PSI	Psmd6	26S protea	K.NWQYQETIK#.K	31.89	6.54	4.87	0.21
Q99JI4_PSI	Psmd6	26S protea	K.SLDWQM*DVDLLSK#.M	13.46	5.78	2.33	0.43
Q99JI4_PSI	Psmd6	26S protea	K.ANEEELK#.R	8.54	1.31	6.54	0.15
Q99JI4_PSI	Psmd6	26S protea	K.GAEILEVLHSLPAVR.Q	29.53	19.44	1.52	0.66
Q99JI4_PSI	Psmd6	26S protea	R.LDEELEDAEK#.N	22.38	2.72	8.24	0.12
Q99JI4_PSI	Psmd6	26S protea	K.NWQYQETIK#.K	39.71	5.62	7.07	0.14
Q99JI4_PSI	Psmd6	26S protea	K.SLDWQM*DVDLLSK#.M	17.93	4.50	3.98	0.25
P26516_P	Psmd7	26S protea	R.DIKDTTVGTLSQR.I	19.51	11.72	1.66	0.60
P26516_P	Psmd7	26S protea	R.ITNQVHGLK#.G	55.79	9.11	6.13	0.16
P26516_P	Psmd7	26S protea	R.SVVALHNLINNK#.I	79.25	17.76	4.46	0.22
P26516_P	Psmd7	26S protea	R.VVGVLLGSWQK#.K	148.18	26.12	5.67	0.18
P26516_P	Psmd7	26S protea	R.SVVALHNLINNK#.I	8.51	12.44	0.68	1.46
P26516_P	Psmd7	26S protea	R.VVGVLLGSWQK#.K	15.76	28.54	0.55	1.81
Q9CX56_P	Psmd8	26S protea	K.DIQTNVYIK#.H	71.77	8.59	8.35	0.12
Q9CX56_P	Psmd8	26S protea	K.HPVSLEQYLM*EGSYNK#.V	20.31	7.06	2.88	0.35
Q9CX56_P	Psmd8	26S protea	K.HPVSLEQYLMEGSYNK#.V	13.81	3.26	4.24	0.24
Q9CX56_P	Psmd8	26S protea	K.ILFAEATR.I	26.95	27.76	0.97	1.03
Q9CX56_P	Psmd8	26S protea	R.ILFFSTPK#.K	124.16	17.06	7.28	0.14
Q9CR00_P	Psmd9	26S protea	K.ANYDVLESQK#.G	25.54	8.09	3.16	0.32
P97371_P	Psme1	Proteasom	K.APLDIPVPDPVK#.E	23.80	7.66	3.11	0.32
P97371_P	Psme1	Proteasom	K.APLDIPVPDPVK#EK#.E	113.23	18.70	6.05	0.17
P97371_P	Psme1	Proteasom	R.IEDGNNFGVAVQEK#.V	141.54	25.65	5.52	0.18
P97371_P	Psme1	Proteasom	K.ISELDAFLK#EPALNEANLSNLK#.A	82.26	9.92	8.29	0.12
P97371_P	Psme1	Proteasom	K.K#ISELDAFLK#EPALNEANLSNLK#.A	81.86	10.98	7.46	0.13
P97371_P	Psme1	Proteasom	R.NAYAVLYDIILK#.N	233.34	31.28	7.46	0.13
P97371_P	Psme1	Proteasom	K.TENLLGSYFPK#.K	97.20	16.57	5.87	0.17
P97371_P	Psme1	Proteasom	K.VFELMTNLHTK#.L	48.75	5.98	8.15	0.12
P97371_P	Psme1	Proteasom	K.APLDIPVPDPVK#EK#.E	26.38	7.17	3.68	0.27
P97371_P	Psme1	Proteasom	R.IEDGNNFGVAVQEK#.V	72.64	13.19	5.51	0.18
P97371_P	Psme1	Proteasom	K.ISELDAFLK#EPALNEANLSNLK#.A	7.65	2.63	2.91	0.34
P97372_P	Psme2	Proteasom	R.AFYAELYHIISSNLEK#.I	140.26	26.35	5.32	0.19
P97372_P	Psme2	Proteasom	K.GEEK#PSM*Y.-	16.08	2.20	7.32	0.14
P97372_P	Psme2	Proteasom	K.IEDGNDFGVAIQEK#.V	86.07	15.54	5.54	0.18
P97372_P	Psme2	Proteasom	K.TK#VEAFQTTISK#.Y	57.69	9.03	6.39	0.16
P97372_P	Psme2	Proteasom	K.VEAFQTTISK#.Y	25.48	4.17	6.11	0.16
P97372_P	Psme2	Proteasom	K.IEDGNDFGVAIQEK#.V	27.91	4.63	6.03	0.17
P97372_P	Psme2	Proteasom	K.TK#VEAFQTTISK#.Y	27.73	3.41	8.12	0.12
P97372_P	Psme2	Proteasom	K.VEAFQTTISK#.Y	9.26	1.77	5.24	0.19
P97372_P	Psme2	Proteasom	R.AFYAELYHIISSNLEK#.I	104.89	18.72	5.60	0.18
P97372_P	Psme2	Proteasom	K.IEDGNDFGVAIQEK#.V	34.47	6.81	5.06	0.20
P97372_P	Psme2	Proteasom	R.KIISLSQLLQEDSLNVADLSSLR.A	19.46	16.42	1.18	0.84
P97372_P	Psme2	Proteasom	K.TK#VEAFQTTISK#.Y	36.77	5.26	6.99	0.14
P97372_P	Psme2	Proteasom	R.AFYAELYHIISSNLEK#.I	71.45	16.27	4.39	0.23
P97372_P	Psme2	Proteasom	K.IEDGNDFGVAIQEK#.V	53.68	9.87	5.44	0.18
P97372_P	Psme2	Proteasom	R.KIISLSQLLQEDSLNVADLSSLR.A	11.71	8.00	1.46	0.68
P97372_P	Psme2	Proteasom	K.TK#VEAFQTTISK#.Y	54.32	14.40	3.77	0.27
P97372_P	Psme2	Proteasom	K.VEAFQTTISK#.Y	17.32	11.47	1.51	0.66
P61290_P	Psme3	Proteasom	R.ITSEAEDLVANFFPK#.K	11.96	5.92	2.02	0.50
P61290_P	Psme3	Proteasom	K.SNQQLVDIIEK#.V	34.45	11.74	2.93	0.34
P61290_P	Psme3	Proteasom	R.TVESEAASYLDQISR.Y	4.16	5.65	0.74	1.36
Q9CZH3_P	Psmg3	Proteasom	K.M*GTLVSLEPSNVANDISKPVLTTR.V	1.73	2.91	0.59	1.69
Q8R326_P	Pspc1	Paraspeckl	K.AELDGTILK#.S	62.30	19.83	3.14	0.32
Q8R326_P	Pspc1	Paraspeckl	K.AVVVVDDR.G	12.46	16.91	0.74	1.36
Q8R326_P	Pspc1	Paraspeckl	R.FAQPGTFEFEYASR.W	19.13	22.90	0.84	1.20
Q8R326_P	Pspc1	Paraspeckl	R.LFVGNLPTDITEEDFK#.R	14.79	7.48	1.98	0.51
Q8R326_P	Pspc1	Paraspeckl	K.NLSPVVSNELLEQAFSQFGPVEK#.A	30.62	11.65	2.63	0.38
Q8R326_P	Pspc1	Paraspeckl	R.YGEPSEVFINR.D	13.33	24.53	0.54	1.84
Q99LS3_SE	Psph	Phosphose	R.LALIQPSR.D	11.40	13.87	0.82	1.22
Q8BGJ5_Q	Ptbp1	MCG13402	R.AQAALQAVNSVQSGNLALAASAAAVDAGM*AM*AGQSPVLR.I	14.04	16.00	0.88	1.14
Q8BGJ5_Q	Ptbp1	MCG13402	R.AQAALQAVNSVQSGNLALAASAAAVDAGMAM*AGQSPVLR.I	5.56	8.22	0.68	1.48
Q8BGJ5_Q	Ptbp1	MCG13402	K.DYGSSPLHR.F	146.45	315.60	0.46	2.16
Q8BGJ5_Q	Ptbp1	MCG13402	K.GKNQAFIEM*NTEEAANTM*VNYYTSVAPVLR.G	2.48	5.66	0.44	2.28
Q8BGJ5_Q	Ptbp1	MCG13402	K.GKNQAFIEMNTEEAANTM*VNYYTSVAPVLR.G	3.45	4.23	0.82	1.23
Q8BGJ5_Q	Ptbp1	MCG13402	K.GKNQAFIEM*NTEEAANTMVNYYTSVAPVLR.G	2.27	5.05	0.45	2.22
Q8BGJ5_Q	Ptbp1	MCG13402	K.HQSVQLPR.E	121.59	236.68	0.51	1.95
Q8BGJ5_Q	Ptbp1	MCG13402	R.IAIPGLAGAGNSVLLVSNLNPER.V	131.29	260.34	0.50	1.98
Q8BGJ5_Q	Ptbp1	MCG13402	R.IIVENLFYPVTLDVLHQIFSK#.F	151.00	52.28	2.89	0.35
Q8BGJ5_Q	Ptbp1	MCG13402	R.KLPSDVTEGEVISLGLPFGK.V	746.98	319.78	2.34	0.43
Q8BGJ5_Q	Ptbp1	MCG13402	R.K#LPSDVTEGEVISLGLPFGK#.V	89.76	40.27	2.23	0.45
Q8BGJ5_Q	Ptbp1	MCG13402	R.KM*ALIQM*GSVEEAVQALIELHNHDLGENHHLR.V	2.10	6.96	0.30	3.31
Q8BGJ5_Q	Ptbp1	MCG13402	K.LPSDVTEGEVISLGLPFGK#.V	76.69	38.84	1.97	0.51
Q8BGJ5_Q	Ptbp1	MCG13402	K.NFQNIFPPSATLHLSNIPPSVSEDDLK#.S	176.88	76.54	2.31	0.43
Q8BGJ5_Q	Ptbp1	MCG13402	K.NNQFQALLQYADPVSAQHAK#.L	657.21	282.12	2.33	0.43
Q8BGJ5_Q	Ptbp1	MCG13402	K.NNQFQALLQYADPVSAQHAK#.L	10.72	5.54	1.93	0.52
Q8BGJ5_Q	Ptbp1	MCG13402	K.NNQFQALLQYADPVSAQHAK#.L	45.94	17.55	2.62	0.38
Q8BGJ5_Q	Ptbp1	MCG13402	K.NQAFIEM*NTEEAANTM*VNYYTSVAPVLR.G	3.17	4.03	0.79	1.27
Q8BGJ5_Q	Ptbp1	MCG13402	K.TDSSPNQAR.A	6.21	10.72	0.58	1.73
Q8BGJ5_Q	Ptbp1	MCG13402	R.IAIPGLAGAGNSVLLVSNLNPER.V	3.72	10.59	0.35	2.85
Q8BGJ5_Q	Ptbp1	MCG13402	R.KLPSDVTEGEVISLGLPFGK.V	57.70	26.21	2.20	0.45
Q8BGJ5_Q	Ptbp1	MCG13402	K.NNQFQALLQYADPVSAQHAK.L	3.21	1.96	1.63	0.61
Q8BGJ5_Q	Ptbp1	MCG13402	R.IAIPGLAGAGNSVLLVSNLNPER.V	21.67	46.66	0.46	2.15
Q8BGJ5_Q	Ptbp1	MCG13402	R.K#LPSDVTEGEVISLGLPFGK#.V	110.84	49.90	2.22	0.45
Q8BGJ5_Q	Ptbp1	MCG13402	K.LPSDVTEGEVISLGLPFGK#.V	7.31	3.13	2.34	0.43
Q8BGJ5_Q	Ptbp1	MCG13402	K.NFQNIFPPSATLHLSNIPPSVSEDDLK#.S	13.27	6.17	2.15	0.46
Q8BGJ5_Q	Ptbp1	MCG13402	K.NNQFQALLQYADPVSAQHAK#.L	52.92	19.70	2.69	0.37
Q91Z31_P	Ptbp2	Polypyrimi	R.AQVVLQAVTAVQTANTPLSGTTVSESAVTPAQSPVLR.I	3.76	5.73	0.66	1.52
Q91Z31_P	Ptbp2	Polypyrimi	R.DYTRPDLPSGDGQPALDPAIAAAFAK.E	11.45	32.61	0.35	2.85
Q91Z31_P	Ptbp2	Polypyrimi	R.K#LPGEVTETEVIALGLPFGK#.V	73.72	48.35	1.52	0.66
Q91Z31_P	Ptbp2	Polypyrimi	K.LVNLNVK#.Y	87.45	56.86	1.54	0.65
Q91Z31_P	Ptbp2	Polypyrimi	K.NNQFQALLQYGDPVNAQQAK#.L	25.32	13.64	1.86	0.54
Q91Z31_P	Ptbp2	Polypyrimi	R.NQPIYIQYSNHK#.E	23.82	15.97	1.49	0.67

Q91Z31_P	Ptbp2	Polypyrimi	K.TDNTLNQR.A	114.81	16.68	6.88	0.15
Q91Z31_P	Ptbp2	Polypyrimi	R.TLFANTGGTVK#.A	63.47	43.32	1.47	0.68
Q91Z31_P	Ptbp2	Polypyrimi	R.EGLDDQGLTK#.D	35.82	8.37	4.28	0.23
Q91Z31_P	Ptbp2	Polypyrimi	R.TLFANTGGTVK#.A	57.66	17.17	3.36	0.30
Q91Z31_P	Ptbp2	Polypyrimi	K.VTNLLM*LK#.G	43.52	14.89	2.92	0.34
Q91Z31_P	Ptbp2	Polypyrimi	K.IITFTK#.N	78.99	40.97	1.93	0.52
Q91Z31_P	Ptbp2	Polypyrimi	K.VTNLLM*LK#.G	35.86	14.08	2.55	0.39
Q91Z31_P	Ptbp2	Polypyrimi	K.VTNLLMLK#.G	22.16	11.46	1.93	0.52
Q8BHD7_P	Ptbp3	Polypyrimi	R.AQAALQAVSAVQSGNLSLPGATANEGTLLPGQSPVLR.I	9.51	19.15	0.50	2.01
Q8BHD7_P	Ptbp3	Polypyrimi	K.DFSNSPLHR.F	15.97	40.78	0.39	2.55
Q8BHD7_P	Ptbp3	Polypyrimi	R.EGQEDQGLTK#.D	379.98	178.70	2.13	0.47
Q8BHD7_P	Ptbp3	Polypyrimi	R.ELKTDNLPNQAR.A	6.43	18.86	0.34	2.93
Q8BHD7_P	Ptbp3	Polypyrimi	K.ENALVQMADASQAQLAMNHLSGQR.L	7.66	15.58	0.49	2.03
Q8BHD7_P	Ptbp3	Polypyrimi	K.LTSLNVK#.Y	1198.58	499.10	2.40	0.42
Q8BHD7_P	Ptbp3	Polypyrimi	K.NFQNIFPPSATLHLSNIPPSVTM*DDLK#.N	10.68	7.61	1.40	0.71
Q8BHD7_P	Ptbp3	Polypyrimi	K.NFQNIFPPSATLHLSNIPPSVTMDDLK#.N	11.29	5.54	2.04	0.49
Q8BHD7_P	Ptbp3	Polypyrimi	K.NNQFQALLQYADPVNAQYAK#.M	94.19	61.86	1.52	0.66
Q8BHD7_P	Ptbp3	Polypyrimi	K.TDNLPNQAR.A	16.19	51.60	0.31	3.19
Q8BHD7_P	Ptbp3	Polypyrimi	R.EGQEDQGLTK#.D	30.48	12.58	2.42	0.41
P34152_F	Ptk2	Focal adhe	K.GFLNQFTEDK#PTLNFFYQQVK#.S	9.17	3.13	2.93	0.34
P34152_F	Ptk2	Focal adhe	K.LLNSDLGELISK#.M	14.81	4.03	3.67	0.27
P34152_F	Ptk2	Focal adhe	K.GFLNQFTEDK#PTLNFFYQQVK#.S	14.16	5.80	2.44	0.41
P34152_F	Ptk2	Focal adhe	K.LLNSDLGELISK#.M	15.96	5.23	3.05	0.33
Q8BKG3_P	Ptk7	Inactive tyr	K.AQGVEEGATETLVLVK#.S	11.81	1.67	7.09	0.14
Q8BKG3_P	Ptk7	Inactive tyr	R.ASLQPITTLGK#.S	29.40	10.37	2.84	0.35
P35235_P	Ptpn11	Tyrosine-pr	R.FDSLTDLVEHYK#.K	13.52	2.91	4.65	0.22
P35235_P	Ptpn11	Tyrosine-pr	R.VVLHDGDPNEPVSDYINANIIM*PEFETK#.C	3.73	2.04	1.83	0.55
P35235_P	Ptpn11	Tyrosine-pr	R.VVLHDGDPNEPVSDYINANIIMPEFETK#.C	5.03	1.90	2.65	0.38
P35235_P	Ptpn11	Tyrosine-pr	R.VVLHDGDPNEPVSDYINANIIM*PEFETK#.C	5.93	2.41	2.46	0.41
P35235_P	Ptpn11	Tyrosine-pr	K.LAETTDK#VK#.Q	8.11	7.98	1.02	0.98
P35235_P	Ptpn11	Tyrosine-pr	R.VVLHDGDPNEPVSDYINANIIM*PEFETK#.C	8.54	2.09	4.08	0.24
P35235_P	Ptpn11	Tyrosine-pr	R.VVLHDGDPNEPVSDYINANIIMPEFETK#.C	3.27	4.61	0.71	1.41
P35831_P	Ptpn12	Tyrosine-pr	K.TPSQDSDYINANFIK#.G	4.95	3.40	1.46	0.69
Q6PB44_P	Ptpn23	Tyrosine-pr	R.AALPTPALTPEDK#.A	37.06	22.33	1.66	0.60
Q6PB44_P	Ptpn23	Tyrosine-pr	R.ALENPDTASLLGR.I	9.73	22.95	0.42	2.36
Q6PB44_P	Ptpn23	Tyrosine-pr	R.DLLEEDELQEQK#.L	14.27	5.17	2.76	0.36
Q6PB44_P	Ptpn23	Tyrosine-pr	K.DNDFIYHEAVPALDTLQPVK#.G	12.99	8.20	1.58	0.63
Q6PB44_P	Ptpn23	Tyrosine-pr	R.FAMDVIGGK#.Y	15.87	5.71	2.78	0.36
Q6PB44_P	Ptpn23	Tyrosine-pr	R.GAAAADLLSSSPESQHGGTQPPGGGQPLLQPTK#.V	13.41	4.91	2.73	0.37
Q6PB44_P	Ptpn23	Tyrosine-pr	K.GAPLVK#PLPVNPTDPAVTGPDIFAK#.L	54.05	30.42	1.78	0.56
Q6PB44_P	Ptpn23	Tyrosine-pr	R.HGVPPPGK#PVASVNISQK#.N	16.64	10.84	1.54	0.65
Q6PB44_P	Ptpn23	Tyrosine-pr	R.HQDVM*PYDSNR.V	2.49	4.16	0.60	1.67
Q6PB44_P	Ptpn23	Tyrosine-pr	K.K#DNDFIYHEAVPALDTLQPVK#.G	10.69	4.17	2.56	0.39
Q6PB44_P	Ptpn23	Tyrosine-pr	K.LQETLGQAGAGPGPSVAK#.A	25.79	13.24	1.95	0.51
Q6PB44_P	Ptpn23	Tyrosine-pr	R.LQQLQQELEAFR.G	7.56	22.02	0.34	2.91
Q6PB44_P	Ptpn23	Tyrosine-pr	R.M*PM*IWLDLK#.E	9.91	6.56	1.51	0.66
Q6PB44_P	Ptpn23	Tyrosine-pr	K.NHLPQDSQDLVLGGDVPISSIQATIAK#.L	36.65	20.39	1.80	0.56
Q6PB44_P	Ptpn23	Tyrosine-pr	K.NYGENPEAYNEELK#.K	15.69	10.27	1.53	0.65
Q6PB44_P	Ptpn23	Tyrosine-pr	R.REEGEAVEAGDTPEELR.S	2.37	33.69	0.07	14.22
Q6PB44_P	Ptpn23	Tyrosine-pr	K.SQEGK#DFYADLESK#.V	19.97	8.59	2.33	0.43
Q6PB44_P	Ptpn23	Tyrosine-pr	R.VLSLQFR.D	7.81	15.47	0.50	1.98
Q6PB44_P	Ptpn23	Tyrosine-pr	R.VPM*GSGQEAAVAVTWTEIFSGK#.S	23.32	10.33	2.26	0.44
Q6PB44_P	Ptpn23	Tyrosine-pr	K.VYLEQNLAAQDNVLR.A	5.34	14.46	0.37	2.71
Q64487_P	Ptprd	Receptor-t	K.TVDIYGHVTLM*R@.A	113.09	2.09	54.20	0.02
O54724_P	Ptrf	Polymeras	K.AHATTSNTVSK.L	16.36	14.04	1.17	0.86
O54724_P	Ptrf	Polymeras	R.ATEEPSGTGSDELIK#.S	163.79	110.85	1.48	0.68
O54724_P	Ptrf	Polymeras	K.ATEM*VEVGPEDDEVGAER.G	7.93	31.53	0.25	3.97
O54724_P	Ptrf	Polymeras	K.ATEMVEVGPEDDEVGAER.G	6.07	29.65	0.20	4.89
O54724_P	Ptrf	Polymeras	K.ATEM*VEVGPEDDEVGAERGEATDLLR.G	4.68	27.19	0.17	5.81
O54724_P	Ptrf	Polymeras	R.EGEVEVLK#.A	65.20	51.77	1.26	0.79
O54724_P	Ptrf	Polymeras	R.GEATDLLR.G	11.45	38.59	0.30	3.37
O54724_P	Ptrf	Polymeras	K.IIGAVDQIQLTQAQLEER.Q	58.55	179.45	0.33	3.06
O54724_P	Ptrf	Polymeras	K.IIGAVDQIQLTQAQLEER.Q	16.10	63.04	0.26	3.91
O54724_P	Ptrf	Polymeras	K.IREGEVEVLK.A	65.40	62.87	1.04	0.96
O54724_P	Ptrf	Polymeras	K.KLEVNEAELLR.R	35.61	138.12	0.26	3.88
O54724_P	Ptrf	Polymeras	R.KSFTPDHVVYAR.S	24.00	84.61	0.28	3.53
O54724_P	Ptrf	Polymeras	R.QAEM*EGAVQSIQGELSK#.L	47.14	30.27	1.56	0.64
O54724_P	Ptrf	Polymeras	R.QAEMEGAVQSIQGELSK.L	11.89	6.61	1.80	0.56
O54724_P	Ptrf	Polymeras	K.SDQVNGVLVLSLLDK#.I	76.64	61.65	1.24	0.80
O54724_P	Ptrf	Polymeras	K.VMIYQDEVK.L	54.18	46.64	1.16	0.86
O54724_P	Ptrf	Polymeras	K.VM*IYQDEVKLPAK.L	74.41	57.30	1.30	0.77
Q8R2Y8_P	Ptrh2	Peptidyl-tR	K.APDEDTLIQLLTHAK#.T	15.55	10.00	1.55	0.64
D3Z4S3_PT	Ptrhd1	Putative pe	K.EEVSQYLK#.K	22.51	9.48	2.37	0.42
D3Z4S3_PT	Ptrhd1	Putative pe	K.VVLEAADETTLK#.E	17.19	6.83	2.52	0.40
D3Z4S3_PT	Ptrhd1	Putative pe	K.VVLEAADETTLK#ELAETLQQK#.N	21.82	11.06	1.97	0.51
Q3UEB3_P	Puf60	Poly(U)-bin	K.AQSSQDAVSSM*NLFDLGGQYLR.V	2.17	4.45	0.49	2.05
Q3UEB3_P	Puf60	Poly(U)-bin	K.AQSSQDAVSSM*NLFDLGGQYLR.V	13.34	20.73	0.64	1.55
Q3UEB3_P	Puf60	Poly(U)-bin	K.AQSSQDAVSSMNLFDLGGQYLR.V	13.48	17.33	0.78	1.29
Q3UEB3_P	Puf60	Poly(U)-bin	K.AVTPPMPLLTPATPGGLPPAAAVAAAAATAK#.I	135.78	61.43	2.21	0.45
Q3UEB3_P	Puf60	Poly(U)-bin	K.GYGFIEYEK#.A	97.53	42.07	2.32	0.43
Q3UEB3_P	Puf60	Poly(U)-bin	R.IYVASVHQDLSDDDIK#SVFEAFGK#.I	10.85	2.99	3.63	0.28
Q3UEB3_P	Puf60	Poly(U)-bin	R.KVVAEVYDQER.F	9.85	20.21	0.49	2.05
Q3UEB3_P	Puf60	Poly(U)-bin	K.LGLPPLTPEQQEALQK#.A	124.14	57.21	2.17	0.46
Q3UEB3_P	Puf60	Poly(U)-bin	R.QAFAPFGPIK#.S	118.39	45.13	2.62	0.38
Q3UEB3_P	Puf60	Poly(U)-bin	K.QGEEEDAEIIVK#.I	92.47	18.20	5.08	0.20
Q3UEB3_P	Puf60	Poly(U)-bin	K.SIDM*SWDSVTM*K#.H	18.19	8.13	2.24	0.45
Q3UEB3_P	Puf60	Poly(U)-bin	K.SIDM*SWDSVTMK#.H	9.29	3.49	2.66	0.38
Q3UEB3_P	Puf60	Poly(U)-bin	K.SIDMSWDSVTM*K#.H	19.25	6.53	2.95	0.34
Q3UEB3_P	Puf60	Poly(U)-bin	K.SIDMSWDSVTMK#.H	22.51	7.94	2.84	0.35
Q3UEB3_P	Puf60	Poly(U)-bin	K.VGRPSNIGQAQPIIDQLAEEAR.A	9.35	51.39	0.18	5.49
Q3UEB3_P	Puf60	Poly(U)-bin	R.VIIYQEK#.Q	141.52	49.74	2.85	0.35
Q3UEB3_P	Puf60	Poly(U)-bin	K.VVAEVYDQER.F	12.83	20.22	0.63	1.58
Q3UEB3_P	Puf60	Poly(U)-bin	R.VYVGSIYYELGEDTIR.Q	18.81	31.63	0.59	1.68
Q3UEB3_P	Puf60	Poly(U)-bin	K.YAMEQSIK#.S	54.55	17.70	3.08	0.32
Q3UEB3_P	Puf60	Poly(U)-bin	K.YAM*EQSIK#.S	203.20	27.93	7.28	0.14
Q3UEB3_P	Puf60	Poly(U)-bin	K.GYGFIEYEK#.A	18.07	7.04	2.57	0.39
Q3UEB3_P	Puf60	Poly(U)-bin	K.LGLPPLTPEQQEALQK#.A	3.34	1.70	1.96	0.51
Q3UEB3_P	Puf60	Poly(U)-bin	K.VGRPSNIGQAQPIIDQLAEEAR.A	2.70	7.51	0.36	2.78
Q3UEB3_P	Puf60	Poly(U)-bin	K.LGLPPLTPEQQEALQK#.A	18.34	6.95	2.64	0.38
Q3UEB3_P	Puf60	Poly(U)-bin	R.QAFAPFGPIK#.S	13.54	7.77	1.74	0.57
Q3UEB3_P	Puf60	Poly(U)-bin	K.VGRPSNIGQAQPIIDQLAEEAR.A	3.03	12.57	0.24	4.14
Q3UR91_Q	Pum2	Pumilio ho	K.ALESISSDQQSEMVK#.E	8.19	5.51	1.49	0.67
Q3UR91_Q	Pum2	Pumilio ho	R.DLIGHIVEFSQDQHGSR.F	4.64	16.98	0.27	3.66

Q3UR91_Q	Pum2	Pumilio ho	K.DQYANYVVQK#.M	230.00	18.19	12.65	0.08
Q3UR91_Q	Pum2	Pumilio ho	R.YISAAPGAEAK#.Y	49.86	43.83	1.14	0.88
Q3UR91_Q	Pum2	Pumilio ho	K.DQYANYVVQK#.M	22.27	26.30	0.85	1.18
Q3UR91_Q	Pum2	Pumilio ho	R.YISAAPGAEAK.Y	27.02	21.54	1.25	0.80
P42669_P	Pura	Transcripti	R.DYLGDFIEHYAQLGPSQPPDLAQAQDEPR.R	3.00	13.12	0.23	4.37
P42669_P	Pura	Transcripti	R.DYLGDFIEHYAQLGPSQPPDLAQAQDEPRR.A	2.04	6.05	0.34	2.96
P42669_P	Pura	Transcripti	R.FFFDVGSNK.Y	63.13	57.62	1.10	0.91
P42669_P	Pura	Transcripti	R.GPGLGSTQGQTIALPAQGLIEFR.D	15.80	64.36	0.25	4.07
P42669_P	Pura	Transcripti	K.IAEVGAGGNK#.S	85.13	86.99	0.98	1.02
P42669_P	Pura	Transcripti	K.LIDDYGVEEEPAELPEGTSLTVDNKR.F	11.85	72.42	0.16	6.11
P42669_P	Pura	Transcripti	R.NSITVPYK#.V	29.29	35.54	0.82	1.21
P42669_P	Pura	Transcripti	K.SEFLVR.E	20.38	110.34	0.18	5.41
P42669_P	Pura	Transcripti	K.YGVFMR.V	3.87	18.54	0.21	4.80
P42669_P	Pura	Transcripti	R.FFFDVGSNK#.Y	13.37	13.37	1.00	1.00
P42669_P	Pura	Transcripti	R.FYLDVK.Q	16.40	18.44	0.89	1.12
P42669_P	Pura	Transcripti	R.GPGLGSTQGQTIALPAQGLIEFR.D	5.41	20.73	0.26	3.83
P42669_P	Pura	Transcripti	K.LIDDYGVEEEPAELPEGTSLTVDNKR.F	3.03	10.50	0.29	3.47
O35295_P	Purb	Transcripti	R.DSLGDFIEHYAQLGPSSPEQLAAGAEEGGGPR.R	3.71	12.97	0.29	3.49
O35295_P	Purb	Transcripti	R.GGGGGGGGGPGGFQPAPR.G	15.38	81.92	0.19	5.33
O35295_P	Purb	Transcripti	R.GGGGGGGGPGGEQETQELASK#.R	53.63	67.20	0.80	1.25
O35295_P	Purb	Transcripti	R.GGGSGGGDESEGEEVDED.-	3.15	3.15	1.00	1.00
O35295_P	Purb	Transcripti	K.IAEVGAGGSK#.S	252.54	117.80	2.14	0.47
O35295_P	Purb	Transcripti	R.K#YYLDLK#.E	17.61	20.51	0.86	1.16
O35295_P	Purb	Transcripti	K.YGVFLR.V	6.29	34.77	0.18	5.53
O35295_P	Purb	Transcripti	K.YYLDLK#.E	8.64	9.97	0.87	1.15
O35295_P	Purb	Transcripti	R.GGGGGGGGGPGGFQPAPR.G	2.23	9.35	0.24	4.18
O35295_P	Purb	Transcripti	K.IAEVGAGGSK#.S	209.26	125.42	1.67	0.60
Q8K094_Q	Pvr	Nectin-2 O	K.NTAEALEPSPTLILQDVAK#.C	7.10	5.49	1.29	0.77
Q8BU03_P	Pwp2	Periodic tr	R.AGQLLPVVQFLQK#.G	15.96	14.07	1.13	0.88
Q8VI36_PA	Pxn	Paxillin OS	R.ELDELM*ASLSDFK#.M	13.70	12.53	1.09	0.91
Q8VI36_PA	Pxn	Paxillin OS	R.ELDELMASLSDFK#.M	9.19	3.14	2.93	0.34
Q8VI36_PA	Pxn	Paxillin OS	K.LGVATVAK#.G	35.96	19.82	1.81	0.55
Q8VI36_PA	Pxn	Paxillin OS	R.YAHQQPPSPLPVYSSSAK#.N	21.33	16.50	1.29	0.77
Q922W5_P	Pycr1	Pyrroline-5	R.LGAQALLGAAK#.M	92.02	12.97	7.10	0.14
Q9DCC4_P	Pycrl	Pyrroline-5	R.IAAQTLLGTAK#.M	64.72	30.44	2.13	0.47
Q9DCC4_P	Pycrl	Pyrroline-5	R.IAAQTLLGTAK#.M	236.05	93.42	2.53	0.40
Q9DCC4_P	Pycrl	Pyrroline-5	R.RVGFVGAGR.M	4.43	28.05	0.16	6.33
Q8CI94_PY	Pygb	Glycogen p	R.IGEGFLTDLSQLK#.K	11.60	4.82	2.41	0.42
Q8CI94_PY	Pygb	Glycogen p	R.IGEGFLTDLSQLK#K#.L	41.71	10.63	3.92	0.25
Q8CI94_PY	Pygb	Glycogen p	R.VEDVEALDQK#.G	31.78	13.22	2.40	0.42
Q8CI94_PY	Pygb	Glycogen p	R.VEHTPDGVLWLDTQVVLAM*PYDTPVPGYK#.N	6.86	2.40	2.86	0.35
Q8CI94_PY	Pygb	Glycogen p	R.EIWGVEPSDLQIPPPNLPK#D.-	7.96	4.44	1.79	0.56
Q8CI94_PY	Pygb	Glycogen p	R.GIAGLGDVAEVR.K	7.50	9.94	0.75	1.32
Q8CI94_PY	Pygb	Glycogen p	R.IGEGFLTDLSQLK#.K	15.42	4.64	3.32	0.30
Q8CI94_PY	Pygb	Glycogen p	R.IGEGFLTDLSQLK#K#.L	61.82	17.26	3.58	0.28
Q8CI94_PY	Pygb	Glycogen p	R.QAVDQISSGFFSPK#.D	10.33	2.94	3.51	0.28
Q8CI94_PY	Pygb	Glycogen p	R.VEDVEALDQK#.G	35.95	9.44	3.81	0.26
Q8CI94_PY	Pygb	Glycogen p	R.YEFGIFNQK#.I	25.15	4.45	5.65	0.18
Q8BML9_Q	Qars	Glutaminyl	K.ATGVLLYDLVSR.L	11.76	12.03	0.98	1.02
Q8BML9_Q	Qars	Glutaminyl	R.FDDTNPEK#EEAK#.F	16.24	3.41	4.77	0.21
Q8BML9_Q	Qars	Glutaminyl	R.LNLHYAVVSK#.R	33.10	2.55	12.97	0.08
Q8BML9_Q	Qars	Glutaminyl	K.TPGYVITPYTM*DLLK#.Q	15.60	4.31	3.62	0.28
Q8BML9_Q	Qars	Glutaminyl	K.TPGYVITPYTMDLLK#.Q	5.99	3.24	1.85	0.54
Q8BML9_Q	Qars	Glutaminyl	R.VPNFPADETK#.G	20.72	3.88	5.34	0.19
Q8BML9_Q	Qars	Glutaminyl	K.AINFNFGYAK#.A	43.49	9.14	4.76	0.21
Q8BML9_Q	Qars	Glutaminyl	K.ATGVLLYDLVSR.L	30.78	17.92	1.72	0.58
Q8BML9_Q	Qars	Glutaminyl	R.LNLHYAVVSK#.R	35.60	9.37	3.80	0.26
Q8BML9_Q	Qars	Glutaminyl	R.SFLVSYIANK#.K	17.48	9.89	1.77	0.57
Q8BML9_Q	Qars	Glutaminyl	R.SHPQDPIDTK#.D	17.73	3.48	5.10	0.20
Q8BML9_Q	Qars	Glutaminyl	K.TPGYVITPYTM*DLLK#.Q	25.94	3.84	6.75	0.15
Q8BML9_Q	Qars	Glutaminyl	R.VPNFPADETK#.G	41.64	9.61	4.33	0.23
Q9QYS9_Q	Qki	Protein qu	K.EYPDFNFVGR.I	4.10	12.28	0.33	2.99
Q9QYS9_Q	Qki	Protein qu	R.SAELPDAVGPIVQLQEK#.L	28.52	21.24	1.34	0.74
Q9QYS9_Q	Qki	Protein qu	R.SAELPDAVGPIVQLQEK#.L	9.59	9.40	1.02	0.98
Q9QYS9_Q	Qki	Protein qu	K.LYVPVKEYPDFNFVGR.I	3.48	20.23	0.17	5.81
Q9QYS9_Q	Qki	Protein qu	R.SAELPDAVGPIVQLQEK#.L	15.32	13.18	1.16	0.86
Q3UA37_Q	Qrich1	Glutamine-	R.EIQEAIAVANATTM*H.-	5.85	5.85	1.00	1.00
Q3UA37_Q	Qrich1	Glutamine-	K.LYDFYLFK#.C	10.61	7.99	1.33	0.75
Q3UA37_Q	Qrich1	Glutamine-	K.NAELEKDAQNR.L	2.65	3.55	0.74	1.34
P61027_R	Rab10	Ras-related	K.AFLTLAEDILR.K	1.68	15.00	0.11	8.92
P61027_R	Rab10	Ras-related	K.IKLQIWDTAGQER.F	4.75	9.22	0.52	1.94
P61027_R	Rab10	Ras-related	K.LLLIGDSGVGK#.T	30.41	19.53	1.56	0.64
P61027_R	Rab10	Ras-related	K.LQIWDTAGQER.F	3.75	23.35	0.16	6.23
P61027_R	Rab10	Ras-related	K.TPVK#EPNSENVDISSGGGVTGWK#.S	4.85	3.04	1.59	0.63
P46638_R	Rab11b	Ras-related	K.AQIWDTAGQER.Y	9.32	36.78	0.25	3.95
P46638_R	Rab11b	Ras-related	R.DHADSNIVIMLVGNK.S	16.19	19.89	0.81	1.23
P46638_R	Rab11b	Ras-related	R.GAVGALLVYDIAK.H	147.84	140.77	1.05	0.95
P46638_R	Rab11b	Ras-related	K.HLTYENVER.W	6.61	41.82	0.16	6.33
P46638_R	Rab11b	Ras-related	R.NEFNLESK#.S	65.10	60.44	1.08	0.93
P46638_R	Rab11b	Ras-related	K.NILTEIYR.I	2.01	10.56	0.19	5.26
P46638_R	Rab11b	Ras-related	K.NNLSFIETSALDSTNVEEAFK#.N	15.06	10.94	1.38	0.73
P46638_R	Rab11b	Ras-related	K.NNLSFIETSALDSTNVEEAFK#.N	25.04	18.07	1.39	0.72
P46638_R	Rab11b	Ras-related	K.STIGVEFATR.S	23.28	114.41	0.20	4.92
P46638_R	Rab11b	Ras-related	K.VVLIGDSGVGK#.S	36.83	22.53	1.63	0.61
P35283_R	Rab12	Ras-related	K.DNFNVDEIFLK#.L	14.15	5.14	2.75	0.36
Q91V41_R	Rab14	Ras-related	R.GAAGALM*VYDITR.R	2.92	4.67	0.62	1.60
Q91V41_R	Rab14	Ras-related	R.IIEVSGQK#.I	26.36	16.77	1.57	0.64
Q91V41_R	Rab14	Ras-related	R.NLTNPNTVIILIGNK#.A	54.53	44.57	1.22	0.82
Q91V41_R	Rab14	Ras-related	K.TGENVEDAFLEAAK#.K	7.00	8.18	0.86	1.17
Q91V41_R	Rab14	Ras-related	K.TGENVEDAFLEAAK#K#.I	38.09	27.76	1.37	0.73
P35293_R	Rab18	Ras-related	R.FTDDTFDPELAATIGVDFK#.V	5.93	5.48	1.08	0.92
P35293_R	Rab18	Ras-related	R.GAQGVILVYDVTR.R	57.23	10.27	5.57	0.18
P35293_R	Rab18	Ras-related	K.IIQTPGLWESENQNK#.G	8.46	6.55	1.29	0.77
P35293_R	Rab18	Ras-related	K.ILIIGESGVGK#.S	39.66	36.62	1.08	0.92
P35293_R	Rab18	Ras-related	K.LAIWDTAGQER.F	4.54	14.70	0.31	3.24
P62821_R	Rab1A	Ras-related	K.EFADSLGIPFLETSAK#.N	59.90	37.84	1.58	0.63
P62821_R	Rab1A	Ras-related	R.FADDTYTESYISTIGVDFK#.I	33.72	23.81	1.42	0.71
P62821_R	Rab1A	Ras-related	R.GAHGIIVVYDVTDQESFNNVK#.Q	38.06	21.77	1.75	0.57
P62821_R	Rab1A	Ras-related	R.M*GPGATAGGAEK#.S	5.68	4.23	1.34	0.75
P62821_R	Rab1A	Ras-related	K.NATNVEQSFM*TM*AAEIK#.K	11.55	7.63	1.51	0.66
P62821_R	Rab1A	Ras-related	K.QWLQEIDR.Y	13.17	42.51	0.31	3.23
P62821_R	Rab1A	Ras-related	K.EFADSLGIPFLETSAK#.N	7.88	5.94	1.33	0.75
P62821_R	Rab1A	Ras-related	R.FADDTYTESYISTIGVDFK#.I	6.11	2.82	2.17	0.46

Q9D1G1_R	Rab1b	Ras-related	K.EFADSLGVPFLETSAK#.N	26.15	20.81	1.26	0.80
Q9D1G1_R	Rab1b	Ras-related	R.GAHGIIVVYDVTDQESYANVK#.Q	13.48	5.99	2.25	0.44
Q9D1G1_R	Rab1b	Ras-related	R.M*GPGAASGGERPNLK.I	2.49	5.16	0.48	2.08
Q9D1G1_R	Rab1b	Ras-related	K.NATNVEQAFM*TM*AAEIK#.K	5.83	2.75	2.12	0.47
P35288_R	Rab23	Ras-related	K.VVAEVGDIPTALVQNK#.I	5.51	3.20	1.72	0.58
P53994_R	Rab2a	Ras-related	R.DTFNHLTTWLEDAR.Q	4.76	27.00	0.18	5.67
P53994_R	Rab2a	Ras-related	R.EHGLIFM*ETSAK#.T	2.58	3.54	0.73	1.37
P53994_R	Rab2a	Ras-related	R.GAAGALLVYDITR.R	8.33	34.26	0.24	4.11
P53994_R	Rab2a	Ras-related	K.LQIWDTAGQESFR@.S	3.51	13.26	0.26	3.78
P53994_R	Rab2a	Ras-related	K.TASNVEEAFINTAK#.E	42.57	29.99	1.42	0.70
P53994_R	Rab2a	Ras-related	K.YIIIGDTGVGK#.S	17.86	12.55	1.42	0.70
Q921E2_R	Rab31	Ras-related	K.NAINIEELFQGISR.Q	6.65	6.62	1.00	1.00
Q9CZT8_R	Rab3b	Ras-related	R.YADDTFTPAFVSTVGIDFK#.V	6.59	2.48	2.66	0.38
Q80UJ7_R	Rab3gap1	Rab3 GTPas	R.LAGAFSSDTSFF.-	10.66	10.66	1.00	1.00
Q80UJ7_R	Rab3gap1	Rab3 GTPas	R.STFEEEGREVADITHALSK.L	3.69	7.28	0.51	1.97
Q80UJ7_R	Rab3gap1	Rab3 GTPas	K.TSLSDSTTSAYPGDAGK#.T	14.78	6.66	2.22	0.45
Q80UJ7_R	Rab3gap1	Rab3 GTPas	K.VPSQYTHLSGLLDIFK#.S	7.56	5.87	1.29	0.78
Q8BMG7_	Rab3gap2	Rab3 GTPas	K.AM*NPQDLQNTGVPIAATAK#.L	8.77	2.89	3.03	0.33
Q8BMG7_	Rab3gap2	Rab3 GTPas	R.FSAATYLM*DK#.V	11.04	4.45	2.48	0.40
Q8BMG7_	Rab3gap2	Rab3 GTPas	K.GGFSPFGNTQGPSR.V	5.04	12.08	0.42	2.40
Q8BMG7_	Rab3gap2	Rab3 GTPas	R.VILLDVAR.G	5.83	16.93	0.34	2.90
Q68EF0_R	Rab3ip	Rab-3A-int	K.IDVLQAEVAALK#.T	9.02	1.21	7.46	0.13
Q9CQD1_R	Rab5a	Ras-related	R.GVDLTEPAQPAR.S	15.73	26.51	0.59	1.69
Q9CQD1_R	Rab5a	Ras-related	K.LVLLGESAVGK#.S	59.11	56.68	1.04	0.96
Q9CQD1_R	Rab5a	Ras-related	K.TSMNVNEIFMAIAK#.K	2.87	3.23	0.89	1.13
P61021_R	Rab5b	Ras-related	R.QASPSIVIALAGNK#.A	10.91	6.87	1.59	0.63
P61021_R	Rab5b	Ras-related	K.TAM*NVNDLFLAIAK#.K	15.57	10.94	1.42	0.70
P35278_R	Rab5c	Ras-related	R.AVEFQEAQAYADDNSLLFM*ETSAK.T	10.93	8.29	1.32	0.76
P35278_R	Rab5c	Ras-related	R.GAQAAIVVYDITNTDTFAR.A	1.91	15.13	0.13	7.91
P35278_R	Rab5c	Ras-related	R.GVDLQESNPASR.S	7.30	30.51	0.24	4.18
P35278_R	Rab5c	Ras-related	K.NEPQNAAGAPGR.T	2.84	12.68	0.22	4.47
P35278_R	Rab5c	Ras-related	R.QASPNIVIALAGNK.A	19.87	22.99	0.86	1.16
P35278_R	Rab5c	Ras-related	K.TAM*NVNEIFMAIAK#.K	5.44	5.87	0.93	1.08
P35279_R	Rab6a	Ras-related	K.ELNVM*FIETSAK#.A	7.70	9.73	0.79	1.26
P35279_R	Rab6a	Ras-related	K.ELNVMFIETSAK#.A	16.22	6.48	2.50	0.40
P35279_R	Rab6a	Ras-related	R.GSDVIIM*LVGNK#.T	11.79	9.13	1.29	0.77
P35279_R	Rab6a	Ras-related	R.GSDVIIMLVGNK#.T	28.18	22.69	1.24	0.81
P35279_R	Rab6a	Ras-related	K.LVFLGEQSVGK#.T	56.93	17.01	3.35	0.30
P35279_R	Rab6a	Ras-related	R.VAAALPGM*ESTQDR.S	1.36	21.74	0.06	16.00
P51150_R	Rab7a	Ras-related	K.ATIGADFLTK#.E	26.87	20.55	1.31	0.76
P51150_R	Rab7a	Ras-related	R.DPENFPFVVLGNK#.I	66.05	53.47	1.24	0.81
P51150_R	Rab7a	Ras-related	K.EAINVEQAFQTIAR.N	14.65	52.22	0.28	3.56
P51150_R	Rab7a	Ras-related	R.FQSLGVAFYR.G	9.64	47.09	0.20	4.88
P51150_R	Rab7a	Ras-related	R.LVTM*QIWDTAGQER.F	1.55	4.44	0.35	2.86
P51150_R	Rab7a	Ras-related	R.NALK#QETEVELYNEFPEPIK#.L	6.41	5.72	1.12	0.89
P51150_R	Rab7a	Ras-related	R.NALK#QETEVELYNEFPEPIK#LDK#.N	9.06	6.43	1.41	0.71
P51150_R	Rab7a	Ras-related	K.NNIPYFETSAK#.E	29.98	21.30	1.41	0.71
P51150_R	Rab7a	Ras-related	K.QETEVELYNEFPEPIK.L	3.14	3.26	0.96	1.04
P51150_R	Rab7a	Ras-related	K.TLDSWRDEFLIQASPR.D	3.37	36.12	0.09	10.72
P51150_R	Rab7a	Ras-related	K.VIILGDSGVGK.T	52.49	40.53	1.29	0.77
P55258_R	Rab8a	Ras-related	K.ANINVENAFFTLAR.D	6.29	10.28	0.61	1.63
P55258_R	Rab8a	Ras-related	R.NIEEHASADVEK#.M	10.99	7.89	1.39	0.72
P61028_R	Rab8b	Ras-related	K.SSTNVEEAFFTLAR.D	4.07	8.28	0.49	2.03
O35551_R	Rabep1	Rab GTPase	R.AQSTDSLGTSSSLQSK#.A	8.85	4.34	2.04	0.49
A2AWA9_R	Rabgap1	Rab GTPase	R.LLDPQTNTEIANYPIYK#.I	5.21	2.26	2.31	0.43
A2AWA9_R	Rabgap1	Rab GTPase	K.TSK#DDLLLTDFEGALK#.F	9.97	3.50	2.85	0.35
A2AWA9_R	Rabgap1	Rab GTPase	K.DDLLLTDFEGALK#.F	10.42	4.53	2.30	0.43
A2AWA9_R	Rabgap1	Rab GTPase	K.DTGGDGQDSLYK#.I	16.19	3.71	4.36	0.23
A2AWA9_R	Rabgap1	Rab GTPase	R.EM*ELELAQTK#.L	23.09	4.81	4.80	0.21
A2AWA9_R	Rabgap1	Rab GTPase	R.EQQAQQEDPIER.F	3.55	7.68	0.46	2.16
A2AWA9_R	Rabgap1	Rab GTPase	K.GVSDEDTDEEK#ETLK#.N	6.49	9.77	0.66	1.50
A2AWA9_R	Rabgap1	Rab GTPase	K.ILETWGELLSK#.W	22.89	4.22	5.43	0.18
A2AWA9_R	Rabgap1	Rab GTPase	K.IQDLEHHLGLALSEVQAAK.K	9.74	2.08	4.68	0.21
A2AWA9_R	Rabgap1	Rab GTPase	K.IVGNGSEQQLQK#.E	11.10	3.04	3.65	0.27
A2AWA9_R	Rabgap1	Rab GTPase	R.LEEESAQLK#.E	10.82	6.64	1.63	0.61
A2AWA9_R	Rabgap1	Rab GTPase	R.LFWPFSK#.R	12.40	3.08	4.03	0.25
A2AWA9_R	Rabgap1	Rab GTPase	R.LLDPQTNTEIANYPIYK#.I	15.08	4.44	3.39	0.29
A2AWA9_R	Rabgap1	Rab GTPase	K.NSSIIGDYK#.Q	20.97	6.59	3.18	0.31
A2AWA9_R	Rabgap1	Rab GTPase	K.SPHFQVVNEETPK#DK#.V	29.04	4.20	6.92	0.14
A2AWA9_R	Rabgap1	Rab GTPase	K.TSK#DDLLLTDFEGALK#.F	54.14	10.76	5.03	0.20
Q9JM13_R	Rabgef1	Rab5 GDP/	K.DLIDWTDGIAK#.E	12.34	7.09	1.74	0.57
Q9JM13_R	Rabgef1	Rab5 GDP/	R.LQREEEEAFASSQSSQGAQSLTFSK.F	2.59	2.83	0.92	1.09
P63001_R	Rac1	Ras-related	K.LTPITYPQGLAM*AK#.E	8.26	14.64	0.56	1.77
Q9WVM1_	Racgap1	Rac GTPase	R.LSTIDESGSILSDISFDK#TDESLDWDSSLVK#.N	3.69	4.93	0.75	1.34
Q9WVM1_	Racgap1	Rac GTPase	K.VSLLGPVTTPEFQLVK.T	4.55	10.42	0.44	2.29
Q9QXK2_R	Rad18	E3 ubiquiti	R.THLLQFALESPPISPVSSTSK#.K	3.56	4.75	0.75	1.34
Q61550_R	Rad21	Double-stra	R.AQLSDYSDIVTTLDLAPPTK.K	7.66	7.47	1.02	0.98
Q61550_R	Rad21	Double-stra	R.DVIDEPIIEEPSR.L	10.01	43.63	0.23	4.36
Q61550_R	Rad21	Double-stra	R.EGSAFEDDDMLVSTSASNLLLEPEQSTSNLNEK#.M	5.08	4.55	1.12	0.90
Q61550_R	Rad21	Double-stra	K.FYSFLVLK.K	38.96	29.33	1.33	0.75
Q61550_R	Rad21	Double-stra	K.KQQAIELTQEEPYSDIIATPGPR.F	3.20	7.65	0.42	2.39
Q61550_R	Rad21	Double-stra	K.LFFLPAQPLWNNR.L	8.91	42.21	0.21	4.74
Q61550_R	Rad21	Double-stra	K.LIVDSVK#.E	45.63	27.96	1.63	0.61
Q61550_R	Rad21	Double-stra	K.MAFRPGVVDLPEENR.E	2.45	22.33	0.11	9.13
Q61550_R	Rad21	Double-stra	K.QQAIELTQEEPYSDIIATPGPR.F	3.27	6.00	0.55	1.83
Q61550_R	Rad21	Double-stra	R.TSGHLLLGVVR.I	11.66	36.56	0.32	3.14
Q61550_R	Rad21	Double-stra	R.TTIEESAM*PPPPPQGVK#.R	9.22	8.31	1.11	0.90
Q61550_R	Rad21	Double-stra	R.AQLSDYSDIVTTLDLAPPTK#.K	6.45	9.11	0.71	1.41
Q61550_R	Rad21	Double-stra	R.EGSAFEDDDM*LVSTSASNLLLEPEQSTSNLNEK#.M	12.44	6.35	1.96	0.51
Q61550_R	Rad21	Double-stra	K.GGEADNLDEFLKEFENPEVPREEQQPQQQQPQPQR.D	4.73	4.62	1.02	0.98
Q61550_R	Rad21	Double-stra	K.LFFLPAQPLWNNR.L	7.07	28.86	0.25	4.08
Q61550_R	Rad21	Double-stra	K.LIVDSVK#.E	30.84	21.10	1.46	0.68
Q61550_R	Rad21	Double-stra	R.TTIEESAM*PPPPPQGVK#.R	7.25	7.84	0.93	1.08
P70388_R	Rad50	DNA repair	R.DSLIQSLATHLELDGFER.G	5.62	20.09	0.28	3.58
P70388_R	Rad50	DNA repair	K.EQISPLETALEK#.L	29.32	16.66	1.76	0.57
P70388_R	Rad50	DNA repair	R.GQDIEYIEIR.S	8.49	18.82	0.45	2.22
P70388_R	Rad50	DNA repair	R.HSDELTSLLGYFPNK#K#.Q	33.95	17.96	1.89	0.53
P70388_R	Rad50	DNA repair	R.VFQTEAELQEVISDLQSK#.L	43.73	25.98	1.68	0.59
P70388_R	Rad50	DNA repair	R.VFQTEAELQEVISDLQSK#.L	6.60	11.68	0.57	1.77
P70388_R	Rad50	DNA repair	K.AEVM*SLQNEK#.A	12.43	4.80	2.59	0.39
P70388_R	Rad50	DNA repair	K.DLDIYYK#.T	13.88	5.04	2.75	0.36
P70388_R	Rad50	DNA repair	K.EQISPLETALEK#.L	23.82	20.51	1.16	0.86
P70388_R	Rad50	DNA repair	R.HSDELTSLLGYFPNK#K#.Q	26.05	9.40	2.77	0.36

P70388_R	Rad50	DNA repair	R.ILELDQELTK#.A	59.55	18.98	3.14	0.32
P70388_R	Rad50	DNA repair	R.K#LIQDQQEQIQHLK#.S	22.92	12.00	1.91	0.52
P70388_R	Rad50	DNA repair	R.SDADENVSASDK#.R	7.64	6.09	1.25	0.80
P70388_R	Rad50	DNA repair	K.TLDQAIM*K#.F	21.88	23.66	0.92	1.08
P70388_R	Rad50	DNA repair	R.VFQTEAELQEVISDLQSK#.L	50.09	28.09	1.78	0.56
Q8C570_R	Rae1	mRNA expo	K.DNFTFK#.C	17.18	12.81	1.34	0.75
Q8C570_R	Rae1	mRNA expo	R.NAAEELKPR.N	3.04	15.74	0.19	5.17
Q8C570_R	Rae1	mRNA expo	R.VAIHYINPPNPAK#.D	16.22	10.96	1.48	0.68
Q9EP71_R	Rai14	Ankycorbin	K.LQASLESEVNALATK#.L	7.32	5.50	1.33	0.75
Q9EP71_R	Rai14	Ankycorbin	K.LSENAGIQNLLLSK#.I	9.38	4.24	2.21	0.45
Q9EP71_R	Rai14	Ankycorbin	K.YQQAQEEIM*K#.L	16.08	12.09	1.33	0.75
Q9EP71_R	Rai14	Ankycorbin	K.LQASLESEVNALATK#.L	8.39	8.52	0.99	1.01
P63321_R	Rala	Ras-related	R.ADQWNVNYVETSAK#.T	5.73	6.96	0.82	1.22
P63321_R	Rala	Ras-related	K.SALTLQFM*YDEFVEDYEPTKADSYR.K	2.01	4.89	0.41	2.44
P63321_R	Rala	Ras-related	K.VIM*VGSGGVGK#.S	30.46	24.14	1.26	0.79
P63321_R	Rala	Ras-related	R.VKEDENVPFLLVGNK.S	3.38	4.14	0.82	1.22
Q9JIW9_R	Ralb	Ras-related	R.GK#AEEWGVQYVETSAK#.T	5.98	5.34	1.12	0.89
Q9JIW9_R	Ralb	Ras-related	K.SQGSLVLHK#.V	11.73	11.10	1.06	0.95
Q64012_R	Raly	RNA-bindin	R.DDGDEEGLLTHSEEELEHSQDTDAEDGALQ.-	40.58	40.58	1.00	1.00
Q64012_R	Raly	RNA-bindin	K.GYAFVQYANER.H	38.81	205.39	0.19	5.29
Q64012_R	Raly	RNA-bindin	K.IQTSNVTNK#.N	131.96	187.12	0.71	1.42
Q64012_R	Raly	RNA-bindin	K.K#SDVETIFSK#.Y	98.58	121.98	0.81	1.24
Q64012_R	Raly	RNA-bindin	R.LEQIAEEQK#.A	342.90	356.96	0.96	1.04
Q64012_R	Raly	RNA-bindin	R.LEQIAEEQK#ANPDGK#.K	13.68	18.86	0.73	1.38
Q64012_R	Raly	RNA-bindin	R.LPAPQEDTASEAGTPQGEVQTR.D	15.50	73.87	0.21	4.77
Q64012_R	Raly	RNA-bindin	K.SDVETIFSK#.Y	24.29	30.05	0.81	1.24
Q64012_R	Raly	RNA-bindin	K.SNIDALLGR.L	38.93	204.25	0.19	5.25
Q64012_R	Raly	RNA-bindin	K.SSELQTIK.T	176.28	180.17	0.98	1.02
Q64012_R	Raly	RNA-bindin	R.STAVTTGSAK.I	40.61	56.99	0.71	1.40
Q64012_R	Raly	RNA-bindin	K.TELTQIK#.S	131.68	179.20	0.73	1.36
Q64012_R	Raly	RNA-bindin	R.VFIGNLNTAVVK#.K	250.18	278.98	0.90	1.12
Q64012_R	Raly	RNA-bindin	R.VLAGQTLDINM*AGEPKPNRPK.G	34.37	154.60	0.22	4.50
Q64012_R	Raly	RNA-bindin	R.VLAGQTLDINMAGEPKPNRPK.G	10.50	71.51	0.15	6.81
Q64012_R	Raly	RNA-bindin	R.VTVPLVR.R	36.20	210.07	0.17	5.80
Q64012_R	Raly	RNA-bindin	K.GYAFVQYANER.H	2.09	8.64	0.24	4.14
Q64012_R	Raly	RNA-bindin	K.IQTSNVTNKNDPK.S	7.13	11.05	0.65	1.55
Q64012_R	Raly	RNA-bindin	R.LPAPQEDTASEAGTPQGEVQTR.D	2.72	16.27	0.17	5.99
Q64012_R	Raly	RNA-bindin	K.SSELQTIK#.T	25.46	30.24	0.84	1.19
Q64012_R	Raly	RNA-bindin	R.VFIGNLNTAVVK.K	23.26	27.29	0.85	1.17
Q64012_R	Raly	RNA-bindin	R.VTVPLVR.R	10.88	63.69	0.17	5.86
Q64012_R	Raly	RNA-bindin	K.KSDVETIFSK.Y	9.20	11.61	0.79	1.26
Q64012_R	Raly	RNA-bindin	R.LEQIAEEQK.A	18.74	25.92	0.72	1.38
Q64012_R	Raly	RNA-bindin	R.LPAPQEDTASEAGTPQGEVQTR.D	4.08	19.86	0.21	4.87
Q64012_R	Raly	RNA-bindin	R.VFIGNLNTAVVK#.K	25.81	28.13	0.92	1.09
Q64012_R	Raly	RNA-bindin	R.VLAGQTLDINM*AGEPKPNRPK.G	4.05	24.68	0.16	6.10
P62827_R	Ran	GTP-bindin	K.LVLVGDGGTGK#.T	99.81	45.30	2.20	0.45
P62827_R	Ran	GTP-bindin	K.NLQYYDISAK#.S	106.63	15.70	6.79	0.15
P62827_R	Ran	GTP-bindin	K.SNYNFEKPFLWLAR.K	44.92	29.15	1.54	0.65
P62827_R	Ran	GTP-bindin	K.LVLVGDGGTGK#.T	19.52	5.04	3.88	0.26
P62827_R	Ran	GTP-bindin	K.NLQYYDISAK#.S	12.73	2.90	4.38	0.23
P34022_R	Ranbp1	Ran-specifi	K.TLEEDEEELFK#.M	14.70	1.41	10.45	0.10
Q6VN19_R	Ranbp10	Ran-bindin	R.VGEAIETTQR.F	6.98	95.90	0.07	13.73
Q6VN19_R	Ranbp10	Ran-bindin	R.M*TETPIQEEQASIK#.N	10.03	4.96	2.02	0.49
Q6VN19_R	Ranbp10	Ran-bindin	R.VGEAIETTQR.F	4.41	16.31	0.27	3.70
Q9ERU9_R	Ranbp2	E3 SUMO-p	K.SK#PEDLPSDNDILIVYELTPTPEQK#.A	4.59	3.64	1.26	0.79
P69566_R	Ranbp9	Ran-bindin	R.LYPAVDEQETPLPR.S	4.80	10.35	0.46	2.16
P69566_R	Ranbp9	Ran-bindin	R.NPNLLFTLK#.V	17.50	10.86	1.61	0.62
P69566_R	Ranbp9	Ran-bindin	R.STDQTVLEELASIK#.N	17.93	10.49	1.71	0.59
P46061_R	Rangap1	Ran GTPase	K.DVIKEIEEFDGLEALR.L	5.02	8.90	0.56	1.77
P46061_R	Rangap1	Ran GTPase	K.GAVAIADAVR.G	11.58	38.65	0.30	3.34
P46061_R	Rangap1	Ran GTPase	R.GFEALLK.S	23.36	21.25	1.10	0.91
P46061_R	Rangap1	Ran GTPase	K.GGVAM*AETLK#.T	20.39	9.66	2.11	0.47
P46061_R	Rangap1	Ran GTPase	R.GSGEEPATPSR.K	4.59	15.81	0.29	3.44
P46061_R	Rangap1	Ran GTPase	R.HNLLQTLYNI.-	40.33	40.33	1.00	1.00
P46061_R	Rangap1	Ran GTPase	K.ILDPNSGEPAPVLSSPTPTDLSTFLSFPSPEK#.L	14.21	3.71	3.82	0.26
P46061_R	Rangap1	Ran GTPase	R.LEGNTVGVEAAR.V	13.60	47.24	0.29	3.47
P46061_R	Rangap1	Ran GTPase	K.SSAQGK#PLALK#.V	7.80	8.06	0.97	1.03
P46061_R	Rangap1	Ran GTPase	K.TAVLDAIDALMK#.K	28.25	28.41	0.99	1.01
P46061_R	Rangap1	Ran GTPase	K.TQVAGGQLSFK#.G	54.65	47.42	1.15	0.87
P46061_R	Rangap1	Ran GTPase	R.VINLNDNTFTEK#.G	64.08	35.70	1.80	0.56
P46061_R	Rangap1	Ran GTPase	K.VSVLIVQQTDTSDPEK#.V	14.41	12.01	1.20	0.83
P46061_R	Rangap1	Ran GTPase	K.VSVLIVQQTDTSDPEK#VVSAFLK#.V	10.70	6.67	1.60	0.62
P46061_R	Rangap1	Ran GTPase	K.GAVAIADAVR.G	9.96	20.91	0.48	2.10
P46061_R	Rangap1	Ran GTPase	R.GFEALLK#.S	33.98	15.80	2.15	0.47
P46061_R	Rangap1	Ran GTPase	K.GGVAM*AETLK.T	44.26	22.63	1.96	0.51
P46061_R	Rangap1	Ran GTPase	R.HNLLQTLYNI.-	55.75	55.75	1.00	1.00
P46061_R	Rangap1	Ran GTPase	R.K#ILDPNSGEPAPVLSSPTPTDLSTFLSFPSPEK#.L	3.35	3.23	1.04	0.96
P46061_R	Rangap1	Ran GTPase	K.LAETLAK#.T	58.71	43.55	1.35	0.74
P46061_R	Rangap1	Ran GTPase	K.TAVLDAIDALM*K#.K	18.94	13.30	1.42	0.70
P46061_R	Rangap1	Ran GTPase	K.TQVAGGQLSFK#.G	62.93	34.49	1.82	0.55
P46061_R	Rangap1	Ran GTPase	R.VINLNDNTFTEK#.G	81.57	50.64	1.61	0.62
P46061_R	Rangap1	Ran GTPase	K.VSVLIVQQTDTSDPEK#.V	13.96	7.99	1.75	0.57
P46061_R	Rangap1	Ran GTPase	K.VSVLIVQQTDTSDPEK#VVSAFLK#.V	23.21	18.64	1.25	0.80
P46061_R	Rangap1	Ran GTPase	R.HNLLQTLYNI.-	13.29	13.29	1.00	1.00
P62835_R	Rap1a	Ras-related	K.INVNEIFYDLVR.Q	11.09	48.19	0.23	4.34
P62835_R	Rap1a	Ras-related	K.LVVLGSGGVGK#.S	75.02	81.17	0.92	1.08
P62835_R	Rap1a	Ras-related	K.NGQGFALVYSITAQSTFNDLQDLR.E	4.98	7.54	0.66	1.52
P62835_R	Rap1a	Ras-related	K.SALTVQFVQGIFVEK#.Y	17.07	15.14	1.13	0.89
P62835_R	Rap1a	Ras-related	K.SKINVNEIFYDLVR.Q	5.76	19.90	0.29	3.46
P62835_R	Rap1a	Ras-related	K.YDPTIEDSYR.K	6.42	22.53	0.28	3.51
Q80ZJ1_RA	Rap2a	Ras-related	K.VVVLGSGGVGK#.S	23.98	19.84	1.21	0.83
Q8CHG7_R	Rapgef2	Rap guanin	R.NIEPTEYIDDLFK#.L	12.22	10.18	1.20	0.83
Q8CHG7_R	Rapgef2	Rap guanin	K.VDGLVNFEK#.L	10.98	18.48	0.59	1.68
Q9D0I9_SY	Rars	Arginine--t	R.LNDYIFSFDK#.M	15.43	2.41	6.40	0.16
Q9D0I9_SY	Rars	Arginine--t	K.SDGGYTYDTSDLAAIK#.Q	13.01	2.53	5.15	0.19
Q9D0I9_SY	Rars	Arginine--t	R.AAYPDLENPPLIVTPSQQPK#.F	7.24	1.69	4.27	0.23
Q9D0I9_SY	Rars	Arginine--t	R.DK#VLTEEELK#.A	26.61	3.49	7.63	0.13
Q9D0I9_SY	Rars	Arginine--t	R.EIAENITK#.H	24.45	8.49	2.88	0.35
Q9D0I9_SY	Rars	Arginine--t	R.FPEILQK#.I	20.49	3.04	6.74	0.15
Q9D0I9_SY	Rars	Arginine--t	R.LFEFAGYDVLR.L	13.31	9.28	1.43	0.70
Q9D0I9_SY	Rars	Arginine--t	R.LNDYIFSFDK#.M	27.91	3.32	8.41	0.12
Q9D0I9_SY	Rars	Arginine--t	K.SDGGYTYDTSDLAAIK#.Q	26.44	4.07	6.50	0.15
Q9D0I9_SY	Rars	Arginine--t	K.VIVDFSSPNIAK#.E	42.79	17.81	2.40	0.42

Q9D0I9_SY	Rars	Arginine--t	R.AAYPDLENPPLIVTPSQQPK#.F	43.85	9.54	4.60	0.22
Q9D0I9_SY	Rars	Arginine--t	R.EIAENITK#.H	77.60	9.85	7.88	0.13
Q9D0I9_SY	Rars	Arginine--t	R.FPEILQK#.I	63.24	12.86	4.92	0.20
Q9D0I9_SY	Rars	Arginine--t	R.LFEFAGYDVLR.L	20.49	19.31	1.06	0.94
Q9D0I9_SY	Rars	Arginine--t	R.LNDYIFSFDK#.M	81.66	12.81	6.38	0.16
Q9D0I9_SY	Rars	Arginine--t	K.VLTEEELK#.A	48.28	9.10	5.31	0.19
E9PYG6_E9	Rasa1	Protein Ras	K.LLAITELLQQK#.Q	6.85	1.34	5.12	0.20
Q6PFQ7_R	Rasa4	Ras GTPase-	K.AVQNIGNM*DTPVSR.A	1.54	7.99	0.19	5.19
Q61820_R	Rasl2-9	GTP-bindin	K.FNVWDTAGQEK#.F	13.24	2.52	5.25	0.19
Q61820_R	Rasl2-9	GTP-bindin	K.FNVWDTAGQEK#.F	109.79	17.83	6.16	0.16
Q61820_R	Rasl2-9	GTP-bindin	R.GPIK#FNVWDTAGQEK#.F	35.36	5.82	6.08	0.16
Q61820_R	Rasl2-9	GTP-bindin	K.FNVWDTAGQEK#.F	7.10	2.05	3.46	0.29
Q61820_R	Rasl2-9	GTP-bindin	K.VDVKDM*K#.V	3.48	191.79	0.02	55.04
Q9CW46_	Raver1	Ribonucle	K.GFAVLEYETAEMAEAAQER.A	5.38	10.60	0.51	1.97
Q9CW46_	Raver1	Ribonucle	K.GYGFAEYM*K#.K	21.36	9.78	2.18	0.46
Q9CW46_	Raver1	Ribonucle	K.GYGFAEYMK#.K	15.31	5.72	2.68	0.37
Q9CW46_	Raver1	Ribonucle	R.SMLAALIAAQATALNR.G	5.32	15.29	0.35	2.88
Q9CW46_	Raver1	Ribonucle	R.SGGGSGGPLSHFYSGSPTSYFTSGLQAGLK.Q	9.48	8.55	1.11	0.90
Q60972_R	Rbbp4	Histone-bi	K.GEFGGFGSVSGK#.I	104.01	62.60	1.66	0.60
Q60972_R	Rbbp4	Histone-bi	K.IGEEQSPEDAEDGPPELLFIHGGHTAK#.I	125.56	71.61	1.75	0.57
Q60972_R	Rbbp4	Histone-bi	K.IGEEQSPEDAEDGPPELLFIHGGHTAK#.I	28.64	21.62	1.32	0.75
Q60972_R	Rbbp4	Histone-bi	K.INHEGEVNR.A	12.65	34.27	0.37	2.71
Q60972_R	Rbbp4	Histone-bi	K.LM*IWDTR.S	28.03	52.72	0.53	1.88
Q60972_R	Rbbp4	Histone-bi	K.LMIWDTR.S	16.49	39.38	0.42	2.39
Q60972_R	Rbbp4	Histone-bi	R.LNVWDLSK#.I	88.49	50.80	1.74	0.57
Q60972_R	Rbbp4	Histone-bi	R.LVLGTHTSDEQNHLVIASVQLPNDDAQFDASHYDSEK#.G	11.18	3.82	2.92	0.34
Q60972_R	Rbbp4	Histone-bi	R.RLNVWDLSK.I	40.02	124.36	0.32	3.11
Q60972_R	Rbbp4	Histone-bi	K.TIFTGHTAVVEDVSWHLLHESLFGSVADDQK#.L	42.87	21.63	1.98	0.50
Q60972_R	Rbbp4	Histone-bi	K.TIFTGHTAVVEDVSWHLLHESLFGSVADDQK#.L	5.05	2.46	2.05	0.49
Q60972_R	Rbbp4	Histone-bi	K.TPSSDVLVFDYTK#.H	304.47	188.86	1.61	0.62
Q60972_R	Rbbp4	Histone-bi	K.TVALWDLR.N	67.51	187.57	0.36	2.78
Q60972_R	Rbbp4	Histone-bi	R.VINEEYK#.I	346.48	164.13	2.11	0.47
Q8BX09_R	Rbbp5	Retinoblast	K.SAPVM*LTLSDSK#.H	7.94	4.21	1.89	0.53
Q8BX09_R	Rbbp5	Retinoblast	R.VTTGTSNTTAIK#.S	15.19	8.93	1.70	0.59
Q8BX09_R	Rbbp5	Retinoblast	K.HVVLPVDDDSDLNVVASFDR.R	3.09	8.96	0.34	2.90
Q8BX09_R	Rbbp5	Retinoblast	R.IVIWDFLTR.G	4.60	18.01	0.26	3.91
Q8BX09_R	Rbbp5	Retinoblast	K.SAPVM*LTLSDSK.H	11.77	13.96	0.84	1.19
Q8BX09_R	Rbbp5	Retinoblast	K.TTNIELQGVPNDEVHPLLGVK#.G	14.35	16.16	0.89	1.13
Q8BX09_R	Rbbp5	Retinoblast	R.VTTGTSNTTAIK#.S	34.49	28.81	1.20	0.84
P97868_R	Rbbp6	E3 ubiquiti	K.AIDDASASISLAQLTK#.T	14.23	11.24	1.27	0.79
P97868_R	Rbbp6	E3 ubiquiti	K.GASSIAITALM*EEK#.G	12.49	6.65	1.88	0.53
P97868_R	Rbbp6	E3 ubiquiti	K.LGYLVSPPQQIR.R	6.90	14.46	0.48	2.10
P97868_R	Rbbp6	E3 ubiquiti	K.AIDDASASISLAQLTK.T	6.36	11.48	0.55	1.81
Q60973_R	Rbbp7	Histone-bi	K.DYALHWLVLGTHTSDEQNHLVVAR.V	1.77	4.64	0.38	2.63
Q60973_R	Rbbp7	Histone-bi	K.EM*FEDTVEER.V	12.33	28.08	0.44	2.28
Q60973_R	Rbbp7	Histone-bi	K.LHTFESHKDEIFQVHWSPHNETILASSGTDR.R	2.87	5.74	0.50	2.00
Q60973_R	Rbbp7	Histone-bi	R.YM*PQNPHIIATK#.T	23.06	10.85	2.13	0.47
Q8BP71_R	Rbfox2	RNA bindin	R.ESEVELPVPGAGADGPEPGLSK.R	5.99	6.61	0.91	1.10
Q8BP71_R	Rbfox2	RNA bindin	K.GFGFVTFENSADADR.A	10.13	60.03	0.17	5.92
Q8BP71_R	Rbfox2	RNA bindin	K.ILDVEIIFNER.G	4.16	18.07	0.23	4.34
Q8BP71_R	Rbfox2	RNA bindin	R.KIEVNNATAR.V	8.40	35.49	0.24	4.23
Q8BP71_R	Rbfox2	RNA bindin	K.RLHVSNIPFR.F	2.91	56.10	0.05	19.28
Q8BP71_R	Rbfox2	RNA bindin	R.YAQPATATAATAAAAAAAAYSDGYGR.V	7.75	23.50	0.33	3.03
Q64701_R	Rbl1	Retinoblast	K.EAVTTPVASATQSVSR.L	2.14	7.16	0.30	3.35
Q64701_R	Rbl1	Retinoblast	K.LSLIQFFSK#.M	22.96	12.37	1.86	0.54
Q99KG3_R	Rbm10	RNA-bindin	R.DGLGSDNIGSR.M	8.59	52.23	0.16	6.08
Q99KG3_R	Rbm10	RNA-bindin	R.ESATADAGYAILEK#.K	18.06	18.45	0.98	1.02
Q99KG3_R	Rbm10	RNA-bindin	K.GDPAGTGPEASLEAGADSVSLQAFSR.A	3.06	10.95	0.28	3.58
Q99KG3_R	Rbm10	RNA-bindin	R.GSSYGVTSTESYK.E	8.74	13.59	0.64	1.55
Q99KG3_R	Rbm10	RNA-bindin	R.KYGGISTASVDFEQPTR.D	1.72	13.92	0.12	8.11
Q99KG3_R	Rbm10	RNA-bindin	R.NLNPHSTM*DSILGALAPYAVLSSSNVR.V	3.79	13.51	0.28	3.56
Q99KG3_R	Rbm10	RNA-bindin	K.NSFQPISALR.D	2.64	24.12	0.11	9.12
Q99KG3_R	Rbm10	RNA-bindin	K.QGIVTPIEAQTR.V	8.03	26.90	0.30	3.35
Q99KG3_R	Rbm10	RNA-bindin	K.TINVEFAK.G	37.74	41.29	0.91	1.09
Q99KG3_R	Rbm10	RNA-bindin	K.YGGISTASVDFEQPTR.D	5.12	21.29	0.24	4.16
Q8R4X3_R	Rbm12	RNA-bindin	R.EIEK#NPPAQGK#.K	5.10	1.58	3.22	0.31
Q8R4X3_R	Rbm12	RNA-bindin	R.ELVLNPEGEVSSAK#.V	44.82	10.42	4.30	0.23
Q8R4X3_R	Rbm12	RNA-bindin	R.LQNFSYDQR.E	10.49	10.66	0.98	1.02
Q8R4X3_R	Rbm12	RNA-bindin	K.VTLLLSSK#.T	13.77	5.71	2.41	0.41
Q80YR9_R	Rbm12b1	RNA-bindin	K.AENPYLFLR.G	2.36	8.71	0.27	3.70
Q8C2Q3_R	Rbm14	RNA-bindin	R.LSESQLSFR.R	2.89	7.24	0.40	2.51
Q8C2Q3_R	Rbm14	RNA-bindin	R.AQPSASLGVGYR.T	40.90	67.09	0.61	1.64
Q8C2Q3_R	Rbm14	RNA-bindin	R.AQPSVSLGAAYR.A	25.97	54.01	0.48	2.08
Q8C2Q3_R	Rbm14	RNA-bindin	R.AQPSVSLGAPYR.G	14.54	56.39	0.26	3.88
Q8C2Q3_R	Rbm14	RNA-bindin	R.ASYDDPYKK.A	22.64	19.92	1.14	0.88
Q8C2Q3_R	Rbm14	RNA-bindin	R.ASYVAPLTAQPATYR.A	15.59	65.60	0.24	4.21
Q8C2Q3_R	Rbm14	RNA-bindin	R.INVELSTK#.G	67.90	62.60	1.08	0.92
Q8C2Q3_R	Rbm14	RNA-bindin	K.K#GPALAIQSGDK#.T	33.32	36.41	0.92	1.09
Q8C2Q3_R	Rbm14	RNA-bindin	K.KGPALAIQSGDKTK.K	24.44	19.08	1.28	0.78
Q8C2Q3_R	Rbm14	RNA-bindin	K.KPGAGDTAFPGTGGFSATFDYQQAFGNSTGGFDGQAR.Q	2.42	9.29	0.26	3.83
Q8C2Q3_R	Rbm14	RNA-bindin	R.LAELSDYR.R	5.63	14.09	0.40	2.50
Q8C2Q3_R	Rbm14	RNA-bindin	R.LSESQLSFR.R	21.85	89.33	0.24	4.09
Q8C2Q3_R	Rbm14	RNA-bindin	R.TQSSASLAASYAAQQHPQAAASYR.G	21.59	81.09	0.27	3.76
Q8C2Q3_R	Rbm14	RNA-bindin	R.YSGSYNDYLR.A	15.32	56.73	0.27	3.70
Q0VBL3_Q	Rbm15	Protein Rb	R.AATSAVTAYEPLDSLDR.R	5.48	13.63	0.40	2.49
Q0VBL3_Q	Rbm15	Protein Rb	R.EVDEISPEDDQR.A	3.84	11.83	0.32	3.08
Q0VBL3_Q	Rbm15	Protein Rb	R.FGVITEVDIK#.R	17.44	9.91	1.76	0.57
Q0VBL3_Q	Rbm15	Protein Rb	K.QAAGVISLPVGGNK#.D	10.76	8.25	1.30	0.77
Q0VBL3_Q	Rbm15	Protein Rb	R.SDGNAPSASTSSSK.Q	1.57	3.72	0.42	2.37
Q0VBL3_Q	Rbm15	Protein Rb	R.VAFVNFR.R	5.56	17.31	0.32	3.11
Q0VBL3_Q	Rbm15	Protein Rb	R.VGAGAGAAPFR.E	7.25	23.29	0.31	3.21
Q0VBL3_Q	Rbm15	Protein Rb	R.VGAGAGAAPFREVDEISPEDDQR.A	1.42	9.10	0.16	6.42
Q6PHZ5_R	Rbm15b	Putative R	R.ALDYYGLYDDR.G	1.78	7.46	0.24	4.19
Q6PHZ5_R	Rbm15b	Putative R	R.LWVGGLGPNTSLAALAR.E	2.62	10.28	0.26	3.92
Q6PHZ5_R	Rbm15b	Putative R	R.NLVSYLK#.Q	14.79	11.31	1.31	0.76
Q8JZX4_SP	Rbm17	Splicing fac	R.DFPYEEDSRPR.S	2.05	9.46	0.22	4.62
Q8JZX4_SP	Rbm17	Splicing fac	K.HEQGLSTALSVEK#.T	24.83	14.09	1.76	0.57
Q8JZX4_SP	Rbm17	Splicing fac	K.K#SDSNPLTEILK#.C	14.34	9.09	1.58	0.63
Q8JZX4_SP	Rbm17	Splicing fac	K.LLQSQLQVK#.K	114.57	70.45	1.63	0.61
Q8JZX4_SP	Rbm17	Splicing fac	R.QIADTPPHVAAGLKDPVPSGFSAGEVLIPLADEYDPM*FPNDYEK.V	8.73	3.72	2.35	0.43
Q8JZX4_SP	Rbm17	Splicing fac	K.QSTVLAPVIDLK#.R	56.46	44.30	1.27	0.78
Q8JZX4_SP	Rbm17	Splicing fac	K.SDSNPLTEILK#.C	15.53	10.05	1.55	0.65
Q8JZX4_SP	Rbm17	Splicing fac	R.SM*GGAAIAPPTSLVEK#.D	28.28	22.45	1.26	0.79

Q8JZX4_SP	Rbm17	Splicing fac	R.SMGGAAIAPPTSLVEK#.D	19.00	7.25	2.62	0.38
Q8JZX4_SP	Rbm17	Splicing fac	R.VLDLAEQV.-	36.85	36.85	1.00	1.00
Q8R3C6_RI	Rbm19	Probable RI	K.EASQEANAPGSSYK#.K	8.97	5.58	1.61	0.62
Q8R3C6_RI	Rbm19	Probable RI	R.GFGFVDFITK#.Q	17.67	17.12	1.03	0.97
Q8R3C6_RI	Rbm19	Probable RI	K.NLNFSTTEETLK#.G	10.76	8.25	1.30	0.77
Q8R3C6_RI	Rbm19	Probable RI	K.NLPAGTLAAEIQETFSR.F	5.86	24.19	0.24	4.13
Q8R3C6_RI	Rbm19	Probable RI	R.TLGENEEEEDLADSGR.L	5.20	14.50	0.36	2.79
Q8R3C6_RI	Rbm19	Probable RI	R.TQVATWANDALEAK#.L	7.57	5.92	1.28	0.78
Q8R3C6_RI	Rbm19	Probable RI	R.VALGETQLVQEVR.S	2.67	15.06	0.18	5.64
Q8BHS3_RI	Rbm22	Pre-mRNA-	K.ATSTSDM*LLK#.L	16.53	23.24	0.71	1.41
Q8BHS3_RI	Rbm22	Pre-mRNA-	K.ATSTSDMLLK.L	17.07	20.55	0.83	1.20
Q8BHS3_RI	Rbm22	Pre-mRNA-	R.EISNSDGTRPVGM*LGK.A	1.98	9.61	0.21	4.85
Q8BHS3_RI	Rbm22	Pre-mRNA-	R.NHFYQFGEIR.T	5.27	83.45	0.06	15.84
Q8BHS3_RI	Rbm22	Pre-mRNA-	K.SDVNKEYYTQNM*ER.E	7.15	31.08	0.23	4.35
Q8BHS3_RI	Rbm22	Pre-mRNA-	K.TITTLYVGGLGDTITETDLR.N	2.28	14.45	0.16	6.33
Q8BHS3_RI	Rbm22	Pre-mRNA-	R.YYGINDPVADK.L	47.38	52.76	0.90	1.11
B2RY56_RE	Rbm25	RNA-bindin	R.LLIYETEAK#.K	13.31	5.76	2.31	0.43
B2RY56_RE	Rbm25	RNA-bindin	K.LPVDSVFNKFEDEDSDDVPR.K	3.59	18.78	0.19	5.23
B2RY56_RE	Rbm25	RNA-bindin	R.DREEDEEDAYER.R	2.91	20.01	0.15	6.88
B2RY56_RE	Rbm25	RNA-bindin	R.DREEDEEDAYERR.K	2.34	42.27	0.06	18.06
B2RY56_RE	Rbm25	RNA-bindin	K.EDINAIEM*EEDKR.D	2.57	9.26	0.28	3.61
B2RY56_RE	Rbm25	RNA-bindin	R.EKEELEEIR.Q	14.95	47.96	0.31	3.21
B2RY56_RE	Rbm25	RNA-bindin	K.GAIEVLIR.E	16.23	50.21	0.32	3.09
B2RY56_RE	Rbm25	RNA-bindin	K.KLPVDSVFNKFEDEDSDDVPR.K	3.55	6.56	0.54	1.85
B2RY56_RE	Rbm25	RNA-bindin	K.LGASNSPGQPNSVK#.R	56.18	30.11	1.87	0.54
B2RY56_RE	Rbm25	RNA-bindin	R.LLAEGHPDPDAELQR.M	41.17	129.57	0.32	3.15
B2RY56_RE	Rbm25	RNA-bindin	R.LLHDLQIGEK#.K	105.50	78.33	1.35	0.74
B2RY56_RE	Rbm25	RNA-bindin	K.LPVDSVFNKFEDEDSDDVPR.K	5.09	13.40	0.38	2.63
B2RY56_RE	Rbm25	RNA-bindin	R.RFPVAPLIPYPLITK.E	7.60	18.64	0.41	2.45
B2RY56_RE	Rbm25	RNA-bindin	K.TK#AQLDEWK#.A	11.81	6.79	1.74	0.57
B2RY56_RE	Rbm25	RNA-bindin	K.LGASNSPGQPNSVK#.R	11.76	7.74	1.52	0.66
Q6NZN0_RI	Rbm26	RNA-bindin	K.AISSTEAVLNNR.F	7.86	23.62	0.33	3.00
Q6NZN0_RI	Rbm26	RNA-bindin	R.EGTTQQLQTTSPK#.V	31.55	12.51	2.52	0.40
Q6NZN0_RI	Rbm26	RNA-bindin	R.LGPVPSATTEPAEAQSATSELPQNVTK#.L	13.91	6.93	2.01	0.50
Q6NZN0_RI	Rbm26	RNA-bindin	K.TLSVSTPAVDNNEAQK#.K	10.31	3.80	2.72	0.37
Q6NZN0_RI	Rbm26	RNA-bindin	K.VIQPLVQQPILPVVK#.Q	13.79	5.28	2.61	0.38
Q6NZN0_RI	Rbm26	RNA-bindin	K.YVLALVK#.K	11.64	3.23	3.60	0.28
Q5SFM8_RI	Rbm27	RNA-bindin	R.LQLGTPPPLLAAR.L	4.07	15.58	0.26	3.82
Q5SFM8_RI	Rbm27	RNA-bindin	K.LSQLQVEAAR.L	3.52	10.31	0.34	2.93
Q5SFM8_RI	Rbm27	RNA-bindin	K.VPSISTETEEEEVKEEETETSDLFLHDDDDEDEDEYESR.S	2.50	3.00	0.83	1.20
Q8CGC6_RI	Rbm28	RNA-bindin	K.AAEGVSAADMAK#.R	26.56	10.80	2.46	0.41
Q8CGC6_RI	Rbm28	RNA-bindin	K.AEVEQVELPDGK#.K	59.75	28.88	2.07	0.48
Q8CGC6_RI	Rbm28	RNA-bindin	K.AGSTSWSGFQTK#.A	42.52	22.75	1.87	0.54
Q8CGC6_RI	Rbm28	RNA-bindin	K.AVFTHYGTVLEVNIPK#.K	29.23	14.72	1.99	0.50
Q8CGC6_RI	Rbm28	RNA-bindin	R.FNQLVEQYK#.Q	51.60	34.31	1.50	0.66
Q8CGC6_RI	Rbm28	RNA-bindin	R.GFAFVQFK#.N	29.58	15.96	1.85	0.54
Q8CGC6_RI	Rbm28	RNA-bindin	R.GFGYVTFSM*LEDVQR.A	2.41	5.06	0.48	2.10
Q8CGC6_RI	Rbm28	RNA-bindin	R.HFNNNPEIFGSQK#.R	19.50	8.62	2.26	0.44
Q8CGC6_RI	Rbm28	RNA-bindin	R.K#LPSDVTEGK#.T	26.03	18.87	1.38	0.72
Q8CGC6_RI	Rbm28	RNA-bindin	K.K#QQLASSVQAPK#.R	7.18	3.83	1.87	0.53
Q8CGC6_RI	Rbm28	RNA-bindin	K.QQLASSVQAPK#.R	34.00	19.22	1.77	0.57
Q8CGC6_RI	Rbm28	RNA-bindin	R.SDQLEELFSQVGPVK#.Q	18.86	9.86	1.91	0.52
Q8CGC6_RI	Rbm28	RNA-bindin	R.TVAVDWAVAK#.D	52.54	20.64	2.55	0.39
Q8CGC6_RI	Rbm28	RNA-bindin	K.VVQSATQDQSK#.A	10.30	7.25	1.42	0.70
Q8C5L7_RE	Rbm34	RNA-bindin	R.LAALFSTAEPSAPPVFVPVPQETSK#.K	16.03	7.67	2.09	0.48
Q8C5L7_RE	Rbm34	RNA-bindin	R.SVFVGNLPYK#.I	22.70	19.62	1.16	0.86
Q8C5L7_RE	Rbm34	RNA-bindin	K.VADGEALDVALSLAK#.D	12.50	10.48	1.19	0.84
Q8VH51_RI	Rbm39	RNA-bindin	R.AAAM*ANNLQK#.G	42.54	33.03	1.29	0.78
Q8VH51_RI	Rbm39	RNA-bindin	R.AAAMANNLQK#.G	36.70	37.67	0.97	1.03
Q8VH51_RI	Rbm39	RNA-bindin	R.DLEEFFSTVGK#.V	157.30	122.03	1.29	0.78
Q8VH51_RI	Rbm39	RNA-bindin	R.GIFEPFGR.I	20.68	69.52	0.30	3.36
Q8VH51_RI	Rbm39	RNA-bindin	K.HGGVIHIYVDK#.N	32.36	26.66	1.21	0.82
Q8VH51_RI	Rbm39	RNA-bindin	R.IESIQLM*M*DSETGR.S	5.34	14.90	0.36	2.79
Q8VH51_RI	Rbm39	RNA-bindin	R.IESIQLM*MDSETGR.S	4.34	10.96	0.40	2.53
Q8VH51_RI	Rbm39	RNA-bindin	R.IESIQLMMDSETGR.S	5.72	12.33	0.46	2.16
Q8VH51_RI	Rbm39	RNA-bindin	K.IGLPHSIK#.L	28.43	14.61	1.95	0.51
Q8VH51_RI	Rbm39	RNA-bindin	K.M*ITAAYVPLPTYHNLFPDSMTATQLLVPSR.R	1.50	3.84	0.39	2.55
Q8VH51_RI	Rbm39	RNA-bindin	K.NSAQGNVYVK#.C	43.59	32.61	1.34	0.75
Q8VH51_RI	Rbm39	RNA-bindin	R.TDASSASSFLDSDELER.T	23.10	81.33	0.28	3.52
Q8VH51_RI	Rbm39	RNA-bindin	R.TGIDLGTTGR.L	50.02	151.07	0.33	3.02
Q8VH51_RI	Rbm39	RNA-bindin	R.VLGVPIIVQASQAEK#.N	199.78	152.77	1.31	0.76
Q8VH51_RI	Rbm39	RNA-bindin	R.IESIQLM*M*DSETGR.S	3.12	3.62	0.86	1.16
Q8VH51_RI	Rbm39	RNA-bindin	K.NSAQGNVYVK#.C	82.20	40.55	2.03	0.49
Q8VH51_RI	Rbm39	RNA-bindin	R.TDASSASSFLDSDELER.T	4.66	16.97	0.27	3.64
Q8VH51_RI	Rbm39	RNA-bindin	R.VLGVPIIVQASQAEK.N	5.78	9.46	0.61	1.64
Q8VH51_RI	Rbm39	RNA-bindin	R.AAAM*ANNLQK#.G	32.31	14.56	2.22	0.45
Q8VH51_RI	Rbm39	RNA-bindin	R.DLEEFFSTVGK#.V	108.88	68.68	1.59	0.63
Q8VH51_RI	Rbm39	RNA-bindin	R.GIFEPFGR.I	17.99	41.68	0.43	2.32
Q8VH51_RI	Rbm39	RNA-bindin	K.HGGVIHIYVDK#.N	26.51	10.91	2.43	0.41
Q8VH51_RI	Rbm39	RNA-bindin	R.IESIQLM*M*DSETGR.S	4.39	8.82	0.50	2.01
Q8VH51_RI	Rbm39	RNA-bindin	R.IESIQLM*MDSETGR.S	3.25	7.87	0.41	2.42
Q8VH51_RI	Rbm39	RNA-bindin	R.IESIQLMMDSETGR.S	3.57	7.71	0.46	2.16
Q8VH51_RI	Rbm39	RNA-bindin	K.IGLPHSIK#.L	10.68	14.43	0.74	1.35
Q8VH51_RI	Rbm39	RNA-bindin	K.NSAQGNVYVK#.C	43.44	22.62	1.92	0.52
Q8VH51_RI	Rbm39	RNA-bindin	R.SKGIAYVEFVDVSSVPLAIGLTGQR.V	2.55	9.86	0.26	3.87
Q8VH51_RI	Rbm39	RNA-bindin	R.TDASSASSFLDSDELER.T	16.83	45.59	0.37	2.71
Q8VH51_RI	Rbm39	RNA-bindin	R.TGIDLGTTGR.L	24.29	65.56	0.37	2.70
Q8VH51_RI	Rbm39	RNA-bindin	R.VLGVPIIVQASQAEK#.N	152.28	90.68	1.68	0.60
Q8VH51_RI	Rbm39	RNA-bindin	R.DLEEFFSTVGK#.V	12.51	13.66	0.92	1.09
Q8VH51_RI	Rbm39	RNA-bindin	R.TDASSASSFLDSDELER.T	1.71	6.52	0.26	3.81
Q8VH51_RI	Rbm39	RNA-bindin	R.VLGVPIIVQASQAEK#.N	12.73	9.22	1.38	0.72
Q8C7Q4_RI	Rbm4	RNA-bindin	R.ATGPVLTVGEGYGYGHDSELSQASAAAR.N	2.40	7.25	0.33	3.02
Q8C7Q4_RI	Rbm4	RNA-bindin	R.GLDNTEFQGK.R	16.49	18.58	0.89	1.13
Q8C7Q4_RI	Rbm4	RNA-bindin	K.LFIGNLPR.E	2.52	15.72	0.16	6.24
Q8C7Q4_RI	Rbm4	RNA-bindin	R.VADLTEQYNEQYGAVR.T	2.30	8.40	0.27	3.65
Q91V81_RI	Rbm42	RNA-bindin	R.ELGLGLGLGLK#.D	16.95	16.57	1.02	0.98
Q91V81_RI	Rbm42	RNA-bindin	R.GHLDSPEAR.E	2.49	13.44	0.18	5.41
Q91V81_RI	Rbm42	RNA-bindin	K.GYGFVSFKDPSDYVR.A	2.92	15.73	0.19	5.38
Q91V81_RI	Rbm42	RNA-bindin	R.TAAGSSWEDPSLLEWDADDFR.I	2.79	7.16	0.39	2.56
Q91YE7_RE	Rbm5	RNA-bindin	K.DLVLPDGNR.V	2.73	12.78	0.21	4.69
Q91YE7_RE	Rbm5	RNA-bindin	R.ESAAADAGFALFEK.K	9.78	12.91	0.76	1.32
Q91YE7_RE	Rbm5	RNA-bindin	R.GLPITITESDIR.E	4.43	30.07	0.15	6.78
Q91YE7_RE	Rbm5	RNA-bindin	R.HQQLSDLHK#.Q	198.47	43.10	4.60	0.22

Q91YE7_R	Rbm5	RNA-bindin	K.QFDAGTVNYEQPTK#.D	7.79	11.08	0.70	1.42
S4R1W5_S	Rbm6	Protein Rb	R.DAQQDLQDQDYR.T	4.06	15.36	0.26	3.79
S4R1W5_S	Rbm6	Protein Rb	R.GGDFSSSDFQSR.D	1.75	11.12	0.16	6.37
S4R1W5_S	Rbm6	Protein Rb	K.ILQNLDPPFSIDGK.M	9.93	9.59	1.03	0.97
S4R1W5_S	Rbm6	Protein Rb	R.LPGNQIFGYGQSK#.S	11.72	6.55	1.79	0.56
Q9CQT2_R	Rbm7	RNA-bindin	R.EDFYYDDR.N	1.35	6.43	0.21	4.76
Q9CQT2_R	Rbm7	RNA-bindin	R.SFSSPEDYQR.Q	11.60	30.35	0.38	2.62
Q9CQT2_R	Rbm7	RNA-bindin	R.TLFVGNLETK#.V	37.12	32.42	1.14	0.87
Q9CQT2_R	Rbm7	RNA-bindin	R.TVGNVSPTAQM*VQR.S	5.74	23.09	0.25	4.02
Q9CQT2_R	Rbm7	RNA-bindin	R.TVGNVSPTAQMVQR.S	3.59	10.81	0.33	3.01
Q9CQT2_R	Rbm7	RNA-bindin	K.VTEELLFELFHQAGPVIK#.V	65.10	32.91	1.98	0.51
Q9CWZ3_R	Rbm8a	RNA-bindin	K.FAEYGEIK#.N	73.56	71.27	1.03	0.97
Q9CWZ3_R	Rbm8a	RNA-bindin	K.GYTLVEYETYK#.E	85.18	85.10	1.00	1.00
Q9CWZ3_R	Rbm8a	RNA-bindin	R.M*REDYDSVEQDGDEPGPQR.S	7.62	178.66	0.04	23.46
Q91W59_	Rbms1	RNA-bindin	R.GLPPNTTDQDLVK.L	54.00	11.22	4.81	0.21
Q91W59_	Rbms1	RNA-bindin	K.GYGFVDFDSPAAAQK.A	28.09	40.61	0.69	1.45
Q8VC70_R	Rbms2	RNA-bindin	K.ASGVQAQM*AK#.Q	11.26	12.69	0.89	1.13
Q8VC70_R	Rbms2	RNA-bindin	K.ASGVQAQMAK.Q	31.20	39.17	0.80	1.26
Q8VC70_R	Rbms2	RNA-bindin	K.GYGFVDFDSPSSAQK#.A	49.58	50.23	0.99	1.01
Q8VC70_R	Rbms2	RNA-bindin	K.LYVAQQM*APPSPR.N	3.37	18.52	0.18	5.50
Q8R0F5_R	Rbmx2	RNA-bindin	R.APQESEDVDDVTR.E	8.16	27.70	0.29	3.40
Q91VM5_R	Rbmxl1	RNA bindin	K.AIKVEQATKPSFESGR.R	13.21	55.21	0.24	4.18
Q91VM5_R	Rbmxl1	RNA bindin	K.ALEAVFGK#.Y	183.98	212.43	0.87	1.15
Q91VM5_R	Rbmxl1	RNA bindin	R.DSYESYGNSR.S	20.26	111.04	0.18	5.48
Q91VM5_R	Rbmxl1	RNA bindin	R.GFAFVTFESPADAK#.D	151.29	194.57	0.78	1.29
Q91VM5_R	Rbmxl1	RNA bindin	R.GGYM*DDGGYSM*NFNM*SSSR.G	2.71	14.25	0.19	5.26
Q91VM5_R	Rbmxl1	RNA bindin	R.IVEILLM*K#.D	43.59	43.90	0.99	1.01
Q91VM5_R	Rbmxl1	RNA bindin	R.IVEILLMK#.D	52.23	60.11	0.87	1.15
Q91VM5_R	Rbmxl1	RNA bindin	K.LFIGGLNTETNEK.A	174.25	206.49	0.84	1.19
Q91VM5_R	Rbmxl1	RNA bindin	R.REPLPSR.R	4.50	136.07	0.03	30.21
Q91VM5_R	Rbmxl1	RNA bindin	R.RGPPPPPR.S	4.20	83.13	0.05	19.79
Q91VM5_R	Rbmxl1	RNA bindin	R.SDLYSSGR.D	30.75	162.75	0.19	5.29
Q91VM5_R	Rbmxl1	RNA bindin	R.YDDYSSSR.D	16.22	24.73	0.66	1.52
Q05186_R	Rcn1	Reticulocal	K.ASDLDGDLTATR.E	5.25	27.04	0.19	5.15
Q05186_R	Rcn1	Reticulocal	R.HWILPQDYDHAQAEAR.H	1.81	14.28	0.13	7.88
Q05186_R	Rcn1	Reticulocal	R.IDSDGDGLVTTEELK.L	6.37	12.76	0.50	2.00
Q05186_R	Rcn1	Reticulocal	K.IVDRIDSDGDGLVTTEELK.L	1.20	13.52	0.09	11.29
Q8BP92_R	Rcn2	Reticulocal	R.DPTANEDPEWILVEK.D	5.86	5.36	1.09	0.92
Q8BP92_R	Rcn2	Reticulocal	R.EALLGVQEDVDEYVK.L	27.05	20.02	1.35	0.74
Q8BP92_R	Rcn2	Reticulocal	K.KLSEEEILENQDLFLTSEATDYGR.Q	3.11	4.51	0.69	1.45
Q8BP92_R	Rcn2	Reticulocal	R.VIDFDENTALDDTEEGSFR.Q	2.69	10.17	0.26	3.78
Q8BH97_R	Rcn3	Reticulocal	R.DIVVAETLEDLDK.N	2.85	7.04	0.40	2.47
Q8BH97_R	Rcn3	Reticulocal	R.M*DLAGDSDGWVSLAELR.A	2.59	7.72	0.34	2.98
Q8BH97_R	Rcn3	Reticulocal	R.MDLAGDSDGWVSLAELR.A	1.97	7.21	0.27	3.67
Q8CFE3_R	Rcor1	REST corep	R.DFQAISDVIGNK#.S	29.18	17.33	1.68	0.59
Q8CFE3_R	Rcor1	REST corep	R.DNLGMLVWSPNQSLSEAK#.L	6.59	2.42	2.73	0.37
Q8CFE3_R	Rcor1	REST corep	K.LDEYIAIAK#.E	34.54	35.32	0.98	1.02
Q8CFE3_R	Rcor1	REST corep	K.NFFVNYR.R	3.82	12.22	0.31	3.20
Q8CFE3_R	Rcor1	REST corep	K.SIASLVK#.F	25.89	18.40	1.41	0.71
Q8CFE3_R	Rcor1	REST corep	R.VGPQYQAAVPDFDPAK#.L	25.30	18.56	1.36	0.73
Q8CFE3_R	Rcor1	REST corep	R.WTTEEQLLAVQAIR.K	3.27	8.37	0.39	2.56
G3X8R0_G	Reep5	Receptor a	K.ATVNLLGDEK#.K	13.99	9.13	1.53	0.65
O54916_R	Reps1	RalBP1-ass	K.TATNVPANVSK#.G	7.52	2.76	2.72	0.37
Q9CQU3_R	Rer1	Protein RE	R.LGQIYQSWLDK#.S	20.53	10.43	1.97	0.51
Q9CQU3_R	Rer1	Protein RE	K.VDPSLM*EDSDDGPSLPTK#.Q	10.93	8.34	1.31	0.76
Q9D8S4_O	Rexo2	Oligoribon	R.ALDDISESIK#.E	10.01	7.35	1.36	0.73
P35601_RF	Rfc1	Replication	R.GGIQELIGLIK#.H	11.85	12.17	0.97	1.03
P35601_RF	Rfc1	Replication	R.GYM*TQFPSFPSWLGK#.H	5.85	3.24	1.81	0.55
P35601_RF	Rfc1	Replication	K.AALLSGPPGVGK#.T	45.67	38.11	1.20	0.83
P35601_RF	Rfc1	Replication	K.AKEESSYNETELLAAR.R	8.15	35.24	0.23	4.32
P35601_RF	Rfc1	Replication	K.ALTYDQAK#.A	28.97	17.21	1.68	0.59
P35601_RF	Rfc1	Replication	K.AVVAESLNNTSIK#.G	57.46	51.40	1.12	0.89
P35601_RF	Rfc1	Replication	K.EAHLTPYSLQVVK#.T	5.14	38.96	0.13	7.58
P35601_RF	Rfc1	Replication	K.EAHLTPYSLQVVK.T	22.44	23.29	0.96	1.04
P35601_RF	Rfc1	Replication	K.GFYTSGAAPSVSAR.H	12.34	53.87	0.23	4.36
P35601_RF	Rfc1	Replication	R.GGIQELIGLIK#.H	83.82	62.93	1.33	0.75
P35601_RF	Rfc1	Replication	R.GYM*TQFPSFPSWLGK#.H	12.45	12.79	0.97	1.03
P35601_RF	Rfc1	Replication	K.ILDEDGLLDLIR.T	14.03	68.24	0.21	4.86
P35601_RF	Rfc1	Replication	R.K#DSEEGEESFSSVQDDLSK#.A	8.96	8.32	1.08	0.93
P35601_RF	Rfc1	Replication	K.LTPTSVLDYFGTESVQR.S	5.70	17.58	0.32	3.08
P35601_RF	Rfc1	Replication	K.QLQLDEDAELER.Q	4.46	18.70	0.24	4.19
P35601_RF	Rfc1	Replication	K.SAMLSIAFK.E	7.26	8.02	0.91	1.10
P35601_RF	Rfc1	Replication	R.TLALLDEEPK#.I	27.26	27.80	0.98	1.02
P35601_RF	Rfc1	Replication	R.DALVRPLTSQGVEGAQHVIK.L	4.64	9.53	0.49	2.06
P35601_RF	Rfc1	Replication	K.GFYTSGAAPSVSAR.H	3.71	18.39	0.20	4.96
P35601_RF	Rfc1	Replication	R.GGIQELIGLIK#.H	27.69	20.10	1.38	0.73
P35601_RF	Rfc1	Replication	K.ILDEDGLLDLIR.T	3.77	19.55	0.19	5.19
Q9WUK4_	Rfc2	Replication	R.EGNVPNIIIAGPPGTGK#.T	52.17	30.35	1.72	0.58
Q9WUK4_	Rfc2	Replication	K.EKVPYTDDGLEAIIFTAQGDM*R.Q	4.21	9.26	0.45	2.20
Q9WUK4_	Rfc2	Replication	K.IIILDEADSMTDGAQQALR.R	2.70	5.33	0.51	1.97
Q9WUK4_	Rfc2	Replication	K.LNEIVGNEDTVSR.L	19.93	58.63	0.34	2.94
Q9WUK4_	Rfc2	Replication	K.LTDAQVLTR.L	15.39	57.39	0.27	3.73
Q9WUK4_	Rfc2	Replication	K.TAGHYELPWVEK#.Y	29.94	18.62	1.61	0.62
Q9WUK4_	Rfc2	Replication	R.EGNVPNIIIAGPPGTGK#.T	6.26	3.90	1.60	0.62
Q9WUK4_	Rfc2	Replication	R.EGNVPNIIIAGPPGTGK#.T	13.88	8.34	1.66	0.60
Q9WUK4_	Rfc2	Replication	K.LNEIVGNEDTVSR.L	4.42	10.17	0.43	2.30
Q8R323_R	Rfc3	Replication	K.EGLALPSTLAR.R	4.79	19.97	0.24	4.17
Q8R323_R	Rfc3	Replication	R.ETANAIVSQQTPQR.L	4.72	15.85	0.30	3.36
Q8R323_R	Rfc3	Replication	K.TVAQSQQLETSSQR.D	8.72	28.72	0.30	3.29
Q8R323_R	Rfc3	Replication	R.VQQYPFTEDQEIPETDWEVYLR.E	3.23	8.14	0.40	2.52
Q8R323_R	Rfc3	Replication	R.ETANAIVSQQTPQR.L	3.35	8.57	0.39	2.56
Q8R323_R	Rfc3	Replication	K.TVAQSQQLETSSQR.D	4.67	14.14	0.33	3.02
Q8R323_R	Rfc3	Replication	R.ETANAIVSQQTPQR.L	5.81	18.01	0.32	3.10
Q8R323_R	Rfc3	Replication	K.TVAQSQQLETSSQR.D	10.07	30.70	0.33	3.05
Q99J62_RF	Rfc4	Replication	K.AITFLQSATR.L	12.76	28.67	0.45	2.25
Q99J62_RF	Rfc4	Replication	K.DRGTPATAGSSGETK.K	1.34	3.76	0.36	2.80
Q99J62_RF	Rfc4	Replication	R.ELFGPELFR.L	25.22	60.70	0.42	2.41
Q99J62_RF	Rfc4	Replication	R.GTPATAGSSGETK#.K	8.49	6.18	1.37	0.73
Q99J62_RF	Rfc4	Replication	K.IGNEEIAYLVK#.I	71.59	43.22	1.66	0.60
Q99J62_RF	Rfc4	Replication	K.IVILDEADSM*TSAAQAALR.R	2.38	5.72	0.42	2.40
Q99J62_RF	Rfc4	Replication	K.IVILDEADSMTSAAQAALR.R	8.60	26.09	0.33	3.03
Q99J62_RF	Rfc4	Replication	R.K#SLEGADLPNLLFYGPPGTGK#.T	39.59	21.78	1.82	0.55
Q99J62_RF	Rfc4	Replication	R.LLDIAEK#ENVK#.I	108.13	65.56	1.65	0.61

Q99J62_RF	Rfc4	Replication	K.NFAQLTVSGSR.S	16.68	40.38	0.41	2.42
Q99J62_RF	Rfc4	Replication	K.SLEGADLPNLLFYGPPGTGK#.T	55.54	41.63	1.33	0.75
Q99J62_RF	Rfc4	Replication	K.TSTILAAAR.E	21.02	45.91	0.46	2.18
Q99J62_RF	Rfc4	Replication	R.VLELNASDER.G	47.90	116.15	0.41	2.42
Q99J62_RF	Rfc4	Replication	K.SLEGADLPNLLFYGPPGTGK#.T	3.57	4.13	0.86	1.16
Q99J62_RF	Rfc4	Replication	K.IGNEEIAYLVK#.I	9.98	6.71	1.49	0.67
Q99J62_RF	Rfc4	Replication	K.SLEGADLPNLLFYGPPGTGK#.T	5.59	4.55	1.23	0.81
Q9D0F6_RI	Rfc5	Replication	R.ALNILQSTNM*AFGK#.V	17.46	11.67	1.50	0.67
Q9D0F6_RI	Rfc5	Replication	K.ALVTLSSGDM*R.R	10.46	29.37	0.36	2.81
Q9D0F6_RI	Rfc5	Replication	K.ALVTLSSGDMR.R	4.08	11.05	0.37	2.71
Q9D0F6_RI	Rfc5	Replication	R.FGPLTPELM*VPR.L	10.07	27.18	0.37	2.70
Q9D0F6_RI	Rfc5	Replication	R.FGPLTPELMVPR.L	6.45	14.11	0.46	2.19
Q9D0F6_RI	Rfc5	Replication	R.GPILSFASTR.T	21.28	40.83	0.52	1.92
Q9D0F6_RI	Rfc5	Replication	K.IQLSSLIAAFQVTR.D	3.93	10.78	0.36	2.74
Q9D0F6_RI	Rfc5	Replication	R.LPHLLLYGPPGTGK#.T	13.05	7.86	1.66	0.60
Q9D0F6_RI	Rfc5	Replication	R.LSVGTSEK#.I	44.31	29.88	1.48	0.67
Q9D0F6_RI	Rfc5	Replication	K.LVILDEADAM*TQDAQNALR.R	1.63	4.17	0.39	2.55
Q9D0F6_RI	Rfc5	Replication	R.ALNILQSTNM*AFGK#.V	7.31	5.42	1.35	0.74
Q9D0F6_RI	Rfc5	Replication	R.FGPLTPELM*VPR.L	4.19	11.02	0.38	2.63
Q9D0F6_RI	Rfc5	Replication	R.GPILSFASTR.T	7.31	11.06	0.66	1.51
Q9D0F6_RI	Rfc5	Replication	R.LEHVVQEENVDISEDGM*K#.A	15.06	18.37	0.82	1.22
Q9D0F6_RI	Rfc5	Replication	R.ALNILQSTNM*AFGK#.V	12.69	6.64	1.91	0.52
Q9D0F6_RI	Rfc5	Replication	R.FGPLTPELM*VPR.L	9.88	28.31	0.35	2.86
Q9D0F6_RI	Rfc5	Replication	R.GPILSFASTR.T	11.12	28.09	0.40	2.53
Q9D0F6_RI	Rfc5	Replication	K.IQLSSLIAAFQVTR.D	3.58	6.89	0.52	1.93
Q9D0F6_RI	Rfc5	Replication	R.LEHVVQEENVDISEDGM*K#.A	45.01	35.30	1.28	0.78
Q9D0F6_RI	Rfc5	Replication	R.LEHVVQEENVDISEDGMK#.A	11.73	6.26	1.87	0.53
Q9D0F6_RI	Rfc5	Replication	R.VDFPSSVR.I	4.30	14.46	0.30	3.36
Q9D0F6_RI	Rfc5	Replication	K.YRPQTLADLISHQDILSTIQK.F	3.03	7.65	0.40	2.53
P48377_RF	Rfx1	MHC class I	R.ASPATVQWLLDNYETAEGVSLPR.S	3.23	11.58	0.28	3.59
P48377_RF	Rfx1	MHC class I	R.SVVQATPQTK#.A	15.83	11.27	1.40	0.71
P48377_RF	Rfx1	MHC class I	R.SLPDFAELDLQGK#.V	11.31	5.36	2.11	0.47
Q99PG4_R	Rgs18	Regulator c	K.EPQQIILK.A	13.48	14.48	0.93	1.07
Q921J2_RH	Rheb	GTP-bindin	K.ALAESWNAAFLESSAK#.E	92.15	34.64	2.66	0.38
Q921J2_RH	Rheb	GTP-bindin	R.IILEAEK#IDGAASQGK#.S	128.54	44.93	2.86	0.35
Q921J2_RH	Rheb	GTP-bindin	K.SSLTIQFVEGQFVDSYDPTIENTFTK#.L	33.32	11.60	2.87	0.35
Q9QUI0_RH	Rhoa	Transformi	K.QVELALWDTAGQEDYDR.L	3.15	9.33	0.34	2.96
P84096_RH	Rhog	Rho-relatec	K.EYIPTVFDNYSAQSAVDGR.T	1.69	3.79	0.45	2.24
P84096_RH	Rhog	Rho-relatec	R.LK#EQGQAPITPQQGQALAK#.Q	16.07	9.15	1.76	0.57
Q3TIR3_RI	Ric8a	Synembryn	K.LLVSVLEQGLSPK#.H	14.62	3.17	4.61	0.22
Q6PR54_RI	Rif1	Telomere-a	R.FASDLIEPVTLDTPLSK.N	13.68	7.48	1.83	0.55
Q6PR54_RI	Rif1	Telomere-a	K.AQM*STEIDSAR.V	29.52	4.85	6.09	0.16
Q6PR54_RI	Rif1	Telomere-a	R.FASDLIEPVTLDTPLSK#.N	9.44	10.71	0.88	1.13
Q6PR54_RI	Rif1	Telomere-a	K.SPQRSSDWSR.K	17.11	16.99	1.01	0.99
Q6PR54_RI	Rif1	Telomere-a	R.SQEDEISPVNK#.I	10.92	12.14	0.90	1.11
Q6PR54_RI	Rif1	Telomere-a	R.FASDLIEPVTLDTPLSK#.N	13.22	15.26	0.87	1.15
Q6PR54_RI	Rif1	Telomere-a	K.FDGSETRPFSPSPLNNISSTVTVR.N	6.01	5.63	1.07	0.94
Q6PR54_RI	Rif1	Telomere-a	R.GATALEM*GM*PLLLQK#.Q	7.87	7.50	1.05	0.95
Q6PR54_RI	Rif1	Telomere-a	R.GLEEIPIFDISEK#.A	16.14	16.24	0.99	1.01
Q6PR54_RI	Rif1	Telomere-a	K.ILLLLPGLENVEM*M*DESSEPYSESTENSQLNVK#.I	7.26	5.44	1.33	0.75
Q6PR54_RI	Rif1	Telomere-a	K.IVLSLEPLEHPLISSPSFFSK#.Y	34.39	29.97	1.15	0.87
Q6PR54_RI	Rif1	Telomere-a	R.LIEQAPVQM*GEESVR.W	1.92	6.11	0.31	3.18
Q6PR54_RI	Rif1	Telomere-a	K.LTDESPIQENLTEK#.G	13.64	16.84	0.81	1.23
Q6PR54_RI	Rif1	Telomere-a	R.NDAFVAADSEK#.S	12.80	8.13	1.57	0.64
Q6PR54_RI	Rif1	Telomere-a	K.SGSEVLTLLLK#.S	29.95	23.19	1.29	0.77
Q6PR54_RI	Rif1	Telomere-a	R.SQEDEISPVNK.I	13.70	15.37	0.89	1.12
Q6PR54_RI	Rif1	Telomere-a	K.TIGDLSTLTASEIK#.T	8.88	10.21	0.87	1.15
Q9JJC6_RIF	Rilpl1	RILP-like pr	R.DDGYTEQGQEALQHL.-	10.34	10.34	1.00	1.00
Q9JJC6_RIF	Rilpl1	RILP-like pr	K.VELEADLQTK#.E	21.67	11.40	1.90	0.53
Q9JJC6_RIF	Rilpl1	RILP-like pr	K.VFLLQEELAYYK#.S	14.23	7.78	1.83	0.55
Q9JJC6_RIF	Rilpl1	RILP-like pr	R.TSPQPESGIK#R@.L	77.59	1.81	42.83	0.02
Q99LE1_RI	Rilpl2	RILP-like pr	K.AGVSGAQVNLGPDK#.M	8.86	8.30	1.07	0.94
Q921Q7_R	Rin1	Ras and Ral	R.VTQPDAFGLFLYK#.D	9.95	3.78	2.63	0.38
O35730_RI	Ring1	E3 ubiquiti	R.GVAGGGEGPEEPALPSLEGVSEK#.Q	5.51	4.95	1.11	0.90
O35730_RI	Ring1	E3 ubiquiti	R.GVAGGGEGPEEPALPSLEGVSEK#.Q	5.71	7.63	0.75	1.34
O35730_RI	Ring1	E3 ubiquiti	R.SLRPDPNFDALISK.I	10.56	32.26	0.33	3.05
Q922Q2_RI	Riok1	Serine/thre	K.LNVTDSVTNK#.V	25.14	7.83	3.21	0.31
Q9CQS5_RI	Riok2	Serine/thre	K.ESDIYIVANEAGQQLALK#.L	17.22	5.07	3.40	0.29
Q9CQS5_RI	Riok2	Serine/thre	R.LTNAGYDYLALK#.T	19.16	9.14	2.10	0.48
Q9CQS5_RI	Riok2	Serine/thre	R.QVVESVGNQM*GVGK#.E	12.20	5.45	2.24	0.45
Q9CQS5_RI	Riok2	Serine/thre	R.SVTEFSEESR.R	3.11	9.38	0.33	3.02
Q60855_RI	Ripk1	Receptor-ir	R.AEYNEVLLEEGK#.M	8.40	5.70	1.47	0.68
Q60855_RI	Ripk1	Receptor-ir	R.AEYNEVLLEEGK#.M	8.46	5.76	1.47	0.68
Q9QZL0_RI	Ripk3	Receptor-ir	K.DK#VDAAVSEVK#.H	18.97	13.02	1.46	0.69
Q9CWY8_R	Rnaseh2a	Ribonuclea	R.FSWSTAQAILEK#.E	18.91	3.40	5.57	0.18
Q9CWY8_R	Rnaseh2a	Ribonuclea	R.LADLEALK#.V	21.60	2.21	9.76	0.10
Q9CWY8_R	Rnaseh2a	Ribonuclea	R.LQQHFPGIEVTVK#.A	18.18	6.16	2.95	0.34
Q9CQE0_RI	Rnf138	E3 ubiquiti	R.ALDLENIM*R.R	2.68	7.57	0.35	2.82
Q9CQE0_RI	Rnf138	E3 ubiquiti	R.ALDLENIM*R.R	18.52	48.69	0.38	2.63
Q9CQJ4_RI	Rnf2	E3 ubiquiti	K.HNNQQALSHSIEEGLK#.I	25.78	23.25	1.11	0.90
Q9CQJ4_RI	Rnf2	E3 ubiquiti	R.SK#GESNQM*NLDTASEK#.Q	10.46	5.53	1.89	0.53
Q9CQJ4_RI	Rnf2	E3 ubiquiti	R.TPQEAITDGLEIVVSPR.S	6.25	18.33	0.34	2.93
Q5DTM8_B	Rnf20	E3 ubiquiti	R.AVEEQIEYLQK#.K	24.37	25.37	0.96	1.04
Q5DTM8_B	Rnf20	E3 ubiquiti	K.LGGVSSTEELDIR.T	6.23	21.36	0.29	3.43
Q5DTM8_B	Rnf20	E3 ubiquiti	K.LHDFQDEIVENSVTK.E	12.87	15.83	0.81	1.23
Q5DTM8_B	Rnf20	E3 ubiquiti	K.LLKEEKEELADQVLTLK.T	12.09	12.36	0.98	1.02
Q5DTM8_B	Rnf20	E3 ubiquiti	R.LQELTDLLQEK#.H	22.05	16.71	1.32	0.76
Q5DTM8_B	Rnf20	E3 ubiquiti	K.LRTEVIQLEDTLAQVR.K	1.25	14.66	0.09	11.76
Q5DTM8_B	Rnf20	E3 ubiquiti	R.SGSALLQSQSSTEDPKDEPTELKQDSEDLATHSSALK.A	4.27	5.93	0.72	1.39
Q5DTM8_B	Rnf20	E3 ubiquiti	K.TAVEDSGTTVETIK#.L	22.80	19.35	1.18	0.85
Q5DTM8_B	Rnf20	E3 ubiquiti	R.TEVIQLEDTLAQVR.K	3.29	12.75	0.26	3.87
E9Q555_R	Rnf213	E3 ubiquiti	K.DLNTSK#PSVDK#.G	17.20	10.59	1.62	0.62
E9Q555_R	Rnf213	E3 ubiquiti	K.DNIQALSIFTASLPEAR.Y	2.01	13.47	0.15	6.71
E9Q555_R	Rnf213	E3 ubiquiti	K.FGTLLSAVITK#.S	38.87	17.77	2.19	0.46
E9Q555_R	Rnf213	E3 ubiquiti	K.FLPEILALQR.D	7.94	33.48	0.24	4.22
E9Q555_R	Rnf213	E3 ubiquiti	K.FSEVFSNM*QR.L	2.32	5.09	0.46	2.19
E9Q555_R	Rnf213	E3 ubiquiti	K.GLPLDGGPALSAFK#.G	25.56	20.16	1.27	0.79
E9Q555_R	Rnf213	E3 ubiquiti	R.GM*EFVQSFSK.Q	14.04	19.00	0.74	1.35
E9Q555_R	Rnf213	E3 ubiquiti	R.IASVEYLQEVAR.V	5.25	21.60	0.24	4.12
E9Q555_R	Rnf213	E3 ubiquiti	R.ILTIHPQVLSSLSQAAEK#.H	27.28	19.19	1.42	0.70
E9Q555_R	Rnf213	E3 ubiquiti	K.QFPVPLINR.L	5.21	11.71	0.45	2.25
E9Q555_R	Rnf213	E3 ubiquiti	K.SLSPFDDVVDQTPVIR.S	2.34	10.67	0.22	4.55
E9Q555_R	Rnf213	E3 ubiquiti	R.SLVDNTLPLLK#.I	29.56	23.53	1.26	0.80

E9Q555_RI	Rnf213	E3 ubiquiti	R.SPGHLYLVEIPQGLSVQPK.R	19.38	11.69	1.66	0.60
E9Q555_RI	Rnf213	E3 ubiquiti	R.TDAQSNLAPSDLAEVK#.D	13.52	11.70	1.16	0.87
E9Q555_RI	Rnf213	E3 ubiquiti	K.TQQAAAPQQAAAPEPTSAFNPR.D	3.67	8.31	0.44	2.26
E9Q555_RI	Rnf213	E3 ubiquiti	R.TQTGHVLGSPQSSGVAEVSDR.G	6.72	19.78	0.34	2.94
E9Q555_RI	Rnf213	E3 ubiquiti	K.VGFVGISNWALDPAK#.M	17.54	14.96	1.17	0.85
E9Q555_RI	Rnf213	E3 ubiquiti	K.VPLVPQAPLPNIQAYLQSHYQVPK#.R	16.17	10.00	1.62	0.62
E9Q555_RI	Rnf213	E3 ubiquiti	R.YKEEVSTVELIK.Q	12.96	6.69	1.94	0.52
E9Q555_RI	Rnf213	E3 ubiquiti	K.YTAINEINK#.T	19.05	12.41	1.54	0.65
Q3U319_BI	Rnf40	E3 ubiquiti	R.EGPSLGPPPAASTLSR.A	3.07	13.84	0.22	4.51
Q3U319_BI	Rnf40	E3 ubiquiti	R.ISLEYSELQDK.V	10.56	10.70	0.99	1.01
Q3U319_BI	Rnf40	E3 ubiquiti	R.K#VEVYADADEILQEEIK#EYK#.A	6.69	7.84	0.85	1.17
Q3U319_BI	Rnf40	E3 ubiquiti	K.LLREEKDELGEQVLGLK.S	6.18	11.37	0.54	1.84
O55236_M	Rngtt	mRNA-capp	K.GVTQVTTQPK#.L	12.32	5.57	2.21	0.45
O55236_M	Rngtt	mRNA-capp	K.LGAIFLEGITVK#.G	14.24	5.85	2.43	0.41
Q99M28_R	Rnps1	RNA-bindin	K.DHIM*EIFSTYGK#.I	29.79	27.09	1.10	0.91
Q99M28_R	Rnps1	RNA-bindin	K.DHIMEIFSTYGK#.I	33.81	35.56	0.95	1.05
Q99M28_R	Rnps1	RNA-bindin	K.GYAYVEFENPDEAEK#.A	123.13	120.22	1.02	0.98
Q99M28_R	Rnps1	RNA-bindin	K.HM*DGGQIDGQEITATAVLAPWPRPPPR.R	2.87	41.98	0.07	14.65
Q99M28_R	Rnps1	RNA-bindin	K.HMDGGQIDGQEITATAVLAPWPRPPPR.R	2.01	6.85	0.29	3.41
Q99M28_R	Rnps1	RNA-bindin	K.MIDM*PVER.M	7.25	27.47	0.26	3.79
Q99M28_R	Rnps1	RNA-bindin	K.M*IDMPVER.M	5.86	27.89	0.21	4.76
Q99M28_R	Rnps1	RNA-bindin	K.M*IDM*PVER.M	14.17	67.12	0.21	4.74
Q99M28_R	Rnps1	RNA-bindin	R.M*LPPPPMWR.R	6.09	27.61	0.22	4.53
Q99M28_R	Rnps1	RNA-bindin	R.NVTK#DHIM*EIFSTYGK#.I	19.88	12.99	1.53	0.65
Q99M28_R	Rnps1	RNA-bindin	R.NVTK#DHIMEIFSTYGK#.I	14.08	9.36	1.50	0.67
Q99M28_R	Rnps1	RNA-bindin	K.GYAYVEFENPDEAEK#.A	24.77	26.36	0.94	1.06
P70335_R(	Rock1	Rho-associa	R.LLEFELAQLTK#.Q	7.34	10.24	0.72	1.39
P70335_R(	Rock1	Rho-associa	R.ELQDQLEAEQYFSTLYK#.T	5.95	3.05	1.95	0.51
P70335_R(	Rock1	Rho-associa	R.GAFGEVQLVR.H	7.79	11.59	0.67	1.49
P70335_R(	Rock1	Rho-associa	R.LLEFELAQLTK#.Q	11.94	4.65	2.57	0.39
P70336_R(	Rock2	Rho-associa	K.EQSNPYM*VLDIDK.L	3.31	1.82	1.82	0.55
P70336_R(	Rock2	Rho-associa	K.NLLLLANSTEEQQK#.W	7.10	3.21	2.22	0.45
Q8VEE4_RF	Rpa1	Replication	R.ATAFNEQVDK#.F	45.23	25.03	1.81	0.55
Q8VEE4_RF	Rpa1	Replication	R.ATAFNEQVDK#FFPLIEVNK#.V	30.16	19.64	1.54	0.65
Q8VEE4_RF	Rpa1	Replication	K.AYGASK#PFGK#PAGTGLLQPSGGTQSK#.V	6.64	5.46	1.22	0.82
Q8VEE4_RF	Rpa1	Replication	K.EKNEQAFEEVFQNANFR.S	7.04	12.31	0.57	1.75
Q8VEE4_RF	Rpa1	Replication	K.LFSLELVDESGEIR.A	8.96	22.70	0.39	2.53
Q8VEE4_RF	Rpa1	Replication	R.NIYLM*DM*SGK#.V	10.21	6.09	1.68	0.60
Q8VEE4_RF	Rpa1	Replication	K.SENLGQGDKADYFSTVAAVVFLR.K	6.01	12.90	0.47	2.15
Q8VEE4_RF	Rpa1	Replication	R.SLSVLSSSTVIVNPDIPEAYK#.L	27.14	13.02	2.08	0.48
Q8VEE4_RF	Rpa1	Replication	R.VKLETYNDESR.I	4.47	12.74	0.35	2.85
Q8VEE4_RF	Rpa1	Replication	K.VVPIASLTPYQSK#.W	48.51	32.40	1.50	0.67
Q8VEE4_RF	Rpa1	Replication	K.VVVLMDLEVM*K#.S	6.23	4.29	1.45	0.69
Q8VEE4_RF	Rpa1	Replication	K.VVVLMDLEVMK#.S	7.64	4.94	1.55	0.65
Q8VEE4_RF	Rpa1	Replication	K.LFSLELVDESGEIRATAFNEQVDK#FFPLIEVNK#.V	2.56	5.36	0.48	2.09
Q8VEE4_RF	Rpa1	Replication	R.ATAFNEQVDK#.F	24.00	11.86	2.02	0.49
Q8VEE4_RF	Rpa1	Replication	R.ATAFNEQVDK#FFPLIEVNK#.V	47.68	32.81	1.45	0.69
Q8VEE4_RF	Rpa1	Replication	K.LFSLELVDESGEIR.A	7.73	22.25	0.35	2.88
Q8VEE4_RF	Rpa1	Replication	K.NEQAFEEVFQNANFR.S	2.63	4.57	0.57	1.74
Q8VEE4_RF	Rpa1	Replication	R.SGGAGGGNTNWK#.T	17.00	7.58	2.24	0.45
Q8VEE4_RF	Rpa1	Replication	R.SLSVLSSSTVIVNPDIPEAYK#.L	21.82	12.43	1.76	0.57
Q8VEE4_RF	Rpa1	Replication	K.SYEDSIK#.I	23.38	9.15	2.56	0.39
Q8VEE4_RF	Rpa1	Replication	R.VKLETYNDESR.I	4.03	10.76	0.37	2.67
Q8VEE4_RF	Rpa1	Replication	K.VVPIASLTPYQSK#.W	64.68	28.03	2.31	0.43
Q8VEE4_RF	Rpa1	Replication	R.ATAFNEQVDK#FFPLIEVNK#.V	21.97	10.90	2.02	0.50
Q8VEE4_RF	Rpa1	Replication	K.LFSLELVDESGEIR.A	5.07	12.24	0.41	2.41
Q8VEE4_RF	Rpa1	Replication	R.SLSVLSSSTVIVNPDIPEAYK#.L	7.13	4.53	1.57	0.64
Q8VEE4_RF	Rpa1	Replication	R.SLSVLSSSTVIVNPDIPEAYK#.L	4.71	3.08	1.53	0.65
Q8VEE4_RF	Rpa1	Replication	K.VVPIASLTPYQSK#.W	13.35	5.79	2.30	0.43
Q62193_RI	Rpa2	Replication	K.APTNIVYK#.I	131.66	53.76	2.45	0.41
Q62193_RI	Rpa2	Replication	K.IDDM*TAPPM*DVR.Q	8.83	17.41	0.51	1.97
Q62193_RI	Rpa2	Replication	R.IGDVEISQVTIVGIIR.H	7.83	23.83	0.33	3.04
Q62193_RI	Rpa2	Replication	R.QWVDTDDASGENAVVPPETYVK#.V	6.39	2.67	2.39	0.42
Q62193_RI	Rpa2	Replication	R.SQLQHMPVPSIK#.Q	6.52	4.35	1.50	0.67
Q62193_RI	Rpa2	Replication	K.IDDM*TAPPM*DVR.Q	2.16	3.80	0.57	1.76
Q62193_RI	Rpa2	Replication	R.QWVDTDDASGENAVVPPETYVK#.V	3.41	1.64	2.09	0.48
Q9CQ71_RI	Rpa3	Replication	R.FDLELYNEAVK#.I	25.41	11.19	2.27	0.44
Q9CQ71_RI	Rpa3	Replication	K.IINELPQFFPVGLPQHE.-	131.10	131.10	1.00	1.00
Q9CQ71_RI	Rpa3	Replication	K.M*FILSDGEGK#.N	44.42	20.75	2.14	0.47
Q9D706_RI	Rpap3	RNA polym	K.AVELQLQVK#.H	14.80	9.99	1.48	0.68
Q9D706_RI	Rpap3	RNA polym	R.EKPALIFEVLER.L	5.68	12.13	0.47	2.14
Q9D706_RI	Rpap3	RNA polym	K.IEAVSDTSAPQAQVGVK#.Q	38.32	19.81	1.93	0.52
Q9D706_RI	Rpap3	RNA polym	K.ILHDFYIER.E	4.73	10.98	0.43	2.32
Q9D706_RI	Rpap3	RNA polym	K.INQALTSK#.E	14.70	8.99	1.64	0.61
Q9D706_RI	Rpap3	RNA polym	K.NLDPDVFNQIIK#.I	22.02	15.34	1.44	0.70
Q9D706_RI	Rpap3	RNA polym	K.SDLK#EDSVEELK#K#.R	16.59	8.63	1.92	0.52
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDM*VAEK#.R	20.84	6.28	3.32	0.30
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDMVAEK#.R	13.43	9.29	1.45	0.69
Q6ZWV3_R	Rpl10	60S ribosor	K.DGFHIR.V	30.52	53.33	0.57	1.75
Q6ZWV3_R	Rpl10	60S ribosor	K.EHVIEALR.R	35.44	55.08	0.64	1.55
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDM*VAEK#.R	200.43	81.96	2.45	0.41
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDMVAEK#.R	112.23	48.35	2.32	0.43
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDM*VAEKR.L	62.16	97.16	0.64	1.56
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDM*VAEKR.L	9.11	11.61	0.78	1.27
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDMVAEKR.L	66.57	96.79	0.69	1.45
Q6ZWV3_R	Rpl10	60S ribosor	R.GAFGKPQGTVAR.V	70.70	125.55	0.56	1.78
Q6ZWV3_R	Rpl10	60S ribosor	R.IFDLGR.K	234.07	411.56	0.57	1.76
Q6ZWV3_R	Rpl10	60S ribosor	K.K#WGFTK#.F	59.18	19.18	3.09	0.32
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDM*VAEK#.R	14.04	6.94	2.02	0.49
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDM*VAEK#.R	21.56	7.24	2.98	0.34
Q6ZWV3_R	Rpl10	60S ribosor	K.FNADEFEDMVAEK#.R	13.59	4.38	3.10	0.32
P53026_RL	Rpl10a	60S ribosor	K.AGK#FPSLLTHNENM*VAK#.V	38.98	9.79	3.98	0.25
P53026_RL	Rpl10a	60S ribosor	R.DTLYEAVR.E	33.23	58.75	0.57	1.77
P53026_RL	Rpl10a	60S ribosor	K.FPSLLTHNENM*VAK#.V	11.06	5.18	2.14	0.47
P53026_RL	Rpl10a	60S ribosor	R.ILGPGLNK#.A	213.27	76.61	2.78	0.36
P53026_RL	Rpl10a	60S ribosor	K.K#YDAFLASESLIK#.Q	100.60	36.76	2.74	0.37
P53026_RL	Rpl10a	60S ribosor	K.KYDAFLASESLIK.Q	71.83	28.66	2.51	0.40
P53026_RL	Rpl10a	60S ribosor	K.AGKFPSLLTHNENM*VAK.V	331.29	96.20	3.44	0.29
P53026_RL	Rpl10a	60S ribosor	K.AGK#FPSLLTHNENMVAK#.V	79.17	23.57	3.36	0.30
P53026_RL	Rpl10a	60S ribosor	R.DTLYEAVR.E	267.80	384.35	0.70	1.44
P53026_RL	Rpl10a	60S ribosor	K.FLETVELQISLK#.N	30.66	11.18	2.74	0.36
P53026_RL	Rpl10a	60S ribosor	R.ILGPGLNK#.A	1438.58	533.44	2.70	0.37
P53026_RL	Rpl10a	60S ribosor	K.K#YDAFLASESLIK#.Q	248.40	84.87	2.93	0.34

P53026_Rl	Rpl10a	60S ribosor	K.KYDAFLASESLIKQIPR.I	4.23	6.37	0.66	1.50
P53026_Rl	Rpl10a	60S ribosor	K.YDAFLASESLIK#.Q	323.24	113.33	2.85	0.35
P53026_Rl	Rpl10a	60S ribosor	R.DTLYEAVR.E	37.02	53.41	0.69	1.44
P53026_Rl	Rpl10a	60S ribosor	R.ILGPGLNK#.A	236.71	89.72	2.64	0.38
P53026_Rl	Rpl10a	60S ribosor	K.K#YDAFLASESLIK#.Q	66.83	20.55	3.25	0.31
P53026_Rl	Rpl10a	60S ribosor	K.YDAFLASESLIK#.Q	15.27	4.48	3.41	0.29
P53026_Rl	Rpl10a	60S ribosor	K.AGK#FPSLLTHNENM*VAK#.V	44.19	11.45	3.86	0.26
P53026_Rl	Rpl10a	60S ribosor	R.ILGPGLNK#.A	325.92	109.64	2.97	0.34
P53026_Rl	Rpl10a	60S ribosor	K.K#YDAFLASESLIK#.Q	116.39	37.07	3.14	0.32
P53026_Rl	Rpl10a	60S ribosor	K.KYDAFLASESLIK.Q	54.46	23.02	2.37	0.42
P53026_Rl	Rpl10a	60S ribosor	K.YDAFLASESLIK#.Q	29.55	11.42	2.59	0.39
Q9CXW4_F	Rpl11	60S ribosor	K.AEEILEK#.G	34.93	88.19	0.40	2.52
Q9CXW4_F	Rpl11	60S ribosor	K.VLEQLTGQTPVFSK#.A	34.26	16.36	2.09	0.48
Q9CXW4_F	Rpl11	60S ribosor	R.AAK#VLEQLTGQTPVFSK#.A	6.00	3.53	1.70	0.59
Q9CXW4_F	Rpl11	60S ribosor	K.AEEILEK#.G	884.04	365.94	2.42	0.41
Q9CXW4_F	Rpl11	60S ribosor	R.GAK#AEEILEK#.G	154.92	62.84	2.47	0.41
Q9CXW4_F	Rpl11	60S ribosor	R.KNNFSDTGNFGFGIQEHIDLGIK.Y	22.74	9.28	2.45	0.41
Q9CXW4_F	Rpl11	60S ribosor	K.NNFSDTGNFGFGIQEHIDLGIK#.Y	115.08	38.27	3.01	0.33
Q9CXW4_F	Rpl11	60S ribosor	K.VLEQLTGQTPVFSK#.A	1908.83	662.75	2.88	0.35
Q9CXW4_F	Rpl11	60S ribosor	K.VREYELR.K	11.18	54.90	0.20	4.91
Q9CXW4_F	Rpl11	60S ribosor	K.YDGIILPGK#.-	1722.17	670.35	2.57	0.39
Q9CXW4_F	Rpl11	60S ribosor	K.VLEQLTGQTPVFSK#.A	36.62	15.56	2.35	0.42
Q9CXW4_F	Rpl11	60S ribosor	K.YDGIILPGK#.-	48.20	22.27	2.16	0.46
Q9CXW4_F	Rpl11	60S ribosor	K.VLEQLTGQTPVFSK#.A	55.96	20.28	2.76	0.36
Q9CXW4_F	Rpl11	60S ribosor	K.YDGIILPGK#.-	39.99	13.07	3.06	0.33
P35979_Rl	Rpl12	60S ribosor	K.HSGNITFDEIVNIAR.Q	13.73	19.28	0.71	1.40
P35979_Rl	Rpl12	60S ribosor	R.QAQIEVVPSASALIIK#.A	40.36	13.62	2.96	0.34
P35979_Rl	Rpl12	60S ribosor	R.ELSGTIK#.E	346.92	128.83	2.69	0.37
P35979_Rl	Rpl12	60S ribosor	K.HSGNITFDEIVNIAR.Q	314.35	542.10	0.58	1.72
P35979_Rl	Rpl12	60S ribosor	K.IGPLGLSPK#.K	1516.87	671.91	2.26	0.44
P35979_Rl	Rpl12	60S ribosor	K.K#VGDDIAK#.A	486.58	210.73	2.31	0.43
P35979_Rl	Rpl12	60S ribosor	R.QAQIEVVPSASALIIK#.A	1071.57	360.05	2.98	0.34
P35979_Rl	Rpl12	60S ribosor	K.VGDDIAK#.A	113.78	55.64	2.05	0.49
P35979_Rl	Rpl12	60S ribosor	K.HSGNITFDEIVNIAR.Q	7.42	14.71	0.50	1.98
P35979_Rl	Rpl12	60S ribosor	R.QAQIEVVPSASALIIK#.A	30.54	8.99	3.40	0.29
P35979_Rl	Rpl12	60S ribosor	R.QAQIEVVPSASALIIK#.A	19.07	10.40	1.83	0.55
P47963_Rl	Rpl13	60S ribosor	R.AKEAAEQDVEK.K	86.94	35.29	2.46	0.41
P47963_Rl	Rpl13	60S ribosor	K.EAAEQDVEK#.K	109.16	32.95	3.31	0.30
P47963_Rl	Rpl13	60S ribosor	R.GFSLEELR.V	104.51	126.26	0.83	1.21
P47963_Rl	Rpl13	60S ribosor	K.KGDSSAEELK.L	122.23	34.84	3.51	0.29
P47963_Rl	Rpl13	60S ribosor	K.LATQLTGPVM*PIR.N	78.73	103.63	0.76	1.32
P47963_Rl	Rpl13	60S ribosor	K.LATQLTGPVMPIR.N	56.78	67.60	0.84	1.19
P47963_Rl	Rpl13	60S ribosor	K.STESLQANVQR.L	176.27	197.38	0.89	1.12
P47963_Rl	Rpl13	60S ribosor	R.TIGISVDPR.R	50.56	57.71	0.88	1.14
P47963_Rl	Rpl13	60S ribosor	R.VDTWFNQPAR.K	62.40	75.97	0.82	1.22
P47963_Rl	Rpl13	60S ribosor	R.VITEEEK#.N	120.95	41.43	2.92	0.34
P47963_Rl	Rpl13	60S ribosor	R.AK#EAAEQDVEK#.K	37.64	11.98	3.14	0.32
P47963_Rl	Rpl13	60S ribosor	K.EAAEQDVEK#.K	50.28	14.11	3.56	0.28
P47963_Rl	Rpl13	60S ribosor	R.GFSLEELR.V	164.16	196.23	0.84	1.20
P47963_Rl	Rpl13	60S ribosor	K.KGDSSAEELK.L	45.71	14.80	3.09	0.32
P47963_Rl	Rpl13	60S ribosor	K.KGDSSAEELKLATQLTGPVM*PIR.N	49.49	46.91	1.05	0.95
P47963_Rl	Rpl13	60S ribosor	K.LATQLTGPVM*PIR.N	126.41	165.64	0.76	1.31
P47963_Rl	Rpl13	60S ribosor	K.LATQLTGPVMPIR.N	39.16	57.23	0.68	1.46
P47963_Rl	Rpl13	60S ribosor	K.LILFPR.K	125.59	147.10	0.85	1.17
P47963_Rl	Rpl13	60S ribosor	R.NKSTESLQANVQR.L	3.94	3.31	1.19	0.84
P47963_Rl	Rpl13	60S ribosor	K.STESLQANVQR.L	211.71	256.98	0.82	1.21
P47963_Rl	Rpl13	60S ribosor	R.TIGISVDPR.R	123.40	173.96	0.71	1.41
P47963_Rl	Rpl13	60S ribosor	R.VDTWFNQPAR.K	122.33	163.02	0.75	1.33
P47963_Rl	Rpl13	60S ribosor	R.VITEEEK#.N	75.89	20.94	3.62	0.28
P47963_Rl	Rpl13	60S ribosor	R.VITEEEK#NFK#.A	222.83	52.32	4.26	0.23
P47963_Rl	Rpl13	60S ribosor	R.AK#EAAEQDVEK#.K	3.97	3.26	1.22	0.82
P19253_Rl	Rpl13a	60S ribosor	R.LAHEVGWK#.Y	54.52	14.58	3.74	0.27
P19253_Rl	Rpl13a	60S ribosor	R.M*VVPAALK#.V	78.56	25.11	3.13	0.32
P19253_Rl	Rpl13a	60S ribosor	R.MVVPAALK#.V	43.22	12.65	3.42	0.29
P19253_Rl	Rpl13a	60S ribosor	K.VLDGIPPPYDK#.K	25.16	9.37	2.69	0.37
P19253_Rl	Rpl13a	60S ribosor	K.YQAVTATLEEK#.R	216.67	48.55	4.46	0.22
P19253_Rl	Rpl13a	60S ribosor	R.LAHEVGWK#.Y	78.95	18.33	4.31	0.23
P19253_Rl	Rpl13a	60S ribosor	R.M*VVPAALK#.V	218.41	68.27	3.20	0.31
P19253_Rl	Rpl13a	60S ribosor	R.MVVPAALK#.V	68.03	14.31	4.76	0.21
P19253_Rl	Rpl13a	60S ribosor	K.VLDGIPPPYDK#.K	75.72	22.78	3.32	0.30
P19253_Rl	Rpl13a	60S ribosor	K.YLAFLR.K	32.58	36.19	0.90	1.11
P19253_Rl	Rpl13a	60S ribosor	K.YQAVTATLEEK#.R	316.76	87.08	3.64	0.27
P19253_Rl	Rpl13a	60S ribosor	R.LAHEVGWK#.Y	26.22	19.92	1.32	0.76
P19253_Rl	Rpl13a	60S ribosor	K.YQAVTATLEEK#.R	124.18	42.15	2.95	0.34
P19253_Rl	Rpl13a	60S ribosor	R.MVVPAALK#.V	13.99	3.98	3.52	0.28
P19253_Rl	Rpl13a	60S ribosor	K.YQAVTATLEEK#.R	100.91	29.27	3.45	0.29
Q9CR57_Rl	Rpl14	60S ribosor	K.AAIAAAAAAAAAK#.A	270.62	81.75	3.31	0.30
Q9CR57_Rl	Rpl14	60S ribosor	K.LVAIVDVIDQNR.A	47.87	57.47	0.83	1.20
Q9CR57_Rl	Rpl14	60S ribosor	K.AAIAAAAAAAAAK#.A	1999.66	514.52	3.89	0.26
Q9CR57_Rl	Rpl14	60S ribosor	R.IIK#TEVK#.K	14.04	3.12	4.50	0.22
Q9CR57_Rl	Rpl14	60S ribosor	K.LVAIVDVIDQNR.A	393.67	474.65	0.83	1.21
Q9CR57_Rl	Rpl14	60S ribosor	R.VAYISFGPHAGK#.L	742.65	200.66	3.70	0.27
Q9CR57_Rl	Rpl14	60S ribosor	K.AAIAAAAAAAAAK#.A	100.51	27.62	3.64	0.27
Q9CR57_Rl	Rpl14	60S ribosor	K.LVAIVDVIDQNR.A	14.03	13.48	1.04	0.96
Q9CR57_Rl	Rpl14	60S ribosor	K.AAIAAAAAAAAAK#.A	108.28	32.52	3.33	0.30
Q9CR57_Rl	Rpl14	60S ribosor	K.LVAIVDVIDQNR.A	19.81	18.74	1.06	0.95
Q9CZM2_R	Rpl15	60S ribosor	K.FFEVILIDPFHK#.A	129.17	37.75	3.42	0.29
Q9CZM2_R	Rpl15	60S ribosor	K.FHHTIGGSR.R	15.47	21.39	0.72	1.38
Q9CZM2_R	Rpl15	60S ribosor	K.GATYGK#PVHHGVNQLK#.F	168.89	38.28	4.41	0.23
Q9CZM2_R	Rpl15	60S ribosor	R.SLQSVAEER.A	104.22	116.54	0.89	1.12
Q9CZM2_R	Rpl15	60S ribosor	R.VLNSYWVGEDSTYK#.F	235.41	67.46	3.49	0.29
Q9CZM2_R	Rpl15	60S ribosor	K.FFEVILIDPFHK#.A	94.80	35.89	2.64	0.38
Q9CZM2_R	Rpl15	60S ribosor	K.GATYGK#PVHHGVNQLK#.F	118.17	29.79	3.97	0.25
Q9CZM2_R	Rpl15	60S ribosor	R.NTLQLHR.Y	13.03	15.29	0.85	1.17
Q9CZM2_R	Rpl15	60S ribosor	R.SLQSVAEER.A	108.44	150.35	0.72	1.39
Q9CZM2_R	Rpl15	60S ribosor	R.VLNSYWVGEDSTYK#.F	173.02	59.40	2.91	0.34
Q9CZM2_R	Rpl15	60S ribosor	K.FFEVILIDPFHK#.A	85.50	17.91	4.77	0.21
Q9CZM2_R	Rpl15	60S ribosor	K.GATYGKPVHHGVNQLK.F	10.62	2.74	3.88	0.26
Q9CZM2_R	Rpl15	60S ribosor	K.GATYGK#PVHHGVNQLK#.F	66.27	17.04	3.89	0.26
Q9CZM2_R	Rpl15	60S ribosor	R.SLQSVAEER.A	75.77	91.00	0.83	1.20
Q9CZM2_R	Rpl15	60S ribosor	R.VLNSYWVGEDSTYK#.F	103.89	34.01	3.06	0.33
Q9CZM2_R	Rpl15	60S ribosor	K.GATYGK#PVHHGVNQLK#.F	94.25	28.67	3.29	0.30
Q9CZM2_R	Rpl15	60S ribosor	R.SLQSVAEER.A	49.41	69.43	0.71	1.41

Q9CZM2_R	Rpl15	60S ribosor	R.VLNSYWVGEDSTYK#.F	103.78	29.78	3.49	0.29
Q9CPR4_Rl	Rpl17	60S ribosor	K.EQIVPK#PEEEVAQK#.K	13.42	4.35	3.08	0.32
Q9CPR4_Rl	Rpl17	60S ribosor	K.NAESNAELK#.G	14.68	8.87	1.66	0.60
Q9CPR4_Rl	Rpl17	60S ribosor	R.YSLDPENPTK#.S	46.11	20.45	2.26	0.44
Q9CPR4_Rl	Rpl17	60S ribosor	K.EQIVPK#PEEEVAQK#.K	235.49	93.13	2.53	0.40
Q9CPR4_Rl	Rpl17	60S ribosor	R.ETAQAIK#.G	251.88	91.79	2.74	0.36
Q9CPR4_Rl	Rpl17	60S ribosor	K.GLDVDSLVIEHIQVNK#.A	1371.91	494.48	2.77	0.36
Q9CPR4_Rl	Rpl17	60S ribosor	K.K#SAEFLLHM*LK#.N	241.65	81.24	2.97	0.34
Q9CPR4_Rl	Rpl17	60S ribosor	K.K#SAEFLLHMLK#.N	171.15	62.16	2.75	0.36
Q9CPR4_Rl	Rpl17	60S ribosor	K.NAESNAELK#.G	404.01	135.59	2.98	0.34
Q9CPR4_Rl	Rpl17	60S ribosor	K.NAESNAELK#GLDVDSLVIEHIQVNK#.A	11.77	6.92	1.70	0.59
Q9CPR4_Rl	Rpl17	60S ribosor	K.NAESNAELK#GLDVDSLVIEHIQVNK#APK#.M	16.39	2.91	5.63	0.18
Q9CPR4_Rl	Rpl17	60S ribosor	K.QWGWTQGR.W	74.59	116.90	0.64	1.57
Q9CPR4_Rl	Rpl17	60S ribosor	K.SAEFLLHM*LK#.N	112.73	42.94	2.63	0.38
Q9CPR4_Rl	Rpl17	60S ribosor	K.YLK#DVTLK#.K	366.48	140.22	2.61	0.38
Q9CPR4_Rl	Rpl17	60S ribosor	K.YLK#DVTLK#K#.Q	347.93	96.36	3.61	0.28
Q9CPR4_Rl	Rpl17	60S ribosor	R.YSLDPENPTK#.S	1084.69	419.41	2.59	0.39
Q9CPR4_Rl	Rpl17	60S ribosor	K.GLDVDSLVIEHIQVNK#.A	34.04	14.92	2.28	0.44
Q9CPR4_Rl	Rpl17	60S ribosor	R.YSLDPENPTK#.S	21.34	9.57	2.23	0.45
P35980_Rl	Rpl18	60S ribosor	K.APGTPHSHTKPYVR.S	1.59	2.58	0.62	1.62
P35980_Rl	Rpl18	60S ribosor	K.ILTFDQLALESPK#.G	143.86	42.11	3.42	0.29
P35980_Rl	Rpl18	60S ribosor	K.TAVVVGTVTDDVR.I	53.86	62.48	0.86	1.16
P35980_Rl	Rpl18	60S ribosor	R.TNRPPLSLSR.M	32.45	51.74	0.63	1.59
P35980_Rl	Rpl18	60S ribosor	R.TNSTFNQVVLK.R	64.17	121.63	0.53	1.90
P35980_Rl	Rpl18	60S ribosor	K.AGGK#ILTFDQLALESPK#.G	17.97	2.76	6.50	0.15
P35980_Rl	Rpl18	60S ribosor	R.GTVLLSGPR.K	93.13	138.00	0.67	1.48
P35980_Rl	Rpl18	60S ribosor	K.ILTFDQLALESPK#.G	829.79	241.98	3.43	0.29
P35980_Rl	Rpl18	60S ribosor	R.RTNSTFNQVVLK.R	6.85	8.68	0.79	1.27
P35980_Rl	Rpl18	60S ribosor	R.RTNSTFNQVVLKR.L	7.74	23.03	0.34	2.98
P35980_Rl	Rpl18	60S ribosor	K.SQDIYLR.L	169.22	204.08	0.83	1.21
P35980_Rl	Rpl18	60S ribosor	K.TAVVVGTVTDDVR.I	260.44	302.09	0.86	1.16
P35980_Rl	Rpl18	60S ribosor	R.TNRPPLSLSR.M	112.60	438.42	0.26	3.89
P35980_Rl	Rpl18	60S ribosor	R.TNSTFNQVVLK#.R	770.17	217.37	3.54	0.28
P35980_Rl	Rpl18	60S ribosor	K.ILTFDQLALESPK#.G	67.29	25.17	2.67	0.37
P35980_Rl	Rpl18	60S ribosor	K.TAVVVGTVTDDVR.I	18.30	20.23	0.90	1.11
P35980_Rl	Rpl18	60S ribosor	R.TNSTFNQVVLK#.R	21.79	15.33	1.42	0.70
P35980_Rl	Rpl18	60S ribosor	K.ILTFDQLALESPK#.G	110.85	37.77	2.94	0.34
P35980_Rl	Rpl18	60S ribosor	K.TAVVVGTVTDDVR.I	18.72	27.67	0.68	1.48
P35980_Rl	Rpl18	60S ribosor	R.TNSTFNQVVLK#.R	34.22	10.53	3.25	0.31
P62717_Rl	Rpl18a	60S ribosor	R.AHSIQIMK#.V	13.68	7.38	1.85	0.54
P62717_Rl	Rpl18a	60S ribosor	R.FWYFVSQLK#.K	18.29	8.23	2.22	0.45
P62717_Rl	Rpl18a	60S ribosor	K.NFGIWLR.Y	13.85	16.25	0.85	1.17
P62717_Rl	Rpl18a	60S ribosor	R.AHSIQIM*K#VEEIAAGK#.C	47.36	18.21	2.60	0.38
P62717_Rl	Rpl18a	60S ribosor	R.FWYFVSQLK#.K	114.12	45.58	2.50	0.40
P62717_Rl	Rpl18a	60S ribosor	R.FWYFVSQLK#K#.M	61.57	21.38	2.88	0.35
P62717_Rl	Rpl18a	60S ribosor	K.NFGIWLR.Y	97.20	146.75	0.66	1.51
P62717_Rl	Rpl18a	60S ribosor	K.SRFWYFVSQLKK.M	13.00	12.44	1.05	0.96
P62717_Rl	Rpl18a	60S ribosor	K.VEEIAAGK#.C	512.94	188.87	2.72	0.37
P62717_Rl	Rpl18a	60S ribosor	R.AHSIQIMK#.V	23.87	46.66	0.51	1.95
P62717_Rl	Rpl18a	60S ribosor	R.IFAPNHVVAK#.S	50.59	16.35	3.09	0.32
P62717_Rl	Rpl18a	60S ribosor	K.NFGIWLR.Y	11.84	16.69	0.71	1.41
P62717_Rl	Rpl18a	60S ribosor	K.VEEIAAGK#.C	59.37	20.45	2.90	0.34
P62717_Rl	Rpl18a	60S ribosor	R.AHSIQIM*K#.V	152.44	38.30	3.98	0.25
P62717_Rl	Rpl18a	60S ribosor	R.FWYFVSQLK#.K	19.54	17.64	1.11	0.90
P62717_Rl	Rpl18a	60S ribosor	R.IFAPNHVVAK#.S	111.42	33.74	3.30	0.30
P62717_Rl	Rpl18a	60S ribosor	K.NFGIWLR.Y	21.36	24.10	0.89	1.13
P62717_Rl	Rpl18a	60S ribosor	K.RPNTFF.-	34.93	47.46	0.74	1.36
P62717_Rl	Rpl18a	60S ribosor	K.VEEIAAGK#.C	206.05	52.37	3.93	0.25
P84099_Rl	Rpl19	60S ribosor	R.HM*YHSLYLK#.V	55.23	16.98	3.25	0.31
P84099_Rl	Rpl19	60S ribosor	R.HMYHSLYLK#.V	37.60	15.70	2.40	0.42
P84099_Rl	Rpl19	60S ribosor	R.ILM*EHIHK#.L	21.97	11.90	1.85	0.54
P84099_Rl	Rpl19	60S ribosor	K.TLSK#EEETK#K#.-	5.88	2.89	2.04	0.49
P84099_Rl	Rpl19	60S ribosor	K.VWLDPNETNEIANANSR.Q	24.47	31.98	0.77	1.31
P84099_Rl	Rpl19	60S ribosor	R.HMYHSLYLK#.V	145.35	35.54	4.09	0.24
P84099_Rl	Rpl19	60S ribosor	R.HM*YHSLYLK#.V	127.29	27.57	4.62	0.22
P84099_Rl	Rpl19	60S ribosor	R.ILM*EHIHK#.L	64.99	19.05	3.41	0.29
P84099_Rl	Rpl19	60S ribosor	R.ILMEHIHK#.L	24.67	8.58	2.88	0.35
P84099_Rl	Rpl19	60S ribosor	K.KLLADQAEAR.R	9.19	17.31	0.53	1.88
P84099_Rl	Rpl19	60S ribosor	K.KVWLDPNETNEIANANSR.Q	39.90	50.70	0.79	1.27
P84099_Rl	Rpl19	60S ribosor	R.LASSVLR.C	33.81	38.60	0.88	1.14
P84099_Rl	Rpl19	60S ribosor	K.LLADQAEAR.R	324.43	432.56	0.75	1.33
P84099_Rl	Rpl19	60S ribosor	K.TLSK#EEETK#K#.-	14.08	4.65	3.03	0.33
P84099_Rl	Rpl19	60S ribosor	K.VK#GNVFK#.N	142.71	46.48	3.07	0.33
P84099_Rl	Rpl19	60S ribosor	K.VWLDPNETNEIANANSR.Q	116.82	159.25	0.73	1.36
P84099_Rl	Rpl19	60S ribosor	K.LLADQAEAR.R	8.56	19.53	0.44	2.28
O09167_Rl	Rpl21	60S ribosor	K.GTWVQLK#.R	47.74	19.73	2.42	0.41
O09167_Rl	Rpl21	60S ribosor	R.VYNVTQHAVGIIVNK#.Q	19.82	7.58	2.61	0.38
O09167_Rl	Rpl21	60S ribosor	R.VYNVTQHAVGIIVNK#.Q	79.65	30.08	2.65	0.38
O09167_Rl	Rpl21	60S ribosor	K.EK#GTWVQLK#.R	87.70	22.65	3.87	0.26
O09167_Rl	Rpl21	60S ribosor	K.EPELLEPIPYEFM*A.-	185.99	185.99	1.00	1.00
O09167_Rl	Rpl21	60S ribosor	K.GDIVDIKGM*GTVQK.G	10.82	3.60	3.01	0.33
O09167_Rl	Rpl21	60S ribosor	K.GTWVQLK#.R	441.63	110.89	3.98	0.25
O09167_Rl	Rpl21	60S ribosor	K.HGVVPLATYM*R.I	36.05	71.81	0.50	1.99
O09167_Rl	Rpl21	60S ribosor	K.HGVVPLATYMR.I	45.00	65.08	0.69	1.45
O09167_Rl	Rpl21	60S ribosor	K.K#GDIVDIK#.G	1271.74	388.01	3.28	0.31
O09167_Rl	Rpl21	60S ribosor	R.TNGK#EPELLEPIPYEFM*A.-	216.39	81.62	2.65	0.38
O09167_Rl	Rpl21	60S ribosor	R.TNGK#EPELLEPIPYEFMA.-	38.27	16.00	2.39	0.42
O09167_Rl	Rpl21	60S ribosor	R.VYNVTQHAVGIIVNK#.Q	1488.81	541.27	2.75	0.36
O09167_Rl	Rpl21	60S ribosor	R.VYNVTQHAVGIIVNK#.Q	62.66	24.52	2.56	0.39
P67984_Rl	Rpl22	60S ribosor	K.AGNLGGGVVTIER.S	8.82	11.90	0.74	1.35
P67984_Rl	Rpl22	60S ribosor	R.YFQINQDEEEEEDED.-	5.71	5.71	1.00	1.00
P67984_Rl	Rpl22	60S ribosor	K.AGNLGGGVVTIER.S	232.10	360.39	0.64	1.55
P67984_Rl	Rpl22	60S ribosor	K.ITVTSEVPFSK#.R	248.09	99.27	2.50	0.40
P67984_Rl	Rpl22	60S ribosor	K.SK#ITVTSEVPFSK#.R	79.91	33.76	2.37	0.42
P67984_Rl	Rpl22	60S ribosor	K.SKITVTSEVPFSKR.Y	17.28	27.02	0.64	1.56
P67984_Rl	Rpl22	60S ribosor	R.VVANSKESYELR.Y	4.73	7.23	0.65	1.53
P67984_Rl	Rpl22	60S ribosor	R.YFQINQDEEEEEDED.-	190.55	190.55	1.00	1.00
Q9D7S7_Rl	Rpl22l1	60S ribosor	R.YFQISQDEDGSESED.-	12.64	12.64	1.00	1.00
P62830_Rl	Rpl23	60S ribosor	R.LPAAGVGDM*VM*ATVK#.K	14.63	10.39	1.41	0.71
P62830_Rl	Rpl23	60S ribosor	K.DGVFLYFEDNAGVIVNNK#.G	8.75	4.29	2.04	0.49
P62830_Rl	Rpl23	60S ribosor	K.DGVFLYFEDNAGVIVNNK#GEM*K#.G	40.77	25.81	1.58	0.63
P62830_Rl	Rpl23	60S ribosor	K.GSAITGPVAK#.E	301.95	152.70	1.98	0.51
P62830_Rl	Rpl23	60S ribosor	R.IASNAGSIA.-	62.62	62.62	1.00	1.00

P62830_Rl	Rpl23	60S ribosor	R.K#DGVFLYFEDNAGVIVNNK#.G	10.81	2.23	4.85	0.21
P62830_Rl	Rpl23	60S ribosor	R.LNRLPAAGVGDM*VM*ATVK.K	4.38	9.43	0.46	2.15
P62830_Rl	Rpl23	60S ribosor	R.LNRLPAAGVGDM*VMATVK.K	6.57	12.62	0.52	1.92
P62830_Rl	Rpl23	60S ribosor	R.LNRLPAAGVGDMVMATVK.K	14.17	33.70	0.42	2.38
P62830_Rl	Rpl23	60S ribosor	R.LPAAGVGDM*VM*ATVK#.K	515.43	272.96	1.89	0.53
P62830_Rl	Rpl23	60S ribosor	R.LPAAGVGDMVM*ATVK#.K	52.18	31.56	1.65	0.60
P62830_Rl	Rpl23	60S ribosor	R.LPAAGVGDMVMATVK#.K	89.98	47.17	1.91	0.52
P62830_Rl	Rpl23	60S ribosor	K.NLYIISVK#.G	1858.11	553.46	3.36	0.30
P62830_Rl	Rpl23	60S ribosor	R.LPAAGVGDM*VM*ATVK#.K	8.39	6.31	1.33	0.75
P62830_Rl	Rpl23	60S ribosor	K.NLYIISVK#.G	20.11	8.64	2.33	0.43
P62751_Rl	Rpl23a	60S ribosor	K.EAPAPPKAEAK.A	300.71	74.02	4.06	0.25
P62751_Rl	Rpl23a	60S ribosor	K.FPLTTESAM*K#.K	353.40	477.17	0.74	1.35
P62751_Rl	Rpl23a	60S ribosor	K.FPLTTESAMK#.K	138.67	41.95	3.31	0.30
P62751_Rl	Rpl23a	60S ribosor	K.FPLTTESAM*K#K#.I	162.53	48.12	3.38	0.30
P62751_Rl	Rpl23a	60S ribosor	K.IEDNNTLVFIVDVK#.A	397.91	112.92	3.52	0.28
P62751_Rl	Rpl23a	60S ribosor	K.IEDNNTLVFIVDVK#.A	68.80	16.97	4.06	0.25
P62751_Rl	Rpl23a	60S ribosor	K.K#EAPAPPK#AEAK#.A	273.93	48.48	5.65	0.18
P62751_Rl	Rpl23a	60S ribosor	K.K#IEDNNTLVFIVDVK#.A	686.75	170.93	4.02	0.25
P62751_Rl	Rpl23a	60S ribosor	K.K#LYDIDVAK#.V	501.67	154.79	3.24	0.31
P62751_Rl	Rpl23a	60S ribosor	R.LAPDYDALDVANK#.I	1971.99	506.02	3.90	0.26
P62751_Rl	Rpl23a	60S ribosor	R.LAPDYDALDVANK#IGII.-	18.56	5.94	3.12	0.32
P62751_Rl	Rpl23a	60S ribosor	K.LDHYAIIK#.F	143.04	39.02	3.67	0.27
P62751_Rl	Rpl23a	60S ribosor	K.LDHYAIIK#FPLTTESAM*K#.K	44.25	9.51	4.65	0.22
P62751_Rl	Rpl23a	60S ribosor	K.LDHYAIIKFPLTTESAMK.K	23.76	16.22	1.46	0.68
P62751_Rl	Rpl23a	60S ribosor	K.LYDIDVAK#.V	532.43	178.04	2.99	0.33
P62751_Rl	Rpl23a	60S ribosor	R.NK#LDHYAIIK#.F	501.30	132.14	3.79	0.26
P62751_Rl	Rpl23a	60S ribosor	R.NK#LDHYAIIK#FPLTTESAMK#.K	57.39	14.85	3.86	0.26
P62751_Rl	Rpl23a	60S ribosor	K.VNTLIRPDGEK.K	59.22	79.93	0.74	1.35
P62751_Rl	Rpl23a	60S ribosor	K.VNTLIRPDGEKK.A	17.33	22.52	0.77	1.30
Q8BP67_Rl	Rpl24	60S ribosor	R.AITGASLADIM*AK#.R	32.20	10.04	3.21	0.31
Q8BP67_Rl	Rpl24	60S ribosor	R.AITGASLADIMAK#.R	26.81	6.74	3.98	0.25
Q8BP67_Rl	Rpl24	60S ribosor	K.VFQFLNAK#.C	37.59	10.69	3.52	0.28
Q8BP67_Rl	Rpl24	60S ribosor	R.AITGASLADIM*AK#.R	806.15	263.93	3.05	0.33
Q8BP67_Rl	Rpl24	60S ribosor	R.AITGASLADIMAK#.R	701.30	218.02	3.22	0.31
Q8BP67_Rl	Rpl24	60S ribosor	K.GQSEEIQK#.K	27.32	11.93	2.29	0.44
Q8BP67_Rl	Rpl24	60S ribosor	R.QINWTVLYR.R	209.08	308.63	0.68	1.48
Q8BP67_Rl	Rpl24	60S ribosor	R.TDGK#VFQFLNAK#.C	29.82	9.18	3.25	0.31
Q8BP67_Rl	Rpl24	60S ribosor	K.VFQFLNAK#.C	695.71	248.14	2.80	0.36
Q8BP67_Rl	Rpl24	60S ribosor	R.AITGASLADIMAK#.R	10.07	3.37	2.99	0.33
Q8BP67_Rl	Rpl24	60S ribosor	K.VFQFLNAK#.C	14.50	6.35	2.28	0.44
Q8BP67_Rl	Rpl24	60S ribosor	K.VFQFLNAK#.C	9.43	5.63	1.67	0.60
P61255_Rl	Rpl26	60S ribosor	K.DDEVQVVR.G	285.67	472.07	0.61	1.65
P61255_Rl	Rpl26	60S ribosor	K.EETIEK#M*QE.-	8.11	4.04	2.01	0.50
P61255_Rl	Rpl26	60S ribosor	K.FNPFVTSDR.S	166.16	273.95	0.61	1.65
P61255_Rl	Rpl26	60S ribosor	K.GK#YK#EETIEK#.M	43.75	13.42	3.26	0.31
P61255_Rl	Rpl26	60S ribosor	R.HFNAPSHIR.R	66.50	108.62	0.61	1.63
P61255_Rl	Rpl26	60S ribosor	R.HFNAPSHIR.R	11.59	22.23	0.52	1.92
P61255_Rl	Rpl26	60S ribosor	K.IM*SSPLSK#.E	712.04	293.20	2.43	0.41
P61255_Rl	Rpl26	60S ribosor	R.K#IMSSPLSK#.E	64.23	22.49	2.86	0.35
P61255_Rl	Rpl26	60S ribosor	R.K#IM*SSPLSK#.E	757.72	291.61	2.60	0.38
P61255_Rl	Rpl26	60S ribosor	K.KYVIYIER.V	20.14	38.06	0.53	1.89
P61255_Rl	Rpl26	60S ribosor	-.MKFNPFVTSDR.S	2.62	4.05	0.65	1.54
P61255_Rl	Rpl26	60S ribosor	K.YK#EETIEK#.M	557.65	185.21	3.01	0.33
P61255_Rl	Rpl26	60S ribosor	K.YKEETIEKM*QE.-	120.41	37.05	3.25	0.31
P61255_Rl	Rpl26	60S ribosor	K.YVIYIER.V	174.77	237.66	0.74	1.36
P61358_Rl	Rpl27	60S ribosor	K.DVFRDPALK.R	38.24	80.03	0.48	2.09
P61358_Rl	Rpl27	60S ribosor	K.NK#WFFQK#.L	100.55	37.36	2.69	0.37
P61358_Rl	Rpl27	60S ribosor	K.VVLVLAGR.Y	455.84	785.85	0.58	1.72
P61358_Rl	Rpl27	60S ribosor	R.YSVDIPLDK#.T	1696.88	642.12	2.64	0.38
P14115_Rl	Rpl27a	60S ribosor	R.INFDK#YHPGYFGK#.V	240.12	67.21	3.57	0.28
P14115_Rl	Rpl27a	60S ribosor	K.LWTLVSEQTR.V	122.61	176.63	0.69	1.44
P14115_Rl	Rpl27a	60S ribosor	K.NKTGVAPIIDVVR.S	64.95	53.51	1.21	0.82
P14115_Rl	Rpl27a	60S ribosor	K.TGVAPIIDVVR.S	427.75	700.26	0.61	1.64
P41105_Rl	Rpl28	60S ribosor	R.K#TVGVEPAADGK#.G	14.11	9.13	1.55	0.65
P41105_Rl	Rpl28	60S ribosor	K.QTYSTEPNNLK#.A	42.89	14.53	2.95	0.34
P41105_Rl	Rpl28	60S ribosor	R.SQK#PVVVK#.R	25.68	7.53	3.41	0.29
P41105_Rl	Rpl28	60S ribosor	K.TVGVEPAADGK#.G	105.07	32.73	3.21	0.31
P41105_Rl	Rpl28	60S ribosor	K.GVVVVMK#.R	66.75	50.79	1.31	0.76
P41105_Rl	Rpl28	60S ribosor	K.GVVVVM*K#.R	991.41	234.33	4.23	0.24
P41105_Rl	Rpl28	60S ribosor	R.KPATSYVR.T	89.03	97.37	0.91	1.09
P41105_Rl	Rpl28	60S ribosor	R.K#TVGVEPAADGK#.G	57.19	12.83	4.46	0.22
P41105_Rl	Rpl28	60S ribosor	R.NK#QTYSTEPNNLK#.A	313.68	69.62	4.51	0.22
P41105_Rl	Rpl28	60S ribosor	K.QTYSTEPNNLK#.A	493.78	140.89	3.50	0.29
P41105_Rl	Rpl28	60S ribosor	R.RASAILR.S	19.51	89.23	0.22	4.57
P41105_Rl	Rpl28	60S ribosor	R.SQK#PVVVK#.R	121.04	35.13	3.45	0.29
P41105_Rl	Rpl28	60S ribosor	K.TVGVEPAADGK#.G	1029.41	290.88	3.54	0.28
P47915_Rl	Rpl29	60S ribosor	K.AQASAPAQAPK#.G	247.09	65.15	3.79	0.26
P47915_Rl	Rpl29	60S ribosor	K.GAQAPVK#AP.-	67.98	20.27	3.35	0.30
P47915_Rl	Rpl29	60S ribosor	R.LAFIAHPK#.L	88.33	21.02	4.20	0.24
P47915_Rl	Rpl29	60S ribosor	K.AQASAPAQAPK#.G	1291.43	427.05	3.02	0.33
P47915_Rl	Rpl29	60S ribosor	K.GAQAPVK#AP.-	760.10	220.60	3.45	0.29
P47915_Rl	Rpl29	60S ribosor	R.LAFIAHPK#.L	714.65	203.31	3.52	0.28
P47915_Rl	Rpl29	60S ribosor	R.YESLK#GVDPK#.F	76.97	16.51	4.66	0.21
P47915_Rl	Rpl29	60S ribosor	K.AQASAPAQAPK#.G	29.16	19.89	1.47	0.68
P27659_Rl	Rpl3	60S ribosor	K.AFM*GPLK#.K	30.14	11.37	2.65	0.38
P27659_Rl	Rpl3	60S ribosor	K.AFMGPLK#.K	15.78	4.45	3.54	0.28
P27659_Rl	Rpl3	60S ribosor	K.AFM*GPLK#K#.D	55.27	18.56	2.98	0.34
P27659_Rl	Rpl3	60S ribosor	K.AFMGPLK#K#.D	23.68	29.73	0.80	1.26
P27659_Rl	Rpl3	60S ribosor	K.AHLM*EIQVNGGTVAEK#.L	28.49	7.97	3.58	0.28
P27659_Rl	Rpl3	60S ribosor	K.AHLMEIQVNGGTVAEK#.L	24.49	8.45	2.90	0.35
P27659_Rl	Rpl3	60S ribosor	K.DDASK#PVHLTAFLGYK#.A	47.52	13.97	3.40	0.29
P27659_Rl	Rpl3	60S ribosor	R.ERLEQQVPVNQVFGQDEM*IDVIGVTK.G	30.74	45.01	0.68	1.46
P27659_Rl	Rpl3	60S ribosor	R.ERLEQQVPVNQVFGQDEMIDVIGVTK.G	28.48	35.76	0.80	1.26
P27659_Rl	Rpl3	60S ribosor	R.FQTMEEK#.K	143.45	42.17	3.40	0.29
P27659_Rl	Rpl3	60S ribosor	R.FQTM*EEK#K#.A	15.76	7.81	2.02	0.50
P27659_Rl	Rpl3	60S ribosor	R.HGSLGFLPR.K	114.58	146.19	0.78	1.28
P27659_Rl	Rpl3	60S ribosor	K.IGQGYLIK#.D	695.40	233.78	2.97	0.34
P27659_Rl	Rpl3	60S ribosor	K.K#AHLM*EIQVNGGTVAEK#.L	26.47	10.12	2.62	0.38
P27659_Rl	Rpl3	60S ribosor	R.K#SLLVQTK#.R	198.29	54.26	3.65	0.27
P27659_Rl	Rpl3	60S ribosor	R.LEQQVPVNQVFGQDEM*IDVIGVTK#.G	149.38	44.35	3.37	0.30
P27659_Rl	Rpl3	60S ribosor	R.LEQQVPVNQVFGQDEMIDVIGVTK#.G	108.13	32.99	3.28	0.31
P27659_Rl	Rpl3	60S ribosor	K.NNASTDYDLSDK#.S	642.80	166.53	3.86	0.26
P27659_Rl	Rpl3	60S ribosor	K.SFPK#DDASK#PVHLTAFLGYK#.A	13.87	2.60	5.33	0.19

P27659_Rl	Rpl3	60S ribosor	K.SINPLGGFVHYGEVTNDFIM*LK#.G	193.05	52.99	3.64	0.27
P27659_Rl	Rpl3	60S ribosor	K.SINPLGGFVHYGEVTNDFIM*LK#.G	13.54	2.94	4.61	0.22
P27659_Rl	Rpl3	60S ribosor	K.SINPLGGFVHYGEVTNDFIMLK#.G	249.14	75.61	3.29	0.30
P27659_Rl	Rpl3	60S ribosor	K.SLLVQTK#.R	463.94	218.28	2.13	0.47
P27659_Rl	Rpl3	60S ribosor	R.VAFSVAR.A	119.74	164.75	0.73	1.38
P27659_Rl	Rpl3	60S ribosor	K.AFM*GPLK#K#.D	24.27	27.02	0.90	1.11
P27659_Rl	Rpl3	60S ribosor	K.DDASK#PVHLTAFLGYK#.A	89.09	28.80	3.09	0.32
P27659_Rl	Rpl3	60S ribosor	R.ERLEQQVPVNQVFGQDEM*IDVIGVTK.G	12.34	13.71	0.90	1.11
P27659_Rl	Rpl3	60S ribosor	R.ERLEQQVPVNQVFGQDEMIDVIGVTK.G	6.92	11.15	0.62	1.61
P27659_Rl	Rpl3	60S ribosor	R.FQTMEEK#.K	22.49	6.95	3.24	0.31
P27659_Rl	Rpl3	60S ribosor	K.IGQGYLIK#.D	175.35	51.68	3.39	0.29
P27659_Rl	Rpl3	60S ribosor	R.K#SLLVQTK#.R	37.51	10.01	3.75	0.27
P27659_Rl	Rpl3	60S ribosor	R.LEQQVPVNQVFGQDEM*IDVIGVTK#.G	35.39	17.06	2.07	0.48
P27659_Rl	Rpl3	60S ribosor	R.LEQQVPVNQVFGQDEMIDVIGVTK#.G	18.78	4.14	4.54	0.22
P27659_Rl	Rpl3	60S ribosor	K.NNASTDYDLSDK#.S	125.76	36.65	3.43	0.29
P27659_Rl	Rpl3	60S ribosor	K.SINPLGGFVHYGEVTNDFIM*LK#.G	104.08	24.31	4.28	0.23
P27659_Rl	Rpl3	60S ribosor	K.SINPLGGFVHYGEVTNDFIMLK#.G	70.71	24.36	2.90	0.34
P27659_Rl	Rpl3	60S ribosor	K.SLLVQTK#.R	53.59	5.01	10.69	0.09
P27659_Rl	Rpl3	60S ribosor	R.VAFSVAR.A	44.15	51.45	0.86	1.17
P27659_Rl	Rpl3	60S ribosor	K.DDASK#PVHLTAFLGYK#.A	67.70	22.49	3.01	0.33
P27659_Rl	Rpl3	60S ribosor	R.ERLEQQVPVNQVFGQDEM*IDVIGVTK.G	14.84	16.99	0.87	1.15
P27659_Rl	Rpl3	60S ribosor	R.ERLEQQVPVNQVFGQDEMIDVIGVTK.G	5.98	9.41	0.64	1.57
P27659_Rl	Rpl3	60S ribosor	K.FIDTTSK#.F	165.31	59.42	2.78	0.36
P27659_Rl	Rpl3	60S ribosor	K.IGQGYLIK#.D	130.34	37.36	3.49	0.29
P27659_Rl	Rpl3	60S ribosor	R.LEQQVPVNQVFGQDEM*IDVIGVTK#.G	62.64	15.90	3.94	0.25
P27659_Rl	Rpl3	60S ribosor	K.NNASTDYDLSDK#.S	126.05	44.42	2.84	0.35
P27659_Rl	Rpl3	60S ribosor	K.SINPLGGFVHYGEVTNDFIM*LK#.G	101.16	35.77	2.83	0.35
P27659_Rl	Rpl3	60S ribosor	K.SINPLGGFVHYGEVTNDFIMLK#.G	40.87	13.51	3.03	0.33
P27659_Rl	Rpl3	60S ribosor	K.SLLVQTK#.R	112.80	21.59	5.23	0.19
P27659_Rl	Rpl3	60S ribosor	R.VAFSVAR.A	43.55	54.92	0.79	1.26
P62889_Rl	Rpl30	60S ribosor	R.K#SEIEYYAM*LAK#.T	158.67	62.65	2.53	0.39
P62889_Rl	Rpl30	60S ribosor	R.KSEIEYYAM*LAK.T	180.87	55.61	3.25	0.31
P62889_Rl	Rpl30	60S ribosor	R.KSEIEYYAMLAK.T	74.90	21.03	3.56	0.28
P62889_Rl	Rpl30	60S ribosor	K.KSLESINSR.L	36.77	49.30	0.75	1.34
P62889_Rl	Rpl30	60S ribosor	R.LQLVM*K#.S	1820.64	648.31	2.81	0.36
P62889_Rl	Rpl30	60S ribosor	R.LQLVMK#.S	281.93	97.37	2.90	0.35
P62889_Rl	Rpl30	60S ribosor	K.SEIEYYAM*LAK#.T	166.37	60.54	2.75	0.36
P62889_Rl	Rpl30	60S ribosor	K.SEIEYYAMLAK#.T	103.71	31.90	3.25	0.31
P62889_Rl	Rpl30	60S ribosor	K.SLESINSR.L	178.29	278.07	0.64	1.56
P62889_Rl	Rpl30	60S ribosor	R.LQLVMK#.S	13.45	4.97	2.71	0.37
P62900_Rl	Rpl31	60S ribosor	K.EM*GTPDVR.I	129.77	237.35	0.55	1.83
P62900_Rl	Rpl31	60S ribosor	R.EYTINIHK#.R	238.49	102.43	2.33	0.43
P62900_Rl	Rpl31	60S ribosor	K.LYTLVTYVPVTTFK#.N	529.17	204.20	2.59	0.39
P62900_Rl	Rpl31	60S ribosor	R.NEDEDSPNK#LYTLVTYVPVTTFK#.N	140.46	59.32	2.37	0.42
P62900_Rl	Rpl31	60S ribosor	K.NLQTVNVDEN.-	922.16	922.16	1.00	1.00
P62900_Rl	Rpl31	60S ribosor	K.RNEDEDSPNKLYTLVTYVPVTTFK.N	10.01	13.32	0.75	1.33
P62900_Rl	Rpl31	60S ribosor	R.SAINEVVTR.E	499.45	920.42	0.54	1.84
P62911_Rl	Rpl32	60S ribosor	R.AAQLAIR.V	123.71	141.40	0.87	1.14
P62911_Rl	Rpl32	60S ribosor	R.FK#GQILM*PNIGYGSNK#.K	148.63	41.83	3.55	0.28
P62911_Rl	Rpl32	60S ribosor	R.FKGQILM*PNIGYGSNK.K	19.75	5.09	3.88	0.26
P62911_Rl	Rpl32	60S ribosor	R.FK#GQILMPNIGYGSNK#.K	33.64	11.87	2.83	0.35
P62911_Rl	Rpl32	60S ribosor	R.FKGQILM*PNIGYGSNKK.T	90.71	29.85	3.04	0.33
P62911_Rl	Rpl32	60S ribosor	R.FK#GQILMPNIGYGSNK#K#.T	45.43	12.59	3.61	0.28
P62911_Rl	Rpl32	60S ribosor	K.FLVHNVK#.E	397.49	72.82	5.46	0.18
P62911_Rl	Rpl32	60S ribosor	K.GQILM*PNIGYGSNK#.K	72.36	25.62	2.82	0.35
P62911_Rl	Rpl32	60S ribosor	K.GQILMPNIGYGSNK#.K	43.01	14.79	2.91	0.34
P62911_Rl	Rpl32	60S ribosor	K.GQILM*PNIGYGSNK#K#.T	11.37	3.45	3.30	0.30
P62911_Rl	Rpl32	60S ribosor	K.HMLPSGFR.K	20.02	20.62	0.97	1.03
P62911_Rl	Rpl32	60S ribosor	K.HM*LPSGFR.K	63.00	35.57	1.77	0.56
Q9D1R9_Rl	Rpl34	60S ribosor	R.AFLIEEQK#.I	13.97	5.40	2.59	0.39
Q9D1R9_Rl	Rpl34	60S ribosor	R.LSYNTASNK#.T	19.47	7.68	2.53	0.39
Q9D1R9_Rl	Rpl34	60S ribosor	R.AFLIEEQK#.I	875.27	288.93	3.03	0.33
Q9D1R9_Rl	Rpl34	60S ribosor	R.AFLIEEQK#IVVK#.V	6.68	2.30	2.91	0.34
Q9D1R9_Rl	Rpl34	60S ribosor	K.AQAQSQK#.A	14.33	4.11	3.49	0.29
Q9D1R9_Rl	Rpl34	60S ribosor	R.IVYLYTK#.K	1013.75	325.91	3.11	0.32
Q9D1R9_Rl	Rpl34	60S ribosor	R.IVYLYTK#K#.V	25.43	7.71	3.30	0.30
Q9D1R9_Rl	Rpl34	60S ribosor	R.LSYNTASNK#.T	264.51	81.34	3.25	0.31
Q9D1R9_Rl	Rpl34	60S ribosor	R.RLSYNTASNK.T	38.88	43.14	0.90	1.11
Q6ZWV7_R	Rpl35	60S ribosor	K.K#K#EELLK#.Q	101.09	28.66	3.53	0.28
Q6ZWV7_R	Rpl35	60S ribosor	K.KYKPLDLRPK.K	36.08	32.50	1.11	0.90
Q6ZWV7_R	Rpl35	60S ribosor	R.VLTVINQTQK#.E	1476.39	352.17	4.19	0.24
Q6ZWV7_R	Rpl35	60S ribosor	R.VLTVINQTQKENLRK.F	3.08	3.11	0.99	1.01
Q6ZWV7_R	Rpl35	60S ribosor	K.YKPLDLRPK.K	27.08	34.26	0.79	1.27
O55142_Rl	Rpl35a	60S ribosor	K.AIFAGYK#.R	302.77	101.10	2.99	0.33
O55142_Rl	Rpl35a	60S ribosor	R.DETEFYLGK#.R	112.93	56.19	2.01	0.50
O55142_Rl	Rpl35a	60S ribosor	R.DETEFYLGKR.C	68.54	117.12	0.59	1.71
O55142_Rl	Rpl35a	60S ribosor	K.IEGVYAR.D	125.05	218.87	0.57	1.75
O55142_Rl	Rpl35a	60S ribosor	K.IEGVYARDETEFYLGKR.C	2.39	10.73	0.22	4.48
O55142_Rl	Rpl35a	60S ribosor	K.NNTVTPGGK#PNK#.T	75.73	37.17	2.04	0.49
O55142_Rl	Rpl35a	60S ribosor	R.VM*LYPSRI.-	175.69	320.36	0.55	1.82
O55142_Rl	Rpl35a	60S ribosor	R.VMLYPSRI.-	24.42	43.61	0.56	1.79
O55142_Rl	Rpl35a	60S ribosor	K.NNTVTPGGK#PNK#.T	8.15	4.08	2.00	0.50
Q6ZWZ4_Q	Rpl36	60S ribosor	R.YPM*AVGLNK#.G	63.42	15.01	4.23	0.24
Q6ZWZ4_Q	Rpl36	60S ribosor	R.YPMAVGLNK#.G	29.29	7.85	3.73	0.27
Q6ZWZ4_Q	Rpl36	60S ribosor	R.EELSNVLAAM*R.K	96.78	129.23	0.75	1.34
Q6ZWZ4_Q	Rpl36	60S ribosor	R.EELSNVLAAMR.K	31.00	40.37	0.77	1.30
Q6ZWZ4_Q	Rpl36	60S ribosor	R.KREELSNVLAAM*R.K	34.83	167.72	0.21	4.82
Q6ZWZ4_Q	Rpl36	60S ribosor	R.KREELSNVLAAMR.K	15.14	78.48	0.19	5.18
Q6ZWZ4_Q	Rpl36	60S ribosor	R.YPM*AVGLNK#.G	422.61	142.79	2.96	0.34
Q6ZWZ4_Q	Rpl36	60S ribosor	R.YPMAVGLNK#.G	101.43	25.95	3.91	0.26
P83882_Rl	Rpl36a	60S ribosor	K.DSLYAQGK#.R	248.48	85.74	2.90	0.35
P83882_Rl	Rpl36a	60S ribosor	K.GK#DSLYAQGK#.R	151.85	53.56	2.83	0.35
P83882_Rl	Rpl36a	60S ribosor	K.HFELGGDK#.K	84.29	29.93	2.82	0.36
P83882_Rl	Rpl36a	60S ribosor	R.K#GQVIQF.-	378.43	113.39	3.34	0.30
P61514_Rl	Rpl37a	60S ribosor	K.TVAGGAWTYNTTSAVTVK#.S	6.09	2.72	2.24	0.45
P61514_Rl	Rpl37a	60S ribosor	K.IEISQHAK#.Y	33.79	12.41	2.72	0.37
P61514_Rl	Rpl37a	60S ribosor	K.K#IEISQHAK#.Y	705.83	326.03	2.16	0.46
P61514_Rl	Rpl37a	60S ribosor	K.KIEISQHAK.Y	179.59	87.04	2.06	0.48
P61514_Rl	Rpl37a	60S ribosor	K.KVGIVGK.Y	219.63	103.57	2.12	0.47
P61514_Rl	Rpl37a	60S ribosor	K.TVAGGAWTYNTTSAVTVK#.S	375.25	120.32	3.12	0.32
P61514_Rl	Rpl37a	60S ribosor	R.YGASLRK.M	49.28	82.64	0.60	1.68
P61514_Rl	Rpl37a	60S ribosor	K.TVAGGAWTYNTTSAVTVK#.S	10.94	3.54	3.09	0.32
Q9JJI8_RL3	Rpl38	60S ribosor	K.IEEIKDFLLTAR.R	15.58	47.07	0.33	3.02

Q9JJI8_RL3	Rpl38	60S ribosor	R.KIEEIKDFLLTAR.R	85.25	238.55	0.36	2.80
Q9JJI8_RL3	Rpl38	60S ribosor	K.LK#QSLPPGLAVK#.D	3.96	3.01	1.31	0.76
P62892_RL	Rpl39	60S ribosor	K.QNRPIPQWIR.M	2.82	18.91	0.15	6.70
Q9D8E6_RI	Rpl4	60S ribosor	K.APIRPDIVNFVHTNLR.K	20.17	118.99	0.17	5.90
Q9D8E6_RI	Rpl4	60S ribosor	K.APIRPDIVNFVHTNLRK.N	11.38	43.46	0.26	3.82
Q9D8E6_RI	Rpl4	60S ribosor	K.EAVQLLK#K#.L	72.61	22.92	3.17	0.32
Q9D8E6_RI	Rpl4	60S ribosor	K.GHRIEEVPELPLVVEDK.V	9.83	15.95	0.62	1.62
Q9D8E6_RI	Rpl4	60S ribosor	R.IEEVPELPLVVEDK#.V	259.33	86.70	2.99	0.33
Q9D8E6_RI	Rpl4	60S ribosor	R.IEEVPELPLVVEDK#VEGYK#K#.T	444.01	133.96	3.31	0.30
Q9D8E6_RI	Rpl4	60S ribosor	R.KLDELYGTWR.K	74.64	83.49	0.89	1.12
Q9D8E6_RI	Rpl4	60S ribosor	K.K#LEAAATALATK#.S	579.92	195.14	2.97	0.34
Q9D8E6_RI	Rpl4	60S ribosor	K.LDELYGTWR.K	17.75	22.83	0.78	1.29
Q9D8E6_RI	Rpl4	60S ribosor	K.LEAAATALATK#.S	477.23	137.09	3.48	0.29
Q9D8E6_RI	Rpl4	60S ribosor	K.MMNTDLSR.I	19.87	20.76	0.96	1.04
Q9D8E6_RI	Rpl4	60S ribosor	K.M*M*NTDLSR.I	56.98	66.28	0.86	1.16
Q9D8E6_RI	Rpl4	60S ribosor	R.NIPGITLLNVSK#.L	1207.67	327.29	3.69	0.27
Q9D8E6_RI	Rpl4	60S ribosor	K.NVTLPAVFK#.A	525.77	164.28	3.20	0.31
Q9D8E6_RI	Rpl4	60S ribosor	R.QPYAVSELAGHQTSAESWGTGR.A	71.68	82.95	0.86	1.16
Q9D8E6_RI	Rpl4	60S ribosor	K.SNYNLPMHK#.M	46.78	16.44	2.85	0.35
Q9D8E6_RI	Rpl4	60S ribosor	K.TKEAVQLLK.K	91.69	24.80	3.70	0.27
Q9D8E6_RI	Rpl4	60S ribosor	K.APIRPDIVNFVHTNLR.K	4.79	31.12	0.15	6.50
Q9D8E6_RI	Rpl4	60S ribosor	K.EAVQLLK#K#.L	21.96	5.32	4.13	0.24
Q9D8E6_RI	Rpl4	60S ribosor	R.IEEVPELPLVVEDK#.V	39.83	14.30	2.79	0.36
Q9D8E6_RI	Rpl4	60S ribosor	R.IEEVPELPLVVEDK#VEGYK#K#.T	140.62	44.37	3.17	0.32
Q9D8E6_RI	Rpl4	60S ribosor	K.K#LEAAATALATK#.S	205.12	50.22	4.08	0.24
Q9D8E6_RI	Rpl4	60S ribosor	K.K#PTTEEK#.K	5.02	6.27	0.80	1.25
Q9D8E6_RI	Rpl4	60S ribosor	K.LEAAATALATK#.S	156.90	43.25	3.63	0.28
Q9D8E6_RI	Rpl4	60S ribosor	K.M*M*NTDLSR.I	12.52	12.79	0.98	1.02
Q9D8E6_RI	Rpl4	60S ribosor	R.NIPGITLLNVSK#.L	276.20	79.57	3.47	0.29
Q9D8E6_RI	Rpl4	60S ribosor	K.NVTLPAVFK#.A	156.79	45.05	3.48	0.29
Q9D8E6_RI	Rpl4	60S ribosor	K.TK#EAVQLLK#.K	30.53	9.05	3.37	0.30
Q9D8E6_RI	Rpl4	60S ribosor	R.IEEVPELPLVVEDK#.V	37.96	16.04	2.37	0.42
Q9D8E6_RI	Rpl4	60S ribosor	K.K#LEAAATALATK#.S	70.88	22.89	3.10	0.32
Q9D8E6_RI	Rpl4	60S ribosor	K.LEAAATALATK#.S	55.41	15.96	3.47	0.29
Q9D8E6_RI	Rpl4	60S ribosor	R.NIPGITLLNVSK#.L	142.08	52.10	2.73	0.37
Q9D8E6_RI	Rpl4	60S ribosor	K.NVTLPAVFK#.A	87.54	32.72	2.68	0.37
Q9D8E6_RI	Rpl4	60S ribosor	K.TK#EAVQLLK#.K	12.26	4.07	3.02	0.33
P47962_RL	Rpl5	60S ribosor	K.EFNAEVHR.K	25.38	41.67	0.61	1.64
P47962_RL	Rpl5	60S ribosor	R.FPGYDSESK#.E	87.28	26.65	3.28	0.31
P47962_RL	Rpl5	60S ribosor	K.HIMGQNVADYM*R.Y	10.07	8.34	1.21	0.83
P47962_RL	Rpl5	60S ribosor	K.HIM*GQNVADYMR.Y	15.36	15.75	0.97	1.03
P47962_RL	Rpl5	60S ribosor	K.HIMGQNVADYMR.Y	8.42	7.13	1.18	0.85
P47962_RL	Rpl5	60S ribosor	K.HIM*GQNVADYM*R.Y	28.96	38.14	0.76	1.32
P47962_RL	Rpl5	60S ribosor	K.NNVTPDM*M*EEMYK#.K	7.06	2.00	3.54	0.28
P47962_RL	Rpl5	60S ribosor	K.NNVTPDMMEEM*YK#.K	11.05	5.44	2.03	0.49
P47962_RL	Rpl5	60S ribosor	K.NNVTPDMMEEMYK#.K	12.06	4.46	2.71	0.37
P47962_RL	Rpl5	60S ribosor	K.QFSQYIK#.N	280.96	102.30	2.75	0.36
P47962_RL	Rpl5	60S ribosor	K.RFPGYDSESK.E	40.26	52.20	0.77	1.30
P47962_RL	Rpl5	60S ribosor	R.YLM*EEDEDAYK#.K	7.91	2.59	3.05	0.33
P47962_RL	Rpl5	60S ribosor	R.YLM*EEDEDAYK#K#.Q	140.21	39.45	3.55	0.28
P47962_RL	Rpl5	60S ribosor	R.YLM*EEDEDAYK#K#.Q	412.09	113.66	3.63	0.28
P47962_RL	Rpl5	60S ribosor	K.HIM*GQNVADYM*R.Y	13.31	15.14	0.88	1.14
P47962_RL	Rpl5	60S ribosor	K.NNVTPDM*M*EEM*YKK.A	8.49	2.85	2.98	0.34
P47962_RL	Rpl5	60S ribosor	K.QFSQYIK#.N	126.78	34.45	3.68	0.27
P47962_RL	Rpl5	60S ribosor	K.RFPGYDSESK.E	16.22	17.93	0.90	1.11
P47962_RL	Rpl5	60S ribosor	R.YLM*EEDEDAYKK.Q	37.20	8.58	4.34	0.23
P47962_RL	Rpl5	60S ribosor	R.FPGYDSESK#.E	27.44	9.30	2.95	0.34
P47962_RL	Rpl5	60S ribosor	K.GAVDGGLSIPHSTK#.R	260.43	89.97	2.89	0.35
P47962_RL	Rpl5	60S ribosor	K.QFSQYIK#.N	143.35	38.97	3.68	0.27
P47962_RL	Rpl5	60S ribosor	K.RFPGYDSESK.E	23.32	18.51	1.26	0.79
P47962_RL	Rpl5	60S ribosor	R.YLM*EEDEDAYKK.Q	133.22	44.43	3.00	0.33
P47911_RL	Rpl6	60S ribosor	K.AVDLQILPK#.I	836.30	272.01	3.07	0.33
P47911_RL	Rpl6	60S ribosor	K.AVPQLQGYLR.S	214.73	337.16	0.64	1.57
P47911_RL	Rpl6	60S ribosor	K.EKVLATVTK.T	114.84	31.78	3.61	0.28
P47911_RL	Rpl6	60S ribosor	K.EKYEITEQR.K	51.31	59.46	0.86	1.16
P47911_RL	Rpl6	60S ribosor	K.FVIATSTK#.V	670.18	207.11	3.24	0.31
P47911_RL	Rpl6	60S ribosor	K.HLTDAYFK#.K	844.62	250.32	3.37	0.30
P47911_RL	Rpl6	60S ribosor	R.HQEGEIFDTEK#.E	112.51	43.46	2.59	0.39
P47911_RL	Rpl6	60S ribosor	R.HQEGEIFDTEK#EK#.Y	607.85	200.33	3.03	0.33
P47911_RL	Rpl6	60S ribosor	R.HQEGEIFDTEKEKYEITEQR.K	108.94	179.79	0.61	1.65
P47911_RL	Rpl6	60S ribosor	K.QLDSGLLLVTGPLVINR.V	40.28	56.63	0.71	1.41
P47911_RL	Rpl6	60S ribosor	R.SQFSLTNGM*YPHK#.L	12.69	3.84	3.31	0.30
P47911_RL	Rpl6	60S ribosor	R.SSITPGTVLIILTGR.H	53.61	73.77	0.73	1.38
P47911_RL	Rpl6	60S ribosor	K.VDISDVK#.I	895.66	258.29	3.47	0.29
P47911_RL	Rpl6	60S ribosor	K.YEITEQR.K	84.63	119.33	0.71	1.41
P47911_RL	Rpl6	60S ribosor	R.YYPTEDVPR.K	169.45	236.95	0.72	1.40
P47911_RL	Rpl6	60S ribosor	K.HLTDAYFK#.K	66.32	25.99	2.55	0.39
P47911_RL	Rpl6	60S ribosor	K.VDISDVK#.I	47.94	19.97	2.40	0.42
P47911_RL	Rpl6	60S ribosor	R.YYPTEDVPR.K	15.21	22.45	0.68	1.48
P47911_RL	Rpl6	60S ribosor	K.VDISDVK#.I	30.53	6.38	4.79	0.21
P14148_RL	Rpl7	60S ribosor	K.AGNFYVPAEPK#.L	227.01	77.09	2.94	0.34
P14148_RL	Rpl7	60S ribosor	K.ASINM*LR.I	52.64	78.59	0.67	1.49
P14148_RL	Rpl7	60S ribosor	K.ASINMLR.I	46.70	60.68	0.77	1.30
P14148_RL	Rpl7	60S ribosor	K.EANNFLWPFK#.L	286.60	87.62	3.27	0.31
P14148_RL	Rpl7	60S ribosor	R.FK#EANNFLWPFK#.L	166.98	45.02	3.71	0.27
P14148_RL	Rpl7	60S ribosor	R.IALTDNSLIAR.S	228.54	309.43	0.74	1.35
P14148_RL	Rpl7	60S ribosor	R.IVEPYIAWGYPNLK#.S	415.83	141.61	2.94	0.34
P14148_RL	Rpl7	60S ribosor	R.K#AGNFYVPAEPK#.L	150.66	41.77	3.61	0.28
P14148_RL	Rpl7	60S ribosor	K.KTTHFVEGGDAGNREDQINR.L	5.96	22.11	0.27	3.71
P14148_RL	Rpl7	60S ribosor	K.K#VATVPGTLK#K#.K	131.55	114.36	1.15	0.87
P14148_RL	Rpl7	60S ribosor	K.KVPAVPETLK.K	246.87	91.43	2.70	0.37
P14148_RL	Rpl7	60S ribosor	K.K#VPAVPETLK#K#.K	117.48	53.57	2.19	0.46
P14148_RL	Rpl7	60S ribosor	K.LAFVIR.I	102.28	113.31	0.90	1.11
P14148_RL	Rpl7	60S ribosor	R.NFAELK#.V	369.96	104.53	3.54	0.28
P14148_RL	Rpl7	60S ribosor	K.SVNELIYK#.R	230.08	86.88	2.65	0.38
P14148_RL	Rpl7	60S ribosor	K.TTHFVEGGDAGNR.E	2.47	3.73	0.66	1.51
P14148_RL	Rpl7	60S ribosor	K.TTHFVEGGDAGNREDQINR.L	30.79	139.27	0.22	4.52
P14148_RL	Rpl7	60S ribosor	K.VATVPGTLK#.K	193.74	84.30	2.30	0.44
P14148_RL	Rpl7	60S ribosor	K.VATVPGTLK#K#.K	109.92	39.86	2.76	0.36
P14148_RL	Rpl7	60S ribosor	K.VPAVPETLK#.K	132.04	52.71	2.51	0.40
P14148_RL	Rpl7	60S ribosor	K.EANNFLWPFK#.L	7.84	3.18	2.46	0.41
P14148_RL	Rpl7	60S ribosor	R.IALTDNSLIAR.S	8.38	10.15	0.83	1.21
P14148_RL	Rpl7	60S ribosor	R.IVEPYIAWGYPNLK#.S	30.87	8.48	3.64	0.27

P14148_Rl	Rpl7	60S ribosor	K.SVNELIYK#.R	4.84	1.51	3.20	0.31
P14148_Rl	Rpl7	60S ribosor	K.AGNFYVPAEPK#.L	32.22	9.57	3.37	0.30
P14148_Rl	Rpl7	60S ribosor	K.EANNFLWPFK#.L	41.12	8.99	4.57	0.22
P14148_Rl	Rpl7	60S ribosor	R.FK#EANNFLWPFK#.L	21.90	6.79	3.22	0.31
P14148_Rl	Rpl7	60S ribosor	R.IALTDNSLIAR.S	26.73	37.24	0.72	1.39
P14148_Rl	Rpl7	60S ribosor	R.IVEPYIAWGYPNLK#.S	68.77	21.47	3.20	0.31
P14148_Rl	Rpl7	60S ribosor	K.K#VPAVPETLK#.K	50.99	15.28	3.34	0.30
P14148_Rl	Rpl7	60S ribosor	K.LAFVIR.I	13.43	20.04	0.67	1.49
P14148_Rl	Rpl7	60S ribosor	K.EANNFLWPFK#.L	32.15	11.82	2.72	0.37
P14148_Rl	Rpl7	60S ribosor	R.FK#EANNFLWPFK#.L	13.13	6.26	2.10	0.48
P14148_Rl	Rpl7	60S ribosor	R.IALTDNSLIAR.S	19.44	26.91	0.72	1.38
P14148_Rl	Rpl7	60S ribosor	R.IVEPYIAWGYPNLK#.S	47.48	15.52	3.06	0.33
P14148_Rl	Rpl7	60S ribosor	R.K#AGNFYVPAEPK#.L	13.24	5.16	2.57	0.39
P14148_Rl	Rpl7	60S ribosor	K.LAFVIR.I	10.15	16.61	0.61	1.64
P14148_Rl	Rpl7	60S ribosor	K.TTHFVEGGDAGNREDQINR.L	27.83	26.08	1.07	0.94
P14148_Rl	Rpl7	60S ribosor	K.VPAVPETLK#.K	18.55	5.03	3.69	0.27
P12970_Rl	Rpl7a	60S ribosor	R.AGVNTVTTLVENK#.K	858.38	291.92	2.94	0.34
P12970_Rl	Rpl7a	60S ribosor	R.AGVNTVTTLVENKK.A	118.96	27.36	4.35	0.23
P12970_Rl	Rpl7a	60S ribosor	R.HWGGNVLGPK#.S	382.66	144.66	2.65	0.38
P12970_Rl	Rpl7a	60S ribosor	K.K#VAPAPAVVK#.K	90.60	36.30	2.50	0.40
P12970_Rl	Rpl7a	60S ribosor	K.K#VVNPLFEK#.R	750.35	185.18	4.05	0.25
P12970_Rl	Rpl7a	60S ribosor	R.LKVPPAINQFTQALDR.Q	149.31	207.21	0.72	1.39
P12970_Rl	Rpl7a	60S ribosor	R.LKVPPAINQFTQALDR.Q	16.03	22.16	0.72	1.38
P12970_Rl	Rpl7a	60S ribosor	K.NFGIGQDIQPK#.R	854.14	281.51	3.03	0.33
P12970_Rl	Rpl7a	60S ribosor	R.RHWGGNVLGPK.S	25.44	27.69	0.92	1.09
P12970_Rl	Rpl7a	60S ribosor	K.RPPVLR.A	98.05	551.79	0.18	5.63
P12970_Rl	Rpl7a	60S ribosor	R.TNYNDRYDEIR.R	11.78	49.66	0.24	4.22
P12970_Rl	Rpl7a	60S ribosor	K.VPPAINQFTQALDR.Q	23.18	34.36	0.67	1.48
P12970_Rl	Rpl7a	60S ribosor	K.VVNPLFEK#.R	269.75	85.09	3.17	0.32
P12970_Rl	Rpl7a	60S ribosor	R.AGVNTVTTLVENK#.K	192.72	60.46	3.19	0.31
P12970_Rl	Rpl7a	60S ribosor	R.AGVNTVTTLVENKK.A	260.66	89.62	2.91	0.34
P12970_Rl	Rpl7a	60S ribosor	R.AGVNTVTTLVENK#K#.A	30.83	13.63	2.26	0.44
P12970_Rl	Rpl7a	60S ribosor	K.K#VAPAPAVVK#.K	17.39	6.02	2.89	0.35
P12970_Rl	Rpl7a	60S ribosor	K.K#VVNPLFEK#.R	26.29	5.73	4.59	0.22
P12970_Rl	Rpl7a	60S ribosor	K.KVVNPLFEK.R	49.06	23.99	2.04	0.49
P12970_Rl	Rpl7a	60S ribosor	R.LKVPPAINQFTQALDR.Q	38.50	69.91	0.55	1.82
P12970_Rl	Rpl7a	60S ribosor	K.NFGIGQDIQPK#.R	267.74	90.57	2.96	0.34
P12970_Rl	Rpl7a	60S ribosor	K.VPPAINQFTQALDR.Q	4.64	6.20	0.75	1.34
P12970_Rl	Rpl7a	60S ribosor	R.AGVNTVTTLVENK#.K	88.47	24.64	3.59	0.28
P12970_Rl	Rpl7a	60S ribosor	R.HWGGNVLGPK#.S	59.48	20.62	2.88	0.35
P12970_Rl	Rpl7a	60S ribosor	R.LKVPPAINQFTQALDR.Q	15.23	26.15	0.58	1.72
P12970_Rl	Rpl7a	60S ribosor	K.NFGIGQDIQPK#.R	96.78	31.11	3.11	0.32
P12970_Rl	Rpl7a	60S ribosor	K.VVNPLFEK#.R	20.87	6.95	3.00	0.33
P12970_Rl	Rpl7a	60S ribosor	R.AGVNTVTTLVENK#.K	70.18	18.11	3.88	0.26
P12970_Rl	Rpl7a	60S ribosor	K.K#VVNPLFEK#.R	37.29	11.31	3.30	0.30
P12970_Rl	Rpl7a	60S ribosor	R.LKVPPAINQFTQALDR.Q	19.03	19.99	0.95	1.05
P12970_Rl	Rpl7a	60S ribosor	K.NFGIGQDIQPK#.R	79.94	21.42	3.73	0.27
P12970_Rl	Rpl7a	60S ribosor	K.VVNPLFEK#.R	28.41	8.15	3.49	0.29
P62918_Rl	Rpl8	60S ribosor	R.AVDFAER.H	174.40	201.87	0.86	1.16
P62918_Rl	Rpl8	60S ribosor	R.AVVGVVAGGGR.I	300.67	384.44	0.78	1.28
P62918_Rl	Rpl8	60S ribosor	K.DIIHDPGR.G	46.54	64.76	0.72	1.39
P62918_Rl	Rpl8	60S ribosor	R.IDK#PILK#.A	289.73	111.58	2.60	0.39
P62918_Rl	Rpl8	60S ribosor	K.VGLIAAR.R	81.22	109.20	0.74	1.34
P62918_Rl	Rpl8	60S ribosor	R.ASGNYATVISHNPETK#.K	221.83	85.01	2.61	0.38
P62918_Rl	Rpl8	60S ribosor	R.ASGNYATVISHNPETKK.T	11.16	3.58	3.12	0.32
P62918_Rl	Rpl8	60S ribosor	R.AVDFAER.H	104.57	192.86	0.54	1.84
P62918_Rl	Rpl8	60S ribosor	R.AVVGVVAGGGR.I	127.46	236.12	0.54	1.85
P62918_Rl	Rpl8	60S ribosor	R.ASGNYATVISHNPETK#.K	13.16	2.71	4.85	0.21
P51410_Rl	Rpl9	60S ribosor	K.FLDGIYVSEK#.G	33.77	11.45	2.95	0.34
P51410_Rl	Rpl9	60S ribosor	K.GVTLGFR.Y	8.36	16.60	0.50	1.99
P51410_Rl	Rpl9	60S ribosor	K.TILSNQTVDIPENVEITLK#.G	8.29	3.81	2.18	0.46
P51410_Rl	Rpl9	60S ribosor	R.DFNHINVELSLLGK#.K	52.68	19.16	2.75	0.36
P51410_Rl	Rpl9	60S ribosor	R.DFNHINVELSLLGK#K#.K	32.62	10.66	3.06	0.33
P51410_Rl	Rpl9	60S ribosor	K.FLDGIYVSEK#.G	984.71	306.69	3.21	0.31
P51410_Rl	Rpl9	60S ribosor	K.GVTLGFR.Y	93.67	153.33	0.61	1.64
P51410_Rl	Rpl9	60S ribosor	R.K#FLDGIYVSEK#.G	255.66	82.59	3.10	0.32
P51410_Rl	Rpl9	60S ribosor	-.M*K#TILSNQTVDIPENVEITLK#.G	34.23	11.96	2.86	0.35
P51410_Rl	Rpl9	60S ribosor	R.SVYAHFPINVVIQENGSLVEIR.N	17.83	32.81	0.54	1.84
P51410_Rl	Rpl9	60S ribosor	K.TILSNQTVDIPENVEITLK#.G	292.82	118.55	2.47	0.40
P51410_Rl	Rpl9	60S ribosor	K.TILSNQTVDIPENVEITLK#.G	188.52	72.79	2.59	0.39
P51410_Rl	Rpl9	60S ribosor	R.DFNHINVELSLLGK#.K	14.32	5.63	2.55	0.39
P51410_Rl	Rpl9	60S ribosor	K.FLDGIYVSEK#.G	29.45	9.18	3.21	0.31
P51410_Rl	Rpl9	60S ribosor	R.NFLGEK#.Y	32.98	9.33	3.53	0.28
P51410_Rl	Rpl9	60S ribosor	K.TILSNQTVDIPENVEITLK#.G	9.15	2.11	4.34	0.23
P51410_Rl	Rpl9	60S ribosor	R.DFNHINVELSLLGK#.K	10.16	1.54	6.59	0.15
P51410_Rl	Rpl9	60S ribosor	K.FLDGIYVSEK#.G	67.89	19.51	3.48	0.29
P51410_Rl	Rpl9	60S ribosor	K.GVTLGFR.Y	13.76	16.03	0.86	1.16
P14869_Rl	Rplp0	60S acidic r	K.AEAK#EESEESDEDM*GFGLFD.-	10.98	5.67	1.94	0.52
P14869_Rl	Rplp0	60S acidic r	K.AEAK#EESEESDEDMGFGLFD.-	6.31	2.46	2.57	0.39
P14869_Rl	Rplp0	60S acidic r	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#.A	458.44	261.58	1.75	0.57
P14869_Rl	Rplp0	60S acidic r	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#AEAK#.E	18.21	10.64	1.71	0.58
P14869_Rl	Rplp0	60S acidic r	K.AVVLM*GK#.N	195.85	98.30	1.99	0.50
P14869_Rl	Rplp0	60S acidic r	K.AVVLMGK#.N	187.90	91.21	2.06	0.49
P14869_Rl	Rplp0	60S acidic r	R.DMLLANK#.V	72.46	35.69	2.03	0.49
P14869_Rl	Rplp0	60S acidic r	K.EESEESDEDM*GFGLFD.-	10.41	10.41	1.00	1.00
P14869_Rl	Rplp0	60S acidic r	R.GHLENNPALEK#.L	544.05	210.58	2.58	0.39
P14869_Rl	Rplp0	60S acidic r	R.GNVGFVFTK#.E	384.30	149.83	2.56	0.39
P14869_Rl	Rplp0	60S acidic r	R.GNVGFVFTKEDLTEIR.D	30.89	58.51	0.53	1.89
P14869_Rl	Rplp0	60S acidic r	R.GTIEILSDVQLIK#.T	490.55	258.91	1.89	0.53
P14869_Rl	Rplp0	60S acidic r	K.IIQLLDDYPK#.C	644.58	294.73	2.19	0.46
P14869_Rl	Rplp0	60S acidic r	K.TSFFQALGITTK#.I	745.89	293.01	2.55	0.39
P14869_Rl	Rplp0	60S acidic r	K.AEAK#EESEESDEDM*GFGLFD.-	4.26	2.22	1.92	0.52
P14869_Rl	Rplp0	60S acidic r	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#.A	36.83	20.92	1.76	0.57
P14869_Rl	Rplp0	60S acidic r	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#AEAK#.E	103.88	41.09	2.53	0.40
P14869_Rl	Rplp0	60S acidic r	K.AVVLMGK#.N	52.45	7.29	7.19	0.14
P14869_Rl	Rplp0	60S acidic r	K.AVVLM*GK#.N	153.23	27.79	5.51	0.18
P14869_Rl	Rplp0	60S acidic r	R.DM*LLANK#.V	20.45	4.76	4.30	0.23
P14869_Rl	Rplp0	60S acidic r	R.DM*LLANKVPAAAR.A	2.28	6.72	0.34	2.95
P14869_Rl	Rplp0	60S acidic r	K.EDLTEIR.D	46.72	49.20	0.95	1.05
P14869_Rl	Rplp0	60S acidic r	R.FLEGVR.N	185.23	141.90	1.31	0.77
P14869_Rl	Rplp0	60S acidic r	R.GHLENNPALEK#.L	348.68	14.80	23.56	0.04
P14869_Rl	Rplp0	60S acidic r	R.GK#AVVLM*GK#.N	9.08	1.78	5.10	0.20
P14869_Rl	Rplp0	60S acidic r	R.GNVGFVFTK#.E	168.59	41.34	4.08	0.25

P14869_Rl	Rplp0	60S acidic r	R.GTIEILSDVQLIK#.T	724.88	135.52	5.35	0.19
P14869_Rl	Rplp0	60S acidic r	K.IIQLLDDYPK#.C	714.06	133.71	5.34	0.19
P14869_Rl	Rplp0	60S acidic r	K.TSFFQALGITTK#.I	1399.34	224.27	6.24	0.16
P14869_Rl	Rplp0	60S acidic r	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#.A	76.60	33.05	2.32	0.43
P14869_Rl	Rplp0	60S acidic r	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#AEAK#.E	5.90	2.35	2.51	0.40
P14869_Rl	Rplp0	60S acidic r	R.GHLENNPALEK#.L	160.27	48.41	3.31	0.30
P14869_Rl	Rplp0	60S acidic r	R.GNVGFVFTK#.E	86.86	27.04	3.21	0.31
P14869_Rl	Rplp0	60S acidic r	R.GNVGFVFTKEDLTEIR.D	11.78	19.08	0.62	1.62
P14869_Rl	Rplp0	60S acidic r	R.GTIEILSDVQLIK#.T	243.89	66.05	3.69	0.27
P14869_Rl	Rplp0	60S acidic r	K.IIQLLDDYPK#.C	173.61	53.72	3.23	0.31
P14869_Rl	Rplp0	60S acidic r	K.TSFFQALGITTK#.I	207.29	50.45	4.11	0.24
P14869_Rl	Rplp0	60S acidic r	K.AFLADPSAFAAAAPAAAATTAAPAAAAAPAK#.A	117.42	49.11	2.39	0.42
P14869_Rl	Rplp0	60S acidic r	R.GHLENNPALEK#.L	241.44	72.61	3.33	0.30
P14869_Rl	Rplp0	60S acidic r	R.GNVGFVFTK#.E	101.34	25.91	3.91	0.26
P14869_Rl	Rplp0	60S acidic r	R.GNVGFVFTKEDLTEIR.D	14.50	11.91	1.22	0.82
P14869_Rl	Rplp0	60S acidic r	R.GTIEILSDVQLIK#.T	230.31	55.15	4.18	0.24
P14869_Rl	Rplp0	60S acidic r	K.IIQLLDDYPK#.C	271.07	69.82	3.88	0.26
P14869_Rl	Rplp0	60S acidic r	K.TSFFQALGITTK#.I	312.00	87.43	3.57	0.28
P47955_Rl	Rplp1	60S acidic r	K.AAGVSVEPFWPGLFAK#.A	49.23	25.89	1.90	0.53
P47955_Rl	Rplp1	60S acidic r	K.AAGVSVEPFWPGLFAK#.A	1576.40	1181.32	1.33	0.75
P47955_Rl	Rplp1	60S acidic r	K.K#EESEESEDDM*GFGLFD.-	160.72	103.84	1.55	0.65
P47955_Rl	Rplp1	60S acidic r	K.K#EESEESEDDMGFGLFD.-	42.56	30.20	1.41	0.71
P47955_Rl	Rplp1	60S acidic r	K.AAGVSVEPFWPGLFAK#.A	20.37	12.92	1.58	0.63
P47955_Rl	Rplp1	60S acidic r	K.AAGVSVEPFWPGLFAK#.A	21.17	10.88	1.95	0.51
P99027_Rl	Rplp2	60S acidic r	K.EESEESDDDM*GFGLFD.-	13.95	13.95	1.00	1.00
P99027_Rl	Rplp2	60S acidic r	K.ILDSVGIEADDDR.L	43.52	177.02	0.25	4.07
P99027_Rl	Rplp2	60S acidic r	K.KEESEESDDDM*GFGLFD.-	50.34	40.92	1.23	0.81
P99027_Rl	Rplp2	60S acidic r	K.KEESEESDDDMGFGLFD.-	14.53	14.79	0.98	1.02
P99027_Rl	Rplp2	60S acidic r	K.KILDSVGIEADDDR.L	3.93	3.25	1.21	0.83
P99027_Rl	Rplp2	60S acidic r	K.KILDSVGIEADDDRLNK.V	46.85	212.17	0.22	4.53
P99027_Rl	Rplp2	60S acidic r	K.KILDSVGIEADDDRLNK.V	2.81	10.48	0.27	3.73
P99027_Rl	Rplp2	60S acidic r	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKK.D	91.94	90.68	1.01	0.99
P99027_Rl	Rplp2	60S acidic r	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEK.K	203.19	186.67	1.09	0.92
P99027_Rl	Rplp2	60S acidic r	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK#K#DEK#.K	29.27	35.61	0.82	1.22
P99027_Rl	Rplp2	60S acidic r	-.M*RYVASYLLAALGGNSSPSAK.D	18.34	39.50	0.46	2.15
P99027_Rl	Rplp2	60S acidic r	K.NIEDVIAQGVGK#.L	1579.59	1369.67	1.15	0.87
P99027_Rl	Rplp2	60S acidic r	K.VISELNGK#NIEDVIAQGVGK#.L	10.51	9.72	1.08	0.92
P99027_Rl	Rplp2	60S acidic r	R.YVASYLLAALGGNSSPSAK#.D	473.31	420.57	1.13	0.89
P99027_Rl	Rplp2	60S acidic r	R.YVASYLLAALGGNSSPSAK#.D	3.69	5.50	0.67	1.49
Q8R040_RI	Rpp21	Ribonuclea	K.ENIQTQALNTSE.-	8.40	8.40	1.00	1.00
Q99JH1_RF	Rpp25l	Ribonuclea	R.NLLGLALGR.L	6.38	20.61	0.31	3.23
Q8VDS4_RI	Rprd1a	Regulation	K.DFAPVIVEAFK#.H	50.65	28.87	1.75	0.57
Q8VDS4_RI	Rprd1a	Regulation	R.IASLPVEVQEVSLLEK#.I	43.68	27.62	1.58	0.63
Q8VDS4_RI	Rprd1a	Regulation	R.IASLPVEVQEVSLLEK#.I	9.79	6.82	1.43	0.70
Q8VDS4_RI	Rprd1a	Regulation	R.K#LTFLYLANDVIQNSK#.R	73.05	18.31	3.99	0.25
Q8VDS4_RI	Rprd1a	Regulation	K.LTFLYLANDVIQNSK#.R	21.08	10.46	2.02	0.50
Q8VDS4_RI	Rprd1a	Regulation	K.LTFLYLANDVIQNSK#.R	31.67	12.85	2.47	0.41
Q8VDS4_RI	Rprd1a	Regulation	R.SVYENDVLEQLK#.H	33.27	21.92	1.52	0.66
Q9CSU0_RI	Rprd1b	Regulation	K.ALQDLENAASGDATVR.Q	12.26	21.04	0.58	1.72
Q9CSU0_RI	Rprd1b	Regulation	K.IASLPQEVQDVSLLEK#.I	60.83	17.27	3.52	0.28
Q9CSU0_RI	Rprd1b	Regulation	R.LLNIWQER.S	16.38	26.38	0.62	1.61
Q9CSU0_RI	Rprd1b	Regulation	R.M*LVEYTQNQK#.E	47.77	15.44	3.09	0.32
Q9CSU0_RI	Rprd1b	Regulation	R.MLVEYTQNQK#.E	22.37	7.74	2.89	0.35
Q9CSU0_RI	Rprd1b	Regulation	R.SVYGGEFIQQLK#.L	69.57	23.89	2.91	0.34
Q6NXI6_RF	Rprd2	Regulation	K.ASVGQSPVLPSTTFK#.L	8.07	4.44	1.82	0.55
Q6NXI6_RF	Rprd2	Regulation	K.VEITPESILSALSK.T	16.79	11.87	1.41	0.71
Q6NXI6_RF	Rprd2	Regulation	R.APQFQESVTSFR.S	2.46	18.87	0.13	7.67
Q6NXI6_RF	Rprd2	Regulation	K.ASVGQSPVLPSTTFK.L	14.28	13.29	1.07	0.93
Q6NXI6_RF	Rprd2	Regulation	R.ESFADVLPEAAALVK#.D	18.64	13.63	1.37	0.73
Q6NXI6_RF	Rprd2	Regulation	K.GTSSDGVSLSNLTQPSLPTTDQQQEEHYR.I	1.65	5.36	0.31	3.26
Q6NXI6_RF	Rprd2	Regulation	K.ISSILSSLTSVMK.N	9.06	9.39	0.96	1.04
Q6NXI6_RF	Rprd2	Regulation	R.NLLSSTQSFIPK#.S	12.06	11.50	1.05	0.95
P63325_RS	Rps10	40S ribosor	R.IAIYELLFK#.E	16.02	9.60	1.67	0.60
P63325_RS	Rps10	40S ribosor	K.AEAGAGSATEFQFR.G	105.23	227.04	0.46	2.16
P63325_RS	Rps10	40S ribosor	R.DYLHLPPEIVPATLR.R	43.97	98.50	0.45	2.24
P63325_RS	Rps10	40S ribosor	K.EQFAWR.H	51.74	117.14	0.44	2.26
P63325_RS	Rps10	40S ribosor	R.HFYWYLTNEGIQYLR.D	28.08	58.02	0.48	2.07
P63325_RS	Rps10	40S ribosor	K.HPELADK#NVPNLHVM*K#.A	119.72	67.00	1.79	0.56
P63325_RS	Rps10	40S ribosor	K.HPELADK#NVPNLHVM*K#.A	18.29	10.95	1.67	0.60
P63325_RS	Rps10	40S ribosor	R.IAIYELLFK#.E	1707.00	770.86	2.21	0.45
P63325_RS	Rps10	40S ribosor	K.KAEAGAGSATEFQFR.G	81.63	175.57	0.46	2.15
P62281_RS	Rps11	40S ribosor	K.EAIEGTYIDK#K#.C	19.86	10.44	1.90	0.53
P62281_RS	Rps11	40S ribosor	R.AYQK#QPTIFQNK#.K	65.83	100.46	0.66	1.53
P62281_RS	Rps11	40S ribosor	R.DYLHYIR.K	81.30	140.75	0.58	1.73
P62281_RS	Rps11	40S ribosor	K.EAIEGTYIDK#.K	211.40	87.76	2.41	0.42
P62281_RS	Rps11	40S ribosor	K.EAIEGTYIDK#K#.C	196.71	82.16	2.39	0.42
P62281_RS	Rps11	40S ribosor	R.ILSGVVTK#.M	1058.42	389.78	2.72	0.37
P62281_RS	Rps11	40S ribosor	K.K#QFQK#F.-	35.43	294.54	0.12	8.31
P62281_RS	Rps11	40S ribosor	K.NIGLGFK#.T	805.19	301.09	2.67	0.37
P62281_RS	Rps11	40S ribosor	R.VLLGETGK#.E	255.62	100.06	2.55	0.39
P62281_RS	Rps11	40S ribosor	R.VLLGETGK#EK#.L	328.76	158.05	2.08	0.48
P63323_RS	Rps12	40S ribosor	K.DVIEEYFK#.C	423.47	149.48	2.83	0.35
P63323_RS	Rps12	40S ribosor	K.DYGK#ESQAK#DVIEEYFK#.C	20.91	8.21	2.55	0.39
P63323_RS	Rps12	40S ribosor	K.ESQAK#DVIEEYFK#.C	130.85	43.28	3.02	0.33
P63323_RS	Rps12	40S ribosor	K.ESQAKDVIEEYFK.C	37.91	18.40	2.06	0.49
P62301_RS	Rps13	40S ribosor	K.GLSQSALPYR.R	334.32	628.78	0.53	1.88
P62301_RS	Rps13	40S ribosor	K.GLTPSQIGVILR.D	158.98	320.18	0.50	2.01
P62301_RS	Rps13	40S ribosor	K.KGLTPSQIGVILR.D	248.98	401.03	0.62	1.61
P62301_RS	Rps13	40S ribosor	R.LILIESR.I	414.89	709.29	0.58	1.71
P62301_RS	Rps13	40S ribosor	K.LTSDDVK#EQIYK#.L	277.43	112.75	2.46	0.41
P62301_RS	Rps13	40S ribosor	K.SK#GLAPDLPEDLYHLIK#.K	207.42	93.60	2.22	0.45
P62301_RS	Rps13	40S ribosor	K.YESSTASALVA.-	315.15	315.15	1.00	1.00
P62264_RS	Rps14	40S ribosor	K.ADRDESSPYAAM*LAAQDVAQR.C	15.62	78.75	0.20	5.04
P62264_RS	Rps14	40S ribosor	K.ADRDESSPYAAMLAAQDVAQR.C	16.61	82.55	0.20	4.97
P62264_RS	Rps14	40S ribosor	R.DESSPYAAM*LAAQDVAQR.C	5.59	8.86	0.63	1.58
P62264_RS	Rps14	40S ribosor	R.DESSPYAAM*LAAQDVAQR.C	3.86	10.02	0.39	2.60
P62264_RS	Rps14	40S ribosor	K.ELGITALHIK#.L	111.53	58.92	1.89	0.53
P62264_RS	Rps14	40S ribosor	R.IEDVTPIPSDSTR.R	227.86	494.23	0.46	2.17
P62264_RS	Rps14	40S ribosor	R.TKTPGPGAQSALR.A	37.92	73.05	0.52	1.93
P62264_RS	Rps14	40S ribosor	K.TPGPGAQSALR.A	220.90	477.36	0.46	2.16
P62264_RS	Rps14	40S ribosor	K.VKADRDESSPYAAM*LAAQDVAQR.C	7.23	33.07	0.22	4.57
P62264_RS	Rps14	40S ribosor	R.IEDVTPIPSDSTR.R	5.04	17.13	0.29	3.40
P62843_RS	Rps15	40S ribosor	R.DM*IILPEMVGSMVGVYNGK#.T	7.93	2.81	2.82	0.36

P62843_RS	Rps15	40S ribosor	K.KEAPPM*EKPEVVK.T	89.97	47.09	1.91	0.52
P62843_RS	Rps15	40S ribosor	K.K#EAPPMEK#PEVVK#.T	29.61	16.18	1.83	0.55
P62843_RS	Rps15	40S ribosor	K.TFNQVEIKPEM*IGHYLGEFSITYKPVK.H	18.35	9.53	1.93	0.52
P62843_RS	Rps15	40S ribosor	K.TFNQVEIK#PEMIGHYLGEFSITYK#PVK#.H	8.22	3.51	2.34	0.43
P62245_RS	Rps15a	40S ribosor	R.FDVQLK#.D	89.12	25.47	3.50	0.29
P62245_RS	Rps15a	40S ribosor	K.HGYIGEFEIIDDHR.A	18.62	29.71	0.63	1.60
P62245_RS	Rps15a	40S ribosor	R.M*NVLADALK#.S	53.92	28.03	1.92	0.52
P62245_RS	Rps15a	40S ribosor	R.MNVLADALK#.S	17.68	9.98	1.77	0.56
P62245_RS	Rps15a	40S ribosor	R.FDVQLK#.D	348.86	80.79	4.32	0.23
P62245_RS	Rps15a	40S ribosor	R.FDVQLK#DLEK#.W	179.91	64.04	2.81	0.36
P62245_RS	Rps15a	40S ribosor	R.FDVQLKDLEKWQNNLLPSR.Q	4.92	16.78	0.29	3.41
P62245_RS	Rps15a	40S ribosor	K.HGYIGEFEIIDDHR.A	44.23	64.55	0.69	1.46
P62245_RS	Rps15a	40S ribosor	K.IVVNLTGR.L	116.76	189.45	0.62	1.62
P62245_RS	Rps15a	40S ribosor	R.M*NVLADALK#.S	493.47	198.43	2.49	0.40
P62245_RS	Rps15a	40S ribosor	R.MNVLADALK#.S	82.86	21.26	3.90	0.26
P62245_RS	Rps15a	40S ribosor	R.QFGFIVLTTSAGIM*DHEEAR.R	18.41	26.61	0.69	1.45
P62245_RS	Rps15a	40S ribosor	R.QFGFIVLTTSAGIMDHEEAR.R	6.62	11.15	0.59	1.68
P62245_RS	Rps15a	40S ribosor	K.WQNNLLPSR.Q	85.97	178.75	0.48	2.08
P62245_RS	Rps15a	40S ribosor	R.FDVQLK#.D	81.00	22.33	3.63	0.28
P62245_RS	Rps15a	40S ribosor	R.FDVQLK#DLEK#.W	37.86	15.08	2.51	0.40
P62245_RS	Rps15a	40S ribosor	K.HGYIGEFEIIDDHR.A	23.94	43.60	0.55	1.82
P62245_RS	Rps15a	40S ribosor	K.IVVNLTGR.L	25.44	47.45	0.54	1.87
P62245_RS	Rps15a	40S ribosor	R.M*NVLADALK#.S	58.32	19.88	2.93	0.34
P62245_RS	Rps15a	40S ribosor	R.MNVLADALK#.S	24.03	8.85	2.72	0.37
P62245_RS	Rps15a	40S ribosor	K.WQNNLLPSR.Q	14.31	35.38	0.40	2.47
P62245_RS	Rps15a	40S ribosor	R.FDVQLK#.D	117.00	42.69	2.74	0.36
P62245_RS	Rps15a	40S ribosor	R.FDVQLK#DLEK#.W	43.28	13.86	3.12	0.32
P62245_RS	Rps15a	40S ribosor	K.HGYIGEFEIIDDHR.A	12.47	19.20	0.65	1.54
P62245_RS	Rps15a	40S ribosor	K.IVVNLTGR.L	34.09	48.26	0.71	1.42
P62245_RS	Rps15a	40S ribosor	R.M*NVLADALK#.S	73.84	26.21	2.82	0.35
P62245_RS	Rps15a	40S ribosor	K.WQNNLLPSR.Q	19.84	24.83	0.80	1.25
P14131_RS	Rps16	40S ribosor	K.ALVAYYQK#.Y	16.41	5.00	3.28	0.30
P14131_RS	Rps16	40S ribosor	R.FAGVDIR.V	10.64	16.93	0.63	1.59
P14131_RS	Rps16	40S ribosor	K.LLEPVLLLGK#.E	76.67	35.97	2.13	0.47
P14131_RS	Rps16	40S ribosor	K.ALVAYYQK#.Y	630.77	227.10	2.78	0.36
P14131_RS	Rps16	40S ribosor	K.DILIQYDR.T	48.46	110.23	0.44	2.27
P14131_RS	Rps16	40S ribosor	K.EIKDILIQYDR.T	90.39	137.44	0.66	1.52
P14131_RS	Rps16	40S ribosor	R.FAGVDIR.V	130.21	219.34	0.59	1.68
P14131_RS	Rps16	40S ribosor	K.GPLQSVQVFGR.K	138.94	260.33	0.53	1.87
P14131_RS	Rps16	40S ribosor	K.LLEPVLLLGK#.E	1091.57	414.43	2.63	0.38
P14131_RS	Rps16	40S ribosor	R.TLLVADPR.R	96.54	192.72	0.50	2.00
P14131_RS	Rps16	40S ribosor	R.VKGGGHVAQIYAIR.Q	71.56	111.65	0.64	1.56
P14131_RS	Rps16	40S ribosor	K.VNGRPLEM*IEPR.T	3.31	49.78	0.07	15.02
P14131_RS	Rps16	40S ribosor	K.VNGRPLEMIEPR.T	1.24	11.37	0.11	9.16
P14131_RS	Rps16	40S ribosor	K.ALVAYYQK#.Y	19.11	9.96	1.92	0.52
P14131_RS	Rps16	40S ribosor	K.LLEPVLLLGK#.E	50.89	21.04	2.42	0.41
P14131_RS	Rps16	40S ribosor	K.ALVAYYQK#.Y	25.71	14.21	1.81	0.55
P14131_RS	Rps16	40S ribosor	K.LLEPVLLLGK#.E	101.88	44.99	2.26	0.44
P63276_RS	Rps17	40S ribosor	R.DNYVPEVSALDQEIIEVDPDTK#.E	5.39	6.49	0.83	1.20
P63276_RS	Rps17	40S ribosor	K.IAGYVTHLM*K#.R	19.97	5.95	3.36	0.30
P63276_RS	Rps17	40S ribosor	K.LLDFGSLSNLQVTQPTVGM*NFK#.T	4.47	3.21	1.39	0.72
P63276_RS	Rps17	40S ribosor	R.DNYVPEVSALDQEIIEVDPDTK#.E	60.29	28.05	2.15	0.47
P63276_RS	Rps17	40S ribosor	R.DNYVPEVSALDQEIIEVDPDTK#EM*LK#.L	539.39	240.17	2.25	0.45
P63276_RS	Rps17	40S ribosor	K.IAGYVTHLMK#.R	47.00	22.00	2.14	0.47
P63276_RS	Rps17	40S ribosor	R.LGNDFHTNKR.V	20.10	33.74	0.60	1.68
P63276_RS	Rps17	40S ribosor	K.LLDFGSLSNLQVTQPTVGM*NFK#.T	463.77	178.73	2.59	0.39
P63276_RS	Rps17	40S ribosor	K.LLDFGSLSNLQVTQPTVGMNFK#.T	368.69	132.35	2.79	0.36
P63276_RS	Rps17	40S ribosor	K.LLDFGSLSNLQVTQPTVGM*NFKTPR.G	1.88	5.13	0.37	2.72
P63276_RS	Rps17	40S ribosor	K.LLDFGSLSNLQVTQPTVGM*NFK#.T	13.69	6.60	2.07	0.48
P62270_RS	Rps18	40S ribosor	R.AGELTEDEVER.V	178.82	316.90	0.56	1.77
P62270_RS	Rps18	40S ribosor	R.HFWGLR.V	138.22	226.18	0.61	1.64
P62270_RS	Rps18	40S ribosor	K.IAFAITAIK#.G	1019.26	295.06	3.45	0.29
P62270_RS	Rps18	40S ribosor	K.IPDWFLNR.Q	524.18	944.57	0.55	1.80
P62270_RS	Rps18	40S ribosor	R.K#ADIDLTK#.R	539.75	181.17	2.98	0.34
P62270_RS	Rps18	40S ribosor	R.KADIDLTKR.A	3.43	5.04	0.68	1.47
P62270_RS	Rps18	40S ribosor	R.K#IAFAITAIK#.G	249.72	77.32	3.23	0.31
P62270_RS	Rps18	40S ribosor	K.LREDLER.L	30.77	182.31	0.17	5.92
P62270_RS	Rps18	40S ribosor	K.RAGELTEDEVER.V	20.53	132.24	0.16	6.44
P62270_RS	Rps18	40S ribosor	R.VITIM*QNPR.Q	200.70	375.09	0.54	1.87
P62270_RS	Rps18	40S ribosor	R.VITIMQNPR.Q	36.65	61.74	0.59	1.68
P62270_RS	Rps18	40S ribosor	R.VLNTNIDGR.R	305.85	503.63	0.61	1.65
P62270_RS	Rps18	40S ribosor	K.YSQVLANGLDNK#.L	358.04	127.13	2.82	0.36
Q9CZX8_RS	Rps19	40S ribosor	R.ALAAFLK#.K	314.84	161.24	1.95	0.51
Q9CZX8_RS	Rps19	40S ribosor	R.ALAAFLK#K#.S	75.62	37.74	2.00	0.50
Q9CZX8_RS	Rps19	40S ribosor	K.DVNQQEFVR.A	237.56	467.18	0.51	1.97
Q9CZX8_RS	Rps19	40S ribosor	K.ELAPYDENWFYTR.A	58.50	111.72	0.52	1.91
Q9CZX8_RS	Rps19	40S ribosor	K.HKELAPYDENWFYTR.A	25.41	46.89	0.54	1.85
Q9CZX8_RS	Rps19	40S ribosor	R.IAGQVAAANK#.K	81.53	36.84	2.21	0.45
Q9CZX8_RS	Rps19	40S ribosor	R.IAGQVAAANK#K#.H	43.00	18.66	2.30	0.43
Q9CZX8_RS	Rps19	40S ribosor	K.LK#VPEWVDTVK#.L	615.58	294.04	2.09	0.48
Q9CZX8_RS	Rps19	40S ribosor	R.RVLQALEGLK.M	20.28	33.64	0.60	1.66
Q9CZX8_RS	Rps19	40S ribosor	R.VLQALEGLK#.M	1057.36	440.14	2.40	0.42
Q8C6B9_AI	Rps19bp1	Active regu	K.AEGTVFTEEDFQK#.F	15.38	36.19	0.42	2.35
Q8C6B9_AI	Rps19bp1	Active regu	R.AVPGQVQASGTPAK#.R	13.46	13.61	0.99	1.01
Q8C6B9_AI	Rps19bp1	Active regu	R.STVPESVTQQILQQNQGR.K	11.17	32.86	0.34	2.94
P25444_RS	Rps2	40S ribosor	K.AEDK#EWIPVTK#.L	374.18	142.34	2.63	0.38
P25444_RS	Rps2	40S ribosor	K.ATFDAISK#.T	479.89	161.21	2.98	0.34
P25444_RS	Rps2	40S ribosor	R.GTGIVSAPVPK#.K	533.95	196.10	2.72	0.37
P25444_RS	Rps2	40S ribosor	R.GYWGNK#.I	75.41	31.13	2.42	0.41
P25444_RS	Rps2	40S ribosor	K.IM*PVQK#.Q	218.61	92.65	2.36	0.42
P25444_RS	Rps2	40S ribosor	K.IMPVQK#.Q	181.70	62.77	2.89	0.35
P25444_RS	Rps2	40S ribosor	K.LSIVPVR.R	54.84	97.93	0.56	1.79
P25444_RS	Rps2	40S ribosor	K.LSIVPVRR.G	9.99	44.03	0.23	4.41
P25444_RS	Rps2	40S ribosor	K.SLEEIYLFSLPIK#.E	851.79	328.18	2.60	0.39
P25444_RS	Rps2	40S ribosor	K.SPYQEFTDHLVK#.T	375.22	146.68	2.56	0.39
P25444_RS	Rps2	40S ribosor	K.TYSYLTPDLWK#.E	339.17	132.97	2.55	0.39
P25444_RS	Rps2	40S ribosor	R.GTGIVSAPVPK#.K	93.57	24.76	3.78	0.26
P25444_RS	Rps2	40S ribosor	K.LSIVPVR.R	9.19	13.73	0.67	1.49
P25444_RS	Rps2	40S ribosor	K.SLEEIYLFSLPIK#.E	31.60	7.02	4.50	0.22
P25444_RS	Rps2	40S ribosor	K.AEDK#EWIPVTK#.L	48.46	17.24	2.81	0.36
P25444_RS	Rps2	40S ribosor	K.ATFDAISK#.T	47.22	20.14	2.34	0.43
P25444_RS	Rps2	40S ribosor	R.GTGIVSAPVPK#.K	58.87	24.92	2.36	0.42
P25444_RS	Rps2	40S ribosor	K.SLEEIYLFSLPIK#.E	63.80	28.31	2.25	0.44

P25444_RS	Rps2	40S riboso	K.SPYQEFTDHLVK#.T	70.93	25.49	2.78	0.36
P25444_RS	Rps2	40S riboso	K.TYSYLTPDLWK#.E	40.28	17.51	2.30	0.43
P25444_RS	Rps2	40S riboso	K.AEDK#EWIPVTK#.L	61.64	24.71	2.49	0.40
P25444_RS	Rps2	40S riboso	K.ATFDAISK#.T	46.97	15.28	3.07	0.33
P25444_RS	Rps2	40S riboso	R.GTGIVSAPVPK#.K	85.33	32.00	2.67	0.37
P25444_RS	Rps2	40S riboso	K.SPYQEFTDHLVK#.T	83.38	29.46	2.83	0.35
P25444_RS	Rps2	40S riboso	K.TYSYLTPDLWK#.E	44.94	17.32	2.59	0.39
P60867_RS	Rps20	40S riboso	K.DTGKTPVEPEVAIHR.I	76.13	148.64	0.51	1.95
P60867_RS	Rps20	40S riboso	R.LIDLHSPSEIVK#.Q	427.65	205.72	2.08	0.48
P60867_RS	Rps20	40S riboso	K.QITSISIEPGVEVEVTIADA.-	11.56	11.56	1.00	1.00
P60867_RS	Rps20	40S riboso	K.TPVEPEVAIHR.I	98.73	215.59	0.46	2.18
Q9CQR2_R	Rps21	40S riboso	K.DHASIQM*NVAEVDR.T	8.69	16.35	0.53	1.88
Q9CQR2_R	Rps21	40S riboso	K.DHASIQMNVAEVDR.T	2.66	6.19	0.43	2.33
Q9CQR2_R	Rps21	40S riboso	R.FNGQFK#.T	29.28	60.97	0.48	2.08
Q9CQR2_R	Rps21	40S riboso	R.M*GESDDSILR.L	46.36	77.75	0.60	1.68
P62267_RS	Rps23	40S riboso	K.VANVSLLALYK#.G	72.22	24.66	2.93	0.34
P62267_RS	Rps23	40S riboso	K.ANPFGGASHAK#.G	583.51	251.44	2.32	0.43
P62267_RS	Rps23	40S riboso	K.GHAVGDIPGVR.F	16.15	97.45	0.17	6.04
P62267_RS	Rps23	40S riboso	K.K#AHLGTALK#.A	27.09	4.91	5.52	0.18
P62267_RS	Rps23	40S riboso	R.KGHAVGDIPGVR.F	22.92	60.32	0.38	2.63
P62267_RS	Rps23	40S riboso	K.VANVSLLALYK#.G	2124.38	813.30	2.61	0.38
P62267_RS	Rps23	40S riboso	K.VANVSLLALYK#.G	25.55	11.90	2.15	0.47
P62267_RS	Rps23	40S riboso	K.VANVSLLALYK#.G	24.55	8.44	2.91	0.34
P62849_RS	Rps24	40S riboso	R.K#QM*VIDVLHPGK#.A	53.45	14.43	3.70	0.27
P62849_RS	Rps24	40S riboso	R.K#QM*VIDVLHPGK#.A	2.22	1.61	1.38	0.73
P62849_RS	Rps24	40S riboso	R.K#QMVIDVLHPGK#.A	68.99	26.72	2.58	0.39
P62849_RS	Rps24	40S riboso	K.QM*VIDVLHPGK#.A	60.30	27.49	2.19	0.46
P62849_RS	Rps24	40S riboso	K.TTGFGM*IYDSLDYAK#.K	413.42	120.15	3.44	0.29
P62849_RS	Rps24	40S riboso	K.TTGFGMIYDSLDYAK#.K	186.69	59.54	3.14	0.32
P62849_RS	Rps24	40S riboso	K.TTPDVIFVFGFR.T	74.17	102.45	0.72	1.38
P62852_RS	Rps25	40S riboso	R.DK#LNNLVLFDK#.A	15.31	5.80	2.64	0.38
P62852_RS	Rps25	40S riboso	K.LNNLVLFDK#.A	12.57	4.56	2.76	0.36
P62852_RS	Rps25	40S riboso	R.AALQELLSK#.G	1000.78	447.51	2.24	0.45
P62852_RS	Rps25	40S riboso	R.AQVIYTR.N	118.98	239.64	0.50	2.01
P62852_RS	Rps25	40S riboso	R.DKLNNLVLFDK.A	81.97	20.46	4.01	0.25
P62852_RS	Rps25	40S riboso	K.LITPAVVSER.L	307.16	592.66	0.52	1.93
P62852_RS	Rps25	40S riboso	K.LNNLVLFDK#.A	218.59	99.56	2.20	0.46
P62852_RS	Rps25	40S riboso	R.NTK#GGDAPAAGEDA.-	9.93	3.84	2.59	0.39
P62852_RS	Rps25	40S riboso	K.VRDKLNNLVLFDK.A	18.08	42.88	0.42	2.37
P62855_RS	Rps26	40S riboso	R.DISEASVFDAYVLPK#.L	41.35	9.87	4.19	0.24
P62855_RS	Rps26	40S riboso	R.DISEASVFDAYVLPK#.L	1173.03	475.98	2.46	0.41
P62855_RS	Rps26	40S riboso	R.GHVQPIR.C	28.79	50.13	0.57	1.74
P62855_RS	Rps26	40S riboso	R.NIVEAAAVR.D	233.78	359.78	0.65	1.54
P62855_RS	Rps26	40S riboso	R.NIVEAAAVR.D	14.03	22.68	0.62	1.62
Q6ZWU9_	Rps27	40S riboso	K.DLLHPSPEEEK#.R	49.71	25.45	1.95	0.51
Q6ZWU9_	Rps27	40S riboso	K.DLLHPSPEEEK#.R	7.63	4.52	1.69	0.59
Q6ZWY3_R	Rps27l	40S riboso	R.LVQSPNSYFM*DVK#.C	15.68	6.92	2.27	0.44
Q6ZWY3_R	Rps27l	40S riboso	R.DLLHPSLEEEK#.K	26.83	10.68	2.51	0.40
Q6ZWY3_R	Rps27l	40S riboso	R.DLLHPSLEEEK#K#K#.H	64.19	27.21	2.36	0.42
Q6ZWY3_R	Rps27l	40S riboso	R.LVQSPNSYFM*DVK#.C	366.79	150.70	2.43	0.41
Q6ZWY3_R	Rps27l	40S riboso	R.LVQSPNSYFMDVK#.C	63.54	28.00	2.27	0.44
Q6ZWY3_R	Rps27l	40S riboso	R.LVQSPNSYFM*DVK#.C	20.69	8.21	2.52	0.40
Q6ZWY3_R	Rps27l	40S riboso	R.LVQSPNSYFMDVK#.C	14.97	7.76	1.93	0.52
Q6ZWY3_R	Rps27l	40S riboso	R.LVQSPNSYFM*DVK#.C	44.18	18.09	2.44	0.41
Q6ZWY3_R	Rps27l	40S riboso	R.LVQSPNSYFMDVK#.C	16.23	8.58	1.89	0.53
P62858_RS	Rps28	40S riboso	R.EGDVLTLLESER.E	142.52	293.95	0.48	2.06
P62858_RS	Rps28	40S riboso	K.GPVREGDVLTLLESER.E	11.52	65.34	0.18	5.67
P62858_RS	Rps28	40S riboso	R.VEFMDDTSR.S	14.52	27.82	0.52	1.92
P62858_RS	Rps28	40S riboso	R.VEFM*DDTSR.S	48.20	104.63	0.46	2.17
P62274_RS	Rps29	40S riboso	K.DIGFIK#LD.-	588.35	289.06	2.04	0.49
P62908_RS	Rps3	40S riboso	K.AELNEFLTR.E	136.08	245.98	0.55	1.81
P62908_RS	Rps3	40S riboso	K.DEILPTTPISEQK#.G	361.28	173.99	2.08	0.48
P62908_RS	Rps3	40S riboso	R.ELAEDGYSGVEVR.V	114.47	209.47	0.55	1.83
P62908_RS	Rps3	40S riboso	R.ELTAVVQK#.R	295.14	140.00	2.11	0.47
P62908_RS	Rps3	40S riboso	R.FGFPEGSVELYAEK#.V	433.60	176.74	2.45	0.41
P62908_RS	Rps3	40S riboso	R.FIM*ESGAK#.G	326.98	122.07	2.68	0.37
P62908_RS	Rps3	40S riboso	K.FVADGIFK#.A	270.90	94.11	2.88	0.35
P62908_RS	Rps3	40S riboso	K.FVDGLM*IHSGDPVNYYVDTAVR.H	37.05	53.76	0.69	1.45
P62908_RS	Rps3	40S riboso	K.FVDGLMIHSGDPVNYYVDTAVR.H	14.89	26.52	0.56	1.78
P62908_RS	Rps3	40S riboso	K.GGK#PEPPAM*PQPVPTA.-	216.00	101.32	2.13	0.47
P62908_RS	Rps3	40S riboso	K.GGK#PEPPAMPQPVPTA.-	190.67	110.58	1.72	0.58
P62908_RS	Rps3	40S riboso	K.IM*LPWDPSGK#.I	115.52	52.65	2.19	0.46
P62908_RS	Rps3	40S riboso	R.IRELTAVVQK.R	18.95	35.99	0.53	1.90
P62908_RS	Rps3	40S riboso	R.K#FVADGIFK#.A	282.33	117.36	2.41	0.42
P62908_RS	Rps3	40S riboso	K.K#PLPDHVSIVEPK#.D	167.91	85.90	1.95	0.51
P62908_RS	Rps3	40S riboso	K.K#PLPDHVSIVEPK#.D	18.13	8.67	2.09	0.48
P62908_RS	Rps3	40S riboso	K.KPLPDHVSIVEPKDEILPTTPISEQK.G	89.59	38.91	2.30	0.43
P62908_RS	Rps3	40S riboso	K.KPLPDHVSIVEPKDEILPTTPISEQK.G	12.16	3.79	3.21	0.31
P62908_RS	Rps3	40S riboso	R.QGVLGIK#.V	339.15	130.00	2.61	0.38
P62908_RS	Rps3	40S riboso	K.RFGFPEGSVELYAEK.V	9.43	20.82	0.45	2.21
P62908_RS	Rps3	40S riboso	R.TEIIILATR.T	158.20	276.78	0.57	1.75
P62908_RS	Rps3	40S riboso	R.TQNVLGEK#.G	359.01	149.73	2.40	0.42
P62908_RS	Rps3	40S riboso	R.ELAEDGYSGVEVR.V	15.39	27.52	0.56	1.79
P62908_RS	Rps3	40S riboso	R.ELTAVVQK#.R	28.43	11.19	2.54	0.39
P62908_RS	Rps3	40S riboso	R.FGFPEGSVELYAEK#.V	43.90	13.91	3.16	0.32
P62908_RS	Rps3	40S riboso	K.FVADGIFK#.A	30.18	9.54	3.16	0.32
P62908_RS	Rps3	40S riboso	K.FVDGLM*IHSGDPVNYYVDTAVR.H	7.62	11.80	0.65	1.55
P62908_RS	Rps3	40S riboso	K.GGK#PEPPAM*PQPVPTA.-	17.93	9.60	1.87	0.54
P62908_RS	Rps3	40S riboso	K.IMLPWDPSGK#.I	14.12	5.96	2.37	0.42
P62908_RS	Rps3	40S riboso	R.K#FVADGIFK#.A	22.63	11.30	2.00	0.50
P62908_RS	Rps3	40S riboso	K.K#PLPDHVSIVEPK#.D	15.08	11.59	1.30	0.77
P62908_RS	Rps3	40S riboso	R.TEIIILATR.T	10.86	15.29	0.71	1.41
P62908_RS	Rps3	40S riboso	K.DEILPTTPISEQK#.G	35.43	11.38	3.11	0.32
P62908_RS	Rps3	40S riboso	R.ELAEDGYSGVEVR.V	17.80	28.63	0.62	1.61
P62908_RS	Rps3	40S riboso	R.FGFPEGSVELYAEK#.V	56.54	19.67	2.87	0.35
P62908_RS	Rps3	40S riboso	K.FVDGLM*IHSGDPVNYYVDTAVR.H	7.66	11.98	0.64	1.56
P62908_RS	Rps3	40S riboso	K.GGK#PEPPAM*PQPVPTA.-	28.09	16.18	1.74	0.58
P62908_RS	Rps3	40S riboso	K.GGK#PEPPAMPQPVPTA.-	69.18	35.48	1.95	0.51
P62908_RS	Rps3	40S riboso	K.K#PLPDHVSIVEPK#.D	18.27	11.17	1.64	0.61
P62908_RS	Rps3	40S riboso	R.TEIIILATR.T	11.41	19.81	0.58	1.74
P97351_RS	Rps3a	40S riboso	R.ADGYEPPVQESV.-	239.21	239.21	1.00	1.00
P97351_RS	Rps3a	40S riboso	K.APAM*FNIR.N	61.68	131.59	0.47	2.13
P97351_RS	Rps3a	40S riboso	K.APAMFNIR.N	29.57	54.23	0.55	1.83

P97351_RS	Rps3a	40S ribosor	K.DWYDVK#.A	156.61	54.16	2.89	0.35
P97351_RS	Rps3a	40S ribosor	R.EVQTNDLK#.E	423.30	182.40	2.32	0.43
P97351_RS	Rps3a	40S ribosor	R.EVQTNDLK#EVVNK#.L	51.01	21.81	2.34	0.43
P97351_RS	Rps3a	40S ribosor	K.K#DWYDVK#.A	97.05	43.67	2.22	0.45
P97351_RS	Rps3a	40S ribosor	K.K#VVDPFSK#.K	34.46	18.30	1.88	0.53
P97351_RS	Rps3a	40S ribosor	K.K#WQTMIEAHVDVK#.T	28.65	10.82	2.65	0.38
P97351_RS	Rps3a	40S ribosor	K.LITEDVQGK#.N	561.05	275.84	2.03	0.49
P97351_RS	Rps3a	40S ribosor	K.LM*ELHGEGGSSGK#.A	13.51	2.99	4.52	0.22
P97351_RS	Rps3a	40S ribosor	K.M*M*EIM*TR.E	16.67	32.21	0.52	1.93
P97351_RS	Rps3a	40S ribosor	K.TSYAQHQQVR.Q	22.83	41.46	0.55	1.82
P97351_RS	Rps3a	40S ribosor	K.TTDGYLLR.L	128.77	217.15	0.59	1.69
P97351_RS	Rps3a	40S ribosor	R.VFEVSLADLQNDEVAFR.K	55.43	109.46	0.51	1.97
P97351_RS	Rps3a	40S ribosor	R.VFEVSLADLQNDEVAFRK.F	32.37	66.37	0.49	2.05
P97351_RS	Rps3a	40S ribosor	K.VVDPFSK#.K	405.43	183.53	2.21	0.45
P97351_RS	Rps3a	40S ribosor	K.WQTMIEAHVDVK#.T	12.72	21.41	0.59	1.68
P97351_RS	Rps3a	40S ribosor	K.LITEDVQGK#.N	59.72	20.16	2.96	0.34
P97351_RS	Rps3a	40S ribosor	K.LM*ELHGEGGSSGK#.A	9.43	4.16	2.26	0.44
P97351_RS	Rps3a	40S ribosor	K.TTDGYLLR.L	13.39	40.20	0.33	3.00
P97351_RS	Rps3a	40S ribosor	R.EVQTNDLK#.E	17.98	8.46	2.13	0.47
P97351_RS	Rps3a	40S ribosor	K.LITEDVQGK#.N	60.97	16.79	3.63	0.28
P97351_RS	Rps3a	40S ribosor	R.VFEVSLADLQNDEVAFR.K	41.68	4.91	8.49	0.12
P97351_RS	Rps3a	40S ribosor	R.VFEVSLADLQNDEVAFR.K	3.81	9.96	0.38	2.61
P62702_RS	Rps4x	40S ribosor	R.ERHPGSFDVVHVK.D	13.34	25.82	0.52	1.94
P62702_RS	Rps4x	40S ribosor	K.GIPHLVTHDAR.T	27.50	16.45	1.67	0.60
P62702_RS	Rps4x	40S ribosor	K.GNKPWISLPR.G	31.33	55.70	0.56	1.78
P62702_RS	Rps4x	40S ribosor	R.HPGSFDVVHVK#.D	108.64	38.84	2.80	0.36
P62702_RS	Rps4x	40S ribosor	R.IGVITNR.E	109.61	184.81	0.59	1.69
P62702_RS	Rps4x	40S ribosor	R.K#IFVGTK#.G	120.08	70.05	1.71	0.58
P62702_RS	Rps4x	40S ribosor	R.LIYDTK#.G	306.86	103.84	2.96	0.34
P62702_RS	Rps4x	40S ribosor	R.LSNIFVIGK#.G	361.29	112.88	3.20	0.31
P62702_RS	Rps4x	40S ribosor	R.TDITYPAGFM*DVISIDK#.T	62.31	21.43	2.91	0.34
P62702_RS	Rps4x	40S ribosor	R.TDITYPAGFMDVISIDK#.T	68.01	29.42	2.31	0.43
P62702_RS	Rps4x	40S ribosor	K.VNDTIQIDLETGK#.I	85.69	36.84	2.33	0.43
P62702_RS	Rps4x	40S ribosor	K.VNDTIQIDLETGK#ITDFIK#.F	8.99	5.99	1.50	0.67
P62702_RS	Rps4x	40S ribosor	K.YALTGDEVK#.K	152.78	62.45	2.45	0.41
P62702_RS	Rps4x	40S ribosor	K.YALTGDEVKK.I	67.15	33.38	2.01	0.50
P62702_RS	Rps4x	40S ribosor	R.YPDPLIK#.V	86.81	27.86	3.12	0.32
P62702_RS	Rps4x	40S ribosor	K.DANGNSFATR.L	9.06	16.09	0.56	1.78
P62702_RS	Rps4x	40S ribosor	R.ERHPGSFDVVHVK.D	26.46	36.51	0.72	1.38
P62702_RS	Rps4x	40S ribosor	R.FIK#IDGK#.V	13.71	1.51	9.06	0.11
P62702_RS	Rps4x	40S ribosor	K.GNKPWISLPR.G	38.32	61.60	0.62	1.61
P62702_RS	Rps4x	40S ribosor	R.HPGSFDVVHVK#.D	167.09	53.99	3.09	0.32
P62702_RS	Rps4x	40S ribosor	K.HWM*LDK#.L	83.36	31.80	2.62	0.38
P62702_RS	Rps4x	40S ribosor	R.IGVITNR.E	197.27	390.08	0.51	1.98
P62702_RS	Rps4x	40S ribosor	R.K#IFVGTK#.G	71.05	31.35	2.27	0.44
P62702_RS	Rps4x	40S ribosor	R.LK#YALTGDEVK#.K	14.55	5.62	2.59	0.39
P62702_RS	Rps4x	40S ribosor	R.LSNIFVIGK#.G	1032.65	378.77	2.73	0.37
P62702_RS	Rps4x	40S ribosor	R.LTIAEER.D	104.46	201.25	0.52	1.93
P62702_RS	Rps4x	40S ribosor	R.TDITYPAGFM*DVISIDK#.T	113.19	54.27	2.09	0.48
P62702_RS	Rps4x	40S ribosor	R.TDITYPAGFMDVISIDK#.T	79.24	35.26	2.25	0.44
P62702_RS	Rps4x	40S ribosor	K.VNDTIQIDLETGK#.I	137.49	82.39	1.67	0.60
P62702_RS	Rps4x	40S ribosor	K.VNDTIQIDLETGK#ITDFIK#.F	29.25	14.91	1.96	0.51
P62702_RS	Rps4x	40S ribosor	K.VRTDITYPAGFM*DVISIDK.T	12.65	23.36	0.54	1.85
P62702_RS	Rps4x	40S ribosor	K.VRTDITYPAGFMDVISIDK.T	13.07	18.32	0.71	1.40
P62702_RS	Rps4x	40S ribosor	K.YALTGDEVK#.K	202.24	83.64	2.42	0.41
P62702_RS	Rps4x	40S ribosor	R.YPDPLIK#.V	221.04	115.25	1.92	0.52
P62702_RS	Rps4x	40S ribosor	K.GNKPWISLPR.G	9.51	16.06	0.59	1.69
P62702_RS	Rps4x	40S ribosor	R.HPGSFDVVHVK#.D	29.62	13.67	2.17	0.46
P62702_RS	Rps4x	40S ribosor	R.IGVITNR.E	35.09	51.16	0.69	1.46
P62702_RS	Rps4x	40S ribosor	R.K#IFVGTK#.G	25.61	9.12	2.81	0.36
P62702_RS	Rps4x	40S ribosor	R.LSNIFVIGK#.G	80.45	27.72	2.90	0.34
P62702_RS	Rps4x	40S ribosor	R.TDITYPAGFM*DVISIDK#.T	9.16	4.71	1.95	0.51
P62702_RS	Rps4x	40S ribosor	K.VNDTIQIDLETGK#.I	19.24	17.14	1.12	0.89
P62702_RS	Rps4x	40S ribosor	K.YALTGDEVK#.K	40.99	18.17	2.26	0.44
P62702_RS	Rps4x	40S ribosor	R.HPGSFDVVHVK#.D	25.98	7.50	3.46	0.29
P62702_RS	Rps4x	40S ribosor	R.LSNIFVIGK#.G	87.53	30.12	2.91	0.34
P62702_RS	Rps4x	40S ribosor	R.TDITYPAGFM*DVISIDK#.T	10.29	4.12	2.50	0.40
P62702_RS	Rps4x	40S ribosor	R.TDITYPAGFMDVISIDK#.T	13.55	5.06	2.68	0.37
P62702_RS	Rps4x	40S ribosor	K.YALTGDEVK#.K	28.37	12.37	2.29	0.44
P97461_RS	Rps5	40S ribosor	K.GSSNSYAIK#.K	16.86	5.48	3.08	0.33
P97461_RS	Rps5	40S ribosor	K.WSTDDVQINDISLQDYIAVK#.E	9.80	3.02	3.25	0.31
P97461_RS	Rps5	40S ribosor	K.GSSNSYAIK#.K	240.51	107.01	2.25	0.44
P97461_RS	Rps5	40S ribosor	K.GSSNSYAIK#K#.K	11.55	4.76	2.42	0.41
P97461_RS	Rps5	40S ribosor	R.QAVDVSPLR.R	57.47	103.22	0.56	1.80
P97461_RS	Rps5	40S ribosor	K.WSTDDVQINDISLQDYIAVK#.E	72.91	27.56	2.65	0.38
P97461_RS	Rps5	40S ribosor	K.WSTDDVQINDISLQDYIAVK#.E	10.58	2.99	3.54	0.28
P97461_RS	Rps5	40S ribosor	K.WSTDDVQINDISLQDYIAVK#.E	11.44	4.06	2.82	0.36
P97461_RS	Rps5	40S ribosor	K.WSTDDVQINDISLQDYIAVK#.E	18.97	6.26	3.03	0.33
P62754_RS	Rps6	40S ribosor	K.KGEKDIPGLTDTTVPR.R	13.48	23.28	0.58	1.73
P62754_RS	Rps6	40S ribosor	R.K#LFNLSK#.E	31.39	40.97	0.77	1.31
P62754_RS	Rps6	40S ribosor	K.K#NK#EEAAEYAK#.L	3.42	1.36	2.52	0.40
P62754_RS	Rps6	40S ribosor	K.LIEVDDER.K	130.34	161.42	0.81	1.24
P62754_RS	Rps6	40S ribosor	R.M*ATEVAADALGEEWK#.G	201.13	55.56	3.62	0.28
P62754_RS	Rps6	40S ribosor	R.MATEVAADALGEEWK#.G	99.95	29.93	3.34	0.30
P62754_RS	Rps6	40S ribosor	R.M*ATEVAADALGEEWKGYVVR.I	7.43	6.22	1.20	0.84
P62754_RS	Rps6	40S ribosor	K.NK#EEAAEYAK#.L	166.56	50.47	3.30	0.30
P62754_RS	Rps6	40S ribosor	R.M*ATEVAADALGEEWK#.G	22.66	6.50	3.49	0.29
P62754_RS	Rps6	40S ribosor	R.M*ATEVAADALGEEWKGYVVR.I	3.85	5.93	0.65	1.54
P18653_KS	Rps6ka1	Ribosomal	K.ADPSQFELLK#.V	37.04	12.11	3.06	0.33
P18653_KS	Rps6ka1	Ribosomal	K.DK#LPQSQLSHQDLQLVK#.G	22.72	8.46	2.68	0.37
P18653_KS	Rps6ka1	Ribosomal	R.DLK#PENILLDEEGHIK#.L	64.27	37.50	1.71	0.58
P18653_KS	Rps6ka1	Ribosomal	K.EVM*FTEEDVK#.F	18.26	6.98	2.62	0.38
P18653_KS	Rps6ka1	Ribosomal	K.FTLSGGNWNTVSETAK#.D	13.45	7.10	1.89	0.53
P18653_KS	Rps6ka1	Ribosomal	R.DLK#PENILLDEEGHIK#.L	36.18	13.72	2.64	0.38
P18653_KS	Rps6ka1	Ribosomal	K.FTLSGGNWNTVSETAK#.D	7.60	4.19	1.81	0.55
P18654_KS	Rps6ka3	Ribosomal	R.DLKPSNILYVDESGNPESIR.I	4.32	5.95	0.73	1.38
P18654_KS	Rps6ka3	Ribosomal	R.EASAVLFTITK#.T	50.00	19.27	2.59	0.39
P18654_KS	Rps6ka3	Ribosomal	K.FSLSGGYWNSVSDTAK#.D	17.22	4.55	3.79	0.26
P18654_KS	Rps6ka3	Ribosomal	R.HSFFSTIDWNK#.L	13.96	6.27	2.23	0.45
P18654_KS	Rps6ka3	Ribosomal	K.LGM*PQFLSPEAQSLLR.M	2.27	6.58	0.35	2.90
P18654_KS	Rps6ka3	Ribosomal	R.EASAVLFTITK#.T	19.65	7.93	2.48	0.40
Q9Z2B9_KS	Rps6ka4	Ribosomal	R.DLK#PENILYADDTPGAPVK#.I	6.23	7.58	0.82	1.22
Q8C050_KS	Rps6ka5	Ribosomal	K.TLQPSNPTEGSNPDTLFQFSD.-	4.48	4.48	1.00	1.00

P62082_RS	Rps7	40S ribosor	K.AIIIFVPVPQLK#.S	784.02	322.67	2.43	0.41
P62082_RS	Rps7	40S ribosor	K.AQQNNVEHKVETFSGVYK.K	72.58	29.91	2.43	0.41
P62082_RS	Rps7	40S ribosor	K.AQQNNVEHK#VETFSGVYK#K#.L	15.32	4.43	3.46	0.29
P62082_RS	Rps7	40S ribosor	R.ELNITAAK#.E	325.71	101.64	3.20	0.31
P62082_RS	Rps7	40S ribosor	K.HVVFIAQR.R	76.85	141.84	0.54	1.85
P62082_RS	Rps7	40S ribosor	K.IVKPNGEKPDEFESGISQALLELEM*NSDLK.A	16.10	6.33	2.54	0.39
P62082_RS	Rps7	40S ribosor	K.IVK#PNGEK#PDEFESGISQALLELEMNSDLK#.A	103.80	39.01	2.66	0.38
P62082_RS	Rps7	40S ribosor	K.IVK#PNGEK#PDEFESGISQALLELEMNSDLK#.A	10.77	3.28	3.29	0.30
P62082_RS	Rps7	40S ribosor	R.K#AIIIFVPVPQLK#.S	35.89	13.91	2.58	0.39
P62082_RS	Rps7	40S ribosor	K.LTGK#DVNFEFPEFQL.-	90.54	38.83	2.33	0.43
P62082_RS	Rps7	40S ribosor	R.TLTAVHDAILEDLVFPSEIVGK#.R	619.41	247.29	2.50	0.40
P62082_RS	Rps7	40S ribosor	K.VETFSGVYK#.K	126.59	49.06	2.58	0.39
P62242_RS	Rps8	40S ribosor	R.ADGYVLEGK#.E	128.96	42.92	3.00	0.33
P62242_RS	Rps8	40S ribosor	R.IIDVVYNASNNELVR.T	26.50	37.24	0.71	1.41
P62242_RS	Rps8	40S ribosor	K.ISSLLEEQFQQGK#.L	178.03	82.01	2.17	0.46
P62242_RS	Rps8	40S ribosor	K.LTPEEEEILNK#.K	222.26	149.37	1.49	0.67
P62242_RS	Rps8	40S ribosor	R.ADGYVLEGK#.E	383.67	96.43	3.98	0.25
P62242_RS	Rps8	40S ribosor	R.ADGYVLEGKELEFYLR.K	13.86	21.93	0.63	1.58
P62242_RS	Rps8	40S ribosor	K.ELEFYLR.K	53.60	68.16	0.79	1.27
P62242_RS	Rps8	40S ribosor	R.IIDVVYNASNNELVR.T	44.12	61.68	0.72	1.40
P62242_RS	Rps8	40S ribosor	R.IIDVVYNASNNELVR@.T	2.99	6.58	0.45	2.20
P62242_RS	Rps8	40S ribosor	K.ISSLLEEQFQQGK#.L	757.26	231.63	3.27	0.31
P62242_RS	Rps8	40S ribosor	K.LTPEEEEILNK#.K	754.30	267.93	2.82	0.36
P62242_RS	Rps8	40S ribosor	K.YELGRPAANTK.I	18.56	43.04	0.43	2.32
P62242_RS	Rps8	40S ribosor	R.ADGYVLEGK#.E	24.46	6.17	3.96	0.25
P62242_RS	Rps8	40S ribosor	K.ISSLLEEQFQQGK#.L	41.77	13.49	3.10	0.32
P62242_RS	Rps8	40S ribosor	R.ADGYVLEGK#.E	33.11	7.24	4.57	0.22
P62242_RS	Rps8	40S ribosor	K.ISSLLEEQFQQGK#.L	28.09	10.27	2.74	0.37
Q6ZWN5_R	Rps9	40S ribosor	K.IEDFLER.R	22.51	26.29	0.86	1.17
Q6ZWN5_R	Rps9	40S ribosor	K.LDYILGLK#.I	13.83	6.80	2.03	0.49
Q6ZWN5_R	Rps9	40S ribosor	R.LFEGNALLR.R	11.89	18.34	0.65	1.54
Q6ZWN5_R	Rps9	40S ribosor	K.QVVNIPSFIVR.L	6.37	10.39	0.61	1.63
Q6ZWN5_R	Rps9	40S ribosor	K.HIDFSLR.S	101.59	162.12	0.63	1.60
Q6ZWN5_R	Rps9	40S ribosor	K.IEDFLER.R	113.11	163.92	0.69	1.45
Q6ZWN5_R	Rps9	40S ribosor	R.IGVLDEGK#.M	889.59	293.20	3.03	0.33
Q6ZWN5_R	Rps9	40S ribosor	R.IGVLDEGKM*K.L	20.62	21.61	0.95	1.05
Q6ZWN5_R	Rps9	40S ribosor	K.K#GQGGAGAGDDEEED.-	9.99	4.42	2.26	0.44
Q6ZWN5_R	Rps9	40S ribosor	R.KQVVNIPSFIVR.L	32.91	53.33	0.62	1.62
Q6ZWN5_R	Rps9	40S ribosor	K.LDYILGLK#.I	417.50	144.81	2.88	0.35
Q6ZWN5_R	Rps9	40S ribosor	R.LFEGNALLR.R	245.50	388.16	0.63	1.58
Q6ZWN5_R	Rps9	40S ribosor	K.LIGEYGLR.N	216.17	321.65	0.67	1.49
Q6ZWN5_R	Rps9	40S ribosor	R.LQTQVFK#.L	500.48	183.04	2.73	0.37
Q6ZWN5_R	Rps9	40S ribosor	K.M*K#LDYILGLK#.I	318.95	119.98	2.66	0.38
Q6ZWN5_R	Rps9	40S ribosor	K.M*KLDYILGLK.I	185.61	69.63	2.67	0.38
Q6ZWN5_R	Rps9	40S ribosor	K.MK#LDYILGLK#.I	52.56	20.02	2.63	0.38
Q6ZWN5_R	Rps9	40S ribosor	K.MKLDYILGLK.I	66.48	24.03	2.77	0.36
Q6ZWN5_R	Rps9	40S ribosor	K.QVVNIPSFIVR.L	48.57	80.74	0.60	1.66
Q6ZWN5_R	Rps9	40S ribosor	R.RLFEGNALLR.R	11.58	71.32	0.16	6.16
Q6ZWN5_R	Rps9	40S ribosor	R.RLQTQVFK.L	103.29	186.96	0.55	1.81
Q6ZWN5_R	Rps9	40S ribosor	R.SPYGGGRPGR.V	5.09	22.85	0.22	4.49
Q6ZWN5_R	Rps9	40S ribosor	K.SRLDQELK.L	92.23	145.21	0.64	1.57
Q6ZWN5_R	Rps9	40S ribosor	R.VK#FTLAK#.I	89.14	19.84	4.49	0.22
Q6ZWN5_R	Rps9	40S ribosor	K.IEDFLER.R	12.64	22.53	0.56	1.78
Q6ZWN5_R	Rps9	40S ribosor	R.IGVLDEGK#.M	35.27	19.60	1.80	0.56
Q6ZWN5_R	Rps9	40S ribosor	K.LDYILGLK#.I	25.49	10.41	2.45	0.41
Q6ZWN5_R	Rps9	40S ribosor	R.LFEGNALLR.R	9.40	16.26	0.58	1.73
Q6ZWN5_R	Rps9	40S ribosor	K.M*K#LDYILGLK#.I	12.46	5.23	2.38	0.42
Q6ZWN5_R	Rps9	40S ribosor	K.IEDFLER.R	18.14	30.78	0.59	1.70
Q6ZWN5_R	Rps9	40S ribosor	R.IGVLDEGK#.M	92.49	33.16	2.79	0.36
Q6ZWN5_R	Rps9	40S ribosor	K.LDYILGLK#.I	38.02	14.30	2.66	0.38
Q6ZWN5_R	Rps9	40S ribosor	R.LFEGNALLR.R	20.73	28.38	0.73	1.37
Q6ZWN5_R	Rps9	40S ribosor	R.LQTQVFK#.L	76.19	21.22	3.59	0.28
Q6ZWN5_R	Rps9	40S ribosor	K.M*K#LDYILGLK#.I	17.97	6.35	2.83	0.35
Q6ZWN5_R	Rps9	40S ribosor	K.QVVNIPSFIVR.L	17.08	24.25	0.70	1.42
P14206_RS	Rpsa	40S ribosor	R.AIVAIENPADVSVISSR.N	87.38	131.97	0.66	1.51
P14206_RS	Rpsa	40S ribosor	R.DPEEIEK#EEQAAAEK#.A	14.81	8.83	1.68	0.60
P14206_RS	Rpsa	40S ribosor	K.FAAATGATPIAGR.F	161.20	265.60	0.61	1.65
P14206_RS	Rpsa	40S ribosor	K.FLAAGTHLGGTNLDFQM*EQYIYK#.R	164.56	45.24	3.64	0.27
P14206_RS	Rpsa	40S ribosor	K.FLAAGTHLGGTNLDFQMEQYIYK#.R	81.31	25.64	3.17	0.32
P14206_RS	Rpsa	40S ribosor	R.FTPGTFTNQIQAAFR.E	53.83	85.38	0.63	1.59
P14206_RS	Rpsa	40S ribosor	R.K#SDGIYIINLK#.R	90.71	22.95	3.95	0.25
P14206_RS	Rpsa	40S ribosor	R.LLVVTDPR.A	78.67	123.44	0.64	1.57
P14206_RS	Rpsa	40S ribosor	K.SDGIYIINLK#.R	158.15	49.11	3.22	0.31
P14206_RS	Rpsa	40S ribosor	R.AIVAIENPADVSVISSR.N	5.79	12.32	0.47	2.13
P14206_RS	Rpsa	40S ribosor	K.FLAAGTHLGGTNLDFQM*EQYIYK#.R	9.22	2.23	4.13	0.24
P14206_RS	Rpsa	40S ribosor	R.FTPGTFTNQIQAAFR.E	6.49	6.54	0.99	1.01
P14206_RS	Rpsa	40S ribosor	R.K#SDGIYIINLK#.R	10.30	3.77	2.73	0.37
P14206_RS	Rpsa	40S ribosor	R.LLVVTDPR.A	9.39	13.23	0.71	1.41
P14206_RS	Rpsa	40S ribosor	R.AIVAIENPADVSVISSR.N	7.17	15.12	0.47	2.11
P14206_RS	Rpsa	40S ribosor	K.FLAAGTHLGGTNLDFQM*EQYIYK#.R	7.52	4.13	1.82	0.55
Q9JKY0_RC	Rqcd1	Cell differer	R.LTSLGVIGALVK#.T	42.89	26.13	1.64	0.61
Q9JKY0_RC	Rqcd1	Cell differer	K.TVATFILQK#.I	19.54	12.42	1.57	0.64
Q9JKY0_RC	Rqcd1	Cell differer	R.ENALLELSK#.K	20.75	14.25	1.46	0.69
Q9JKY0_RC	Rqcd1	Cell differer	R.IM*ESGSELSK#.T	10.46	7.72	1.35	0.74
Q9JKY0_RC	Rqcd1	Cell differer	R.LTSLGVIGALVK#.T	51.20	32.52	1.57	0.64
Q9JKY0_RC	Rqcd1	Cell differer	K.TVATFILQK#.I	39.56	25.34	1.56	0.64
Q9JKY0_RC	Rqcd1	Cell differer	R.LTSLGVIGALVK#.T	18.54	8.00	2.32	0.43
Q9JKY0_RC	Rqcd1	Cell differer	R.LTSLGVIGALVK#.T	31.15	16.42	1.90	0.53
Q9JKY0_RC	Rqcd1	Cell differer	K.TVATFILQK#.I	19.55	11.71	1.67	0.60
Q99K70_RI	Rragc	Ras-related	K.AFLFDVVSK#.I	22.79	10.40	2.19	0.46
Q99K70_RI	Rragc	Ras-related	R.ANDDLADAGLEK#.L	15.95	3.56	4.49	0.22
Q99K70_RI	Rragc	Ras-related	K.M*SPNETLFLESTNK#.I	4.11	1.70	2.42	0.41
Q99K70_RI	Rragc	Ras-related	K.MSPNETLFLESTNK#.I	6.08	4.24	1.43	0.70
Q99K70_RI	Rragc	Ras-related	K.AFLFDVVSK#.I	17.00	6.60	2.57	0.39
Q99K70_RI	Rragc	Ras-related	K.AFLFDVVSK#.I	25.10	11.58	2.17	0.46
P62071_RF	Rras2	Ras-related	R.LDILDTAGQEEFGAM*R.E	1.23	10.68	0.11	8.70
P62071_RF	Rras2	Ras-related	R.LVVVGGGGVGK#.S	37.04	10.68	3.47	0.29
P62071_RF	Rras2	Ras-related	R.QVTQEEGQQLAR.Q	1.44	10.07	0.14	6.99
Q99PL5_RF	Rrbp1	Ribosome-l	K.ASM*VQSQEAPK#.Q	6.57	3.50	1.88	0.53
Q99PL5_RF	Rrbp1	Ribosome-l	R.DALNQATSQVESK#.Q	38.31	11.22	3.41	0.29
Q99PL5_RF	Rrbp1	Ribosome-l	R.LIEILSEK#.T	25.30	6.86	3.69	0.27
Q99PL5_RF	Rrbp1	Ribosome-l	K.LLATEQEDAAVAK#.S	45.38	10.87	4.17	0.24
Q99PL5_RF	Rrbp1	Ribosome-l	R.DALNQATSQVESK#.Q	14.36	4.75	3.02	0.33

Q99PL5_RI	Rrbp1	Ribosome-l	K.LQSSEVEVK#.S	13.09	1.48	8.85	0.11
P07742_RI	Rrm1	Ribonuclec	R.GAFIDQSQSLNIHIAEPNYGK#.L	22.99	11.21	2.05	0.49
P07742_RI	Rrm1	Ribonuclec	K.GILQYDM*WNVAPTDLWDWK#PLK#.E	6.97	6.73	1.03	0.97
P07742_RI	Rrm1	Ribonuclec	K.SNQQNLGTIK#.C	23.01	25.41	0.91	1.10
P07742_RI	Rrm1	Ribonuclec	R.VSVGIHK#EDIDAAIETYNLLSEK#.W	4.10	4.41	0.93	1.08
P07742_RI	Rrm1	Ribonuclec	R.YPFESPEAQLLNK#.Q	22.37	16.84	1.33	0.75
P07742_RI	Rrm1	Ribonuclec	R.GAFIDQSQSLNIHIAEPNYGK#.L	20.61	9.62	2.14	0.47
P07742_RI	Rrm1	Ribonuclec	K.GILQYDM*WNVAPTDLWDWK#PLK#.E	2.79	3.53	0.79	1.27
P07742_RI	Rrm1	Ribonuclec	K.SNQQNLGTIK#.C	25.87	17.22	1.50	0.67
P07742_RI	Rrm1	Ribonuclec	R.VSVGIHK#EDIDAAIETYNLLSEK#.W	4.14	3.76	1.10	0.91
P07742_RI	Rrm1	Ribonuclec	R.YPFESPEAQLLNK#.Q	22.04	26.23	0.84	1.19
P56183_RI	Rrp1	Ribosomal	R.ATGGFTPDELLK#.V	19.46	11.57	1.68	0.59
P56183_RI	Rrp1	Ribosomal	R.ELAGGTFPEDDVPEK#.A	8.72	6.61	1.32	0.76
P56183_RI	Rrp1	Ribosomal	R.M*VLSESLK.A	17.34	10.85	1.60	0.63
Q6P5B0_RI	Rrp12	RRP12-like	R.ALSQAAVEEEEEEEEEEEPVQSK#.G	14.34	5.89	2.43	0.41
Q6P5B0_RI	Rrp12	RRP12-like	K.AM*DLAQAGSTVESK#.I	9.49	7.65	1.24	0.81
Q6P5B0_RI	Rrp12	RRP12-like	K.EGGGDEPLNFLDPK#.V	8.70	6.26	1.39	0.72
Q6P5B0_RI	Rrp12	RRP12-like	K.SDLTVDAVK#.L	17.10	5.87	2.91	0.34
Q6P5B0_RI	Rrp12	RRP12-like	K.VLDPASSDFTR.L	3.45	12.29	0.28	3.56
Q9CYX7_RI	Rrp15	RRP15-like	R.GVVQLFNAVQK#.H	24.48	10.49	2.33	0.43
Q91YK2_RI	Rrp1b	Ribosomal	K.LGALPDSSSDLPVQK#.S	8.52	3.18	2.68	0.37
Q91YK2_RI	Rrp1b	Ribosomal	K.VPDSESEPDTAQR.Q	2.28	5.95	0.38	2.61
Q9D1C9_RI	Rrp7a	Ribosomal	K.GPLLVSTESHLVK#.S	16.69	8.34	2.00	0.50
Q9D1C9_RI	Rrp7a	Ribosomal	K.TVELQEK#PDLAESPTEPK#.S	39.24	39.09	1.00	1.00
Q9D1C9_RI	Rrp7a	Ribosomal	K.WISDYEDSVLDPEALR.M	2.56	7.73	0.33	3.02
Q91WM3_	Rrp9	U3 small nu	R.AK#PAPGPGAAPVAGK#.R	7.88	3.09	2.55	0.39
Q91WM3_	Rrp9	U3 small nu	K.EIQAPAPTDIR.V	2.54	9.36	0.27	3.69
Q91WM3_	Rrp9	U3 small nu	R.K#TEEEEEEELEETAQEK#.K	15.10	5.22	2.89	0.35
E9PWW9_	Rsf1	Protein Rsf	R.DSQPSALPSEQESSK#.K	8.90	5.22	1.71	0.59
E9PWW9_	Rsf1	Protein Rsf	R.NSTASENTEITSER.K	4.62	12.01	0.38	2.60
E9PWW9_	Rsf1	Protein Rsf	K.AQIDPVLLK#.N	32.06	21.80	1.47	0.68
E9PWW9_	Rsf1	Protein Rsf	R.DSQPSALPSEQESSK#.K	20.21	24.26	0.83	1.20
E9PWW9_	Rsf1	Protein Rsf	R.FDEFDEAIDEAIEDDIKEADGGGVGR.G	4.34	17.57	0.25	4.04
E9PWW9_	Rsf1	Protein Rsf	K.GIDSSVPDIESLSQK#.A	29.43	24.60	1.20	0.84
E9PWW9_	Rsf1	Protein Rsf	K.LDNAQTSGM*EDTSETK#.G	14.15	17.92	0.79	1.27
E9PWW9_	Rsf1	Protein Rsf	K.LEK#PLPETEEK#.K	27.77	19.22	1.44	0.69
E9PWW9_	Rsf1	Protein Rsf	K.LSPIPEEVVR.G	5.23	36.80	0.14	7.03
E9PWW9_	Rsf1	Protein Rsf	R.NRNELAETLALLK.A	2.76	17.30	0.16	6.27
E9PWW9_	Rsf1	Protein Rsf	R.NSTASENTEITSER.K	11.69	38.95	0.30	3.33
E9PWW9_	Rsf1	Protein Rsf	R.RADGEDGVEGEPASLQTADKK.D	1.39	11.37	0.12	8.19
Q8BVY0_RL	Rsl1d1	Ribosomal	K.ALLATETPEASAPGTSGK#.K	58.16	45.83	1.27	0.79
Q8BVY0_RL	Rsl1d1	Ribosomal	K.ATSLLTQSGLASSAPAK#.S	49.75	28.30	1.76	0.57
Q8BVY0_RL	Rsl1d1	Ribosomal	K.AVEVISNR.S	12.64	19.12	0.66	1.51
Q8BVY0_RL	Rsl1d1	Ribosomal	K.DEFDSPEQTEGFYK#.K	6.14	2.87	2.14	0.47
Q8BVY0_RL	Rsl1d1	Ribosomal	K.GSASESPSASVAEATTTDVQVTPTALLQLDR.E	3.00	7.19	0.42	2.40
Q8BVY0_RL	Rsl1d1	Ribosomal	K.HGVNTISQIIPFK#.T	32.96	21.59	1.53	0.66
Q8BVY0_RL	Rsl1d1	Ribosomal	R.K#ALLATETPEASAPGTSGK#K#.Q	4.57	3.59	1.27	0.78
Q8BVY0_RL	Rsl1d1	Ribosomal	K.K#ATSLLTQSGLASSAPAK#.S	14.03	7.78	1.80	0.55
Q8BVY0_RL	Rsl1d1	Ribosomal	K.K#HGVNTISQIIPFK#.T	14.35	9.10	1.58	0.63
Q8BVY0_RL	Rsl1d1	Ribosomal	R.KKVPVSVNLLAK.N	37.66	26.75	1.41	0.71
Q8BVY0_RL	Rsl1d1	Ribosomal	K.K#VPVSVNLLAK#.N	24.22	15.31	1.58	0.63
Q8BVY0_RL	Rsl1d1	Ribosomal	R.LLGSFEVFITDAR.I	8.97	21.12	0.42	2.35
Q8BVY0_RL	Rsl1d1	Ribosomal	K.SVSLPIFSSFVTSQDENAVSLR.S	4.45	12.73	0.35	2.86
Q8BVY0_RL	Rsl1d1	Ribosomal	K.GSASESPSASVAEATTTDVQVTPTALLQLDR.E	2.34	4.12	0.57	1.76
Q8BVY0_RL	Rsl1d1	Ribosomal	K.HGVNTISQIIPFK#.T	14.20	9.51	1.49	0.67
Q8BVY0_RL	Rsl1d1	Ribosomal	K.VPVSVNLLAK#.N	10.80	6.86	1.57	0.64
Q8BVY0_RL	Rsl1d1	Ribosomal	K.ALLATETPEASAPGTSGK#.K	13.86	8.55	1.62	0.62
Q8BVY0_RL	Rsl1d1	Ribosomal	K.ATSLLTQSGLASSAPAK#.S	18.75	8.02	2.34	0.43
Q8BVY0_RL	Rsl1d1	Ribosomal	K.HGVNTISQIIPFK#.T	21.26	8.30	2.56	0.39
Q8BVY0_RL	Rsl1d1	Ribosomal	K.ALLATETPEASAPGTSGK#.K	18.22	9.84	1.85	0.54
Q8BVY0_RL	Rsl1d1	Ribosomal	K.ATSLLTQSGLASSAPAK#.S	16.64	9.98	1.67	0.60
Q8BVY0_RL	Rsl1d1	Ribosomal	K.GSASESPSASVAEATTTDVQVTPTALLQLDR.E	3.94	2.79	1.41	0.71
Q8BVY0_RL	Rsl1d1	Ribosomal	K.HGVNTISQIIPFK#.T	12.51	5.88	2.13	0.47
Q8BVY0_RL	Rsl1d1	Ribosomal	K.SVSLPIFSSFVTSQDENAVSLR.S	11.66	18.38	0.63	1.58
Q99L28_RL	Rsl24d1	Probable ri	K.ELTVDNSFEFEK#.R	25.16	19.16	1.31	0.76
Q99L28_RL	Rsl24d1	Probable ri	K.M*VQQLQEDVDM*EEAS.-	8.76	8.76	1.00	1.00
Q99L28_RL	Rsl24d1	Probable ri	K.MVQQLQEDVDM*EEAS.-	2.97	2.97	1.00	1.00
A2RTL5_RS	Rsrc2	Arginine/se	K.ALAETGIAVPSYYNPAAVNPM*K.F	13.95	19.39	0.72	1.39
A2RTL5_RS	Rsrc2	Arginine/se	K.ALAETGIAVPSYYNPAAVNPMK.F	4.78	6.51	0.73	1.36
A2RTL5_RS	Rsrc2	Arginine/se	R.GM*GLGFTSSM*R.G	2.61	14.49	0.18	5.56
A2RTL5_RS	Rsrc2	Arginine/se	R.NLDAQYEMAR.S	1.57	9.73	0.16	6.20
A2RTL5_RS	Rsrc2	Arginine/se	R.NTAM*DAQEALAR.R	84.79	65.17	1.30	0.77
A2RTL5_RS	Rsrc2	Arginine/se	R.NTAMDAQEALAR.R	80.92	30.74	2.63	0.38
A2RTL5_RS	Rsrc2	Arginine/se	K.SQSAEIWEK.L	22.37	36.22	0.62	1.62
Q01730_RS	Rsu1	Ras suppres	R.DNDLISLPK#.E	24.29	6.50	3.74	0.27
Q01730_RS	Rsu1	Ras suppres	R.LTVLPPELGNLDLTGQK#.Q	12.88	3.35	3.84	0.26
Q01730_RS	Rsu1	Ras suppres	R.ALYLSDNDFEILPPDIGK#.L	6.96	3.55	1.96	0.51
Q01730_RS	Rsu1	Ras suppres	R.DNDLISLPK#.E	24.68	6.08	4.06	0.25
Q01730_RS	Rsu1	Ras suppres	K.EIGELTQLK#.E	29.22	6.80	4.29	0.23
Q9D7H3_R	RtcA	RNA 3'-term	R.AFVAGVLPLK#.V	40.39	23.77	1.70	0.59
Q9D7H3_R	RtcA	RNA 3'-term	K.GGGEVIVR.V	5.61	15.59	0.36	2.78
Q9D7H3_R	RtcA	RNA 3'-term	K.TGSVTLHTQTAIHFAEQLAK#.A	9.04	6.32	1.43	0.70
Q9D7H3_R	RtcA	RNA 3'-term	R.VEVDGGIM*EGGGQILR.V	3.17	7.97	0.40	2.51
Q9D7H3_R	RtcA	RNA 3'-term	R.VEVDGGIMEGGGQILR.V	3.08	7.17	0.43	2.33
Q9D7H3_R	RtcA	RNA 3'-term	R.AFVAGVLPLK#.V	12.89	4.65	2.77	0.36
Q99LF4_RT	Rtcb	tRNA-splici	K.DLEEALEM*GVDWSLR.E	2.24	12.21	0.18	5.46
Q99LF4_RT	Rtcb	tRNA-splici	K.GFVPNM*QVEGVFYVNDALEK#.L	12.41	2.50	4.97	0.20
Q99LF4_RT	Rtcb	tRNA-splici	K.GFVPNMQVEGVFYVNDALEK#.L	5.79	5.44	1.06	0.94
Q99LF4_RT	Rtcb	tRNA-splici	R.GGGVGGFLPAM*K#.Q	71.78	41.41	1.73	0.58
Q99LF4_RT	Rtcb	tRNA-splici	R.GGGVGGFLPAMK#.Q	27.47	12.87	2.13	0.47
Q99LF4_RT	Rtcb	tRNA-splici	R.GLGHQVATDALVAM*EK#.A	68.27	39.12	1.75	0.57
Q99LF4_RT	Rtcb	tRNA-splici	R.GLGHQVATDALVAMEK#.A	75.43	143.99	0.52	1.91
Q99LF4_RT	Rtcb	tRNA-splici	R.GLPQLGTLGAGNHYAEIQVVDEIFNEYAAK#.K	95.96	47.12	2.04	0.49
Q99LF4_RT	Rtcb	tRNA-splici	K.GMAAAGNYAWVNR.S	5.60	15.64	0.36	2.79
Q99LF4_RT	Rtcb	tRNA-splici	R.IASPEGQDYLK#.G	180.93	105.26	1.72	0.58
Q99LF4_RT	Rtcb	tRNA-splici	K.KGFVPNM*QVEGVFYVNDALEK.L	7.63	6.29	1.21	0.82
Q99LF4_RT	Rtcb	tRNA-splici	K.LADMGIAIR.V	11.14	21.19	0.53	1.90
Q99LF4_RT	Rtcb	tRNA-splici	K.LVM*EEAPESYK#.N	91.37	60.14	1.52	0.66
Q99LF4_RT	Rtcb	tRNA-splici	K.LVMEEAPESYK#.N	51.27	39.00	1.31	0.76
Q99LF4_RT	Rtcb	tRNA-splici	R.NLDFQDVLDK#.L	72.08	36.46	1.98	0.51
Q99LF4_RT	Rtcb	tRNA-splici	R.NYNDELQFLDK#.I	56.35	35.53	1.59	0.63
Q99LF4_RT	Rtcb	tRNA-splici	K.QIGNVAALPGIVHR.S	16.57	53.86	0.31	3.25
Q99LF4_RT	Rtcb	tRNA-splici	R.SSM*TFLTR.Q	9.25	31.22	0.30	3.38

Q99LF4_RT	Rtcb	tRNA-splici	R.TNLDESDVQPVK#EQLAQAM*FDHIPVGVGSK#.G	9.50	4.12	2.30	0.43
Q99LF4_RT	Rtcb	tRNA-splici	R.TNLDESDVQPVK#EQLAQAMFDHIPVGVGSK#.G	4.09	3.38	1.21	0.83
Q99LF4_RT	Rtcb	tRNA-splici	K.VEQHVVDGK#.E	62.58	35.91	1.74	0.57
Q99LF4_RT	Rtcb	tRNA-splici	K.VFNTTPDDLDLHVIYDVSHNIAK#.V	141.24	72.55	1.95	0.51
A2AQ19_R	Rtf1	RNA polym	K.AM*AEDLGDQDK#.A	6.09	2.41	2.53	0.40
A2AQ19_R	Rtf1	RNA polym	K.FNDQDIEEIVK#.E	9.30	4.83	1.92	0.52
A2AQ19_R	Rtf1	RNA polym	K.IDLQVPSSESK#.A	26.59	14.66	1.81	0.55
A2AQ19_R	Rtf1	RNA polym	R.LEFVSNQEFTESEFM*K#.W	9.84	2.52	3.90	0.26
A2AQ19_R	Rtf1	RNA polym	R.LEFVSNQEFTESEFMK#.W	8.50	3.02	2.81	0.36
A2AQ19_R	Rtf1	RNA polym	R.VAEITGVVETAK#.V	67.79	20.96	3.23	0.31
A2AQ19_R	Rtf1	RNA polym	K.YGSGVLPDAPK#.E	22.36	7.68	2.91	0.34
Q99K95_R	Rtfdc1	Protein RT	R.SIADSEESETYK.S	7.24	9.11	0.79	1.26
Q8BH78_Q	Rtn4	RTN4 OS=	R.AYLESEVAISEELVQK#.Y	11.94	9.31	1.28	0.78
Q8BH78_Q	Rtn4	RTN4 OS=	R.AYLESEVAISEELVQK.Y	9.57	10.01	0.96	1.05
Q8BH78_Q	Rtn4	RTN4 OS=	R.GPLPAAPPTAPER.Q	21.28	70.86	0.30	3.33
Q8BH78_Q	Rtn4	RTN4 OS=	R.GSGSVVVDLLYWR.D	9.01	18.64	0.48	2.07
Q8BH78_Q	Rtn4	RTN4 OS=	K.GVIQAIQK#.S	51.54	32.74	1.57	0.64
Q8BH78_Q	Rtn4	RTN4 OS=	R.HQAQIDHYLGLANK#.S	65.05	48.04	1.35	0.74
Q8BH78_Q	Rtn4	RTN4 OS=	R.SPAASAPSLPPAAAVLPSK#.L	8.74	5.57	1.57	0.64
Q9ER80_R	Rtp4	Receptor-t	K.IALTSNASLGEK#.V	14.09	14.14	1.00	1.00
P60122_R	Ruvbl1	RuvB-like 1	R.ALESSIAPIVIFASNR.G	21.19	65.30	0.32	3.08
P60122_R	Ruvbl1	RuvB-like 1	R.AVLLAGPPGTGK#.T	290.35	197.38	1.47	0.68
P60122_R	Ruvbl1	RuvB-like 1	K.DSIEK#EHVEEISELFYDAK#.S	34.76	21.08	1.65	0.61
P60122_R	Ruvbl1	RuvB-like 1	K.DSIEK#EHVEEISELFYDAK#.S	3.70	2.54	1.46	0.69
P60122_R	Ruvbl1	RuvB-like 1	K.EHVEEISELFYDAK#.S	13.22	3.84	3.44	0.29
P60122_R	Ruvbl1	RuvB-like 1	K.GLGLDESGLAK#.Q	212.46	126.27	1.68	0.59
P60122_R	Ruvbl1	RuvB-like 1	K.ILADQQDK#.Y	77.12	52.43	1.47	0.68
P60122_R	Ruvbl1	RuvB-like 1	K.KTEVLM*ENFR.R	8.34	39.28	0.21	4.71
P60122_R	Ruvbl1	RuvB-like 1	K.LDPSIFESLQK#.E	165.86	115.59	1.43	0.70
P60122_R	Ruvbl1	RuvB-like 1	K.QAASGLVGQENAR.E	27.60	99.96	0.28	3.62
P60122_R	Ruvbl1	RuvB-like 1	K.TALALAIAQELGSK#.V	52.09	39.00	1.34	0.75
P60122_R	Ruvbl1	RuvB-like 1	K.TEVLM*ENFR.R	8.28	14.79	0.56	1.79
P60122_R	Ruvbl1	RuvB-like 1	K.TEVLMENFR.R	5.45	11.90	0.46	2.18
P60122_R	Ruvbl1	RuvB-like 1	R.TM*LYTPQEM*K#.Q	45.96	33.04	1.39	0.72
P60122_R	Ruvbl1	RuvB-like 1	R.TMLYTPQEM*K#.Q	26.37	17.27	1.53	0.65
P60122_R	Ruvbl1	RuvB-like 1	R.TM*LYTPQEMK#.Q	17.78	9.95	1.79	0.56
P60122_R	Ruvbl1	RuvB-like 1	R.VEAGDVIYIEANSGAVK#.R	48.30	30.14	1.60	0.62
P60122_R	Ruvbl1	RuvB-like 1	R.VEAGDVIYIEANSGAVK#.R	17.47	5.90	2.96	0.34
P60122_R	Ruvbl1	RuvB-like 1	R.YSVQLLTPANLLAK#.I	134.75	90.92	1.48	0.67
P60122_R	Ruvbl1	RuvB-like 1	R.ALESSIAPIVIFASNR.G	2.06	4.81	0.43	2.34
P60122_R	Ruvbl1	RuvB-like 1	K.GLGLDESGLAK#.Q	25.12	10.95	2.29	0.44
P60122_R	Ruvbl1	RuvB-like 1	K.LDPSIFESLQK#.E	12.48	11.88	1.05	0.95
P60122_R	Ruvbl1	RuvB-like 1	K.QAASGLVGQENAR.E	1.67	6.29	0.27	3.76
P60122_R	Ruvbl1	RuvB-like 1	R.YSVQLLTPANLLAK#.I	16.77	9.76	1.72	0.58
P60122_R	Ruvbl1	RuvB-like 1	R.ALESSIAPIVIFASNR.G	2.90	7.13	0.41	2.46
P60122_R	Ruvbl1	RuvB-like 1	K.LDPSIFESLQK#.E	10.79	7.79	1.39	0.72
P60122_R	Ruvbl1	RuvB-like 1	K.TALALAIAQELGSK#.V	17.81	8.48	2.10	0.48
P60122_R	Ruvbl1	RuvB-like 1	R.YSVQLLTPANLLAK#.I	17.56	11.46	1.53	0.65
Q9WTM5_	Ruvbl2	RuvB-like 2	R.AAGVVLEMIR.E	15.73	44.94	0.35	2.86
Q9WTM5_	Ruvbl2	RuvB-like 2	R.ALESDM*APVLIM*ATNR.G	4.38	7.28	0.60	1.66
Q9WTM5_	Ruvbl2	RuvB-like 2	R.ALESDM*APVLIMATNR.G	4.82	23.66	0.20	4.91
Q9WTM5_	Ruvbl2	RuvB-like 2	R.ALESDMAPVLIM*ATNR.G	3.69	6.22	0.59	1.68
Q9WTM5_	Ruvbl2	RuvB-like 2	R.AVLIAGQPGTGK#.T	253.36	149.76	1.69	0.59
Q9WTM5_	Ruvbl2	RuvB-like 2	K.DK#VQAGDVITIDK#.A	77.55	54.00	1.44	0.70
Q9WTM5_	Ruvbl2	RuvB-like 2	R.DYDAM*GSQTK#.F	11.76	5.37	2.19	0.46
Q9WTM5_	Ruvbl2	RuvB-like 2	R.DYDAMGSQTK#.F	11.48	7.25	1.58	0.63
Q9WTM5_	Ruvbl2	RuvB-like 2	K.EYQDAFLFNELK#.G	12.59	7.94	1.59	0.63
Q9WTM5_	Ruvbl2	RuvB-like 2	K.EYQDAFLFNELK#GETM*DTS.-	17.94	11.11	1.61	0.62
Q9WTM5_	Ruvbl2	RuvB-like 2	K.EYQDAFLFNELK#GETMDTS.-	11.52	8.34	1.38	0.72
Q9WTM5_	Ruvbl2	RuvB-like 2	R.IGLETSLR.Y	36.51	125.46	0.29	3.44
Q9WTM5_	Ruvbl2	RuvB-like 2	R.KGTEVQVDDIKR.V	20.79	108.34	0.19	5.21
Q9WTM5_	Ruvbl2	RuvB-like 2	R.LLIVSTSPYSEK#.D	129.86	91.64	1.42	0.71
Q9WTM5_	Ruvbl2	RuvB-like 2	R.QASQGM*VGQLAAR.R	17.76	47.31	0.38	2.66
Q9WTM5_	Ruvbl2	RuvB-like 2	R.QASQGMVGQLAAR.R	11.62	35.53	0.33	3.06
Q9WTM5_	Ruvbl2	RuvB-like 2	R.RAAGVVLEM*IR.E	1.29	17.26	0.07	13.43
Q9WTM5_	Ruvbl2	RuvB-like 2	K.TEALTQAFR.R	49.55	103.77	0.48	2.09
Q9WTM5_	Ruvbl2	RuvB-like 2	R.TQGFLALFSGDTGEIK#.S	120.41	63.84	1.89	0.53
Q9WTM5_	Ruvbl2	RuvB-like 2	R.TQGFLALFSGDTGEIKSEVR.E	7.01	8.38	0.84	1.20
Q9WTM5_	Ruvbl2	RuvB-like 2	K.TTEM*ETIYDLGTK#.M	91.98	54.31	1.69	0.59
Q9WTM5_	Ruvbl2	RuvB-like 2	K.TTEMETIYDLGTK#.M	52.71	37.86	1.39	0.72
Q9WTM5_	Ruvbl2	RuvB-like 2	K.VQAGDVITIDK#.A	61.94	41.36	1.50	0.67
Q9WTM5_	Ruvbl2	RuvB-like 2	R.VYSLFLDESR.S	34.96	95.16	0.37	2.72
Q9WTM5_	Ruvbl2	RuvB-like 2	R.TQGFLALFSGDTGEIK.S	6.11	5.78	1.06	0.95
Q9WTM5_	Ruvbl2	RuvB-like 2	R.TQGFLALFSGDTGEIK#.S	9.34	16.14	0.58	1.73
Q9CQK7_R	Rwdd1	RWD doma	K.AK#FDAELLEIK#.K	19.95	7.70	2.59	0.39
Q9CQK7_R	Rwdd1	RWD doma	K.LFHGTPVTIENFLSWK#.A	66.37	17.82	3.72	0.27
Q9CQK7_R	Rwdd1	RWD doma	K.LNEIVDQIK#.T	129.28	34.10	3.79	0.26
Q9CPR1_R	Rwdd4	RWD doma	K.DHK#EQFM*ENHHPGNSATPVANIISVETPTTAPSSK#.K	10.16	3.34	3.04	0.33
Q9CPR1_R	Rwdd4	RWD doma	R.ELSPVSFQYR.I	10.19	27.41	0.37	2.69
Q9CPR1_R	Rwdd4	RWD doma	R.GWNWVDVVK#.H	57.01	29.40	1.94	0.52
P50543_S1	S100a11	Protein S1	K.DPGVLDR.M	10.26	17.84	0.58	1.74
P50543_S1	S100a11	Protein S1	K.TEFLSFM*NTELAAFTK#.N	6.36	3.02	2.10	0.48
P50543_S1	S100a11	Protein S1	K.TEFLSFM*NTELAAFTK#.N	36.85	14.64	2.52	0.40
Q9D708_Q	S100a16	Protein S1	K.AVVVLVENFYK#.Y	12.41	10.30	1.21	0.83
Q9R1T2_S	Sae1	SUMO-acti	R.AK#LDSSETTM*VK#.K	8.41	4.42	1.90	0.53
Q9R1T2_S	Sae1	SUMO-acti	R.AQNLNPM*VDVK#.V	15.48	8.37	1.85	0.54
Q9R1T2_S	Sae1	SUMO-acti	R.DPPHNNFFFFDGM*K#.G	10.52	5.94	1.77	0.57
Q9R1T2_S	Sae1	SUMO-acti	K.FFTGDVFGYHGYTFANLGEHEFVEEK#.T	5.95	2.49	2.39	0.42
Q9R1T2_S	Sae1	SUMO-acti	K.GLTM*LDHEQVSPEDPGAQFLIQTGSVGR.N	2.00	3.60	0.55	1.80
Q9R1T2_S	Sae1	SUMO-acti	K.LDSSETTM*VK#.K	21.37	7.27	2.94	0.34
Q9R1T2_S	Sae1	SUMO-acti	K.VDTEDVEK#K#PESFFTK#.F	13.38	6.99	1.91	0.52
Q9R1T2_S	Sae1	SUMO-acti	K.LDSSETTM*VK#.K	4.94	2.00	2.48	0.40
D3YXK2_S	Safb	Scaffold att	R.APTAALSPEPQDSK#EDVK#K#.F	35.93	28.69	1.25	0.80
D3YXK2_S	Safb	Scaffold att	R.AWQGTADGGM*M*ER.D	4.17	16.55	0.25	3.97
D3YXK2_S	Safb	Scaffold att	R.LQAQWER.E	13.77	57.76	0.24	4.19
D3YXK2_S	Safb	Scaffold att	K.MSSVEEDSDTKR.L	19.32	7.42	2.60	0.38
D3YXK2_S	Safb	Scaffold att	R.NFWVSGLSSTTR.A	11.44	45.59	0.25	3.99
D3YXK2_S	Safb	Scaffold att	K.REPADAPGGGTGM*DREPVGLEEPVEQSSTAAQLPEATSQELVR.A	2.64	11.39	0.23	4.31
D3YXK2_S	Safb	Scaffold att	K.SEPVKEEGSELEQPFAQATSSVGPDR.K	2.65	18.86	0.14	7.13
D3YXK2_S	Safb	Scaffold att	K.SEPVKEEGSELEQPFAQATSSVGPDRK.L	1.69	10.82	0.16	6.41
D3YXK2_S	Safb	Scaffold att	K.SKDADDQKPGPSER.S	1.55	2.87	0.54	1.84
D3YXK2_S	Safb	Scaffold att	R.SVVSFDK#.V	48.92	52.64	0.93	1.08
D3YXK2_S	Safb	Scaffold att	K.SEPVKEEGSELEQPFAQATSSVGPDR.K	1.77	6.86	0.26	3.89

Q80YR5_SA	Safb2	Scaffold att	K.EKDQDELTPGAAGHSR.V	7.66	20.92	0.37	2.73
Q80YR5_SA	Safb2	Scaffold att	R.ELADAPGGGGGTR.H	3.45	23.81	0.15	6.89
Q80YR5_SA	Safb2	Scaffold att	R.LDAFQER.R	4.16	16.42	0.25	3.95
Q80YR5_SA	Safb2	Scaffold att	R.LEGGGM*ASQDQGGR.V	1.30	3.92	0.33	3.01
Q80YR5_SA	Safb2	Scaffold att	R.NLWVSGLSSSTR.A	2.60	14.81	0.18	5.70
F7ARK3_F7	Sall2	Sal-like pro	-.XSPHYQLSR.S	1.36	44.54	0.03	32.72
Q8BX22_SA	Sall4	Sal-like pro	K.SRSPEGHKAEGVESCR@.V	2.07	1.67	1.24	0.81
Q8CBY1_SN	Samd4a	Protein Sm	R.DQVGVLAGWFK#.G	10.01	4.13	2.43	0.41
Q69Z37_SA	Samd9l	Sterile alph	R.ETGQNEEQEPSLTK#.E	8.39	2.80	3.00	0.33
Q69Z37_SA	Samd9l	Sterile alph	K.LFAVLDFDPYSHIK#.G	14.31	6.84	2.09	0.48
Q69Z37_SA	Samd9l	Sterile alph	K.ATDFVEIGEQVSK#.L	59.66	14.77	4.04	0.25
Q69Z37_SA	Samd9l	Sterile alph	K.DK#PHGEIVGVQVTSK#.D	61.79	16.52	3.74	0.27
Q69Z37_SA	Samd9l	Sterile alph	K.EHGAETDTLFSPLIEELQNEETEK#.V	68.11	21.09	3.23	0.31
Q69Z37_SA	Samd9l	Sterile alph	K.ELDEDSTLIEK#.Y	30.51	6.82	4.47	0.22
Q69Z37_SA	Samd9l	Sterile alph	K.ELTELLLSK#.K	52.27	13.80	3.79	0.26
Q69Z37_SA	Samd9l	Sterile alph	K.ESM*AEFLSGK#.G	25.20	5.72	4.41	0.23
Q69Z37_SA	Samd9l	Sterile alph	R.GPALLIK#.R	33.95	12.83	2.65	0.38
Q69Z37_SA	Samd9l	Sterile alph	K.HSISTLNIELVNNTILK#.L	24.71	4.15	5.95	0.17
Q69Z37_SA	Samd9l	Sterile alph	K.LANSISLK#.Y	45.56	8.23	5.54	0.18
Q69Z37_SA	Samd9l	Sterile alph	R.LISFLTDENIIVK#.G	36.56	5.03	7.27	0.14
Q69Z37_SA	Samd9l	Sterile alph	K.NFSTALVWANLAK#.R	24.32	8.75	2.78	0.36
Q69Z37_SA	Samd9l	Sterile alph	K.NSYISDTLGQVYK.S	36.86	7.62	4.84	0.21
Q69Z37_SA	Samd9l	Sterile alph	K.TKNEEENSVSSNSDHGLR.E	8.54	8.04	1.06	0.94
Q69Z37_SA	Samd9l	Sterile alph	R.VAETGPLNLIDPIHEFK#.A	108.94	25.32	4.30	0.23
Q69Z37_SA	Samd9l	Sterile alph	K.YFEDSEISEAR.A	8.66	17.39	0.50	2.01
Q69Z37_SA	Samd9l	Sterile alph	K.YILPFSTLK#.K	49.77	12.98	3.84	0.26
Q60710_SA	Samhd1	Deoxynucle	K.FAEQLIR.V	8.96	21.18	0.42	2.36
Q60710_SA	Samhd1	Deoxynucle	K.IAGSFLPFLDEDR.L	5.90	14.54	0.41	2.46
Q60710_SA	Samhd1	Deoxynucle	R.IIDTPQFQR.L	14.03	37.72	0.37	2.69
Q60710_SA	Samhd1	Deoxynucle	R.INK#EQVSQLLPEK#.F	12.71	7.87	1.62	0.62
Q60710_SA	Samhd1	Deoxynucle	R.ISTAIDDM*EAFTK#.L	34.81	26.32	1.32	0.76
Q60710_SA	Samhd1	Deoxynucle	R.LEDLGVSSLEER.K	6.05	11.38	0.53	1.88
Q60710_SA	Samhd1	Deoxynucle	K.NYGLVPEEDITFIK#.E	33.64	20.83	1.61	0.62
Q60710_SA	Samhd1	Deoxynucle	K.ADPYVEITGTAGK#.K	89.26	43.40	2.06	0.49
Q60710_SA	Samhd1	Deoxynucle	K.APDVELK#.A	30.19	17.81	1.70	0.59
Q60710_SA	Samhd1	Deoxynucle	K.APDVELKAEDFIVDVINVDYGM*EDKNPIDR.V	9.48	16.09	0.59	1.70
Q60710_SA	Samhd1	Deoxynucle	K.APDVELKAEDFIVDVINVDYGM*EDKNPIDR.V	1.73	5.44	0.32	3.14
Q60710_SA	Samhd1	Deoxynucle	K.APDVELKAEDFIVDVINVDYGMEDKNPIDR.V	2.88	6.84	0.42	2.38
Q60710_SA	Samhd1	Deoxynucle	R.DFTKPQDGDIIAPLITPLK.W	83.24	42.63	1.95	0.51
Q60710_SA	Samhd1	Deoxynucle	R.EKEVGNLYDMFHTR.N	2.94	8.22	0.36	2.79
Q60710_SA	Samhd1	Deoxynucle	K.EQVSQLLPEK#.F	39.66	23.71	1.67	0.60
Q60710_SA	Samhd1	Deoxynucle	K.FAEQLIR.V	28.39	70.03	0.41	2.47
Q60710_SA	Samhd1	Deoxynucle	K.HEQGSIEM*FEHLVNSNELK#.L	9.80	4.93	1.99	0.50
Q60710_SA	Samhd1	Deoxynucle	K.HEQGSIEMFEHLVNSNELK#.L	8.15	4.27	1.91	0.52
Q60710_SA	Samhd1	Deoxynucle	K.IAGSFLPFLDEDRLEDLGVSSLEER.K	26.66	134.43	0.20	5.04
Q60710_SA	Samhd1	Deoxynucle	R.IIDTPQFQR.L	41.35	90.50	0.46	2.19
Q60710_SA	Samhd1	Deoxynucle	R.INK#EQVSQLLPEK#.F	64.22	34.59	1.86	0.54
Q60710_SA	Samhd1	Deoxynucle	K.ISNLIDIM*ITDAFLK#.A	44.08	22.59	1.95	0.51
Q60710_SA	Samhd1	Deoxynucle	R.ISTAIDDM*EAFTK#.L	102.82	58.64	1.75	0.57
Q60710_SA	Samhd1	Deoxynucle	R.ISTAIDDMEAFTK#.L	50.10	26.24	1.91	0.52
Q60710_SA	Samhd1	Deoxynucle	R.LPQEVAK#.A	165.75	93.74	1.77	0.57
Q60710_SA	Samhd1	Deoxynucle	R.NGIDVDKWDYFAR.D	4.04	9.28	0.43	2.30
Q60710_SA	Samhd1	Deoxynucle	K.NYGLVPEEDITFIK#.E	92.00	41.31	2.23	0.45
Q60710_SA	Samhd1	Deoxynucle	K.QLGGGYYVFPGASHNR.F	11.30	34.42	0.33	3.05
Q60710_SA	Samhd1	Deoxynucle	K.WK#HEQGSIEMFEHLVNSNELK#.L	14.58	8.34	1.75	0.57
Q60710_SA	Samhd1	Deoxynucle	K.YLGETQPK#.R	136.15	60.23	2.26	0.44
Q60710_SA	Samhd1	Deoxynucle	K.ADPYVEITGTAGK#.K	53.84	20.51	2.62	0.38
Q60710_SA	Samhd1	Deoxynucle	R.DFTK#PQDGDIIAPLITPLK#.W	36.47	20.33	1.79	0.56
Q60710_SA	Samhd1	Deoxynucle	K.EQVSQLLPEK#.F	13.11	8.64	1.52	0.66
Q60710_SA	Samhd1	Deoxynucle	K.FAEQLIR.V	11.59	19.68	0.59	1.70
Q60710_SA	Samhd1	Deoxynucle	K.IAGSFLPFLDEDRLEDLGVSSLEER.K	9.21	36.10	0.26	3.92
Q60710_SA	Samhd1	Deoxynucle	R.IIDTPQFQR.L	11.66	27.68	0.42	2.37
Q60710_SA	Samhd1	Deoxynucle	R.INK#EQVSQLLPEK#.F	32.12	9.62	3.34	0.30
Q60710_SA	Samhd1	Deoxynucle	R.ISTAIDDM*EAFTK#.L	42.12	22.69	1.86	0.54
Q60710_SA	Samhd1	Deoxynucle	R.ISTAIDDMEAFTK#.L	12.80	9.16	1.40	0.72
Q60710_SA	Samhd1	Deoxynucle	K.NYGLVPEEDITFIK#.E	59.11	23.68	2.50	0.40
Q60710_SA	Samhd1	Deoxynucle	K.YLGETQPK#.R	37.78	15.69	2.41	0.42
Q8BIH0_SP	Sap130	Histone dea	R.INELIQGNM*QR.C	2.42	6.64	0.36	2.74
Q8BIH0_SP	Sap130	Histone dea	R.LTNLQEGIIPK#.K	15.41	14.23	1.08	0.92
O55128_SA	Sap18	Histone dea	K.ELTSLVK.E	87.55	77.42	1.13	0.88
O55128_SA	Sap18	Histone dea	K.FQIGDYLDIAITPPNR.A	33.51	167.35	0.20	4.99
O55128_SA	Sap18	Histone dea	K.FQIGDYLDIAITPPNR.A	15.94	82.15	0.19	5.15
O55128_SA	Sap18	Histone dea	R.GNVPSSELQIYTWM*DATLK#.E	52.91	50.27	1.05	0.95
O55128_SA	Sap18	Histone dea	R.GNVPSSELQIYTWM*DATLK.E	28.06	29.75	0.94	1.06
O55128_SA	Sap18	Histone dea	R.GNVPSSELQIYTWMDATLK#.E	38.11	32.43	1.17	0.85
O55128_SA	Sap18	Histone dea	R.GNVPSSELQIYTWMDATLK.E	43.78	42.67	1.03	0.97
O55128_SA	Sap18	Histone dea	K.GTDDSMTLQSQK#.F	27.54	10.84	2.54	0.39
O55128_SA	Sap18	Histone dea	K.GTHFNFAIVFM*DLK.R	9.14	15.59	0.59	1.71
O55128_SA	Sap18	Histone dea	R.KGTDDSM*TLQSQK.F	26.95	29.11	0.93	1.08
O55128_SA	Sap18	Histone dea	R.K#GTDDSMTLQSQK#.F	14.81	14.39	1.03	0.97
O55128_SA	Sap18	Histone dea	R.VFTTNNGR.H	4.45	16.16	0.28	3.63
Q99JZ4_QS	Sar1a	GTP-bindin	R.EIFGLYGQTTGK#.G	27.07	23.47	1.15	0.87
Q99JZ4_QS	Sar1a	GTP-bindin	K.LVFLGLDNAGK#.T	93.99	88.08	1.07	0.94
Q99JZ4_QS	Sar1a	GTP-bindin	K.VELNALM*TDETISNVPILILGNK#.I	29.50	17.25	1.71	0.58
Q99JZ4_QS	Sar1a	GTP-bindin	K.LVFLGLDNAGK.T	6.71	8.20	0.82	1.22
Q99JZ4_QS	Sar1a	GTP-bindin	K.LVFLGLDNAGK.T	13.33	14.93	0.89	1.12
Q9D1J3_SA	Sarnp	SAP domai	R.FGIVTSSAGTGTTEDTEAK#.K	6.89	3.38	2.04	0.49
Q9Z315_SN	Sart1	U4/U6.U5 t	R.ADDLLPLGDQTQDGDFGSR.L	6.60	17.67	0.37	2.68
Q9Z315_SN	Sart1	U4/U6.U5 t	K.ASSGDASSLSIEETNK#.L	26.83	24.70	1.09	0.92
Q9Z315_SN	Sart1	U4/U6.U5 t	K.DKGVLQDGEDVLVNVNMVDKER.A	3.83	5.64	0.68	1.47
Q9Z315_SN	Sart1	U4/U6.U5 t	K.EAAGTTAAAGTGGTTEQPPR.H	11.90	48.32	0.25	4.06
Q9Z315_SN	Sart1	U4/U6.U5 t	K.EAGTKEEPVAADVINPM*ALR.Q	4.24	19.78	0.21	4.66
Q9Z315_SN	Sart1	U4/U6.U5 t	K.GLLETTVQK#.V	52.89	38.48	1.37	0.73
Q9Z315_SN	Sart1	U4/U6.U5 t	K.IEYVDETGR.K	31.10	30.08	1.03	0.97
Q9Z315_SN	Sart1	U4/U6.U5 t	K.IKTLGEDDPWLDDTAAWIER.S	5.55	2.91	1.91	0.52
Q9Z315_SN	Sart1	U4/U6.U5 t	K.KKPDYLPYAEDESVDDLAQQKPR.S	2.86	5.20	0.55	1.82
Q9Z315_SN	Sart1	U4/U6.U5 t	K.K#LDEEALLK#K#.M	41.74	51.69	0.81	1.24
Q9Z315_SN	Sart1	U4/U6.U5 t	R.LASEYLSPEEM*VTFK.K	6.41	8.39	0.76	1.31
Q9Z315_SN	Sart1	U4/U6.U5 t	R.LEQGGM*ADGLR.E	9.31	38.81	0.24	4.17
Q9Z315_SN	Sart1	U4/U6.U5 t	K.LGLK#PLEVNAVK#.K	23.73	26.72	0.89	1.13
Q9Z315_SN	Sart1	U4/U6.U5 t	K.LLEEMDQEFGVSTLVEEEFEQR.R	3.59	3.32	1.08	0.93
Q9Z315_SN	Sart1	U4/U6.U5 t	R.LQAQSLSSVGPR.L	15.59	71.31	0.22	4.57
Q9Z315_SN	Sart1	U4/U6.U5 t	K.M*SSSDTPLGTVALLQEK#.Q	14.85	14.03	1.06	0.94

Q9Z315_SN	Sart1	U4/U6.U5 t	K.MSSSDTPLGTVALLQEK.Q	7.79	8.39	0.93	1.08
Q9Z315_SN	Sart1	U4/U6.U5 t	K.QHQDFSASSTTILDEEPIVNR.G	4.80	13.44	0.36	2.80
Q9Z315_SN	Sart1	U4/U6.U5 t	R.QLQQLQQLR.D	11.95	39.08	0.31	3.27
Q9Z315_SN	Sart1	U4/U6.U5 t	K.RDDGYEAAASSK.A	1.63	4.07	0.40	2.49
Q9Z315_SN	Sart1	U4/U6.U5 t	R.RQDLYSAR.D	1.67	27.13	0.06	16.25
Q9Z315_SN	Sart1	U4/U6.U5 t	K.TPYIVLSGSGK#.S	48.74	52.07	0.94	1.07
Q9JLI8_SAF	Sart3	Squamous (	R.ALEYLQQEVEER.F	14.03	12.85	1.09	0.92
Q9JLI8_SAF	Sart3	Squamous (	K.DSVTVFVSNLPYSIEEPEVK#.L	9.34	3.13	2.98	0.34
Q9JLI8_SAF	Sart3	Squamous (	K.DSVTVFVSNLPYSIEEPEVK#.L	3.47	3.16	1.10	0.91
Q9JLI8_SAF	Sart3	Squamous (	R.K#VLSGAVAAEAAEAK#.G	14.66	2.88	5.09	0.20
Q9JLI8_SAF	Sart3	Squamous (	R.LAEYQAYIDFEM*K#.I	7.95	1.58	5.02	0.20
Q9JLI8_SAF	Sart3	Squamous (	R.LAEYQAYIDFEMK#.I	3.91	1.77	2.20	0.45
Q9JLI8_SAF	Sart3	Squamous (	R.QGAAPQAENGPAPGPAVAPSVATEAPK#.M	6.39	3.63	1.76	0.57
Q9JLI8_SAF	Sart3	Squamous (	R.TEGTLEDWDLAIQK#.T	54.39	6.67	8.16	0.12
Q9JLI8_SAF	Sart3	Squamous (	K.VLSGAVAAEAAEAK#.G	55.93	8.45	6.62	0.15
Q9JLI8_SAF	Sart3	Squamous (	R.ALEYLQQEVEER.F	10.84	7.18	1.51	0.66
Q9JLI8_SAF	Sart3	Squamous (	K.ALGQLEK#.Y	39.50	7.95	4.97	0.20
Q9JLI8_SAF	Sart3	Squamous (	K.GLAYVEYENESQASQAVM*K#.M	12.12	2.51	4.83	0.21
Q9JLI8_SAF	Sart3	Squamous (	R.LAEYQAYIDFEM*K#.I	6.76	2.08	3.25	0.31
Q9JLI8_SAF	Sart3	Squamous (	R.TEGTLEDWDLAIQK#.T	42.33	4.08	10.37	0.10
Q9JLI8_SAF	Sart3	Squamous (	K.VLSGAVAAEAAEAK#.G	68.40	10.13	6.75	0.15
Q689Z5_SE	Sbno1	Protein stra	R.FQQAADLIDAEQR.M	1.86	6.24	0.30	3.36
Q689Z5_SE	Sbno1	Protein stra	K.GVLQSLIEK#.H	19.61	6.31	3.11	0.32
Q689Z5_SE	Sbno1	Protein stra	R.SELDVPVEILNITEK#.Q	13.77	15.27	0.90	1.11
Q689Z5_SE	Sbno1	Protein stra	K.SIDPDSIQSALLASGLGSK#.R	9.92	10.58	0.94	1.07
Q689Z5_SE	Sbno1	Protein stra	K.TGLAVLELQNK#.L	17.67	10.44	1.69	0.59
Q689Z5_SE	Sbno1	Protein stra	R.TLEALEEGGGELNDFVSTAK#.G	6.23	8.78	0.71	1.41
Q689Z5_SE	Sbno1	Protein stra	R.VVSNDDGSISYESR.S	2.57	9.05	0.28	3.53
Q689Z5_SE	Sbno1	Protein stra	R.VVYASATGASEPR.N	4.18	20.43	0.20	4.88
Q6DID3_SC	Scaf8	Protein SC/	R.FSNNIISTFQNLYR.C	1.35	2.92	0.46	2.16
Q6DID3_SC	Scaf8	Protein SC/	R.VLNLWQK#.N	12.01	7.04	1.71	0.59
Q6DID3_SC	Scaf8	Protein SC/	K.VPGLYVIDSIVR.Q	7.54	20.72	0.36	2.75
O35609_S(	Scamp3	Secretory c	K.AQQEFAAGVFSNPAVR.T	2.24	4.25	0.53	1.90
O35609_S(	Scamp3	Secretory c	R.NYGSYSTQASAAAATAELLK#.K	6.14	4.56	1.35	0.74
O35609_S(	Scamp3	Secretory c	R.TAAANAAAGAAENAFR.A	6.04	15.00	0.40	2.48
Q8BRF7_SC	Scfd1	Sec1 family	R.FGQDIISPLLSVK#.E	9.96	8.34	1.19	0.84
Q8BRF7_SC	Scfd1	Sec1 family	K.LTSAVSSLPELLEK#.K	9.34	11.92	0.78	1.28
Q8BRF7_SC	Scfd1	Sec1 family	K.SLLDVISDPDAGTPEDK.M	3.16	5.82	0.54	1.84
Q8BRF7_SC	Scfd1	Sec1 family	K.LTSAVSSLPELLEK.K	10.19	11.18	0.91	1.10
Q8BRF7_SC	Scfd1	Sec1 family	R.SKLEDIANAALAASAVTQVAK.V	8.39	10.30	0.81	1.23
Q8BRF7_SC	Scfd1	Sec1 family	R.VM*NTGSQFVM*EGVK#.N	7.14	4.98	1.43	0.70
Q8BTY8_SC	Scfd2	Sec1 family	R.VIATDLANYAPAK#.N	11.07	3.51	3.15	0.32
Q78YZ6_SC	Scoc	Short coile	R.LINQVLELQHTLEDLSAR.V	7.99	22.27	0.36	2.79
Q80U72_S(	Scrib	Protein scri	R.FQTEDDAQTGEK#.V	3.55	1.26	2.82	0.36
Q80U72_S(	Scrib	Protein scri	R.FQTEDDAQTGEK#.V	7.91	4.89	1.62	0.62
Q9JJS0_SCI	Scube2	Signal pept	K.EVTASCNLSCVVK#.R	16.44	15.04	1.09	0.92
Q64124_S(	Scx	Basic helix-	R.TNSVNTAFTALR.T	14.61	10.94	1.34	0.75
Q9EQC5_N'	Scyl1	N-terminal	R.AEAGGLK#EQELSWGLHQIVK#.A	7.62	6.31	1.21	0.83
Q9EQC5_N'	Scyl1	N-terminal	K.ATGSAVSIFVYDVK#PGAEEQTQVAK#.A	15.30	9.73	1.57	0.64
Q9EQC5_N'	Scyl1	N-terminal	R.DPVRDFPFELSPEPPEGGPPGPWILHR.G	2.70	2.31	1.17	0.86
Q9EQC5_N'	Scyl1	N-terminal	K.DVHAASSPGTGGAAASWAGWAVTGVSSLTSK#.L	3.99	4.72	0.85	1.18
Q9EQC5_N'	Scyl1	N-terminal	R.FVETNLFLEEIQIK#EPAEK#.Q	20.52	19.87	1.03	0.97
Q9EQC5_N'	Scyl1	N-terminal	K.GIPELEQYDPPELADSSSR.A	1.51	5.55	0.27	3.67
Q9EQC5_N'	Scyl1	N-terminal	K.IGSYLSASTR.H	3.56	15.14	0.23	4.26
Q9EQC5_N'	Scyl1	N-terminal	R.LLQQM*EQFIQYLDEPTVNTQIFPHVTHGFLDTNPAIR.E	1.60	2.76	0.58	1.72
Q9EQC5_N'	Scyl1	N-terminal	K.LNEANLNVELM*K#.H	16.20	14.33	1.13	0.88
Q9EQC5_N'	Scyl1	N-terminal	R.AEAGGLK#EQELSWGLHQIVK#.A	5.78	5.96	0.97	1.03
Q9EQC5_N'	Scyl1	N-terminal	K.ATGSAVSIFVYDVK#PGAEEQTQVAK#.A	10.50	9.57	1.10	0.91
Q9EQC5_N'	Scyl1	N-terminal	K.IGSYLSASTR.H	3.58	10.63	0.34	2.97
Q9EQC5_N'	Scyl1	N-terminal	K.LNEANLNVELM*K#.H	13.63	8.18	1.67	0.60
Q8CFE4_SC	Scyl2	SCY1-like pı	K.LILPELGPVFK#.Q	27.97	18.33	1.53	0.66
Q8CFE4_SC	Scyl2	SCY1-like pı	K.VTADVTSAVM*GNPVTR.E	1.23	5.01	0.25	4.07
Q8CFE4_SC	Scyl2	SCY1-like pı	K.YGLLQVSEGLSFLHSSVK#.M	17.01	7.83	2.17	0.46
Q8CFE4_SC	Scyl2	SCY1-like pı	K.LILPELGPVFK#.Q	34.89	15.46	2.26	0.44
Q8CFE4_SC	Scyl2	SCY1-like pı	K.VTADVTSAVM*GNPVTR.E	3.46	6.30	0.55	1.82
Q80UZ2_SI	Sdad1	Protein SD/	R.VLTQDDFQK#.I	11.45	8.67	1.32	0.76
Q9DCT5_SI	Sdf2	Stromal cel	R.AEVHHAEL.-	8.32	8.32	1.00	1.00
Q9DCT5_SI	Sdf2	Stromal cel	K.HSSTDVLLSVTGEQYGRPISGQK.E	2.06	4.82	0.43	2.35
Q9ESP1_SD	Sdf2l1	Stromal cel	K.AM*EGIFIK#PGADLSTGHDEL.-	43.59	15.16	2.88	0.35
Q9ESP1_SD	Sdf2l1	Stromal cel	K.AMEGIFIK#PGADLSTGHDEL.-	11.65	7.59	1.54	0.65
Q9ESP1_SD	Sdf2l1	Stromal cel	R.FQHVGTSVFLSVTGEQYGNPIR.G	6.10	9.73	0.63	1.59
Q9ESP1_SD	Sdf2l1	Stromal cel	K.YGSGSGQQSVTGVEESDDANSYWR.I	1.95	3.87	0.50	1.99
Q63918_SI	Sdpr	Serum depr	R.DNSQVNAVTVHTLLDK#.L	28.93	15.02	1.93	0.52
Q63918_SI	Sdpr	Serum depr	K.GIQNDLTK#.L	45.08	21.96	2.05	0.49
Q63918_SI	Sdpr	Serum depr	K.LVNMLDAVR.E	6.14	13.55	0.45	2.21
Q63918_SI	Sdpr	Serum depr	K.VLIFQEESEIPASVFVK#.E	36.18	18.49	1.96	0.51
Q63918_SI	Sdpr	Serum depr	K.YQASTSNTVSK#.L	52.76	22.75	2.32	0.43
Q63918_SI	Sdpr	Serum depr	K.EPVPSAAEGK#EELADENK#.S	47.88	26.83	1.79	0.56
Q63918_SI	Sdpr	Serum depr	K.GIQNDLTK#.L	65.59	30.01	2.19	0.46
Q63918_SI	Sdpr	Serum depr	K.QVQPAVLHVDQTA.-	67.57	67.57	1.00	1.00
Q63918_SI	Sdpr	Serum depr	R.RGNNSAVGSNADLTIEEDEEEEPVALQQAQQVR.Y	1.95	6.62	0.29	3.39
Q63918_SI	Sdpr	Serum depr	K.VLIFQEESEIPASVFVK#.E	47.17	29.07	1.62	0.62
Q63918_SI	Sdpr	Serum depr	K.VLIFQEESEIPASVFVK#EPVPSAAEGK#EELADENK#.S	7.31	3.07	2.38	0.42
Q63918_SI	Sdpr	Serum depr	K.YQASTSNTVSK#.L	63.95	35.27	1.81	0.55
Q9D1M0_S	Sec13	Protein SEC	K.GQGSVSASITEGQQNEQ.-	61.17	61.17	1.00	1.00
Q9D1M0_S	Sec13	Protein SEC	R.NGGQILIADLR.G	12.75	18.19	0.70	1.43
Q9D1M0_S	Sec13	Protein SEC	K.GQGSVSASITEGQQNEQ.-	7.56	7.56	1.00	1.00
Q9D1M0_S	Sec13	Protein SEC	K.GQGSVSASITEGQQNEQ.-	10.87	10.87	1.00	1.00
O08547_S(	Sec22b	Vesicle-traf	R.IMVANIEEVLQR.G	1.98	8.17	0.24	4.12
O08547_S(	Sec22b	Vesicle-traf	R.NLGSINTELQDVQR.I	1.79	4.24	0.42	2.37
Q01405_S(	Sec23a	Protein trai	R.AETEEGPDVLR.W	12.13	17.15	0.71	1.41
Q01405_S(	Sec23a	Protein trai	R.FLQPVQK#.I	36.37	12.77	2.85	0.35
Q01405_S(	Sec23a	Protein trai	R.FSWNVWPSSR.L	11.95	13.36	0.89	1.12
Q01405_S(	Sec23a	Protein trai	R.GPQVQQPPPSNR.F	9.83	15.37	0.64	1.56
Q01405_S(	Sec23a	Protein trai	K.IDMNLTDLLGELQR.D	3.51	8.53	0.41	2.43
Q01405_S(	Sec23a	Protein trai	K.MGFGGTLEIK#.T	15.49	3.78	4.10	0.24
Q01405_S(	Sec23a	Protein trai	R.M*VVPVAALFTPLK#.E	39.78	10.18	3.91	0.26
Q01405_S(	Sec23a	Protein trai	R.SPFLQVFNNSPDESSYYR.H	9.32	12.03	0.77	1.29
Q01405_S(	Sec23a	Protein trai	R.FLQPVQK#.I	32.92	7.01	4.69	0.21
Q01405_S(	Sec23a	Protein trai	R.GPQVQQPPPSNR.F	9.47	9.73	0.97	1.03
Q01405_S(	Sec23a	Protein trai	K.IDM*NLTDLLGELQR.D	5.30	6.02	0.88	1.14
Q01405_S(	Sec23a	Protein trai	R.M*VVPVAALFTPLK#.E	37.51	10.20	3.68	0.27
Q9D662_S(	Sec23b	Protein trai	R.AESEEGPDVLR.W	12.82	18.15	0.71	1.42

Q9D662_S	Sec23b	Protein tra	K.AGYQDM*PEYENFK#.H	11.48	5.44	2.11	0.47
Q9D662_S	Sec23b	Protein tra	R.DPWPVTQGK#.R	12.75	5.22	2.44	0.41
Q9D662_S	Sec23b	Protein tra	K.FGQYNKEDPTSFR.L	11.59	19.29	0.60	1.66
Q9D662_S	Sec23b	Protein tra	R.GAIQFVTQYQHSSTQK#.R	13.56	5.01	2.71	0.37
Q9D662_S	Sec23b	Protein tra	K.HLLQAPLDDAQEILQAR.F	19.31	26.52	0.73	1.37
Q9D662_S	Sec23b	Protein tra	R.M*AFGATLDVK#.T	26.65	9.18	2.90	0.34
Q9D662_S	Sec23b	Protein tra	R.MAFGATLDVK#.T	17.91	5.40	3.31	0.30
Q9D662_S	Sec23b	Protein tra	K.AGYQDM*PEYENFK#.H	8.41	3.37	2.49	0.40
Q9D662_S	Sec23b	Protein tra	K.HLLQAPLDDAQEILQAR.F	12.49	21.29	0.59	1.71
Q9D662_S	Sec23b	Protein tra	R.IM*LFTGGPPTQGPGM*VVGDELK#.T	9.95	11.38	0.87	1.14
Q9D662_S	Sec23b	Protein tra	R.M*AFGATLDVK#.T	18.84	7.34	2.57	0.39
G3X928_G	Sec23ip	SEC23-inte	R.AHTSTTQLQEELEK#.V	39.10	9.99	3.92	0.26
G3X928_G	Sec23ip	SEC23-inte	R.LEPM*IAPDLDLK#.A	21.57	6.15	3.51	0.28
G3X928_G	Sec23ip	SEC23-inte	K.SAWQTLNEFAR.A	8.98	8.06	1.11	0.90
G3X928_G	Sec23ip	SEC23-inte	R.TM*NISPEQPQH.-	18.90	18.90	1.00	1.00
G3X928_G	Sec23ip	SEC23-inte	R.TMNISPEQPQH.-	12.44	12.44	1.00	1.00
G3X928_G	Sec23ip	SEC23-inte	K.VANQIK#EEEEK#QVVEAEK#.I	28.71	7.35	3.91	0.26
G3X928_G	Sec23ip	SEC23-inte	R.AHTSTTQLQEELEK#.V	47.60	8.99	5.30	0.19
G3X928_G	Sec23ip	SEC23-inte	R.LEPM*IAPDLDLK#.A	24.33	6.34	3.84	0.26
G3X928_G	Sec23ip	SEC23-inte	R.TM*NISPEQPQH.-	17.55	17.55	1.00	1.00
Q3U2P1_S	Sec24a	Protein tra	K.TLETQSALGPALQAAFK#.L	5.30	4.33	1.23	0.82
Q3U2P1_S	Sec24a	Protein tra	K.ELVQDLLK#.T	16.78	9.37	1.79	0.56
Q3U2P1_S	Sec24a	Protein tra	R.TESALSYYEFLLHIQQQVNK#.-	5.18	17.69	0.29	3.42
Q3U2P1_S	Sec24a	Protein tra	K.TLETQSALGPALQAAFK#.L	9.59	5.78	1.66	0.60
Q80ZX0_Q	Sec24b	Protein Sec	R.DALVNAVVDPLSAYSSAVASVPR.S	9.05	11.23	0.81	1.24
Q80ZX0_Q	Sec24b	Protein Sec	R.ETHSALGPALQAAFK#.L	12.51	3.45	3.63	0.28
Q80ZX0_Q	Sec24b	Protein Sec	R.VNDVPEEFLYNPLTR.S	7.53	6.59	1.14	0.88
Q80ZX0_Q	Sec24b	Protein Sec	K.VVHHLGPATDFYK#.K	28.34	3.27	8.67	0.12
Q80ZX0_Q	Sec24b	Protein Sec	R.DALVNAVVDPLSAYSSAVASVPR.S	11.79	11.19	1.05	0.95
Q80ZX0_Q	Sec24b	Protein Sec	R.M*PPAPSHPVGPVPSAPPPPEQM*QTK#.G	6.61	3.69	1.79	0.56
Q80ZX0_Q	Sec24b	Protein Sec	R.NQM*GSLATANSHPTNNENVQPPK#.S	7.49	3.23	2.32	0.43
Q80ZX0_Q	Sec24b	Protein Sec	R.VNDVPEEFLYNPLTR.S	7.52	8.16	0.92	1.09
G3X972_G	Sec24c	Protein Sec	R.GQVPPLVTTNFLVK#.D	19.60	4.33	4.53	0.22
G3X972_G	Sec24c	Protein Sec	K.LFLFHTSLPIAEAPGK#.L	17.96	5.59	3.22	0.31
G3X972_G	Sec24c	Protein Sec	R.VGFVTYNK#.V	14.37	6.44	2.23	0.45
G3X972_G	Sec24c	Protein Sec	R.ETETVFAPVIQAGM*EALK#.A	5.55	2.84	1.95	0.51
G3X972_G	Sec24c	Protein Sec	R.GQVPPLVTTNFLVK#.D	43.10	10.41	4.14	0.24
G3X972_G	Sec24c	Protein Sec	K.LFLFHTSLPIAEAPGK#.L	51.44	14.65	3.51	0.28
G3X972_G	Sec24c	Protein Sec	K.TLFQPQTGTYQTLAK#.E	18.45	4.69	3.94	0.25
G3X972_G	Sec24c	Protein Sec	R.VGFVTYNK#.V	22.89	18.70	1.22	0.82
Q6NXL1_Q	Sec24d	Protein Sec	R.KLDPDSIPSPIQVIENDR.A	6.64	8.69	0.76	1.31
Q6NXL1_Q	Sec24d	Protein Sec	K.LFIFHSSLPTAEAPGK#.L	46.23	15.12	3.06	0.33
Q6NXL1_Q	Sec24d	Protein Sec	R.M*IM*NNIQQK#.K	8.03	2.91	2.76	0.36
Q6NXL1_Q	Sec24d	Protein Sec	R.VGFITYNK#.V	38.36	11.71	3.28	0.31
Q6NXL1_Q	Sec24d	Protein Sec	K.AVLNQPLK#.A	39.27	8.25	4.76	0.21
Q6NXL1_Q	Sec24d	Protein Sec	K.ILFQPQTAVYESLAK#.D	27.24	9.40	2.90	0.34
Q6NXL1_Q	Sec24d	Protein Sec	K.LFIFHSSLPTAEAPGK#.L	46.71	11.09	4.21	0.24
Q3UPL0_S	Sec31a	Protein tra	K.AQDGSSPLSLQDLIEK#.V	8.93	12.30	0.73	1.38
Q3UPL0_S	Sec31a	Protein tra	K.IIAGDK#EVVIAQK#.D	14.36	6.69	2.15	0.47
Q3UPL0_S	Sec31a	Protein tra	K.TTFEDLIQR.C	5.56	17.93	0.31	3.23
Q3UPL0_S	Sec31a	Protein tra	K.VVLSQASK#.L	26.21	12.50	2.10	0.48
Q3UPL0_S	Sec31a	Protein tra	K.AQDGSSPLSLQDLIEK#.V	79.87	40.36	1.98	0.51
Q3UPL0_S	Sec31a	Protein tra	K.AQGKPVSGQESSQSPYER.Q	25.38	50.03	0.51	1.97
Q3UPL0_S	Sec31a	Protein tra	R.ATVWDLR.K	12.88	27.13	0.47	2.11
Q3UPL0_S	Sec31a	Protein tra	K.AVQLTQALDTNTVGALLAEK#.M	24.87	8.71	2.86	0.35
Q3UPL0_S	Sec31a	Protein tra	K.GDVSGVLIAGGENGNIILYDPSK#.I	9.90	3.28	3.02	0.33
Q3UPL0_S	Sec31a	Protein tra	K.IALALNK#.V	65.75	21.58	3.05	0.33
Q3UPL0_S	Sec31a	Protein tra	K.IALALNK#VDGPDVALK#.D	41.01	17.72	2.31	0.43
Q3UPL0_S	Sec31a	Protein tra	K.IALALNKVDGPDVALKDSDQVAQSDGEESPAAEEQLLGER.I	2.21	2.87	0.77	1.30
Q3UPL0_S	Sec31a	Protein tra	K.IEASQTEFEK#.N	57.47	20.93	2.75	0.36
Q3UPL0_S	Sec31a	Protein tra	R.ISVYSIM*GGSIDGLR.Q	12.40	23.48	0.53	1.89
Q3UPL0_S	Sec31a	Protein tra	R.K#AVQLTQALDTNTVGALLAEK#.M	49.13	18.35	2.68	0.37
Q3UPL0_S	Sec31a	Protein tra	K.K#IEASQTEFEK#.N	47.97	22.38	2.14	0.47
Q3UPL0_S	Sec31a	Protein tra	R.K#NEPIIK#.V	11.72	6.51	1.80	0.56
Q3UPL0_S	Sec31a	Protein tra	K.K#PIPEEHLILK#.T	63.76	28.41	2.24	0.45
Q3UPL0_S	Sec31a	Protein tra	R.LITAVVM*K#.N	37.36	18.32	2.04	0.49
Q3UPL0_S	Sec31a	Protein tra	K.LSSSFGNLDPFGTGQPLPPLQIPQQSAQHSIVLPLK#.K	17.15	6.13	2.80	0.36
Q3UPL0_S	Sec31a	Protein tra	K.LVTFESVAVPLQQGAEQQR.R	25.15	56.17	0.45	2.23
Q3UPL0_S	Sec31a	Protein tra	R.M*ADAIILAIAGGQELLAQTQK#K#.Y	16.60	4.94	3.36	0.30
Q3UPL0_S	Sec31a	Protein tra	R.NPAVLSAASFDGR.I	13.11	26.92	0.49	2.05
Q3UPL0_S	Sec31a	Protein tra	K.NVWSFLK#.V	65.00	21.09	3.08	0.32
Q3UPL0_S	Sec31a	Protein tra	R.QVQHILASASPSGR.A	6.70	9.80	0.68	1.46
Q3UPL0_S	Sec31a	Protein tra	R.RPVGASFSFGGK.L	10.76	22.06	0.49	2.05
Q3UPL0_S	Sec31a	Protein tra	R.RQPVFISQVVTEKDFLNR.S	4.19	24.87	0.17	5.94
Q3UPL0_S	Sec31a	Protein tra	K.TTFEDLIQR.C	14.52	23.51	0.62	1.62
Q3UPL0_S	Sec31a	Protein tra	K.VNFEEDSR.G	17.65	28.64	0.62	1.62
Q3UPL0_S	Sec31a	Protein tra	K.VVLSQASK#.L	54.96	28.80	1.91	0.52
Q3UPL0_S	Sec31a	Protein tra	K.YLELLGYR.K	19.26	28.04	0.69	1.46
S4R2A9_S4	Sec31a	Protein tra	R.IAPTVTTWSNK#.T	8.63	3.35	2.57	0.39
Q3UPL0_S	Sec31a	Protein tra	K.AQDGSSPLSLQDLIEK#.V	60.13	27.70	2.17	0.46
Q3UPL0_S	Sec31a	Protein tra	K.AQGKPVSGQESSQSPYER.Q	13.93	29.35	0.47	2.11
Q3UPL0_S	Sec31a	Protein tra	K.AVQLTQALDTNTVGALLAEK#.M	36.59	14.57	2.51	0.40
Q3UPL0_S	Sec31a	Protein tra	K.IALALNK#.V	37.50	15.54	2.41	0.41
Q3UPL0_S	Sec31a	Protein tra	K.IEASQTEFEK#.N	28.28	20.10	1.41	0.71
Q3UPL0_S	Sec31a	Protein tra	R.ISVYSIM*GGSIDGLR.Q	5.53	12.15	0.45	2.20
Q3UPL0_S	Sec31a	Protein tra	R.K#AVQLTQALDTNTVGALLAEK#.M	33.17	10.08	3.29	0.30
Q3UPL0_S	Sec31a	Protein tra	K.K#PIPEEHLILK#.T	33.26	18.45	1.80	0.55
Q3UPL0_S	Sec31a	Protein tra	K.LVTFESVAVPLQQGAEQQR.R	20.60	25.19	0.82	1.22
Q3UPL0_S	Sec31a	Protein tra	R.M*ADAIILAIAGGQELLAQTQK#K#.Y	11.55	4.99	2.32	0.43
Q3UPL0_S	Sec31a	Protein tra	R.NPAVLSAASFDGR.I	13.65	22.37	0.61	1.64
Q3UPL0_S	Sec31a	Protein tra	R.QVQHILASASPSGR.A	3.61	7.30	0.49	2.02
Q3UPL0_S	Sec31a	Protein tra	R.RQPVFISQVVTEKDFLNR.S	1.26	10.60	0.12	8.38
Q3UPL0_S	Sec31a	Protein tra	K.VNFEEDSR.G	10.75	19.64	0.55	1.83
Q3UQA7_S	Selh	Selenoprot	K.FPEPQEVVEELK#K#.Y	9.99	21.22	0.47	2.12
Q3UQA7_S	Selh	Selenoprot	R.HAAALSQALQLEAPELPVQVNPSKPR.R	9.14	25.61	0.36	2.80
Q3UQA7_S	Selh	Selenoprot	R.VELWTGIK.K	15.23	34.13	0.45	2.24
Q9WTM3_	Sema6c	Semaphori	R.IIGLELDTEGHR.L	2.65	7.19	0.37	2.71
Q9EP97_SE	Senp3	Sentrin-spe	K.SGGGFGPDPGSGTTVPTR.R	1.91	13.01	0.15	6.81
Q8BUH8_S	Senp7	Sentrin-spe	R.SFAAGQEPDASAASGR.A	5.02	7.31	0.69	1.46
Q8BH69_S	Sephs1	Selenide, w	R.ESFNPETYELDK#.S	12.75	1.90	6.70	0.15
Q8BH69_S	Sephs1	Selenide, w	R.NEVSFVIHNLPVLAK#.M	15.02	4.29	3.50	0.29
Q8C1B7_SE	Sept11	Septin-11	K.AAAQLLQSQAQQSGAQQTK#.K	56.25	20.27	2.78	0.36
Q8C1B7_SE	Sept11	Septin-11	K.DTDPDSK#PFSLQETYEAK#.R	8.41	6.85	1.23	0.81

Q8C1B7_SE	Sept11	Septin-11	K.ELEEEVSNFQK#.K	25.33	9.02	2.81	0.36
Q8C1B7_SE	Sept11	Septin-11	K.K#AAAQLLQSQAQQSGAQQTK#.K	14.99	4.12	3.64	0.27
Q8C1B7_SE	Sept11	Septin-11	K.LTIVDTVGFGDQINK#.D	6.14	3.06	2.01	0.50
Q8C1B7_SE	Sept11	Septin-11	K.STLM*DTLFNTK#.F	15.13	10.86	1.39	0.72
Q8C1B7_SE	Sept11	Septin-11	K.STLMDTLFNTK#.F	19.28	7.50	2.57	0.39
Q9ERR7_SE	Sept15	15 kDa sele	K.LLDDNGNIAEELSILK#.W	30.03	17.62	1.70	0.59
Q9ERR7_SE	Sept15	15 kDa sele	K.WNTDSVEEFLSEK#.L	30.36	16.82	1.80	0.55
P42208_SE	Sept2	Septin-2 O	K.ADTLTLK#.E	54.65	15.72	3.48	0.29
P42208_SE	Sept2	Septin-2 O	K.ASIPFSVVGSNQLIEAK#.G	79.76	18.89	4.22	0.24
P42208_SE	Sept2	Septin-2 O	K.GFEFTLMVVGESGLGK#.S	6.47	1.86	3.48	0.29
P42208_SE	Sept2	Septin-2 O	R.K#VENEDMNK#DQILLEK#.E	46.93	10.80	4.34	0.23
P42208_SE	Sept2	Septin-2 O	K.QQPTQFINPETPGYVGFANLPNQVHR.K	9.11	10.47	0.87	1.15
P42208_SE	Sept2	Septin-2 O	K.TIISYIDEQFER.Y	17.46	18.87	0.93	1.08
P42208_SE	Sept2	Septin-2 O	K.VNIVPVIAK#.A	92.27	21.10	4.37	0.23
Q9Z2Q6_SE	Sept5	Septin-5 O	K.ESAPFAVIGSNTVVEAK#.G	7.84	4.79	1.64	0.61
Q9Z2Q6_SE	Sept5	Septin-5 O	K.HTVDIEEK#.G	44.50	13.12	3.39	0.29
Q9Z2Q6_SE	Sept5	Septin-5 O	K.LATPEDK#QDIDK#.Q	5.96	1.97	3.03	0.33
Q9Z2Q6_SE	Sept5	Septin-5 O	K.STLVHSLFLTDLYK#.D	12.95	2.68	4.82	0.21
O55131_SE	Sept7	Septin-7 O	K.FEDYLNAESR.V	12.03	10.71	1.12	0.89
O55131_SE	Sept7	Septin-7 O	K.IYEFPETDDEEENK#LVK#.K	6.75	11.54	0.58	1.71
O55131_SE	Sept7	Septin-7 O	K.LAAVTYNGVDNNK#.N	7.46	9.34	0.80	1.25
O55131_SE	Sept7	Septin-7 O	K.STLINSLFLTDLYSPEYPGPSHR.I	10.90	7.24	1.51	0.66
Q80UG5_S	Sept9	Septin-9 O	K.FINDQYEK#.Y	50.21	10.69	4.70	0.21
Q80UG5_S	Sept9	Septin-9 O	K.IPEGSAVPATDAAPK#.R	50.90	12.28	4.15	0.24
Q80UG5_S	Sept9	Septin-9 O	K.SITHDIEEK#.G	56.56	11.18	5.06	0.20
Q80UG5_S	Sept9	Septin-9 O	K.STLINTLFK#.S	50.52	10.38	4.87	0.21
Q80UG5_S	Sept9	Septin-9 O	K.VVNIVPVIAK#.A	66.38	10.16	6.53	0.15
Q80UG5_S	Sept9	Septin-9 O	K.YLQEEVNINR.K	6.68	6.58	1.02	0.99
Q80UG5_S	Sept9	Septin-9 O	K.FINDQYEK#.Y	55.49	15.94	3.48	0.29
Q80UG5_S	Sept9	Septin-9 O	K.IPEGSAVPATDAAPK#.R	70.49	17.21	4.10	0.24
Q80UG5_S	Sept9	Septin-9 O	K.SITHDIEEK#.G	73.10	14.51	5.04	0.20
Q80UG5_S	Sept9	Septin-9 O	K.STLINTLFK#.S	75.46	15.65	4.82	0.21
Q80UG5_S	Sept9	Septin-9 O	K.VVNIVPVIAK#.A	92.80	19.64	4.73	0.21
Q80UG5_S	Sept9	Septin-9 O	K.IPEGSAVPATDAAPK#.R	10.88	3.93	2.76	0.36
Q80UG5_S	Sept9	Septin-9 O	K.STLINTLFK#.S	22.28	2.36	9.45	0.11
Q80UG5_S	Sept9	Septin-9 O	K.VVNIVPVIAK#.A	15.52	3.95	3.93	0.25
Q9CY58_P	Serbp1	Plasminoge	K.EAGGGGVGGPGAK#.S	9.86	10.22	0.96	1.04
Q9CY58_P	Serbp1	Plasminoge	R.FDQLFDDESDPFEVLK#.A	11.37	8.22	1.38	0.72
Q9CY58_P	Serbp1	Plasminoge	K.SAAQAAAQTNSNAAGK#.Q	29.62	18.88	1.57	0.64
Q9CY58_P	Serbp1	Plasminoge	K.SSASAPDVDDPEAFPALA.-	20.89	20.89	1.00	1.00
P19324_SE	Serpinh1	Serpin H1	K.AVAISLPK#.G	348.01	246.06	1.41	0.71
P19324_SE	Serpinh1	Serpin H1	K.AVLSAEK#.L	327.04	249.08	1.31	0.76
P19324_SE	Serpinh1	Serpin H1	R.DNQSGSLLFIGR.L	117.96	429.04	0.27	3.64
P19324_SE	Serpinh1	Serpin H1	K.GVVEVTHDLQK#.H	411.70	263.57	1.56	0.64
P19324_SE	Serpinh1	Serpin H1	K.HLAGLGLTEAIDK#.N	155.12	112.58	1.38	0.73
P19324_SE	Serpinh1	Serpin H1	K.HLAGLGLTEAIDK#.N	127.31	90.92	1.40	0.71
P19324_SE	Serpinh1	Serpin H1	K.HLAGLGLTEAIDK#NK#.A	608.16	451.55	1.35	0.74
P19324_SE	Serpinh1	Serpin H1	K.K#AVAISLPK#.G	158.22	124.48	1.27	0.79
P19324_SE	Serpinh1	Serpin H1	K.K#PLEAAAPGTAEK#.L	23.20	87.20	0.27	3.76
P19324_SE	Serpinh1	Serpin H1	K.LQM*VEM*PLAHK#.L	36.64	25.03	1.46	0.68
P19324_SE	Serpinh1	Serpin H1	K.LQM*VEM*PLAHK#.L	156.47	113.20	1.38	0.72
P19324_SE	Serpinh1	Serpin H1	K.LQMVEM*PLAHK#.L	30.85	18.16	1.70	0.59
P19324_SE	Serpinh1	Serpin H1	K.LQM*VEMPLAHK#.L	82.05	56.67	1.45	0.69
P19324_SE	Serpinh1	Serpin H1	K.LQM*VEMPLAHK.L	16.76	15.55	1.08	0.93
P19324_SE	Serpinh1	Serpin H1	K.LQMVEMPLAHK.L	171.12	110.50	1.55	0.65
P19324_SE	Serpinh1	Serpin H1	K.LQMVEMPLAHK#.L	44.96	53.81	0.84	1.20
P19324_SE	Serpinh1	Serpin H1	K.LRDEEVHTGLGELLR.S	23.98	351.29	0.07	14.65
P19324_SE	Serpinh1	Serpin H1	K.LSSLIILMPHHVEPLER.L	22.58	85.59	0.26	3.79
P19324_SE	Serpinh1	Serpin H1	K.LSSLIILMPHHVEPLER.L	35.93	128.50	0.28	3.58
P19324_SE	Serpinh1	Serpin H1	R.LYGPSSVSFADDFVR.S	133.62	480.85	0.28	3.60
P19324_SE	Serpinh1	Serpin H1	R.SALQSINEWASQTTDGK#.L	53.22	36.31	1.47	0.68
P19324_SE	Serpinh1	Serpin H1	R.SALQSINEWASQTTDGK#LPEVTK#.D	508.95	317.41	1.60	0.62
P19324_SE	Serpinh1	Serpin H1	R.STGLAFSLYQAM*AK#.D	148.07	118.79	1.25	0.80
P19324_SE	Serpinh1	Serpin H1	R.STGLAFSLYQAMAK#.D	170.33	118.33	1.44	0.69
P19324_SE	Serpinh1	Serpin H1	R.SYTVGVTM*M*HR.T	28.61	70.03	0.41	2.45
P19324_SE	Serpinh1	Serpin H1	R.SYTVGVTM*MHR.T	7.52	23.71	0.32	3.15
P19324_SE	Serpinh1	Serpin H1	R.SYTVGVTMMHR.T	8.19	26.31	0.31	3.21
P19324_SE	Serpinh1	Serpin H1	R.TDGALLVNAMFFK#PHWDEK#.F	82.69	58.64	1.41	0.71
P19324_SE	Serpinh1	Serpin H1	R.TDGALLVNAMFFKPHWDEK.F	65.40	57.94	1.13	0.89
P19324_SE	Serpinh1	Serpin H1	R.TGLYNYYDDEK#.E	71.08	60.94	1.17	0.86
P19324_SE	Serpinh1	Serpin H1	R.TGLYNYYDDEK#EK#.L	499.99	341.82	1.46	0.68
P19324_SE	Serpinh1	Serpin H1	R.TGLYNYYDDEKEK.L	162.66	116.09	1.40	0.71
P19324_SE	Serpinh1	Serpin H1	K.AVAISLPK#.G	249.25	191.88	1.30	0.77
P19324_SE	Serpinh1	Serpin H1	R.DNQSGSLLFIGR.L	161.98	503.00	0.32	3.11
P19324_SE	Serpinh1	Serpin H1	K.GVVEVTHDLQK#.H	423.84	280.53	1.51	0.66
P19324_SE	Serpinh1	Serpin H1	K.HLAGLGLTEAIDK#.N	64.56	48.97	1.32	0.76
P19324_SE	Serpinh1	Serpin H1	K.HLAGLGLTEAIDK#NK#.A	415.45	239.08	1.74	0.58
P19324_SE	Serpinh1	Serpin H1	K.K#AVAISLPK#.G	62.16	35.49	1.75	0.57
P19324_SE	Serpinh1	Serpin H1	K.LQM*VEMPLAHK#.L	24.07	20.08	1.20	0.83
P19324_SE	Serpinh1	Serpin H1	K.LQMVEMPLAHK#.L	21.33	15.76	1.35	0.74
P19324_SE	Serpinh1	Serpin H1	K.LRDEEVHTGLGELLR.S	4.53	98.46	0.05	21.73
P19324_SE	Serpinh1	Serpin H1	K.LSSLIILM*PHHVEPLER.L	15.67	60.98	0.26	3.89
P19324_SE	Serpinh1	Serpin H1	K.LSSLIILMPHHVEPLER.L	23.70	74.09	0.32	3.13
P19324_SE	Serpinh1	Serpin H1	R.LYGPSSVSFADDFVR.S	17.93	86.87	0.21	4.84
P19324_SE	Serpinh1	Serpin H1	R.SALQSINEWASQTTDGKLPEVTK.D	45.10	38.63	1.17	0.86
P19324_SE	Serpinh1	Serpin H1	R.STGLAFSLYQAM*AK#.D	20.44	18.88	1.08	0.92
P19324_SE	Serpinh1	Serpin H1	R.SYTVGVTM*MHR.T	34.21	8.18	4.18	0.24
P19324_SE	Serpinh1	Serpin H1	R.SYTVGVTMMHR.T	7.51	25.51	0.29	3.40
P19324_SE	Serpinh1	Serpin H1	R.SYTVGVTM*M*HR.T	14.21	48.93	0.29	3.44
P19324_SE	Serpinh1	Serpin H1	R.TGLYNYYDDEK#.E	49.21	34.44	1.43	0.70
P19324_SE	Serpinh1	Serpin H1	R.TGLYNYYDDEKEK.L	33.95	15.59	2.18	0.46
P19324_SE	Serpinh1	Serpin H1	R.TGLYNYYDDEKEKLQM*VEM*PLAHK.L	26.97	20.58	1.31	0.76
P19324_SE	Serpinh1	Serpin H1	R.TGLYNYYDDEK#EK#LQMVEMPLAHK#.L	10.26	7.15	1.43	0.70
P19324_SE	Serpinh1	Serpin H1	K.AVAISLPK#.G	40.84	28.44	1.44	0.70
P19324_SE	Serpinh1	Serpin H1	R.DNQSGSLLFIGR.L	16.57	60.50	0.27	3.65
P19324_SE	Serpinh1	Serpin H1	K.GVVEVTHDLQK#.H	91.05	76.94	1.18	0.84
P19324_SE	Serpinh1	Serpin H1	K.HLAGLGLTEAIDK#.N	15.44	46.47	0.33	3.01
P19324_SE	Serpinh1	Serpin H1	K.HLAGLGLTEAIDK#NK#.A	102.62	84.95	1.21	0.83
P19324_SE	Serpinh1	Serpin H1	K.KAVAISLPK.G	23.01	21.05	1.09	0.91
P19324_SE	Serpinh1	Serpin H1	R.LYGPSSVSFADDFVR.S	28.33	85.05	0.33	3.00
P19324_SE	Serpinh1	Serpin H1	R.STGLAFSLYQAM*AK#.D	18.21	11.59	1.57	0.64
P19324_SE	Serpinh1	Serpin H1	R.TDGALLVNAMFFK#PHWDEK#.F	12.89	9.44	1.37	0.73
P19324_SE	Serpinh1	Serpin H1	K.AVAISLPK#.G	23.74	20.92	1.13	0.88

P19324_SE	Serpinh1	Serpin H1 C	R.DNQSGSLLFIGR.L	8.83	27.20	0.32	3.08
P19324_SE	Serpinh1	Serpin H1 C	K.DQAVENILLSPLVVASSLGLVSLGGK#.A	47.45	63.75	0.74	1.34
P19324_SE	Serpinh1	Serpin H1 C	K.HLAGLGLTEAIDKNK.A	53.40	29.92	1.78	0.56
P19324_SE	Serpinh1	Serpin H1 C	R.LYGPSSVSFADDFVR.S	12.06	38.02	0.32	3.15
P19324_SE	Serpinh1	Serpin H1 C	R.STGLAFSLYQAM*AK#.D	9.97	8.19	1.22	0.82
Q9EQU5_SI	Set	Protein SET	R.IDFYFDENPYFENK#.V	5.05	2.05	2.47	0.41
E9PYH6_E9	Setd1a	Protein Set	K.FQGSGAAAETTEAR.R	4.18	10.96	0.38	2.62
E9PYH6_E9	Setd1a	Protein Set	R.EAYHLPLPM*AAEPLPSSSVSGEEAR.L	2.65	6.37	0.42	2.40
E9PYH6_E9	Setd1a	Protein Set	K.FQGSGAAAETTEAR.R	7.11	18.81	0.38	2.64
E9PYH6_E9	Setd1a	Protein Set	K.LIVDPALDPALR.R	6.54	20.07	0.33	3.07
E9PYH6_E9	Setd1a	Protein Set	R.LLSAIGTSAIM*DSDLLK#.L	9.67	8.69	1.11	0.90
E9PYH6_E9	Setd1a	Protein Set	R.VLATLVQEM*K#.S	32.11	21.45	1.50	0.67
E9PYH6_E9	Setd1a	Protein Set	R.YVQEGIGSSYLFR.V	3.79	8.01	0.47	2.11
E9Q5F9_SE	Setd2	Histone-lys	R.HAYEEEYESK.G	3.73	5.04	0.74	1.35
E9Q5F9_SE	Setd2	Histone-lys	K.LFEQEVAQR.E	2.75	16.10	0.17	5.85
E9Q5F9_SE	Setd2	Histone-lys	K.LPTSEPEADTETEPK.D	7.43	10.45	0.71	1.41
E9Q5F9_SE	Setd2	Histone-lys	K.LVPSGSELTFDYQFQR.Y	1.62	7.42	0.22	4.57
E9Q5F9_SE	Setd2	Histone-lys	K.TSRPQELPVYSDDFEDLPNK.S	6.53	17.41	0.38	2.67
E9Q5F9_SE	Setd2	Histone-lys	K.VESEATIEVSK.L	6.15	13.66	0.45	2.22
Q91WC0_S	Setd3	Histone-lys	K.EILNLTSELLQK#.C	9.23	4.29	2.15	0.47
Q91WC0_S	Setd3	Histone-lys	R.IFTLGNAEFPVSWDNEVK#.L	4.34	3.94	1.10	0.91
Q64213_SF	Sf1	Splicing fac	R.HTLITEMVALNPDFKPPADYKPPATR.V	4.20	10.72	0.39	2.55
Q64213_SF	Sf1	Splicing fac	K.TVIPGMPTVIPPGLTR.E	2.55	5.12	0.50	2.01
Q64213_SF	Sf1	Splicing fac	R.WNQDTMEQK#.T	11.46	5.89	1.95	0.51
Q64213_SF	Sf1	Splicing fac	R.AYIVQLQIEDLTR.K	3.60	13.75	0.26	3.82
Q64213_SF	Sf1	Splicing fac	K.FQRPGDPQSAQDK.A	10.57	17.87	0.59	1.69
Q64213_SF	Sf1	Splicing fac	R.HTLITEM*VALNPDFKPPADYKPPATR.V	7.27	4.69	1.55	0.65
Q64213_SF	Sf1	Splicing fac	R.HTLITEMVALNPDFKPPADYKPPATR.V	8.64	26.52	0.33	3.07
Q64213_SF	Sf1	Splicing fac	K.TVIPGMPTVIPPGLTR.E	3.88	10.79	0.36	2.78
Q8K4Z5_SF	Sf3a1	Splicing fac	K.VQAQVIQETIVPK#.E	22.82	4.78	4.78	0.21
Q8K4Z5_SF	Sf3a1	Splicing fac	K.AQEPSAAIPK#.V	70.81	28.44	2.49	0.40
Q8K4Z5_SF	Sf3a1	Splicing fac	K.ASK#PLPPAPAPDEYLVSPITGEK#.I	64.18	38.16	1.68	0.59
Q8K4Z5_SF	Sf3a1	Splicing fac	R.EK#QSDDEVYAPGLDIESSLK#.Q	30.27	12.29	2.46	0.41
Q8K4Z5_SF	Sf3a1	Splicing fac	K.FNFLNPNDPYHAYYR.H	12.60	23.42	0.54	1.86
Q8K4Z5_SF	Sf3a1	Splicing fac	K.IGEEEIQKPEEK.V	26.70	12.01	2.22	0.45
Q8K4Z5_SF	Sf3a1	Splicing fac	R.IGLLDPR.W	13.19	26.57	0.50	2.01
Q8K4Z5_SF	Sf3a1	Splicing fac	K.IHEATGM*PAGK#.Q	11.65	9.09	1.28	0.78
Q8K4Z5_SF	Sf3a1	Splicing fac	R.IRQNEINNPK.F	6.10	12.16	0.50	1.99
Q8K4Z5_SF	Sf3a1	Splicing fac	K.K#IGEEEIQK#PEEK#.V	40.03	16.18	2.47	0.40
Q8K4Z5_SF	Sf3a1	Splicing fac	K.LQYEGIFIK#.D	44.57	22.60	1.97	0.51
Q8K4Z5_SF	Sf3a1	Splicing fac	K.LTAQFVAR.N	29.11	58.18	0.50	2.00
Q8K4Z5_SF	Sf3a1	Splicing fac	R.QFLTQLM*QK#.E	25.34	9.70	2.61	0.38
Q8K4Z5_SF	Sf3a1	Splicing fac	R.QFLTQLMQK#.E	24.98	11.63	2.15	0.47
Q8K4Z5_SF	Sf3a1	Splicing fac	K.QSDDEVYAPGLDIESSLK#.Q	16.22	5.59	2.90	0.34
Q8K4Z5_SF	Sf3a1	Splicing fac	R.RTDIFGVEETAIGK.K	5.65	4.34	1.30	0.77
Q8K4Z5_SF	Sf3a1	Splicing fac	R.RTDIFGVEETAIGKK.I	14.71	29.36	0.50	2.00
Q8K4Z5_SF	Sf3a1	Splicing fac	R.TDIFGVEETAIGK#.K	16.60	5.30	3.13	0.32
Q8K4Z5_SF	Sf3a1	Splicing fac	R.TDIFGVEETAIGK#K#.I	22.83	12.07	1.89	0.53
Q8K4Z5_SF	Sf3a1	Splicing fac	R.TQQAAQANITLQEQIEAIHK#.A	93.44	32.56	2.87	0.35
Q8K4Z5_SF	Sf3a1	Splicing fac	K.VM*QQQQQATQQQLPQK#.V	74.66	24.63	3.03	0.33
Q8K4Z5_SF	Sf3a1	Splicing fac	K.VMQQQQQATQQQLPQK#.V	25.12	7.77	3.23	0.31
Q8K4Z5_SF	Sf3a1	Splicing fac	K.VQAQVIQETIVPK#.E	140.13	59.92	2.34	0.43
Q8K4Z5_SF	Sf3a1	Splicing fac	K.ASK#PLPPAPAPDEYLVSPITGEK#.I	10.94	4.70	2.33	0.43
Q8K4Z5_SF	Sf3a1	Splicing fac	K.VM*QQQQQATQQQLPQK#.V	7.30	8.43	0.87	1.15
Q8K4Z5_SF	Sf3a1	Splicing fac	K.VQAQVIQETIVPK#.E	16.25	6.88	2.36	0.42
G3UVU2_G	Sf3a2	Splicing fac	K.EAPAQPAPEK#.V	57.97	36.41	1.59	0.63
G3UVU2_G	Sf3a2	Splicing fac	R.FM*SAYEQR.I	11.11	22.24	0.50	2.00
G3UVU2_G	Sf3a2	Splicing fac	K.MEK#PPAPPSLPAGPPGVK#.R	35.94	16.83	2.13	0.47
G3UVU2_G	Sf3a2	Splicing fac	R.QLALETIDINK#DPYFMK#.N	19.11	9.00	2.12	0.47
G3UVU2_G	Sf3a2	Splicing fac	K.TGSGGVASSSESNR.D	2.57	7.51	0.34	2.92
G3UVU2_G	Sf3a2	Splicing fac	R.WQYLLM*AAEPYETIAFK#.V	15.13	9.27	1.63	0.61
G3UVU2_G	Sf3a2	Splicing fac	R.WQYLLMAAEPYETIAFK#.V	19.91	10.93	1.82	0.55
G3UVU2_G	Sf3a2	Splicing fac	K.EAPAQPAPEK#.V	17.37	11.03	1.57	0.64
G3UVU2_G	Sf3a2	Splicing fac	R.WQYLLM*AAEPYETIAFK#.V	4.82	3.33	1.45	0.69
Q9D554_SI	Sf3a3	Splicing fac	K.EELNAISGPNEFAEFYNR.L	5.65	8.54	0.66	1.51
Q9D554_SI	Sf3a3	Splicing fac	R.ENPSEEAQNLVEFTDEEGYGR.Y	5.10	6.48	0.79	1.27
Q9D554_SI	Sf3a3	Splicing fac	K.ETSSALTHAGAHLDLSAFSSWEELASLGLDR.L	1.91	2.66	0.72	1.39
Q9D554_SI	Sf3a3	Splicing fac	K.IQTDFEK#.K	95.21	30.68	3.10	0.32
Q9D554_SI	Sf3a3	Splicing fac	R.KEELNAISGPNEFAEFYNR.L	13.51	17.99	0.75	1.33
Q9D554_SI	Sf3a3	Splicing fac	K.NLPLGWDGK#PIPYWLYK#.L	6.00	2.55	2.35	0.43
Q9D554_SI	Sf3a3	Splicing fac	K.SALLALGLK#.C	73.06	25.61	2.85	0.35
Q9D554_SI	Sf3a3	Splicing fac	K.SLESLDTSLFAK#.N	179.00	55.72	3.21	0.31
Q9D554_SI	Sf3a3	Splicing fac	R.VK#PLQDQNELFGK#.I	143.38	54.26	2.64	0.38
Q9D554_SI	Sf3a3	Splicing fac	R.WQPDTEEEYEDSSGNVVNK#.K	10.92	2.80	3.90	0.26
Q9D554_SI	Sf3a3	Splicing fac	R.YMEVSGNLR.D	10.26	17.11	0.60	1.67
Q9D554_SI	Sf3a3	Splicing fac	K.SALLALGLK#.C	12.83	4.79	2.68	0.37
Q9D554_SI	Sf3a3	Splicing fac	R.VK#PLQDQNELFGK#.I	19.56	5.01	3.90	0.26
Q99NB9_SI	Sf3b1	Splicing fac	K.AAGLATM*ISTM*RPDIDNM*DEYVR.N	2.87	12.90	0.22	4.49
Q99NB9_SI	Sf3b1	Splicing fac	K.AIGPHDVLATLLNNLK#.V	83.42	54.30	1.54	0.65
Q99NB9_SI	Sf3b1	Splicing fac	R.AK#GSETPGATPGSK#.I	4.27	3.42	1.25	0.80
Q99NB9_SI	Sf3b1	Splicing fac	R.ATVNTFGYIAK#.A	60.21	41.60	1.45	0.69
Q99NB9_SI	Sf3b1	Splicing fac	R.EFQSPDEEM*K#K#.I	9.52	6.14	1.55	0.65
Q99NB9_SI	Sf3b1	Splicing fac	R.EVM*LILIR.E	1.63	13.81	0.12	8.49
Q99NB9_SI	Sf3b1	Splicing fac	R.FAGYVTSIAATELEDDDDDYSSSTSLLGQK#.K	24.69	10.83	2.28	0.44
Q99NB9_SI	Sf3b1	Splicing fac	R.GDTPGHATPGHGGATSSAR.K	8.71	19.22	0.45	2.21
Q99NB9_SI	Sf3b1	Splicing fac	R.GGDSIGETPTPGASK#.R	38.53	29.77	1.29	0.77
Q99NB9_SI	Sf3b1	Splicing fac	R.GK#GLAAFLK#.A	12.82	6.69	1.92	0.52
Q99NB9_SI	Sf3b1	Splicing fac	K.GLAAFLK#.A	19.08	9.80	1.95	0.51
Q99NB9_SI	Sf3b1	Splicing fac	K.GSETPGATPGSK#.I	8.43	5.41	1.56	0.64
Q99NB9_SI	Sf3b1	Splicing fac	K.IYNSIYIGSQDALIAHYPR.I	6.13	19.91	0.31	3.25
Q99NB9_SI	Sf3b1	Splicing fac	K.KAALDEAQGVGLDSTGYYDQEIYGGSDSR.F	2.97	6.98	0.43	2.35
Q99NB9_SI	Sf3b1	Splicing fac	K.LLVDVDESTLSPEEQK#.E	10.48	8.42	1.24	0.80
Q99NB9_SI	Sf3b1	Splicing fac	R.NRPLSDEELDAM*FPEGYK.V	3.89	19.56	0.20	5.03
Q99NB9_SI	Sf3b1	Splicing fac	R.NRPLSDEELDAMFPEGYK.V	11.70	15.64	0.75	1.34
Q99NB9_SI	Sf3b1	Splicing fac	R.QLVDTTVELANK#.V	35.41	21.06	1.68	0.59
Q99NB9_SI	Sf3b1	Splicing fac	R.SLVEIIEHGLVDEQQK#.V	114.70	81.68	1.40	0.71
Q99NB9_SI	Sf3b1	Splicing fac	K.SRWDETPASQM*GGSTPVLTPGK.T	3.18	9.07	0.35	2.85
Q99NB9_SI	Sf3b1	Splicing fac	R.TDRGGDSIGETPTPGASK.R	3.35	9.84	0.34	2.94
Q99NB9_SI	Sf3b1	Splicing fac	K.TEILPPFFK#.H	65.29	49.77	1.31	0.76
Q99NB9_SI	Sf3b1	Splicing fac	K.THEDIEAQIR.E	10.45	30.72	0.34	2.94
Q99NB9_SI	Sf3b1	Splicing fac	K.VGAAEIISR.I	24.36	68.34	0.36	2.81
Q99NB9_SI	Sf3b1	Splicing fac	R.VPELNVQNGVLK#.S	17.88	14.98	1.19	0.84
Q99NB9_SI	Sf3b1	Splicing fac	R.WDQTADQTPGATPK#.K	24.64	17.59	1.40	0.71

Q99NB9_SI	Sf3b1	Splicing fac	K.AAGLATM*ISTM*RPDIDNM*DEYVR.N	4.73	28.61	0.17	6.04
Q99NB9_SI	Sf3b1	Splicing fac	K.AALDEAQGVGLDSTGYYDQEIYGGSDSR.F	4.42	12.02	0.37	2.72
Q99NB9_SI	Sf3b1	Splicing fac	K.AIGPHDVLATLLNNLK#.V	149.01	69.68	2.14	0.47
Q99NB9_SI	Sf3b1	Splicing fac	K.AIGYLIPLM*DAEYANYYTR.E	2.30	6.08	0.38	2.65
Q99NB9_SI	Sf3b1	Splicing fac	K.AIGYLIPLM*DAEYANYYTR.E	3.09	7.95	0.39	2.57
Q99NB9_SI	Sf3b1	Splicing fac	K.AIGYLIPLMDAEYANYYTR.E	3.30	6.19	0.53	1.88
Q99NB9_SI	Sf3b1	Splicing fac	R.AK#GSETPGATPGSK#.I	6.84	3.92	1.74	0.57
Q99NB9_SI	Sf3b1	Splicing fac	R.ATVNTFGYIAK#.A	111.43	55.71	2.00	0.50
Q99NB9_SI	Sf3b1	Splicing fac	R.DTPGHGSGWAETPR.T	17.47	57.15	0.31	3.27
Q99NB9_SI	Sf3b1	Splicing fac	R.EFQSPDEEM*K#K#.I	14.93	9.32	1.60	0.62
Q99NB9_SI	Sf3b1	Splicing fac	R.EVM*LILIR.E	9.08	21.35	0.43	2.35
Q99NB9_SI	Sf3b1	Splicing fac	R.FAGYVTSIAATELEDDDDDYSSSTSLLGQK#.K	59.58	25.64	2.32	0.43
Q99NB9_SI	Sf3b1	Splicing fac	R.GDTPGHATPGHGGATSSAR.K	15.40	43.79	0.35	2.84
Q99NB9_SI	Sf3b1	Splicing fac	R.GGDSIGETPTPGASK#.R	112.36	60.32	1.86	0.54
Q99NB9_SI	Sf3b1	Splicing fac	R.GK#GLAAFLK#.A	17.03	9.27	1.84	0.54
Q99NB9_SI	Sf3b1	Splicing fac	K.GLAAFLK#.A	38.08	17.74	2.15	0.47
Q99NB9_SI	Sf3b1	Splicing fac	K.KAALDEAQGVGLDSTGYYDQEIYGGSDSR.F	5.13	10.61	0.48	2.07
Q99NB9_SI	Sf3b1	Splicing fac	K.LLVDVDESTLSPEEQK#.E	34.73	25.37	1.37	0.73
Q99NB9_SI	Sf3b1	Splicing fac	K.M*VM*ETIEK#.I	59.03	33.03	1.79	0.56
Q99NB9_SI	Sf3b1	Splicing fac	R.NRPLSDEELDAM*FPEGYK.V	11.94	28.15	0.42	2.36
Q99NB9_SI	Sf3b1	Splicing fac	R.NRPLSDEELDAMFPEGYK.V	5.82	14.22	0.41	2.44
Q99NB9_SI	Sf3b1	Splicing fac	R.QLVDTTVELANK#.V	70.46	30.77	2.29	0.44
Q99NB9_SI	Sf3b1	Splicing fac	R.QQAADLISR.T	19.00	41.91	0.45	2.21
Q99NB9_SI	Sf3b1	Splicing fac	R.SLVEIIEHGLVDEQQK#.V	162.35	81.54	1.99	0.50
Q99NB9_SI	Sf3b1	Splicing fac	K.SRWDETPASQM*GGSTPVLTPGK.T	4.83	16.37	0.30	3.39
Q99NB9_SI	Sf3b1	Splicing fac	R.TDRGGDSIGETPTPGASK.R	8.59	18.12	0.47	2.11
Q99NB9_SI	Sf3b1	Splicing fac	K.TEILPPFFK#.H	232.14	119.44	1.94	0.51
Q99NB9_SI	Sf3b1	Splicing fac	K.THEDIEAQIR.E	11.55	40.43	0.29	3.50
Q99NB9_SI	Sf3b1	Splicing fac	K.VGAAEIISR.I	40.64	93.29	0.44	2.30
Q99NB9_SI	Sf3b1	Splicing fac	R.VPELNVQNGVLK#.S	53.88	22.98	2.35	0.43
Q99NB9_SI	Sf3b1	Splicing fac	R.WDETPASQMGGSTPVLTPGK.T	4.08	4.91	0.83	1.20
Q99NB9_SI	Sf3b1	Splicing fac	R.WDQTADQTPGATPK#.K	50.18	33.35	1.50	0.66
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.EALQEK#EEQK#.T	9.37	10.06	0.93	1.07
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.GIEK#PPFELPDFIK#.R	31.62	38.41	0.82	1.21
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.IDIDYQK#.L	39.92	35.43	1.13	0.89
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.ISLGMPVGPNAHK#.V	15.05	11.98	1.26	0.80
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.YGPPPSYPNLK#.I	16.35	16.51	0.99	1.01
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.EALQEK#EEQK#.T	27.19	14.35	1.89	0.53
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.EQQAQVEK#EDFSDM*VAEHAAK#.Q	20.87	11.83	1.77	0.57
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.EQQAQVEKEDFSDMVAEHAAK.Q	17.41	7.78	2.24	0.45
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.FTVAELK#.Q	143.57	68.21	2.10	0.48
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.GIEK#PPFELPDFIK#.R	129.38	88.50	1.46	0.68
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.GPPPPPGDENR.E	5.19	11.19	0.46	2.15
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.IDIDYQK#.L	154.25	82.43	1.87	0.53
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.IFEAFK#.L	122.04	60.00	2.03	0.49
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.IPQALEK#.I	144.18	87.11	1.66	0.60
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.KGPAPELQGVEVALAPEELELDPM*AM*TQK.Y	17.64	9.76	1.81	0.55
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.KGPAPELQGVEVALAPEELELDPM*AMTQK.Y	10.39	6.28	1.65	0.60
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.K#GPAPELQGVEVALAPEELELDPMAMTQK#.Y	13.45	8.78	1.53	0.65
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.KPGDLSDELR.I	16.79	46.54	0.36	2.77
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.LAEIGAPIQGSR.E	33.25	95.02	0.35	2.86
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.LAQQQAALLM*QQEER.A	4.59	14.68	0.31	3.20
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.LAQQQAALLMQQEER.A	6.78	27.57	0.25	4.06
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.LHDAFFK#.W	82.30	62.13	1.32	0.75
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.LLVHLK#.A	44.88	21.67	2.07	0.48
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.LTIHGDLYYEGK#.E	61.16	37.88	1.61	0.62
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.MESSAVPK#.K	22.61	14.04	1.61	0.62
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.QAAVLMEQER.Q	10.76	25.91	0.42	2.41
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.SSLGQSASETEEDTVSISK#.K	31.42	17.85	1.76	0.57
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.TEEEEIDR.T	8.44	11.19	0.75	1.33
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.VAAPVGPVVPTPTVLPM*GAPVPRPR.G	1.48	3.99	0.37	2.70
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.VGEPVALSEEER.L	30.90	84.34	0.37	2.73
Q3UJB0_Q:	Sf3b2	Protein Sf3	K.VPPPWLIAMQR.Y	12.75	28.94	0.44	2.27
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.YGPPPSYPNLK#.I	66.64	47.09	1.42	0.71
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.EALQEK#EEQK#.T	3.48	1.55	2.24	0.45
Q3UJB0_Q:	Sf3b2	Protein Sf3	R.GIEK#PPFELPDFIK#.R	17.32	9.25	1.87	0.53
Q921M3_S	Sf3b3	Splicing fac	K.AEVIM*NYHVGETVLSLQK#.T	18.93	27.46	0.69	1.45
Q921M3_S	Sf3b3	Splicing fac	K.AEVIMNYHVGETVLSLQK.T	15.66	18.39	0.85	1.17
Q921M3_S	Sf3b3	Splicing fac	R.AVM*ISAIEK#.Q	16.16	20.06	0.81	1.24
Q921M3_S	Sf3b3	Splicing fac	R.AVMISAIEK#.Q	20.15	23.36	0.86	1.16
Q921M3_S	Sf3b3	Splicing fac	K.DYIVVGSDSGR.I	15.71	31.25	0.50	1.99
Q921M3_S	Sf3b3	Splicing fac	R.FLAVGLVDNTVR.I	20.32	134.53	0.15	6.62
Q921M3_S	Sf3b3	Splicing fac	R.FSNTGEDWYVLVGVAK.D	17.90	22.24	0.80	1.24
Q921M3_S	Sf3b3	Splicing fac	R.HGLEVSEM*AVSELPGNPNAVWTVR.R	4.54	12.81	0.35	2.82
Q921M3_S	Sf3b3	Splicing fac	R.HGLEVSEMAVSELPGNPNAVWTVR.R	2.72	16.87	0.16	6.21
Q921M3_S	Sf3b3	Splicing fac	K.HIANYISGIQTIGHR.V	7.64	49.87	0.15	6.53
Q921M3_S	Sf3b3	Splicing fac	K.ITLETDEDM*VTEIR.L	5.62	27.73	0.20	4.93
Q921M3_S	Sf3b3	Splicing fac	K.ITLETDEDMVTEIR.L	1.92	7.48	0.26	3.90
Q921M3_S	Sf3b3	Splicing fac	R.IVPGQFLAVDPK.G	40.16	153.44	0.26	3.82
Q921M3_S	Sf3b3	Splicing fac	R.KFVIHPESNNLIIIETDHNAYTEATK.A	25.02	29.24	0.86	1.17
Q921M3_S	Sf3b3	Splicing fac	K.LGAVFNQVAFPLQYTPR.K	29.85	28.89	1.03	0.97
Q921M3_S	Sf3b3	Splicing fac	R.LPPNTNDEVDEDPTGNK.A	11.68	17.53	0.67	1.50
Q921M3_S	Sf3b3	Splicing fac	K.LVYILNR.D	10.29	61.52	0.17	5.98
Q921M3_S	Sf3b3	Splicing fac	R.M*QGQEAVLAM*SSR.S	2.55	14.52	0.18	5.70
Q921M3_S	Sf3b3	Splicing fac	R.NENQLIIFADDTYPR.W	4.09	22.34	0.18	5.47
Q921M3_S	Sf3b3	Splicing fac	R.SVAGGFVYTYK#.L	54.81	52.81	1.04	0.96
Q921M3_S	Sf3b3	Splicing fac	R.SWLSYSYQSR.F	4.49	23.20	0.19	5.17
Q921M3_S	Sf3b3	Splicing fac	R.SYYFPVK.N	30.46	30.44	1.00	1.00
Q921M3_S	Sf3b3	Splicing fac	K.TPVEEVPAAIAPFQGR.V	6.80	38.01	0.18	5.59
Q921M3_S	Sf3b3	Splicing fac	R.TVLDPVTGDLSDTR.T	12.67	74.49	0.17	5.88
Q921M3_S	Sf3b3	Splicing fac	R.VIVSDVQESFIWVR.Y	4.29	26.20	0.16	6.11
Q921M3_S	Sf3b3	Splicing fac	R.WVTTASLLDYDTVAGADK.F	9.82	9.48	1.04	0.97
Q921M3_S	Sf3b3	Splicing fac	R.FLAVGLVDNTVR.I	12.34	52.99	0.23	4.29
Q921M3_S	Sf3b3	Splicing fac	R.HGLEVSEM*AVSELPGNPNAVWTVR.R	3.59	12.05	0.30	3.36
Q921M3_S	Sf3b3	Splicing fac	K.ITLETDEDM*VTEIR.L	5.54	21.44	0.26	3.87
Q921M3_S	Sf3b3	Splicing fac	R.IVILEYQPSK#.N	39.99	39.31	1.02	0.98
Q921M3_S	Sf3b3	Splicing fac	K.LGAVFNQVAFPLQYTPR.K	9.58	31.12	0.31	3.25
Q921M3_S	Sf3b3	Splicing fac	R.LPPNTNDEVDEDPTGNK#.A	10.79	13.10	0.82	1.21
Q921M3_S	Sf3b3	Splicing fac	K.LVYILNR.D	6.80	37.66	0.18	5.54
Q921M3_S	Sf3b3	Splicing fac	R.M*QGQEAVLAM*SSR.S	1.87	9.09	0.21	4.86
Q921M3_S	Sf3b3	Splicing fac	R.NENQLIIFADDTYPR.W	5.53	17.74	0.31	3.21
Q921M3_S	Sf3b3	Splicing fac	K.SM*FFFLAQTEQGDIFK#.I	11.02	10.62	1.04	0.96
Q921M3_S	Sf3b3	Splicing fac	R.SVAGGFVYTYK#.L	36.00	32.12	1.12	0.89

Q921M3_S	Sf3b3	Splicing fac	R.SYYFPVK#.N	17.29	17.44	0.99	1.01
Q921M3_S	Sf3b3	Splicing fac	R.TVLDPVTGDLSDTR.T	10.00	53.32	0.19	5.33
Q8QZY9_SF	Sf3b4	Splicing fac	K.NLDVGANIFIGNLDPEIDEK#.L	14.02	11.83	1.18	0.84
Q8QZY9_SF	Sf3b4	Splicing fac	R.NQDATVYVGGLDEK#.V	89.54	67.39	1.33	0.75
Q8QZY9_SF	Sf3b4	Splicing fac	R.VTGQHQGYGFVEFLSEEDADYAIK#.I	60.73	45.49	1.33	0.75
Q923D4_SI	Sf3b5	Splicing fac	K.MLQPSGPPADK#PEEN.-	11.78	16.18	0.73	1.37
Q923D4_SI	Sf3b5	Splicing fac	K.M*LQPSGPPADK#PEEN.-	29.86	42.65	0.70	1.43
Q923D4_SI	Sf3b5	Splicing fac	R.YTIHSQLEHLQSK#.Y	22.26	26.31	0.85	1.18
P59708_SF	Sf3b6	Splicing fac	R.GTAYVVYEDIFDAK#.N	137.06	82.55	1.66	0.60
P59708_SF	Sf3b6	Splicing fac	K.ITAEEM*YDIFGK#.Y	58.11	34.84	1.67	0.60
P59708_SF	Sf3b6	Splicing fac	K.ITAEEMYDIFGK#.Y	122.36	79.27	1.54	0.65
P59708_SF	Sf3b6	Splicing fac	K.YGINTDPPK#.-	130.51	88.81	1.47	0.68
P59708_SF	Sf3b6	Splicing fac	R.YLVVLYYNANR.A	10.50	21.20	0.50	2.02
Q8VIJ6_SFF	Sfpq	Splicing fac	K.AELDDTPM*R.G	29.87	74.61	0.40	2.50
Q8VIJ6_SFF	Sfpq	Splicing fac	K.AELDDTPMR.G	8.49	10.56	0.80	1.24
Q8VIJ6_SFF	Sfpq	Splicing fac	R.FAQHGTFEYEYSQR.W	25.63	59.63	0.43	2.33
Q8VIJ6_SFF	Sfpq	Splicing fac	R.FATHAAALSVR.N	28.30	55.92	0.51	1.98
Q8VIJ6_SFF	Sfpq	Splicing fac	R.FGQGGAGPVGGQGPR.G	43.48	91.38	0.48	2.10
Q8VIJ6_SFF	Sfpq	Splicing fac	R.GM*GPGTPAGYGR.G	6.27	24.87	0.25	3.97
Q8VIJ6_SFF	Sfpq	Splicing fac	K.ISDSEGFK#.A	87.68	42.51	2.06	0.48
Q8VIJ6_SFF	Sfpq	Splicing fac	R.LFVGNLPADITEDEFK#.R	20.71	13.17	1.57	0.64
Q8VIJ6_SFF	Sfpq	Splicing fac	R.MGGGGTM*NM*GDPYGSGGQK#.F	4.66	2.23	2.09	0.48
Q8VIJ6_SFF	Sfpq	Splicing fac	K.QQR@EQVEK#NMK#.D	10.62	1.87	5.69	0.18
Q8VIJ6_SFF	Sfpq	Splicing fac	K.YGEPGEVFINK#.G	163.80	84.78	1.93	0.52
Q3USH5_SI	Sfswap	Splicing fac	R.EK#NEAENLEENEEPFIAPLGLSVPSDVELPPTAK#.M	4.28	1.91	2.24	0.45
Q3USH5_SI	Sfswap	Splicing fac	K.SGPTSDNEEEDDEEDGSYLHPSLFASK#.K	4.38	2.01	2.18	0.46
Q8BJU0_SG	Sgta	Small gluta	R.AIGIDPGYSK#.A	31.75	11.60	2.74	0.37
Q8BJU0_SG	Sgta	Small gluta	K.HAEAVAYYK#.K	138.55	10.09	13.74	0.07
Q8BJU0_SG	Sgta	Small gluta	K.LENFEAAVHLYGK#.A	24.35	8.89	2.74	0.37
Q8BJU0_SG	Sgta	Small gluta	R.MGLALSSLNK#.H	16.48	6.82	2.42	0.41
Q8BJU0_SG	Sgta	Small gluta	K.ALELDPDNDTYK#.S	11.16	4.36	2.56	0.39
A2A5V4_A2	Sh3bp1	SH3 domai	K.FLALLAEEQDVNK#.M	23.21	9.13	2.54	0.39
A2A5V4_A2	Sh3bp1	SH3 domai	K.SLTSLDTALAELR.D	6.12	8.52	0.72	1.39
A2A5V4_A2	Sh3bp1	SH3 domai	R.DVLQPLSR.L	19.26	7.45	2.59	0.39
A2A5V4_A2	Sh3bp1	SH3 domai	R.LSEEELPAILK#.H	25.58	13.05	1.96	0.51
A2A5V4_A2	Sh3bp1	SH3 domai	R.TPETAEFLGEDLLQVEQR.L	16.56	28.66	0.58	1.73
A2A5V4_A2	Sh3bp1	SH3 domai	K.FLALLAEEQDVNK#.M	48.57	15.69	3.09	0.32
A2A5V4_A2	Sh3bp1	SH3 domai	R.LAAGASVLK#.R	45.78	17.80	2.57	0.39
A2A5V4_A2	Sh3bp1	SH3 domai	R.LSEEELPAILK#.H	65.35	18.05	3.62	0.28
A2A5V4_A2	Sh3bp1	SH3 domai	K.LVSDWNTLK#.S	64.23	17.85	3.60	0.28
A2A5V4_A2	Sh3bp1	SH3 domai	R.NPTETAASAEDMTR.K	7.59	11.27	0.67	1.48
A2A5V4_A2	Sh3bp1	SH3 domai	R.NPTETAASAEDM*TR.K	9.09	19.89	0.46	2.19
A2A5V4_A2	Sh3bp1	SH3 domai	R.RLPASPVISNM*PAQVDQGVATEDR.G	3.02	7.58	0.40	2.51
A2A5V4_A2	Sh3bp1	SH3 domai	R.RLPASPVISNMPAQVDQGVATEDR.G	2.74	4.46	0.62	1.62
A2A5V4_A2	Sh3bp1	SH3 domai	R.TPETAEFLGEDLLQVEQR.L	15.83	23.67	0.67	1.50
A2A5V4_A2	Sh3bp1	SH3 domai	K.VSSQQVSEELPPVTVPAPATTPAPTPAPASM*AVR.E	2.26	3.17	0.72	1.40
A2A5V4_A2	Sh3bp1	SH3 domai	K.FLALLAEEQDVNK#.M	11.51	5.79	1.99	0.50
Q62419_SH	Sh3gl1	Endophilin	K.ALYDFEPENDGELGFR.E	20.50	48.39	0.42	2.36
Q62419_SH	Sh3gl1	Endophilin	K.ASQLVSEK#.V	133.21	62.63	2.13	0.47
Q62419_SH	Sh3gl1	Endophilin	K.AVAEVLVR.T	21.90	814.61	0.03	37.20
Q62419_SH	Sh3gl1	Endophilin	K.DSLDIEVK#.Q	46.45	23.99	1.94	0.52
Q62419_SH	Sh3gl1	Endophilin	K.ELGGESNFGDALLDAGESM*K#.R	22.99	10.82	2.12	0.47
Q62419_SH	Sh3gl1	Endophilin	K.ELGGESNFGDALLDAGESMK#.R	24.08	8.85	2.72	0.37
Q62419_SH	Sh3gl1	Endophilin	K.ITASSSFR.S	40.31	73.25	0.55	1.82
Q62419_SH	Sh3gl1	Endophilin	R.LAEVK#DSLDIEVK#.Q	6.45	2.35	2.75	0.36
Q62419_SH	Sh3gl1	Endophilin	K.LTM*LNTVSK#.I	76.07	34.02	2.24	0.45
Q62419_SH	Sh3gl1	Endophilin	K.LTMLNTVSK#.I	100.68	41.42	2.43	0.41
Q62419_SH	Sh3gl1	Endophilin	R.QAVQILEELADK#.L	45.21	24.56	1.84	0.54
Q62419_SH	Sh3gl1	Endophilin	R.QAVQILEELADK#LK#.R	97.16	50.37	1.93	0.52
Q62419_SH	Sh3gl1	Endophilin	R.TIEYLQPNPASR.A	28.17	60.68	0.46	2.15
Q62419_SH	Sh3gl1	Endophilin	K.VGGAEGTK#LDDDFK#DMEK#.K	26.92	12.16	2.21	0.45
Q9JK48_SH	Sh3glb1	Endophilin	R.ELIQTSALNFLTPLR.N	8.19	19.50	0.42	2.38
Q9JK48_SH	Sh3glb1	Endophilin	K.GK#VPITYLELLN.-	24.32	14.73	1.65	0.61
Q9JK48_SH	Sh3glb1	Endophilin	K.LAADAGTFLSR.A	7.54	18.13	0.42	2.40
A2AAY5_SP	Sh3pxd2b	SH3 and PX	R.GAVVEVVQK#.N	24.65	4.30	5.73	0.17
P98083_SH	Shc1	SHC-transfc	R.ELFDDPSYVNIQNLDK#.A	24.85	14.50	1.71	0.58
P98083_SH	Shc1	SHC-transfc	R.ESTTTPGQYVLTGLQSGQPK#.H	10.24	4.38	2.34	0.43
P98083_SH	Shc1	SHC-transfc	R.VEGGQLGGEEWTR.H	7.32	11.30	0.65	1.54
P98083_SH	Shc1	SHC-transfc	K.VM*GPGVSYLVR.Y	2.49	5.99	0.41	2.41
P98083_SH	Shc1	SHC-transfc	K.VMGPGVSYLVR.Y	64.80	2.28	28.40	0.04
P50431_GI	Shmt1	Serine hydr	R.ALSDALTELGYK#.I	21.74	5.87	3.70	0.27
P50431_GI	Shmt1	Serine hydr	K.ISATSIFFESM*PYK#.V	63.73	16.22	3.93	0.25
P50431_GI	Shmt1	Serine hydr	K.ISATSIFFESMPYK#.V	102.55	23.73	4.32	0.23
P50431_GI	Shmt1	Serine hydr	K.ISATSIFFESM*PYK#.V	9.58	2.97	3.23	0.31
P50431_GI	Shmt1	Serine hydr	K.ISATSIFFESMPYK#.V	15.19	3.20	4.75	0.21
Q9CZN7_Q!	Shmt2	Protein Shr	R.AHLLADM*AHISGLVAAK#.V	36.39	12.34	2.95	0.34
Q9CZN7_Q!	Shmt2	Protein Shr	R.GFPM*PGFDER.-	12.59	14.92	0.84	1.19
Q9CZN7_Q!	Shmt2	Protein Shr	R.LGAPALTSR.Q	73.34	76.92	0.95	1.05
Q9CZN7_Q!	Shmt2	Protein Shr	R.LIIAGTSAYAR.L	63.42	68.70	0.92	1.08
Q9CZN7_Q!	Shmt2	Protein Shr	K.LNPQTGLIDYDQLALTAR.L	22.15	27.18	0.81	1.23
Q9CZN7_Q!	Shmt2	Protein Shr	R.NAQAM*ADALLK#.R	45.21	14.14	3.20	0.31
Q9CZN7_Q!	Shmt2	Protein Shr	R.NAQAMADALLK#.R	42.65	11.80	3.61	0.28
Q9CZN7_Q!	Shmt2	Protein Shr	R.QQVEQFAR.G	22.02	27.04	0.81	1.23
Q9CZN7_Q!	Shmt2	Protein Shr	R.SAITPGGLR.L	36.50	45.15	0.81	1.24
Q9CZN7_Q!	Shmt2	Protein Shr	R.SGLIFYR.K	23.51	34.01	0.69	1.45
Q9CZN7_Q!	Shmt2	Protein Shr	K.VAQTQAGEAAGGWTGQESLSDSDPEM*WELLQR.E	4.47	4.47	1.00	1.00
Q9CZN7_Q!	Shmt2	Protein Shr	K.VAQTQAGEAAGGWTGQESLSDSDPEMWELLQR.E	4.96	5.71	0.87	1.15
Q9CZN7_Q!	Shmt2	Protein Shr	R.VLELVSITANK#.N	179.77	48.20	3.73	0.27
Q9CZN7_Q!	Shmt2	Protein Shr	R.VVDFIDEGVNIGLEVK#.R	40.35	8.62	4.68	0.21
Q9CZN7_Q!	Shmt2	Protein Shr	K.YADVVTTTTHK#.T	118.72	27.17	4.37	0.23
Q9CZN7_Q!	Shmt2	Protein Shr	K.YSEGYPGK#.R	37.32	12.07	3.09	0.32
Q9CZN7_Q!	Shmt2	Protein Shr	R.VLELVSITANK#.N	20.19	6.56	3.08	0.32
Q9CZN7_Q!	Shmt2	Protein Shr	R.VVDFIDEGVNIGLEVK#.R	8.17	2.31	3.54	0.28
Q9CZN7_Q!	Shmt2	Protein Shr	R.VLELVSITANK#.N	30.79	6.94	4.44	0.23
O88520_SH	Shoc2	Leucine-ric	R.ELDLEENK#LESLPNEIAYLK#.D	13.82	11.00	1.26	0.80
O88520_SH	Shoc2	Leucine-ric	K.ESSAAQPGVAFSVDNTIK#.R	11.92	6.31	1.89	0.53
O88520_SH	Shoc2	Leucine-ric	K.LVLTNNQLSTLPR.G	2.18	6.34	0.34	2.92
O88520_SH	Shoc2	Leucine-ric	K.ESSAAQPGVAFSVDNTIK#.R	5.67	3.46	1.64	0.61
O88520_SH	Shoc2	Leucine-ric	K.LVLTNNQLSTLPR.G	4.06	7.64	0.53	1.88
Q60520_SI	Sin3a	Paired amp	K.LLFSNTAAQK#.L	16.98	9.12	1.86	0.54
Q60520_SI	Sin3a	Paired amp	K.EAGGNYTPALTEQEVYAQVAR.L	3.07	7.21	0.43	2.35
Q60520_SI	Sin3a	Paired amp	R.HSGTGATPPVK#.K	14.32	9.73	1.47	0.68
Q60520_SI	Sin3a	Paired amp	R.LK#VEDALSYLDQVK#.L	4.62	2.09	2.21	0.45

Q60520_SI	Sin3a	Paired amp	R.LKVEDALSYLDQVK.L	19.01	11.98	1.59	0.63
Q60520_SI	Sin3a	Paired amp	R.SLLESAYQR.K	8.98	15.41	0.58	1.72
Q60520_SI	Sin3a	Paired amp	K.SLLNEIESIYDER.Q	2.15	5.69	0.38	2.64
Q60520_SI	Sin3a	Paired amp	R.SPPVQPHTPVTISLGTAPSLQNNQPVEFNHAINYVNK#.I	5.57	4.08	1.37	0.73
Q60520_SI	Sin3a	Paired amp	R.YM*SSDTTSPELR.E	3.24	9.49	0.34	2.93
P46062_SI	Sipa1	Signal-indu	R.EGQPISESGDPK#.E	7.80	5.21	1.50	0.67
P59941_SI	Sirt6	NAD-depen	R.LVIVNLQPTK#.H	9.23	6.20	1.49	0.67
Q6NZR5_Q	Skiv2l	Protein Ski	R.FLLSDQSLLLLPEYHQR.V	5.95	5.54	1.07	0.93
Q6NZR5_Q	Skiv2l	Protein Ski	R.LIPQPAFQWAFEPDVFQK#.Q	6.02	2.75	2.19	0.46
Q6NZR5_Q	Skiv2l	Protein Ski	K.LQPGDVAAISTK#.V	24.16	10.43	2.32	0.43
Q6NZR5_Q	Skiv2l	Protein Ski	R.TLGYVDEAGTVK#.L	10.35	3.34	3.10	0.32
Q6NZR5_Q	Skiv2l	Protein Ski	K.TVVAEYAIALAQK#.H	11.67	4.32	2.70	0.37
Q6NZR5_Q	Skiv2l	Protein Ski	R.DK#GPATPDVPHPDDLIGFK#.L	16.89	5.88	2.87	0.35
Q6NZR5_Q	Skiv2l	Protein Ski	R.LAQSYPAGPPTLDPINDLQLK#.D	15.62	8.35	1.87	0.53
Q6NZR5_Q	Skiv2l	Protein Ski	R.LIPQPAFQWAFEPDVFQK#.Q	10.92	4.05	2.69	0.37
Q6NZR5_Q	Skiv2l	Protein Ski	R.LIPQPAFQWAFEPDVFQK#.Q	28.49	12.71	2.24	0.45
Q6NZR5_Q	Skiv2l	Protein Ski	R.TLGYVDEAGTVK#.L	25.85	11.85	2.18	0.46
Q6NZR5_Q	Skiv2l	Protein Ski	K.TVVAEYAIALAQK#.H	22.04	6.22	3.54	0.28
Q9CZU3_S	Skiv2l2	Superkiller	K.AIGNTELENK#.F	59.10	34.34	1.72	0.58
Q9CZU3_S	Skiv2l2	Superkiller	R.DLDVEGTDEPIFGK#.K	45.22	26.43	1.71	0.58
Q9CZU3_S	Skiv2l2	Superkiller	K.ETIEILFSEGLIK#.A	28.49	15.47	1.84	0.54
Q9CZU3_S	Skiv2l2	Superkiller	K.EYPFILDAFQR.E	13.24	32.38	0.41	2.44
Q9CZU3_S	Skiv2l2	Superkiller	R.GIVILMVDEK#.M	18.46	8.48	2.18	0.46
Q9CZU3_S	Skiv2l2	Superkiller	K.IVIPNEENVVIYYK#.I	63.29	37.06	1.71	0.59
Q9CZU3_S	Skiv2l2	Superkiller	R.K#AQIALDIK#.S	39.10	19.98	1.96	0.51
Q9CZU3_S	Skiv2l2	Superkiller	R.LGFATSSDVIEM*K#.G	27.38	9.61	2.85	0.35
Q9CZU3_S	Skiv2l2	Superkiller	R.LGFATSSDVIEMK#.G	15.52	7.81	1.99	0.50
Q9CZU3_S	Skiv2l2	Superkiller	K.LPQVEHVLPLLK#.R	15.75	11.60	1.36	0.74
Q9CZU3_S	Skiv2l2	Superkiller	K.M*TDVFEGSIIR.C	5.67	9.47	0.60	1.67
Q9CZU3_S	Skiv2l2	Superkiller	R.RLEELLR.Q	3.53	20.35	0.17	5.77
Q9CZU3_S	Skiv2l2	Superkiller	R.TVLQM*DELK#.C	19.67	10.36	1.90	0.53
Q9CZU3_S	Skiv2l2	Superkiller	R.VEEINPEYM*LEK#.S	15.82	12.34	1.28	0.78
Q9CZU3_S	Skiv2l2	Superkiller	R.VIFTSPIK#.A	48.38	22.89	2.11	0.47
Q9CZU3_S	Skiv2l2	Superkiller	K.VK#NEGDDFGWGVVVNFSK#.K	18.54	11.33	1.64	0.61
Q9CZU3_S	Skiv2l2	Superkiller	R.WISSGEYIQM*SGR.A	6.54	9.64	0.68	1.47
Q9CZU3_S	Skiv2l2	Superkiller	K.AIGNTELENK#.F	82.33	37.24	2.21	0.45
Q9CZU3_S	Skiv2l2	Superkiller	R.DLDVEGTDEPIFGK#.K	54.23	28.20	1.92	0.52
Q9CZU3_S	Skiv2l2	Superkiller	K.EYPFILDAFQR.E	11.74	28.04	0.42	2.39
Q9CZU3_S	Skiv2l2	Superkiller	K.FAEGITK#.I	61.93	35.67	1.74	0.58
Q9CZU3_S	Skiv2l2	Superkiller	R.GIVILMVDEK#.M	9.61	4.92	1.95	0.51
Q9CZU3_S	Skiv2l2	Superkiller	R.IEDSINEDLSLADLM*PR.V	2.33	7.66	0.30	3.29
Q9CZU3_S	Skiv2l2	Superkiller	K.IVIPNEENVVIYYK#.I	52.72	26.22	2.01	0.50
Q9CZU3_S	Skiv2l2	Superkiller	R.K#AQIALDIK#.S	18.83	8.36	2.25	0.44
Q9CZU3_S	Skiv2l2	Superkiller	R.LGFATSSDVIEM*K#.G	27.70	10.23	2.71	0.37
Q9CZU3_S	Skiv2l2	Superkiller	R.LGFATSSDVIEMK#.G	15.74	6.61	2.38	0.42
Q9CZU3_S	Skiv2l2	Superkiller	K.LPQVEHVLPLLK#.R	17.25	8.64	2.00	0.50
Q9CZU3_S	Skiv2l2	Superkiller	K.LTEQLAGPLR.Q	9.53	20.47	0.47	2.15
Q9CZU3_S	Skiv2l2	Superkiller	R.NFQPVIIFSFSK#.K	22.23	8.98	2.48	0.40
Q9CZU3_S	Skiv2l2	Superkiller	R.TVLQM*DELK#.C	22.25	11.98	1.86	0.54
Q9CZU3_S	Skiv2l2	Superkiller	R.VEEINPEYM*LEK#.S	17.35	7.97	2.18	0.46
Q9CZU3_S	Skiv2l2	Superkiller	R.VEEINPEYMLEK#.S	12.50	7.89	1.58	0.63
Q9WTX5_S	Skp1	S-phase kin	K.LQSSDGEIFEVDVEIAK#.Q	30.04	15.52	1.94	0.52
Q9WTX5_S	Skp1	S-phase kin	K.NDFTEEEEAQVR.K	23.31	66.99	0.35	2.87
Q9WTX5_S	Skp1	S-phase kin	K.RTDDIPVWDQEFLK.V	13.25	52.92	0.25	3.99
Q9WTX5_S	Skp1	S-phase kin	R.TDDIPVWDQEFLK#.V	77.42	61.55	1.26	0.80
Q9WTX5_S	Skp1	S-phase kin	K.TM*LEDLGM*DDEGDDDPVPLPNVNAAILK#.K	26.66	19.19	1.39	0.72
Q9WTX5_S	Skp1	S-phase kin	K.TM*LEDLGMDDEGDDDPVPLPNVNAAILK#K#.V	4.71	3.43	1.37	0.73
Q9WTX5_S	Skp1	S-phase kin	K.TMLEDLGM*DDEGDDDPVPLPNVNAAILK#K#.V	9.69	4.27	2.27	0.44
Q8CI08_SL	Slain2	SLAIN moti	R.VGVSTPSSGAASPR.G	15.52	21.37	0.73	1.38
Q8CI08_SL	Slain2	SLAIN moti	K.LNDVTDVQILAR.M	1.43	15.47	0.09	10.85
P53986_M	Slc16a1	Monocarb	K.AAQSPQQHSSGDPTEEESPV.-	21.64	21.64	1.00	1.00
P53986_M	Slc16a1	Monocarb	K.SDANTDLIGGSPK#.G	10.12	10.30	0.98	1.02
Q8VEM8_M	Slc25a3	Phosphate	K.FGFYEVFK#.A	7.09	7.82	0.91	1.10
Q8VEM8_M	Slc25a3	Phosphate	R.IQTQPGYANTLR.E	8.88	15.41	0.58	1.74
P48962_A	Slc25a4	ADP/ATP tr	R.YFPTQALNFAFK#.D	29.67	15.79	1.88	0.53
P48962_A	Slc25a4	ADP/ATP tr	K.DFLAGGIAAAVSK#.T	12.72	1.47	8.68	0.12
P48962_A	Slc25a4	ADP/ATP tr	R.YFPTQALNFAFK#.D	28.02	10.37	2.70	0.37
P51881_A	Slc25a5	ADP/ATP tr	K.DFLAGGVAAAISK#.T	20.82	8.63	2.41	0.41
P51881_A	Slc25a5	ADP/ATP tr	K.DFLAGGVAAAISK#.T	17.88	7.51	2.38	0.42
P17809_G	Slc2a1	Solute carri	K.VTILELFR.S	4.07	14.07	0.29	3.45
P10852_4	Slc3a2	4F2 cell-sur	R.DAGGIAGLK#.S	15.05	9.67	1.56	0.64
P10852_4	Slc3a2	4F2 cell-sur	K.FTGLSK#EELLK#.V	11.42	6.63	1.72	0.58
P10852_4	Slc3a2	4F2 cell-sur	K.GLVLGPIHK#.N	14.62	9.94	1.47	0.68
P10852_4	Slc3a2	4F2 cell-sur	R.LGASNLPAGISLPASAK#.L	28.17	22.40	1.26	0.80
P10852_4	Slc3a2	4F2 cell-sur	K.VAEDETEAGVK#.F	34.02	14.87	2.29	0.44
P10852_4	Slc3a2	4F2 cell-sur	K.GLVLGPIHK#.N	17.66	10.22	1.73	0.58
P10852_4	Slc3a2	4F2 cell-sur	R.LGASNLPAGISLPASAK#.L	25.36	21.51	1.18	0.85
P10852_4	Slc3a2	4F2 cell-sur	K.NQK#DEINETDLK#.Q	8.28	5.38	1.54	0.65
P10852_4	Slc3a2	4F2 cell-sur	K.QINPTLGSQEDFK#DLLQSAK#.K	21.86	24.17	0.90	1.11
E9Q585_E	Slc4a1ap	Protein Slc	K.TELQTTNAENK#.T	5.34	2.91	1.84	0.54
Q9Z127_L	Slc7a5	Large neutr	K.DM*GQGDASNLQQK.L	4.13	5.10	0.81	1.23
B1ARD6_B	Slfn9	Protein Slf	K.GVYTLNTEEWVR.M	3.18	10.09	0.31	3.18
B1ARD6_B	Slfn9	Protein Slf	K.SLESNPAFEIFQSK.K	413.24	33.87	12.20	0.08
B1ARD6_B	Slfn9	Protein Slf	R.SYPDLIIYAGEVTLGEK.V	4.72	6.67	0.71	1.41
B1ARD6_B	Slfn9	Protein Slf	R.DAFYFLK.K	9.51	11.97	0.79	1.26
B1ARD6_B	Slfn9	Protein Slf	R.FQHIIIDEAQNFR.T	1.56	15.20	0.10	9.75
B1ARD6_B	Slfn9	Protein Slf	R.NADKIAEFLQQELQK.I	9.97	17.83	0.56	1.79
B1ARD6_B	Slfn9	Protein Slf	K.SLESNPAFEIFQSK.K	16.35	22.53	0.73	1.38
O54988_SL	Slk	STE20-like	K.AGNILFTLDGDIK#.L	9.31	2.15	4.33	0.23
O54988_SL	Slk	STE20-like	K.LADFGVSAK#.N	8.37	5.32	1.57	0.64
O54988_SL	Slk	STE20-like	R.SSEVGTDEALDDTQK#.A	20.32	4.41	4.61	0.22
O54988_SL	Slk	STE20-like	K.AEVTEEVEDGK#EEDEEEEAENALPIPANK#.R	12.01	4.57	2.63	0.38
O54988_SL	Slk	STE20-like	K.AGNILFTLDGDIK#.L	58.61	14.53	4.03	0.25
O54988_SL	Slk	STE20-like	R.ALGSEGEAAATEVDLER.K	8.59	12.81	0.67	1.49
O54988_SL	Slk	STE20-like	K.DSGSVSLQETR.R	12.07	9.01	1.34	0.75
O54988_SL	Slk	STE20-like	K.EADFQAVDNEVGLTK#.E	8.83	4.02	2.20	0.45
O54988_SL	Slk	STE20-like	K.IVTDSDSKTEELR.F	4.09	8.96	0.46	2.19
O54988_SL	Slk	STE20-like	R.K#LQEQEVFFK#.M	16.27	23.55	0.69	1.45
O54988_SL	Slk	STE20-like	K.LADFGVSAK#.N	55.40	20.90	2.65	0.38
O54988_SL	Slk	STE20-like	K.LIQSEEINDTHIQTM*DLVSQETGEK#.E	6.52	2.65	2.46	0.41
O54988_SL	Slk	STE20-like	R.QYDQEIENLEK#.Q	23.36	5.65	4.14	0.24
O54988_SL	Slk	STE20-like	R.SSEVGTDEALDDTQK#.A	87.44	21.47	4.07	0.25
O54988_SL	Slk	STE20-like	R.TEQSTSEDK#FSNK#.I	16.04	3.83	4.19	0.24

Q8CH25_SI	Sltm	SAFB-like tr	K.DVQDAIAQSPEK#.E	8.52	4.99	1.71	0.59
Q8CH25_SI	Sltm	SAFB-like tr	R.IVQM*SGNSLPR.G	5.33	9.53	0.56	1.79
Q8CH25_SI	Sltm	SAFB-like tr	K.NIWVSGLSSNTK#.A	14.70	7.61	1.93	0.52
Q8CH25_SI	Sltm	SAFB-like tr	R.TELHGQLISVEK#.V	29.59	21.45	1.38	0.72
Q8BHJ9_SL	Slu7	Pre-mRNA-	K.YGGQEHLDAPPAELLLAQTEDYVEYSR.H	2.56	5.90	0.43	2.30
Q3TKT4_SN	Smarca4	Transcripti	K.EVDYSDSLTEK#.Q	15.15	8.20	1.85	0.54
Q3TKT4_SN	Smarca4	Transcripti	K.FNVLLTTYEYIIK#.D	12.27	7.22	1.70	0.59
Q3TKT4_SN	Smarca4	Transcripti	K.AENAEGQTPAIGPDGEPLDETSQM*SDLPVK.V	3.76	2.17	1.73	0.58
Q3TKT4_SN	Smarca4	Transcripti	R.AFLQAILEHEEQDEEEDEVPDDETVNQM*IAR.H	3.15	5.81	0.54	1.84
Q3TKT4_SN	Smarca4	Transcripti	R.AFLQAILEHEEQDEEEDEVPDDETVNQMIAR.H	2.29	2.61	0.88	1.14
Q3TKT4_SN	Smarca4	Transcripti	K.AIEEGTLEEIEEEVR.Q	18.45	45.45	0.41	2.46
Q3TKT4_SN	Smarca4	Transcripti	K.AVATYHANTER.E	4.38	13.84	0.32	3.16
Q3TKT4_SN	Smarca4	Transcripti	R.DSEAGSSTPTTSTR.S	10.72	28.70	0.37	2.68
Q3TKT4_SN	Smarca4	Transcripti	R.DTALETALNAK#.A	77.27	57.86	1.34	0.75
Q3TKT4_SN	Smarca4	Transcripti	K.ELPEYYELIR.K	17.64	52.96	0.33	3.00
Q3TKT4_SN	Smarca4	Transcripti	K.EVDYSDSLTEK#.Q	76.52	48.63	1.57	0.64
Q3TKT4_SN	Smarca4	Transcripti	R.GLDPVEILQER.E	21.07	73.29	0.29	3.48
Q3TKT4_SN	Smarca4	Transcripti	K.HQEYLNSILQHAK#.D	28.39	18.47	1.54	0.65
Q3TKT4_SN	Smarca4	Transcripti	R.IGQQNEVR.V	23.12	41.68	0.55	1.80
Q3TKT4_SN	Smarca4	Transcripti	R.ILLTGTPLQNK#.L	25.11	17.41	1.44	0.69
Q3TKT4_SN	Smarca4	Transcripti	K.IPDPDSDDVSEVDAR.H	5.40	15.75	0.34	2.92
Q3TKT4_SN	Smarca4	Transcripti	R.IQELENLPGSLAGDLR.T	10.40	38.58	0.27	3.71
Q3TKT4_SN	Smarca4	Transcripti	K.IVDAVIK#.Y	54.88	50.71	1.08	0.92
Q3TKT4_SN	Smarca4	Transcripti	K.KAENAEGQTPAIGPDGEPLDETSQM*SDLPVK.V	6.70	5.90	1.13	0.88
Q3TKT4_SN	Smarca4	Transcripti	K.K#AENAEGQTPAIGPDGEPLDETSQMSDLPVK#.V	2.90	2.70	1.07	0.93
Q3TKT4_SN	Smarca4	Transcripti	R.LM*EEDELPSWIIKDDAEVER.L	8.08	22.68	0.36	2.81
Q3TKT4_SN	Smarca4	Transcripti	K.QDVDDEYGVSQALAR.G	6.65	12.76	0.52	1.92
Q3TKT4_SN	Smarca4	Transcripti	R.QLSEVFIQLPSR.K	4.40	20.56	0.21	4.68
Q3TKT4_SN	Smarca4	Transcripti	R.RAFVPQLR.S	2.24	23.99	0.09	10.70
Q3TKT4_SN	Smarca4	Transcripti	K.TLM*NTIM*QLR.K	7.50	21.72	0.35	2.90
Q3TKT4_SN	Smarca4	Transcripti	R.VDLNEEETILIIR.R	9.39	29.91	0.31	3.18
Q3TKT4_SN	Smarca4	Transcripti	K.VIQAGM*FDQK#.S	51.87	38.45	1.35	0.74
Q3TKT4_SN	Smarca4	Transcripti	K.YK#LNVDQK#.V	15.32	14.40	1.06	0.94
Q91ZW3_S	Smarca5	SWI/SNF-re	R.ANRFEYLLK.Q	12.29	17.63	0.70	1.43
Q91ZW3_S	Smarca5	SWI/SNF-re	K.ANYAVDAYFR.E	3.32	20.81	0.16	6.26
Q91ZW3_S	Smarca5	SWI/SNF-re	R.DFNQFIK#.A	43.80	40.04	1.09	0.91
Q91ZW3_S	Smarca5	SWI/SNF-re	K.DIDILNSAGK.M	35.27	61.50	0.57	1.74
Q91ZW3_S	Smarca5	SWI/SNF-re	K.EIQEPDPTYEEK#.M	38.48	42.80	0.90	1.11
Q91ZW3_S	Smarca5	SWI/SNF-re	R.ENM*ELEEK#EK#.A	5.07	3.42	1.48	0.67
Q91ZW3_S	Smarca5	SWI/SNF-re	K.ESEITDEDIDGILER.G	17.25	70.35	0.25	4.08
Q91ZW3_S	Smarca5	SWI/SNF-re	R.FDWFIK#.S	34.95	30.49	1.15	0.87
Q91ZW3_S	Smarca5	SWI/SNF-re	R.FEDSPSYVK#.W	80.75	78.62	1.03	0.97
Q91ZW3_S	Smarca5	SWI/SNF-re	R.FEYLLK#.Q	12.72	10.76	1.18	0.85
Q91ZW3_S	Smarca5	SWI/SNF-re	R.FITDNTVEER.I	26.48	114.89	0.23	4.34
Q91ZW3_S	Smarca5	SWI/SNF-re	R.HGATHVFASK#.E	44.64	39.96	1.12	0.90
Q91ZW3_S	Smarca5	SWI/SNF-re	R.ILM*K#DIDILNSAGK#.M	15.55	9.46	1.64	0.61
Q91ZW3_S	Smarca5	SWI/SNF-re	R.KANYAVDAYFR.E	7.83	25.65	0.31	3.28
Q91ZW3_S	Smarca5	SWI/SNF-re	R.LDGQTPHDER.Q	2.16	8.66	0.25	4.00
Q91ZW3_S	Smarca5	SWI/SNF-re	R.LDSIVIQQGR.L	7.62	25.97	0.29	3.41
Q91ZW3_S	Smarca5	SWI/SNF-re	R.LFELLEK#.E	50.98	54.31	0.94	1.07
Q91ZW3_S	Smarca5	SWI/SNF-re	R.LLNILM*QLR.K	8.42	28.31	0.30	3.36
Q91ZW3_S	Smarca5	SWI/SNF-re	K.LLTQGFTNWNK#.R	20.12	20.33	0.99	1.01
Q91ZW3_S	Smarca5	SWI/SNF-re	K.LRLDSIVIQQGR.L	1.92	23.18	0.08	12.06
Q91ZW3_S	Smarca5	SWI/SNF-re	R.LVDQNLNK#.I	104.06	99.26	1.05	0.95
Q91ZW3_S	Smarca5	SWI/SNF-re	R.QDSINAYNEPNSTK#.F	17.59	17.77	0.99	1.01
Q91ZW3_S	Smarca5	SWI/SNF-re	K.QTELFAHFIQPAAQK#.T	21.81	18.41	1.18	0.84
Q91ZW3_S	Smarca5	SWI/SNF-re	R.SPDLPNAAQAQK.E	15.88	15.95	1.00	1.00
Q91ZW3_S	Smarca5	SWI/SNF-re	R.TEQEEDEELLTESSK#.A	34.33	35.96	0.95	1.05
Q91ZW3_S	Smarca5	SWI/SNF-re	K.TLQTISLLGYM*K#.H	25.21	23.04	1.09	0.91
Q91ZW3_S	Smarca5	SWI/SNF-re	K.TLQTISLLGYMK#.H	15.44	12.14	1.27	0.79
Q91ZW3_S	Smarca5	SWI/SNF-re	K.TPEEVIEYSAVFWER.C	2.59	15.24	0.17	5.88
Q91ZW3_S	Smarca5	SWI/SNF-re	K.TPTSPLK#.M	31.92	21.70	1.47	0.68
Q91ZW3_S	Smarca5	SWI/SNF-re	R.VLIFSQM*TR.L	13.87	43.21	0.32	3.12
Q91ZW3_S	Smarca5	SWI/SNF-re	R.VLIFSQMTR.L	8.14	20.29	0.40	2.49
Q91ZW3_S	Smarca5	SWI/SNF-re	K.WGRDDIENIAR.E	3.86	26.20	0.15	6.79
Q91ZW3_S	Smarca5	SWI/SNF-re	R.ANRFEYLLK.Q	14.90	46.04	0.32	3.09
Q91ZW3_S	Smarca5	SWI/SNF-re	K.ANYAVDAYFR.E	7.73	30.00	0.26	3.88
Q91ZW3_S	Smarca5	SWI/SNF-re	R.DFNQFIK#.A	94.00	72.72	1.29	0.77
Q91ZW3_S	Smarca5	SWI/SNF-re	K.DIDILNSAGK#.M	80.46	89.53	0.90	1.11
Q91ZW3_S	Smarca5	SWI/SNF-re	K.EIQEPDPTYEEK#.M	69.32	72.81	0.95	1.05
Q91ZW3_S	Smarca5	SWI/SNF-re	R.ENM*ELEEKEK.A	7.86	9.44	0.83	1.20
Q91ZW3_S	Smarca5	SWI/SNF-re	K.ESEITDEDIDGILER.G	26.65	109.87	0.24	4.12
Q91ZW3_S	Smarca5	SWI/SNF-re	R.FDWFIK#.S	82.74	64.42	1.28	0.78
Q91ZW3_S	Smarca5	SWI/SNF-re	R.FEDSPSYVK#.W	142.32	107.97	1.32	0.76
Q91ZW3_S	Smarca5	SWI/SNF-re	R.FEYLLK#.Q	30.80	25.87	1.19	0.84
Q91ZW3_S	Smarca5	SWI/SNF-re	R.FITDNTVEER.I	51.39	185.09	0.28	3.60
Q91ZW3_S	Smarca5	SWI/SNF-re	K.FVFM*LSTR.A	4.24	9.26	0.46	2.19
Q91ZW3_S	Smarca5	SWI/SNF-re	R.HGATHVFASK#.E	122.56	90.89	1.35	0.74
Q91ZW3_S	Smarca5	SWI/SNF-re	K.IDEAEPLNDEELEEK#.E	40.56	33.69	1.20	0.83
Q91ZW3_S	Smarca5	SWI/SNF-re	R.ILM*K#DIDILNSAGK#.M	23.29	15.58	1.49	0.67
Q91ZW3_S	Smarca5	SWI/SNF-re	K.IM*AQIER.G	17.44	59.35	0.29	3.40
Q91ZW3_S	Smarca5	SWI/SNF-re	K.IYVGLSK#.M	149.58	106.89	1.40	0.71
Q91ZW3_S	Smarca5	SWI/SNF-re	R.KANYAVDAYFR.E	16.48	69.53	0.24	4.22
Q91ZW3_S	Smarca5	SWI/SNF-re	R.LDSIVIQQGR.L	17.47	63.66	0.27	3.64
Q91ZW3_S	Smarca5	SWI/SNF-re	R.LFELLEK#.E	79.88	65.12	1.23	0.82
Q91ZW3_S	Smarca5	SWI/SNF-re	K.LGFDKENVYDELR.Q	14.19	48.68	0.29	3.43
Q91ZW3_S	Smarca5	SWI/SNF-re	R.LLNILM*QLR.K	12.37	55.07	0.22	4.45
Q91ZW3_S	Smarca5	SWI/SNF-re	K.LLTQGFTNWNK#.R	55.36	46.68	1.19	0.84
Q91ZW3_S	Smarca5	SWI/SNF-re	K.LRLDSIVIQQGR.L	2.91	48.87	0.06	16.78
Q91ZW3_S	Smarca5	SWI/SNF-re	K.LSEIVR.E	24.46	103.09	0.24	4.22
Q91ZW3_S	Smarca5	SWI/SNF-re	R.LVDQNLNK#.I	235.53	209.55	1.12	0.89
Q91ZW3_S	Smarca5	SWI/SNF-re	K.M*VVLDK#.L	34.56	30.52	1.13	0.88
Q91ZW3_S	Smarca5	SWI/SNF-re	R.NFTM*DTESSVYNFEGEDYREK.Q	12.56	43.62	0.29	3.47
Q91ZW3_S	Smarca5	SWI/SNF-re	R.QDSINAYNEPNSTK#.F	40.21	35.08	1.15	0.87
Q91ZW3_S	Smarca5	SWI/SNF-re	K.QNLLSVGDYR.H	18.12	64.32	0.28	3.55
Q91ZW3_S	Smarca5	SWI/SNF-re	R.RTEQEEDEELLTESSK.A	60.43	81.89	0.74	1.36
Q91ZW3_S	Smarca5	SWI/SNF-re	R.SPDLPNAAQAQK#.E	42.60	42.37	1.01	0.99
Q91ZW3_S	Smarca5	SWI/SNF-re	K.STLHNWM*SEFK#K#.W	28.24	18.66	1.51	0.66
Q91ZW3_S	Smarca5	SWI/SNF-re	R.TEQEEDEELLTESSK#.A	79.62	53.08	1.50	0.67
Q91ZW3_S	Smarca5	SWI/SNF-re	K.TLQTISLLGYM*K#.H	63.59	44.86	1.42	0.71
Q91ZW3_S	Smarca5	SWI/SNF-re	K.TLQTISLLGYMK#.H	30.29	33.01	0.92	1.09
Q91ZW3_S	Smarca5	SWI/SNF-re	R.VLIFSQM*TR.L	29.93	78.95	0.38	2.64
Q91ZW3_S	Smarca5	SWI/SNF-re	R.VLIFSQMTR.L	8.33	42.54	0.20	5.10

Q91ZW3_S	Smarca5	SWI/SNF-re	K.WGRDDIENIAR.E	2.28	15.54	0.15	6.83
Q91ZW3_S	Smarca5	SWI/SNF-re	R.YKAPFHQLR.I	10.55	56.28	0.19	5.34
Q04692_S	Smarcad1	SWI/SNF-re	K.LISQGTIEESM*LK#.I	9.19	7.20	1.28	0.78
Q04692_S	Smarcad1	SWI/SNF-re	K.LKLEQDM*TTVDEADEGSM*PADIATLLK.T	2.64	3.17	0.83	1.20
Q9Z0H3_S	Smarcb1	SWI/SNF-re	K.ASEVEEILDGNDEK#.Y	14.79	11.49	1.29	0.78
Q9Z0H3_S	Smarcb1	SWI/SNF-re	K.ASEVEEILDGNDEK#YK#.A	32.81	21.41	1.53	0.65
Q9Z0H3_S	Smarcb1	SWI/SNF-re	K.AVSISTEPPTYLR.E	18.10	75.23	0.24	4.16
Q9Z0H3_S	Smarcb1	SWI/SNF-re	K.DHGYTTLATSVTLLK#.A	5.63	2.47	2.28	0.44
Q9Z0H3_S	Smarcb1	SWI/SNF-re	K.FQLEDDGEFYM*IGSEVGNYLR.M	3.69	4.85	0.76	1.32
Q9Z0H3_S	Smarcb1	SWI/SNF-re	R.GQLSWHQK#.T	30.58	19.13	1.60	0.63
Q9Z0H3_S	Smarcb1	SWI/SNF-re	R.LDM*EIDGQK#.L	22.99	16.39	1.40	0.71
Q9Z0H3_S	Smarcb1	SWI/SNF-re	R.QQIESYPTDSILEDQSDQR.V	3.51	5.34	0.66	1.52
Q9Z0H3_S	Smarcb1	SWI/SNF-re	K.TFGQK#PVK#.F	22.38	23.04	0.97	1.03
P97496_S	Smarcc1	SWI/SNF c	K.AALEEFSR.V	15.05	55.45	0.27	3.68
P97496_S	Smarcc1	SWI/SNF c	R.FDLQNPSR.M	1.91	12.96	0.15	6.80
P97496_S	Smarcc1	SWI/SNF c	K.FWESPDTVSQLDSVR.V	8.52	22.53	0.38	2.64
P97496_S	Smarcc1	SWI/SNF c	K.HLAAVEER.K	29.36	113.69	0.26	3.87
P97496_S	Smarcc1	SWI/SNF c	R.HQGTFTDEK#.S	8.95	9.28	0.96	1.04
P97496_S	Smarcc1	SWI/SNF c	K.HVTNPAFTK#.L	53.59	46.14	1.16	0.86
P97496_S	Smarcc1	SWI/SNF c	K.KKVEHEISEGNVATAAAAALASAATK.A	12.47	13.58	0.92	1.09
P97496_S	Smarcc1	SWI/SNF c	K.K#VEHEISEGNVATAAAAALASAATK#.A	9.73	15.45	0.63	1.59
P97496_S	Smarcc1	SWI/SNF c	R.NFM*IDTYR.L	16.50	49.06	0.34	2.97
P97496_S	Smarcc1	SWI/SNF c	R.NFMIDTYR.L	6.64	17.62	0.38	2.65
P97496_S	Smarcc1	SWI/SNF c	R.NVEM*FMNIEK#.T	7.28	2.81	2.59	0.39
P97496_S	Smarcc1	SWI/SNF c	K.SKTPEIYLAYR.N	18.13	53.04	0.34	2.93
P97496_S	Smarcc1	SWI/SNF c	K.SLVALLVETQM*K#.K	45.42	38.90	1.17	0.86
P97496_S	Smarcc1	SWI/SNF c	K.SLVALLVETQMK#.K	45.72	40.61	1.13	0.89
P97496_S	Smarcc1	SWI/SNF c	R.SPQVPAAQQM*LNFPEK#.N	14.42	16.52	0.87	1.15
P97496_S	Smarcc1	SWI/SNF c	R.SPQVPAAQQM*LNFPEK.N	8.76	7.99	1.10	0.91
P97496_S	Smarcc1	SWI/SNF c	R.SPQVPAAQQMLNFPEK.N	7.63	8.61	0.89	1.13
P97496_S	Smarcc1	SWI/SNF c	K.TPEIYLAYR.N	12.63	35.76	0.35	2.83
P97496_S	Smarcc1	SWI/SNF c	R.VREEVPLELVEAHVK.K	12.17	41.04	0.30	3.37
P97496_S	Smarcc1	SWI/SNF c	K.FWESPDTVSQLDSVR.V	3.78	9.87	0.38	2.61
P97496_S	Smarcc1	SWI/SNF c	K.HLAAVEER.K	8.41	32.72	0.26	3.89
P97496_S	Smarcc1	SWI/SNF c	R.NFM*IDTYR.L	4.80	14.82	0.32	3.09
P97496_S	Smarcc1	SWI/SNF c	K.SLVALLVETQM*K#.K	20.10	16.24	1.24	0.81
Q6PDG5_S	Smarcc2	SWI/SNF c	R.DIGEGNLSTAAAAALAAAAVK#.A	93.42	53.99	1.73	0.58
Q6PDG5_S	Smarcc2	SWI/SNF c	R.DIGEGNLSTAAAAALAAAAVK.A	40.41	21.76	1.86	0.54
Q6PDG5_S	Smarcc2	SWI/SNF c	R.EGGGAVEEEAKEEISEVPK.K	26.45	18.58	1.42	0.70
Q6PDG5_S	Smarcc2	SWI/SNF c	K.HVSNAPLTK#.L	49.44	26.38	1.87	0.53
Q6PDG5_S	Smarcc2	SWI/SNF c	K.K#GPSTPYTK#.S	34.31	24.81	1.38	0.72
Q6PDG5_S	Smarcc2	SWI/SNF c	R.NVEM*FM*TIEK#.S	23.55	10.06	2.34	0.43
Q6PDG5_S	Smarcc2	SWI/SNF c	R.NVEMFM*TIEK#.S	9.75	5.46	1.79	0.56
Q6PDG5_S	Smarcc2	SWI/SNF c	K.SALEEFSK#.M	48.53	27.41	1.77	0.56
Q6PDG5_S	Smarcc2	SWI/SNF c	K.WILDTDTFNEWM*NEEDYEVSDDKSPVSR.R	1.56	3.43	0.46	2.19
Q6PDG5_S	Smarcc2	SWI/SNF c	K.YIQAEPPTNK#.S	42.87	24.51	1.75	0.57
Q6PDG5_S	Smarcc2	SWI/SNF c	K.YYEAADTVTQFDNVR.L	7.97	19.56	0.41	2.45
Q6PDG5_S	Smarcc2	SWI/SNF c	R.DIGEGNLSTAAAAALAAAAVK#.A	55.48	29.61	1.87	0.53
Q6PDG5_S	Smarcc2	SWI/SNF c	R.DIGEGNLSTAAAAALAAAAVK#.A	21.02	14.00	1.50	0.67
Q6PDG5_S	Smarcc2	SWI/SNF c	K.K#GPSTPYTK#.S	17.98	13.07	1.38	0.73
Q6PDG5_S	Smarcc2	SWI/SNF c	R.NVEM*FM*TIEK#.S	14.00	6.52	2.15	0.47
Q6PDG5_S	Smarcc2	SWI/SNF c	R.YDFQNPSR.M	4.29	9.90	0.43	2.31
Q6PDG5_S	Smarcc2	SWI/SNF c	K.YIQAEPPTNK#.S	27.76	19.00	1.46	0.68
Q6PDG5_S	Smarcc2	SWI/SNF c	K.YYEAADTVTQFDNVR.L	5.71	14.53	0.39	2.55
Q61466_S	Smarcd1	SWI/SNF-re	K.FSEIPQR.L	3.50	14.98	0.23	4.28
Q61466_S	Smarcd1	SWI/SNF-re	R.LLEDAALSK#.Y	18.92	12.66	1.49	0.67
Q99JR8_S	Smarcd2	SWI/SNF-re	K.ADGDNAGTAGTPGGTPAADK#.V	16.55	13.10	1.26	0.79
Q99JR8_S	Smarcd2	SWI/SNF-re	K.IHETIESINQLK#.T	42.07	25.60	1.64	0.61
Q99JR8_S	Smarcd2	SWI/SNF-re	R.M*PTTQETDGFQVK.R	7.41	7.77	0.95	1.05
Q6P9Z1_S	Smarcd3	SWI/SNF-re	R.LYISNTFNPAKPDAEDSDGSIASWELR.V	2.52	5.49	0.46	2.18
Q6P9Z1_S	Smarcd3	SWI/SNF-re	R.SAIVQALWQYVK#.T	11.56	8.73	1.32	0.76
Q6P9Z1_S	Smarcd3	SWI/SNF-re	R.TPTTQETDGFQVK#.R	16.11	9.61	1.68	0.60
Q6P9Z1_S	Smarcd3	SWI/SNF-re	K.VM*TDVAGNPEEER.R	2.52	7.61	0.33	3.02
O54941_S	Smarce1	SWI/SNF-re	K.AYHNSPAYLAYINAK#.S	11.94	9.04	1.32	0.76
O54941_S	Smarce1	SWI/SNF-re	R.DLTDEEK#QEYLNEYEAEK#.I	5.08	5.85	0.87	1.15
O54941_S	Smarce1	SWI/SNF-re	R.DLTDEEK#QEYLNEYEAEK#IEYNESMK#.A	2.82	1.89	1.49	0.67
O54941_S	Smarce1	SWI/SNF-re	K.FLESTDSFNNELK.R	9.39	11.16	0.84	1.19
O54941_S	Smarce1	SWI/SNF-re	R.KLEAELLQIEER.H	23.38	18.86	1.24	0.81
O54941_S	Smarce1	SWI/SNF-re	R.K#VWDQVK#.A	19.27	22.72	0.85	1.18
O54941_S	Smarce1	SWI/SNF-re	R.LGGNPGTNSR.V	3.65	17.31	0.21	4.74
O54941_S	Smarce1	SWI/SNF-re	K.LWEIGK#.I	32.89	22.54	1.46	0.69
O54941_S	Smarce1	SWI/SNF-re	R.SQSSM*APEEEQVANK#.A	6.64	4.41	1.51	0.66
Q9CU62_S	Smc1a	Structural r	R.AATLAQELEK#.F	115.85	84.50	1.37	0.73
Q9CU62_S	Smc1a	Structural r	K.ADQDRLDLEER.K	3.50	63.99	0.05	18.30
Q9CU62_S	Smc1a	Structural r	R.AFVSM*VYSEEGAEDR.T	3.78	15.39	0.25	4.07
Q9CU62_S	Smc1a	Structural r	R.AFVSMVYSEEGAEDR.T	7.93	22.23	0.36	2.80
Q9CU62_S	Smc1a	Structural r	R.AQVQLQLFK#.L	41.76	37.00	1.13	0.89
Q9CU62_S	Smc1a	Structural r	R.DKFQETSDEFEAAR.K	12.41	56.09	0.22	4.52
Q9CU62_S	Smc1a	Structural r	R.DLTLEENQVK#.K	42.74	40.98	1.04	0.96
Q9CU62_S	Smc1a	Structural r	R.DLTLEENQVK#K#.Y	26.33	21.25	1.24	0.81
Q9CU62_S	Smc1a	Structural r	K.EM*VKAEEDTQFNYHR.K	2.48	11.06	0.22	4.45
Q9CU62_S	Smc1a	Structural r	K.EVTAIETK#.L	67.80	45.92	1.48	0.68
Q9CU62_S	Smc1a	Structural r	K.FQETSDEFEAAR.K	3.63	8.80	0.41	2.42
Q9CU62_S	Smc1a	Structural r	R.FRPM*DNLSGGEK.T	2.61	15.07	0.17	5.77
Q9CU62_S	Smc1a	Structural r	R.GEPETFLPLDYLEVK#PTDEK#.L	5.83	6.66	0.88	1.14
Q9CU62_S	Smc1a	Structural r	K.GTM*DDISQEEGSSQGEESVSGSQR.T	6.99	18.65	0.37	2.67
Q9CU62_S	Smc1a	Structural r	R.HLALNLQEK#.S	99.58	65.76	1.51	0.66
Q9CU62_S	Smc1a	Structural r	R.IAAPNMK#.A	38.16	26.77	1.43	0.70
Q9CU62_S	Smc1a	Structural r	R.IAAPNM*K#.A	45.49	43.40	1.05	0.95
Q9CU62_S	Smc1a	Structural r	R.IEK#LEEYITTSK#.Q	53.46	37.98	1.41	0.71
Q9CU62_S	Smc1a	Structural r	K.IIDETM*AQLQDLK#.N	51.83	40.93	1.27	0.79
Q9CU62_S	Smc1a	Structural r	K.IIDETMAQLQDLK#.N	32.35	26.93	1.20	0.83
Q9CU62_S	Smc1a	Structural r	K.K#DENEIEK#.L	16.04	11.47	1.40	0.72
Q9CU62_S	Smc1a	Structural r	K.K#LEGELTEEVEM*AK#.R	17.36	13.77	1.26	0.79
Q9CU62_S	Smc1a	Structural r	K.KLEGELTEEVEM*AK.R	7.32	9.26	0.79	1.26
Q9CU62_S	Smc1a	Structural r	K.LEEYITTSK#.Q	26.35	27.91	0.94	1.06
Q9CU62_S	Smc1a	Structural r	R.LGIQLDFEK#.N	51.45	41.43	1.24	0.81
Q9CU62_S	Smc1a	Structural r	K.LIEIENFK#.S	116.79	96.15	1.21	0.82
Q9CU62_S	Smc1a	Structural r	R.LK#YSQSDLEQTK#.T	32.87	19.57	1.68	0.60
Q9CU62_S	Smc1a	Structural r	K.LNEQQSVLQR.I	26.62	95.07	0.28	3.57
Q9CU62_S	Smc1a	Structural r	K.LREIEENQK.R	5.16	44.27	0.12	8.58
Q9CU62_S	Smc1a	Structural r	R.LTEELKEQM*K.A	60.80	45.97	1.32	0.76
Q9CU62_S	Smc1a	Structural r	R.LTEELK#EQMK#.A	21.55	17.99	1.20	0.83

Q9CU62_SI	Smc1a	Structural r	K.LVIDVIR.Y	26.56	72.86	0.36	2.74
Q9CU62_SI	Smc1a	Structural r	K.LYHNEVEIEK#.L	110.60	86.21	1.28	0.78
Q9CU62_SI	Smc1a	Structural r	R.NFLVFQGAVESIAM*K.N	27.15	21.06	1.29	0.78
Q9CU62_SI	Smc1a	Structural r	K.NM*DAIIVDSEK#.T	57.98	51.51	1.13	0.89
Q9CU62_SI	Smc1a	Structural r	R.QIIGPFQR.F	16.89	44.05	0.38	2.61
Q9CU62_SI	Smc1a	Structural r	K.RLEFENQK.T	13.73	60.48	0.23	4.40
Q9CU62_SI	Smc1a	Structural r	R.SGELAQEYDKR.K	9.70	29.48	0.33	3.04
Q9CU62_SI	Smc1a	Structural r	K.SGVISGGASDLK#.A	165.96	92.06	1.80	0.55
Q9CU62_SI	Smc1a	Structural r	K.SKLESELANFGPR.I	8.88	35.48	0.25	3.99
Q9CU62_SI	Smc1a	Structural r	K.SKLESELANFGPR.I	6.82	26.34	0.26	3.86
Q9CU62_SI	Smc1a	Structural r	K.SNLM*DAISFVLGEK#.T	32.83	33.68	0.97	1.03
Q9CU62_SI	Smc1a	Structural r	K.SNLM*DAISFVLGEK#.T	21.31	15.45	1.38	0.73
Q9CU62_SI	Smc1a	Structural r	R.TALFEEISR.S	27.73	80.81	0.34	2.91
Q9CU62_SI	Smc1a	Structural r	K.TVALDGTLFQK#.S	90.87	70.80	1.28	0.78
Q9CU62_SI	Smc1a	Structural r	K.VANYIK#.E	60.04	48.43	1.24	0.81
Q9CU62_SI	Smc1a	Structural r	R.VIVGGSSEYK#.I	147.21	123.14	1.20	0.84
Q9CU62_SI	Smc1a	Structural r	K.VLTFDLTK#.Y	34.36	25.79	1.33	0.75
Q9CU62_SI	Smc1a	Structural r	K.VLTFDLTK#YPDANPNPNEQ.-	38.63	29.14	1.33	0.75
Q9CU62_SI	Smc1a	Structural r	K.VLTFDLTK#YPDANPNPNEQ.-	23.09	19.97	1.16	0.86
Q9CU62_SI	Smc1a	Structural r	K.YPDANPNPNEQ.-	9.93	9.93	1.00	1.00
Q9CU62_SI	Smc1a	Structural r	K.YSQSDLEQTK#.T	129.05	96.91	1.33	0.75
Q9CU62_SI	Smc1a	Structural r	R.AATLAQELEK#.F	32.87	22.76	1.44	0.69
Q9CU62_SI	Smc1a	Structural r	K.ADQDRLDLEER.K	1.12	13.59	0.08	12.08
Q9CU62_SI	Smc1a	Structural r	R.AFVSM*VYSEEGAEDR.T	2.54	9.31	0.27	3.67
Q9CU62_SI	Smc1a	Structural r	R.DKFQETSDEFEAAR.K	6.79	24.29	0.28	3.58
Q9CU62_SI	Smc1a	Structural r	R.DLTLEENQVK#.K	18.25	15.69	1.16	0.86
Q9CU62_SI	Smc1a	Structural r	R.DLTLEENQVK#K#.Y	10.48	4.51	2.32	0.43
Q9CU62_SI	Smc1a	Structural r	K.GTM*DDISQEEGSSQGEESVSGSQR.T	2.46	8.19	0.30	3.33
Q9CU62_SI	Smc1a	Structural r	R.HLALNLQEK#.S	33.16	31.33	1.06	0.94
Q9CU62_SI	Smc1a	Structural r	K.IIDETM*AQLQDLK#.N	12.68	10.77	1.18	0.85
Q9CU62_SI	Smc1a	Structural r	K.IIDETMAQLQDLK#.N	12.97	7.22	1.80	0.56
Q9CU62_SI	Smc1a	Structural r	R.LGIQLDFEK#.N	15.92	8.23	1.93	0.52
Q9CU62_SI	Smc1a	Structural r	K.LIEIENFK#.S	27.18	27.55	0.99	1.01
Q9CU62_SI	Smc1a	Structural r	K.LNEQQSVLQR.I	13.37	37.42	0.36	2.80
Q9CU62_SI	Smc1a	Structural r	K.LVIDVIR.Y	7.57	25.67	0.29	3.39
Q9CU62_SI	Smc1a	Structural r	R.NFLVFQGAVESIAM*K#.N	5.02	5.40	0.93	1.08
Q9CU62_SI	Smc1a	Structural r	K.NM*DAIIVDSEK#.T	17.35	14.10	1.23	0.81
Q9CU62_SI	Smc1a	Structural r	R.SGELAQEYDKR.K	2.64	10.64	0.25	4.03
Q9CU62_SI	Smc1a	Structural r	K.SKLESELANFGPR.I	1.55	8.04	0.19	5.18
Q9CU62_SI	Smc1a	Structural r	K.SNLM*DAISFVLGEK#.T	10.66	7.91	1.35	0.74
Q9CU62_SI	Smc1a	Structural r	R.TALFEEISR.S	12.91	26.07	0.49	2.02
Q9CU62_SI	Smc1a	Structural r	K.TVALDGTLFQK#.S	30.93	24.92	1.24	0.81
Q9CU62_SI	Smc1a	Structural r	R.VIVGGSSEYK#.I	44.65	27.60	1.62	0.62
Q9CU62_SI	Smc1a	Structural r	K.VLTFDLTK#.Y	10.70	7.12	1.50	0.67
Q9CU62_SI	Smc1a	Structural r	K.VLTFDLTK#YPDANPNPNEQ.-	9.16	7.08	1.29	0.77
Q9CU62_SI	Smc1a	Structural r	K.VVQLHEYSEELEK#.L	39.95	39.55	1.01	0.99
Q9CU62_SI	Smc1a	Structural r	K.YQIAVTK#.V	16.86	8.71	1.94	0.52
Q9CU62_SI	Smc1a	Structural r	K.YSQSDLEQTK#.T	31.19	25.69	1.21	0.82
Q8CG48_SI	Smc2	Structural r	K.AEEKYEALENK.M	24.00	10.81	2.22	0.45
Q8CG48_SI	Smc2	Structural r	R.AM*NVLTEAEER.Y	11.13	26.57	0.42	2.39
Q8CG48_SI	Smc2	Structural r	R.ASNLQDLVYK#.N	86.21	54.23	1.59	0.63
Q8CG48_SI	Smc2	Structural r	K.AYEGQIEK#.M	51.50	25.87	1.99	0.50
Q8CG48_SI	Smc2	Structural r	K.DNSTATALEVVAGER.L	11.90	32.13	0.37	2.70
Q8CG48_SI	Smc2	Structural r	K.DQDAFEAVK#.K	20.05	34.11	0.59	1.70
Q8CG48_SI	Smc2	Structural r	R.EHASNEQQLDAVNEAIK#.A	110.63	60.17	1.84	0.54
Q8CG48_SI	Smc2	Structural r	K.ELQNSMAEDSK#.A	24.33	12.22	1.99	0.50
Q8CG48_SI	Smc2	Structural r	K.ENLTELSGGQR.S	20.92	59.75	0.35	2.86
Q8CG48_SI	Smc2	Structural r	K.FPNLQFAYK#.D	10.43	6.86	1.52	0.66
Q8CG48_SI	Smc2	Structural r	K.FPNLQFAYK#DPEK#.N	35.14	22.97	1.53	0.65
Q8CG48_SI	Smc2	Structural r	K.FQEVK#DVQDELR@TK#.E	9.48	10.45	0.91	1.10
Q8CG48_SI	Smc2	Structural r	K.FVDGVSTVAR.F	35.91	45.01	0.80	1.25
Q8CG48_SI	Smc2	Structural r	K.GLVASLINVK#.D	84.82	33.03	2.57	0.39
Q8CG48_SI	Smc2	Structural r	K.HLFGQPNSAYDFK#.T	21.27	9.81	2.17	0.46
Q8CG48_SI	Smc2	Structural r	K.HNLQNNESQLK#.I	50.16	27.73	1.81	0.55
Q8CG48_SI	Smc2	Structural r	K.IK#ELDHSISK#.H	80.50	38.32	2.10	0.48
Q8CG48_SI	Smc2	Structural r	K.ILATIEDLDQK#.K	40.33	23.27	1.73	0.58
Q8CG48_SI	Smc2	Structural r	K.IVNLQEVLSENEK#.K	35.12	16.28	2.16	0.46
Q8CG48_SI	Smc2	Structural r	K.K#AEEK#YEALENK#.M	79.23	38.72	2.05	0.49
Q8CG48_SI	Smc2	Structural r	R.K#DK#ETGGK#.L	70.37	5.80	12.13	0.08
Q8CG48_SI	Smc2	Structural r	K.K#NQALNIAWQK#.V	6.78	4.46	1.52	0.66
Q8CG48_SI	Smc2	Structural r	R.LYNVVVDTEVTAK#.K	44.06	22.03	2.00	0.50
Q8CG48_SI	Smc2	Structural r	K.M*LSDYDWINAEK#.H	28.01	18.23	1.54	0.65
Q8CG48_SI	Smc2	Structural r	K.MLSDYDWINAEK#.H	12.45	5.70	2.19	0.46
Q8CG48_SI	Smc2	Structural r	K.QIITAQDNIIK#.D	21.96	10.65	2.06	0.48
Q8CG48_SI	Smc2	Structural r	R.SAGELK#EM*QDK#.I	8.81	4.76	1.85	0.54
Q8CG48_SI	Smc2	Structural r	K.SIILEGFK#.S	68.14	37.27	1.83	0.55
Q8CG48_SI	Smc2	Structural r	R.SQAASILTK#.F	91.91	46.11	1.99	0.50
Q8CG48_SI	Smc2	Structural r	R.SSYLEYQK#.V	61.40	34.67	1.77	0.56
Q8CG48_SI	Smc2	Structural r	K.TEEGDLLQTK#.L	47.10	28.19	1.67	0.60
Q8CG48_SI	Smc2	Structural r	K.TIEESEETLK#.S	125.52	65.95	1.90	0.53
Q8CG48_SI	Smc2	Structural r	K.TILEEEITPTIQK#.L	85.65	46.20	1.85	0.54
Q8CG48_SI	Smc2	Structural r	K.VALGNTWK#.E	44.19	23.81	1.86	0.54
Q8CG48_SI	Smc2	Structural r	R.VAQNLVGPDNVHVALSLVDYK#PELQK#.G	11.14	7.53	1.48	0.68
Q8CG48_SI	Smc2	Structural r	K.VLNM*KPPEILSM*IEEAAGTR.M	4.23	10.55	0.40	2.50
Q8CG48_SI	Smc2	Structural r	K.VLNM*KPPEILSMIEEAAGTR.M	4.43	6.28	0.71	1.42
Q8CG48_SI	Smc2	Structural r	R.ALEEELAGLK#.N	52.22	21.53	2.43	0.41
Q8CG48_SI	Smc2	Structural r	R.ASNLQDLVYK#.N	32.08	15.42	2.08	0.48
Q8CG48_SI	Smc2	Structural r	K.DNSTATALEVVAGER.L	5.57	14.24	0.39	2.56
Q8CG48_SI	Smc2	Structural r	R.EHASNEQQLDAVNEAIK#.A	38.00	15.53	2.45	0.41
Q8CG48_SI	Smc2	Structural r	K.ELQNSM*AEDSK#.A	5.12	2.75	1.86	0.54
Q8CG48_SI	Smc2	Structural r	K.ENLTELSGGQR.S	7.14	17.78	0.40	2.49
Q8CG48_SI	Smc2	Structural r	K.FVDGVSTVAR.F	29.77	15.09	1.97	0.51
Q8CG48_SI	Smc2	Structural r	K.GLVASLINVK#.D	32.44	19.24	1.69	0.59
Q8CG48_SI	Smc2	Structural r	K.HNLQNNESQLK#.I	31.75	15.81	2.01	0.50
Q8CG48_SI	Smc2	Structural r	K.ILATIEDLDQK#.K	15.42	9.97	1.55	0.65
Q8CG48_SI	Smc2	Structural r	K.IVNLQEVLSENEK#.K	15.75	9.66	1.63	0.61
Q8CG48_SI	Smc2	Structural r	K.K#AEEK#YEALENK#.M	20.65	18.37	1.12	0.89
Q8CG48_SI	Smc2	Structural r	R.LYNVVVDTEVTAK#.K	18.07	11.18	1.62	0.62
Q8CG48_SI	Smc2	Structural r	K.M*LSDYDWINAEK#.H	13.23	6.62	2.00	0.50
Q8CG48_SI	Smc2	Structural r	R.SAGELK#EM*QDK#.I	3.41	1.64	2.07	0.48
Q8CG48_SI	Smc2	Structural r	K.SIILEGFK#.S	39.53	19.12	2.07	0.48
Q8CG48_SI	Smc2	Structural r	R.SQAASILTK#.F	32.98	15.65	2.11	0.47
Q8CG48_SI	Smc2	Structural r	R.SSYLEYQK#.V	23.76	13.15	1.81	0.55

Q8CG48_SI	Smc2	Structural r	K.TIEESEETLK#.S	60.86	31.07	1.96	0.51
Q8CG48_SI	Smc2	Structural r	K.TILEEEITPTIQK#.L	44.05	23.73	1.86	0.54
Q9CW03_S	Smc3	Structural r	K.AELGTDLLSQLSLEDQK#.R	11.01	10.27	1.07	0.93
Q9CW03_S	Smc3	Structural r	K.AELGTDLLSQLSLEDQK#.R	11.20	5.86	1.91	0.52
Q9CW03_S	Smc3	Structural r	K.AKDLQDELAGNSEQR.K	7.32	30.30	0.24	4.14
Q9CW03_S	Smc3	Structural r	R.AK#LDELSAK#.R	58.81	37.85	1.55	0.64
Q9CW03_S	Smc3	Structural r	K.ALDQFVNFSEQK#.E	54.45	47.91	1.14	0.88
Q9CW03_S	Smc3	Structural r	R.ALEYTIYNQELNETR.A	7.92	27.62	0.29	3.49
Q9CW03_S	Smc3	Structural r	K.DFVEDDTTHG.-	80.33	80.33	1.00	1.00
Q9CW03_S	Smc3	Structural r	R.DKMEDIER.Q	5.37	11.72	0.46	2.18
Q9CW03_S	Smc3	Structural r	K.DLEDTEANK#EK#.N	18.30	13.50	1.36	0.74
Q9CW03_S	Smc3	Structural r	K.DLQDELAGNSEQR.K	10.32	24.42	0.42	2.37
Q9CW03_S	Smc3	Structural r	R.DQTIVDPFSSK#.H	33.29	27.10	1.23	0.81
Q9CW03_S	Smc3	Structural r	R.DSILSEMK#.M	18.17	12.55	1.45	0.69
Q9CW03_S	Smc3	Structural r	R.DTAYPETNDAIPM*ISK#.L	22.40	15.51	1.44	0.69
Q9CW03_S	Smc3	Structural r	R.EENAEQQALAAK#.R	112.69	83.46	1.35	0.74
Q9CW03_S	Smc3	Structural r	R.ELGSLPQEAFEK#.Y	80.54	69.86	1.15	0.87
Q9CW03_S	Smc3	Structural r	R.EMQQLSGGQK#.S	11.06	7.69	1.44	0.70
Q9CW03_S	Smc3	Structural r	R.ESLKAELGTDLLSQLSLEDQK.R	7.35	5.81	1.27	0.79
Q9CW03_S	Smc3	Structural r	R.GSGSQSSVPSVDQFTGVGIR.V	9.01	34.14	0.26	3.79
Q9CW03_S	Smc3	Structural r	R.GSQFTSKEER.D	5.25	6.01	0.87	1.14
Q9CW03_S	Smc3	Structural r	R.IKLEGIITR.V	9.07	32.05	0.28	3.53
Q9CW03_S	Smc3	Structural r	K.ILM*EFNK#.M	58.24	39.56	1.47	0.68
Q9CW03_S	Smc3	Structural r	K.ILMEFNK#.M	24.61	15.79	1.56	0.64
Q9CW03_S	Smc3	Structural r	R.INNEIDQLM*NQM*QQIETQQR.K	1.68	6.75	0.25	4.03
Q9CW03_S	Smc3	Structural r	R.INNEIDQLMNQMQQIETQQR.K	7.44	25.85	0.29	3.48
Q9CW03_S	Smc3	Structural r	K.INQMATAPDSQR.L	4.20	11.79	0.36	2.81
Q9CW03_S	Smc3	Structural r	K.INQM*ATAPDSQR.L	18.83	61.21	0.31	3.25
Q9CW03_S	Smc3	Structural r	K.ISAMKEEKEQLSAER.Q	10.97	16.11	0.68	1.47
Q9CW03_S	Smc3	Structural r	R.K#AEEELGELEAK#.L	35.09	35.21	1.00	1.00
Q9CW03_S	Smc3	Structural r	K.K#DQYFLDK#K#.M	52.38	41.62	1.26	0.79
Q9CW03_S	Smc3	Structural r	R.K#EESISLM*K#.E	38.00	22.98	1.65	0.60
Q9CW03_S	Smc3	Structural r	K.KGDVEGSQSQDEGEGSGESER.G	5.67	19.44	0.29	3.43
Q9CW03_S	Smc3	Structural r	R.K#YEAIQLTFK#.Q	26.27	24.61	1.07	0.94
Q9CW03_S	Smc3	Structural r	R.KYEAIQLTFK.Q	38.68	24.01	1.61	0.62
Q9CW03_S	Smc3	Structural r	R.LAQATQER.T	4.31	19.24	0.22	4.46
Q9CW03_S	Smc3	Structural r	K.LDQDLNEVK#.A	25.35	19.57	1.30	0.77
Q9CW03_S	Smc3	Structural r	R.LFYHIVDSDEVSTK#.I	101.76	80.34	1.27	0.79
Q9CW03_S	Smc3	Structural r	R.LHTLEEEKEELAQYQK.W	8.70	9.01	0.97	1.04
Q9CW03_S	Smc3	Structural r	K.M*NLPGEVTFLPLNK#.L	37.51	30.11	1.25	0.80
Q9CW03_S	Smc3	Structural r	K.MNLPGEVTFLPLNK#.L	30.85	21.34	1.45	0.69
Q9CW03_S	Smc3	Structural r	K.NDVM*NLLESAGFSR.S	4.48	11.76	0.38	2.63
Q9CW03_S	Smc3	Structural r	K.NDVMNLLESAGFSR.S	4.88	11.24	0.43	2.30
Q9CW03_S	Smc3	Structural r	K.NFSEVFQK#.L	60.40	45.35	1.33	0.75
Q9CW03_S	Smc3	Structural r	K.NLEQYNKLDQDLNEVK.A	72.07	50.88	1.42	0.71
Q9CW03_S	Smc3	Structural r	K.NLEQYNK#LDQDLNEVK#.A	13.78	8.14	1.69	0.59
Q9CW03_S	Smc3	Structural r	R.SEDLDNSIDKTEAGIK.E	26.04	19.22	1.35	0.74
Q9CW03_S	Smc3	Structural r	K.SIM*ELM*NVLELR.K	2.94	11.75	0.25	4.00
Q9CW03_S	Smc3	Structural r	K.SIM*ELMNVLELR.K	2.15	6.19	0.35	2.87
Q9CW03_S	Smc3	Structural r	K.SLDQAINDK#.K	73.81	57.42	1.29	0.78
Q9CW03_S	Smc3	Structural r	R.SM*EVSTQLAR.A	15.65	32.72	0.48	2.09
Q9CW03_S	Smc3	Structural r	R.SMEVSTQLAR.A	7.16	20.62	0.35	2.88
Q9CW03_S	Smc3	Structural r	R.SNPYYIVK#.Q	45.82	33.40	1.37	0.73
Q9CW03_S	Smc3	Structural r	R.VDALNDEIR.Q	17.10	57.44	0.30	3.36
Q9CW03_S	Smc3	Structural r	R.VETYLNENLR.K	21.72	70.69	0.31	3.26
Q9CW03_S	Smc3	Structural r	K.VSHIDVITAEM*AK#.D	9.28	6.25	1.48	0.67
Q9CW03_S	Smc3	Structural r	K.AILNGIDSINK#.V	11.92	5.04	2.36	0.42
Q9CW03_S	Smc3	Structural r	K.ALDQFVNFSEQK#.E	28.25	16.23	1.74	0.57
Q9CW03_S	Smc3	Structural r	R.ALEYTIYNQELNETR.A	5.26	11.32	0.46	2.15
Q9CW03_S	Smc3	Structural r	K.DFVEDDTTHG.-	33.68	33.68	1.00	1.00
Q9CW03_S	Smc3	Structural r	K.DLQDELAGNSEQR.K	5.35	9.45	0.57	1.77
Q9CW03_S	Smc3	Structural r	R.DQTIVDPFSSK#.H	21.55	13.94	1.55	0.65
Q9CW03_S	Smc3	Structural r	R.DTAYPETNDAIPM*ISK#.L	8.17	9.36	0.87	1.15
Q9CW03_S	Smc3	Structural r	R.DTAYPETNDAIPMISK#.L	6.83	4.35	1.57	0.64
Q9CW03_S	Smc3	Structural r	R.EENAEQQALAAK#.R	58.46	32.37	1.81	0.55
Q9CW03_S	Smc3	Structural r	R.ELGSLPQEAFEK#.Y	28.35	22.43	1.26	0.79
Q9CW03_S	Smc3	Structural r	R.GSGSQSSVPSVDQFTGVGIR.V	7.11	13.86	0.51	1.95
Q9CW03_S	Smc3	Structural r	K.INQM*ATAPDSQR.L	15.32	44.50	0.34	2.90
Q9CW03_S	Smc3	Structural r	R.K#AEEELGELEAK#.L	21.39	21.06	1.02	0.98
Q9CW03_S	Smc3	Structural r	K.K#DQYFLDK#K#.M	21.55	16.13	1.34	0.75
Q9CW03_S	Smc3	Structural r	K.LDQDLNEVK#.A	16.29	22.79	0.71	1.40
Q9CW03_S	Smc3	Structural r	R.LFYHIVDSDEVSTK#.I	56.13	35.71	1.57	0.64
Q9CW03_S	Smc3	Structural r	R.LHTLEEEK#EELAQYQK#.W	34.16	25.44	1.34	0.74
Q9CW03_S	Smc3	Structural r	K.M*NLPGEVTFLPLNK#.L	19.71	15.93	1.24	0.81
Q9CW03_S	Smc3	Structural r	K.NLEQYNKLDQDLNEVK.A	37.26	22.03	1.69	0.59
Q9CW03_S	Smc3	Structural r	K.SLDQAINDK#.K	35.70	28.43	1.26	0.80
Q9CW03_S	Smc3	Structural r	R.SYRDQTIVDPFSSK.H	3.93	9.16	0.43	2.33
Q9CW03_S	Smc3	Structural r	R.VDALNDEIR.Q	8.06	25.16	0.32	3.12
Q8CG47_SI	Smc4	Structural r	K.AK#EALITASETLK#.E	17.85	11.15	1.60	0.62
Q8CG47_SI	Smc4	Structural r	R.DTLVANNLDQATR.V	10.37	28.23	0.37	2.72
Q8CG47_SI	Smc4	Structural r	R.FLILQGEVEQIAMMK#PK#.G	9.54	3.81	2.50	0.40
Q8CG47_SI	Smc4	Structural r	K.FTQLDLEDVQVR.E	8.06	18.99	0.42	2.36
Q8CG47_SI	Smc4	Structural r	K.HNIGIATFIGLDK#.M	13.91	9.17	1.52	0.66
Q8CG47_SI	Smc4	Structural r	R.HNTAVSQLSK#.A	94.23	50.31	1.87	0.53
Q8CG47_SI	Smc4	Structural r	R.IAEITTQK#.E	58.22	22.93	2.54	0.39
Q8CG47_SI	Smc4	Structural r	K.IFNLSGGEK#.T	28.55	14.74	1.94	0.52
Q8CG47_SI	Smc4	Structural r	K.IHEDTK#EITEK#.S	4.55	3.48	1.30	0.77
Q8CG47_SI	Smc4	Structural r	K.IIDKEGDDYEVLPNSNFYVSR.T	9.66	15.18	0.64	1.57
Q8CG47_SI	Smc4	Structural r	R.IPGIYGR.L	10.58	35.56	0.30	3.36
Q8CG47_SI	Smc4	Structural r	R.LGDLGAIDEK#.Y	27.37	6.03	4.54	0.22
Q8CG47_SI	Smc4	Structural r	R.LM*ITHIVNQNFK#.S	7.26	5.54	1.31	0.76
Q8CG47_SI	Smc4	Structural r	R.LNEFMAGFYVITNK#.L	7.20	4.12	1.75	0.57
Q8CG47_SI	Smc4	Structural r	K.LTQEEINLK#.S	62.22	35.20	1.77	0.57
Q8CG47_SI	Smc4	Structural r	K.NIAIEFLTLENEM*FK#.K	13.92	9.67	1.44	0.69
Q8CG47_SI	Smc4	Structural r	K.NIEDK#AEEVINNTK#.T	32.80	22.41	1.46	0.68
Q8CG47_SI	Smc4	Structural r	R.NLLQELK#.V	32.46	16.51	1.97	0.51
Q8CG47_SI	Smc4	Structural r	R.QAFYFALR.D	5.56	14.21	0.39	2.55
Q8CG47_SI	Smc4	Structural r	K.SLVHDLFQK#.V	19.51	13.53	1.44	0.69
Q8CG47_SI	Smc4	Structural r	K.SNVIDSM*LFVFGYR.A	4.01	7.05	0.57	1.76
Q8CG47_SI	Smc4	Structural r	K.SNVLSNEM*K#.A	18.36	9.88	1.86	0.54
Q8CG47_SI	Smc4	Structural r	K.TAETSLPEIQK#.E	50.75	28.38	1.79	0.56
Q8CG47_SI	Smc4	Structural r	K.TVINETTTR.N	18.40	47.63	0.39	2.59
Q8CG47_SI	Smc4	Structural r	K.VLDAIIQEK#.K	59.32	34.55	1.72	0.58

Q8CG47_SI	Smc4	Structural r	K.VQHEEAVVK#.L	19.04	9.71	1.96	0.51
Q8CG47_SI	Smc4	Structural r	R.VVTLQGQIIEQSGTM*SGGGSK#.V	19.03	52.87	0.36	2.78
Q8CG47_SI	Smc4	Structural r	R.VVTLQGQIIEQSGTMSGGGSK#.V	9.29	7.11	1.31	0.76
Q8CG47_SI	Smc4	Structural r	K.DK#EK#VEELK#.S	7.58	6.47	1.17	0.85
Q8CG47_SI	Smc4	Structural r	R.DSTSVYHISGK#.K	40.17	21.29	1.89	0.53
Q8CG47_SI	Smc4	Structural r	K.DTEK#EINDLK#TELK#.N	7.78	4.38	1.78	0.56
Q8CG47_SI	Smc4	Structural r	R.DTLVANNLDQATR.V	20.06	51.70	0.39	2.58
Q8CG47_SI	Smc4	Structural r	K.ELEANVLTTAPDR.K	7.66	17.67	0.43	2.30
Q8CG47_SI	Smc4	Structural r	K.ELM*GFNK#.S	39.11	21.21	1.84	0.54
Q8CG47_SI	Smc4	Structural r	K.FTQLDLEDVQVR.E	15.42	30.44	0.51	1.97
Q8CG47_SI	Smc4	Structural r	K.HNIGIATFIGLDK#.M	22.14	13.21	1.68	0.60
Q8CG47_SI	Smc4	Structural r	R.HNTAVSQLSK#.A	124.65	85.85	1.45	0.69
Q8CG47_SI	Smc4	Structural r	R.IAEITTQK#.E	81.17	44.48	1.82	0.55
Q8CG47_SI	Smc4	Structural r	K.IFNLSGGEK#.T	60.47	27.30	2.21	0.45
Q8CG47_SI	Smc4	Structural r	K.IHEDTK#EITEK#.S	93.61	38.06	2.46	0.41
Q8CG47_SI	Smc4	Structural r	K.IIDKEGDDYEVLPNSNFYVSR.T	11.09	21.41	0.52	1.93
Q8CG47_SI	Smc4	Structural r	R.IPGIYGR.L	17.35	44.36	0.39	2.56
Q8CG47_SI	Smc4	Structural r	K.IQTPENTPR.L	24.37	72.92	0.33	2.99
Q8CG47_SI	Smc4	Structural r	K.K#IFNLSGGEK#.T	13.56	6.34	2.14	0.47
Q8CG47_SI	Smc4	Structural r	R.LIGIYK#.T	60.73	35.86	1.69	0.59
Q8CG47_SI	Smc4	Structural r	K.LLEENVSVFK#.K	41.07	26.98	1.52	0.66
Q8CG47_SI	Smc4	Structural r	R.LM*ITHIVNQNFK#.S	28.48	13.63	2.09	0.48
Q8CG47_SI	Smc4	Structural r	R.LMITHIVNQNFK#.S	10.07	7.05	1.43	0.70
Q8CG47_SI	Smc4	Structural r	R.LNEFMAGFYVITNK#.L	6.31	3.45	1.83	0.55
Q8CG47_SI	Smc4	Structural r	K.LPQTQQELK#.E	129.00	68.37	1.89	0.53
Q8CG47_SI	Smc4	Structural r	K.LTQEEINLK#.S	122.97	59.76	2.06	0.49
Q8CG47_SI	Smc4	Structural r	R.M*GSSVIDEISVEEVNK#.M	14.96	7.13	2.10	0.48
Q8CG47_SI	Smc4	Structural r	K.NIAIEFLTLENEM*FK#.K	19.89	8.58	2.32	0.43
Q8CG47_SI	Smc4	Structural r	K.NIEDK#AEEVINNTK#.T	47.95	34.42	1.39	0.72
Q8CG47_SI	Smc4	Structural r	K.NIEDKAEEVINNTK.T	24.41	16.84	1.45	0.69
Q8CG47_SI	Smc4	Structural r	R.NLLQELK#.V	72.39	42.04	1.72	0.58
Q8CG47_SI	Smc4	Structural r	K.SLVHDLFQK#.V	29.07	19.74	1.47	0.68
Q8CG47_SI	Smc4	Structural r	K.SLVHDLFQK#VEEAK#.S	29.95	16.40	1.83	0.55
Q8CG47_SI	Smc4	Structural r	K.SNVIDSM*LFVFGYR.A	7.32	7.02	1.04	0.96
Q8CG47_SI	Smc4	Structural r	K.SNVLSNEM*K#.A	34.75	18.18	1.91	0.52
Q8CG47_SI	Smc4	Structural r	K.TAETSLPEIQK#.E	72.84	49.92	1.46	0.69
Q8CG47_SI	Smc4	Structural r	K.TVINETTTR.N	30.14	60.18	0.50	2.00
Q8CG47_SI	Smc4	Structural r	K.VIQENEHALQK#.D	31.44	19.47	1.61	0.62
Q8CG47_SI	Smc4	Structural r	K.VLDAIIQEK#.K	80.86	51.05	1.58	0.63
Q8CG47_SI	Smc4	Structural r	R.VVTLQGQIIEQSGTM*SGGGSK#.V	19.33	10.07	1.92	0.52
Q8CG47_SI	Smc4	Structural r	R.VVTLQGQIIEQSGTMSGGGSK#.V	16.21	9.24	1.76	0.57
Q8CG46_SI	Smc5	Structural r	R.EVEIQQLTEELQGK.K	5.44	8.11	0.67	1.49
Q8CG46_SI	Smc5	Structural r	K.ELQQALTVK#.Q	11.23	9.82	1.14	0.87
Q8CG46_SI	Smc5	Structural r	R.EVEIQQLTEELQGK#.K	13.50	14.54	0.93	1.08
Q8CG46_SI	Smc5	Structural r	K.IELLEATEK.S	12.45	12.63	0.99	1.01
Q8CG46_SI	Smc5	Structural r	R.TSGNLIITR.E	3.37	9.30	0.36	2.76
Q924W5_S	Smc6	Structural r	R.EAFTADGDQVFAGR.Y	2.12	9.12	0.23	4.30
Q924W5_S	Smc6	Structural r	R.ELENIEEHQSVDIATLEDEAEENKIK.M	1.54	2.81	0.55	1.82
Q924W5_S	Smc6	Structural r	K.SAVLTALIVGLGGK.A	9.04	10.57	0.86	1.17
Q924W5_S	Smc6	Structural r	R.DVDSEISDLETEIENK#.K	7.70	6.02	1.28	0.78
Q924W5_S	Smc6	Structural r	R.FQNIAGLSTM*K#.T	8.54	4.60	1.85	0.54
Q924W5_S	Smc6	Structural r	R.GQTTLPFRPVTQEEDDSAS.-	1.89	9.32	0.20	4.94
Q924W5_S	Smc6	Structural r	K.INQLSELADPLKDELNLADSEVDSQKR.G	4.23	14.79	0.29	3.50
Q924W5_S	Smc6	Structural r	K.SAVLTALIVGLGGK.A	12.44	14.01	0.89	1.13
Q924W5_S	Smc6	Structural r	R.SIETVLLIK#.N	12.86	10.36	1.24	0.81
Q6P5D8_SI	Smchd1	Structural r	K.AHVEGDGVVEGVIR.Y	12.50	15.71	0.80	1.26
Q6P5D8_SI	Smchd1	Structural r	R.AIYDETQGR.Q	25.13	31.09	0.81	1.24
Q6P5D8_SI	Smchd1	Structural r	K.AYNIDIPATQQTTHIEALLEK#.K	120.07	37.26	3.22	0.31
Q6P5D8_SI	Smchd1	Structural r	R.EINITPSLAEK#.I	18.69	5.40	3.46	0.29
Q6P5D8_SI	Smchd1	Structural r	K.FSFGLLDSPFR.V	30.79	40.57	0.76	1.32
Q6P5D8_SI	Smchd1	Structural r	R.GM*VFGAPVPK#.Q	28.57	11.62	2.46	0.41
Q6P5D8_SI	Smchd1	Structural r	K.HQDEVTWVAGDVIR.N	10.96	13.89	0.79	1.27
Q6P5D8_SI	Smchd1	Structural r	R.IDFLPHYDTLVK#.S	50.52	18.83	2.68	0.37
Q6P5D8_SI	Smchd1	Structural r	R.ISGALFTNDK#FQVSTNK#.L	45.52	11.20	4.06	0.25
Q6P5D8_SI	Smchd1	Structural r	K.ITLEANSQSVSVQGIR.F	6.21	11.72	0.53	1.89
Q6P5D8_SI	Smchd1	Structural r	K.K#ITEQNELK#.K	23.68	12.63	1.87	0.53
Q6P5D8_SI	Smchd1	Structural r	K.LGNYTLK#.L	56.51	17.10	3.30	0.30
Q6P5D8_SI	Smchd1	Structural r	K.LLFDETQGKPAVAVVDNGR.G	12.02	11.94	1.01	0.99
Q6P5D8_SI	Smchd1	Structural r	K.LLLM*DWPELK#.E	25.04	9.71	2.58	0.39
Q6P5D8_SI	Smchd1	Structural r	R.LSITDNYGNHTGM*DLVGTVVATIK#.G	30.04	12.24	2.45	0.41
Q6P5D8_SI	Smchd1	Structural r	R.LSITDNYGNHTGMDLVGTVVATIK#.G	11.18	5.69	1.96	0.51
Q6P5D8_SI	Smchd1	Structural r	R.LSSVNEDLDNQLQYLHTPDMK#.K	19.36	5.88	3.29	0.30
Q6P5D8_SI	Smchd1	Structural r	R.LSTVSGTLESYSLPFM*FYNDVK#.K	4.89	2.24	2.18	0.46
Q6P5D8_SI	Smchd1	Structural r	K.LTFM*DLELK#.L	14.97	71.56	0.21	4.78
Q6P5D8_SI	Smchd1	Structural r	K.LVPDSQPATPAVSNVR.S	18.19	29.76	0.61	1.64
Q6P5D8_SI	Smchd1	Structural r	R.NLIFQM*YDEGEREINITPSLAEK.I	4.46	9.37	0.48	2.10
Q6P5D8_SI	Smchd1	Structural r	R.SLNSDISYFGVGGK#.Q	47.48	17.26	2.75	0.36
Q6P5D8_SI	Smchd1	Structural r	K.STIEGPTIK#.L	45.02	10.13	4.44	0.23
Q6P5D8_SI	Smchd1	Structural r	K.TNILSSQQVIVDVLPNQPM*K#.L	13.21	3.88	3.40	0.29
Q6P5D8_SI	Smchd1	Structural r	K.VNWTPEVNK#EHLVQGLLPDVQVPTSVK#.D	29.60	14.07	2.10	0.48
Q6P5D8_SI	Smchd1	Structural r	R.VQLVSGPPTK#.L	107.61	35.35	3.04	0.33
Q6P2K6_P4	Smek1	Serine/thre	R.AESDGSLLLESK#.I	19.93	5.20	3.84	0.26
Q6P2K6_P4	Smek1	Serine/thre	K.ALEDVDYVQTFK#.G	12.42	48.00	0.26	3.87
Q6P2K6_P4	Smek1	Serine/thre	K.SFLFEPVVK#.A	13.53	5.21	2.60	0.38
Q6P2K6_P4	Smek1	Serine/thre	K.STSQTAAITTK#.G	10.00	3.51	2.85	0.35
Q6P2K6_P4	Smek1	Serine/thre	R.AESDGSLLLESK#.I	20.43	5.37	3.80	0.26
Q6P2K6_P4	Smek1	Serine/thre	K.FK#EVIPISDPELK#.Q	14.57	2.55	5.70	0.18
Q6P2K6_P4	Smek1	Serine/thre	K.SFLFEPVVK#.A	16.94	3.60	4.70	0.21
Q6P2K6_P4	Smek1	Serine/thre	R.TLVDPENM*LATANK#.T	6.57	2.10	3.13	0.32
Q922R5_P4	Smek2	Serine/thre	K.ALESIEYVQTFK#.G	7.03	7.46	0.94	1.06
Q922R5_P4	Smek2	Serine/thre	K.SVVSQTTPASSNVASSK#.T	11.91	1.56	7.62	0.13
Q8VE18_SN	Smg8	Protein SM	K.LYEVAIDGK#EEDLGSPTGELTSK#.I	5.35	4.74	1.13	0.89
Q8VE18_SN	Smg8	Protein SM	K.LYEVAIDGK#EEDLGSPTGELTSK#.I	14.71	3.43	4.29	0.23
P97801_SN	Smn1	Survival mc	K.AAPWTSFLPPPPPM*PGSGLGPGK#PGLK#.F	6.73	7.59	0.89	1.13
P97801_SN	Smn1	Survival mc	K.AAPWTSFLPPPPPMPGSGLGPGKPGLK.F	7.13	6.45	1.11	0.90
P97801_SN	Smn1	Survival mc	R.GTGQSDDSDIWDDTALIK.A	5.37	4.54	1.19	0.84
P97801_SN	Smn1	Survival mc	K.AAPWTSFLPPPPPMPGSGLGPGKPGLK.F	5.19	11.45	0.45	2.21
Q3UKJ7_SN	Smu1	WD40 repe	R.DTEM*LATGAQDGK#.I	5.68	4.85	1.17	0.85
Q3UKJ7_SN	Smu1	WD40 repe	R.GHSSFVNEATFTQDGHYIISASSDGTVK#.I	13.24	6.96	1.90	0.53
Q3UKJ7_SN	Smu1	WD40 repe	R.LM*ALLGQALK#.W	9.26	5.85	1.58	0.63
Q3UKJ7_SN	Smu1	WD40 repe	R.AAIAQALAGEVSVVPPSR.L	7.61	19.66	0.39	2.58
Q3UKJ7_SN	Smu1	WD40 repe	R.LM*ALLGQALK#.W	18.23	15.45	1.18	0.85
Q3UKJ7_SN	Smu1	WD40 repe	R.LMALLGQALK#.W	8.90	6.83	1.30	0.77

Q3UKJ7_SN	Smu1	WD40 repe	R.YIHLENLLAR.S	9.24	18.62	0.50	2.02
O09044_SN	Snap23	Synaptosor	K.ATWGDGGDNSPSNVVSK.Q	5.02	7.18	0.70	1.43
O09044_SN	Snap23	Synaptosor	R.ILGLAIESQDAGIK.T	7.51	7.73	0.97	1.03
Q8R570_SN	Snap47	Synaptosor	R.ELPTGGQEGEQLQLQK#.N	5.84	3.51	1.66	0.60
Q9Z266_SN	Snapin	SNARE-asso	R.AM*LDSGVYPPGSPSK#.-	4.18	2.39	1.75	0.57
Q9Z266_SN	Snapin	SNARE-asso	K.VALDLDPYVK.K	28.89	26.74	1.08	0.93
Q9Z266_SN	Snapin	SNARE-asso	K.VALDLDPYVK#K#.L	11.46	4.67	2.45	0.41
Q9Z266_SN	Snapin	SNARE-asso	R.VVLVNNILQNAQER.L	10.15	23.83	0.43	2.35
Q78PY7_SN	Snd1	Staphyloco	R.ETDGSETPEPFAAEAK#.F	22.89	3.59	6.38	0.16
Q78PY7_SN	Snd1	Staphyloco	R.EVEVEVESM*DK#.A	24.12	2.96	8.15	0.12
Q78PY7_SN	Snd1	Staphyloco	R.LEGDNIQDK#.N	25.20	4.73	5.32	0.19
Q78PY7_SN	Snd1	Staphyloco	R.NLPGLVQEGEPFSEEATLFTK#.E	16.62	4.44	3.75	0.27
Q78PY7_SN	Snd1	Staphyloco	R.SAYYK#PLLSAEEAAK#.Q	7.79	2.25	3.45	0.29
Q78PY7_SN	Snd1	Staphyloco	R.VADISGDTQK#.A	31.90	12.93	2.47	0.41
Q78PY7_SN	Snd1	Staphyloco	K.VITEYLNAQESAK#.S	28.87	4.69	6.16	0.16
Q78PY7_SN	Snd1	Staphyloco	K.VM*QVLNADAIVVK#.L	10.71	34.54	0.31	3.23
Q78PY7_SN	Snd1	Staphyloco	K.VMQVLNADAIVVK#.L	17.50	2.33	7.52	0.13
Q78PY7_SN	Snd1	Staphyloco	R.ETDGSETPEPFAAEAK#.F	11.40	1.89	6.03	0.17
Q78PY7_SN	Snd1	Staphyloco	R.EVEVEVESM*DK#.A	7.30	1.92	3.80	0.26
Q78PY7_SN	Snd1	Staphyloco	R.VADISGDTQK#.A	22.76	11.40	2.00	0.50
Q78PY7_SN	Snd1	Staphyloco	K.VITEYLNAQESAK#.S	13.07	2.69	4.86	0.21
Q9CZ28_SN	Snf8	Vacuolar-sc	K.FAQDVSQDDLIR.A	3.69	8.15	0.45	2.21
Q9CZ28_SN	Snf8	Vacuolar-sc	R.GTVLAEDQLAQM*SK#.Q	3.58	2.32	1.54	0.65
Q9CZ28_SN	Snf8	Vacuolar-sc	K.TNLEEFASK#.H	13.59	5.27	2.58	0.39
Q8BIZ6_SN	Snip1	Smad nucle	R.DSQNLQAQEEER.D	5.33	15.85	0.34	2.97
Q8BIZ6_SN	Snip1	Smad nucle	K.EKPSFELSGALLEDTNTFR.G	3.70	11.70	0.32	3.16
Q6P4T2_U5	Snrnp200	U5 small nu	K.ADEVLEILK#.T	30.58	18.11	1.69	0.59
Q6P4T2_U5	Snrnp200	U5 small nu	R.AIFEIVLNR.G	9.78	19.82	0.49	2.03
Q6P4T2_U5	Snrnp200	U5 small nu	K.ANSNLVLQADR.S	32.15	74.63	0.43	2.32
Q6P4T2_U5	Snrnp200	U5 small nu	R.DEPTGEVLSLVGK#.L	118.29	65.79	1.80	0.56
Q6P4T2_U5	Snrnp200	U5 small nu	R.DIDAFWLQR.Q	28.83	69.22	0.42	2.40
Q6P4T2_U5	Snrnp200	U5 small nu	K.DTLGLFLR.E	10.75	30.34	0.35	2.82
Q6P4T2_U5	Snrnp200	U5 small nu	R.EEEK#LELQK#.L	58.83	25.46	2.31	0.43
Q6P4T2_U5	Snrnp200	U5 small nu	R.EEGWWVVIGDAK#.S	63.98	29.09	2.20	0.45
Q6P4T2_U5	Snrnp200	U5 small nu	R.EGSASTEVLR.T	41.00	71.74	0.57	1.75
Q6P4T2_U5	Snrnp200	U5 small nu	R.EIDLLLGQTDDTR.Y	14.00	33.16	0.42	2.37
Q6P4T2_U5	Snrnp200	U5 small nu	K.ESIEEPSAK#.I	103.92	55.00	1.89	0.53
Q6P4T2_U5	Snrnp200	U5 small nu	R.FQIM*NEIVYEK#.I	40.48	20.19	2.00	0.50
Q6P4T2_U5	Snrnp200	U5 small nu	R.FYDDAIVSQK#.K	179.55	63.33	2.84	0.35
Q6P4T2_U5	Snrnp200	U5 small nu	K.GLFYFDNSFRPVPLEQTYVGITEK.K	20.39	40.34	0.51	1.98
Q6P4T2_U5	Snrnp200	U5 small nu	R.GLIEIISNAAEYENIPIR.H	65.63	130.59	0.50	1.99
Q6P4T2_U5	Snrnp200	U5 small nu	K.GNIIISTPEK#.W	79.34	36.74	2.16	0.46
Q6P4T2_U5	Snrnp200	U5 small nu	K.GNIIISTPEKWDILSR.R	14.93	30.01	0.50	2.01
Q6P4T2_U5	Snrnp200	U5 small nu	K.GTQVYSPEK#.G	108.26	54.63	1.98	0.50
Q6P4T2_U5	Snrnp200	U5 small nu	K.GVESVFDIM*EM*EDEER.N	2.27	5.90	0.39	2.60
Q6P4T2_U5	Snrnp200	U5 small nu	R.GWAQLTDK#.T	56.14	24.07	2.33	0.43
Q6P4T2_U5	Snrnp200	U5 small nu	K.GYEEVHVPALK#PK#PFGSEEQLLPVEK#.L	32.92	12.30	2.68	0.37
Q6P4T2_U5	Snrnp200	U5 small nu	R.HLILPEK#.Y	53.44	23.84	2.24	0.45
Q6P4T2_U5	Snrnp200	U5 small nu	R.HLILPEKYPPPTELLDLQPLPVSALR.N	11.32	21.43	0.53	1.89
Q6P4T2_U5	Snrnp200	U5 small nu	R.IASHYYITNDTVQTYNQLLKPTLSEIELFR.V	9.07	14.46	0.63	1.59
Q6P4T2_U5	Snrnp200	U5 small nu	R.IVALSSSLSNAK#.D	160.43	70.51	2.28	0.44
Q6P4T2_U5	Snrnp200	U5 small nu	K.K#ADEVLEILK#.T	88.86	46.94	1.89	0.53
Q6P4T2_U5	Snrnp200	U5 small nu	K.KADEVLEILK.T	52.31	23.09	2.27	0.44
Q6P4T2_U5	Snrnp200	U5 small nu	K.KADEVLEILK#TASDDR.E	1.99	15.42	0.13	7.73
Q6P4T2_U5	Snrnp200	U5 small nu	R.KGYEEVHVPALKPKPFGSEEQLLPVEK.L	13.17	25.68	0.51	1.95
Q6P4T2_U5	Snrnp200	U5 small nu	K.KPVIVFVPSR.K	14.73	33.51	0.44	2.27
Q6P4T2_U5	Snrnp200	U5 small nu	K.LPDM*LNAEIVLGNVQNAK#.D	32.28	17.67	1.83	0.55
Q6P4T2_U5	Snrnp200	U5 small nu	R.M*DTDLETM*DLDQGGEALAPR.Q	9.98	20.44	0.49	2.05
Q6P4T2_U5	Snrnp200	U5 small nu	K.MEADPELSK#.F	33.49	18.11	1.85	0.54
Q6P4T2_U5	Snrnp200	U5 small nu	K.M*EADPELSK#.F	73.69	38.34	1.92	0.52
Q6P4T2_U5	Snrnp200	U5 small nu	R.M*QLSAELQSDTEEILSK#.A	55.29	26.94	2.05	0.49
Q6P4T2_U5	Snrnp200	U5 small nu	R.MQLSAELQSDTEEILSK#.A	17.36	28.45	0.61	1.64
Q6P4T2_U5	Snrnp200	U5 small nu	R.NALLQLTDSQIADVAR.F	15.72	27.94	0.56	1.78
Q6P4T2_U5	Snrnp200	U5 small nu	R.NIEM*TQEDVR.L	36.45	83.04	0.44	2.28
Q6P4T2_U5	Snrnp200	U5 small nu	R.NIEMTQEDVR.L	6.86	14.86	0.46	2.16
Q6P4T2_U5	Snrnp200	U5 small nu	K.NQVLVFVHSR.K	11.85	21.68	0.55	1.83
Q6P4T2_U5	Snrnp200	U5 small nu	R.SLQYEYK#.A	77.73	40.39	1.92	0.52
Q6P4T2_U5	Snrnp200	U5 small nu	R.SLVQEM*VGSFGK#.R	92.96	37.79	2.46	0.41
Q6P4T2_U5	Snrnp200	U5 small nu	K.SNSLISIK#.R	105.63	43.20	2.45	0.41
Q6P4T2_U5	Snrnp200	U5 small nu	K.TGNFQVTELGR.I	44.15	89.39	0.49	2.02
Q6P4T2_U5	Snrnp200	U5 small nu	K.VELTITPDFQWDEK#.V	71.99	32.41	2.22	0.45
Q6P4T2_U5	Snrnp200	U5 small nu	R.VFSLSSEFK#.N	174.67	74.09	2.36	0.42
Q6P4T2_U5	Snrnp200	U5 small nu	K.VVLLTGETSTDLK#.L	219.49	99.41	2.21	0.45
Q6P4T2_U5	Snrnp200	U5 small nu	K.YAQAGFEGFK#.T	194.72	91.37	2.13	0.47
Q6P4T2_U5	Snrnp200	U5 small nu	R.YHVLVNLGK#.K	21.93	12.66	1.73	0.58
Q6P4T2_U5	Snrnp200	U5 small nu	R.YPNIELSYEVVDKDSIR.S	6.43	15.02	0.43	2.33
Q6P4T2_U5	Snrnp200	U5 small nu	K.YPPPTELLDLQPLPVSALR.N	4.52	11.68	0.39	2.59
Q8K194_SN	Snrnp27	U4/U6.U5 s	K.VDGSVNAYAINVSQK#.R	5.87	3.80	1.54	0.65
Q6PE01_SN	Snrnp40	U5 small nu	R.FVYVWDTTSR.R	16.20	63.66	0.25	3.93
Q6PE01_SN	Snrnp40	U5 small nu	R.GHADSVTGLSLSSEGSYLLSNAM*DNTVR.V	7.62	17.77	0.43	2.33
Q6PE01_SN	Snrnp40	U5 small nu	K.GHSGAVM*ELHYNTDGSM*LFSASTDK#.T	7.11	3.41	2.08	0.48
Q6PE01_SN	Snrnp40	U5 small nu	K.GPELPLVPVK#.R	11.55	9.60	1.20	0.83
Q6PE01_SN	Snrnp40	U5 small nu	R.HELLLGAAGAGPGAGPQQATPGALLQAGPPR.C	17.89	52.58	0.34	2.94
Q6PE01_SN	Snrnp40	U5 small nu	K.IFQGNVHNFEK#.N	60.18	33.97	1.77	0.56
Q6PE01_SN	Snrnp40	U5 small nu	R.K#GPELPLVPVK#.R	68.04	40.79	1.67	0.60
Q6PE01_SN	Snrnp40	U5 small nu	K.LPGHAGSINEVAFHPDEPIILSASSDK.R	2.38	3.32	0.72	1.40
Q6PE01_SN	Snrnp40	U5 small nu	K.LPGHAGSINEVAFHPDEPIILSASSDKR.L	2.66	5.00	0.53	1.88
Q6PE01_SN	Snrnp40	U5 small nu	K.TVAVWDSETGER.V	20.09	58.02	0.35	2.89
Q62376_RU	Snrnp70	U1 small nu	R.DPIPYLPPLEK#.L	74.65	58.01	1.29	0.78
Q62376_RU	Snrnp70	U1 small nu	R.GGGGSGQDNGLEGLGSDGR.D	4.47	10.14	0.44	2.27
Q62376_RU	Snrnp70	U1 small nu	R.LGGGLGGTR.R	33.26	38.54	0.86	1.16
Q62376_RU	Snrnp70	U1 small nu	K.M*WDPHNDPNAQGDAFK#.T	22.41	12.10	1.85	0.54
Q62376_RU	Snrnp70	U1 small nu	R.VNYDTTESK#.L	43.78	19.46	2.25	0.44
Q62189_SN	Snrpa	U1 small nu	R.ANHTIYINNLNEK#.I	43.54	9.32	4.67	0.21
Q62189_SN	Snrpa	U1 small nu	K.KAVQGGAAAPVVGAVQPVPGM*PPM*PQAPR.I	1.93	3.23	0.60	1.67
Q62189_SN	Snrpa	U1 small nu	K.TDSDIIAK#.M	84.91	21.54	3.94	0.25
P57784_RU	Snrpa1	U2 small nu	K.GGPSAGDVEAIK#.N	45.63	23.84	1.91	0.52
P57784_RU	Snrpa1	U2 small nu	K.GLLQSGQIPGR.E	12.88	22.99	0.56	1.78
P57784_RU	Snrpa1	U2 small nu	K.LTAELIEQAAQYTNAVR.D	3.06	9.68	0.32	3.16
P57784_RU	Snrpa1	U2 small nu	K.NAIANASTLAEVER.L	11.78	28.83	0.41	2.45
P57784_RU	Snrpa1	U2 small nu	K.SLTYLSILR.N	4.61	13.22	0.35	2.87
P57784_RU	Snrpa1	U2 small nu	K.GGPSAGDVEAIK#.N	41.55	24.34	1.71	0.59
P57784_RU	Snrpa1	U2 small nu	K.GLLQSGQIPGR.E	16.19	26.22	0.62	1.62

P57784_R	Snrpa1	U2 small n	K.LTAELIEQAAQYTNAVR.D	3.92	5.32	0.74	1.36
P57784_R	Snrpa1	U2 small n	K.LTAELIEQAAQYTNAVR.D	1.82	2.99	0.61	1.65
P57784_R	Snrpa1	U2 small n	K.NAIANASTLAEVER.L	13.72	29.97	0.46	2.18
P27048_R	Snrpb	Small nucl	R.GENLVSM*TVEGPPPK#.D	6.30	3.99	1.58	0.63
P27048_R	Snrpb	Small nucl	R.IFIGTFK#.A	195.91	27.73	7.06	0.14
P27048_R	Snrpb	Small nucl	R.VLGLVLLR.G	6.56	22.80	0.29	3.48
P27048_R	Snrpb	Small nucl	R.GENLVSM*TVEGPPPK#.D	27.68	19.02	1.46	0.69
P27048_R	Snrpb	Small nucl	R.GENLVSMTVEGPPPK#.D	20.95	27.62	0.76	1.32
P27048_R	Snrpb	Small nucl	R.GENLVSM*TVEGPPPKDTGIAR.V	23.73	54.20	0.44	2.28
P27048_R	Snrpb	Small nucl	R.GENLVSMTVEGPPPKDTGIAR.V	17.56	82.39	0.21	4.69
P27048_R	Snrpb	Small nucl	R.IFIGTFK#.A	327.02	165.43	1.98	0.51
P27048_R	Snrpb	Small nucl	K.RVLGLVLLR.G	8.59	72.48	0.12	8.44
P27048_R	Snrpb	Small nucl	R.VLGLVLLR.G	86.61	189.11	0.46	2.18
P27048_R	Snrpb	Small nucl	R.VLGLVLLR.G	4.62	16.63	0.28	3.60
Q9CQI7_R	Snrpb2	U2 small n	R.DALQGFK#.I	62.02	20.62	3.01	0.33
Q9CQI7_R	Snrpb2	U2 small n	R.GQAFVIFK#.E	95.31	28.12	3.39	0.30
Q9CQI7_R	Snrpb2	U2 small n	K.TMEQAAAAANK#.K	12.27	8.93	1.37	0.73
Q62241_R	Snrpc	U1 small n	K.WM*EEQAQSLIDK.T	12.95	16.89	0.77	1.30
Q62241_R	Snrpc	U1 small n	K.WM*EEQAQSLIDKTTAAFQQGK.I	6.28	7.24	0.87	1.15
P62315_S	Snrpd1	Small nucl	R.EPVQLETLSIR.G	3.87	11.02	0.35	2.85
P62315_S	Snrpd1	Small nucl	K.LSHETVTIELK#.N	154.22	94.46	1.63	0.61
P62315_S	Snrpd1	Small nucl	K.LSHETVTIELK.N	51.45	29.71	1.73	0.58
P62315_S	Snrpd1	Small nucl	K.NGTQVHGTITGVDVSM*NTHLK.A	9.92	11.51	0.86	1.16
P62315_S	Snrpd1	Small nucl	K.NGTQVHGTITGVDVSMNTHLK#.A	9.93	3.50	2.84	0.35
P62315_S	Snrpd1	Small nucl	K.NREPVQLETLSIR.G	4.03	41.56	0.10	10.31
P62315_S	Snrpd1	Small nucl	K.NREPVQLETLSIR.G	13.20	139.24	0.09	10.55
P62315_S	Snrpd1	Small nucl	K.LSHETVTIELK.N	26.28	24.24	1.08	0.92
P62315_S	Snrpd1	Small nucl	K.NREPVQLETLSIR.G	2.22	31.15	0.07	14.04
P62317_S	Snrpd2	Small nucl	R.EEEEFNTGPLSVLTQSVK#.N	38.23	24.10	1.59	0.63
P62317_S	Snrpd2	Small nucl	R.EEEEFNTGPLSVLTQSVK#.N	25.27	20.74	1.22	0.82
P62317_S	Snrpd2	Small nucl	K.EM*WTEVPK#.S	62.04	40.11	1.55	0.65
P62317_S	Snrpd2	Small nucl	R.GDSVIVVLR.N	68.26	138.21	0.49	2.02
P62317_S	Snrpd2	Small nucl	K.M*FLRGDSVIVVLR.N	3.85	17.96	0.21	4.67
P62317_S	Snrpd2	Small nucl	R.NPLIAGK#.-	389.18	252.79	1.54	0.65
P62317_S	Snrpd2	Small nucl	K.REEEEFNTGPLSVLTQSVK.N	71.89	125.23	0.57	1.74
P62317_S	Snrpd2	Small nucl	K.SEMTPEELQK#.R	59.12	42.98	1.38	0.73
P62317_S	Snrpd2	Small nucl	K.SEM*TPEELQK#.R	175.76	97.73	1.80	0.56
P62317_S	Snrpd2	Small nucl	K.SEM*TPEELQKR.E	3.14	6.93	0.45	2.20
P62317_S	Snrpd2	Small nucl	K.SEM*TPEELQKREEEEFNTGPLSVLTQSVK.N	11.67	18.52	0.63	1.59
P62317_S	Snrpd2	Small nucl	K.SEM*TPEELQKREEEEFNTGPLSVLTQSVK.N	1.92	4.91	0.39	2.56
P62317_S	Snrpd2	Small nucl	K.SEMTPEELQKREEEEFNTGPLSVLTQSVK.N	3.01	6.52	0.46	2.17
P62317_S	Snrpd2	Small nucl	R.EEEEFNTGPLSVLTQSVK#.N	3.55	4.76	0.75	1.34
P62317_S	Snrpd2	Small nucl	R.NPLIAGK#.-	33.87	22.99	1.47	0.68
P62317_S	Snrpd2	Small nucl	K.REEEEFNTGPLSVLTQSVK.N	2.48	8.23	0.30	3.32
P62317_S	Snrpd2	Small nucl	K.SEM*TPEELQK#.R	15.62	16.23	0.96	1.04
P62320_S	Snrpd3	Small nucl	R.FLILPDM*LK#.N	308.18	188.82	1.63	0.61
P62320_S	Snrpd3	Small nucl	R.FLILPDMLK#.N	143.88	81.59	1.76	0.57
P62320_S	Snrpd3	Small nucl	R.VAQLEQVYIR.G	107.95	279.27	0.39	2.59
P62320_S	Snrpd3	Small nucl	R.FLILPDMLK#.N	32.68	24.75	1.32	0.76
P62320_S	Snrpd3	Small nucl	R.VAQLEQVYIR.G	11.37	47.32	0.24	4.16
P62305_R	Snrpe	Small nucl	K.GDNITLLQSVSN.-	7.02	7.02	1.00	1.00
P62305_R	Snrpe	Small nucl	K.VM*VQPINLIFR.Y	3.64	10.84	0.34	2.98
P62305_R	Snrpe	Small nucl	K.GDNITLLQSVSN.-	87.42	87.42	1.00	1.00
P62305_R	Snrpe	Small nucl	R.IM*LK#GDNITLLQSVSN.-	38.45	22.72	1.69	0.59
P62305_R	Snrpe	Small nucl	R.IMLK#GDNITLLQSVSN.-	7.28	3.10	2.35	0.43
P62305_R	Snrpe	Small nucl	R.IQVWLYEQVNM*R.I	4.80	15.56	0.31	3.24
P62305_R	Snrpe	Small nucl	K.VM*VQPINLIFR.Y	118.47	302.96	0.39	2.56
P62305_R	Snrpe	Small nucl	K.VMVQPINLIFR.Y	18.32	49.37	0.37	2.69
P62305_R	Snrpe	Small nucl	K.GDNITLLQSVSN.-	14.81	14.81	1.00	1.00
P62305_R	Snrpe	Small nucl	K.VM*VQPINLIFR.Y	11.22	42.17	0.27	3.76
P62305_R	Snrpe	Small nucl	K.VMVQPINLIFR.Y	7.21	25.30	0.29	3.51
P62305_R	Snrpe	Small nucl	K.VM*VQPINLIFR.Y	1.91	7.92	0.24	4.16
P62307_R	Snrpf	Small nucl	R.GVEEEEEDGEM*RE.-	14.63	31.16	0.47	2.13
P62307_R	Snrpf	Small nucl	R.GVEEEEEDGEMRE.-	5.02	13.77	0.36	2.74
P62307_R	Snrpf	Small nucl	R.GVEEEEEDGEM*RE.-	4.05	15.78	0.26	3.90
P62309_R	Snrpg	Small nucl	R.GNSIIM*LEALER.V	10.72	29.81	0.36	2.78
P62309_R	Snrpg	Small nucl	R.GNSIIMLEALER.V	3.17	7.97	0.40	2.52
P62309_R	Snrpg	Small nucl	R.GNSIIM*LEALERV.-	7.50	11.35	0.66	1.51
P62309_R	Snrpg	Small nucl	R.GNSIIMLEALERV.-	11.72	25.73	0.46	2.20
Q61234_S	Snta1	Alpha-1-sy	R.HGVDTHLFSVESPQELAAWTR.Q	2.06	3.86	0.53	1.88
Q61234_S	Snta1	Alpha-1-sy	R.K#ADAGGLGISIK#.G	7.81	3.63	2.15	0.46
Q61235_S	Sntb2	Beta-2-synt	K.K#PSLVSDLPWEGASPQSPSFSGSEDSGSPK#.H	1.89	2.69	0.70	1.42
Q61235_S	Sntb2	Beta-2-synt	R.SPSLGSDLTFATR.T	2.39	5.54	0.43	2.32
Q61235_S	Sntb2	Beta-2-synt	K.K#PSLVSDLPWEGASPQSPSFSGSEDSGSPK#.H	4.61	3.06	1.51	0.66
Q9CSN1_S	Snw1	SNW doma	R.GREGPVQFEEDPFGLDKFLEEAK.Q	1.29	9.39	0.14	7.25
Q9CSN1_S	Snw1	SNW doma	K.LAEALYIADR.K	6.85	35.66	0.19	5.21
Q9CSN1_S	Snw1	SNW doma	K.LAEALYIADRK.A	7.38	26.45	0.28	3.59
Q9CSN1_S	Snw1	SNW doma	R.LLEDFGDGGAFPEIHVAQYPLDM*GR.K	5.38	18.28	0.29	3.40
Q9CSN1_S	Snw1	SNW doma	R.LLEDFGDGGAFPEIHVAQYPLDMGR.K	2.97	13.85	0.21	4.66
Q9CSN1_S	Snw1	SNW doma	K.M*SNALAIQVDPEGK.I	22.71	24.81	0.92	1.09
Q9CSN1_S	Snw1	SNW doma	K.MSNALAIQVDPEGK#.I	9.95	9.78	1.02	0.98
Q9CSN1_S	Snw1	SNW doma	R.SLQTSLVSSR.R	13.92	53.30	0.26	3.83
Q9CSN1_S	Snw1	SNW doma	R.TSNEVQYDQR.L	10.46	42.31	0.25	4.04
Q9CSN1_S	Snw1	SNW doma	K.VAAAMPVR.A	5.84	24.20	0.24	4.15
Q9CSN1_S	Snw1	SNW doma	K.YTDLVPK#.E	17.53	205.41	0.09	11.72
Q9CSN1_S	Snw1	SNW doma	R.YTPSQQGVAFNSGAK.Q	60.37	63.93	0.94	1.06
Q9CSN1_S	Snw1	SNW doma	R.DISEVIALGVPNPR.T	5.39	12.61	0.43	2.34
Q9CSN1_S	Snw1	SNW doma	K.LAEALYIADR.K	45.52	22.61	2.01	0.50
Q9CSN1_S	Snw1	SNW doma	R.LLEDFGDGGAFPEIHVAQYPLDM*GR.K	3.10	10.28	0.30	3.31
Q9CSN1_S	Snw1	SNW doma	R.LLEDFGDGGAFPEIHVAQYPLDMGR.K	2.11	9.48	0.22	4.48
Q9CSN1_S	Snw1	SNW doma	K.M*SNALAIQVDPEGK#.I	6.79	9.24	0.73	1.36
Q9CSN1_S	Snw1	SNW doma	R.SLQTSLVSSR.R	19.70	50.19	0.39	2.55
Q9CSN1_S	Snw1	SNW doma	R.TSNEVQYDQR.L	5.75	16.22	0.35	2.82
Q9WV80_S	Snx1	Sorting nex	R.ALSQLAEVEEK#.I	54.08	23.65	2.29	0.44
Q9WV80_S	Snx1	Sorting nex	R.AVGTQALSGAGLLK#.M	69.76	29.44	2.37	0.42
Q9WV80_S	Snx1	Sorting nex	K.EDSSSAEFLEK#.R	18.27	4.86	3.76	0.27
Q9WV80_S	Snx1	Sorting nex	K.ELALNTALFAK#.S	31.15	15.15	2.06	0.49
Q9WV80_S	Snx1	Sorting nex	R.FSDFLGLYEK#.L	26.86	12.95	2.07	0.48
Q9WV80_S	Snx1	Sorting nex	K.IGDGM*NAYVAYK#.V	12.87	8.09	1.59	0.63
Q9WV80_S	Snx1	Sorting nex	R.LLWANK#PDK#.L	12.96	6.41	2.02	0.49
Q9WV80_S	Snx1	Sorting nex	K.M*NESDIWFEEK#.L	11.95	4.87	2.45	0.41
Q9WV80_S	Snx1	Sorting nex	K.SLAM*LGSSEDNTALSR.A	4.29	10.40	0.41	2.42
Q9WV80_S	Snx1	Sorting nex	K.VGK#EDSSSAEFLEK#.R	7.60	3.69	2.06	0.49

Q9WV80_S	Snx1	Sorting nex	R.WQDAQATLQK#.K	51.59	21.28	2.42	0.41
Q9WV80_S	Snx1	Sorting nex	K.YWEAFLPEAK#.A	54.25	18.14	2.99	0.33
Q9WV80_S	Snx1	Sorting nex	R.ALSQLAEVEEK#.I	7.89	3.62	2.18	0.46
Q9WV80_S	Snx1	Sorting nex	R.AVGTQALSGAGLLK#.M	7.82	4.72	1.66	0.60
Q9WV80_S	Snx1	Sorting nex	R.FSDFLGLYEK#.L	8.52	3.60	2.37	0.42
Q9WV80_S	Snx1	Sorting nex	K.M*NESDIWFEEK#.L	1.85	2.17	0.85	1.17
Q9WV80_S	Snx1	Sorting nex	K.SLAM*LGSSEDNTALSR.A	1.28	4.23	0.30	3.31
Q9WV80_S	Snx1	Sorting nex	R.ALSQLAEVEEK#.I	97.72	27.29	3.58	0.28
Q9WV80_S	Snx1	Sorting nex	R.AVGTQALSGAGLLK#.M	39.62	16.84	2.35	0.42
Q9WV80_S	Snx1	Sorting nex	K.ELALNTALFAK#.S	24.02	10.38	2.31	0.43
Q9WV80_S	Snx1	Sorting nex	R.FSDFLGLYEK#.L	24.19	12.61	1.92	0.52
Q9WV80_S	Snx1	Sorting nex	K.SLAM*LGSSEDNTALSR.A	3.62	6.36	0.57	1.76
Q9WV80_S	Snx1	Sorting nex	K.VGK#EDSSSAEFLEK#.R	18.77	8.05	2.33	0.43
Q9WV80_S	Snx1	Sorting nex	R.WQDAQATLQK#.K	21.76	7.12	3.05	0.33
Q9WV80_S	Snx1	Sorting nex	K.YWEAFLPEAK#.A	45.57	17.82	2.56	0.39
Q9WV80_S	Snx1	Sorting nex	R.ALSQLAEVEEK#.I	14.20	4.54	3.13	0.32
O70493_S	Snx12	Sorting nex	R.GDEGIFEESFIEER.R	6.46	18.13	0.36	2.81
O70493_S	Snx12	Sorting nex	R.LNSKPQDLTDAYGPPSNFLEIDIFNPQTVGVGR.A	2.40	13.76	0.17	5.74
O70493_S	Snx12	Sorting nex	R.RLNSKPQDLTDAYGPPSNFLEIDIFNPQTVGVGR.A	1.71	10.75	0.16	6.28
O70493_S	Snx12	Sorting nex	R.RQGLEQFINK.I	10.07	29.96	0.34	2.98
O70493_S	Snx12	Sorting nex	R.TNLPIFK#.L	48.92	47.54	1.03	0.97
O70493_S	Snx12	Sorting nex	R.YSDFEWLK#.N	5.89	4.36	1.35	0.74
O70493_S	Snx12	Sorting nex	R.YSDFEWLKNELER.D	7.00	34.84	0.20	4.98
Q8BVL3_S	Snx17	Sorting nex	K.VLVTVLTSDQTEDVLEAVAAK#.L	7.55	5.30	1.42	0.70
Q8C788_Q	Snx18	Sorting nex	K.SGGEAFVLGEASGFVK#.D	9.29	6.97	1.33	0.75
Q8C788_Q	Snx18	Sorting nex	R.APEPGPPADGGPGAPAR.Y	2.81	19.22	0.15	6.83
Q8C788_Q	Snx18	Sorting nex	R.GLFPASYVQVIR.A	8.62	28.00	0.31	3.25
Q8C788_Q	Snx18	Sorting nex	K.SENPGEISLR.E	6.28	24.58	0.26	3.91
Q8C788_Q	Snx18	Sorting nex	K.SGGEAFVLGEASGFVK#.D	21.79	16.70	1.30	0.77
Q9CWK8_S	Snx2	Sorting nex	R.AVNTQALSGAGILR.M	14.58	19.30	0.76	1.32
Q9CWK8_S	Snx2	Sorting nex	K.EDSSSTEFVEK#.R	15.00	2.73	5.49	0.18
Q9CWK8_S	Snx2	Sorting nex	R.ELILSSEPSPAVTPVTPTTLIAPR.I	6.48	16.92	0.38	2.61
Q9CWK8_S	Snx2	Sorting nex	K.M*NESDAWFEEK#.Q	17.39	3.30	5.27	0.19
Q9CWK8_S	Snx2	Sorting nex	K.VGK#EDSSSTEFVEK#.R	27.25	5.94	4.59	0.22
Q9CWK8_S	Snx2	Sorting nex	K.WEDAQITLLK#.K	33.88	6.96	4.87	0.21
Q9CWK8_S	Snx2	Sorting nex	K.YLESLVQTQQQLIK#.Y	21.67	5.85	3.71	0.27
Q78ZM0_Q	Snx3	Sorting nex	R.FTTYEIR.V	11.60	64.49	0.18	5.56
Q78ZM0_Q	Snx3	Sorting nex	R.GDDGIFDDNFIEER.K	10.08	45.98	0.22	4.56
Q78ZM0_Q	Snx3	Sorting nex	R.K#QGLEQFINK#.V	56.08	56.74	0.99	1.01
Q78ZM0_Q	Snx3	Sorting nex	R.KQGLEQFINK.V	67.63	60.11	1.13	0.89
Q78ZM0_Q	Snx3	Sorting nex	R.QLPFRGDDGIFDDNFIEER.K	2.49	29.32	0.09	11.76
Q78ZM0_Q	Snx3	Sorting nex	R.VKTNLPIFK.L	6.48	5.27	1.23	0.81
Q78ZM0_Q	Snx3	Sorting nex	R.YSDFEWLR.S	14.89	73.08	0.20	4.91
Q91YJ2_SN	Snx4	Sorting nex	R.DK#IFYSFLTQEGNWK#.E	8.26	3.41	2.42	0.41
Q91YJ2_SN	Snx4	Sorting nex	K.ETVNETGFQLK#.A	39.35	16.64	2.37	0.42
Q91YJ2_SN	Snx4	Sorting nex	R.HYSDELQSVISHLLR.V	15.82	24.48	0.65	1.55
Q91YJ2_SN	Snx4	Sorting nex	K.IFYSFLTQEGNWK#.E	11.66	5.56	2.10	0.48
Q91YJ2_SN	Snx4	Sorting nex	R.K#HELMQYDLETAAQDLAAK#.K	9.49	4.53	2.10	0.48
Q91YJ2_SN	Snx4	Sorting nex	K.LFGQETPEQR.E	14.70	23.95	0.61	1.63
Q91YJ2_SN	Snx4	Sorting nex	K.LLQPGPLEPLGGPGAVLEAAVGEENEGTREDGSGVDTM*TGNNFWLK.K	1.90	5.20	0.37	2.73
Q91YJ2_SN	Snx4	Sorting nex	K.LSADNM*DPDFVER.R	4.70	12.83	0.37	2.73
Q91YJ2_SN	Snx4	Sorting nex	R.NAVNMQETYTAYLIETR.S	2.71	2.43	1.12	0.89
Q91YJ2_SN	Snx4	Sorting nex	R.NYLLVYYPHVVVPPLPEK#.R	9.53	7.85	1.21	0.82
Q91YJ2_SN	Snx4	Sorting nex	R.VGLENFLLR.V	18.59	37.54	0.50	2.02
Q91YJ2_SN	Snx4	Sorting nex	K.VLEEQINEGEQQLK#.S	51.00	20.90	2.44	0.41
Q9D8U8_S	Snx5	Sorting nex	K.ALIDYENSNK#.A	32.44	12.91	2.51	0.40
Q9D8U8_S	Snx5	Sorting nex	K.EVDDFFEQEK#.N	34.96	9.88	3.54	0.28
Q9D8U8_S	Snx5	Sorting nex	K.LGEGEGSM*TK#.E	7.29	3.47	2.10	0.48
Q9D8U8_S	Snx5	Sorting nex	K.LGEGEGSMTK#.E	15.66	6.83	2.29	0.44
Q9D8U8_S	Snx5	Sorting nex	K.M*K#QELEAEYLAVFK#.K	12.35	7.91	1.56	0.64
Q9D8U8_S	Snx5	Sorting nex	K.SADEVLFSGVK#.E	41.24	20.68	1.99	0.50
Q9D8U8_S	Snx5	Sorting nex	K.TTLSTFQSPEFSVTR.Q	17.81	32.18	0.55	1.81
Q9D8U8_S	Snx5	Sorting nex	K.TVSTHEVFLQR.L	3.67	8.65	0.42	2.35
Q9D8U8_S	Snx5	Sorting nex	K.VAELFEK#.L	38.73	13.62	2.84	0.35
Q9D8U8_S	Snx5	Sorting nex	R.YYMLNIEAAK#.D	17.74	5.83	3.04	0.33
Q6P8X1_S	Snx6	Sorting nex	K.LGEGEGSM*TK#EEFTK#.M	13.24	2.70	4.90	0.20
Q6P8X1_S	Snx6	Sorting nex	K.M*K#QELEAEYLAIFK#.K	19.48	4.39	4.44	0.23
Q6P8X1_S	Snx6	Sorting nex	K.NLVELAELELK#.H	67.65	19.52	3.47	0.29
Q6P8X1_S	Snx6	Sorting nex	K.SADGVIVSGVK#.D	50.76	22.54	2.25	0.44
Q6P8X1_S	Snx6	Sorting nex	R.SLVDYENANK#.A	67.21	23.25	2.89	0.35
Q6P8X1_S	Snx6	Sorting nex	R.VSADEDLK#.L	60.85	16.73	3.64	0.27
Q6P8X1_S	Snx6	Sorting nex	K.NLVELAELELK#.H	7.84	1.27	6.18	0.16
F8WI30_F	Snx7	Sorting nex	K.GK#LEEAHPTLIIPPLPEK#.F	17.49	8.99	1.94	0.51
F8WI30_F	Snx7	Sorting nex	R.IADHPTLTFNEDFK#.V	28.75	15.96	1.80	0.56
F8WI30_F	Snx7	Sorting nex	K.INLIDK#.I	33.65	14.52	2.32	0.43
F8WI30_F	Snx7	Sorting nex	R.LASGSSELAVGESPR.G	10.10	25.07	0.40	2.48
F8WI30_F	Snx7	Sorting nex	R.SAFTDTAEQNIR.Y	11.98	26.28	0.46	2.19
F8WI30_F	Snx7	Sorting nex	K.VEALTYK#.K	21.86	4.95	4.42	0.23
F8WI30_F	Snx7	Sorting nex	K.VFLTAQAEELSSYK#.K	11.97	5.34	2.24	0.45
Q8CFD4_S	Snx8	Sorting nex	R.AIDNAADLLIFGK#.E	13.79	7.51	1.84	0.54
Q91VH2_S	Snx9	Sorting nex	K.ALQSLAAVFSSSGYQGETDLNDAITEAGK#.T	7.60	2.77	2.74	0.36
Q91VH2_S	Snx9	Sorting nex	R.LYLEQQVQFYETIAEK#.L	3.21	1.97	1.63	0.61
Q91VH2_S	Snx9	Sorting nex	K.FGSAIPIPSLPDK#.Q	73.03	21.47	3.40	0.29
Q91VH2_S	Snx9	Sorting nex	R.LYLEQQVQFYETIAEK#.L	9.24	2.93	3.16	0.32
Q91VH2_S	Snx9	Sorting nex	K.TYEEIASLVAEQPK#.K	14.69	2.73	5.38	0.19
P09671_S	Sod2	Superoxide	K.GDVTTQVALQPALK#.F	7.46	1.31	5.71	0.18
Q9QX47_S	Son	Protein SO	R.AGIEGPLLASEVER.D	6.10	25.85	0.24	4.24
Q9QX47_S	Son	Protein SO	K.GFEFVTASALISESK#.Y	10.02	9.95	1.01	0.99
Q9QX47_S	Son	Protein SO	R.AGIEGPLLASEVER.D	4.81	32.39	0.15	6.74
Q9QX47_S	Son	Protein SO	K.GM*NLLGGDENLGPEVGM*QETLLHPGEEPR.D	3.13	9.82	0.32	3.13
Q9QX47_S	Son	Protein SO	K.GM*NLLGGDENLGPEVGMQETLLHPGEEPR.D	2.26	3.23	0.70	1.43
Q9QX47_S	Son	Protein SO	K.GMNLLGGDENLGPEVGMQETLLHPGEEPR.D	2.13	6.21	0.34	2.92
Q9QX47_S	Son	Protein SO	K.IEEVLSGVLDTELR.Y	4.83	33.60	0.14	6.95
Q9QX47_S	Son	Protein SO	R.LAQDPYR.L	103.58	130.33	0.79	1.26
Q9QX47_S	Son	Protein SO	R.LGQDPYR.L	4.26	49.14	0.09	11.53
Q9QX47_S	Son	Protein SO	R.LPEQPVEAPSEIADSSMTRPQESLELPK.T	4.90	38.48	0.13	7.85
Q9QX47_S	Son	Protein SO	R.SEGQLNGETNPPIEGNQAGDTAASAR.S	1.24	7.51	0.17	6.04
Q9QX47_S	Son	Protein SO	K.SGGATIEELTEK.C	12.95	14.58	0.89	1.13
Q9QX47_S	Son	Protein SO	K.SLETM*PPETSK.T	28.36	29.75	0.95	1.05
Q9QX47_S	Son	Protein SO	R.SLPNEEIVQK#.I	26.39	36.12	0.73	1.37
Q9QX47_S	Son	Protein SO	R.SLSSQLALELDTVGTSK.G	13.70	17.91	0.77	1.31
Q9QX47_S	Son	Protein SO	R.SM*M*M*SYAAER.S	2.99	9.20	0.32	3.08
Q9QX47_S	Son	Protein SO	R.SM*M*SPM*AER.S	3.12	15.01	0.21	4.81

Q9QX47_S	Son	Protein SO	R.SM*M*SSYSAADR.S	8.94	26.24	0.34	2.93
Q9QX47_S	Son	Protein SO	K.SPEPVVTMSVEYQK.S	11.73	18.75	0.63	1.60
Q9QX47_S	Son	Protein SO	K.TTLVELPIAK#.V	75.43	87.18	0.87	1.16
O89090_S	Sp1	Transcripti	R.VGGLQGSDSLNIQQNQTSGGSLQGSQQK#.E	21.44	9.37	2.29	0.44
E9PUD1_E	Spag9	C-Jun-amin	K.AGSSAQEPSSQTPLK#.S	10.17	1.54	6.62	0.15
E9PUD1_E	Spag9	C-Jun-amin	R.DGGSVVGASVFYK#.D	12.35	5.69	2.17	0.46
E9PUD1_E	Spag9	C-Jun-amin	R.EVENLILENTQLLETK#.N	13.44	3.68	3.65	0.27
E9PUD1_E	Spag9	C-Jun-amin	R.SSTLSQLPGDK#.S	20.83	6.72	3.10	0.32
E9PUD1_E	Spag9	C-Jun-amin	R.VQAFGWSLPQK#.Y	8.72	1.28	6.79	0.15
E9PUD1_E	Spag9	C-Jun-amin	K.AGSSAQEPSSQTPLK#.S	21.28	2.54	8.37	0.12
E9PUD1_E	Spag9	C-Jun-amin	R.DGGSVVGASVFYK#.D	17.35	6.19	2.80	0.36
E9PUD1_E	Spag9	C-Jun-amin	R.ETDYPAGEELSESGQVDK#.A	19.04	3.95	4.83	0.21
E9PUD1_E	Spag9	C-Jun-amin	R.EVENLILENTQLLETK#.N	24.27	4.55	5.33	0.19
E9PUD1_E	Spag9	C-Jun-amin	K.FFVAVPGQVISPQSSSGGADLTADK#.A	15.75	3.39	4.65	0.22
E9PUD1_E	Spag9	C-Jun-amin	K.IYVVQPK#.A	23.01	4.10	5.61	0.18
E9PUD1_E	Spag9	C-Jun-amin	R.M*GDEGGESELLGEDLPLEPSVTK#.A	4.13	1.80	2.29	0.44
E9PUD1_E	Spag9	C-Jun-amin	R.SHTSLK#DELSDISQGGSK#.A	20.54	5.86	3.51	0.29
E9PUD1_E	Spag9	C-Jun-amin	R.VQAFGWSLPQK#.Y	14.26	3.03	4.70	0.21
P07214_S	Sparc	SPARC OS=	K.NVLVTLYER.D	3.02	20.01	0.15	6.62
Q9QYY8_S	Spast	Spastin OS=	K.FDDIAGQELAK#.Q	10.68	5.23	2.04	0.49
Q3UMC0_S	Spata5	Spermatog	K.AGEVLLDVTQSPR.D	2.26	13.82	0.16	6.13
Q3UMC0_S	Spata5	Spermatog	K.ALANESGLNFLAIK#.G	13.35	14.04	0.95	1.05
Q3UMC0_S	Spata5	Spermatog	R.DGSGLGLEESTGLK#.C	9.66	8.29	1.16	0.86
Q3UMC0_S	Spata5	Spermatog	K.EGAEGASPSLSAAPSR.S	7.50	4.33	1.73	0.58
Q3UMC0_S	Spata5	Spermatog	R.EVAIDVPNVSWSDIGGLENIK#.L	4.67	5.27	0.89	1.13
Q3UMC0_S	Spata5	Spermatog	R.SGTSTPFAQPSPAAPGMLVVTNFLEK#.V	10.86	10.10	1.08	0.93
Q8K1N4_S	Spats2	Spermatog	K.SAPIQEEQPASSEK#.G	23.95	18.78	1.28	0.78
Q8K1N4_S	Spats2	Spermatog	K.SK#PK#PASEASGSAPDSSK#.S	7.35	8.10	0.91	1.10
Q8K1N4_S	Spats2	Spermatog	K.SK#PK#PASEASGSAPDSSK#.S	2.87	1.51	1.90	0.53
Q8K1N4_S	Spats2	Spermatog	K.SAPIQEEQPASSEK#.G	31.87	18.54	1.72	0.58
Q9D083_S	Spc24	Kinetochor	R.QGDTELQQLEVELQR.T	1.13	6.10	0.18	5.42
Q9D083_S	Spc24	Kinetochor	R.QLITELQELR.E	2.41	10.42	0.23	4.33
Q3UA16_S	Spc25	Kinetochor	K.GK#EQESEELTAK#.I	4.05	2.62	1.54	0.65
Q3UA16_S	Spc25	Kinetochor	K.LQFIFTSIDPK#.N	14.07	18.87	0.75	1.34
Q6ZWQ7_	Spcs3	Signal pept	K.NNALNQVVLWDK#.I	7.95	7.69	1.03	0.97
Q2KN98_C	Specc1l	Cytospin-A	K.SFDSASQVPNAAAAAIPR.T	4.35	5.18	0.84	1.19
Q8R1X6_S	Spg20	Spartin OS=	R.NDLQDVPK#.L	14.72	10.14	1.45	0.69
Q8R1X6_S	Spg20	Spartin OS=	K.VAHNILSGASWVSWGLVK#.G	6.96	1.56	4.46	0.22
Q61142_S	Spin1	Spindlin-1	K.GTVLDQVPVNPSLYLIK#.Y	6.70	14.65	0.46	2.19
Q61142_S	Spin1	Spindlin-1	R.VSALEVLPDR.V	109.20	11.82	9.24	0.11
Q61142_S	Spin1	Spindlin-1	K.GTVLDQVPVNPSLYLIK.Y	4.70	9.89	0.48	2.10
Q61142_S	Spin1	Spindlin-1	R.VSALEVLPDR.V	3.37	8.81	0.38	2.61
P08032_S	Spta1	Spectrin al	-.M*ETPK#ETAVESSGPK#VLETAEEIQHR.R	0.00	0.00	#DIV/0!	#DIV/0!
P08032_S	Spta1	Spectrin al	K.ADVVESWIGEK#.E	46.83	18.74	2.50	0.40
P08032_S	Spta1	Spectrin al	K.EASLKTK.S	17.63	8.33	2.12	0.47
P16546_S	Sptan1	Spectrin al	K.IAALQAFADQLIAVDHYAK#.G	21.09	6.74	3.13	0.32
P16546_S	Sptan1	Spectrin al	R.AGTFQAFEQFGQQLLAHGHYASPEIK#.E	137.35	56.66	2.42	0.41
P16546_S	Sptan1	Spectrin al	K.AINVQEEK#.I	169.75	68.82	2.47	0.41
P16546_S	Sptan1	Spectrin al	K.AK#LDENSAFLQFNWK#.A	12.51	6.64	1.88	0.53
P16546_S	Sptan1	Spectrin al	K.ALINADELANDVAGAEALLDR.H	68.18	141.68	0.48	2.08
P16546_S	Sptan1	Spectrin al	R.ALSSEGKPYVTKEELYQNLTR.E	6.24	14.06	0.44	2.25
P16546_S	Sptan1	Spectrin al	K.ASAFNSWFENAEEDLTDPVR.C	7.04	12.37	0.57	1.76
P16546_S	Sptan1	Spectrin al	R.DADETK#EWIEEK#.N	59.40	33.76	1.76	0.57
P16546_S	Sptan1	Spectrin al	R.DADETKEWIEEK.N	31.49	19.28	1.63	0.61
P16546_S	Sptan1	Spectrin al	R.DAEELEK#WIQEK#.L	12.47	6.06	2.06	0.49
P16546_S	Sptan1	Spectrin al	R.DLAALEDK#VK#.A	82.14	40.95	2.01	0.50
P16546_S	Sptan1	Spectrin al	R.DLAALGDK#.V	43.79	19.38	2.26	0.44
P16546_S	Sptan1	Spectrin al	R.DLAALGDKVNSLGETAQR.L	16.48	44.63	0.37	2.71
P16546_S	Sptan1	Spectrin al	K.DLASVNNLLK#.K	18.91	10.44	1.81	0.55
P16546_S	Sptan1	Spectrin al	R.DLASVQALLR.K	35.78	41.01	0.87	1.15
P16546_S	Sptan1	Spectrin al	K.DLIGVQNLLK#.K	41.32	14.99	2.76	0.36
P16546_S	Sptan1	Spectrin al	K.DLNSQADSLM*TSSAFDTSQVK#.E	15.12	8.54	1.77	0.56
P16546_S	Sptan1	Spectrin al	K.DLNSQADSLM*TSSAFDTSQVK#.E	7.92	4.30	1.84	0.54
P16546_S	Sptan1	Spectrin al	K.DLNSQADSLMTSSAFDTSQVK#.E	6.65	2.33	2.86	0.35
P16546_S	Sptan1	Spectrin al	R.DLSSVQTLLTK#.Q	145.74	68.45	2.13	0.47
P16546_S	Sptan1	Spectrin al	R.DLTGVQNLR.K	38.04	63.75	0.60	1.68
P16546_S	Sptan1	Spectrin al	K.DLTNVQNLQK#.K	70.61	28.31	2.49	0.40
P16546_S	Sptan1	Spectrin al	R.DLTSWVTEM*K#.A	43.07	20.47	2.10	0.48
P16546_S	Sptan1	Spectrin al	R.DLTSWVTEMK#.A	36.04	14.31	2.52	0.40
P16546_S	Sptan1	Spectrin al	K.DQLLAAK#.H	34.01	16.83	2.02	0.49
P16546_S	Sptan1	Spectrin al	R.DSDELK#SWVNEK#.M	16.26	5.49	2.96	0.34
P16546_S	Sptan1	Spectrin al	R.DTEQVDNWM*SK#.Q	36.11	19.70	1.83	0.55
P16546_S	Sptan1	Spectrin al	R.DTEQVDNWMSK#.Q	10.65	4.80	2.22	0.45
P16546_S	Sptan1	Spectrin al	R.DVDEIEAWISEK#.L	93.76	43.96	2.13	0.47
P16546_S	Sptan1	Spectrin al	R.DVDETIGWIK#.E	65.67	22.79	2.88	0.35
P16546_S	Sptan1	Spectrin al	R.DVEDEETWIR.E	16.85	37.42	0.45	2.22
P16546_S	Sptan1	Spectrin al	K.EAALTNEEVGADLEQVEVLQK#.K	114.67	42.64	2.69	0.37
P16546_S	Sptan1	Spectrin al	R.EAFLNTEDK#GDSLDSVEALIK#.K	188.54	75.32	2.50	0.40
P16546_S	Sptan1	Spectrin al	R.EANELQQWITEK#.E	91.93	45.02	2.04	0.49
P16546_S	Sptan1	Spectrin al	R.EANQQQQFNR.N	13.26	30.51	0.43	2.30
P16546_S	Sptan1	Spectrin al	R.EELITNWEQIR.T	3.75	11.33	0.33	3.02
P16546_S	Sptan1	Spectrin al	R.ELPTAFDYVEFTR.S	20.63	36.26	0.57	1.76
P16546_S	Sptan1	Spectrin al	R.ENLLEEQGSIALR.Q	29.00	62.05	0.47	2.14
P16546_S	Sptan1	Spectrin al	K.EQLM*ASDDFGR.D	4.58	9.24	0.50	2.02
P16546_S	Sptan1	Spectrin al	R.FLADFR.D	18.58	38.88	0.48	2.09
P16546_S	Sptan1	Spectrin al	R.FLSDFR.D	12.20	38.27	0.32	3.14
P16546_S	Sptan1	Spectrin al	R.FNRDVDETIGWIK.E	6.26	11.66	0.54	1.86
P16546_S	Sptan1	Spectrin al	R.GK#DLIGVQNLLK#.K	45.38	17.97	2.52	0.40
P16546_S	Sptan1	Spectrin al	R.GLVSSDELAK#.D	56.78	23.06	2.46	0.41
P16546_S	Sptan1	Spectrin al	K.GNAM*VEEGHFAAEDVK#.A	81.64	32.16	2.54	0.39
P16546_S	Sptan1	Spectrin al	R.GVIDM*GNSLIER.G	16.97	41.75	0.41	2.46
P16546_S	Sptan1	Spectrin al	R.GVIDMGNSLIER.G	8.22	21.16	0.39	2.57
P16546_S	Sptan1	Spectrin al	K.HEAFETDFTVHK#.D	16.08	11.36	1.42	0.71
P16546_S	Sptan1	Spectrin al	K.HQAFEAELHANADR.I	26.87	59.76	0.45	2.22
P16546_S	Sptan1	Spectrin al	K.HQAFEAELSANQSR.I	28.60	37.86	0.76	1.32
P16546_S	Sptan1	Spectrin al	K.HQAFEAEVQANSGAIVK#.L	44.46	18.98	2.34	0.43
P16546_S	Sptan1	Spectrin al	K.HQALQAEIAGHEPR.I	22.32	44.09	0.51	1.98
P16546_S	Sptan1	Spectrin al	K.HQLLEADISAHEDR.L	18.61	29.48	0.63	1.58
P16546_S	Sptan1	Spectrin al	K.IAALQAFADQLIAVDHYAK#.G	354.27	163.09	2.17	0.46
P16546_S	Sptan1	Spectrin al	R.IDGITIQAR.Q	12.42	20.36	0.61	1.64
P16546_S	Sptan1	Spectrin al	K.IEDLGAAM*EEALILDNK#.Y	8.20	3.75	2.19	0.46
P16546_S	Sptan1	Spectrin al	K.ITALDEFATK#.L	145.46	63.29	2.30	0.44
P16546_S	Sptan1	Spectrin al	K.K#FDDFQK#.D	76.89	40.44	1.90	0.53

P16546_SP	Sptan1	Spectrin alp	K.KFEEFQTDLAAHEER.V	8.15	25.43	0.32	3.12
P16546_SP	Sptan1	Spectrin alp	K.K#GDILTLLNSTNK#.D	6.09	3.45	1.77	0.57
P16546_SP	Sptan1	Spectrin alp	K.K#GDILTLLNSTNK#DWWK#.V	27.10	12.70	2.13	0.47
P16546_SP	Sptan1	Spectrin alp	K.K#IEDLGAAM*EEALILDNK#.Y	28.05	9.70	2.89	0.35
P16546_SP	Sptan1	Spectrin alp	K.K#LLEATELK#.G	32.90	13.14	2.50	0.40
P16546_SP	Sptan1	Spectrin alp	K.KLSDDNTIGQEEIQQR.L	4.82	10.27	0.47	2.13
P16546_SP	Sptan1	Spectrin alp	R.K#VEDLFLTFAK#.K	62.18	27.28	2.28	0.44
P16546_SP	Sptan1	Spectrin alp	R.KVEDLFLTFAK.K	56.43	30.95	1.82	0.55
P16546_SP	Sptan1	Spectrin alp	R.LAALADQWQFLVQK#.S	117.19	53.52	2.19	0.46
P16546_SP	Sptan1	Spectrin alp	K.LDENSAFLQFNWK.A	33.73	16.16	2.09	0.48
P16546_SP	Sptan1	Spectrin alp	K.LDETGNLM*ISEGHFASETIR.T	16.29	24.60	0.66	1.51
P16546_SP	Sptan1	Spectrin alp	R.LEAELAAHEPAIQGVLDTGK#.K	18.96	7.37	2.57	0.39
P16546_SP	Sptan1	Spectrin alp	R.LEESLEYQQFVANVEEEEAWINEK#.M	39.55	14.17	2.79	0.36
P16546_SP	Sptan1	Spectrin alp	K.LFGAAEVQR.F	39.40	69.89	0.56	1.77
P16546_SP	Sptan1	Spectrin alp	K.LGDSHDLQR.F	10.18	20.27	0.50	1.99
P16546_SP	Sptan1	Spectrin alp	K.LGESQTLQQFSR.D	14.51	46.23	0.31	3.19
P16546_SP	Sptan1	Spectrin alp	R.LIQSHPESAEDLK#.E	36.79	15.03	2.45	0.41
P16546_SP	Sptan1	Spectrin alp	R.LK#DLNSQADSLM*TSSAFDTSQVK#.E	33.49	14.67	2.28	0.44
P16546_SP	Sptan1	Spectrin alp	R.LK#DLNSQADSLMTSSAFDTSQVK#.E	12.59	4.16	3.03	0.33
P16546_SP	Sptan1	Spectrin alp	K.LLEATELK#.G	89.97	37.37	2.41	0.42
P16546_SP	Sptan1	Spectrin alp	K.LLVSSEDYGR.D	14.74	42.71	0.35	2.90
P16546_SP	Sptan1	Spectrin alp	R.LQQSHPLSASQIQVK#.R	111.49	54.14	2.06	0.49
P16546_SP	Sptan1	Spectrin alp	K.LQTASDESYKDPTNIQSK.H	194.30	104.47	1.86	0.54
P16546_SP	Sptan1	Spectrin alp	K.LSDDNTIGQEEIQQR.L	23.32	56.53	0.41	2.42
P16546_SP	Sptan1	Spectrin alp	K.LSELNQK#.W	73.71	30.01	2.46	0.41
P16546_SP	Sptan1	Spectrin alp	K.LSILSEER.T	17.98	34.09	0.53	1.90
P16546_SP	Sptan1	Spectrin alp	R.M*NEVISLWK#.K	34.86	20.55	1.70	0.59
P16546_SP	Sptan1	Spectrin alp	R.MNEVISLWK#.K	17.71	11.27	1.57	0.64
P16546_SP	Sptan1	Spectrin alp	R.M*QHNLEQQIQAR.N	17.30	44.33	0.39	2.56
P16546_SP	Sptan1	Spectrin alp	K.M*TLVASEDYGDTLAAIQGLLK#.K	102.77	44.48	2.31	0.43
P16546_SP	Sptan1	Spectrin alp	K.NQALNTDNYGHDLASVQALQR.K	28.39	60.89	0.47	2.14
P16546_SP	Sptan1	Spectrin alp	R.NTTGVTEEALK#.E	73.51	23.84	3.08	0.32
P16546_SP	Sptan1	Spectrin alp	K.QDEVNAAWQR.L	8.56	11.10	0.77	1.30
P16546_SP	Sptan1	Spectrin alp	K.QETFDAGLQAFQQEGIANITALK#.D	18.99	13.30	1.43	0.70
P16546_SP	Sptan1	Spectrin alp	R.QGFVPAAYVK#.K	80.30	44.58	1.80	0.56
P16546_SP	Sptan1	Spectrin alp	R.QQVAPM*DDETGK#.E	12.22	6.60	1.85	0.54
P16546_SP	Sptan1	Spectrin alp	R.QQVAPM*DDETGK#ELVLALYDYQEK#.S	24.27	12.04	2.02	0.50
P16546_SP	Sptan1	Spectrin alp	R.RQDLEDSLQAQQYFADANEAESWM*R.E	3.06	8.88	0.34	2.90
P16546_SP	Sptan1	Spectrin alp	K.SADESGQALLAASHYASDEVR.E	32.23	66.28	0.49	2.06
P16546_SP	Sptan1	Spectrin alp	R.SLQQLAEER.S	46.92	89.61	0.52	1.91
P16546_SP	Sptan1	Spectrin alp	K.SSEEIESAFR.A	22.30	48.32	0.46	2.17
P16546_SP	Sptan1	Spectrin alp	R.SSLSSAQADFNQLAELDR.Q	16.22	34.78	0.47	2.14
P16546_SP	Sptan1	Spectrin alp	K.TATDEAYK#DPSNLQGK#.V	163.89	66.88	2.45	0.41
P16546_SP	Sptan1	Spectrin alp	K.TKQDEVNAAWQR.L	4.75	9.28	0.51	1.95
P16546_SP	Sptan1	Spectrin alp	K.VAEDLESEGLM*AEEVQAVQQQEVYGAM*PR.D	5.81	9.83	0.59	1.69
P16546_SP	Sptan1	Spectrin alp	K.VAEDLESEGLMAEEVQAVQQQEVYGAM*PR.D	3.12	5.06	0.62	1.62
P16546_SP	Sptan1	Spectrin alp	K.VEDLFLTFAK#.K	14.20	7.69	1.85	0.54
P16546_SP	Sptan1	Spectrin alp	K.VLETAEDIQER.R	40.49	77.13	0.52	1.90
P16546_SP	Sptan1	Spectrin alp	R.VNEVSQFAAK#.L	127.84	49.49	2.58	0.39
P16546_SP	Sptan1	Spectrin alp	K.YTEHSTVGLAQQWDQLDQLGM*R.M	14.08	18.23	0.77	1.29
P16546_SP	Sptan1	Spectrin alp	K.YTEHSTVGLAQQWDQLDQLGMR.M	2.90	7.07	0.41	2.44
E9Q447_E9	Sptan1	Spectrin alp	R.QGQIDNQYQSLLELGEK#.R	17.96	12.00	1.50	0.67
Q62261_SP	Sptbn1	Spectrin be	R.AFEDEM*SGR.S	9.72	20.90	0.47	2.15
Q62261_SP	Sptbn1	Spectrin be	K.AK#DEQSAVSM*LK#.K	26.05	11.38	2.29	0.44
Q62261_SP	Sptbn1	Spectrin be	K.ALQFLK#.E	74.75	34.60	2.16	0.46
Q62261_SP	Sptbn1	Spectrin be	K.AQQYYFDAAEAEAWMSEQELYM*M*SEEK#.A	4.21	1.50	2.80	0.36
Q62261_SP	Sptbn1	Spectrin be	R.AQTLPTSVVTITSESSPGK#.R	14.33	6.93	2.07	0.48
Q62261_SP	Sptbn1	Spectrin be	R.DASVAEAWLLGQEPYLSSR.E	19.23	35.76	0.54	1.86
Q62261_SP	Sptbn1	Spectrin be	R.DGM*AFNALIHK#.H	41.63	14.42	2.89	0.35
Q62261_SP	Sptbn1	Spectrin be	R.DLDDFQSWLSR.T	19.87	34.34	0.58	1.73
Q62261_SP	Sptbn1	Spectrin be	R.DLM*LWM*EDVIR.Q	4.29	7.65	0.56	1.78
Q62261_SP	Sptbn1	Spectrin be	R.DLVAIEAK#.L	104.38	56.32	1.85	0.54
Q62261_SP	Sptbn1	Spectrin be	R.DQNTVETLQR.M	26.22	52.90	0.50	2.02
Q62261_SP	Sptbn1	Spectrin be	R.DTGNIGQER.V	11.46	24.97	0.46	2.18
Q62261_SP	Sptbn1	Spectrin be	K.DVAEEITNYRPTIDTLHEQASALPQAHAESPDVK.G	5.45	18.96	0.29	3.48
Q62261_SP	Sptbn1	Spectrin be	R.DVEDEILWVGER.M	11.45	25.72	0.45	2.25
Q62261_SP	Sptbn1	Spectrin be	R.EAASELLM*R.L	12.19	23.14	0.53	1.90
Q62261_SP	Sptbn1	Spectrin be	K.EAEKLESEHPDQAQAILSR.L	19.19	41.32	0.46	2.15
Q62261_SP	Sptbn1	Spectrin be	R.EASLGEASK#.L	44.70	24.57	1.82	0.55
Q62261_SP	Sptbn1	Spectrin be	K.EGMQLISEK#PETEAVVK#.E	61.01	33.52	1.82	0.55
Q62261_SP	Sptbn1	Spectrin be	K.EIEELQSQAQALSQEGK#.S	43.34	21.87	1.98	0.50
Q62261_SP	Sptbn1	Spectrin be	R.EIGQSVDEVEK#.L	137.75	75.80	1.82	0.55
Q62261_SP	Sptbn1	Spectrin be	R.ENEVLEAWK#.S	76.48	39.30	1.95	0.51
Q62261_SP	Sptbn1	Spectrin be	R.EQWANLEQLSAIR.K	19.00	36.17	0.53	1.90
Q62261_SP	Sptbn1	Spectrin be	R.EVDDLEQWIAER.E	18.23	45.61	0.40	2.50
Q62261_SP	Sptbn1	Spectrin be	R.EVVAGSHELGQDYEHVTMLQER.F	5.35	6.66	0.80	1.25
Q62261_SP	Sptbn1	Spectrin be	K.FANSLVGVQQQLQAFNTYR.T	3.48	7.47	0.47	2.15
Q62261_SP	Sptbn1	Spectrin be	R.FESLEPEM*NNQASR.V	14.51	29.35	0.49	2.02
Q62261_SP	Sptbn1	Spectrin be	R.FQIQDISVETEDNK#.E	23.22	9.17	2.53	0.40
Q62261_SP	Sptbn1	Spectrin be	K.HLLGVEDLLQK#.H	64.68	25.68	2.52	0.40
Q62261_SP	Sptbn1	Spectrin be	K.HQAFMAELASNK#EWLDK#IEK#.E	12.37	5.58	2.22	0.45
Q62261_SP	Sptbn1	Spectrin be	K.HQILEQAVEDYAETVHQLSK#.T	85.30	44.32	1.92	0.52
Q62261_SP	Sptbn1	Spectrin be	K.HRPDLIDFDK.L	20.33	36.15	0.56	1.78
Q62261_SP	Sptbn1	Spectrin be	K.HYASEEIK#.E	8.34	4.70	1.78	0.56
Q62261_SP	Sptbn1	Spectrin be	R.IDDIFER.S	18.25	40.51	0.45	2.22
Q62261_SP	Sptbn1	Spectrin be	K.INAVVETGR.R	9.65	16.06	0.60	1.66
Q62261_SP	Sptbn1	Spectrin be	K.IVSSNDVGHDEYSTQSLVK#.K	239.61	109.69	2.18	0.46
Q62261_SP	Sptbn1	Spectrin be	K.KHEAIETDIAAYEER.V	70.66	31.25	2.26	0.44
Q62261_SP	Sptbn1	Spectrin be	R.K#HYASEEIK#EK#.L	3.15	5.12	0.61	1.63
Q62261_SP	Sptbn1	Spectrin be	R.K#K#EIEELQSQAQALSQEGK#.S	62.37	39.19	1.59	0.63
Q62261_SP	Sptbn1	Spectrin be	R.LAEISDVWEEM*K#.T	39.43	15.51	2.54	0.39
Q62261_SP	Sptbn1	Spectrin be	R.LAEISDVWEEMK#.T	49.57	20.18	2.46	0.41
Q62261_SP	Sptbn1	Spectrin be	R.LEM*NLGLQK#.I	46.09	23.67	1.95	0.51
Q62261_SP	Sptbn1	Spectrin be	R.LEMNLGLQK#.I	20.85	6.18	3.37	0.30
Q62261_SP	Sptbn1	Spectrin be	K.LLTQHENIK#NEIDNYEEDYQK#.M	40.28	13.20	3.05	0.33
Q62261_SP	Sptbn1	Spectrin be	R.LQAAYAGDK#.A	55.86	22.17	2.52	0.40
Q62261_SP	Sptbn1	Spectrin be	R.LQAAYAGDK#ADDIQK#.R	4.90	3.61	1.36	0.74
Q62261_SP	Sptbn1	Spectrin be	R.LQALDTGWNELHK#.M	175.11	68.47	2.56	0.39
Q62261_SP	Sptbn1	Spectrin be	R.LTTLELLEVR.R	27.21	64.46	0.42	2.37
Q62261_SP	Sptbn1	Spectrin be	R.LVSDGNINSDR.I	25.74	62.61	0.41	2.43
Q62261_SP	Sptbn1	Spectrin be	R.LVSQDNFGFDLPAVEAATK#.K	87.63	40.72	2.15	0.46
Q62261_SP	Sptbn1	Spectrin be	R.LVSQDNFGFDLPAVEAATK#.K	66.30	33.50	1.98	0.51
Q62261_SP	Sptbn1	Spectrin be	R.M*HTTFEHDIQALGTQVR.Q	10.55	21.00	0.50	1.99

Q62261_SF	Sptbn1	Spectrin be	K.M*LTAQDM*SYDEAR.N	7.55	13.25	0.57	1.76
Q62261_SF	Sptbn1	Spectrin be	R.M*PLATSTDHGHNLQTVQLLIK#.K	21.92	10.81	2.03	0.49
Q62261_SF	Sptbn1	Spectrin be	R.MPLATSTDHGHNLQTVQLLIK#.K	11.89	4.20	2.83	0.35
Q62261_SF	Sptbn1	Spectrin be	K.M*WEVLESTTQTK#.A	29.44	14.06	2.09	0.48
Q62261_SF	Sptbn1	Spectrin be	K.NEIDNYEEDYQK#.M	18.03	5.98	3.01	0.33
Q62261_SF	Sptbn1	Spectrin be	K.QAEAFLNNQEYVLAHTEM*PTTLEGAEAAIK#.K	17.07	7.19	2.37	0.42
Q62261_SF	Sptbn1	Spectrin be	K.QALQDTLALYK#.M	64.11	21.58	2.97	0.34
Q62261_SF	Sptbn1	Spectrin be	R.QIEAQEKPR.D	4.80	11.58	0.41	2.41
Q62261_SF	Sptbn1	Spectrin be	R.QLM*HNGHPSEK#.E	4.00	1.64	2.44	0.41
Q62261_SF	Sptbn1	Spectrin be	R.QNLLSQSHAYQQFLR.D	19.80	43.35	0.46	2.19
Q62261_SF	Sptbn1	Spectrin be	K.SAASGIPYHSEVPVSLK#.E	50.72	27.18	1.87	0.54
Q62261_SF	Sptbn1	Spectrin be	K.SALPAQSAATLPAR.T	17.48	43.95	0.40	2.51
Q62261_SF	Sptbn1	Spectrin be	R.SGHFEQAIK#EGEDM*IAEEHFGSEK#.I	16.34	8.86	1.84	0.54
Q62261_SF	Sptbn1	Spectrin be	K.SNAHYNLQNAFNLAEQHLGLTK#.L	22.28	7.54	2.96	0.34
Q62261_SF	Sptbn1	Spectrin be	K.SNAHYNLQNAFNLAEQHLGLTK#.L	67.44	26.19	2.57	0.39
Q62261_SF	Sptbn1	Spectrin be	R.SQNIITDSSSLNAEAIR.Q	16.18	35.59	0.45	2.20
Q62261_SF	Sptbn1	Spectrin be	R.TLETPAAQMEGFLNR.K	10.99	11.46	0.96	1.04
Q62261_SF	Sptbn1	Spectrin be	R.TQILAASYELHK#.F	102.95	44.56	2.31	0.43
Q62261_SF	Sptbn1	Spectrin be	R.TQTAIASEDM*PNTLTEAEK#.L	31.23	13.94	2.24	0.45
Q62261_SF	Sptbn1	Spectrin be	R.TQTAIASEDMPNTLTEAEK#.L	30.71	11.52	2.67	0.38
Q62261_SF	Sptbn1	Spectrin be	R.VAVVNQIAR.Q	34.53	71.13	0.49	2.06
Q62261_SF	Sptbn1	Spectrin be	R.VDTVNNM*ADELINSGHSDAATIAEWK#.D	49.92	16.93	2.95	0.34
Q62261_SF	Sptbn1	Spectrin be	R.VDTVNNMADELINSGHSDAATIAEWK#.D	34.00	16.09	2.11	0.47
Q62261_SF	Sptbn1	Spectrin be	K.VIESTQDLGNDLAGVM*ALQR.K	9.99	24.19	0.41	2.42
Q62261_SF	Sptbn1	Spectrin be	K.VIESTQDLGNDLAGVMALQR.K	3.48	7.37	0.47	2.12
Q62261_SF	Sptbn1	Spectrin be	K.VIESTQDLGNDLAGVMALQR.K	7.03	21.60	0.33	3.07
Q62261_SF	Sptbn1	Spectrin be	K.VLDNAIETEK#.M	114.02	55.00	2.07	0.48
Q62261_SF	Sptbn1	Spectrin be	K.VLLLSQDYGK#.H	164.21	75.48	2.18	0.46
Q62261_SF	Sptbn1	Spectrin be	R.VQAVVAVAR.E	25.43	53.28	0.48	2.10
Q62261_SF	Sptbn1	Spectrin be	K.VSEEAESQQWDTSK#.G	15.97	5.07	3.15	0.32
Q9R112_SC	Sqrdl	Sulfide:qui	K.EGNALFTFPNTPVK#.C	6.89	1.63	4.23	0.24
Q64337_SC	Sqstm1	Sequestoso	K.EVDPSTGELQSLQMPESEGPSSLDPSQEGPTGLK#.E	3.65	1.72	2.13	0.47
Q64337_SC	Sqstm1	Sequestoso	R.LTPTTPESSSTGTEDK#.S	20.16	10.49	1.92	0.52
Q64337_SC	Sqstm1	Sequestoso	K.NYDIGAALDTIQYSK#.H	36.82	17.50	2.10	0.48
Q497V5_SF	Srbd1	S1 RNA-bin	R.LQTTVHTLQVIIDGLSQPK#.T	14.39	5.93	2.43	0.41
A0A087WC	Srcap	Protein Src	K.DLLPVAVDILPESEK#.T	18.33	14.24	1.29	0.78
A0A087WC	Srcap	Protein Src	R.LEQLSEIIER.F	2.86	29.39	0.10	10.26
A0A087WC	Srcap	Protein Src	R.SPFYLDSLEEK#.R	9.89	7.22	1.37	0.73
A0A087WC	Srcap	Protein Src	K.TPIPLLLR.G	4.99	15.46	0.32	3.10
Q8BZX4_SF	Srek1	Splicing reg	R.EAQSFISAAIEPESGK#.S	8.40	3.70	2.27	0.44
Q91Z69_SF	Srgap1	SLIT-ROBO	K.QIGR@SGDPVFHIR.L	3.80	3.65	1.04	0.96
Q91Z67_SF	Srgap2	SLIT-ROBO	R.NEYLLALEATNASVFK#.Y	5.94	1.56	3.82	0.26
Q91Z67_SF	Srgap2	SLIT-ROBO	K.VLNELYSVM*K#.T	13.90	14.77	0.94	1.06
Q6P069_SC	Sri	Sorcin OS=	R.SGTVDPQELQK#.A	19.49	7.78	2.50	0.40
P16254_SF	Srp14	Signal reco	R.K#ISTVVSSK#.E	50.92	16.16	3.15	0.32
P16254_SF	Srp14	Signal reco	R.K#SSVEGLEPAENK#.C	12.58	5.27	2.38	0.42
G5E8T3_G5	Srp19	Signal reco	K.SGGADPSLQQGEGSK#.K	3.37	1.64	2.05	0.49
G5E8T3_G5	Srp19	Signal reco	K.SGGADPSLQQGEGSK#.K	98.74	36.76	2.69	0.37
G5E8T3_G5	Srp19	Signal reco	K.SGGADPSLQQGEGSK#K#.G	1.73	2.24	0.77	1.30
G5E8T3_G5	Srp19	Signal reco	K.SVM*LYVAEM*IPK#.L	9.36	2.84	3.30	0.30
G5E8T3_G5	Srp19	Signal reco	K.SVMLYVAEM*IPK#.L	20.99	8.42	2.49	0.40
G5E8T3_G5	Srp19	Signal reco	K.SVMLYVAEMIPK#.L	4.67	2.21	2.12	0.47
P14576_SF	Srp54	Signal reco	K.AFK#DK#VDVASVIVTK#.L	14.75	3.96	3.73	0.27
P14576_SF	Srp54	Signal reco	R.AGAFDQLK#.Q	71.70	24.36	2.94	0.34
P14576_SF	Srp54	Signal reco	K.DK#VDVASVIVTK#.L	71.84	20.59	3.49	0.29
P14576_SF	Srp54	Signal reco	R.DM*YEQFQNIM*K#.M	23.20	7.51	3.09	0.32
P14576_SF	Srp54	Signal reco	R.DMYEQFQNIM*K#.M	5.89	1.87	3.16	0.32
P14576_SF	Srp54	Signal reco	R.DM*YEQFQNIMK#.M	9.17	1.87	4.89	0.20
P14576_SF	Srp54	Signal reco	R.DMYEQFQNIMK#.M	12.58	3.35	3.75	0.27
P14576_SF	Srp54	Signal reco	R.DVQELLTQYTK#.F	76.09	25.82	2.95	0.34
P14576_SF	Srp54	Signal reco	K.FAQMVK#.K	30.51	18.12	1.68	0.59
P14576_SF	Srp54	Signal reco	K.FKNENFEIIIVDTSGR.H	9.06	11.59	0.78	1.28
P14576_SF	Srp54	Signal reco	K.GGGALSAVAATK#.S	143.91	53.65	2.68	0.37
P14576_SF	Srp54	Signal reco	K.GK#QNVIMFVGLQGSGK#.T	8.31	1.16	7.14	0.14
P14576_SF	Srp54	Signal reco	R.IPFYGSYTEM*DPVIIASEGVEK#.F	20.37	7.24	2.81	0.36
P14576_SF	Srp54	Signal reco	R.IPFYGSYTEM*DPVIIASEGVEK#.F	8.25	2.91	2.83	0.35
P14576_SF	Srp54	Signal reco	R.IPFYGSYTEMDPVIIASEGVEK#.F	17.27	4.35	3.97	0.25
P14576_SF	Srp54	Signal reco	K.LAYYYQR.K	11.53	19.07	0.60	1.65
P14576_SF	Srp54	Signal reco	K.LDDNEALIEK#.L	57.60	28.50	2.02	0.49
P14576_SF	Srp54	Signal reco	K.LLGM*GDIEGLIDK#.V	7.86	5.24	1.50	0.67
P14576_SF	Srp54	Signal reco	K.LLGM*GDIEGLIDK#VNELK#.L	19.95	5.63	3.54	0.28
P14576_SF	Srp54	Signal reco	K.MIQHAVFK#.E	16.28	3.26	5.00	0.20
P14576_SF	Srp54	Signal reco	K.QNVIMFVGLQGSGK#.T	11.86	8.06	1.47	0.68
P14576_SF	Srp54	Signal reco	K.SAIDLEEM*ASGLNK#.R	22.18	16.69	1.33	0.75
P14576_SF	Srp54	Signal reco	K.SAIDLEEMASGLNK#.R	26.34	9.13	2.89	0.35
P14576_SF	Srp54	Signal reco	R.SLSNATIINEEVLNAM*LK#.E	8.22	2.78	2.96	0.34
P14576_SF	Srp54	Signal reco	R.SLSNATIINEEVLNAMLK#.E	24.22	7.60	3.19	0.31
P14576_SF	Srp54	Signal reco	K.SPIIFIGTGEHIDDFEPFK#.T	81.41	26.67	3.05	0.33
P14576_SF	Srp54	Signal reco	K.VDVASVIVTK#.L	55.99	18.14	3.09	0.32
P14576_SF	Srp54	Signal reco	K.VNELK#LDDNEALIEK#.L	3.98	1.94	2.05	0.49
P14576_SF	Srp54	Signal reco	K.GGGALSAVAATK#.S	11.76	4.66	2.53	0.40
P14576_SF	Srp54	Signal reco	K.SPIIFIGTGEHIDDFEPFK#.T	17.22	8.08	2.13	0.47
P14576_SF	Srp54	Signal reco	R.DVQELLTQYTK#.F	10.16	4.26	2.39	0.42
P14576_SF	Srp54	Signal reco	K.GGGALSAVAATK#.S	18.05	3.48	5.18	0.19
P14576_SF	Srp54	Signal reco	R.IPFYGSYTEM*DPVIIASEGVEK#.F	5.76	3.95	1.46	0.69
Q8BMA6_S	Srp68	Signal reco	R.ALLQQQPEDDSK#.R	6.08	2.66	2.28	0.44
Q8BMA6_S	Srp68	Signal reco	K.ANK#EFGDSLSLEILQIIK#.E	25.33	14.80	1.71	0.58
Q8BMA6_S	Srp68	Signal reco	R.AWSYAM*QLK#.Q	26.28	6.89	3.82	0.26
Q8BMA6_S	Srp68	Signal reco	R.IFLLGLADNEAAIVQAESEETK#.E	15.57	7.83	1.99	0.50
Q8BMA6_S	Srp68	Signal reco	R.IFLLGLADNEAAIVQAESEETKER.L	12.23	14.02	0.87	1.15
Q8BMA6_S	Srp68	Signal reco	K.LASAFTEEQAVLYNQR.V	5.02	5.68	0.88	1.13
Q8BMA6_S	Srp68	Signal reco	K.NSLKDLPDVQELITQVR.S	3.63	10.92	0.33	3.01
Q8BMA6_S	Srp68	Signal reco	K.SAIEAFNK#.C	27.37	15.91	1.72	0.58
Q8BMA6_S	Srp68	Signal reco	R.SGGTEGLLAEKLEALITQTR.A	4.45	3.97	1.12	0.89
Q8BMA6_S	Srp68	Signal reco	K.VTEELLTDNR.Y	8.37	10.94	0.77	1.31
Q8BMA6_S	Srp68	Signal reco	K.YANEVSSHGGASK#.N	17.97	7.05	2.55	0.39
Q8BMA6_S	Srp68	Signal reco	K.ANK#EFGDSLSLEILQIIK#.E	26.02	3.34	7.79	0.13
Q8BMA6_S	Srp68	Signal reco	K.NSLKDLPDVQELITQVR.S	3.32	8.72	0.38	2.63
Q8BMA6_S	Srp68	Signal reco	R.SGGTEGLLAEK#.L	17.29	1.70	10.17	0.10
Q8BMA6_S	Srp68	Signal reco	R.SGGTEGLLAEKLEALITQTR.A	6.34	9.69	0.65	1.53
Q8BMA6_S	Srp68	Signal reco	K.YANEVSSHGGASK#.N	7.11	4.10	1.74	0.58
Q8BMA6_S	Srp68	Signal reco	K.DLPDVQELITQVR.S	6.42	14.77	0.43	2.30
Q8BMA6_S	Srp68	Signal reco	R.IFLLGLADNEAAIVQAESEETK#.E	23.36	4.54	5.15	0.19

Q8BMA6_S	Srp68	Signal reco	R.IFLLGLADNEAAIVQAESEETKER.L	22.90	26.62	0.86	1.16
F8VQC1_F8	Srp72	Signal reco	K.AIELLQEFSDQHPENAAEIK#.L	57.32	23.41	2.45	0.41
F8VQC1_F8	Srp72	Signal reco	K.DIHTLAQLISAYSLVDPEK#AK#.A	4.79	3.36	1.43	0.70
F8VQC1_F8	Srp72	Signal reco	K.EAVSDLEQLWK#.Q	24.67	12.45	1.98	0.50
F8VQC1_F8	Srp72	Signal reco	K.GTQGATAGASSELDASK#.A	46.18	22.40	2.06	0.49
F8VQC1_F8	Srp72	Signal reco	K.LTNAEGVEFK#.L	48.46	25.34	1.91	0.52
F8VQC1_F8	Srp72	Signal reco	K.TIESATQQTDK#.L	13.98	3.54	3.94	0.25
F8VQC1_F8	Srp72	Signal reco	K.VLANNSLSFEK#.A	23.00	8.14	2.82	0.35
F8VQC1_F8	Srp72	Signal reco	R.K#TNLSAVVAAQSNWEK#.V	13.48	5.70	2.37	0.42
F8VQC1_F8	Srp72	Signal reco	K.TIESATQQTDK#.L	10.54	4.81	2.19	0.46
F8VQC1_F8	Srp72	Signal reco	K.AIELLQEFSDQHPENAAEIK#.L	90.49	38.98	2.32	0.43
F8VQC1_F8	Srp72	Signal reco	K.AIELLQEFSDQHPENAAEIK#.L	5.43	2.27	2.39	0.42
F8VQC1_F8	Srp72	Signal reco	K.DIHTLAQLISAYSLVDPEK#AK#.A	24.10	6.14	3.92	0.25
F8VQC1_F8	Srp72	Signal reco	K.EAVSDLEQLWK#.Q	41.32	16.87	2.45	0.41
F8VQC1_F8	Srp72	Signal reco	K.GTQGATAGASSELDASK#.A	116.61	41.02	2.84	0.35
F8VQC1_F8	Srp72	Signal reco	K.ISQGNISK#.A	44.54	13.28	3.35	0.30
F8VQC1_F8	Srp72	Signal reco	R.K#TNLSAVVAAQSNWEK#.V	8.88	4.01	2.22	0.45
F8VQC1_F8	Srp72	Signal reco	K.LTM*AQLK#.I	33.43	10.62	3.15	0.32
F8VQC1_F8	Srp72	Signal reco	K.LTMAQLK#.I	33.07	17.91	1.85	0.54
F8VQC1_F8	Srp72	Signal reco	K.LTNAEGVEFK#.L	108.75	38.64	2.81	0.36
F8VQC1_F8	Srp72	Signal reco	R.QLQAIEFNK#.A	43.65	14.19	3.08	0.33
F8VQC1_F8	Srp72	Signal reco	R.TEEALQLYNQIIK#.L	13.60	6.06	2.25	0.45
F8VQC1_F8	Srp72	Signal reco	K.TIESATQQTDK#.L	40.57	13.58	2.99	0.33
F8VQC1_F8	Srp72	Signal reco	K.TIESATQQTDKLK.E	21.47	7.81	2.75	0.36
F8VQC1_F8	Srp72	Signal reco	K.VLANNSLSFEK#.A	89.14	56.86	1.57	0.64
F8VQC1_F8	Srp72	Signal reco	R.YGQNSDFTR.A	12.91	20.74	0.62	1.61
F8VQC1_F8	Srp72	Signal reco	K.AIELLQEFSDQHPENAAEIK#.L	37.57	10.32	3.64	0.27
F8VQC1_F8	Srp72	Signal reco	K.EAVSDLEQLWK#.Q	13.60	3.27	4.16	0.24
F8VQC1_F8	Srp72	Signal reco	K.GTQGATAGASSELDASK#.A	30.47	11.21	2.72	0.37
F8VQC1_F8	Srp72	Signal reco	K.LTNAEGVEFK#.L	31.90	9.50	3.36	0.30
F8VQC1_F8	Srp72	Signal reco	R.TEEALQLYNQIIK#.L	14.70	3.62	4.06	0.25
F8VQC1_F8	Srp72	Signal reco	K.VLANNSLSFEK#.A	26.38	33.42	0.79	1.27
O70551_SF	Srpk1	SRSF protei	K.LK#PWGLLEVLVEK#.Y	11.50	7.06	1.63	0.61
O70551_SF	Srpk1	SRSF protei	K.FSAGNFLINPLEPK#.N	15.91	13.78	1.15	0.87
O70551_SF	Srpk1	SRSF protei	R.LAAEATEWQR.S	5.15	11.02	0.47	2.14
O70551_SF	Srpk1	SRSF protei	K.LEESNSIGQDQTLTER.G	2.99	6.88	0.44	2.30
O54781_SF	Srpk2	SRSF protei	R.AADLLVNPLDPR.N	4.91	8.53	0.58	1.74
O54781_SF	Srpk2	SRSF protei	K.LK#PWSLFDVLVEK#.Y	31.44	8.49	3.70	0.27
O54781_SF	Srpk2	SRSF protei	R.TVSASSTGDLPK#.T	43.27	7.24	5.97	0.17
Q52KI8_SR	Srrm1	Serine/argi	R.APQTSSPPPVR.R	10.09	24.22	0.42	2.40
Q52KI8_SR	Srrm1	Serine/argi	K.AVTIATPATAAPAAVSAATTTSAQEEPAAAPEPR.K	14.20	29.56	0.48	2.08
Q52KI8_SR	Srrm1	Serine/argi	K.DSSVQEATSTSDILK#.A	41.01	21.20	1.93	0.52
Q52KI8_SR	Srrm1	Serine/argi	R.KETESEAEDDNLDDLER.H	25.85	78.08	0.33	3.02
Q52KI8_SR	Srrm1	Serine/argi	R.K#VELSESEEDK#GSK#.M	141.73	53.34	2.66	0.38
Q52KI8_SR	Srrm1	Serine/argi	R.KVELSESEEDKGSK.M	29.40	12.47	2.36	0.42
Q52KI8_SR	Srrm1	Serine/argi	K.M*AAADSVQQR.R	12.68	33.97	0.37	2.68
Q52KI8_SR	Srrm1	Serine/argi	K.MAAADSVQQR.R	24.44	60.33	0.41	2.47
Q52KI8_SR	Srrm1	Serine/argi	R.M*K#DSSVQEATSTSDILK#.A	65.93	32.63	2.02	0.49
Q52KI8_SR	Srrm1	Serine/argi	R.MK#DSSVQEATSTSDILK#.A	10.00	5.50	1.82	0.55
Q52KI8_SR	Srrm1	Serine/argi	K.M*M*QINLTGFLNGK#.N	6.85	3.78	1.81	0.55
Q52KI8_SR	Srrm1	Serine/argi	R.SVSGSPEPAAK#.K	38.73	15.96	2.43	0.41
Q52KI8_SR	Srrm1	Serine/argi	K.VNLEVIK#PWITK#.R	106.26	49.21	2.16	0.46
Q52KI8_SR	Srrm1	Serine/argi	K.DSSVQEATSTSDILK#.A	9.63	5.21	1.85	0.54
Q8BTI8_SR	Srrm2	Serine/argi	R.SVVQTTPVAGSQSLSSGTVAK.S	5.86	7.07	0.83	1.21
Q8BTI8_SR	Srrm2	Serine/argi	R.TPAASAVNLAGAR.T	5.50	21.51	0.26	3.91
Q8BTI8_SR	Srrm2	Serine/argi	R.TPAGLAPTNLSSSR.M	2.67	12.33	0.22	4.61
Q8BTI8_SR	Srrm2	Serine/argi	R.AAFGISDSYVDGSSFDPQR.R	3.83	17.54	0.22	4.58
Q8BTI8_SR	Srrm2	Serine/argi	K.GHTQTWPDTSSPEVMQTQVESPLLQSK.S	11.59	9.25	1.25	0.80
Q8BTI8_SR	Srrm2	Serine/argi	R.HLEAALVK#.R	54.18	55.98	0.97	1.03
Q8BTI8_SR	Srrm2	Serine/argi	R.HSGSTSPYLK.S	15.19	25.27	0.60	1.66
Q8BTI8_SR	Srrm2	Serine/argi	R.IPAASAAAM*NLASAR.T	5.70	19.78	0.29	3.47
Q8BTI8_SR	Srrm2	Serine/argi	R.IPAASAAAMNLASAR.T	1.68	15.74	0.11	9.37
Q8BTI8_SR	Srrm2	Serine/argi	K.MELGTPLR.H	5.29	10.74	0.49	2.03
Q8BTI8_SR	Srrm2	Serine/argi	R.M*SQVPAPVPLM*SLR.T	3.95	16.77	0.24	4.24
Q8BTI8_SR	Srrm2	Serine/argi	R.M*SQVPAPVPLMSLR.T	1.21	10.90	0.11	9.02
Q8BTI8_SR	Srrm2	Serine/argi	K.NSGPVSEVNTGFSPEVK#.E	23.81	27.95	0.85	1.17
Q8BTI8_SR	Srrm2	Serine/argi	K.RPNPDILDHER.K	2.00	62.33	0.03	31.14
Q8BTI8_SR	Srrm2	Serine/argi	K.SEISTDPK.L	44.52	44.65	1.00	1.00
Q8BTI8_SR	Srrm2	Serine/argi	K.SFLVQSR.L	13.94	65.42	0.21	4.69
Q8BTI8_SR	Srrm2	Serine/argi	R.SGSSQELDGKPSASPQER.S	7.21	37.98	0.19	5.27
Q8BTI8_SR	Srrm2	Serine/argi	K.SLLPNSSQDELM*EVEK.S	10.54	10.55	1.00	1.00
Q8BTI8_SR	Srrm2	Serine/argi	K.SLLPNSSQDELMEVEK.S	12.82	11.73	1.09	0.92
Q8BTI8_SR	Srrm2	Serine/argi	K.SM*LQTPPDQNLSGSK.S	11.86	18.16	0.65	1.53
Q8BTI8_SR	Srrm2	Serine/argi	R.SPGM*LEPLGSAR.T	17.90	25.71	0.70	1.44
Q8BTI8_SR	Srrm2	Serine/argi	R.SSSELSPEVVEK#.V	28.21	25.99	1.09	0.92
Q8BTI8_SR	Srrm2	Serine/argi	R.SSVPENHAQSR.I	1.94	7.27	0.27	3.75
Q8BTI8_SR	Srrm2	Serine/argi	R.SVVQTTPVAGSQSLSSGTVAK#.S	7.25	7.75	0.94	1.07
Q8BTI8_SR	Srrm2	Serine/argi	R.TAPAANLASR.I	6.33	48.51	0.13	7.66
Q8BTI8_SR	Srrm2	Serine/argi	R.TAVAPSAVNLADPR.T	2.70	26.48	0.10	9.79
Q8BTI8_SR	Srrm2	Serine/argi	K.TK#PDSSIYPLVDSK#.S	55.84	60.71	0.92	1.09
Q8BTI8_SR	Srrm2	Serine/argi	K.TKPDSSIYPLVDSK.S	21.01	25.35	0.83	1.21
Q8BTI8_SR	Srrm2	Serine/argi	R.TPAAAAAM*NLASPR.T	4.27	12.87	0.33	3.01
Q8BTI8_SR	Srrm2	Serine/argi	R.TPAALAALSLTGSGTPPTAANYPSSSR.T	3.74	13.50	0.28	3.61
Q8BTI8_SR	Srrm2	Serine/argi	R.TPAASAVNLAGAR.T	9.67	58.70	0.16	6.07
Q8BTI8_SR	Srrm2	Serine/argi	R.TPAGLAPTNLSSSR.M	7.40	22.56	0.33	3.05
Q8BTI8_SR	Srrm2	Serine/argi	R.TPM*SVLQQTGGSM*M*DGPGPR.I	4.84	24.55	0.20	5.07
Q8BTI8_SR	Srrm2	Serine/argi	R.TPPVALSSSR.M	2.77	21.14	0.13	7.62
Q8BTI8_SR	Srrm2	Serine/argi	R.TPQAPTPANLVVGPR.S	2.60	21.62	0.12	8.33
Q8BTI8_SR	Srrm2	Serine/argi	K.VGLFSSQK#.V	91.69	83.84	1.09	0.91
Q8BTI8_SR	Srrm2	Serine/argi	K.VSSPVLETVQQR.T	8.72	41.06	0.21	4.71
Q99MR6_S	Srrt	Serrate RN	R.ILEQEEEEEQAGK#.T	13.11	7.05	1.86	0.54
Q99MR6_S	Srrt	Serrate RN	R.AGPALGEGER.K	27.89	46.60	0.60	1.67
Q99MR6_S	Srrt	Serrate RN	R.DLDAPDDVDFF.-	94.01	94.01	1.00	1.00
Q99MR6_S	Srrt	Serrate RN	R.ESLSEEEAQK#.M	196.94	70.41	2.80	0.36
Q99MR6_S	Srrt	Serrate RN	K.EVAFFNNFLTDAK#.R	198.20	73.51	2.70	0.37
Q99MR6_S	Srrt	Serrate RN	K.FVTSNTQELGK#.D	150.22	46.64	3.22	0.31
Q99MR6_S	Srrt	Serrate RN	K.HAEKIEEVKK.E	7.48	2.59	2.88	0.35
Q99MR6_S	Srrt	Serrate RN	R.ILEQEEEEEQAGK#.T	182.88	74.80	2.44	0.41
Q99MR6_S	Srrt	Serrate RN	R.ILEQEEEEEQAGK#TGEASK#.K	15.27	4.40	3.47	0.29
Q99MR6_S	Srrt	Serrate RN	R.ISHGEVLEWQK#.T	107.15	48.30	2.22	0.45
Q99MR6_S	Srrt	Serrate RN	R.K#DPEQEVEK#.F	82.71	31.49	2.63	0.38
Q99MR6_S	Srrt	Serrate RN	R.LGSIAEIDLGVPPPIM*K#.S	23.23	10.01	2.32	0.43
Q99MR6_S	Srrt	Serrate RN	R.LGSIAEIDLGVPPPIMK#.S	19.38	7.61	2.55	0.39

Q99MR6_S	Srrt	Serrate RNA	K.LIHTLDDR.T	17.96	18.42	0.98	1.03
Q99MR6_S	Srrt	Serrate RNA	K.LLLYLR.I	20.52	29.90	0.69	1.46
Q99MR6_S	Srrt	Serrate RNA	K.M*EGGTENDLR.I	11.86	18.92	0.63	1.60
Q99MR6_S	Srrt	Serrate RNA	K.M*LDAAVIK#.M	49.05	20.81	2.36	0.42
Q99MR6_S	Srrt	Serrate RNA	K.SFKEFLLSLDDSVDETEAVKR.Y	5.83	10.55	0.55	1.81
Q99MR6_S	Srrt	Serrate RNA	R.SK#YHPDEVGK#.R	8.36	4.38	1.91	0.52
Q99MR6_S	Srrt	Serrate RNA	R.VALSEPQPER.R	15.31	26.11	0.59	1.70
Q99MR6_S	Srrt	Serrate RNA	R.DLDAPDDVDFF.-	26.09	26.09	1.00	1.00
Q99MR6_S	Srrt	Serrate RNA	R.ESLSEEEAQK#.M	35.17	13.96	2.52	0.40
Q99MR6_S	Srrt	Serrate RNA	K.EVAFFNNFLTDAK#.R	42.20	15.62	2.70	0.37
Q99MR6_S	Srrt	Serrate RNA	K.FVTSNTQELGK#.D	28.11	9.96	2.82	0.35
Q99MR6_S	Srrt	Serrate RNA	R.ILEQEEEEEQAGK#.T	40.16	17.24	2.33	0.43
Q99MR6_S	Srrt	Serrate RNA	R.K#DPEQEVEK#.F	19.80	8.51	2.33	0.43
Q99MR6_S	Srrt	Serrate RNA	R.TQLWASEPGTPPVPTSLPSQNPILK#.N	12.45	5.14	2.42	0.41
Q6PDM2_S	Srsf1	Serine/argi	R.DAEDAVYGR.D	68.85	275.24	0.25	4.00
Q6PDM2_S	Srsf1	Serine/argi	R.DGTGVVEFVR.K	84.60	282.42	0.30	3.34
Q6PDM2_S	Srsf1	Serine/argi	R.DGYDYDGYR.L	42.00	135.98	0.31	3.24
Q6PDM2_S	Srsf1	Serine/argi	K.DIEDVFYK#.Y	53.52	43.76	1.22	0.82
Q6PDM2_S	Srsf1	Serine/argi	R.GGPPFAFVEFEDPR.D	32.36	119.99	0.27	3.71
Q6PDM2_S	Srsf1	Serine/argi	R.GGPPFAFVEFEDPRDAEDAVYGR.D	4.00	28.97	0.14	7.25
Q6PDM2_S	Srsf1	Serine/argi	R.IYVGNLPPDIR.T	16.92	64.27	0.26	3.80
Q6PDM2_S	Srsf1	Serine/argi	R.KEDM*TYAVR.K	21.91	65.78	0.33	3.00
Q6PDM2_S	Srsf1	Serine/argi	R.RGGPPFAFVEFEDPR.D	3.26	22.84	0.14	7.02
Q6PDM2_S	Srsf1	Serine/argi	R.SHEGETAYIR.V	50.45	172.84	0.29	3.43
Q6PDM2_S	Srsf1	Serine/argi	R.TK#DIEDVFYK#.Y	109.36	79.96	1.37	0.73
Q6PDM2_S	Srsf1	Serine/argi	R.TKDIEDVFYK.Y	122.48	72.43	1.69	0.59
Q6PDM2_S	Srsf1	Serine/argi	R.VVVSGLPPSGSWQDLK#.D	50.93	42.96	1.19	0.84
Q9R0U0_S	Srsf10	Serine/argi	R.DAEDALHNLDR.K	4.83	18.51	0.26	3.83
Q9R0U0_S	Srsf10	Serine/argi	R.GFAYVQFEDVR.D	20.75	104.95	0.20	5.06
Q9R0U0_S	Srsf10	Serine/argi	R.QIEIQFAQGDR.K	13.37	57.99	0.23	4.34
Q9R0U0_S	Srsf10	Serine/argi	R.YGPIVDVYVPLDFYTR.R	14.51	90.94	0.16	6.27
Q9R0U0_S	Srsf10	Serine/argi	R.YLRPPNTSLFVR.N	12.80	82.24	0.16	6.42
Q9R0U0_S	Srsf10	Serine/argi	R.GFAYVQFEDVR.D	31.05	141.52	0.22	4.56
Q9R0U0_S	Srsf10	Serine/argi	R.YGPIVDVYVPLDFYTR.R	6.72	33.91	0.20	5.04
Q9R0U0_S	Srsf10	Serine/argi	R.YLRPPNTSLFVR.N	4.37	129.71	0.03	29.65
Q3UIX4_Q3	Srsf11	Protein Srsf	R.ALIVVPYAEGVIPDETK#.A	29.22	14.04	2.08	0.48
Q3UIX4_Q3	Srsf11	Protein Srsf	K.FHDPDSAVVAQHLTNTVFVDR.A	6.99	9.57	0.73	1.37
Q3UIX4_Q3	Srsf11	Protein Srsf	K.LNHVAAGLVSPSLK#.S	54.21	26.63	2.04	0.49
Q3UIX4_Q3	Srsf11	Protein Srsf	R.TLFGFLGK#.I	45.82	19.99	2.29	0.44
Q3UIX4_Q3	Srsf11	Protein Srsf	R.ALIVVPYAEGVIPDETK#.A	102.38	37.03	2.77	0.36
Q3UIX4_Q3	Srsf11	Protein Srsf	K.FHDPDSAVVAQHLTNTVFVDR.A	2.66	2.72	0.98	1.02
Q3UIX4_Q3	Srsf11	Protein Srsf	R.LFPPDDSPLPVSSR.V	6.36	12.99	0.49	2.04
Q3UIX4_Q3	Srsf11	Protein Srsf	R.ALIVVPYAEGVIPDETK#.A	21.99	9.59	2.29	0.44
Q3UIX4_Q3	Srsf11	Protein Srsf	K.FHDPDSAVVAQHLTNTVFVDR.A	3.93	6.90	0.57	1.76
Q3UIX4_Q3	Srsf11	Protein Srsf	K.LNHVAAGLVSPSLK#.S	41.32	15.12	2.73	0.37
Q62093_SR	Srsf2	Serine/argi	R.DAEDAM*DAM*DGAVLDGR.E	3.64	15.34	0.24	4.21
Q62093_SR	Srsf2	Serine/argi	R.DAEDAM*DAMDGAVLDGR.E	1.64	3.83	0.43	2.33
Q62093_SR	Srsf2	Serine/argi	K.VDNLTYR.T	47.97	60.87	0.79	1.27
Q62093_SR	Srsf2	Serine/argi	R.VGDVYIPR.D	41.43	107.89	0.38	2.60
P84104_SR	Srsf3	Serine/argi	R.NPPGFAFVEFEDPR.D	15.87	65.37	0.24	4.12
P84104_SR	Srsf3	Serine/argi	R.AFGYYGPLR.S	144.01	592.43	0.24	4.11
P84104_SR	Srsf3	Serine/argi	R.NPPGFAFVEFEDPR.D	151.59	785.31	0.19	5.18
P84104_SR	Srsf3	Serine/argi	R.NPPGFAFVEFEDPRDAADAVR.E	40.09	564.05	0.07	14.07
P84104_SR	Srsf3	Serine/argi	R.NRGPPPSWGR.R	2.95	24.42	0.12	8.28
P84104_SR	Srsf3	Serine/argi	R.VELSNGEK.R	15.75	17.98	0.88	1.14
P84104_SR	Srsf3	Serine/argi	R.VELSNGEKR.S	3.39	9.93	0.34	2.93
P84104_SR	Srsf3	Serine/argi	R.VRVELSNGEK.R	9.63	57.88	0.17	6.01
P84104_SR	Srsf3	Serine/argi	K.VYVGNLGNNGNK#.T	56.04	64.39	0.87	1.15
Q8VE97_SR	Srsf4	Serine/argi	R.LIVENLSSR.C	96.08	323.53	0.30	3.37
Q8VE97_SR	Srsf4	Serine/argi	R.QAGEVTYADAHK.G	34.12	38.29	0.89	1.12
Q8VE97_SR	Srsf4	Serine/argi	R.AEGESEAPNPEPR.A	24.32	69.58	0.35	2.86
Q8VE97_SR	Srsf4	Serine/argi	K.ILEVDLK#.N	77.55	53.45	1.45	0.69
Q8VE97_SR	Srsf4	Serine/argi	K.LDGTEVNGR.K	3.93	10.21	0.38	2.60
Q8VE97_SR	Srsf4	Serine/argi	R.LIVENLSSR.C	30.72	123.02	0.25	4.00
Q8VE97_SR	Srsf4	Serine/argi	R.LVEDKPGSR.R	5.91	23.07	0.26	3.90
Q8VE97_SR	Srsf4	Serine/argi	K.NGYGFVEFDDLR.D	3.11	8.51	0.37	2.73
Q8VE97_SR	Srsf4	Serine/argi	K.SKDHAEDKLQNNDSAGK.A	5.81	6.17	0.94	1.06
O35326_SR	Srsf5	Serine/argi	R.DADDAVYELDGK#.E	92.74	58.35	1.59	0.63
O35326_SR	Srsf5	Serine/argi	K.LNEGVVEFASYGDLK#.N	92.04	59.83	1.54	0.65
O35326_SR	Srsf5	Serine/argi	R.QAGEVTFADAHRPK.L	2.88	5.77	0.50	2.00
O35326_SR	Srsf5	Serine/argi	R.VSWQDLK#.D	109.54	86.70	1.26	0.79
O35326_SR	Srsf5	Serine/argi	R.DADDAVYELDGK#.E	12.50	10.24	1.22	0.82
Q3TWW8_S	Srsf6	Serine/argi	R.ALDKLDGTEINGR.N	2.77	15.16	0.18	5.46
Q3TWW8_S	Srsf6	Serine/argi	R.DADDAVYELNSK#.E	100.24	93.78	1.07	0.94
Q3TWW8_S	Srsf6	Serine/argi	R.FFSGYGR.L	27.30	86.34	0.32	3.16
Q3TWW8_S	Srsf6	Serine/argi	R.LLEIDLK#.N	55.96	51.48	1.09	0.92
Q3TWW8_S	Srsf6	Serine/argi	K.NGYGFVEFEDSR.D	3.88	16.97	0.23	4.38
Q3TWW8_S	Srsf6	Serine/argi	R.TNEGVIEFR.S	39.25	149.28	0.26	3.80
Q3TWW8_S	Srsf6	Serine/argi	R.LLEIDLK#.N	17.07	12.65	1.35	0.74
Q3TWW8_S	Srsf6	Serine/argi	R.TNEGVIEFR.S	6.55	20.86	0.31	3.18
Q8BL97_SR	Srsf7	Serine/argi	R.AFSYYGPLR.T	21.85	96.73	0.23	4.43
Q8BL97_SR	Srsf7	Serine/argi	R.VELSTGM*PR.R	15.39	57.95	0.27	3.76
Q8BL97_SR	Srsf7	Serine/argi	R.VELSTGMPR.R	5.18	24.33	0.21	4.69
Q8BL97_SR	Srsf7	Serine/argi	K.VYVGNLGTGAGK#.G	208.28	166.19	1.25	0.80
Q8BL97_SR	Srsf7	Serine/argi	K.VYVGNLGTGAGK#.G	12.97	12.62	1.03	0.97
Q9D0B0_S	Srsf9	Serine/argi	R.HGLVPFAFVR.F	2.55	17.47	0.15	6.86
Q9D0B0_S	Srsf9	Serine/argi	R.IYVGNLPSDVR.E	4.79	34.56	0.14	7.21
Q9D0B0_S	Srsf9	Serine/argi	R.DAEDAIYGR.N	2.72	15.31	0.18	5.63
Q9D0B0_S	Srsf9	Serine/argi	K.DGM*GM*VEYLR.K	4.15	28.55	0.15	6.89
Q9D0B0_S	Srsf9	Serine/argi	K.DLEDLFYK#.Y	14.47	18.24	0.79	1.26
Q9D0B0_S	Srsf9	Serine/argi	R.EK#DLEDLFYK#.Y	40.27	44.57	0.90	1.11
Q9D0B0_S	Srsf9	Serine/argi	R.EKDLEDLFYK.Y	67.21	74.13	0.91	1.10
Q9D0B0_S	Srsf9	Serine/argi	R.FEDPRDAEDAIYGR.N	2.33	79.10	0.03	33.91
Q9D0B0_S	Srsf9	Serine/argi	R.HGLVPFAFVR.F	15.42	95.12	0.16	6.17
Q9D0B0_S	Srsf9	Serine/argi	R.IYVGNLPSDVR.E	31.71	209.48	0.15	6.61
Q9D0B0_S	Srsf9	Serine/argi	R.SHEGETSYIR.V	3.13	24.58	0.13	7.85
Q9D0B0_S	Srsf9	Serine/argi	R.STSYGYSR.S	3.58	16.21	0.22	4.52
Q9D0B0_S	Srsf9	Serine/argi	R.VLVSGLPPSGSWQDLK.D	17.61	28.58	0.62	1.62
P32067_LA	Ssb	Lupus La pr	K.DTNLLILFK#.E	13.92	9.28	1.50	0.67
P32067_LA	Ssb	Lupus La pr	K.GNRPGYAGAPK.G	8.54	26.08	0.33	3.05
P32067_LA	Ssb	Lupus La pr	K.GSIFAVFDSIQSAK#.K	177.96	134.78	1.32	0.76
P32067_LA	Ssb	Lupus La pr	K.ITDDQQESLNK#.W	109.79	93.79	1.17	0.85
P32067_LA	Ssb	Lupus La pr	K.K#FVEIPGQK#.Y	62.67	47.58	1.32	0.76

P32067_LA	Ssb	Lupus La pr	K.K#ITDDQQESLNK#.W	11.15	10.54	1.06	0.95
P32067_LA	Ssb	Lupus La pr	K.LDEGWVPLETMIK#.F	52.27	42.21	1.24	0.81
P32067_LA	Ssb	Lupus La pr	K.LM*EVSADK#.T	25.81	29.24	0.88	1.13
P32067_LA	Ssb	Lupus La pr	K.LM*EVSADKTK.I	7.97	8.22	0.97	1.03
P32067_LA	Ssb	Lupus La pr	R.LTTDFNVIVQALSK#.S	97.35	75.24	1.29	0.77
P32067_LA	Ssb	Lupus La pr	K.MTALEAK#.I	34.71	35.17	0.99	1.01
P32067_LA	Ssb	Lupus La pr	R.NANNGNLLLR.N	4.19	20.46	0.20	4.89
P32067_LA	Ssb	Lupus La pr	R.SPSRPLPEVTDEYKNDVK.N	9.26	34.67	0.27	3.74
P32067_LA	Ssb	Lupus La pr	K.YK#DTNLLILFK#.E	58.31	39.69	1.47	0.68
P32067_LA	Ssb	Lupus La pr	K.ITDDQQESLNK#.W	11.50	6.44	1.79	0.56
P32067_LA	Ssb	Lupus La pr	K.GSIFAVFDSIQSAK#.K	5.74	3.49	1.65	0.61
Q9CYR0_SS	Ssbp1	Single-stran	R.SGDSEVYQM*GDVSQK.T	8.32	11.38	0.73	1.37
Q9CY50_SS	Ssr1	Translocon	K.GTEDFIVESLDASFR.Y	3.22	11.36	0.28	3.52
Q9DCF9_SS	Ssr3	Translocon	K.QQSEEDLLLQDFSR.N	2.38	8.38	0.28	3.52
Q62186_SS	Ssr4	Translocon	R.FFDEESYSLLR.K	1.62	4.32	0.37	2.67
Q08943_SS	Ssrp1	FACT comp	K.LFDFVNAK#.K	12.84	5.42	2.37	0.42
Q08943_SS	Ssrp1	FACT comp	R.SFDFEIETK#.Q	10.02	3.75	2.67	0.37
Q08943_SS	Ssrp1	FACT comp	K.ASSGLLYPLER.G	11.17	56.79	0.20	5.09
Q08943_SS	Ssrp1	FACT comp	R.FDEISFVNFAR.G	11.34	48.82	0.23	4.30
Q08943_SS	Ssrp1	FACT comp	R.FYVPPTQEDGVDPVEAFAQNVLSK.A	30.58	25.45	1.20	0.83
Q08943_SS	Ssrp1	FACT comp	K.GWNWGTVK#.F	17.58	18.46	0.95	1.05
Q08943_SS	Ssrp1	FACT comp	K.IKSDHPGISITDLSK.K	21.63	30.41	0.71	1.41
Q08943_SS	Ssrp1	FACT comp	K.IPYTTVLR.L	11.67	59.11	0.20	5.06
Q08943_SS	Ssrp1	FACT comp	K.LFDFVNAK#.K	60.70	47.68	1.27	0.79
Q08943_SS	Ssrp1	FACT comp	K.LSDFFK#.T	34.52	37.80	0.91	1.10
Q08943_SS	Ssrp1	FACT comp	K.NM*SGSLYEM*VSR.V	3.38	12.39	0.27	3.67
Q08943_SS	Ssrp1	FACT comp	K.SDHPGISITDLSK#.K	22.28	21.76	1.02	0.98
Q08943_SS	Ssrp1	FACT comp	R.SFDFEIETK#.Q	48.99	36.09	1.36	0.74
Q08943_SS	Ssrp1	FACT comp	K.TGKVDNIQAGELTEGIWR.R	2.81	16.90	0.17	6.02
Q08943_SS	Ssrp1	FACT comp	K.VDNIQAGELTEGIWR.R	11.83	26.51	0.45	2.24
P56873_SS	Sssca1	Sjoegren sy	K.AAQAPPLPAAPPNTDAVASTQTALLQK#.L	35.95	30.76	1.17	0.86
Q9CY97_SS	Ssu72	RNA polym	K.TTYDQM*YNDLLR.K	3.91	5.35	0.73	1.37
Q9CY97_SS	Ssu72	RNA polym	R.VYDQVVEDLNSR.E	3.03	7.74	0.39	2.55
Q99L47_F1	St13	Hsc70-inter	K.AIDLFTDAIK#.L	30.75	5.36	5.74	0.17
Q99L47_F1	St13	Hsc70-inter	R.AIEINPDSAQPYK#.W	17.78	4.57	3.89	0.26
Q8BZ71_ST	Stac3	SH3 and cys	K.GDEAGGYVK#VYTGR@.K	48.50	5.54	8.75	0.11
Q9D3E6_ST	Stag1	Cohesin sub	R.FALTFGLDQIK#.T	12.22	10.73	1.14	0.88
Q9D3E6_ST	Stag1	Cohesin sub	R.HDPQAEEALAK#.R	20.39	21.74	0.94	1.07
Q9D3E6_ST	Stag1	Cohesin sub	R.LELLLQK#.R	32.73	18.42	1.78	0.56
Q9D3E6_ST	Stag1	Cohesin sub	R.FALTFGLDQIK#.T	18.89	12.97	1.46	0.69
Q9D3E6_ST	Stag1	Cohesin sub	R.FNHSVEDLLQEGEEADDDDIYNVLSTLK#.R	9.24	3.67	2.51	0.40
Q9D3E6_ST	Stag1	Cohesin sub	R.HDPQAEEALAK#.R	27.49	23.97	1.15	0.87
Q9D3E6_ST	Stag1	Cohesin sub	K.M*YSDAFLNDSYLK#.Y	16.89	8.69	1.94	0.51
Q9D3E6_ST	Stag1	Cohesin sub	K.MYSDAFLNDSYLK#.Y	6.10	3.91	1.56	0.64
Q9D3E6_ST	Stag1	Cohesin sub	R.SQLIDEFVDR.F	4.94	19.48	0.25	3.95
Q9D3E6_ST	Stag1	Cohesin sub	R.TDTMIQTPGPLPTPQLTSTVLR.E	2.34	6.80	0.34	2.91
O35638_ST	Stag2	Cohesin sub	R.IVSM*TLDKEYDVAVQAIK.L	25.88	15.58	1.66	0.60
O35638_ST	Stag2	Cohesin sub	R.IVSMTLDK#EYDVAVQAIK#.L	8.05	4.04	1.99	0.50
O35638_ST	Stag2	Cohesin sub	R.LLEDFLQEGEEPDEDDAYQVLSTLK#.R	19.38	11.79	1.64	0.61
P70297_ST	Stam	Signal trans	K.AGEIITVLDDSDPNWWK#.G	6.96	4.14	1.68	0.59
P70297_ST	Stam	Signal trans	R.AVYDFEAAEDNELTFK#.A	9.13	4.05	2.25	0.44
P70297_ST	Stam	Signal trans	K.GETHQGVGLFPSNFVTADLTAEPEM*IK#.T	7.73	7.44	1.04	0.96
P70297_ST	Stam	Signal trans	K.VM*EALSLYTK.L	11.51	8.42	1.37	0.73
P70297_ST	Stam	Signal trans	R.DFASEVSNVLNK#.G	352.66	133.90	2.63	0.38
O88811_ST	Stam2	Signal trans	K.AIELSLQEQK#.Q	10.78	6.93	1.56	0.64
O88811_ST	Stam2	Signal trans	R.ALQILQSIDPK#.E	9.94	6.72	1.48	0.68
O88811_ST	Stam2	Signal trans	R.ALYDFEAVEDNELTFK#.H	25.30	3.70	6.83	0.15
O88811_ST	Stam2	Signal trans	K.LVNEAPVYSVYSK#.L	29.20	52.46	0.56	1.80
O88811_ST	Stam2	Signal trans	K.SM*K#EEGVTFPSAGSQTVAAAAK#.N	5.74	7.96	0.72	1.39
O88811_ST	Stam2	Signal trans	K.VLEALDLYNK#.L	13.56	5.71	2.38	0.42
Q9CQ26_ST	Stambp	STAM-bindi	R.SLKPGALSVIENVPTIEGLR.H	3.64	8.26	0.44	2.27
Q8C3V4_Q8	Stat1	Signal trans	K.ELSAVTFPDIIR.N	6.19	17.36	0.36	2.80
Q8C3V4_Q8	Stat1	Signal trans	K.FTYEPDPITK#.N	15.31	11.83	1.29	0.77
Q8C3V4_Q8	Stat1	Signal trans	R.GLNADQLSM*LGEK#.L	9.90	8.17	1.21	0.83
Q8C3V4_Q8	Stat1	Signal trans	K.K#LEELEQK#.F	20.14	18.55	1.09	0.92
Q8C3V4_Q8	Stat1	Signal trans	K.SDQK#QEQLLLHK#.M	19.61	15.56	1.26	0.79
Q8C3V4_Q8	Stat1	Signal trans	K.TGVQFTVK#.S	23.99	15.58	1.54	0.65
Q8C3V4_Q8	Stat1	Signal trans	K.TLEELQDEYDFK#.C	8.38	6.29	1.33	0.75
Q8C3V4_Q8	Stat1	Signal trans	K.VSFDK#DVNEK#.N	10.41	6.51	1.60	0.62
Q8C3V4_Q8	Stat1	Signal trans	K.ELSAVTFPDIIR.N	4.53	21.25	0.21	4.69
Q8C3V4_Q8	Stat1	Signal trans	R.FHDLLSQLDDQYSR.F	4.06	11.87	0.34	2.93
Q8C3V4_Q8	Stat1	Signal trans	K.FLEQVHQLYDDSFPM*EIR.Q	8.91	21.56	0.41	2.42
Q8C3V4_Q8	Stat1	Signal trans	R.FNQAQEGNIQNTVM*LDK#.Q	14.76	10.70	1.38	0.72
Q8C3V4_Q8	Stat1	Signal trans	R.FNQAQEGNIQNTVMLDK#.Q	8.87	4.87	1.82	0.55
Q8C3V4_Q8	Stat1	Signal trans	R.IVGPEFDSM*M*STV.-	8.06	8.06	1.00	1.00
Q8C3V4_Q8	Stat1	Signal trans	R.QYLAQWLEK#.Q	19.29	14.22	1.36	0.74
Q8C3V4_Q8	Stat1	Signal trans	K.TLEELQDEYDFK#.C	20.41	14.74	1.38	0.72
Q8C3V4_Q8	Stat1	Signal trans	K.VM*AAENIPENPLK#.Y	7.85	7.43	1.06	0.95
Q8C3V4_Q8	Stat1	Signal trans	R.ALLKDQQPGTFLLR.F	20.40	36.24	0.56	1.78
Q8C3V4_Q8	Stat1	Signal trans	K.DQQPGTFLLR.F	13.60	36.20	0.38	2.66
Q8C3V4_Q8	Stat1	Signal trans	R.EGAITFTWVER.S	16.11	52.60	0.31	3.26
Q8C3V4_Q8	Stat1	Signal trans	R.ELLNSIELTQNTLINDELVEWKR.R	3.42	4.96	0.69	1.45
Q8C3V4_Q8	Stat1	Signal trans	K.ELSAVTFPDIIR.N	41.48	96.43	0.43	2.32
Q8C3V4_Q8	Stat1	Signal trans	R.FHDLLSQLDDQYSR.F	11.59	38.47	0.30	3.32
Q8C3V4_Q8	Stat1	Signal trans	K.FLEQVHQLYDDSFPM*EIR.Q	12.31	20.77	0.59	1.69
Q8C3V4_Q8	Stat1	Signal trans	K.FLEQVHQLYDDSFPMEIR.Q	9.55	15.59	0.61	1.63
Q8C3V4_Q8	Stat1	Signal trans	K.FNILGTHTK#.V	38.96	14.49	2.69	0.37
Q8C3V4_Q8	Stat1	Signal trans	R.FNQAQEGNIQNTVM*LDK#.Q	33.17	13.33	2.49	0.40
Q8C3V4_Q8	Stat1	Signal trans	R.FNQAQEGNIQNTVMLDK#.Q	20.10	10.98	1.83	0.55
Q8C3V4_Q8	Stat1	Signal trans	K.FTYEPDPITK#.N	140.74	72.34	1.95	0.51
Q8C3V4_Q8	Stat1	Signal trans	R.GLNADQLSM*LGEK#.L	82.24	62.70	1.31	0.76
Q8C3V4_Q8	Stat1	Signal trans	R.GLNADQLSMLGEK#.L	33.86	7.55	4.49	0.22
Q8C3V4_Q8	Stat1	Signal trans	K.IRELLNSIELTQNTLINDELVEWK.R	5.10	8.78	0.58	1.72
Q8C3V4_Q8	Stat1	Signal trans	R.K#FNILGTHTK#.V	66.31	26.28	2.52	0.40
Q8C3V4_Q8	Stat1	Signal trans	K.K#LEELEQK#.F	127.77	57.10	2.24	0.45
Q8C3V4_Q8	Stat1	Signal trans	K.LQELNYNLK#.V	130.96	66.84	1.96	0.51
Q8C3V4_Q8	Stat1	Signal trans	K.M*FLM*LDNK#.R	63.83	25.49	2.50	0.40
Q8C3V4_Q8	Stat1	Signal trans	K.MFLMLDNK#.R	10.90	4.20	2.60	0.39
Q8C3V4_Q8	Stat1	Signal trans	K.QDWEHAAYDVSFATIR.F	14.81	30.84	0.48	2.08
Q8C3V4_Q8	Stat1	Signal trans	R.QYLAQWLEK#.Q	53.52	21.50	2.49	0.40
Q8C3V4_Q8	Stat1	Signal trans	K.SDQK#QEQLLLHK#.M	170.86	73.38	2.33	0.43
Q8C3V4_Q8	Stat1	Signal trans	K.TGVQFTVK#.S	96.91	48.56	2.00	0.50
Q8C3V4_Q8	Stat1	Signal trans	K.TLEELQDEYDFK#.C	64.61	28.34	2.28	0.44

Q8C3V4_Q	Stat1	Signal trans	K.VM*AAENIPENPLK#.Y	96.56	48.08	2.01	0.50
Q8C3V4_Q	Stat1	Signal trans	K.VMAAENIPENPLK#.Y	45.98	24.70	1.86	0.54
Q8C3V4_Q	Stat1	Signal trans	K.VSFDKDVNEK.N	66.82	39.97	1.67	0.60
Q8C3V4_Q	Stat1	Signal trans	K.YLYPNIDK#DHAFGK#.Y	15.63	5.41	2.89	0.35
Q8C3V4_Q	Stat1	Signal trans	K.DQQPGTFLLR.F	16.66	55.68	0.30	3.34
Q8C3V4_Q	Stat1	Signal trans	R.EGAITFTWVER.S	35.43	79.69	0.44	2.25
Q8C3V4_Q	Stat1	Signal trans	R.ELLNSIELTQNTLINDELVEWK#.R	73.63	31.32	2.35	0.43
Q8C3V4_Q	Stat1	Signal trans	K.ELSAVTFPDIIR.N	74.07	156.74	0.47	2.12
Q8C3V4_Q	Stat1	Signal trans	R.FHDLLSQLDDQYSR.F	25.65	41.39	0.62	1.61
Q8C3V4_Q	Stat1	Signal trans	K.FLEQVHQLYDDSFPM*EIR.Q	13.48	23.06	0.58	1.71
Q8C3V4_Q	Stat1	Signal trans	K.FLEQVHQLYDDSFPMEIR.Q	5.41	15.99	0.34	2.96
Q8C3V4_Q	Stat1	Signal trans	K.FNILGTHTK#.V	64.77	26.42	2.45	0.41
Q8C3V4_Q	Stat1	Signal trans	R.FNQAQEGNIQNTVM*LDK#.Q	45.42	19.92	2.28	0.44
Q8C3V4_Q	Stat1	Signal trans	R.FNQAQEGNIQNTVMLDK#.Q	25.68	14.33	1.79	0.56
Q8C3V4_Q	Stat1	Signal trans	K.FTYEPDPITK#.N	173.22	89.89	1.93	0.52
Q8C3V4_Q	Stat1	Signal trans	R.GLNADQLSM*LGEK#.L	101.26	48.81	2.07	0.48
Q8C3V4_Q	Stat1	Signal trans	K.ILENAQR.F	9.94	26.36	0.38	2.65
Q8C3V4_Q	Stat1	Signal trans	R.K#FNILGTHTK#.V	102.36	47.23	2.17	0.46
Q8C3V4_Q	Stat1	Signal trans	K.K#LEELEQK#.F	231.32	109.36	2.12	0.47
Q8C3V4_Q	Stat1	Signal trans	K.LQELNYNLK#.V	166.00	72.07	2.30	0.43
Q8C3V4_Q	Stat1	Signal trans	K.QDWEHAAYDVSFATIR.F	10.45	23.30	0.45	2.23
Q8C3V4_Q	Stat1	Signal trans	R.QYLAQWLEK#.Q	72.37	29.80	2.43	0.41
Q8C3V4_Q	Stat1	Signal trans	K.SDQK#QEQLLLHK#.M	215.25	97.82	2.20	0.45
Q8C3V4_Q	Stat1	Signal trans	K.TELISVSEVHPSR.L	7.88	17.42	0.45	2.21
Q8C3V4_Q	Stat1	Signal trans	K.TGVQFTVK#.S	125.45	43.47	2.89	0.35
Q8C3V4_Q	Stat1	Signal trans	K.TLEELQDEYDFK#.C	104.36	54.58	1.91	0.52
Q8C3V4_Q	Stat1	Signal trans	K.VM*AAENIPENPLK#.Y	170.85	88.26	1.94	0.52
Q8C3V4_Q	Stat1	Signal trans	K.VM*NM*EESTNGSLAAEFR.H	4.11	6.85	0.60	1.67
Q9QXJ2_Q	Stat2	Signal trans	K.EVLQSLPLTEIIR.H	24.81	38.38	0.65	1.55
Q9QXJ2_Q	Stat2	Signal trans	K.FNILTSNQK#.T	24.13	12.80	1.88	0.53
Q9QXJ2_Q	Stat2	Signal trans	R.QVDELQQPLELK#.Q	9.35	6.05	1.55	0.65
Q9QXJ2_Q	Stat2	Signal trans	K.TSSSDPHQSQQAQLVQATANK#.V	16.00	5.88	2.72	0.37
Q9QXJ2_Q	Stat2	Signal trans	R.YKGDM*FGQGVDLQNAQVM*ELLQR.L	5.03	10.59	0.48	2.10
Q9QXJ2_Q	Stat2	Signal trans	R.YTVFSLK#K#.T	11.85	4.70	2.52	0.40
Q9QXJ2_Q	Stat2	Signal trans	R.AQEVQPPPAPEAVVESQQLEIENR.I	3.15	9.00	0.35	2.86
Q9QXJ2_Q	Stat2	Signal trans	R.EAALGSDDAK#.A	20.33	7.82	2.60	0.38
Q9QXJ2_Q	Stat2	Signal trans	K.EVLQSLPLTEIIR.H	18.39	39.74	0.46	2.16
Q9QXJ2_Q	Stat2	Signal trans	K.FNILTSNQK#.T	22.83	11.98	1.91	0.52
Q9QXJ2_Q	Stat2	Signal trans	R.GLDSEQLGM*LR.T	10.98	17.19	0.64	1.57
Q9QXJ2_Q	Stat2	Signal trans	R.HYQVLAEENIPENPLR.F	8.94	14.25	0.63	1.59
Q9QXJ2_Q	Stat2	Signal trans	R.QVDELQQPLELK#.Q	10.33	5.50	1.88	0.53
Q9QXJ2_Q	Stat2	Signal trans	K.TSSSDPHQSQQAQLVQATANK#.V	26.64	11.74	2.27	0.44
Q9QXJ2_Q	Stat2	Signal trans	R.YKGDM*FGQGVDLQNAQVM*ELLQR.L	7.20	6.87	1.05	0.96
Q9QXJ2_Q	Stat2	Signal trans	R.YTVFSLK#.K	14.79	6.36	2.32	0.43
P42227_ST	Stat3	Signal trans	K.EGGVTFTWVEK.D	6.33	8.19	0.77	1.29
P42227_ST	Stat3	Signal trans	K.VVENLQDDFDFNYK#.T	6.70	7.09	0.95	1.06
P42227_ST	Stat3	Signal trans	K.ESHATLVFHNLLGEIDQQYSR.F	4.67	12.32	0.38	2.64
P42227_ST	Stat3	Signal trans	K.FPELNYQLK.I	23.52	19.81	1.19	0.84
P42227_ST	Stat3	Signal trans	R.GLSIEQLTTLAEK#.L	28.66	27.91	1.03	0.97
P42227_ST	Stat3	Signal trans	R.K#FNILGTNTK#.V	13.94	297.78	0.05	21.36
P42227_ST	Stat3	Signal trans	R.LLQTAATAAQQGGQANHPTAAVVTEK#.Q	50.88	33.78	1.51	0.66
P42227_ST	Stat3	Signal trans	R.QFLAPWIESQDWAYAASK.E	6.55	3.50	1.87	0.53
P42227_ST	Stat3	Signal trans	K.SAFVVER.Q	24.49	16.25	1.51	0.66
P42227_ST	Stat3	Signal trans	K.TLTDEELADWK#.R	17.65	15.11	1.17	0.86
P42227_ST	Stat3	Signal trans	K.TQIQSVEPYTK.Q	36.51	40.72	0.90	1.12
P42227_ST	Stat3	Signal trans	K.VVENLQDDFDFNYK#.T	23.85	17.91	1.33	0.75
P42227_ST	Stat3	Signal trans	R.YLEQLHQLYSDSFPM*ELR.Q	3.70	9.71	0.38	2.62
P42227_ST	Stat3	Signal trans	R.YLEQLHQLYSDSFPMELR.Q	3.17	8.01	0.40	2.53
P42227_ST	Stat3	Signal trans	K.FPELNYQLK#.I	12.06	8.23	1.47	0.68
P42227_ST	Stat3	Signal trans	R.GLSIEQLTTLAEK#.L	14.25	12.49	1.14	0.88
P42227_ST	Stat3	Signal trans	K.TQIQSVEPYTK#.Q	18.29	12.66	1.44	0.69
P42232_ST	Stat5b	Signal trans	K.ATQLLEGLVQELQK#.K	14.02	6.22	2.26	0.44
P42232_ST	Stat5b	Signal trans	R.FSDSEIGGITIAWK#.F	9.92	6.48	1.53	0.65
P42232_ST	Stat5b	Signal trans	R.IQAQFAQLGQLNPQER.M	2.34	5.42	0.43	2.32
Q9DBE7_Q	Stau1	Double-str	R.EAEEENLNKSEISQVFEIALK.R	8.16	9.47	0.86	1.16
Q9DBE7_Q	Stau1	Double-str	R.ELLYGGTSPTAETILK#.S	23.60	19.81	1.19	0.84
Q9DBE7_Q	Stau1	Double-str	K.LLSELDQQSTEM*PR.T	2.24	8.37	0.27	3.74
Q9DBE7_Q	Stau1	Double-str	K.LQTAPDYGQGMNPISR.L	1.81	7.01	0.26	3.88
Q9DBE7_Q	Stau1	Double-str	R.NAAENM*LEILGFK#.V	6.24	7.92	0.79	1.27
Q9DBE7_Q	Stau1	Double-str	R.NAAENMLEILGFK#.V	19.60	17.92	1.09	0.91
Q9DBE7_Q	Stau1	Double-str	R.TLQSEPLPER.L	31.52	49.60	0.64	1.57
Q9DBE7_Q	Stau1	Double-str	R.VSVGEFVGEGEGK#.S	31.37	27.98	1.12	0.89
Q60864_S	Stip1	Stress-indu	K.DPQALSEHLK#.N	16.02	4.94	3.24	0.31
Q60864_S	Stip1	Stress-indu	K.DPQALSEHLK#NPVIAQK#.I	16.90	2.88	5.87	0.17
Q60864_S	Stip1	Stress-indu	R.IGNSYFK#EEK#.Y	11.71	1.43	8.18	0.12
Q60864_S	Stip1	Stress-indu	R.LAYINPDLALEEK#.N	50.86	10.21	4.98	0.20
Q60864_S	Stip1	Stress-indu	K.YK#DAIHFYNK#.S	20.21	4.42	4.57	0.22
Q60864_S	Stip1	Stress-indu	R.LAYINPDLALEEK#.N	12.44	3.46	3.60	0.28
O55098_S	Stk10	Serine/thre	K.FYDVELENLER.Q	2.57	7.53	0.34	2.93
Q99KH8_S	Stk24	Serine/thre	K.GSFGEVFK#.G	22.98	8.01	2.87	0.35
Q99KH8_S	Stk24	Serine/thre	K.LADFGVAGQLTDTQIK#.R	24.68	7.50	3.29	0.30
Q99KH8_S	Stk24	Serine/thre	K.NLENGTLQLSDLER.N	3.02	4.71	0.64	1.56
Q99KH8_S	Stk24	Serine/thre	R.NTFVGTPFWM*APEVIK#.Q	11.04	4.02	2.74	0.36
Q99KH8_S	Stk24	Serine/thre	R.NTFVGTPFWMAPEVIK#.Q	9.81	5.84	1.68	0.60
Q99KH8_S	Stk24	Serine/thre	K.VLFLIPK#.N	39.03	9.87	3.95	0.25
Q99KH8_S	Stk24	Serine/thre	K.LADFGVAGQLTDTQIK#.R	6.87	2.25	3.06	0.33
Q99KH8_S	Stk24	Serine/thre	K.LADFGVAGQLTDTQIK#.R	5.42	2.22	2.44	0.41
Q9JI10_ST	Stk3	Serine/thre	K.LADFGVAGQLTDTM*AK#.R	14.57	6.72	2.17	0.46
Q9JI10_ST	Stk3	Serine/thre	K.LADFGVAGQLTDTMAK#.R	7.06	4.54	1.56	0.64
Q9JI10_ST	Stk3	Serine/thre	K.LSEDSLTK#QPEEVFDVLEK#.L	7.74	6.79	1.14	0.88
Q9JI10_ST	Stk3	Serine/thre	K.TLTEDEIATILK#.S	20.41	9.40	2.17	0.46
Q9JI10_ST	Stk3	Serine/thre	K.LADFGVAGQLTDTM*AK#.R	6.25	3.72	1.68	0.59
Q9JI10_ST	Stk3	Serine/thre	K.LGEGSYGSVFK#.A	7.51	16.85	0.45	2.24
Q9JI10_ST	Stk3	Serine/thre	K.TLTEDEIATILK#.S	7.46	2.09	3.58	0.28
Q91VJ4_ST	Stk38	Serine/thre	R.LGLEDFESLK#.V	8.40	15.72	0.53	1.87
Q91VJ4_ST	Stk38	Serine/thre	R.NLNHSLPSDFTFQNM*NSK.R	14.26	8.36	1.71	0.59
Q91VJ4_ST	Stk38	Serine/thre	K.SIDDTSNFDEFPESDILKPTVTTSSHPETDYK.N	4.22	5.73	0.74	1.36
P54116_ST	Stom	Erythrocyt	K.VIAAEGEM*NASR.A	2.70	8.45	0.32	3.13
Q8CDJ8_ST	Ston1	Stonin-1 O	R.SLGVESDAQPQK#.H	15.11	10.38	1.46	0.69
Q9Z1Z2_ST	Strap	Serine-thre	K.AATAAADFTAK#.V	48.33	26.82	1.80	0.55
Q9Z1Z2_ST	Strap	Serine-thre	K.EFLVAGGEDFK#.L	12.93	9.11	1.42	0.70
Q9Z1Z2_ST	Strap	Serine-thre	R.FSPDGELYASGSEDGTLR.L	5.45	13.01	0.42	2.39
Q9Z1Z2_ST	Strap	Serine-thre	R.IYDLNK#PEAEPK#.E	12.92	6.67	1.94	0.52

Q9Z1Z2_ST	Strap	Serine-thre	R.LWQTVVGK.T	21.47	19.30	1.11	0.90
Q9Z1Z2_ST	Strap	Serine-thre	R.QGDTGDWIGTFLGHK#.G	15.60	12.91	1.21	0.83
Q9Z1Z2_ST	Strap	Serine-thre	K.SFEAPATINSASLHPEK#.E	1.29	2.60	0.50	2.01
Q9Z1Z2_ST	Strap	Serine-thre	K.SFEAPATINSASLHPEK#EFLVAGGEDFK#.L	5.32	4.81	1.11	0.90
Q9Z1Z2_ST	Strap	Serine-thre	K.TVDFTQDSNYLLTGGQDK#.L	20.49	18.34	1.12	0.89
Q9Z1Z2_ST	Strap	Serine-thre	K.YDYNSGEELESYK#.G	19.66	12.97	1.52	0.66
Q8C079_S	Strip1	Striatin-int	R.EVFSK#PISWEELLQ.-	10.34	6.05	1.71	0.59
Q8C079_S	Strip1	Striatin-int	K.ILLAAAPTSK#.A	14.61	7.88	1.85	0.54
Q8C079_S	Strip1	Striatin-int	R.LLDGLEVTAR.E	8.91	15.26	0.58	1.71
Q8C079_S	Strip1	Striatin-int	R.AAGGLLPGGK#.A	14.44	30.44	0.47	2.11
Q8C079_S	Strip1	Striatin-int	R.EVFSK#PISWEELLQ.-	7.73	21.87	0.35	2.83
Q8C079_S	Strip1	Striatin-int	K.ILLAAAPTSK#.A	14.40	9.41	1.53	0.65
O55106_S	Strn	Striatin OS	R.ALAFHPIEPVLITASEDHTLK#.M	10.18	4.37	2.33	0.43
O55106_S	Strn	Striatin OS	K.EALKEFDFLVTSEEGDNESR.S	2.17	6.19	0.35	2.86
O55106_S	Strn	Striatin OS	R.LPEQELSR.A	5.57	12.44	0.45	2.23
Q9ERG2_S	Strn3	Striatin-3 C	R.ALAFHPVEPVLVTASEDHTLK#.L	8.79	3.91	2.25	0.44
Q9ERG2_S	Strn3	Striatin-3 C	K.AYIASAGADALAK#.V	28.85	10.57	2.73	0.37
Q9ERG2_S	Strn3	Striatin-3 C	R.IAFLQGER.K	3.42	14.23	0.24	4.15
P58404_ST	Strn4	Striatin-4 C	K.ALIASAGADALAK#.V	22.86	15.30	1.49	0.67
P58404_ST	Strn4	Striatin-4 C	R.ASPGPGGLSGGESLLVK#.Q	13.90	11.29	1.23	0.81
P58404_ST	Strn4	Striatin-4 C	K.K#TDLSEQVSNGPVESVTLENSPLVWK#.E	2.68	3.36	0.80	1.25
Q9ER00_ST	Stx12	Syntaxin-1	K.ELGSLPLPLSASEQR.Q	2.18	9.31	0.23	4.28
Q9ER00_ST	Stx12	Syntaxin-1	R.ISQATAQIK#.N	33.14	35.29	0.94	1.06
Q8K1E0_ST	Stx5	Syntaxin-5	R.APVSALPLAPNNLGGGPIILGAESR.A	0.90	4.82	0.19	5.35
O70439_S	Stx7	Syntaxin-7	R.LVAEFTTSLTNFQK#.A	4.44	2.49	1.78	0.56
O08599_S	Stxbp1	Syntaxin-bi	R.AIVPILLDANVSTYDK#.I	19.70	9.36	2.11	0.47
O08599_S	Stxbp1	Syntaxin-bi	K.DIM*EDTIEDK#LDTK#.H	16.67	4.15	4.02	0.25
O08599_S	Stxbp1	Syntaxin-bi	R.EPLPSLEAVYLITPSEK#.S	90.20	197.92	0.46	2.19
O08599_S	Stxbp1	Syntaxin-bi	R.ISEQTYQLSR.W	11.13	17.88	0.62	1.61
O08599_S	Stxbp1	Syntaxin-bi	K.LNK#TDEEISS.-	26.10	5.13	5.09	0.20
O08599_S	Stxbp1	Syntaxin-bi	R.REPLPSLEAVYLITPSEK.S	6.83	7.16	0.95	1.05
O08599_S	Stxbp1	Syntaxin-bi	R.VEQDLAM*GTDAEGEK#.I	20.82	4.61	4.52	0.22
O08599_S	Stxbp1	Syntaxin-bi	R.AIVPILLDANVSTYDK#.I	9.91	1.62	6.10	0.16
O08599_S	Stxbp1	Syntaxin-bi	K.LNK#TDEEISS.-	13.11	23.28	0.56	1.78
O08599_S	Stxbp1	Syntaxin-bi	R.REPLPSLEAVYLITPSEK.S	6.36	3.67	1.73	0.58
O08599_S	Stxbp1	Syntaxin-bi	R.VEQDLAM*GTDAEGEK#.I	9.54	1.61	5.94	0.17
Q64324_S	Stxbp2	Syntaxin-bi	R.K#GPEDTAQLAHAVLAK#.L	9.99	13.06	0.77	1.31
Q64324_S	Stxbp2	Syntaxin-bi	K.SVQALIADFQGTPTFTYK#.A	6.39	2.59	2.47	0.41
Q60770_S	Stxbp3	Syntaxin-bi	K.IM*LLDEFTTK#.L	17.42	3.90	4.47	0.22
Q9Z2I9_SU	Sucla2	Succinyl-C	K.AVSSQM*IGQK#.L	10.63	3.34	3.18	0.31
Q9Z2I9_SU	Sucla2	Succinyl-C	K.EQAVTLAQK#.M	22.15	5.74	3.86	0.26
Q9Z2I9_SU	Sucla2	Succinyl-C	K.LHGGTPANFLDVGGGATVQQVTEAFK#.L	18.09	5.25	3.44	0.29
Q9Z2I9_SU	Sucla2	Succinyl-C	K.LYNLFLK#.Y	10.72	4.63	2.32	0.43
Q9WUM5_	Suclg1	Succinyl-C	K.HLGLPVFNTVK#.E	22.89	6.56	3.49	0.29
Q9WUM5_	Suclg1	Succinyl-C	K.QGTFHSQQALEYGTK#.L	23.01	5.84	3.94	0.25
Q9Z2I8_SU	Suclg2	Succinyl-C	R.LEGTNVQEAQNILK#.S	13.19	2.70	4.88	0.20
Q9Z2I8_SU	Suclg2	Succinyl-C	R.M*AENLGFLGSLK#.N	7.62	1.22	6.24	0.16
Q9Z2I8_SU	Suclg2	Succinyl-C	R.SHNGPVIVGSPQGGVDIEEVAASSPELIFK#.E	2.87	1.41	2.04	0.49
Q8BR65_S	Suds3	Sin3 histon	R.QLQQLQEGTLQEYQK#.R	6.02	3.66	1.64	0.61
Q9CX34_S	Sugt1	Suppressor	K.DYASALETFAEGQK#.L	8.55	3.02	2.83	0.35
Q9CX34_S	Sugt1	Suppressor	K.LEGQGDEPTPK#.Q	32.03	15.83	2.02	0.49
P61957_S	Sumo2	Small ubiq	K.VAGQDGSVVQFK#.I	54.59	35.60	1.53	0.65
P61957_S	Sumo2	Small ubiq	K.VAGQDGSVVQFK#.I	52.46	30.49	1.72	0.58
P61957_S	Sumo2	Small ubiq	K.VAGQDGSVVQFK#.I	41.17	25.68	1.60	0.62
Q920B9_S	Supt16h	FACT comp	R.AALLTER.T	7.07	31.29	0.23	4.42
Q920B9_S	Supt16h	FACT comp	K.AASITSEVFNK#.F	29.37	17.79	1.65	0.61
Q920B9_S	Supt16h	FACT comp	K.APGEQTVPALNLQNAFR.I	3.33	16.28	0.20	4.88
Q920B9_S	Supt16h	FACT comp	K.ELAAQLNEEAK#.R	30.24	26.69	1.13	0.88
Q920B9_S	Supt16h	FACT comp	R.HTDVQFYTEVGEITTDLGK#.H	24.84	16.86	1.47	0.68
Q920B9_S	Supt16h	FACT comp	R.LTEQK#GEQQIQK#.A	8.08	31.92	0.25	3.95
Q920B9_S	Supt16h	FACT comp	K.NEDDEEEEEKDEAEDLLGR.G	3.18	11.05	0.29	3.47
Q920B9_S	Supt16h	FACT comp	R.NEGNIFPNPEATFVK.E	19.40	21.21	0.91	1.09
Q920B9_S	Supt16h	FACT comp	K.VEALTKEELEFEVPFR.D	6.11	17.17	0.36	2.81
Q920B9_S	Supt16h	FACT comp	K.YTEGVQSLNWTK#.I	20.29	11.37	1.78	0.56
Q920B9_S	Supt16h	FACT comp	R.AALLTER.T	11.29	21.60	0.52	1.91
Q920B9_S	Supt16h	FACT comp	K.AASITSEVFNK#.F	37.68	24.97	1.51	0.66
Q920B9_S	Supt16h	FACT comp	K.APGEQTVPALNLQNAFR.I	3.76	19.82	0.19	5.27
Q920B9_S	Supt16h	FACT comp	K.ELAAQLNEEAK#.R	37.95	28.09	1.35	0.74
Q920B9_S	Supt16h	FACT comp	R.HTDVQFYTEVGEITTDLGK#.H	18.03	16.62	1.08	0.92
Q920B9_S	Supt16h	FACT comp	R.LTEQK#GEQQIQK#.A	5.69	4.51	1.26	0.79
Q920B9_S	Supt16h	FACT comp	K.NEDDEEEEEKDEAEDLLGR.G	4.41	12.77	0.35	2.89
Q920B9_S	Supt16h	FACT comp	R.NEGNIFPNPEATFVK#.E	31.54	27.28	1.16	0.86
Q920B9_S	Supt16h	FACT comp	K.NISM*SVEGDYTYLR.I	4.33	8.64	0.50	1.99
Q920B9_S	Supt16h	FACT comp	K.YETVIM*PVFGIATPFHIATIK#.N	15.53	15.12	1.03	0.97
Q920B9_S	Supt16h	FACT comp	K.YTEGVQSLNWTK#.I	23.83	15.44	1.54	0.65
Q9Z199_S	Supt4h1b	Transcripti	R.VSNFKPGVYAVSVTGR.L	16.41	40.56	0.40	2.47
O55201_S	Supt5h	Transcripti	R.DVTNLTVGGFTPM*SPR.I	3.92	12.14	0.32	3.10
O55201_S	Supt5h	Transcripti	R.FAVALDSDQNNIHVK#.D	103.40	30.38	3.40	0.29
O55201_S	Supt5h	Transcripti	K.FIAYQFTDTPLQIK#.S	23.30	8.79	2.65	0.38
O55201_S	Supt5h	Transcripti	R.GIYK#DDIAQVDYVEPSQNTISLK#.M	36.53	12.15	3.01	0.33
O55201_S	Supt5h	Transcripti	K.GYIYVEAYK#.Q	42.36	19.14	2.21	0.45
O55201_S	Supt5h	Transcripti	R.K#FIAYQFTDTPLQIK#.S	37.46	18.73	2.00	0.50
O55201_S	Supt5h	Transcripti	R.LGYWNQQM*VPIK#.E	8.11	3.65	2.22	0.45
O55201_S	Supt5h	Transcripti	R.SLGGDVASDGDFLIFEGNR.Y	7.65	16.05	0.48	2.10
O55201_S	Supt5h	Transcripti	R.SSEAEEAEVEEDQR.S	5.70	12.06	0.47	2.11
O55201_S	Supt5h	Transcripti	K.SSVGETVYGGSDELSDDITQQQLLPGVK#DPNLWTVK#.C	11.39	6.67	1.71	0.59
O55201_S	Supt5h	Transcripti	K.SVVAPEHVK#.G	21.51	7.85	2.74	0.36
O55201_S	Supt5h	Transcripti	R.TPM*YGSQTPLQDGSR.T	6.84	11.67	0.59	1.71
O55201_S	Supt5h	Transcripti	K.VLSVDGNK#.I	44.95	19.49	2.31	0.43
O55201_S	Supt5h	Transcripti	R.GIYK#DDIAQVDYVEPSQNTISLK#.M	21.32	10.05	2.12	0.47
O55201_S	Supt5h	Transcripti	K.GYIYVEAYK#.Q	16.64	4.80	3.46	0.29
O55201_S	Supt5h	Transcripti	R.K#FIAYQFTDTPLQIK#.S	15.17	7.88	1.93	0.52
O55201_S	Supt5h	Transcripti	R.SLGGDVASDGDFLIFEGNR.Y	3.15	5.42	0.58	1.72
Q62383_S	Supt6h	Transcripti	K.AAEDDELEEEADWIYR.N	5.58	14.02	0.40	2.51
Q62383_S	Supt6h	Transcripti	K.ETPETFYIGK#.L	44.12	33.43	1.32	0.76
Q62383_S	Supt6h	Transcripti	K.FGLTPEQFGENLR.D	8.61	28.10	0.31	3.26
Q62383_S	Supt6h	Transcripti	K.FLLGYQPR.G	8.79	35.81	0.25	4.07
Q62383_S	Supt6h	Transcripti	K.FVEEEDDDEEEEEENLDDQDER.G	1.99	7.05	0.28	3.55
Q62383_S	Supt6h	Transcripti	K.GVEGYGNDQTYFEEIK#.Q	19.66	14.56	1.35	0.74
Q62383_S	Supt6h	Transcripti	R.HETEQFPAEPLELAK#.D	7.02	5.24	1.34	0.75
Q62383_S	Supt6h	Transcripti	K.IDTASLGDSTDSYIEVLDGSR.V	4.00	17.76	0.23	4.44
Q62383_S	Supt6h	Transcripti	R.IEYVTVTPEGFR.Y	9.27	29.05	0.32	3.13
Q62383_S	Supt6h	Transcripti	R.IKEDGDEEGEGEEAEDEEQRGPELK.Q	9.69	54.02	0.18	5.57

Q62383_SF	Supt6h	Transcripti	K.KFGLTPEQFGENLR.D	7.62	22.55	0.34	2.96
Q62383_SF	Supt6h	Transcripti	K.KFVEEEDDDEEEEEENLDDQDER.G	3.66	13.08	0.28	3.57
Q62383_SF	Supt6h	Transcripti	K.K#LEELLIK#.T	40.19	25.32	1.59	0.63
Q62383_SF	Supt6h	Transcripti	R.KM*AVDALEYDESAEDANPAGALEEILENPER.L	4.49	16.32	0.28	3.63
Q62383_SF	Supt6h	Transcripti	K.KPHVVTIAGENR.D	18.62	48.71	0.38	2.62
Q62383_SF	Supt6h	Transcripti	R.LKDLDLDAFAEELER.Q	12.87	39.80	0.32	3.09
Q62383_SF	Supt6h	Transcripti	K.M*AEQWLQEK#.E	14.41	16.10	0.89	1.12
Q62383_SF	Supt6h	Transcripti	K.M*AVDALEYDESAEDANPAGALEEILENPER.L	4.58	8.90	0.51	1.94
Q62383_SF	Supt6h	Transcripti	K.M*M*ETM*DQGDVIIRPSSK.G	5.04	25.68	0.20	5.09
Q62383_SF	Supt6h	Transcripti	K.M*QAYQYEQISADPDKPLADGIR.A	5.95	19.25	0.31	3.24
Q62383_SF	Supt6h	Transcripti	K.MQAYQYEQISADPDKPLADGIR.A	3.58	10.12	0.35	2.83
Q62383_SF	Supt6h	Transcripti	R.NQHFEVPFIAFYR.K	4.12	22.07	0.19	5.35
Q62383_SF	Supt6h	Transcripti	R.RPQGESYDQAIR.N	2.86	28.07	0.10	9.81
Q62383_SF	Supt6h	Transcripti	R.SIFEMYEPSELESSHLTDQDNEIR.A	2.83	7.77	0.36	2.74
Q62383_SF	Supt6h	Transcripti	R.SPNTEEIFNM*LTK#.E	21.96	23.35	0.94	1.06
Q62383_SF	Supt6h	Transcripti	R.TPASINATPANINLADLTR.A	3.94	16.87	0.23	4.28
Q62383_SF	Supt6h	Transcripti	R.TRTPASINATPANINLADLTR.A	2.92	7.55	0.39	2.59
Q62383_SF	Supt6h	Transcripti	R.VAPYRPDQQVEEDDDFM*DENQGK.G	10.14	35.92	0.28	3.54
Q62383_SF	Supt6h	Transcripti	R.VAPYRPDQQVEEDDDFMDENQGK.G	2.15	7.07	0.30	3.28
Q62383_SF	Supt6h	Transcripti	R.VLGIAFSSAR.D	4.63	13.23	0.35	2.86
Q62383_SF	Supt6h	Transcripti	R.VNEVGVDVNR.A	76.36	54.99	1.39	0.72
Q62383_SF	Supt6h	Transcripti	R.YM*VALQIAR.E	3.23	9.56	0.34	2.96
Q64310_S	Surf4	Surfeit locu	K.SM*FAGVPTM*R.E	9.55	35.63	0.27	3.73
O54864_S	Suv39h1	Histone-lys	K.FAYNDQGQVR.L	5.52	19.09	0.29	3.46
Q80U70_S	Suz12	Polycomb	K.ALETDGVSGVPK#.Q	49.83	30.40	1.64	0.61
Q80U70_S	Suz12	Polycomb	K.ETLTTELQTR.K	6.31	16.14	0.39	2.56
Q80U70_S	Suz12	Polycomb	K.HGGGGGGGSGPSAGSGGGGFGGSAAAVAAAASGGK#.S	8.63	3.10	2.78	0.36
Q80U70_S	Suz12	Polycomb	K.ALETDGVSGVPK#.Q	33.13	19.00	1.74	0.57
Q80U70_S	Suz12	Polycomb	R.ATWETILDGK#.R	9.37	4.76	1.97	0.51
Q80U70_S	Suz12	Polycomb	K.ETLTTELQTR.K	7.56	17.42	0.43	2.30
Q80U70_S	Suz12	Polycomb	K.HGGGGGGGSGPSAGSGGGGFGGSAAAVAAAASGGK#.S	15.28	9.61	1.59	0.63
Q80U70_S	Suz12	Polycomb	R.NSESLHQENKPGSVKPAQTIAVK.E	35.62	17.60	2.02	0.49
Q6A028_S	Swap70	Switch-ass	K.K#QEWIQAIYSTIHLLK#.L	7.13	2.91	2.45	0.41
Q6A028_S	Swap70	Switch-ass	K.LLAEQEELER.Q	6.63	18.49	0.36	2.79
Q6A028_S	Swap70	Switch-ass	R.QTVSM*AINEVFNELILDVLK#.Q	14.66	4.28	3.43	0.29
Q6A028_S	Swap70	Switch-ass	K.SPLLITEDDAFK#.V	22.14	8.07	2.74	0.36
Q6A028_S	Swap70	Switch-ass	R.GLK#DELLK#.A	9.88	6.31	1.57	0.64
Q6A028_S	Swap70	Switch-ass	K.K#LTEAM*GGGWQQEQFEHYK#.I	8.06	2.16	3.74	0.27
Q6A028_S	Swap70	Switch-ass	K.K#LTEAMGGGWQQEQFEHYK#.I	4.60	3.55	1.30	0.77
Q6A028_S	Swap70	Switch-ass	K.LQEALEDER.Q	13.20	25.49	0.52	1.93
Q6A028_S	Swap70	Switch-ass	R.LQTQVELQTR.F	15.91	24.94	0.64	1.57
A0A0A0MC	Swi5	DNA repair	K.ELYPDFDLNLND.-	23.18	23.18	1.00	1.00
A0A0A0MC	Swi5	DNA repair	R.SPQRPFPMIDENNDVSEEALSSDIK.K	2.50	4.48	0.56	1.79
P48025_KS	Syk	Tyrosine-pr	R.SLLTLEDNELGSGNFGTVK#.K	4.01	2.32	1.72	0.58
Q80X82_S	Sympk	Symplekin	K.AAVEQLLK#.F	12.28	6.79	1.81	0.55
Q80X82_S	Sympk	Symplekin	R.AYLGM*STLGDLIFK#.R	10.20	5.60	1.82	0.55
Q80X82_S	Sympk	Symplekin	R.DHPYIQYNVLWEEGK#.A	7.35	4.58	1.60	0.62
Q80X82_S	Sympk	Symplekin	R.LSDVLK#PLTDAQVEAM*K#.L	9.13	6.08	1.50	0.67
Q80X82_S	Sympk	Symplekin	R.SQALLFIK#.R	9.89	10.93	0.91	1.10
Q80X82_S	Sympk	Symplekin	K.VVLEAPLITESALEVIR.K	2.85	14.57	0.20	5.11
Q80X82_S	Sympk	Symplekin	K.AAVEQLLK#.F	31.13	13.95	2.23	0.45
Q80X82_S	Sympk	Symplekin	R.AYLGMSTLGDLIFK#.R	7.99	3.23	2.47	0.40
Q80X82_S	Sympk	Symplekin	R.DHPYIQYNVLWEEGK#.A	9.20	7.07	1.30	0.77
Q80X82_S	Sympk	Symplekin	K.EVIQALPK#.L	18.85	12.64	1.49	0.67
Q80X82_S	Sympk	Symplekin	K.ILASLVTQFDSGFK#.A	8.27	9.17	0.90	1.11
Q80X82_S	Sympk	Symplekin	K.LNPIVVK#.E	19.75	18.94	1.04	0.96
Q80X82_S	Sympk	Symplekin	R.LSDVLK#PLTDAQVEAM*K#.L	23.97	14.65	1.64	0.61
Q80X82_S	Sympk	Symplekin	R.SQALLFIK#.R	21.15	16.18	1.31	0.76
Q80X82_S	Sympk	Symplekin	R.VVDLLNQAALITNDSK#.I	16.03	8.73	1.84	0.54
Q7TMK9_H	Syncrip	Heterogene	R.AIEALK#EFNEDGALAVLQQFK#.D	21.71	18.80	1.15	0.87
Q7TMK9_H	Syncrip	Heterogene	R.DLFEDELVPLFEK#.A	47.45	36.59	1.30	0.77
Q7TMK9_H	Syncrip	Heterogene	K.DSDLSHVQNK#.S	18.25	14.15	1.29	0.78
Q7TMK9_H	Syncrip	Heterogene	R.LFVGSIPK#.S	38.94	27.80	1.40	0.71
Q7TMK9_H	Syncrip	Heterogene	R.LM*M*DPLTGLNR.G	15.35	12.30	1.25	0.80
Q7TMK9_H	Syncrip	Heterogene	K.SFSQFGK#.L	26.66	12.75	2.09	0.48
Q7TMK9_H	Syncrip	Heterogene	R.TGYTLDVTTGQR.K	11.04	25.11	0.44	2.27
Q7TMK9_H	Syncrip	Heterogene	K.TK#EQILEEFSK#.V	10.34	7.58	1.37	0.73
Q7TMK9_H	Syncrip	Heterogene	K.VTEGLTDVILYHQPDDK#.K	31.93	20.25	1.58	0.63
Q7TMK9_H	Syncrip	Heterogene	K.AGPIWDLR.L	11.72	35.02	0.33	2.99
Q7TMK9_H	Syncrip	Heterogene	R.AIEALKEFNEDGALAVLQQFK.D	37.09	28.07	1.32	0.76
Q7TMK9_H	Syncrip	Heterogene	R.DLFEDELVPLFEK#.A	63.02	42.47	1.48	0.67
Q7TMK9_H	Syncrip	Heterogene	K.DSDLSHVQNK#.S	12.71	7.13	1.78	0.56
Q7TMK9_H	Syncrip	Heterogene	R.K#YGGPPPDSVYSGQQPSVGTEIFVGK#.I	5.10	3.88	1.31	0.76
Q7TMK9_H	Syncrip	Heterogene	R.LFVGSIPK#.S	56.89	40.08	1.42	0.70
Q7TMK9_H	Syncrip	Heterogene	R.LM*M*DPLTGLNR.G	5.12	9.20	0.56	1.80
Q7TMK9_H	Syncrip	Heterogene	R.NLANTVTEEILEK#.S	61.91	47.22	1.31	0.76
Q7TMK9_H	Syncrip	Heterogene	R.TGYTLDVTTGQR.K	12.78	43.16	0.30	3.38
Q7TMK9_H	Syncrip	Heterogene	K.TK#EQILEEFSK#.V	19.30	11.04	1.75	0.57
Q7TMK9_H	Syncrip	Heterogene	K.TKEQILEEFSK.V	18.91	7.83	2.42	0.41
Q7TMK9_H	Syncrip	Heterogene	K.VAEKLDEIYVAGLVAHSDLDER.A	2.43	4.30	0.56	1.77
Q7TMK9_H	Syncrip	Heterogene	K.VWGNVGTVEWADPIEDPDPEVM*AK#.V	4.76	2.99	1.59	0.63
O55101_S	Syngr2	Synaptogyr	R.FLSQPQVVTR.L	7.45	10.57	0.70	1.42
Q8CHC4_S	Synj1	Synaptojan	K.GPAVLPEPLK#PQAAFPQQPSLPTPAQK#.L	6.99	2.10	3.33	0.30
Q8CHC4_S	Synj1	Synaptojan	K.NQTLTDWLLDAPK#.L	6.47	3.44	1.88	0.53
Q8CHC4_S	Synj1	Synaptojan	R.SAEDLDLLNASFQDESK#.I	7.84	2.63	2.98	0.34
Q8CF89_TA	Tab1	TGF-beta-a	K.YGYTDIDLLSAAK#.S	7.08	7.71	0.92	1.09
Q9JJG0_TA	Tacc2	Transformi	R.IGSTEVEKPPGLLFQQPDLDSALQVAR.A	1.74	6.17	0.28	3.54
D3Z4Z0_D	Tada2b	MCG49644	K.M*EESAEYEAAR.H	2.90	5.22	0.56	1.80
Q8R0L9_TA	Tada3	Transcripti	K.GLIGPLTELDTK.D	9.54	10.85	0.88	1.14
Q8R0L9_TA	Tada3	Transcripti	R.WAQEDLLEEQK.D	6.51	6.91	0.94	1.06
Q8K0H5_T	Taf10	Transcripti	K.ASPAGTAGGPVAGVATAGTGPVAAR.A	1.57	6.40	0.24	4.08
P61216_TA	Taf13	Transcripti	R.VQVEDIVFLIR.K	5.27	13.20	0.40	2.50
E9QAP7_E	Taf4a	Protein Taf	K.ALSTVSAQAAAAQK.N	12.37	21.08	0.59	1.70
E9QAP7_E	Taf4a	Protein Taf	K.FFEQLDQIEK.Q	8.62	11.80	0.73	1.37
E9QAP7_E	Taf4a	Protein Taf	R.ILATNSELVGTLTR.S	8.15	11.87	0.69	1.46
Q91WQ5_T	Taf5l	TAF5-like R	K.YLASAGEDQR.L	2.34	9.10	0.26	3.89
Q8R2K4_T	Taf6l	TAF6-like R	K.GNLAPQGSVPSAVSSLTDDLLK#.Y	7.52	5.55	1.35	0.74
Q8R2K4_T	Taf6l	TAF6-like R	K.VALQDLQTNSK#.I	8.03	7.01	1.15	0.87
Q8VI33_TA	Taf9	Transcripti	R.DFLLDIAR.Q	2.74	10.58	0.26	3.87
Q9WVA4_T	Tagln2	Transgelin-	R.DDGLFSGDPNWFPK#.K	32.08	16.65	1.93	0.52
Q9WVA4_T	Tagln2	Transgelin-	K.IQASSM*AFK#.Q	28.57	11.97	2.39	0.42
Q9WVA4_T	Tagln2	Transgelin-	K.LINSLYPEGQAPVK#.K	9.74	3.92	2.49	0.40
Q9WVA4_T	Tagln2	Transgelin-	K.NVIGLQM*GTNR.G	7.07	10.50	0.67	1.48

Q9WVA4_T	Tagln2	Transgelin-	R.YGINTTDIFQTVDLWEGK#.N	13.37	6.04	2.21	0.45
Q0VGY8_T	Tanc1	Protein TA	R.ETVAQSGLVM*QPTK#.Q	9.55	2.86	3.34	0.30
Q0VGY8_T	Tanc1	Protein TA	K.LVEEGNVM*YK#.K	10.39	5.27	1.97	0.51
Q0VGY8_T	Tanc1	Protein TA	R.QIASSSPSLSPK#.S	7.83	2.55	3.07	0.33
Q5F2E8_TA	Taok1	Serine/thre	K.AGNILLTEPGQVK#.L	41.62	21.61	1.93	0.52
Q5F2E8_TA	Taok1	Serine/thre	R.LQHQTELTNQLEYNK#.R	22.07	11.80	1.87	0.53
Q5F2E8_TA	Taok1	Serine/thre	K.AGNILLTEPGQVK#.L	13.27	5.41	2.45	0.41
Q8BYC6_T	Taok3	Serine/thre	R.LQHQTELENQLEYNK#.R	13.65	4.41	3.10	0.32
Q9R233_T	Tapbp	Tapasin OS	K.ATAASLTIPR.N	3.17	13.15	0.24	4.15
Q921F2_T	Tardbp	TAR DNA-bi	R.AFAFVTFADDK.V	148.64	243.06	0.61	1.64
Q921F2_T	Tardbp	TAR DNA-bi	K.DYFSTFGEVLM*VQVK.K	22.76	32.81	0.69	1.44
Q921F2_T	Tardbp	TAR DNA-bi	K.DYFSTFGEVLM*VQVK.K	14.54	16.52	0.88	1.14
Q921F2_T	Tardbp	TAR DNA-bi	K.DYFSTFGEVLMVQVK.K	10.67	31.62	0.34	2.96
Q921F2_T	Tardbp	TAR DNA-bi	K.DYFSTFGEVLMVQVK#.K	22.22	30.94	0.72	1.39
Q921F2_T	Tardbp	TAR DNA-bi	R.FGGNPGGFGNQGGFGNSR.G	58.79	387.15	0.15	6.59
Q921F2_T	Tardbp	TAR DNA-bi	R.FTEYETQVK#.V	555.70	701.17	0.79	1.26
Q921F2_T	Tardbp	TAR DNA-bi	K.GISVHISNAEPK#.H	166.27	236.52	0.70	1.42
Q921F2_T	Tardbp	TAR DNA-bi	R.K#M*DETDASSAVK#.V	182.00	292.81	0.62	1.61
Q921F2_T	Tardbp	TAR DNA-bi	R.K#MDETDASSAVK#.V	76.76	114.56	0.67	1.49
Q921F2_T	Tardbp	TAR DNA-bi	R.LVEGILHAPDAGWGNLVYVVNYPK.D	349.92	384.90	0.91	1.10
Q921F2_T	Tardbp	TAR DNA-bi	R.LVEGILHAPDAGWGNLVYVVNYPK.D	23.26	33.52	0.69	1.44
Q921F2_T	Tardbp	TAR DNA-bi	K.M*DETDASSAVK.V	64.58	122.11	0.53	1.89
Q921F2_T	Tardbp	TAR DNA-bi	K.MDETDASSAVK.V	93.51	116.05	0.81	1.24
Q921F2_T	Tardbp	TAR DNA-bi	K.QSPDEPLR.S	68.48	524.76	0.13	7.66
Q921F2_T	Tardbp	TAR DNA-bi	K.TSDLIVLGLPWK.T	433.32	678.22	0.64	1.57
Q921F2_T	Tardbp	TAR DNA-bi	K.TTEQDLKDYFSTFGEVLM*VQVK.K	54.29	96.23	0.56	1.77
Q921F2_T	Tardbp	TAR DNA-bi	R.FGGNPGGFGNQGGFGNSR.G	3.43	18.03	0.19	5.26
Q921F2_T	Tardbp	TAR DNA-bi	R.FTEYETQVK.V	11.84	13.24	0.89	1.12
Q921F2_T	Tardbp	TAR DNA-bi	R.FGGNPGGFGNQGGFGNSR.G	4.56	30.23	0.15	6.62
Q921F2_T	Tardbp	TAR DNA-bi	R.FTEYETQVK.V	32.56	54.57	0.60	1.68
Q921F2_T	Tardbp	TAR DNA-bi	R.KM*DETDASSAVK.V	8.17	12.51	0.65	1.53
Q921F2_T	Tardbp	TAR DNA-bi	R.K#MDETDASSAVK#.V	5.03	6.25	0.80	1.24
Q921F2_T	Tardbp	TAR DNA-bi	R.LVEGILHAPDAGWGNLVYVVNYPK.D	29.20	22.62	1.29	0.77
Q921F2_T	Tardbp	TAR DNA-bi	K.TSDLIVLGLPWK.T	38.65	42.36	0.91	1.10
Q921F2_T	Tardbp	TAR DNA-bi	R.FTEYETQVK.V	19.08	35.07	0.54	1.84
Q921F2_T	Tardbp	TAR DNA-bi	R.KM*DETDASSAVK.V	7.91	9.41	0.84	1.19
Q921F2_T	Tardbp	TAR DNA-bi	R.LVEGILHAPDAGWGNLVYVVNYPK.D	14.59	20.31	0.72	1.39
Q921F2_T	Tardbp	TAR DNA-bi	K.TSDLIVLGLPWK.T	17.64	28.40	0.62	1.61
Q9D0R2_S	Tars	Threonine-	K.FLGDIEIWNQAEK#.Q	12.19	1.46	8.35	0.12
Q9D0R2_S	Tars	Threonine-	R.M*IAILTENYGGK#.W	6.37	5.86	1.09	0.92
Q9D0R2_S	Tars	Threonine-	R.NAQLAQYNFILVVGEK#.E	4.46	0.00	#DIV/0!	0.00
Q9D0R2_S	Tars	Threonine-	K.FLGDIEIWNQAEK#.Q	27.42	14.27	1.92	0.52
Q9D0R2_S	Tars	Threonine-	R.IYGISFPDPK#.L	44.01	4.30	10.24	0.10
Q9D0R2_S	Tars	Threonine-	K.LK#AEHDSILAEK#.A	64.57	4.09	15.79	0.06
Q9D0R2_S	Tars	Threonine-	K.LLK#EWEK#.F	20.41	1.89	10.80	0.09
Q9D0R2_S	Tars	Threonine-	R.M*IAILTENYGGK#.W	16.38	1.39	11.82	0.08
Q9D0R2_S	Tars	Threonine-	K.QLENSLNEFGEK#.W	11.46	1.24	9.26	0.11
Q9D0R2_S	Tars	Threonine-	K.WELNPGDGAFYGPK#.I	9.41	3.45	2.73	0.37
Q9D0R2_S	Tars	Threonine-	K.ETLLEM*FK#.Y	31.84	3.05	10.45	0.10
Q9D0R2_S	Tars	Threonine-	K.ETLLEMFK#.Y	27.25	2.62	10.39	0.10
Q9D0R2_S	Tars	Threonine-	K.FLGDIEIWNQAEK#.Q	123.59	7.44	16.62	0.06
Q9D0R2_S	Tars	Threonine-	R.IYGISFPDPK#.L	117.65	10.64	11.06	0.09
Q9D0R2_S	Tars	Threonine-	K.LK#AEHDSILAEK#.A	26.59	1.44	18.44	0.05
Q9D0R2_S	Tars	Threonine-	K.LLK#EWEK#.F	42.36	11.40	3.72	0.27
Q9D0R2_S	Tars	Threonine-	R.M*IAILTENYGGK#.W	50.86	3.86	13.18	0.08
Q9D0R2_S	Tars	Threonine-	R.NAQLAQYNFILVVGEK#.E	27.80	2.39	11.61	0.09
Q9D0R2_S	Tars	Threonine-	R.NELSGALTGLTR.V	49.49	20.14	2.46	0.41
Q9D0R2_S	Tars	Threonine-	K.NSSTYWEGK#.A	46.07	8.12	5.67	0.18
Q9D0R2_S	Tars	Threonine-	K.QLENSLNEFGEK#.W	16.93	4.27	3.96	0.25
Q9D0R2_S	Tars	Threonine-	K.QVDAESWK#.T	50.83	4.44	11.45	0.09
Q9D0R2_S	Tars	Threonine-	R.SK#QAEEEF.-	19.65	2.35	8.37	0.12
Q9D0R2_S	Tars	Threonine-	K.WELNPGDGAFYGPK#.I	26.21	2.63	9.96	0.10
Q60949_T	Tbc1d1	TBC1 doma	K.HLTTLTNQEQATIFEEVQK#.L	7.39	2.63	2.81	0.36
Q60949_T	Tbc1d1	TBC1 doma	K.QAFTVAAVQQTAK#.A	7.67	40.82	0.19	5.32
Q60949_T	Tbc1d1	TBC1 doma	K.ANHLGDTDGTPVK#.T	7.45	4.94	1.51	0.66
Q60949_T	Tbc1d1	TBC1 doma	R.GLQDHSASVDLDSSTSSTLSNTSK#.E	19.19	7.93	2.42	0.41
Q60949_T	Tbc1d1	TBC1 doma	K.HLTTLTNQEQATIFEEVQK#.L	15.91	3.14	5.07	0.20
Q60949_T	Tbc1d1	TBC1 doma	R.IQSLEATVEK#.L	23.03	8.74	2.63	0.38
Q60949_T	Tbc1d1	TBC1 doma	K.QAFTVAAVQQTAK#.A	6.57	86.52	0.08	13.18
Q60949_T	Tbc1d1	TBC1 doma	R.SLTESLESILSR.G	8.96	11.11	0.81	1.24
Q60949_T	Tbc1d1	TBC1 doma	K.TISQVFEM*DIAK#.Q	11.95	8.23	1.45	0.69
Q9CXF4_T	Tbc1d15	TBC1 doma	K.ANDQDSLISGILR.V	22.79	13.38	1.70	0.59
Q9CXF4_T	Tbc1d15	TBC1 doma	K.TQLIQLSTLLR.L	3.75	7.78	0.48	2.07
A3KGB4_T	Tbc1d8b	TBC1 doma	R.LYVIQTLEETTK#.Q	10.87	5.31	2.05	0.49
A3KGB4_T	Tbc1d8b	TBC1 doma	K.TLSVFDSNEDITNFVQGK#.I	6.58	3.04	2.16	0.46
Q5SVR0_T	Tbc1d9b	TBC1 doma	R.VVGALVDQGIFEELTR.D	5.41	11.32	0.48	2.09
Q9QXE7_T	Tbl1x	F-box-like/	K.GNYILSAGVDK#.T	13.83	8.99	1.54	0.65
Q9QXE7_T	Tbl1x	F-box-like/	K.HQEPVYSVAFSPDGK#.Y	11.94	6.52	1.83	0.55
Q9QXE7_T	Tbl1x	F-box-like/	K.LAQQQANAAAAAAAAATATSTAATTPAAAAQQNPPK#.N	14.12	7.10	1.99	0.50
Q8BHJ5_T	Tbl1xr1	F-box-like/	K.GPIFALK#.W	44.47	36.08	1.23	0.81
Q8BHJ5_T	Tbl1xr1	F-box-like/	K.LAQQHAAAAAAAAAATNQQGSAK#.N	14.29	12.91	1.11	0.90
Q8BHJ5_T	Tbl1xr1	F-box-like/	R.YLASGSFDK#.C	26.93	40.50	0.66	1.50
Q8C4J7_TB	Tbl3	Transducin	K.VNILDVASGALLR.S	1.42	5.71	0.25	4.02
Q8C4J7_TB	Tbl3	Transducin	R.TVPVFESVEASVLLPEQPAPALGVK#.S	20.80	10.27	2.02	0.49
Q8C4J7_TB	Tbl3	Transducin	K.VNILDVASGALLR.S	2.97	16.31	0.18	5.49
P29037_T	Tbp	TATA-box-b	R.AEIYEAFENIYPILK#.G	9.04	8.49	1.06	0.94
P29037_T	Tbp	TATA-box-b	R.TTALIFSSGK#.V	14.56	8.34	1.74	0.57
P29037_T	Tbp	TATA-box-b	R.AEIYEAFENIYPILK#.G	13.48	10.80	1.25	0.80
Q810F8_T	Tbx10	T-box trans	K.LTNNLMDDNGHIILNSM*HR.Y	2.44	17.46	0.14	7.16
O70306_T	Tbx15	T-box trans	R.TPSLISGIPTPPSLPSNSK.M	3.46	6.24	0.55	1.80
P83940_EL	Tceb1	Transcripti	K.AM*LSGPGQFAENETNEVNFR.E	14.36	38.20	0.38	2.66
P83940_EL	Tceb1	Transcripti	K.AMLSGPGQFAENETNEVNFR.E	2.38	5.06	0.47	2.13
P83940_EL	Tceb1	Transcripti	R.EHALTSGTIK#.A	48.56	18.48	2.63	0.38
P62869_EL	Tceb2	Transcripti	R.ADDTFEALR.I	14.35	42.64	0.34	2.97
P62869_EL	Tceb2	Transcripti	K.ESSTVFELK#.R	40.05	23.87	1.68	0.60
P62869_EL	Tceb2	Transcripti	R.IEPFSSPPELPDVM*K#PQDSGGSANEQAVQ.-	32.69	16.52	1.98	0.51
P62869_EL	Tceb2	Transcripti	R.IVEGILK#.R	70.57	36.51	1.93	0.52
P62869_EL	Tceb2	Transcripti	R.LYKDDQLLDDGK.T	37.74	30.85	1.22	0.82
P62869_EL	Tceb2	Transcripti	R.LYK#DDQLLDDGK#.T	12.31	9.80	1.26	0.80
P62869_EL	Tceb2	Transcripti	K.TTIFTDAK#.E	71.69	41.07	1.75	0.57
Q8CB77_El	Tceb3	Transcripti	K.AFSSPQEEEEAGFTGR.R	3.44	8.59	0.40	2.49
Q8CB77_El	Tceb3	Transcripti	K.FGTGGAAVPEK#.V	25.23	10.04	2.51	0.40
Q61286_H	Tcf12	Transcripti	R.GNAAGSSQTGDALGK.A	2.48	4.77	0.52	1.93

Q61286_H	Tcf12	Transcripti	R.GNAAGSSQTGDALGK.A	6.07	11.01	0.55	1.81
Q9EPQ8_T	Tcf20	Transcripti	R.LYGLQEALEIAR.E	21.14	6.99	3.02	0.33
Q9EPQ8_T	Tcf20	Transcripti	K.NVAPVGILAPEANPK#.A	4.06	5.64	0.72	1.39
Q00417_T	Tcf7	Transcripti	K.K#PLNAFM*LYM*KEMRAK.V	1.42	2.20	0.65	1.55
O08784_T	Tcof1	Treacle pro	R.LLEQAWPLSEAQVQASVVK#.V	5.45	2.95	1.85	0.54
O08784_T	Tcof1	Treacle pro	K.VLTELLEQER.L	5.42	18.14	0.30	3.35
O08784_T	Tcof1	Treacle pro	K.AGAVTSSASLSSPALAK#.G	6.11	3.95	1.55	0.65
P11983_T	Tcp1	T-complex	R.AFHNEAQVNPER.K	14.38	22.46	0.64	1.56
P11983_T	Tcp1	T-complex	R.AFHNEAQVNPERK.N	40.59	45.38	0.89	1.12
P11983_T	Tcp1	T-complex	R.AFHNEAQVNPERK.N	1.63	3.96	0.41	2.43
P11983_T	Tcp1	T-complex	K.DDK#HGSYENAVHSGALDD.-	230.65	61.65	3.74	0.27
P11983_T	Tcp1	T-complex	R.EQLAIAEFAR.S	124.03	170.85	0.73	1.38
P11983_T	Tcp1	T-complex	K.FATEAAITILR.I	93.93	127.43	0.74	1.36
P11983_T	Tcp1	T-complex	K.HGSYENAVHSGALDD.-	98.66	98.66	1.00	1.00
P11983_T	Tcp1	T-complex	K.ILATGANVILTTGGIDDM*YLK#.Y	185.19	52.85	3.50	0.29
P11983_T	Tcp1	T-complex	K.ILATGANVILTTGGIDDM*YLK#.Y	76.72	23.33	3.29	0.30
P11983_T	Tcp1	T-complex	K.ILATGANVILTTGGIDDMYLK#.Y	80.43	21.64	3.72	0.27
P11983_T	Tcp1	T-complex	K.LGVQVVITDPEK#.L	31.37	10.08	3.11	0.32
P11983_T	Tcp1	T-complex	K.LGVQVVITDPEKLDQIR.Q	58.45	58.74	1.00	1.00
P11983_T	Tcp1	T-complex	K.LLEVEHPAAK#.V	161.21	42.21	3.82	0.26
P11983_T	Tcp1	T-complex	K.M*LVDDIGDVTITNDGATILK#.L	67.67	18.79	3.60	0.28
P11983_T	Tcp1	T-complex	K.M*LVDDIGDVTITNDGATILK#.L	54.76	17.92	3.06	0.33
P11983_T	Tcp1	T-complex	K.MLVDDIGDVTITNDGATILK#.L	60.98	16.92	3.60	0.28
P11983_T	Tcp1	T-complex	K.NADELVK#.Q	265.01	79.50	3.33	0.30
P11983_T	Tcp1	T-complex	K.QAGVFEPTIVK#.V	393.13	104.01	3.78	0.26
P11983_T	Tcp1	T-complex	R.SLLVIPNTLAVNAAQDSTDLVAK#.L	451.69	137.79	3.28	0.31
P11983_T	Tcp1	T-complex	R.SLLVIPNTLAVNAAQDSTDLVAK#.L	139.42	39.49	3.53	0.28
P11983_T	Tcp1	T-complex	R.SQNVM*AAASIANIVK#.S	192.44	57.06	3.37	0.30
P11983_T	Tcp1	T-complex	R.SQNVMAAASIANIVK#.S	116.99	33.70	3.47	0.29
P11983_T	Tcp1	T-complex	K.SSFGPVGLDK#.M	310.78	103.58	3.00	0.33
P11983_T	Tcp1	T-complex	R.TSASIILR.G	92.20	112.86	0.82	1.22
P11983_T	Tcp1	T-complex	K.YFVEAGAM*AVR.R	39.27	50.09	0.78	1.28
P11983_T	Tcp1	T-complex	K.YFVEAGAMAVR.R	37.55	43.83	0.86	1.17
P11983_T	Tcp1	T-complex	R.YINENLIINTDELGR.D	26.07	35.95	0.73	1.38
P11983_T	Tcp1	T-complex	R.YPVNSVNILK#.A	477.58	118.31	4.04	0.25
P11983_T	Tcp1	T-complex	K.DDK#HGSYENAVHSGALDD.-	9.02	2.87	3.15	0.32
P11983_T	Tcp1	T-complex	R.EQLAIAEFAR.S	21.13	25.61	0.83	1.21
P11983_T	Tcp1	T-complex	K.FATEAAITILR.I	27.31	26.79	1.02	0.98
P11983_T	Tcp1	T-complex	K.HGSYENAVHSGALDD.-	10.67	10.67	1.00	1.00
P11983_T	Tcp1	T-complex	R.IDDLIK#.L	78.75	18.90	4.17	0.24
P11983_T	Tcp1	T-complex	K.ILATGANVILTTGGIDDM*YLK#.Y	10.85	4.93	2.20	0.45
P11983_T	Tcp1	T-complex	K.ILATGANVILTTGGIDDMYLK#.Y	13.11	17.64	0.74	1.35
P11983_T	Tcp1	T-complex	K.LGVQVVITDPEKLDQIR.Q	11.13	22.98	0.48	2.06
P11983_T	Tcp1	T-complex	K.LLEVEHPAAK#.V	36.35	8.81	4.13	0.24
P11983_T	Tcp1	T-complex	K.M*LVDDIGDVTITNDGATILK#.L	11.57	3.89	2.98	0.34
P11983_T	Tcp1	T-complex	K.NADELVK#.Q	40.31	5.76	7.00	0.14
P11983_T	Tcp1	T-complex	R.SLLVIPNTLAVNAAQDSTDLVAK#.L	133.78	38.62	3.46	0.29
P11983_T	Tcp1	T-complex	R.SQNVM*AAASIANIVK#.S	41.69	14.01	2.97	0.34
P11983_T	Tcp1	T-complex	R.SQNVMAAASIANIVK#.S	21.64	9.91	2.18	0.46
P11983_T	Tcp1	T-complex	K.SSFGPVGLDK#.M	75.55	23.91	3.16	0.32
P11983_T	Tcp1	T-complex	R.TSASIILR.G	19.84	20.46	0.97	1.03
P11983_T	Tcp1	T-complex	K.YFVEAGAM*AVR.R	9.46	12.97	0.73	1.37
P11983_T	Tcp1	T-complex	R.YPVNSVNILK#.A	96.23	27.07	3.55	0.28
P11983_T	Tcp1	T-complex	K.DDK#HGSYENAVHSGALDD.-	49.85	14.43	3.45	0.29
P11983_T	Tcp1	T-complex	R.EQLAIAEFAR.S	19.44	30.19	0.64	1.55
P11983_T	Tcp1	T-complex	R.IDDLIK#.L	81.68	28.10	2.91	0.34
P11983_T	Tcp1	T-complex	K.ILATGANVILTTGGIDDM*YLK#.Y	47.81	15.48	3.09	0.32
P11983_T	Tcp1	T-complex	K.LGVQVVITDPEK#.L	7.03	5.61	1.25	0.80
P11983_T	Tcp1	T-complex	K.LLEVEHPAAK#.V	27.86	12.21	2.28	0.44
P11983_T	Tcp1	T-complex	K.M*LVDDIGDVTITNDGATILK#.L	19.33	6.45	3.00	0.33
P11983_T	Tcp1	T-complex	K.NADELVK#.Q	43.53	13.57	3.21	0.31
P11983_T	Tcp1	T-complex	K.QAGVFEPTIVK#.V	63.53	18.99	3.35	0.30
P11983_T	Tcp1	T-complex	R.SLLVIPNTLAVNAAQDSTDLVAK#.L	191.68	53.82	3.56	0.28
P11983_T	Tcp1	T-complex	R.SQNVM*AAASIANIVK#.S	51.68	14.91	3.47	0.29
P11983_T	Tcp1	T-complex	K.SSFGPVGLDK#.M	74.17	23.23	3.19	0.31
P11983_T	Tcp1	T-complex	R.YPVNSVNILK#.A	80.33	23.40	3.43	0.29
Q8K1H1_T	Tdrd7	Tudor dom	R.ALDVQFLDSGNSTSVK#.V	10.81	4.42	2.44	0.41
Q8K1H1_T	Tdrd7	Tudor dom	R.AQIISTDENK#.I	15.44	9.74	1.59	0.63
Q8K1H1_T	Tdrd7	Tudor dom	K.LAGLEVLNDDPDLVK#.A	13.00	7.21	1.80	0.55
Q8K1H1_T	Tdrd7	Tudor dom	R.SLTGDWIPFK#.Q	8.96	4.42	2.03	0.49
Q8K1H1_T	Tdrd7	Tudor dom	K.YSSGLWASALPK#.A	8.37	5.51	1.52	0.66
Q8K1H1_T	Tdrd7	Tudor dom	R.ALDVQFLDSGNSTSVK#.V	7.93	4.21	1.89	0.53
Q8K1H1_T	Tdrd7	Tudor dom	R.AQIISTDENK#.I	14.51	8.20	1.77	0.57
Q8K1H1_T	Tdrd7	Tudor dom	K.ILK#DEGQAQGDFDIK#.S	11.47	6.24	1.84	0.54
Q8K1H1_T	Tdrd7	Tudor dom	K.LAGLEVLNDDPDLVK#.A	13.37	7.94	1.68	0.59
P30051_TE	Tead1	Transcripti	K.GPQNAFFLVK.F	12.67	20.04	0.63	1.58
P70210_TE	Tead3	Transcripti	K.ALQSM*ASM*SSAQIVSASVLQNK.F	4.15	3.85	1.08	0.93
O35144_TE	Terf2	Telomeric r	R.ALNQPHPGEK#.K	4.95	1.96	2.52	0.40
O35144_TE	Terf2	Telomeric r	K.ALSTAQDSEAAFAK#.L	16.53	11.03	1.50	0.67
O35144_TE	Terf2	Telomeric r	R.LLLEEDSQSTEPSPGLNSSHK#.A	7.30	4.45	1.64	0.61
O35144_TE	Terf2	Telomeric r	K.NLAHPVIQNFSYEVFQQK#.M	16.14	6.71	2.40	0.42
O35144_TE	Terf2	Telomeric r	R.TDLLNIIR.E	1.63	7.83	0.21	4.79
Q91VL8_TE	Terf2ip	Telomeric r	R.IAYTDAEDVAILTYVK#.E	5.68	2.55	2.22	0.45
Q91VL8_TE	Terf2ip	Telomeric r	K.VSTQEVGTAIK#.V	11.93	6.04	1.98	0.51
P47226_TE	Tes	Testin OS=	K.FPSEM*NAQGDK.V	6.55	8.12	0.81	1.24
P47226_TE	Tes	Testin OS=	R.NVM*ILTNPVAAK.K	18.19	19.03	0.96	1.05
P47226_TE	Tes	Testin OS=	R.NVMILTNPVAAK#.K	16.09	12.52	1.29	0.78
P47226_TE	Tes	Testin OS=	K.SEALGVGDVK.F	6.10	6.81	0.90	1.12
Q3URQ0_T	Tex10	Testis-expr	R.ASPEELPVVGQLLR.L	1.64	10.06	0.16	6.14
Q3URQ0_T	Tex10	Testis-expr	K.NFVELISHQQLSK#.G	6.85	6.56	1.04	0.96
Q3URQ0_T	Tex10	Testis-expr	K.VLDILLEHYPALITGR.S	2.92	9.26	0.32	3.17
Q3URQ0_T	Tex10	Testis-expr	R.ASPEELPVVGQLLR.L	3.47	19.21	0.18	5.54
Q3URQ0_T	Tex10	Testis-expr	R.IYDPQEGAVVVLPAESQQR.L	6.48	3.36	1.93	0.52
Q3URQ0_T	Tex10	Testis-expr	K.LENATATNFK#.T	16.46	13.45	1.22	0.82
Q3URQ0_T	Tex10	Testis-expr	R.NPELSTQLIDIIHTAASQANK#.D	12.31	11.30	1.09	0.92
P40630_TF	Tfam	Transcripti	R.SAYNIYVSESFQEAK#DDSAQGK#.L	4.48	5.46	0.82	1.22
Q9ERA6_TF	Tfip11	Tuftelin-int	R.ADLAVAIVYPLVK#.D	14.03	8.82	1.59	0.63
Q9ERA6_TF	Tfip11	Tuftelin-int	K.LILQPWK#.E	13.30	9.37	1.42	0.70
Q9ERA6_TF	Tfip11	Tuftelin-int	R.TEQEIIQSDR.Q	2.91	14.46	0.20	4.97
Q9ERA6_TF	Tfip11	Tuftelin-int	K.VYYSYSQISHK#.H	29.31	14.96	1.96	0.51
Q9ERA6_TF	Tfip11	Tuftelin-int	R.ADLAVAIVYPLVK#.D	22.47	11.50	1.95	0.51
Q9ERA6_TF	Tfip11	Tuftelin-int	K.AEEHNIVFM*PVIGK#.R	16.40	8.26	1.99	0.50
Q9ERA6_TF	Tfip11	Tuftelin-int	R.AVSSNVGAYM*QPGAR.E	4.67	7.47	0.63	1.60

Q9ERA6_TF	Tfip11	Tuftelin-int	R.DYSAPVNFISAGLK#.K	11.84	5.71	2.07	0.48
Q9ERA6_TF	Tfip11	Tuftelin-int	K.LILQPWK#.E	14.07	13.22	1.06	0.94
Q9ERA6_TF	Tfip11	Tuftelin-int	K.SLLENDQLLSHSSQDLSSDAFHR.L	7.78	5.99	1.30	0.77
Q9ERA6_TF	Tfip11	Tuftelin-int	R.TTQSLQDFPVADSEEEAEEEFQK#.E	4.49	4.67	0.96	1.04
Q62219_TC	Tgfb1i1	Transformi	K.GSLDTMLGLLQSDLSR.R	2.73	7.56	0.36	2.77
Q9JJD0_TH	Thap11	THAP doma	R.VPTIFPLR.G	1.37	10.93	0.13	7.96
Q8R3N6_TH	Thoc1	THO compl	R.DK#PITGEQIESFANK#.L	14.14	4.33	3.27	0.31
Q8R3N6_TH	Thoc1	THO compl	K.YSEEVLAVFK#.S	17.41	5.14	3.39	0.30
Q8R3N6_TH	Thoc1	THO compl	R.DK#PITGEQIESFANK#.L	3.83	2.15	1.78	0.56
Q8R3N6_TH	Thoc1	THO compl	K.ILIGNEELTR.L	8.96	15.55	0.58	1.74
Q8R3N6_TH	Thoc1	THO compl	K.SSNYVLTDEQSLWIEDTTK#.S	6.12	2.58	2.37	0.42
Q8R3N6_TH	Thoc1	THO compl	K.YSEEVLAVFK#.S	13.26	6.75	1.96	0.51
Q8R3N6_TH	Thoc1	THO compl	R.DK#PITGEQIESFANK#.L	17.48	10.46	1.67	0.60
Q8R3N6_TH	Thoc1	THO compl	K.SGLNLQSQFNLENVTVFNTNEQESTLGQK#.H	6.78	3.01	2.26	0.44
Q8R3N6_TH	Thoc1	THO compl	K.SGLSDLAESLTNDTETNS.-	10.39	10.39	1.00	1.00
B1AZI6_TH	Thoc2	THO compl	R.LDPETLESLGLIK#.Q	15.05	6.88	2.19	0.46
B1AZI6_TH	Thoc2	THO compl	K.LGLLEALLK#.V	19.74	10.43	1.89	0.53
B1AZI6_TH	Thoc2	THO compl	K.SFDLLILK#.E	13.86	4.67	2.97	0.34
B1AZI6_TH	Thoc2	THO compl	R.ATGFDGGNKADQLDYENFR.H	6.22	10.18	0.61	1.64
B1AZI6_TH	Thoc2	THO compl	R.DFQQALYELSYHVIK#.G	45.78	21.82	2.10	0.48
B1AZI6_TH	Thoc2	THO compl	K.FYQEPSGETPSSLYR.V	8.77	6.41	1.37	0.73
B1AZI6_TH	Thoc2	THO compl	R.LDPETLESLGLIK#.Q	59.01	20.30	2.91	0.34
B1AZI6_TH	Thoc2	THO compl	K.LGLLEALLK#.V	75.73	24.75	3.06	0.33
B1AZI6_TH	Thoc2	THO compl	K.LIAELGQDLSGNITSDLILENIK#.S	26.31	12.55	2.10	0.48
B1AZI6_TH	Thoc2	THO compl	R.NILIVLTK#.I	31.79	8.63	3.69	0.27
B1AZI6_TH	Thoc2	THO compl	K.SFDLLILK#.E	42.44	15.58	2.72	0.37
B1AZI6_TH	Thoc2	THO compl	K.VLNLGQALER.R	15.23	25.50	0.60	1.67
B1AZI6_TH	Thoc2	THO compl	K.YDNLITPVVDSLK#.Y	15.69	5.59	2.81	0.36
Q8BKT7_TH	Thoc5	THO compl	K.TPNPANQYQFDK#.V	12.47	3.58	3.48	0.29
Q8BKT7_TH	Thoc5	THO compl	R.LNSIM*QASLPVQEYLFM*PFDQAHK#.Q	5.88	3.50	1.68	0.59
Q8BKT7_TH	Thoc5	THO compl	K.TLSVAIEGSVDEAK#.A	12.14	6.43	1.89	0.53
Q8BKT7_TH	Thoc5	THO compl	K.TPNPANQYQFDK#.V	18.52	8.94	2.07	0.48
Q5U4D9_TH	Thoc6	THO compl	K.GWLWAEILK#.K	20.49	4.64	4.42	0.23
Q5U4D9_TH	Thoc6	THO compl	R.HLLSAGDGEVK#.G	44.17	19.83	2.23	0.45
Q5U4D9_TH	Thoc6	THO compl	R.SPEVLSGGEDGAVR.L	9.34	18.80	0.50	2.01
Q5U4D9_TH	Thoc6	THO compl	R.TSLEVPEINALLLVPK#.E	9.00	4.46	2.02	0.50
Q5U4D9_TH	Thoc6	THO compl	R.VDVFTNLGYR.A	4.46	14.99	0.30	3.36
Q7TMY4_TH	Thoc7	THO compl	R.INLLVK#.S	38.64	16.85	2.29	0.44
Q7TMY4_TH	Thoc7	THO compl	K.LSEVDEAQESTM*EADPK#P.-	2.98	1.36	2.19	0.46
Q7TMY4_TH	Thoc7	THO compl	K.TLLVYDM*NLR.E	5.12	12.93	0.40	2.53
Q7TMY4_TH	Thoc7	THO compl	K.TLLVYDMNLR.E	7.38	11.97	0.62	1.62
Q8C1A5_TH	Thop1	Thimet olig	R.EELGGLPEDFLSSLEK#.A	13.33	1.80	7.41	0.14
Q8C1A5_TH	Thop1	Thimet olig	R.TGSEAPQDLLEK#.L	10.84	2.63	4.11	0.24
Q8C1A5_TH	Thop1	Thimet olig	K.TSQTVATFLDELAQK#.L	10.42	4.50	2.32	0.43
Q8C1A5_TH	Thop1	Thimet olig	R.VGAQNFEDVSYESTLK#.A	11.14	2.47	4.52	0.22
Q569Z6_TR	Thrap3	Thyroid ho	K.AEEM*EDEPFTER.S	4.81	19.07	0.25	3.97
Q569Z6_TR	Thrap3	Thyroid ho	R.ASVSDLSPR.E	20.11	54.43	0.37	2.71
Q569Z6_TR	Thrap3	Thyroid ho	K.DSRPSQAAGDNQGDEAK.E	2.70	13.35	0.20	4.95
Q569Z6_TR	Thrap3	Thyroid ho	R.EAQVNVR.M	38.44	154.13	0.25	4.01
Q569Z6_TR	Thrap3	Thyroid ho	K.EESAASGGAAYSK#.R	16.41	20.45	0.80	1.25
Q569Z6_TR	Thrap3	Thyroid ho	R.EESTSGFDK#.S	69.25	67.28	1.03	0.97
Q569Z6_TR	Thrap3	Thyroid ho	K.EPEFDDEPK#.F	13.55	17.43	0.78	1.29
Q569Z6_TR	Thrap3	Thyroid ho	K.EQTFSGGTSQDIK#.G	83.96	70.58	1.19	0.84
Q569Z6_TR	Thrap3	Thyroid ho	K.GGFSDADVK#.M	176.01	162.40	1.08	0.92
Q569Z6_TR	Thrap3	Thyroid ho	K.GRKEPEFDDEPK.F	25.17	89.50	0.28	3.56
Q569Z6_TR	Thrap3	Thyroid ho	K.GSESSKPWPDATTYGAGSASR.A	32.88	137.37	0.24	4.18
Q569Z6_TR	Thrap3	Thyroid ho	R.KAEEM*EDEPFTER.S	27.39	99.37	0.28	3.63
Q569Z6_TR	Thrap3	Thyroid ho	R.K#EPEFDDEPK#.F	17.96	49.68	0.36	2.77
Q569Z6_TR	Thrap3	Thyroid ho	R.K#HGLTHEELK#.S	6.98	5.20	1.34	0.75
Q569Z6_TR	Thrap3	Thyroid ho	K.LRDDFEKK.M	11.31	41.95	0.27	3.71
Q569Z6_TR	Thrap3	Thyroid ho	R.M*DSFDEDLARPSGLLAQER.K	7.65	111.15	0.07	14.54
Q569Z6_TR	Thrap3	Thyroid ho	R.MDSFDEDLARPSGLLAQER.K	2.45	36.69	0.07	15.00
Q569Z6_TR	Thrap3	Thyroid ho	K.M*K#SDPFAPK#.T	20.00	26.68	0.75	1.33
Q569Z6_TR	Thrap3	Thyroid ho	K.MK#SDPFAPK#.T	14.03	10.85	1.29	0.77
Q569Z6_TR	Thrap3	Thyroid ho	K.SGK#WESLHTGK#.E	62.59	40.30	1.55	0.64
Q569Z6_TR	Thrap3	Thyroid ho	R.SIFQHIQSAQSQR.S	52.01	227.42	0.23	4.37
Q569Z6_TR	Thrap3	Thyroid ho	R.SNWQNYR.Q	2.41	28.72	0.08	11.90
Q569Z6_TR	Thrap3	Thyroid ho	K.SPLQSVVVR.R	41.89	228.63	0.18	5.46
Q569Z6_TR	Thrap3	Thyroid ho	K.SPPATGSAYGSSQK#.E	13.04	12.93	1.01	0.99
Q569Z6_TR	Thrap3	Thyroid ho	K.SPPATGSAYGSSQK#EESAASGGAAYSK#.R	52.08	42.24	1.23	0.81
Q569Z6_TR	Thrap3	Thyroid ho	R.SPSELFAQHIVTIVHHVK#.E	63.80	58.53	1.09	0.92
Q569Z6_TR	Thrap3	Thyroid ho	K.TDSEKPFR.G	18.20	76.34	0.24	4.19
Q569Z6_TR	Thrap3	Thyroid ho	K.WESLHTGK.E	17.31	21.70	0.80	1.25
Q569Z6_TR	Thrap3	Thyroid ho	K.YKDDPVDLR.L	10.56	71.06	0.15	6.73
Q569Z6_TR	Thrap3	Thyroid ho	K.EQTFSGGTSQDIK#.G	17.66	13.86	1.27	0.78
Q569Z6_TR	Thrap3	Thyroid ho	K.GGFSDADVK#.M	22.49	18.85	1.19	0.84
Q569Z6_TR	Thrap3	Thyroid ho	K.GSESSKPWPDATTYGAGSASR.A	4.18	25.77	0.16	6.16
Q569Z6_TR	Thrap3	Thyroid ho	R.KAEEM*EDEPFTER.S	2.67	11.23	0.24	4.21
Q569Z6_TR	Thrap3	Thyroid ho	R.M*DSFDEDLARPSGLLAQER.K	2.37	15.84	0.15	6.68
Q569Z6_TR	Thrap3	Thyroid ho	K.SPPATGSAYGSSQK.E	4.79	4.95	0.97	1.03
P97770_TH	Thumpd3	THUMP do	R.DFGGAIQEYFK#.W	8.36	3.76	2.22	0.45
P52912_TI	Tia1	Nucleolysi	R.QTFSPFGQIM*EIR.V	5.84	10.07	0.58	1.72
P52912_TI	Tia1	Nucleolysi	R.SQDHFHVFVGDLSPEITTEDIK#.A	4.78	1.55	3.08	0.32
P52912_TI	Tia1	Nucleolysi	K.TLYVGNLSR.D	21.83	48.52	0.45	2.22
P52912_TI	Tia1	Nucleolysi	K.VNWATTPSSQK#.K	70.23	34.65	2.03	0.49
P70318_TI	Tial1	Nucleolysi	R.FEDVVNQSSPK#.N	107.94	49.92	2.16	0.46
P70318_TI	Tial1	Nucleolysi	K.GYGFVSFYNK#.L	14.90	6.87	2.17	0.46
P70318_TI	Tial1	Nucleolysi	K.LDAENAIVHMGGQWLGGR.Q	6.15	19.18	0.32	3.12
P70318_TI	Tial1	Nucleolysi	K.SAFAPFGK#.I	30.55	18.44	1.66	0.60
Q9R1X4_TI	Timeless	Protein tim	R.FGGSYIVQGLK#.S	10.08	4.31	2.34	0.43
Q9R1X4_TI	Timeless	Protein tim	K.EFNFLEYLK#.R	21.57	13.10	1.65	0.61
Q9R1X4_TI	Timeless	Protein tim	R.EVWPEGNAFGSPVISPGEEM*QLLK#.Q	6.58	4.17	1.58	0.63
Q9R1X4_TI	Timeless	Protein tim	R.FGGSYIVQGLK#.S	24.10	11.33	2.13	0.47
Q9R1X4_TI	Timeless	Protein tim	K.LLALGLVSER.R	8.71	20.27	0.43	2.33
Q9R1X4_TI	Timeless	Protein tim	R.NILHVPANLEQEK#.S	23.76	11.80	2.01	0.50
Q9WVA2_T	Timm8a1	Mitochond	K.SK#PVFSESLSD.-	6.87	3.22	2.13	0.47
Q99JR5_TI	Tinagl1	Tubulointe	R.LDGAWWFLR.R	5.38	9.48	0.57	1.76
P39447_ZO	Tjp1	Tight juncti	R.AEQLASVQYTLPK#.T	6.60	4.10	1.61	0.62
P39447_ZO	Tjp1	Tight juncti	R.AEQLASVQYTLPK#.T	22.94	19.36	1.18	0.84
P39447_ZO	Tjp1	Tight juncti	R.DGNIQEGDVVLK#.I	29.37	29.94	0.98	1.02
P39447_ZO	Tjp1	Tight juncti	R.EAGFLRPVTIFGPIADVAR.E	4.33	45.82	0.09	10.59
P39447_ZO	Tjp1	Tight juncti	K.EAIQQQQNQLVWVSEGK.A	7.45	8.39	0.89	1.13
P39447_ZO	Tjp1	Tight juncti	K.EAIQQQQNQLVWVSEGK#.A	8.66	7.69	1.13	0.89

P39447_ZO	Tjp1	Tight juncti	R.EEPDIYQIAK#.S	13.45	12.19	1.10	0.91
P39447_ZO	Tjp1	Tight juncti	K.EGLEEGDQILR.V	8.22	27.03	0.30	3.29
P39447_ZO	Tjp1	Tight juncti	K.EISQDSLAAR.D	11.17	40.33	0.28	3.61
P39447_ZO	Tjp1	Tight juncti	R.FEEPAPLSYDSR.T	4.91	20.71	0.24	4.21
P39447_ZO	Tjp1	Tight juncti	K.GGPAEGQLQENDR.V	5.00	28.70	0.17	5.74
P39447_ZO	Tjp1	Tight juncti	R.HEEQPAPAYEVHNR.Y	9.60	49.79	0.19	5.18
P39447_ZO	Tjp1	Tight juncti	R.IVESDVGDSFYIR.T	9.48	21.28	0.45	2.25
P39447_ZO	Tjp1	Tight juncti	R.LAGGNDVGIFVAGVLEDSPAAK#.E	11.17	10.17	1.10	0.91
P39447_ZO	Tjp1	Tight juncti	K.LGSWLAIR.I	3.82	13.48	0.28	3.53
P39447_ZO	Tjp1	Tight juncti	K.SREDLSAQPVQTK.F	5.28	20.14	0.26	3.82
P39447_ZO	Tjp1	Tight juncti	R.SVASSQPAKPTK.V	9.39	11.82	0.79	1.26
P39447_ZO	Tjp1	Tight juncti	R.YEVSSYTDQFSR.N	4.65	21.39	0.22	4.60
P39447_ZO	Tjp1	Tight juncti	K.YQM*NNISTM*PK#.A	12.72	12.11	1.05	0.95
Q9Z0U1_ZO	Tjp2	Tight juncti	R.EDAVLYLLEIPKGETVTILAQSR.A	2.31	15.90	0.15	6.89
Q9Z0U1_ZO	Tjp2	Tight juncti	R.GFEVIEEFDGR.S	2.83	8.87	0.32	3.14
Q9Z0U1_ZO	Tjp2	Tight juncti	K.IAAIVVK#.R	26.49	16.41	1.61	0.62
Q9Z0U1_ZO	Tjp2	Tight juncti	R.LATELPDLFQTAK#.T	25.64	17.11	1.50	0.67
Q9Z0U1_ZO	Tjp2	Tight juncti	R.LGSQIFIK#.E	34.66	18.53	1.87	0.53
Q9Z0U1_ZO	Tjp2	Tight juncti	R.LISDFEDTDGEGGAYTDNELEEPAEEPLVSSITR.S	2.24	5.66	0.39	2.53
Q9Z0U1_ZO	Tjp2	Tight juncti	K.RPVVLFGPIADIAM*ER.L	1.75	14.04	0.12	8.03
Q9Z0U1_ZO	Tjp2	Tight juncti	R.RQQYSDQDYHSSTEK.L	1.52	3.31	0.46	2.18
Q9Z0U1_ZO	Tjp2	Tight juncti	K.SNLPATAGSEIPGGSTK#.G	23.95	21.56	1.11	0.90
Q9Z0U1_ZO	Tjp2	Tight juncti	K.STGDITAAGVTEASR.E	40.21	10.02	4.02	0.25
Q9Z0U1_ZO	Tjp2	Tight juncti	R.VVDTLYDGK#.L	28.16	17.90	1.57	0.64
Q9Z0U1_ZO	Tjp2	Tight juncti	R.VVDTLYDGK#.L	18.20	14.25	1.28	0.78
P40142_TK	Tkt	Transketola	K.AVELAANTK#.G	114.72	20.27	5.66	0.18
P40142_TK	Tkt	Transketola	K.HQPTAIIAK#.T	239.67	57.39	4.18	0.24
P40142_TK	Tkt	Transketola	R.IIALDGDTK#.N	200.65	33.63	5.97	0.17
P40142_TK	Tkt	Transketola	K.ILATPPQEDAPSVDIANIR.M	23.21	20.90	1.11	0.90
P40142_TK	Tkt	Transketola	K.ISSDLDGHPVPK#.Q	29.70	3.74	7.95	0.13
P40142_TK	Tkt	Transketola	R.K#AYGLALAK#.L	141.38	26.31	5.37	0.19
P40142_TK	Tkt	Transketola	R.K#ISSDLDGHPVPK#.Q	61.37	11.67	5.26	0.19
P40142_TK	Tkt	Transketola	R.LAVSQVPR.S	53.91	35.17	1.53	0.65
P40142_TK	Tkt	Transketola	K.LDNLVAIFDINR.L	77.50	29.68	2.61	0.38
P40142_TK	Tkt	Transketola	R.LGQSDPAPLQHQVDIYQK#.R	152.19	28.92	5.26	0.19
P40142_TK	Tkt	Transketola	K.M*FGIDK#DAIVQAVK#.G	70.45	18.36	3.84	0.26
P40142_TK	Tkt	Transketola	K.MFGIDK#DAIVQAVK#.G	48.21	4.44	10.86	0.09
P40142_TK	Tkt	Transketola	R.M*PTPPSYK#.V	48.46	13.73	3.53	0.28
P40142_TK	Tkt	Transketola	K.NM*AEQIIQEIYSQVQSK#.K	95.27	12.89	7.39	0.14
P40142_TK	Tkt	Transketola	K.NSTFSELFK#.K	155.05	24.85	6.24	0.16
P40142_TK	Tkt	Transketola	K.SK#DDQVTVIGAGVTLHEALAAAESLK#K#.D	92.68	16.84	5.50	0.18
P40142_TK	Tkt	Transketola	R.SVPM*STVFYPSDGVATEK#.A	50.75	9.29	5.47	0.18
P40142_TK	Tkt	Transketola	R.SVPMSTVFYPSDGVATEK#.A	35.77	7.72	4.63	0.22
P40142_TK	Tkt	Transketola	R.TSRPENAIIYSNNEDFQVGQAK.V	37.95	24.13	1.57	0.64
P40142_TK	Tkt	Transketola	K.HQPTAIIAK#.T	12.98	2.98	4.35	0.23
P40142_TK	Tkt	Transketola	R.TSRPENAIIYSNNEDFQVGQAK.V	3.99	4.40	0.91	1.10
P40142_TK	Tkt	Transketola	K.AVELAANTK#.G	121.62	18.89	6.44	0.16
P40142_TK	Tkt	Transketola	K.AYGLALAK#.L	39.77	5.36	7.42	0.13
P40142_TK	Tkt	Transketola	K.HQPTAIIAK#.T	237.47	37.48	6.34	0.16
P40142_TK	Tkt	Transketola	R.IIALDGDTK#.N	116.15	19.18	6.06	0.17
P40142_TK	Tkt	Transketola	K.ILATPPQEDAPSVDIANIR.M	17.12	16.06	1.07	0.94
P40142_TK	Tkt	Transketola	R.K#AYGLALAK#.L	83.42	15.62	5.34	0.19
P40142_TK	Tkt	Transketola	R.K#ISSDLDGHPVPK#.Q	44.45	8.54	5.20	0.19
P40142_TK	Tkt	Transketola	K.LDNLVAIFDINR.L	47.68	31.59	1.51	0.66
P40142_TK	Tkt	Transketola	R.LGQSDPAPLQHQVDIYQK#.R	101.99	15.81	6.45	0.16
P40142_TK	Tkt	Transketola	K.M*FGIDK#DAIVQAVK#.G	18.81	3.60	5.23	0.19
P40142_TK	Tkt	Transketola	K.M*FGIDK#DAIVQAVK#.G	51.66	7.97	6.48	0.15
P40142_TK	Tkt	Transketola	K.MFGIDK#DAIVQAVK#.G	45.23	4.51	10.03	0.10
P40142_TK	Tkt	Transketola	R.M*PTPPSYK#.V	53.03	14.86	3.57	0.28
P40142_TK	Tkt	Transketola	R.MPTPPSYK#.V	36.26	10.43	3.48	0.29
P40142_TK	Tkt	Transketola	K.NM*AEQIIQEIYSQVQSK#.K	83.53	12.46	6.70	0.15
P40142_TK	Tkt	Transketola	K.NSTFSELFK#.K	92.09	16.48	5.59	0.18
P40142_TK	Tkt	Transketola	K.NSTFSELFK#K#.E	15.37	6.35	2.42	0.41
P40142_TK	Tkt	Transketola	R.SGK#PAELLK#.M	77.24	10.45	7.39	0.14
P40142_TK	Tkt	Transketola	K.SK#DDQVTVIGAGVTLHEALAAAESLK#.K	6.84	2.14	3.19	0.31
P40142_TK	Tkt	Transketola	K.SK#DDQVTVIGAGVTLHEALAAAESLK#K#.D	107.77	24.11	4.47	0.22
P40142_TK	Tkt	Transketola	R.SVPM*STVFYPSDGVATEK#.A	33.10	5.51	6.01	0.17
P40142_TK	Tkt	Transketola	R.SVPMSTVFYPSDGVATEK#.A	24.34	7.57	3.22	0.31
P40142_TK	Tkt	Transketola	R.TSRPENAIIYSNNEDFQVGQAK.V	26.59	15.64	1.70	0.59
P40142_TK	Tkt	Transketola	K.AVELAANTK#.G	103.52	19.17	5.40	0.19
P40142_TK	Tkt	Transketola	K.HQPTAIIAK#.T	260.78	46.33	5.63	0.18
P40142_TK	Tkt	Transketola	R.IIALDGDTK#.N	150.82	18.07	8.35	0.12
P40142_TK	Tkt	Transketola	K.ILATPPQEDAPSVDIANIR.M	13.06	11.50	1.14	0.88
P40142_TK	Tkt	Transketola	K.ISSDLDGHPVPK#.Q	19.35	5.96	3.24	0.31
P40142_TK	Tkt	Transketola	R.K#AYGLALAK#.L	55.10	11.09	4.97	0.20
P40142_TK	Tkt	Transketola	R.LAVSQVPR.S	33.33	26.45	1.26	0.79
P40142_TK	Tkt	Transketola	K.LDNLVAIFDINR.L	31.32	26.75	1.17	0.85
P40142_TK	Tkt	Transketola	K.M*FGIDK#DAIVQAVK#.G	65.46	9.84	6.65	0.15
P40142_TK	Tkt	Transketola	K.MFGIDK#DAIVQAVK#.G	28.24	4.50	6.28	0.16
P40142_TK	Tkt	Transketola	R.M*PTPPSYK#.V	53.30	12.54	4.25	0.24
P40142_TK	Tkt	Transketola	K.NM*AEQIIQEIYSQVQSK#.K	83.61	15.98	5.23	0.19
P40142_TK	Tkt	Transketola	K.NSTFSELFK#.K	81.19	14.23	5.71	0.18
P40142_TK	Tkt	Transketola	K.SK#DDQVTVIGAGVTLHEALAAAESLK#.K	6.00	1.71	3.51	0.28
P40142_TK	Tkt	Transketola	K.SK#DDQVTVIGAGVTLHEALAAAESLK#K#.D	55.23	8.07	6.85	0.15
P40142_TK	Tkt	Transketola	R.SVPM*STVFYPSDGVATEK#.A	39.96	70.98	0.56	1.78
P40142_TK	Tkt	Transketola	R.SVPMSTVFYPSDGVATEK#.A	18.87	2.83	6.66	0.15
P40142_TK	Tkt	Transketola	R.TSRPENAIIYSNNEDFQVGQAK.V	26.64	20.04	1.33	0.75
P26039_TL	Tln1	Talin-1 OS=	K.AAAFEDQENETVVVK#.E	14.57	41.21	0.35	2.83
P26039_TL	Tln1	Talin-1 OS=	K.LAQAAQSSVATITR.L	3.22	6.40	0.50	1.99
P26039_TL	Tln1	Talin-1 OS=	K.LGAASLGAEDPETQVVLINAVK#.D	6.25	5.40	1.16	0.86
P26039_TL	Tln1	Talin-1 OS=	K.TYGVSFFLVK#.E	28.24	6.39	4.42	0.23
P26039_TL	Tln1	Talin-1 OS=	R.VAGSVTELIQAAEAM*K#.G	5.53	24.72	0.22	4.47
P26039_TL	Tln1	Talin-1 OS=	R.VAGSVTELIQAAEAMK#.G	7.02	4.78	1.47	0.68
P26039_TL	Tln1	Talin-1 OS=	K.VGDDPAVWQLK#.N	8.35	8.25	1.01	0.99
P26039_TL	Tln1	Talin-1 OS=	K.VMVTNVTSLLK#.T	9.59	6.11	1.57	0.64
P26039_TL	Tln1	Talin-1 OS=	K.AAAFEDQENETVVVK#.E	28.81	8.08	3.56	0.28
P26039_TL	Tln1	Talin-1 OS=	R.AAMEPIVISAK#.T	14.03	4.49	3.12	0.32
P26039_TL	Tln1	Talin-1 OS=	K.AIAVTVQEMVTK#.S	28.92	7.01	4.13	0.24
P26039_TL	Tln1	Talin-1 OS=	K.ALGDLISATK#.A	44.93	13.07	3.44	0.29
P26039_TL	Tln1	Talin-1 OS=	K.ALSTDPASPNLK#.S	48.69	16.10	3.02	0.33
P26039_TL	Tln1	Talin-1 OS=	K.AVASAAAALVLK#.A	38.08	11.07	3.44	0.29
P26039_TL	Tln1	Talin-1 OS=	K.EADESLNFEEQILEAAK#.S	31.82	8.52	3.73	0.27
P26039_TL	Tln1	Talin-1 OS=	K.EVANSTANLVK#.T	54.55	18.39	2.97	0.34

P26039_TL Tln1	Talin-1 OS= R.GSQAQPDSPSAQLALIAASQSFLQPGGK#.M	24.32	12.14	2.00	0.50
P26039_TL Tln1	Talin-1 OS= R.ILAQATSDLVNAIK#.A	37.93	13.23	2.87	0.35
P26039_TL Tln1	Talin-1 OS= R.IPEALAGPPNDFGLFLSDDDPK#.K	4.58	2.36	1.95	0.51
P26039_TL Tln1	Talin-1 OS= K.ISIGNVVK#.T	25.14	9.95	2.53	0.40
P26039_TL Tln1	Talin-1 OS= K.LAQAAQSSVATITR.L	13.83	21.56	0.64	1.56
P26039_TL Tln1	Talin-1 OS= R.LASQAK#PAAVAAENEEIGAHIK#.H	28.74	7.42	3.88	0.26
P26039_TL Tln1	Talin-1 OS= K.LGAASLGAEDPETQVVLINAVK#.D	29.42	9.43	3.12	0.32
P26039_TL Tln1	Talin-1 OS= K.LLGEIAQGNENYAGIAAR.D	3.69	10.69	0.35	2.90
P26039_TL Tln1	Talin-1 OS= R.LNEAAAGLNQAATELVQASR.G	3.87	5.39	0.72	1.39
P26039_TL Tln1	Talin-1 OS= R.M*ATNAAAQNAIK#.K	20.42	8.20	2.49	0.40
P26039_TL Tln1	Talin-1 OS= K.NLGTALAELR.T	8.26	15.46	0.53	1.87
P26039_TL Tln1	Talin-1 OS= K.QAAASATQTIAAAQHAASAPK#.A	49.13	19.74	2.49	0.40
P26039_TL Tln1	Talin-1 OS= R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	3.82	4.24	0.90	1.11
P26039_TL Tln1	Talin-1 OS= K.SIAAATSALVK.A	39.58	70.02	0.57	1.77
P26039_TL Tln1	Talin-1 OS= K.TLAESALQLLYTAK#.E	78.44	30.21	2.60	0.39
P26039_TL Tln1	Talin-1 OS= K.TYGVSFFLVK#.E	32.68	11.11	2.94	0.34
P26039_TL Tln1	Talin-1 OS= R.VAGSVTELIQAAEAM*K#.G	7.98	4.96	1.61	0.62
P26039_TL Tln1	Talin-1 OS= R.VAGSVTELIQAAEAMK#.G	14.55	4.61	3.16	0.32
P26039_TL Tln1	Talin-1 OS= K.VGAIPANALDDGQWSQGLISAAR.M	7.19	7.51	0.96	1.05
P26039_TL Tln1	Talin-1 OS= K.VGDDPAVWQLK#.N	29.94	5.99	5.00	0.20
P26039_TL Tln1	Talin-1 OS= K.VLGEAM*TGISQNAK#.N	29.86	10.48	2.85	0.35
P26039_TL Tln1	Talin-1 OS= K.VLVQNAAGSQEK#.L	101.80	25.25	4.03	0.25
P26039_TL Tln1	Talin-1 OS= K.VM*VTNVTSLLK#.T	16.54	13.46	1.23	0.81
P26039_TL Tln1	Talin-1 OS= K.VMVTNVTSLLK#.T	34.52	13.13	2.63	0.38
P26039_TL Tln1	Talin-1 OS= K.VSQM*AQYFEPLTLAAVGAASK#.T	17.02	5.96	2.85	0.35
P26039_TL Tln1	Talin-1 OS= K.AAAFEDQENETVVVK#.E	369.18	139.63	2.64	0.38
P26039_TL Tln1	Talin-1 OS= K.AAAFEDQENETVVVKEK.M	83.78	26.61	3.15	0.32
P26039_TL Tln1	Talin-1 OS= R.AAM*EPIVISAK#.T	471.63	204.82	2.30	0.43
P26039_TL Tln1	Talin-1 OS= R.AAMEPIVISAK#.T	162.76	66.79	2.44	0.41
P26039_TL Tln1	Talin-1 OS= K.ADAEGESDLENSR.K	59.36	117.07	0.51	1.97
P26039_TL Tln1	Talin-1 OS= R.AEASQLGHK#.V	58.35	23.44	2.49	0.40
P26039_TL Tln1	Talin-1 OS= K.AGFLDLK#DFLPK#.E	294.61	116.37	2.53	0.39
P26039_TL Tln1	Talin-1 OS= K.AIAVTVQEM*VTK#.S	334.68	141.75	2.36	0.42
P26039_TL Tln1	Talin-1 OS= K.AIAVTVQEMVTK#.S	262.49	107.54	2.44	0.41
P26039_TL Tln1	Talin-1 OS= K.ALDGDFTEENR.A	88.86	152.62	0.58	1.72
P26039_TL Tln1	Talin-1 OS= K.ALDYYM*LR.N	51.51	84.09	0.61	1.63
P26039_TL Tln1	Talin-1 OS= K.ALDYYMLR.N	14.83	14.52	1.02	0.98
P26039_TL Tln1	Talin-1 OS= K.ALGDLISATK#.A	478.36	161.65	2.96	0.34
P26039_TL Tln1	Talin-1 OS= K.ALSTDPASPNLK#.S	560.35	184.79	3.03	0.33
P26039_TL Tln1	Talin-1 OS= R.AQVVSNLK#.G	675.71	230.40	2.93	0.34
P26039_TL Tln1	Talin-1 OS= R.ASDNLVK#.A	132.67	118.90	1.12	0.90
P26039_TL Tln1	Talin-1 OS= K.ASGHPGDPESQQR.L	6.11	10.40	0.59	1.70
P26039_TL Tln1	Talin-1 OS= K.ASSLIEEAK#.K	102.91	38.71	2.66	0.38
P26039_TL Tln1	Talin-1 OS= K.AVAEQIPLLVQGVR.G	79.40	152.91	0.52	1.93
P26039_TL Tln1	Talin-1 OS= K.AVASAAAALVLK#.A	441.33	164.80	2.68	0.37
P26039_TL Tln1	Talin-1 OS= K.AVEDEATK#.G	63.45	23.71	2.68	0.37
P26039_TL Tln1	Talin-1 OS= K.AVTQALNR.C	125.73	220.10	0.57	1.75
P26039_TL Tln1	Talin-1 OS= K.DHFGLEGDEESTM*LEDSVSPK#.K	58.58	23.77	2.46	0.41
P26039_TL Tln1	Talin-1 OS= R.DLDQASLAAVSQQLAPR.E	31.69	62.34	0.51	1.97
P26039_TL Tln1	Talin-1 OS= R.DPVQLNLLYVQAR.D	19.86	28.90	0.69	1.46
P26039_TL Tln1	Talin-1 OS= K.EADESLNFEEQILEAAK#.S	127.64	50.16	2.54	0.39
P26039_TL Tln1	Talin-1 OS= R.EGAETFADHR.E	38.45	74.81	0.51	1.95
P26039_TL Tln1	Talin-1 OS= R.ERIPEALAGPPNDFGLFLSDDDPK.K	9.24	29.52	0.31	3.20
P26039_TL Tln1	Talin-1 OS= K.EVANSTANLVK#.T	686.01	227.00	3.02	0.33
P26039_TL Tln1	Talin-1 OS= K.EVIQEWSLTNIK#.R	63.43	28.69	2.21	0.45
P26039_TL Tln1	Talin-1 OS= K.FFYSDQNVDSR.D	15.57	38.16	0.41	2.45
P26039_TL Tln1	Talin-1 OS= R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	25.10	38.12	0.66	1.52
P26039_TL Tln1	Talin-1 OS= K.GAAAHPDSEEQQQR.L	23.34	51.67	0.45	2.21
P26039_TL Tln1	Talin-1 OS= K.GITM*ATAK#.A	169.47	58.47	2.90	0.35
P26039_TL Tln1	Talin-1 OS= K.GIWLEAGK#.A	154.05	61.21	2.52	0.40
P26039_TL Tln1	Talin-1 OS= R.GSQAQPDSPSAQLALIAASQSFLQPGGK#.M	501.55	205.39	2.44	0.41
P26039_TL Tln1	Talin-1 OS= R.GVAALTSDPAVQAIVLDTASDVLDK#.A	44.55	15.93	2.80	0.36
P26039_TL Tln1	Talin-1 OS= R.IGITNHDEYSLVR.E	124.05	196.68	0.63	1.59
P26039_TL Tln1	Talin-1 OS= K.ILADATAK#.M	538.00	183.92	2.93	0.34
P26039_TL Tln1	Talin-1 OS= R.ILAQATSDLVNAIK#.A	255.62	114.14	2.24	0.45
P26039_TL Tln1	Talin-1 OS= R.ILAQATSDLVNAIKADAEGESDLENSR.K	6.42	6.38	1.01	0.99
P26039_TL Tln1	Talin-1 OS= R.IPEALAGPPNDFGLFLSDDDPK#.K	80.91	41.23	1.96	0.51
P26039_TL Tln1	Talin-1 OS= R.IPEALAGPPNDFGLFLSDDDPK#K#.G	120.44	50.83	2.37	0.42
P26039_TL Tln1	Talin-1 OS= K.ISIGNVVK#.T	227.06	100.42	2.26	0.44
P26039_TL Tln1	Talin-1 OS= K.K#GIWLEAGK#.A	81.74	28.34	2.88	0.35
P26039_TL Tln1	Talin-1 OS= K.KLEQLKPR.A	9.65	20.19	0.48	2.09
P26039_TL Tln1	Talin-1 OS= K.KSTVLQQQYNR.V	57.04	81.51	0.70	1.43
P26039_TL Tln1	Talin-1 OS= K.LAQAAQSSVATITR.L	166.12	322.71	0.51	1.94
P26039_TL Tln1	Talin-1 OS= R.LASQAK#PAAVAAENEEIGAHIK#.H	432.11	134.66	3.21	0.31
P26039_TL Tln1	Talin-1 OS= R.LASQAKPAAVAAENEEIGAHIK.H	142.35	42.97	3.31	0.30
P26039_TL Tln1	Talin-1 OS= K.LGAASLGAEDPETQVVLINAVK#.D	474.77	187.37	2.53	0.39
P26039_TL Tln1	Talin-1 OS= K.LK#PLPGETM*EK#.C	171.69	69.43	2.47	0.40
P26039_TL Tln1	Talin-1 OS= K.LK#PLPGETMEK#.C	69.60	34.52	2.02	0.50
P26039_TL Tln1	Talin-1 OS= K.LLAALLEDEGGNGRPLLQAAK.G	60.70	99.74	0.61	1.64
P26039_TL Tln1	Talin-1 OS= K.LLGEIAQGNENYAGIAAR.D	60.18	120.88	0.50	2.01
P26039_TL Tln1	Talin-1 OS= R.LLSDSLPPSTGTFQEAQSR.L	11.35	19.17	0.59	1.69
P26039_TL Tln1	Talin-1 OS= R.LNEAAAGLNQAATELVQASR.G	39.59	65.41	0.61	1.65
P26039_TL Tln1	Talin-1 OS= R.LNEAAAGLNQAATELVQASR.G	75.06	140.93	0.53	1.88
P26039_TL Tln1	Talin-1 OS= R.LQAAGNAVK#.R	356.44	151.17	2.36	0.42
P26039_TL Tln1	Talin-1 OS= R.LREAAEGLR.M	8.70	36.46	0.24	4.19
P26039_TL Tln1	Talin-1 OS= R.MATNAAAQNAIK#.K	207.31	81.37	2.55	0.39
P26039_TL Tln1	Talin-1 OS= R.M*ATNAAAQNAIK#.K	300.42	108.57	2.77	0.36
P26039_TL Tln1	Talin-1 OS= R.M*ATNAAAQNAIKK.K	22.37	9.60	2.33	0.43
P26039_TL Tln1	Talin-1 OS= R.M*LDGTVK#.T	156.86	446.03	0.35	2.84
P26039_TL Tln1	Talin-1 OS= K.M*VGGIAQIIAAQEEM*LR.K	10.05	14.47	0.69	1.44
P26039_TL Tln1	Talin-1 OS= K.M*VGGIAQIIAAQEEMLR.K	7.43	13.63	0.55	1.83
P26039_TL Tln1	Talin-1 OS= K.NGNLPEFGDAIATASK#.A	167.69	62.66	2.68	0.37
P26039_TL Tln1	Talin-1 OS= K.NLGTALAELR.T	132.22	210.43	0.63	1.59
P26039_TL Tln1	Talin-1 OS= K.QAAASATQTIAAAQHAASAPK#.A	829.62	291.71	2.84	0.35
P26039_TL Tln1	Talin-1 OS= R.QEDVIATANLSR.R	50.46	83.03	0.61	1.65
P26039_TL Tln1	Talin-1 OS= R.RAIADMLR.A	3.47	239.20	0.01	68.95
P26039_TL Tln1	Talin-1 OS= K.RVAGSVTELIQAAEAM*K.G	12.00	20.17	0.59	1.68
P26039_TL Tln1	Talin-1 OS= K.RVAGSVTELIQAAEAMK.G	4.84	14.81	0.33	3.06
P26039_TL Tln1	Talin-1 OS= R.SAQPASAEPR.Q	47.23	94.27	0.50	2.00
P26039_TL Tln1	Talin-1 OS= R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	42.05	67.17	0.63	1.60
P26039_TL Tln1	Talin-1 OS= R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	7.94	11.48	0.69	1.45
P26039_TL Tln1	Talin-1 OS= R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	14.36	26.38	0.54	1.84
P26039_TL Tln1	Talin-1 OS= R.SGASGPENFQVGSMPPAQQQITSGQM*HR.G	5.22	7.50	0.70	1.44

P26039_TL	Tln1	Talin-1 OS=	R.SGASGPENFQVGSMPPAQQQITSGQMHR.G	5.78	9.62	0.60	1.66
P26039_TL	Tln1	Talin-1 OS=	K.SIAAATSALVK#.A	497.40	183.08	2.72	0.37
P26039_TL	Tln1	Talin-1 OS=	K.SKDHFGLEGDEESTM*LEDSVSPK.K	54.35	20.60	2.64	0.38
P26039_TL	Tln1	Talin-1 OS=	K.SK#DHFGLEGDEESTMLEDSVSPK#.K	36.75	15.33	2.40	0.42
P26039_TL	Tln1	Talin-1 OS=	K.SKDHFGLEGDEESTMLEDSVSPK.K	17.47	7.76	2.25	0.44
P26039_TL	Tln1	Talin-1 OS=	K.SNTSPEELGPLANQLTSDYGR.L	23.67	50.08	0.47	2.12
P26039_TL	Tln1	Talin-1 OS=	K.SQLAAAAR.A	39.10	104.62	0.37	2.68
P26039_TL	Tln1	Talin-1 OS=	K.STVLQQQYNR.V	47.41	97.13	0.49	2.05
P26039_TL	Tln1	Talin-1 OS=	K.TIM*VDDSK#.T	155.28	60.45	2.57	0.39
P26039_TL	Tln1	Talin-1 OS=	K.TK#EVIQEWSLTNIK#.R	75.57	21.61	3.50	0.29
P26039_TL	Tln1	Talin-1 OS=	K.TLAESALQLLYTAK#.E	1177.05	444.71	2.65	0.38
P26039_TL	Tln1	Talin-1 OS=	K.TLSHPQQM*ALLDQTK#.T	374.36	149.80	2.50	0.40
P26039_TL	Tln1	Talin-1 OS=	K.TLSHPQQMALLDQTK#.T	158.53	55.98	2.83	0.35
P26039_TL	Tln1	Talin-1 OS=	K.TM*LESAGGLIQTAR.A	39.39	80.84	0.49	2.05
P26039_TL	Tln1	Talin-1 OS=	K.TMLESAGGLIQTAR.A	34.19	56.04	0.61	1.64
P26039_TL	Tln1	Talin-1 OS=	K.TSTPEDFIR.M	103.70	177.28	0.58	1.71
P26039_TL	Tln1	Talin-1 OS=	R.TVSDSIK#K#.L	76.13	29.37	2.59	0.39
P26039_TL	Tln1	Talin-1 OS=	K.TYGVSFFLVK#.E	286.83	94.78	3.03	0.33
P26039_TL	Tln1	Talin-1 OS=	R.VAGSVTELIQAAEAM*K#.G	192.53	78.72	2.45	0.41
P26039_TL	Tln1	Talin-1 OS=	R.VAGSVTELIQAAEAM*K#.G	159.14	67.72	2.35	0.43
P26039_TL	Tln1	Talin-1 OS=	R.VAGSVTELIQAAEAMK#.G	156.85	56.87	2.76	0.36
P26039_TL	Tln1	Talin-1 OS=	K.VGAIPANALDDGQWSQGLISAAR.M	19.37	38.09	0.51	1.97
P26039_TL	Tln1	Talin-1 OS=	K.VGDDPAVWQLK#.N	439.22	160.15	2.74	0.36
P26039_TL	Tln1	Talin-1 OS=	K.VLGEAM*TGISQNAK#.N	400.50	153.88	2.60	0.38
P26039_TL	Tln1	Talin-1 OS=	K.VLGEAMTGISQNAK#.N	154.65	51.87	2.98	0.34
P26039_TL	Tln1	Talin-1 OS=	K.VLVEDTK#.V	470.44	177.17	2.66	0.38
P26039_TL	Tln1	Talin-1 OS=	K.VLVQNAAGSQEK#.L	1394.95	505.68	2.76	0.36
P26039_TL	Tln1	Talin-1 OS=	K.VM*VTNVTSLLK#.T	219.53	80.30	2.73	0.37
P26039_TL	Tln1	Talin-1 OS=	K.VMVTNVTSLLK#.T	540.29	177.38	3.05	0.33
P26039_TL	Tln1	Talin-1 OS=	K.VSHVLAALQAGNR.G	62.55	109.65	0.57	1.75
P26039_TL	Tln1	Talin-1 OS=	K.VSQM*AQYFEPLTLAAVGAASK#.T	287.67	118.09	2.44	0.41
P26039_TL	Tln1	Talin-1 OS=	K.VSQMAQYFEPLTLAAVGAASK#.T	281.28	104.21	2.70	0.37
P26039_TL	Tln1	Talin-1 OS=	R.WSVLAGHSR.T	25.76	37.11	0.69	1.44
P26039_TL	Tln1	Talin-1 OS=	R.YDQATDTILTVTENIFSSM*GDAGEM*VR.Q	57.67	93.13	0.62	1.61
Q71LX4_TL	Tln2	Talin-2 OS=	R.GQSGELAAASGK#.F	10.55	1.37	7.70	0.13
Q9D1D4_T	Tmed10	Transmemb	R.IPDQLVILDM*K#.H	21.43	17.75	1.21	0.83
Q9D1D4_T	Tmed10	Transmemb	R.IPDQLVILDMK.H	5.55	8.52	0.65	1.53
Q9D1D4_T	Tmed10	Transmemb	K.ITDSAGHILYAK#.E	8.37	9.23	0.91	1.10
Q9D1D4_T	Tmed10	Transmemb	K.LKPLEVELR.R	14.07	47.70	0.29	3.39
Q9D1D4_T	Tmed10	Transmemb	R.RLEDLSESIVNDFAYM*K.K	29.53	15.85	1.86	0.54
Q9D1D4_T	Tmed10	Transmemb	R.RLEDLSESIVNDFAYMK.K	3.65	7.24	0.50	1.98
Q9R0Q3_T	Tmed2	Transmemb	K.IVM*FTIDIGEAPK#.G	17.22	9.85	1.75	0.57
Q9R0Q3_T	Tmed2	Transmemb	K.IVMFTIDIGEAPK#.G	11.61	10.36	1.12	0.89
Q9CXE7_T	Tmed5	Transmemb	K.LEDILESINSIK#.S	9.64	6.78	1.42	0.70
Q3UBX0_T	Tmem109	Transmemb	K.ETSADILTQIGR.S	1.65	69.76	0.02	42.31
Q9DAM7_T	Tmem263	Transmemb	K.GAVGATIGGVAWIGGK.S	3.84	23.32	0.16	6.07
Q9DAM7_T	Tmem263	Transmemb	K.TAVTTVPSM*GIGLVK.G	6.30	11.78	0.54	1.87
Q9DAM7_T	Tmem263	Transmemb	R.VTGGIFSVTK.G	6.80	16.82	0.40	2.47
Q9JHJ0_T	Tmod3	Tropomod	K.DLGDYK#DLDEDELLGK#.L	26.49	71.54	0.37	2.70
Q9JHJ0_T	Tmod3	Tropomod	R.DNETLM*ELK.I	3.71	11.36	0.33	3.06
Q9JHJ0_T	Tmod3	Tropomod	K.DRDDYVPYTGEK.K	3.71	29.51	0.13	7.96
Q9JHJ0_T	Tmod3	Tropomod	K.HFSLAATR.S	4.05	57.34	0.07	14.14
Q9JHJ0_T	Tmod3	Tropomod	K.LSESELK.Q	30.97	81.70	0.38	2.64
Q9JHJ0_T	Tmod3	Tropomod	R.LVEVNLNNIK.N	36.34	63.72	0.57	1.75
Q9JHJ0_T	Tmod3	Tropomod	K.M*LEENTNILK.F	12.41	19.88	0.62	1.60
Q9JHJ0_T	Tmod3	Tropomod	R.QQLGTSVELEM*AK.M	7.59	16.35	0.46	2.15
Q9JHJ0_T	Tmod3	Tropomod	R.QQLGTSVELEMAK.M	2.85	8.47	0.34	2.97
Q9JHJ0_T	Tmod3	Tropomod	R.SNDPVAVAFADMLK.V	6.66	14.45	0.46	2.17
Q9JHJ0_T	Tmod3	Tropomod	K.DLDEDELLGK.L	18.79	54.74	0.34	2.91
Q9JHJ0_T	Tmod3	Tropomod	K.DLGDYKDLDEDELLGK.L	117.61	407.69	0.29	3.47
Q9JHJ0_T	Tmod3	Tropomod	K.DLGDYKDLDEDELLGKLSESELK.Q	8.34	28.03	0.30	3.36
Q9JHJ0_T	Tmod3	Tropomod	K.DRDDYVPYTGEK.K	4.56	55.58	0.08	12.19
Q9JHJ0_T	Tmod3	Tropomod	R.KDLGDYKDLDEDELLGK.L	5.76	20.14	0.29	3.50
Q9JHJ0_T	Tmod3	Tropomod	K.LSESELK.Q	126.46	342.72	0.37	2.71
Q9JHJ0_T	Tmod3	Tropomod	R.LVEVNLNNIK#.N	9.80	4.26	2.30	0.44
Q9JHJ0_T	Tmod3	Tropomod	K.QLETVLDDLDPENALLPAGFR.Q	6.31	43.88	0.14	6.96
Q9JHJ0_T	Tmod3	Tropomod	K.SATGPFDR.E	7.51	107.86	0.07	14.37
Q61033_L	Tmpo	Lamina-ass	R.AEEPGVSDQSVFSSER.E	4.41	11.68	0.38	2.65
Q61033_L	Tmpo	Lamina-ass	R.AQPLRAEEPGVSDQSVFSSER.E	2.30	11.42	0.20	4.97
Q61033_L	Tmpo	Lamina-ass	K.LTVAPFK#.G	26.69	20.35	1.31	0.76
Q61033_L	Tmpo	Lamina-ass	R.LVSAAASPSLIR.E	17.05	45.42	0.38	2.66
Q61033_L	Tmpo	Lamina-ass	R.SLFIPSESSYDR.C	4.69	13.34	0.35	2.84
Q61033_L	Tmpo	Lamina-ass	K.SLQADISQAAQIINSDPSDAQQALR.I	5.18	10.61	0.49	2.05
Q61033_L	Tmpo	Lamina-ass	R.SQVISPPLAQAIR.D	6.38	18.85	0.34	2.96
Q61033_L	Tmpo	Lamina-ass	R.SSTPLPTVSSSAENTR.Q	4.25	9.32	0.46	2.20
Q61033_L	Tmpo	Lamina-ass	K.SVVSHSLTTLGVEVSK#PPPQHDK#IEASEPSFPLHESILK#.V	4.87	1.71	2.85	0.35
Q61033_L	Tmpo	Lamina-ass	R.SYEAAASALQIAAHTAFVAK#.S	29.98	19.43	1.54	0.65
Q61033_L	Tmpo	Lamina-ass	K.VDDEILGFISEATPR.A	2.65	9.41	0.28	3.55
Q61033_L	Tmpo	Lamina-ass	K.VVEEEWQQIDR.Q	6.79	20.03	0.34	2.95
Q61033_L	Tmpo	Lamina-ass	R.YPVSSIEAAR.I	11.37	25.99	0.44	2.29
Q61029_L	Tmpo	Lamina-ass	R.IDGAVISESTPIAETIK#.A	10.13	8.73	1.16	0.86
Q61033_L	Tmpo	Lamina-ass	R.AEEPGVSDQSVFSSER.E	3.01	8.03	0.38	2.66
Q61033_L	Tmpo	Lamina-ass	K.GPPDFSSDEEREPTPVLGSGASVGR.G	3.49	8.58	0.41	2.46
Q61033_L	Tmpo	Lamina-ass	R.LSQSSYQDSESLSPPR.K	2.26	4.01	0.56	1.78
Q61033_L	Tmpo	Lamina-ass	R.LVSAAASPSLIR.E	11.57	42.60	0.27	3.68
Q61033_L	Tmpo	Lamina-ass	R.NRPPLAAGANSK.G	3.71	9.74	0.38	2.62
Q61033_L	Tmpo	Lamina-ass	K.SELVANNVTLPAGEQR.K	2.31	7.44	0.31	3.22
Q61033_L	Tmpo	Lamina-ass	R.SQVISPPLAQAIR.D	5.81	18.18	0.32	3.13
Q61033_L	Tmpo	Lamina-ass	R.SSTPLPTVSSSAENTR.Q	4.14	20.18	0.21	4.87
Q61033_L	Tmpo	Lamina-ass	R.SYEAAASALQIAAHTAFVAK#.S	25.43	24.38	1.04	0.96
Q61033_L	Tmpo	Lamina-ass	K.VDDEILGFISEATPR.A	5.38	14.21	0.38	2.64
Q61033_L	Tmpo	Lamina-ass	K.VVEEEWQQIDR.Q	4.97	33.99	0.15	6.84
Q61033_L	Tmpo	Lamina-ass	R.YPVSSIEAAR.I	11.04	32.15	0.34	2.91
Q921Z5_T	Tnfaip8	Tumor nec	R.NNQFNQDELALM*EK#.F	3.43	2.31	1.49	0.67
Q9WUU8_	Tnip1	TNFAIP3-in	K.GKM*QGIKM*LGELLEESQMEASR@.L	1.66	2.06	0.81	1.24
Q9WUU8_	Tnip1	TNFAIP3-in	K.GVAGQQQASVM*ASK#.V	4.23	2.38	1.77	0.56
P58871_T	Tnks1bp1	182 kDa ta	R.APAIRPGGTLGLSETADSDTR.L	1.87	19.54	0.10	10.43
P58871_T	Tnks1bp1	182 kDa ta	R.ATAQQNQEFGK#.S	40.57	13.58	2.99	0.33
P58871_T	Tnks1bp1	182 kDa ta	R.DVGHLEEGASGGLLSPSTPHSR.D	1.86	7.39	0.25	3.98
P58871_T	Tnks1bp1	182 kDa ta	R.ELGVGQVDWGDDLGLR.N	3.56	9.19	0.39	2.58
P58871_T	Tnks1bp1	182 kDa ta	R.ESGVGEPDWSGAEAGEFLK#.S	9.11	7.06	1.29	0.78
P58871_T	Tnks1bp1	182 kDa ta	R.VGPDLELDPK#.S	14.77	9.90	1.49	0.67
P58871_T	Tnks1bp1	182 kDa ta	R.VLLEEEGLAAGAGQGEPQEPSR.A	5.86	7.88	0.74	1.34

P58871_TE	Tnks1bp1	182 kDa tar	K.VNLFPGLSPSALK#.A	21.24	11.45	1.85	0.54
P58871_TE	Tnks1bp1	182 kDa tar	K.AGAVDWTDQLGLR.N	9.19	32.04	0.29	3.49
P58871_TE	Tnks1bp1	182 kDa tar	R.APAIRPGGTLGLSETADSDTR.L	4.76	38.95	0.12	8.19
P58871_TE	Tnks1bp1	182 kDa tar	R.APLPSSRPQPDGEASQVEEVDGTWSLTGAAR.Q	1.81	10.47	0.17	5.80
P58871_TE	Tnks1bp1	182 kDa tar	R.ATAQQNQEFGK#.S	34.67	23.54	1.47	0.68
P58871_TE	Tnks1bp1	182 kDa tar	K.DEGSWQDGDSSQEITR.L	4.20	14.82	0.28	3.53
P58871_TE	Tnks1bp1	182 kDa tar	R.DSLGSFSTR.D	6.26	22.09	0.28	3.53
P58871_TE	Tnks1bp1	182 kDa tar	R.DSVLDIHGSR.A	4.24	16.67	0.25	3.93
P58871_TE	Tnks1bp1	182 kDa tar	R.DVGHLEEGASGGLLSPSTPHSR.D	3.88	17.05	0.23	4.39
P58871_TE	Tnks1bp1	182 kDa tar	R.ESGVGEPDWSGAEAGEFLK#.S	27.40	18.95	1.45	0.69
P58871_TE	Tnks1bp1	182 kDa tar	R.FSEGVLQPPSQDQEK#.L	7.09	7.65	0.93	1.08
P58871_TE	Tnks1bp1	182 kDa tar	R.GVGQADWTPDLGLR.N	4.07	22.82	0.18	5.60
P58871_TE	Tnks1bp1	182 kDa tar	R.KPISGVQGNDPGISLPQR.D	4.95	13.88	0.36	2.81
P58871_TE	Tnks1bp1	182 kDa tar	R.LANISVPASESPR.L	12.45	44.86	0.28	3.60
P58871_TE	Tnks1bp1	182 kDa tar	R.SAEEGEVTESK.S	17.69	14.07	1.26	0.80
P58871_TE	Tnks1bp1	182 kDa tar	K.SAWFQDYSSGGGGSR.V	4.06	11.59	0.35	2.86
P58871_TE	Tnks1bp1	182 kDa tar	R.SPALLPSTVEGPPGAPLLQAK.E	17.31	10.25	1.69	0.59
P58871_TE	Tnks1bp1	182 kDa tar	R.SPALLPSTVEGPPGAPLLQAK#.E	32.90	28.03	1.17	0.85
P58871_TE	Tnks1bp1	182 kDa tar	R.SPPSGSQSLLEGIMTASSSK#.G	8.59	5.98	1.44	0.70
P58871_TE	Tnks1bp1	182 kDa tar	K.SSGSLSPGLETEDPLEAR.E	5.35	15.81	0.34	2.96
P58871_TE	Tnks1bp1	182 kDa tar	R.VGPDLELDPK.S	35.82	31.19	1.15	0.87
P58871_TE	Tnks1bp1	182 kDa tar	R.VLLEEEGLAAGAGQGEPQEPSR.A	8.14	21.39	0.38	2.63
P58871_TE	Tnks1bp1	182 kDa tar	K.VNLFPGLSPSALK#.A	64.74	48.01	1.35	0.74
P58871_TE	Tnks1bp1	182 kDa tar	R.VPSSDEEVVEEPQSR.R	1.38	7.09	0.20	5.12
P58871_TE	Tnks1bp1	182 kDa tar	R.VSGAGLSPSR.K	81.11	13.55	5.99	0.17
P58871_TE	Tnks1bp1	182 kDa tar	R.WLDDLLASPPPNSGSAR.R	4.33	6.55	0.66	1.51
Q8BFY9_TN	Tnpo1	Transportir	R.ATVGILITTIASK#.G	8.56	4.61	1.86	0.54
Q8BFY9_TN	Tnpo1	Transportir	K.GELQNWPDLLPK#.L	7.59	3.15	2.41	0.41
Q8BFY9_TN	Tnpo1	Transportir	K.YSDIDIILLK#.G	14.00	5.40	2.59	0.39
Q8BFY9_TN	Tnpo1	Transportir	R.ATVGILITTIASK#.G	17.53	6.54	2.68	0.37
Q8BFY9_TN	Tnpo1	Transportir	K.ESQSPDTTIQR.T	11.97	16.66	0.72	1.39
Q8BFY9_TN	Tnpo1	Transportir	R.FSDQFPLPLK#.E	29.43	10.15	2.90	0.34
Q8BFY9_TN	Tnpo1	Transportir	K.GELQNWPDLLPK#.L	13.02	8.48	1.54	0.65
Q8BFY9_TN	Tnpo1	Transportir	R.QSSFALLGDLTK#.A	31.46	12.59	2.50	0.40
Q8BFY9_TN	Tnpo1	Transportir	K.YSDIDIILLK#.G	27.11	6.93	3.91	0.26
Q6P2B1_TN	Tnpo3	Transportir	K.ETTVGAVTVTHK#.Q	23.24	11.29	2.06	0.49
Q6P2B1_TN	Tnpo3	Transportir	R.SVHAWEISDQLLQIR.Q	8.62	9.51	0.91	1.10
Q6P2B1_TN	Tnpo3	Transportir	K.VIQEIWPVLSETLNK#.H	18.37	5.84	3.15	0.32
Q8BKI2_TN	Tnrc6b	Trinucleoti	R.VLSNTGWGQTQIK#.Q	4.88	4.02	1.21	0.82
Q9QZ06_TO	Tollip	Toll-interac	R.GPVYIGELPQDFLR.I	3.78	12.58	0.30	3.33
Q9QZ06_TO	Tollip	Toll-interac	R.LSITVVQAK#.L	9.28	4.18	2.22	0.45
O88746_TO	Tom1	Target of M	R.GDLSQHATPLPTPAVLPGDSPITPTPEQIGK#.L	11.17	5.00	2.23	0.45
Q5SRX1_TN	Tom1l2	TOM1-like p	R.DFIDSVLVK#.I	9.47	2.96	3.20	0.31
Q5SRX1_TN	Tom1l2	TOM1-like p	R.VSNEEVTEELLHVNDDLNNVFLR.Y	4.73	6.90	0.69	1.46
Q9CYG7_TO	Tomm34	Mitochond	R.LK#LPPIPVVPVSAQK#.R	8.33	2.45	3.39	0.29
Q9CYG7_TO	Tomm34	Mitochond	K.YALAYVDYK#.T	16.05	4.52	3.55	0.28
Q9CQN3_T	Tomm6	Mitochond	R.NLSDIDLM*APQPGV.-	5.69	5.69	1.00	1.00
Q04750_TO	Top1	DNA topois	K.ELTAPDENVPAK#.I	42.76	48.64	0.88	1.14
Q04750_TO	Top1	DNA topois	K.FAWAIDM*TDEDYEF.-	11.22	11.22	1.00	1.00
Q04750_TO	Top1	DNA topois	K.FYYDGK.V	17.85	20.43	0.87	1.14
Q04750_TO	Top1	DNA topois	K.GPVFAPPYEPLPESVK.F	34.37	42.76	0.80	1.24
Q04750_TO	Top1	DNA topois	K.HLQDLM*EGLTAK#.V	12.17	10.46	1.16	0.86
Q04750_TO	Top1	DNA topois	R.LEEQLM*K#.L	37.09	36.57	1.01	0.99
Q04750_TO	Top1	DNA topois	R.LRDEDDADYKPK.K	5.66	44.57	0.13	7.88
Q04750_TO	Top1	DNA topois	R.TYNASITLQQQLK#.E	16.24	16.84	0.96	1.04
Q04750_TO	Top1	DNA topois	R.VEHINLHPELDGQEYVVEFDFPGKDSIR.Y	2.94	4.77	0.62	1.62
Q04750_TO	Top1	DNA topois	K.WGVPIEK.I	13.90	14.64	0.95	1.05
Q04750_TO	Top1	DNA topois	K.WWEEERYPEGIK.W	5.73	7.09	0.81	1.24
Q04750_TO	Top1	DNA topois	K.YIM*LNPSSR.I	3.32	16.73	0.20	5.03
Q04750_TO	Top1	DNA topois	K.AEEVATFFAK#.M	13.49	13.73	0.98	1.02
Q04750_TO	Top1	DNA topois	K.GPVFAPPYEPLPESVK.F	12.63	17.77	0.71	1.41
Q01320_TO	Top2a	DNA topois	K.IFDEILVNAADNK#.Q	11.28	10.36	1.09	0.92
Q01320_TO	Top2a	DNA topois	K.DKVDETGNSLK.V	12.63	9.57	1.32	0.76
Q01320_TO	Top2a	DNA topois	R.FLEEFITPIVK#.V	15.20	12.06	1.26	0.79
Q01320_TO	Top2a	DNA topois	R.HVDYVADQIVSK.L	12.26	11.84	1.04	0.97
Q01320_TO	Top2a	DNA topois	K.IFDEILVNAADNK#.Q	14.43	36.13	0.40	2.50
Q01320_TO	Top2a	DNA topois	K.IKSENVEGTPAEDGAEPGSLR.Q	2.46	11.77	0.21	4.78
Q01320_TO	Top2a	DNA topois	K.IM*IM*TDQDQDGSHIK#.G	13.10	12.45	1.05	0.95
Q01320_TO	Top2a	DNA topois	K.IVGLQYK#.K	26.72	15.21	1.76	0.57
Q01320_TO	Top2a	DNA topois	K.NKQEIAFYSLPEFEEWK.S	7.94	11.34	0.70	1.43
Q01320_TO	Top2a	DNA topois	K.QIM*ENAEINNIIK#.I	8.29	4.87	1.70	0.59
Q01320_TO	Top2a	DNA topois	K.TLAVSGLGVVGR.D	4.18	19.66	0.21	4.70
Q01320_TO	Top2a	DNA topois	K.YSGPEDDAAISLAFSK.K	6.35	8.03	0.79	1.26
Q01320_TO	Top2a	DNA topois	K.AKGEEQDFPVDLEDTIAPR.A	4.66	20.23	0.23	4.34
Q01320_TO	Top2a	DNA topois	K.DK#VDETGNSLK#.V	45.77	49.95	0.92	1.09
Q01320_TO	Top2a	DNA topois	K.ELILFSNSDNER.S	28.75	91.10	0.32	3.17
Q01320_TO	Top2a	DNA topois	K.EQELNTLK#.Q	28.22	27.14	1.04	0.96
Q01320_TO	Top2a	DNA topois	R.EVTFVPGLYK#.I	108.39	82.68	1.31	0.76
Q01320_TO	Top2a	DNA topois	K.EWLLGM*LGAESSK.L	2.45	46.40	0.05	18.92
Q01320_TO	Top2a	DNA topois	R.FLEEFITPIVK#.V	142.65	117.23	1.22	0.82
Q01320_TO	Top2a	DNA topois	K.FTVETASR.E	23.34	84.95	0.27	3.64
Q01320_TO	Top2a	DNA topois	K.GEEQDFPVDLEDTIAPR.A	12.18	9.51	1.28	0.78
Q01320_TO	Top2a	DNA topois	R.GFQQISFVNSIATSK#.G	48.99	37.35	1.31	0.76
Q01320_TO	Top2a	DNA topois	R.GFQQISFVNSIATSK.G	25.26	21.72	1.16	0.86
Q01320_TO	Top2a	DNA topois	R.HVDYVADQIVSK#.L	67.40	56.67	1.19	0.84
Q01320_TO	Top2a	DNA topois	K.IFDEILVNAADNK#.Q	55.07	29.89	1.84	0.54
Q01320_TO	Top2a	DNA topois	K.IKSENVEGTPAEDGAEPGSLR.Q	18.26	76.36	0.24	4.18
Q01320_TO	Top2a	DNA topois	K.IM*IM*TDQDQDGSHIK#.G	103.02	76.19	1.35	0.74
Q01320_TO	Top2a	DNA topois	K.IM*IMTDQDQDGSHIK#.G	9.81	4.56	2.15	0.46
Q01320_TO	Top2a	DNA topois	K.IVIENK#PK#.K	40.70	31.35	1.30	0.77
Q01320_TO	Top2a	DNA topois	K.LDDANDAGSR.N	4.02	13.88	0.29	3.45
Q01320_TO	Top2a	DNA topois	R.LLDGEEPLPM*LPSYK#.N	24.87	26.23	0.95	1.05
Q01320_TO	Top2a	DNA topois	R.LLDGEEPLPMLPSYK#.N	10.03	11.02	0.91	1.10
Q01320_TO	Top2a	DNA topois	K.M*QSLDKDIVALMVR.R	2.88	11.45	0.25	3.97
Q01320_TO	Top2a	DNA topois	R.NEK#EQELNTLK#.Q	16.27	12.86	1.27	0.79
Q01320_TO	Top2a	DNA topois	K.NK#QEIAFYSLPEFEEWK#.S	26.47	29.33	0.90	1.11
Q01320_TO	Top2a	DNA topois	K.NYEDEDSLK#.T	54.68	43.93	1.24	0.80
Q01320_TO	Top2a	DNA topois	K.QIM*ENAEINNIIK#.I	33.75	25.17	1.34	0.75
Q01320_TO	Top2a	DNA topois	K.SENVEGTPAEDGAEPGSLR.Q	8.82	31.57	0.28	3.58
Q01320_TO	Top2a	DNA topois	K.SQSSVSTAGTK#.K	12.62	11.06	1.14	0.88
Q01320_TO	Top2a	DNA topois	R.SYVDLYLK.D	48.10	29.75	1.62	0.62
Q01320_TO	Top2a	DNA topois	R.SYVDLYLK#DK#VDETGNSLK#.V	9.74	7.75	1.26	0.80
Q01320_TO	Top2a	DNA topois	K.TLAVSGLGVVGR.D	29.56	110.70	0.27	3.75

Q01320_T	Top2a	DNA topois	K.TPSLITDYR.E	19.93	69.81	0.29	3.50
Q01320_T	Top2a	DNA topois	K.VDETGNSLK#.V	10.06	8.22	1.22	0.82
Q01320_T	Top2a	DNA topois	K.VIHEQVNPR.W	36.59	158.37	0.23	4.33
Q01320_T	Top2a	DNA topois	R.VTIDPENNVISIWNNGK#.G	11.26	11.63	0.97	1.03
Q01320_T	Top2a	DNA topois	K.YDTVLDILR.D	4.31	22.91	0.19	5.32
Q01320_T	Top2a	DNA topois	K.YGVFPLR.G	8.76	25.68	0.34	2.93
Q01320_T	Top2a	DNA topois	R.YIFTMLSPLAR.L	7.35	18.68	0.39	2.54
Q01320_T	Top2a	DNA topois	K.YSGPEDDAAISLAFSK#.K	46.93	50.07	0.94	1.07
Q64511_T	Top2b	DNA topois	R.LLFPAVDDNLLK#.F	22.92	11.30	2.03	0.49
Q64511_T	Top2b	DNA topois	K.SLAVSGLGVIGR.D	2.76	7.78	0.35	2.82
Q64511_T	Top2b	DNA topois	K.ASGSENEGDYNPGR.K	1.71	4.30	0.40	2.52
Q64511_T	Top2b	DNA topois	K.ASPITNDGEDEFVPSDGLDKDEYAFSSGK.S	14.78	5.86	2.52	0.40
Q64511_T	Top2b	DNA topois	K.DK#LDETGVALK#.V	45.74	38.49	1.19	0.84
Q64511_T	Top2b	DNA topois	K.DLIQM*LVQR.G	6.83	15.70	0.44	2.30
Q64511_T	Top2b	DNA topois	K.DLIQMLVQR.G	6.02	20.25	0.30	3.37
Q64511_T	Top2b	DNA topois	K.EK#VEELIK#.Q	52.97	26.12	2.03	0.49
Q64511_T	Top2b	DNA topois	K.FDSNEEDTASVFAPSFGLK#.Q	12.04	6.11	1.97	0.51
Q64511_T	Top2b	DNA topois	K.GFQQISFVNSIATTK#.G	30.85	18.91	1.63	0.61
Q64511_T	Top2b	DNA topois	K.GTIQELGQNQYAVSGEIFVVDR.N	12.34	19.87	0.62	1.61
Q64511_T	Top2b	DNA topois	K.HGFLEEFITPIVK#.A	28.70	13.49	2.13	0.47
Q64511_T	Top2b	DNA topois	K.HLTYNDFINK#.E	26.19	14.42	1.82	0.55
Q64511_T	Top2b	DNA topois	R.HVDYVVDQVVSK#.L	40.55	23.57	1.72	0.58
Q64511_T	Top2b	DNA topois	K.K#EELETANK#NDSTK#.K	18.03	13.05	1.38	0.72
Q64511_T	Top2b	DNA topois	K.KTSFDQDSDVDIFPSDFTSEPPALPR.T	7.60	11.69	0.65	1.54
Q64511_T	Top2b	DNA topois	K.K#YETVQDILK#.E	13.94	9.03	1.54	0.65
Q64511_T	Top2b	DNA topois	K.LAQAEAAGLHK#.V	30.01	18.27	1.64	0.61
Q64511_T	Top2b	DNA topois	R.LHGLPEQFLYGTATK#.H	42.22	23.54	1.79	0.56
Q64511_T	Top2b	DNA topois	R.LLFPAVDDNLLK#.F	162.33	80.32	2.02	0.49
Q64511_T	Top2b	DNA topois	K.LQLEETM*PSPYGR.R	5.69	7.01	0.81	1.23
Q64511_T	Top2b	DNA topois	R.LSYYGLR.K	7.59	19.25	0.39	2.54
Q64511_T	Top2b	DNA topois	K.NK#QELSFYSIPEFDEWK#K#.H	9.48	9.32	1.02	0.98
Q64511_T	Top2b	DNA topois	R.NTVEITELPVR.T	16.72	47.18	0.35	2.82
Q64511_T	Top2b	DNA topois	K.SEDDSAK#FDSNEEDTASVFAPSFGLK#.Q	18.14	9.38	1.93	0.52
Q64511_T	Top2b	DNA topois	K.SLAVSGLGVIGR.D	20.80	46.85	0.44	2.25
Q64511_T	Top2b	DNA topois	K.SQDFGNLFSFPSYSQK#.S	38.25	21.47	1.78	0.56
Q64511_T	Top2b	DNA topois	K.SSLAGSDGALTWVNNATK#.K	22.40	13.59	1.65	0.61
Q64511_T	Top2b	DNA topois	K.SYDDAESLK#.T	44.58	25.54	1.75	0.57
Q64511_T	Top2b	DNA topois	R.YAGPEDDAAITLAFSK#.K	45.98	24.82	1.85	0.54
Q64511_T	Top2b	DNA topois	K.YFAESDEEEDVDFAM*FN.-	5.35	5.35	1.00	1.00
Q64511_T	Top2b	DNA topois	R.YIFTM*LSSLAR.L	7.93	10.78	0.74	1.36
Q64511_T	Top2b	DNA topois	K.YTFDFSEEEDDDAAAADDSNDLEELK#.V	6.32	4.99	1.27	0.79
Q64511_T	Top2b	DNA topois	K.YTFDFSEEEDDDAAAADDSNDLEELK#VK#.A	4.88	3.56	1.37	0.73
O70157_T	Top3a	DNA topois	K.LYTQGYISYPR.T	2.29	7.93	0.29	3.46
Q6ZQF0_T	Topbp1	DNA topois	R.FNQLNEDVTHVIVGDYDDDVR.Q	1.73	5.39	0.32	3.12
Q6ZQF0_T	Topbp1	DNA topois	K.LFKPSFDVTDALAALETPNAASQK.R	3.80	4.71	0.81	1.24
Q6ZQF0_T	Topbp1	DNA topois	R.FNQLNEDVTHVIVGDYDDDVR.Q	1.11	8.07	0.14	7.29
Q6ZQF0_T	Topbp1	DNA topois	R.FVQEEDYEWGSSSILDALPDVTEHQQK#.L	3.91	3.25	1.20	0.83
Q6ZQF0_T	Topbp1	DNA topois	K.LFK#PSFDVTDALAALETPNAASQK#.R	7.73	7.29	1.06	0.94
Q6ZQF0_T	Topbp1	DNA topois	K.MPDDSPSR.K	1.11	11.45	0.10	10.35
Q9ER81_I	Tor1aip2	Torsin-1A-i	R.VAGFNPALQLILSR.T	5.54	20.99	0.26	3.79
Q8BU11_T	Tox4	TOX high m	K.DPNEPQKPVSAYALFFR.D	2.84	12.20	0.23	4.29
Q8BU11_T	Tox4	TOX high m	R.DVFLAWVASR.N	2.76	14.92	0.18	5.41
Q8BU11_T	Tox4	TOX high m	R.GLQVGQTSTATIQPSQQAQIVTR.S	4.19	15.59	0.27	3.72
Q8BU11_T	Tox4	TOX high m	K.GQNPNATFGEVSK#.I	33.04	40.95	0.81	1.24
Q8BU11_T	Tox4	TOX high m	R.INLQQQPPPLQSK#.I	15.83	18.42	0.86	1.16
P02340_P	Tp53	Cellular tur	R.ELNEALELK#.D	111.28	137.02	0.81	1.23
P02340_P	Tp53	Cellular tur	R.HSVVVPYEPPEAGSEYTTIHYK.Y	65.27	70.18	0.93	1.08
P02340_P	Tp53	Cellular tur	K.KPLDGEYFTLK.I	40.15	55.96	0.72	1.39
P02340_P	Tp53	Cellular tur	K.K#PLDGEYFTLK#.I	48.54	55.52	0.87	1.14
P02340_P	Tp53	Cellular tur	R.RPILTIITLEDSSGNLLGR.D	5.46	164.92	0.03	30.21
P02340_P	Tp53	Cellular tur	R.RTEEENFR.K	1.63	39.96	0.04	24.52
P02340_P	Tp53	Cellular tur	K.SQHM*TEVVR.R	7.70	33.92	0.23	4.40
P02340_P	Tp53	Cellular tur	K.SQHMTEVVR.R	17.03	120.64	0.14	7.09
P02340_P	Tp53	Cellular tur	R.TEEENFR.K	15.78	80.66	0.20	5.11
P02340_P	Tp53	Cellular tur	R.VEGNLYPEYLEDR.Q	33.49	194.73	0.17	5.81
P02340_P	Tp53	Cellular tur	R.VSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQK.T	36.82	30.48	1.21	0.83
P02340_P	Tp53	Cellular tur	R.AM*AIYK#.K	23.67	33.74	0.70	1.43
P02340_P	Tp53	Cellular tur	R.ELNEALELK.D	46.83	68.10	0.69	1.45
P02340_P	Tp53	Cellular tur	R.HSVVVPYEPPEAGSEYTTIHYK.Y	46.63	54.21	0.86	1.16
P02340_P	Tp53	Cellular tur	K.KKPLDGEYFTLK.I	7.04	10.44	0.67	1.48
P02340_P	Tp53	Cellular tur	K.KPLDGEYFTLK.I	18.85	33.59	0.56	1.78
P02340_P	Tp53	Cellular tur	R.RPILTIITLEDSSGNLLGR.D	6.52	146.22	0.04	22.43
P02340_P	Tp53	Cellular tur	R.RTEEENFR.K	3.20	31.63	0.10	9.89
P02340_P	Tp53	Cellular tur	K.SQHMTEVVR.R	4.66	17.80	0.26	3.82
P02340_P	Tp53	Cellular tur	R.TEEENFR.K	8.38	49.02	0.17	5.85
P02340_P	Tp53	Cellular tur	K.TYQGNYGFHLGFLQSGTAK#.S	5.67	7.06	0.80	1.25
P02340_P	Tp53	Cellular tur	R.VEGNLYPEYLEDR.Q	21.65	152.55	0.14	7.05
P02340_P	Tp53	Cellular tur	R.VSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQK.T	25.33	18.56	1.37	0.73
P02340_P	Tp53	Cellular tur	R.ELNEALELK.D	31.08	42.28	0.73	1.36
P02340_P	Tp53	Cellular tur	R.HSVVVPYEPPEAGSEYTTIHYK.Y	22.91	42.69	0.54	1.86
P02340_P	Tp53	Cellular tur	K.KKPLDGEYFTLK.I	34.93	57.28	0.61	1.64
P02340_P	Tp53	Cellular tur	K.KPLDGEYFTLK.I	25.25	31.88	0.79	1.26
P02340_P	Tp53	Cellular tur	R.RTEEENFR.K	1.84	27.79	0.07	15.10
P02340_P	Tp53	Cellular tur	R.VEGNLYPEYLEDR.Q	16.77	100.82	0.17	6.01
P02340_P	Tp53	Cellular tur	R.VSGAPAAQDPVTETPGPVAPAPATPWPLSSFVPSQK.T	22.00	19.58	1.12	0.89
P70399_T	Tp53bp1	Tumor sup	K.AADISLDNLVEGK#.R	52.83	22.22	2.38	0.42
P70399_T	Tp53bp1	Tumor sup	K.ASGTEAADFALPSSR.G	10.63	19.08	0.56	1.79
P70399_T	Tp53bp1	Tumor sup	R.ASQEPFSPAEDVM*ETDLLEGLAANQDRPSK.M	3.71	6.43	0.58	1.73
P70399_T	Tp53bp1	Tumor sup	K.ASSSHHTSSGTSLSAIHSSGSSGR.G	16.12	33.65	0.48	2.09
P70399_T	Tp53bp1	Tumor sup	R.DEPVRPDQETQQPQVQEK.E	15.96	47.60	0.34	2.98
P70399_T	Tp53bp1	Tumor sup	K.EAQSEAPPSAPDR.A	3.95	14.56	0.27	3.69
P70399_T	Tp53bp1	Tumor sup	K.ENPVLDIVSNPEQSAVEQGDSNSSFNEHLK#.E	6.42	3.58	1.79	0.56
P70399_T	Tp53bp1	Tumor sup	R.EQYGLGPYEAVTPLTK#.A	12.99	8.31	1.56	0.64
P70399_T	Tp53bp1	Tumor sup	K.ESGELYYSIEK#.E	36.75	14.80	2.48	0.40
P70399_T	Tp53bp1	Tumor sup	R.ETVVSGPLGVEDISPSM*SPDDK#.S	5.96	3.76	1.59	0.63
P70399_T	Tp53bp1	Tumor sup	R.ETVVSGPLGVEDISPSM*SPDDKSFTR.I	1.90	3.99	0.48	2.10
P70399_T	Tp53bp1	Tumor sup	K.LLDGPTGSSEEEEEFLEIPPFNK#.Q	17.06	7.23	2.36	0.42
P70399_T	Tp53bp1	Tumor sup	K.LM*LSTSEYSQSSK#.M	14.23	4.82	2.95	0.34
P70399_T	Tp53bp1	Tumor sup	K.LMLSTSEYSQSSK#.M	20.59	7.40	2.78	0.36
P70399_T	Tp53bp1	Tumor sup	R.LREQYGLGPYEAVTPLTK.A	6.47	21.03	0.31	3.25
P70399_T	Tp53bp1	Tumor sup	R.QSEQPVKPVGPVM*DDAAPEDSASPVSQQR.A	2.48	5.15	0.48	2.07
P70399_T	Tp53bp1	Tumor sup	R.SEALSSVLDQEEAM*DTK#.E	11.15	3.57	3.12	0.32
P70399_T	Tp53bp1	Tumor sup	R.SEALSSVLDQEEAMDTK#.E	8.02	3.97	2.02	0.50

P70399_TP	Tp53bp1	Tumor supp	R.SNISSPVTPTAASSSSTTPTR.K	6.01	10.16	0.59	1.69
P70399_TP	Tp53bp1	Tumor supp	R.VITDVYYVDGTEVER.K	10.63	20.31	0.52	1.91
Q62393_TP	Tpd52	Tumor prot	K.ASAAFSSVGSVITK#.K	11.91	5.52	2.16	0.46
Q62393_TP	Tpd52	Tumor prot	K.LGISSLQEFK#.Q	5.05	6.00	0.84	1.19
Q62393_TP	Tpd52	Tumor prot	K.SFEEK#VENLK#.S	7.29	1.92	3.79	0.26
Q62393_TP	Tpd52	Tumor prot	K.TSETLSQAGQK#.A	7.42	1.33	5.60	0.18
Q9CYZ2_TP	Tpd52l2	Tumor prot	R.LGLSTLGELK#.Q	27.06	17.00	1.59	0.63
Q9CYZ2_TP	Tpd52l2	Tumor prot	K.TQETLSQAGQK#.T	23.94	15.70	1.52	0.66
Q9CYZ2_TP	Tpd52l2	Tumor prot	R.LGLSTLGELK#.Q	64.29	20.10	3.20	0.31
Q9CYZ2_TP	Tpd52l2	Tumor prot	K.TSAALSTM*GSAISR.K	2.89	6.50	0.44	2.25
P17751_TP	Tpi1	Triosephosp	R.HVFGESDELIGQK#.V	26.60	5.07	5.24	0.19
P17751_TP	Tpi1	Triosephosp	K.SNVNDGVAQSTR.I	8.43	11.88	0.71	1.41
P17751_TP	Tpi1	Triosephosp	K.TATPQQAQEVHEK#.L	14.13	3.78	3.74	0.27
P17751_TP	Tpi1	Triosephosp	K.VIADNVK#DWSK#.V	10.59	2.01	5.27	0.19
P17751_TP	Tpi1	Triosephosp	K.VVLAYEPVWAIGTGK#.T	125.38	27.24	4.60	0.22
E9Q450_E9	Tpm1	Tropomyos	R.AELSEGQVR.Q	13.20	30.98	0.43	2.35
E9Q450_E9	Tpm1	Tropomyos	K.ATDAEADVASLNR.R	39.01	66.91	0.58	1.72
E9Q450_E9	Tpm1	Tropomyos	K.GTEDELDKYSEALKDAQEK.L	44.78	15.73	2.85	0.35
E9Q450_E9	Tpm1	Tropomyos	K.QLEDELVSLQK#.K	60.59	38.66	1.57	0.64
E9Q450_E9	Tpm1	Tropomyos	R.SK#QLEDELVSLQK#.K	61.97	19.28	3.21	0.31
G5E8R1_G5	Tpm1	Tropomyos	R.AQK#DEEK#MEIQEIQLK#.E	12.91	5.05	2.56	0.39
G5E8R1_G5	Tpm1	Tropomyos	K.EENLSM*HQM*LDQTLLELNNM*.-	4.18	4.18	1.00	1.00
G5E8R1_G5	Tpm1	Tropomyos	R.ETAEADVASLNR.R	4.65	10.08	0.46	2.17
G5E8R1_G5	Tpm1	Tropomyos	K.HIAEDADR.K	11.97	22.77	0.53	1.90
G5E8R1_G5	Tpm1	Tropomyos	R.IQLVEEELDR.A	73.81	158.18	0.47	2.14
G5E8R1_G5	Tpm1	Tropomyos	R.KLVIIESDLER.A	34.71	66.12	0.52	1.90
G5E8R1_G5	Tpm1	Tropomyos	K.LEEAEKAADESER.G	27.29	42.85	0.64	1.57
G5E8R1_G5	Tpm1	Tropomyos	K.LVIIESDLER.A	21.93	45.57	0.48	2.08
G5E8R1_G5	Tpm1	Tropomyos	R.RIQLVEEELDR.A	2.47	17.42	0.14	7.07
G5E8R1_G5	Tpm1	Tropomyos	K.SIDDLEEK#.V	221.06	110.61	2.00	0.50
G5E8R1_G5	Tpm1	Tropomyos	K.SLEAQAEK#.Y	105.06	43.78	2.40	0.42
G5E8R1_G5	Tpm1	Tropomyos	R.SLQEQADAAEER.A	23.73	35.80	0.66	1.51
G5E8R1_G5	Tpm1	Tropomyos	K.YSQK#EDK#YEEEIK#.V	331.74	147.36	2.25	0.44
G5E8R1_G5	Tpm1	Tropomyos	K.YSQKEDKYEEEIK.V	123.61	44.11	2.80	0.36
G5E8R1_G5	Tpm1	Tropomyos	R.LATALQK#.L	42.21	14.01	3.01	0.33
A2AIM4_A2	Tpm2	Tropomyos	K.DAQEK#LEQAEK#.K	14.32	4.33	3.30	0.30
A2AIM4_A2	Tpm2	Tropomyos	K.GTEDEVEK#YSESVK#.D	6.68	3.15	2.13	0.47
A2AIM4_A2	Tpm2	Tropomyos	K.LVILEGELER.S	5.63	12.77	0.44	2.27
A2AIM4_A2	Tpm2	Tropomyos	K.QLEEEQQALQK#.K	40.46	45.99	0.88	1.14
A2AIM4_A2	Tpm2	Tropomyos	K.SLIASEEEYSTK#.E	21.08	8.04	2.62	0.38
A2AIM4_A2	Tpm2	Tropomyos	K.YSESVK#DAQEK#.L	8.61	3.79	2.27	0.44
D3Z2H9_D3	Tpm3-rs7	Uncharacte	R.ALKDEEKM*ELQEIQLK.E	50.52	21.25	2.38	0.42
D3Z2H9_D3	Tpm3-rs7	Uncharacte	K.HIAEEADR.K	15.62	21.03	0.74	1.35
D3Z2H9_D3	Tpm3-rs7	Uncharacte	K.IQVLQQQADDAEER.A	28.07	53.75	0.52	1.91
D3Z2H9_D3	Tpm3-rs7	Uncharacte	R.KIQVLQQQADDAEER.A	13.47	22.63	0.60	1.68
D3Z2H9_D3	Tpm3-rs7	Uncharacte	R.KLVIIEGDLER.T	30.57	48.06	0.64	1.57
D3Z2H9_D3	Tpm3-rs7	Uncharacte	R.M*LDQTLLDLNEM*.-	50.61	50.61	1.00	1.00
D3Z2H9_D3	Tpm3-rs7	Uncharacte	R.MLDQTLLDLNEM*.-	23.91	23.91	1.00	1.00
D3Z2H9_D3	Tpm3-rs7	Uncharacte	R.MLDQTLLDLNEM.-	5.80	5.80	1.00	1.00
D3Z2H9_D3	Tpm3-rs7	Uncharacte	K.TIDDLEDK#LK#.C	97.87	35.97	2.72	0.37
D3Z2H9_D3	Tpm3-rs7	Uncharacte	K.IQVLQQQADDAEER.A	5.55	9.03	0.62	1.63
Q6IRU2_TP	Tpm4	Tropomyos	K.AEGDAAALNR.R	10.38	14.45	0.72	1.39
Q6IRU2_TP	Tpm4	Tropomyos	R.AEVSELK#.C	97.83	32.63	3.00	0.33
Q6IRU2_TP	Tpm4	Tropomyos	R.AQEQLATALQNLEEAEK#.A	28.52	10.28	2.77	0.36
Q6IRU2_TP	Tpm4	Tropomyos	R.EKAEGDAAALNR.R	10.92	20.11	0.54	1.84
Q6IRU2_TP	Tpm4	Tropomyos	R.IQLLEEELDR.A	11.12	19.35	0.57	1.74
Q6IRU2_TP	Tpm4	Tropomyos	R.KIQALQQQADDAEDR.A	16.85	28.70	0.59	1.70
Q6IRU2_TP	Tpm4	Tropomyos	R.K#LVILEGELK#.R	76.94	23.75	3.24	0.31
Q6IRU2_TP	Tpm4	Tropomyos	R.KLVILEGELKR.A	13.71	19.70	0.70	1.44
Q6IRU2_TP	Tpm4	Tropomyos	K.LVILEGELK#.R	26.63	8.33	3.20	0.31
Q6IRU2_TP	Tpm4	Tropomyos	K.M*EILEM*QLK#.E	15.38	4.94	3.11	0.32
Q6IRU2_TP	Tpm4	Tropomyos	K.MEILEM*QLK#.E	21.96	5.08	4.32	0.23
Q6IRU2_TP	Tpm4	Tropomyos	K.MEILEMQLK#.E	28.03	8.79	3.19	0.31
Q6IRU2_TP	Tpm4	Tropomyos	K.YSEK#EDK#YEEEIK#.L	105.94	32.86	3.22	0.31
Q6IRU2_TP	Tpm4	Tropomyos	R.AQEQLATALQNLEEAEK#.A	4.65	3.45	1.34	0.74
Q6IRU2_TP	Tpm4	Tropomyos	K.IQALQQQADDAEDR.A	9.62	12.21	0.79	1.27
Q6IRU2_TP	Tpm4	Tropomyos	R.K#LVILEGELK#.R	17.75	5.62	3.16	0.32
Q6IRU2_TP	Tpm4	Tropomyos	K.LVILEGELK#.R	6.28	8.10	0.78	1.29
Q6IRU2_TP	Tpm4	Tropomyos	K.YSEK#EDK#YEEEIK#.L	23.04	12.63	1.82	0.55
Q64514_TP	Tpp2	Tripeptidyl	R.DPVQVAAPSDHGVGIEPVFPENTENSEK#.I	6.44	1.90	3.39	0.29
Q64514_TP	Tpp2	Tripeptidyl	K.IIDIIDTTGSGDVNTATEVEPK#.D	7.59	1.98	3.83	0.26
Q64514_TP	Tpp2	Tripeptidyl	K.LIK#EELQSQVELLNSFEK#.K	10.04	3.12	3.21	0.31
Q64514_TP	Tpp2	Tripeptidyl	K.VLIFAYK#.H	18.06	2.50	7.23	0.14
Q64514_TP	Tpp2	Tripeptidyl	R.VPITAVIAAK#.V	46.60	8.36	5.58	0.18
Q64514_TP	Tpp2	Tripeptidyl	K.GTLIEAFPVLGGK#.A	57.91	8.93	6.49	0.15
Q64514_TP	Tpp2	Tripeptidyl	R.GVLIAVLDTGVDPGAPGM*QVTTDGK#PK#.I	12.89	3.77	3.42	0.29
Q64514_TP	Tpp2	Tripeptidyl	R.GVLIAVLDTGVDPGAPGMQVTTDGK#PK#.I	10.27	4.85	2.12	0.47
Q64514_TP	Tpp2	Tripeptidyl	K.IPANWTNPLGK#.Y	25.95	5.00	5.19	0.19
Q64514_TP	Tpp2	Tripeptidyl	K.LIK#EELQSQVELLNSFEK#.K	11.99	2.12	5.65	0.18
Q64514_TP	Tpp2	Tripeptidyl	K.VLIFAYK#.H	31.46	7.08	4.44	0.23
Q64514_TP	Tpp2	Tripeptidyl	R.VPITAVIAAK#.V	74.83	10.46	7.16	0.14
F6ZDS4_TP	Tpr	Nucleoprot	R.NLGIQSQFTR@.A	11.74	2.18	5.38	0.19
F6ZDS4_TP	Tpr	Nucleoprot	R.ASTALSNEQQAR.R	2.83	5.09	0.56	1.80
F6ZDS4_TP	Tpr	Nucleoprot	R.ASTALSNEQQAR.R	10.55	22.22	0.47	2.11
F6ZDS4_TP	Tpr	Nucleoprot	K.DAVQAPLNVSLNEEGK#.S	16.01	7.99	2.00	0.50
F6ZDS4_TP	Tpr	Nucleoprot	K.ELENANDLLSATK#.R	20.86	22.95	0.91	1.10
F6ZDS4_TP	Tpr	Nucleoprot	K.GAILSEEELAAMSPTAAAVAK#.I	5.55	5.78	0.96	1.04
F6ZDS4_TP	Tpr	Nucleoprot	R.GIASTSDPPTANIK#PTPVVSTPSK#.V	30.92	13.35	2.32	0.43
F6ZDS4_TP	Tpr	Nucleoprot	K.HVEDLLTK#.L	25.10	19.52	1.29	0.78
F6ZDS4_TP	Tpr	Nucleoprot	K.IIDIQEK#.V	57.87	28.24	2.05	0.49
F6ZDS4_TP	Tpr	Nucleoprot	R.K#LELDILPLQEANAELSEK#.S	58.08	29.27	1.98	0.50
F6ZDS4_TP	Tpr	Nucleoprot	K.LENSLAELEQLR.E	4.79	17.99	0.27	3.76
F6ZDS4_TP	Tpr	Nucleoprot	R.LEQNLQQM*QAK#.V	27.82	13.21	2.11	0.47
F6ZDS4_TP	Tpr	Nucleoprot	R.LK#ESAEFQTQLEK#.K	29.84	14.16	2.11	0.47
F6ZDS4_TP	Tpr	Nucleoprot	R.LSQEVEYLTEDVKR.L	10.87	28.13	0.39	2.59
F6ZDS4_TP	Tpr	Nucleoprot	K.LTELYNAYVETQDQLLLEK#.Q	18.27	6.08	3.01	0.33
F6ZDS4_TP	Tpr	Nucleoprot	R.NQQLINQQK#.D	13.76	5.98	2.30	0.43
F6ZDS4_TP	Tpr	Nucleoprot	K.SLEGQVENLQK#.T	54.38	20.28	2.68	0.37
F6ZDS4_TP	Tpr	Nucleoprot	R.SLQEQTVQLQSELSR.L	8.61	8.64	1.00	1.00
F6ZDS4_TP	Tpr	Nucleoprot	R.SSTSQTVSTPAPEPVIDSTEAIEAK#.A	15.04	13.41	1.12	0.89
F6ZDS4_TP	Tpr	Nucleoprot	K.TETM*NVVM*ETNK#.M	28.23	12.74	2.22	0.45
F6ZDS4_TP	Tpr	Nucleoprot	K.TLSEKETEAR.S	4.87	8.28	0.59	1.70
F6ZDS4_TP	Tpr	Nucleoprot	K.TSTSNVEQYR.A	9.35	13.66	0.68	1.46

Q8QZZ7_TP	Tprkb	EKC/KEOPS	K.FGISETNTSVLIVYIEDGSK#.Q	4.61	2.77	1.66	0.60
Q8QZZ7_TP	Tprkb	EKC/KEOPS	R.TLSTEIIFNLSPNNNISEALK#K#.F	20.98	4.90	4.28	0.23
Q8QZZ7_TP	Tprkb	EKC/KEOPS	R.VTLLLFK#.D	25.67	5.05	5.08	0.20
A2APB8_TP	Tpx2	Targeting p	R.IFESGPILPK#.R	12.01	10.27	1.17	0.85
A2APB8_TP	Tpx2	Targeting p	R.TFDEAASTYVPIAQQVEAFHK#.R	5.98	6.25	0.96	1.05
Q6PFR5_TF	Tra2a	Transforme	R.GYDRYEDYDYR.R	1.52	26.83	0.06	17.61
Q6PFR5_TF	Tra2a	Transforme	R.IRVDYSITK.R	14.20	57.95	0.25	4.08
Q6PFR5_TF	Tra2a	Transforme	R.YGPLSGVNVVYDQR.T	30.63	158.68	0.19	5.18
Q6PFR5_TF	Tra2a	Transforme	R.GFAFVYFER.I	1.46	5.88	0.25	4.03
Q6PFR5_TF	Tra2a	Transforme	R.YGPLSGVNVVYDQR.T	2.52	7.33	0.34	2.91
P62996_TF	Tra2b	Transforme	R.GFAFVYFENVDDAK#.E	390.99	354.31	1.10	0.91
P62996_TF	Tra2b	Transforme	R.IRVDFSITK.R	17.18	65.31	0.26	3.80
P62996_TF	Tra2b	Transforme	R.VDFSITK#.R	169.49	154.60	1.10	0.91
P62996_TF	Tra2b	Transforme	K.YGPIADVSIVYDQQSR.R	42.08	175.99	0.24	4.18
P62996_TF	Tra2b	Transforme	R.GFAFVYFENVDDAK#.E	31.57	21.30	1.48	0.67
P62996_TF	Tra2b	Transforme	K.YGPIADVSIVYDQQSR.R	4.24	16.59	0.26	3.91
Q9CQN1_TI	Trap1	Heat shock	K.AFLEALQNQAETSSK#.I	12.00	27.21	0.44	2.27
Q9CQN1_TI	Trap1	Heat shock	K.AFLEALQNQAETSSK#.I	7.26	52.48	0.14	7.23
Q3TLI0_TP(	Trappc10	Trafficking	R.LADLLDVDK#DEALVESEDYFSTK#.L	4.37	3.42	1.28	0.78
B2RXC1_TP	Trappc11	Trafficking	K.ASEVLENLTQGK#.M	17.31	5.50	3.15	0.32
B2RXC1_TP	Trappc11	Trafficking	K.QFQAFGDLFDEAIK#.L	7.61	3.69	2.06	0.48
B2RXC1_TP	Trappc11	Trafficking	K.VAVVLIQK#.K	15.89	5.10	3.12	0.32
Q8K2L8_TP	Trappc12	Trafficking	R.ILLQIGDIK#.T	16.30	3.49	4.67	0.21
Q9CQP2_TI	Trappc2	Trafficking	K.FAM*NPFYEPNSPIR.S	2.36	3.56	0.66	1.51
O55013_TF	Trappc3	Trafficking	K.FVQDTLKGDGVTEIR.M	10.17	40.90	0.25	4.02
O55013_TF	Trappc3	Trafficking	R.GALEM*VQM*AVEAK#.F	5.26	5.10	1.03	0.97
O55013_TF	Trappc3	Trafficking	R.RIEDNLPAGEE.-	8.06	24.45	0.33	3.03
Q9ES56_TP	Trappc4	Trafficking	K.AGGLIYQWDSYSPR.A	3.28	8.49	0.39	2.59
Q9ES56_TP	Trappc4	Trafficking	K.YTADGKEVLEYLGNPANYPVSIR.F	1.62	5.19	0.31	3.20
Q9CQA1_TI	Trappc5	Trafficking	R.VLDALVAR.E	5.80	7.57	0.77	1.30
Q9CQA1_TI	Trappc5	Trafficking	K.VLGALLFVK#.G	41.00	21.00	1.95	0.51
E9PWG2_E	Trappc8	Protein Tra	R.ASDEQIPDPWSQYLQK#.N	5.11	1.99	2.57	0.39
Q99PP9_TF	Trim16	Tripartite	R.IVDLGEEPEK#PAGSSVEAAP.-	5.77	5.12	1.13	0.89
Q64127_TI	Trim24	Transcripti	K.FPTQISLAQLR.L	1.23	8.26	0.15	6.72
Q64127_TI	Trim24	Transcripti	R.YQFIEEAFQNQK#.V	8.74	7.77	1.12	0.89
Q61510_TF	Trim25	E3 ubiquiti	K.ASAAQPDSVGVK#.A	16.57	16.43	1.01	0.99
Q61510_TF	Trim25	E3 ubiquiti	K.AVIDAAETSSLR.K	5.50	9.72	0.57	1.77
Q62318_TI	Trim28	Transcripti	K.DIVENYFM*R.D	10.01	31.24	0.32	3.12
Q62318_TI	Trim28	Transcripti	K.DIVENYFMR.D	4.00	20.87	0.19	5.22
Q62318_TI	Trim28	Transcripti	R.FASWALESDNNTALLLSK.K	17.19	16.73	1.03	0.97
Q62318_TI	Trim28	Transcripti	K.FSAVLVEPPPLNLPSAGLSSQELSGPGDGP.-	22.25	22.25	1.00	1.00
Q62318_TI	Trim28	Transcripti	K.IVAERPGTNSTGPGPM*APPR.A	2.13	33.82	0.06	15.90
Q62318_TI	Trim28	Transcripti	K.IVAERPGTNSTGPGPMAPPR.A	2.49	28.12	0.09	11.31
Q62318_TI	Trim28	Transcripti	R.LDLDLTSDSQPPVFK#.V	46.02	55.84	0.82	1.21
Q62318_TI	Trim28	Transcripti	K.LSPPYSSPQEFAQDVGR.M	3.27	19.24	0.17	5.88
Q62318_TI	Trim28	Transcripti	K.M*AILQIMK.E	11.46	16.56	0.69	1.44
Q62318_TI	Trim28	Transcripti	K.MAILQIMK#.E	11.15	9.83	1.13	0.88
Q62318_TI	Trim28	Transcripti	K.M*IVDPVEPHGEM*K.F	24.47	31.37	0.78	1.28
Q62318_TI	Trim28	Transcripti	R.M*NDAFGDTK.F	23.16	16.35	1.42	0.71
Q62318_TI	Trim28	Transcripti	R.SGEGEVSGLLR.K	17.73	101.74	0.17	5.74
Q62318_TI	Trim28	Transcripti	K.VFPGSTTEDYNLIVIER.G	2.67	8.34	0.32	3.12
Q62318_TI	Trim28	Transcripti	K.LSPPYSSPQEFAQDVGR.M	1.79	8.15	0.22	4.55
Q62318_TI	Trim28	Transcripti	K.ADVQSIIGLQR.F	104.76	103.77	1.01	0.99
Q62318_TI	Trim28	Transcripti	K.DHQYQFLEDAVR.N	9.85	43.45	0.23	4.41
Q62318_TI	Trim28	Transcripti	K.DIVENYFM*R.D	71.28	175.60	0.41	2.46
Q62318_TI	Trim28	Transcripti	K.DIVENYFMR.D	14.18	43.59	0.33	3.07
Q62318_TI	Trim28	Transcripti	K.EEDGSLSLDGADSTGVVAK#.L	15.56	18.83	0.83	1.21
Q62318_TI	Trim28	Transcripti	R.FASWALESDNNTALLLSK#.K	131.27	105.79	1.24	0.81
Q62318_TI	Trim28	Transcripti	R.FASWALESDNNTALLLSK.K	73.72	64.46	1.14	0.87
Q62318_TI	Trim28	Transcripti	K.FQWDLNAWTK#.S	227.95	195.10	1.17	0.86
Q62318_TI	Trim28	Transcripti	R.GAAAAAAGQAGTVPPGAPGAPPLPGMAIVK.E	10.62	6.15	1.73	0.58
Q62318_TI	Trim28	Transcripti	K.IVAERPGTNSTGPGPM*APPR.A	9.99	231.33	0.04	23.16
Q62318_TI	Trim28	Transcripti	K.IVAERPGTNSTGPGPMAPPR.A	10.10	147.53	0.07	14.61
Q62318_TI	Trim28	Transcripti	K.KLIYFQLHR.A	10.28	31.38	0.33	3.05
Q62318_TI	Trim28	Transcripti	R.K#LLASLVK#.R	271.27	223.92	1.21	0.83
Q62318_TI	Trim28	Transcripti	R.LDLDLTSDSQPPVFK#.V	355.80	327.04	1.09	0.92
Q62318_TI	Trim28	Transcripti	R.LGDK#HATLQK#.N	12.45	8.05	1.55	0.65
Q62318_TI	Trim28	Transcripti	K.LIYFQLHR.A	16.19	26.29	0.62	1.62
Q62318_TI	Trim28	Transcripti	K.LLASLVK#.R	167.17	131.27	1.27	0.79
Q62318_TI	Trim28	Transcripti	K.LSPPYSSPQEFAQDVGR.M	37.23	175.94	0.21	4.73
Q62318_TI	Trim28	Transcripti	K.LTEDKADVQSIIGLQR.F	8.79	37.38	0.24	4.25
Q62318_TI	Trim28	Transcripti	K.LTEDKADVQSIIGLQR.F	52.49	187.91	0.28	3.58
Q62318_TI	Trim28	Transcripti	K.M*AILQIM*K#.E	104.12	90.90	1.15	0.87
Q62318_TI	Trim28	Transcripti	K.MAILQIM*K#.E	53.13	45.24	1.17	0.85
Q62318_TI	Trim28	Transcripti	K.M*AILQIMK#.E	56.65	62.25	0.91	1.10
Q62318_TI	Trim28	Transcripti	K.MAILQIMK#.E	50.63	58.46	0.87	1.15
Q62318_TI	Trim28	Transcripti	K.M*IVDPVEPHGEM*K#.F	135.35	149.16	0.91	1.10
Q62318_TI	Trim28	Transcripti	K.M*IVDPVEPHGEMK#.F	39.81	34.32	1.16	0.86
Q62318_TI	Trim28	Transcripti	K.MIVDPVEPHGEM*K#.F	59.68	49.20	1.21	0.82
Q62318_TI	Trim28	Transcripti	R.MNDAFGDTK#.F	65.27	48.00	1.36	0.74
Q62318_TI	Trim28	Transcripti	R.M*NDAFGDTK#.F	90.76	84.88	1.07	0.94
Q62318_TI	Trim28	Transcripti	K.QGSGSSQPM*EVQEGYGFGSDDPYSSAEPHVSGMK#.R	21.83	12.18	1.79	0.56
Q62318_TI	Trim28	Transcripti	K.QGSGSSQPMEVQEGYGFGSDDPYSSAEPHVSGM*K.R	21.83	12.18	1.79	0.56
Q62318_TI	Trim28	Transcripti	K.QGSGSSQPM*EVQEGYGFGSDDPYSSAEPHVSGM*KR.S	5.04	24.09	0.21	4.78
Q62318_TI	Trim28	Transcripti	K.QGSGSSQPMEVQEGYGFGSDDPYSSAEPHVSGM*KR.S	2.51	6.29	0.40	2.50
Q62318_TI	Trim28	Transcripti	K.SAEAFGK#.I	155.56	150.26	1.04	0.97
Q62318_TI	Trim28	Transcripti	R.SGEGEVSGLLR.K	84.41	358.37	0.24	4.25
Q62318_TI	Trim28	Transcripti	K.VFPGSTTEDYNLIVIER.G	32.19	127.81	0.25	3.97
Q62318_TI	Trim28	Transcripti	R.VLVNDAQK#.V	341.81	313.27	1.09	0.92
Q62318_TI	Trim28	Transcripti	K.VTEGQQER.L	4.75	15.12	0.31	3.18
Q62318_TI	Trim28	Transcripti	K.DHQYQFLEDAVR.N	3.38	13.73	0.25	4.06
Q62318_TI	Trim28	Transcripti	K.DIVENYFM*R.D	4.44	26.01	0.17	5.86
Q62318_TI	Trim28	Transcripti	K.EEDGSLSLDGADSTGVVAK.L	4.90	6.76	0.72	1.38
Q62318_TI	Trim28	Transcripti	R.FASWALESDNNTALLLSK#.K	22.01	22.29	0.99	1.01
Q62318_TI	Trim28	Transcripti	K.FQWDLNAWTK#.S	21.22	19.26	1.10	0.91
Q62318_TI	Trim28	Transcripti	R.K#LLASLVK#.R	30.37	26.24	1.16	0.86
Q62318_TI	Trim28	Transcripti	R.LDLDLTSDSQPPVFK.V	64.24	70.66	0.91	1.10
Q62318_TI	Trim28	Transcripti	K.LLASLVK#.R	22.74	23.12	0.98	1.02
Q62318_TI	Trim28	Transcripti	K.LSPPYSSPQEFAQDVGR.M	6.24	30.62	0.20	4.91
Q62318_TI	Trim28	Transcripti	K.LTEDKADVQSIIGLQR.F	15.98	56.68	0.28	3.55
Q62318_TI	Trim28	Transcripti	K.M*AILQIM*K#.E	20.51	13.54	1.52	0.66
Q62318_TI	Trim28	Transcripti	R.M*NDAFGDTK#.F	14.85	14.55	1.02	0.98
Q62318_TI	Trim28	Transcripti	R.SGEGEVSGLLR.K	12.86	66.48	0.19	5.17

Q62318_T	Trim28	Transcripti	K.VFPGSTTEDYNLIVIER.G	4.65	18.72	0.25	4.02
Q62318_T	Trim28	Transcripti	R.VLVNDAQK#.V	69.91	66.45	1.05	0.95
Q9R1R2_T	Trim3	Tripartite	R.QALVGQPASLTVTTK#.D	8.38	5.75	1.46	0.69
Q9R1R2_T	Trim3	Tripartite	K.VLQTQLDTLR.Q	4.64	11.15	0.42	2.40
Q99PP7_T	Trim33	E3 ubiquiti	K.LLQQQNDITGLSR.Q	3.45	19.38	0.18	5.61
Q99PP7_T	Trim33	E3 ubiquiti	K.LLQQQNDITGLSR.Q	2.75	10.16	0.27	3.69
Q8CJ53_C	Trip10	Cdc42-inte	R.HTQWGLDLLDK#YVK#.F	8.32	4.26	1.96	0.51
Q8CJ53_C	Trip10	Cdc42-inte	R.IAETLGNIER.L	16.34	14.97	1.09	0.92
Q8CJ53_C	Trip10	Cdc42-inte	R.LDQDINATK#.A	32.30	12.65	2.55	0.39
Q8CJ53_C	Trip10	Cdc42-inte	K.VAAESVDAK#.N	20.24	15.64	1.29	0.77
G5E870_T	Trip12	E3 ubiquiti	K.IDPLALVQAIER.Y	2.98	11.37	0.26	3.81
G5E870_T	Trip12	E3 ubiquiti	R.LVDNFQHEENLLQQVASK#.D	9.22	5.80	1.59	0.63
G5E870_T	Trip12	E3 ubiquiti	R.SSAVVVDAIPVFLEK#.L	8.48	7.45	1.14	0.88
G5E870_T	Trip12	E3 ubiquiti	R.EGQQSFHLS.-	26.05	26.05	1.00	1.00
G5E870_T	Trip12	E3 ubiquiti	K.EIIPTSEFINSK#.L	18.52	8.66	2.14	0.47
G5E870_T	Trip12	E3 ubiquiti	R.FLHVFFSSPLPGEEPVGR.V	13.13	10.54	1.25	0.80
G5E870_T	Trip12	E3 ubiquiti	K.IDPLALVQAIER.Y	14.09	36.31	0.39	2.58
G5E870_T	Trip12	E3 ubiquiti	R.IIEAAHQVGEDEISLSTLGR.V	3.77	68.35	0.06	18.14
G5E870_T	Trip12	E3 ubiquiti	R.LLDTNPEINQSDSQDSR.V	6.41	13.24	0.48	2.07
G5E870_T	Trip12	E3 ubiquiti	R.LVDLPLGLPFYK#.W	59.57	35.34	1.69	0.59
G5E870_T	Trip12	E3 ubiquiti	R.LVDNFQHEENLLQQVASK#.D	47.00	21.74	2.16	0.46
G5E870_T	Trip12	E3 ubiquiti	K.M*ADPESNQETVNSSAAR.T	4.23	6.15	0.69	1.45
G5E870_T	Trip12	E3 ubiquiti	K.NHAVSSHIASM*LSSQDLK#.I	5.94	2.11	2.81	0.36
G5E870_T	Trip12	E3 ubiquiti	R.QFSVQAEDERESTDDESNPLGR.A	1.92	5.81	0.33	3.02
G5E870_T	Trip12	E3 ubiquiti	K.SETSK#PGPSGLQAK#.L	8.45	18.05	0.47	2.14
G5E870_T	Trip12	E3 ubiquiti	R.SLNPPLTIVR.K	5.13	15.10	0.34	2.95
G5E870_T	Trip12	E3 ubiquiti	R.SSAVVVDAIPVFLEK#.L	51.01	23.17	2.20	0.45
G5E870_T	Trip12	E3 ubiquiti	K.SSFLASLNPK#.T	21.97	18.60	1.18	0.85
G5E870_T	Trip12	E3 ubiquiti	K.TLFGVLYEVYSSSAGPAVR.H	6.55	15.46	0.42	2.36
Q3UA06_P	Trip13	Pachytene	R.HSNVVILTTSNITEK#.I	10.60	2.58	4.11	0.24
Q3UA06_P	Trip13	Pachytene	R.NVQSVSIVDTELK#.A	16.35	4.18	3.91	0.26
Q3UA06_P	Trip13	Pachytene	K.QYIGPPSAAAIFK#.I	14.14	7.20	1.96	0.51
Q3UA06_P	Trip13	Pachytene	K.SHLLDYVMTTVLFSDK#.N	6.58	2.29	2.87	0.35
Q3UA06_P	Trip13	Pachytene	R.VVNAVLTQIDQIK#.R	6.90	2.24	3.08	0.33
Q3UA06_P	Trip13	Pachytene	R.NVQSVSIVDTELK#.A	15.53	4.57	3.39	0.29
Q3UA06_P	Trip13	Pachytene	K.QYIGPPSAAAIFK#.I	9.05	5.95	1.52	0.66
Q9QXN3_T	Trip4	Activating	K.GQFIEDLITK#.W	9.27	4.59	2.02	0.49
Q9QXN3_T	Trip4	Activating	R.LDETIQAIASGTLNQSLVTLDR.S	2.51	7.06	0.36	2.81
Q9QXN3_T	Trip4	Activating	R.NK#QEVPAFPEPDVAVEVK#.T	14.01	14.92	0.94	1.07
Q8C1Z8_T	Trmt10a	tRNA meth	K.KEDLVYLTSDSPNVLK#.D	16.95	6.81	2.49	0.40
Q8C1Z8_T	Trmt10a	tRNA meth	R.VDAGAEPISK#.R	17.85	3.27	5.45	0.18
Q9DCG9_T	Trmt112	Multifuncti	R.GIPNM*LLNDEETET.-	24.97	24.97	1.00	1.00
Q9DCG9_T	Trmt112	Multifuncti	R.INPVEFNPEFVAR.M	29.83	72.86	0.41	2.44
Q9DCG9_T	Trmt112	Multifuncti	R.LQATEVR.I	1058.82	5964.56	0.18	5.63
A2RSY6_TR	Trmt1l	TRMT1-like	R.NLGIVSVTSTDISSLYAK#.A	13.45	7.45	1.80	0.55
A2RSY6_TR	Trmt1l	TRMT1-like	K.TTDDTTIDIYSAQGK#.R	8.21	5.73	1.43	0.70
A2RSY6_TR	Trmt1l	TRMT1-like	K.VTINDLNENSVTLIQK#.N	6.02	2.52	2.39	0.42
A2RSY6_TR	Trmt1l	TRMT1-like	R.NLGIVSVTSTDISSLYAK#.A	15.19	9.18	1.66	0.60
A2RSY6_TR	Trmt1l	TRMT1-like	K.TTDDTTIDIYSAQGK#.R	12.71	7.81	1.63	0.61
A2RSY6_TR	Trmt1l	TRMT1-like	K.VTINDLNENSVTLIQK#.N	10.26	5.12	2.01	0.50
A2RSY6_TR	Trmt1l	TRMT1-like	K.VVVDSEEKEEGDALEDDGTLGDIQVTR.M	3.19	7.60	0.42	2.38
Q8BNV1_T	Trmt2a	tRNA (uraci	K.AFQEFIR.S	3.02	7.46	0.41	2.47
Q8BNV1_T	Trmt2a	tRNA (uraci	K.LSSEEVAGLK#.A	12.54	10.01	1.25	0.80
Q8BNV1_T	Trmt2a	tRNA (uraci	K.AFQEFIR.S	4.36	9.28	0.47	2.13
Q8BNV1_T	Trmt2a	tRNA (uraci	K.ASGVTSLYFVEEGQR.K	1.86	6.73	0.28	3.62
O08848_R	Trove2	60 kDa SS-	R.LSHLK#PSSEGLAIVTK#.Y	9.20	2.04	4.51	0.22
Q925H1_T	Trps1	Zinc finger	R.LNPEALQAEQLNK.Q	7.66	14.57	0.53	1.90
Q80YV3_T	Trrap	Transforma	R.LVEDNPSSLSLVEIYK#.Q	6.46	4.25	1.52	0.66
Q8R3W5_S	Tsen15	tRNA-splici	K.LTDGFM*LPDPQNISLR.R	2.12	5.51	0.38	2.60
Q8BMZ5_S	Tsen34	tRNA-splici	K.FGGDFLVYPGDPLR.F	2.10	9.11	0.23	4.34
Q61187_T	Tsg101	Tumor susc	R.ASLISAVSDK#.L	36.30	14.69	2.47	0.40
Q61187_T	Tsg101	Tumor susc	R.DGTISEDTIR.A	7.33	22.39	0.33	3.06
Q61187_T	Tsg101	Tumor susc	R.ELVNLTGTIPVR.Y	11.70	35.53	0.33	3.04
Q61187_T	Tsg101	Tumor susc	R.GVIDLDVFLK#.H	28.14	15.19	1.85	0.54
Q61187_T	Tsg101	Tumor susc	R.LDQEVAEVDK#NIELLK#.K	37.17	21.51	1.73	0.58
Q62348_T	Tsn	Translin OS	R.EILTLLQGVHQGTGFQDIPK#.R	10.31	4.27	2.41	0.41
Q5SWD9_T	Tsr1	Pre-rRNA-p	R.AYLFAHVADFVPSEESDLVGTLK#.I	12.85	6.78	1.89	0.53
Q5SWD9_T	Tsr1	Pre-rRNA-p	R.IFQFQNFVNTR.K	3.94	8.13	0.48	2.07
Q5SWD9_T	Tsr1	Pre-rRNA-p	R.ISLPEAFK#.L	19.55	4.69	4.16	0.24
Q8CD92_T	Ttc27	Tetratricop	R.AM*R@QTQALADQFEDK.A	2.93	2.25	1.30	0.77
Q8CD92_T	Ttc27	Tetratricop	K.NLELNDDTVLNEIK#.L	16.51	5.19	3.18	0.31
Q8CD92_T	Ttc27	Tetratricop	R.SPQLFALAK#.N	19.72	5.85	3.37	0.30
F8VPK0_F8	Ttc37	Protein Ttc	K.VALVDFLDGK#.A	13.23	3.97	3.33	0.30
F8VPK0_F8	Ttc37	Protein Ttc	K.AALNELLK#.H	24.93	17.55	1.42	0.70
F8VPK0_F8	Ttc37	Protein Ttc	K.ASELNPDSTYSVFK#.V	25.26	6.54	3.86	0.26
F8VPK0_F8	Ttc37	Protein Ttc	K.AVDYVEQALGYFTR.A	6.01	6.99	0.86	1.16
F8VPK0_F8	Ttc37	Protein Ttc	K.AVHSNPADPALWSLLSR.I	3.62	9.47	0.38	2.62
F8VPK0_F8	Ttc37	Protein Ttc	K.IM*EDLVTSYPDLAEAHALEGR.V	7.39	9.23	0.80	1.25
F8VPK0_F8	Ttc37	Protein Ttc	K.SNPDQPAVILLLR.Q	11.07	15.19	0.73	1.37
F8VPK0_F8	Ttc37	Protein Ttc	K.VAAIQQILGR.Y	11.08	10.74	1.03	0.97
F8VPK0_F8	Ttc37	Protein Ttc	K.VALVDFLDGK#.A	56.13	15.13	3.71	0.27
F8VPK0_F8	Ttc37	Protein Ttc	R.YSEAIAQYQLIIK#.M	10.76	1.58	6.79	0.15
Q8BYY4_TT	Ttc39b	Tetratricop	K.AAILSM*LPEEEVAATK#.E	5.94	2.78	2.13	0.47
Q8BYY4_TT	Ttc39b	Tetratricop	K.AAILSM*LPEEEVAATK#.E	13.15	4.36	3.02	0.33
Q5NC05_T	Ttf2	Transcripti	K.QVLSGSEGPVTK#.L	7.80	6.57	1.19	0.84
Q5NC05_T	Ttf2	Transcripti	K.VSSLLAELEAIQK#.G	10.74	6.06	1.77	0.56
A2ASS6_TI	Ttn	Titin OS=M	K.DVTVPEK#.R	34.04	17.04	2.00	0.50
P68369_T	Tuba1a	Tubulin alp	R.AFVHWYVGEGM*EEGEFSEAR.E	78.42	177.68	0.44	2.27
P68369_T	Tuba1a	Tubulin alp	R.AFVHWYVGEGM*EEGEFSEAR.E	6.60	17.51	0.38	2.65
P68369_T	Tuba1a	Tubulin alp	R.AFVHWYVGEGMEEGEFSEAR.E	38.48	119.02	0.32	3.09
P68369_T	Tuba1a	Tubulin alp	R.AVFVDLEPTVIDEVR.T	73.21	212.50	0.34	2.90
P68369_T	Tuba1a	Tubulin alp	R.AVFVDLEPTVIDEVR.T	196.32	604.81	0.32	3.08
P68369_T	Tuba1a	Tubulin alp	K.DVNAAIATIK#.T	585.18	415.56	1.41	0.71
P68369_T	Tuba1a	Tubulin alp	K.DYEEVGVDSVEGEGEEEGEEY.-	79.68	79.68	1.00	1.00
P68369_T	Tuba1a	Tubulin alp	K.EDAANNYAR.G	30.73	86.07	0.36	2.80
P68369_T	Tuba1a	Tubulin alp	R.EDMAALEK#.D	115.24	70.15	1.64	0.61
P68369_T	Tuba1a	Tubulin alp	R.EDM*AALEK#.D	247.23	179.95	1.37	0.73
P68369_T	Tuba1a	Tubulin alp	R.EDM*AALEK#DYEEVGVDSVEGEGEEEGEEY.-	19.20	7.88	2.44	0.41
P68369_T	Tuba1a	Tubulin alp	K.EIIDLVLDR.I	113.37	356.97	0.32	3.15
P68369_T	Tuba1a	Tubulin alp	R.FDGALNVDLTEFQTNLVPYPR.I	68.33	233.92	0.29	3.42
P68369_T	Tuba1a	Tubulin alp	K.FDLM*YAK#.R	220.84	132.79	1.66	0.60
P68369_T	Tuba1a	Tubulin alp	K.FDLMYAK#.R	80.34	59.40	1.35	0.74
P68369_T	Tuba1a	Tubulin alp	R.IHFPLATYAPVISAEK#.A	352.94	248.27	1.42	0.70

P68369_TE	Tuba1a	Tubulin alp	R.LDHK#FDLM*YAK#.R	127.66	85.94	1.49	0.67
P68369_TE	Tuba1a	Tubulin alp	R.LDHKFDLM*YAK.R	3.27	59.63	0.05	18.26
P68369_TE	Tuba1a	Tubulin alp	R.LDHK#FDLMYAK#.R	85.62	56.65	1.51	0.66
P68369_TE	Tuba1a	Tubulin alp	R.LIGQIVSSITASLR.F	15.35	37.55	0.41	2.45
P68369_TE	Tuba1a	Tubulin alp	R.LSVDYGK#.K	370.44	268.51	1.38	0.72
P68369_TE	Tuba1a	Tubulin alp	R.LSVDYGK#K#.S	214.77	100.31	2.14	0.47
P68369_TE	Tuba1a	Tubulin alp	K.TIGGGDDSFNTFFSETGAGK#.H	521.68	317.27	1.64	0.61
P68369_TE	Tuba1a	Tubulin alp	K.VGINYQPPTVVPGGDLAK#.V	371.93	246.67	1.51	0.66
P68369_TE	Tuba1a	Tubulin alp	K.VGINYQPPTVVPGGDLAK.V	71.53	57.88	1.24	0.81
P68369_TE	Tuba1a	Tubulin alp	R.AFVHWYVGEGM*EEGEFSEAR.E	7.63	23.18	0.33	3.04
P68369_TE	Tuba1a	Tubulin alp	R.AFVHWYVGEGMEEGEFSEAR.E	2.77	8.50	0.33	3.07
P68369_TE	Tuba1a	Tubulin alp	R.AVFVDLEPTVIDEVR.T	26.26	115.73	0.23	4.41
P68369_TE	Tuba1a	Tubulin alp	K.DVNAAIATIK#.T	95.70	72.78	1.31	0.76
P68369_TE	Tuba1a	Tubulin alp	K.DYEEVGVDSVEGEGEEEGEEY.-	8.67	8.67	1.00	1.00
P68369_TE	Tuba1a	Tubulin alp	R.EDMAALEK#.D	11.65	7.59	1.53	0.65
P68369_TE	Tuba1a	Tubulin alp	K.EIIDLVLDR.I	77.69	38.49	2.02	0.50
P68369_TE	Tuba1a	Tubulin alp	R.LDHK#FDLMYAK#.R	9.18	6.46	1.42	0.70
P68369_TE	Tuba1a	Tubulin alp	K.TIGGGDDSFNTFFSETGAGK#.H	69.15	58.72	1.18	0.85
P68369_TE	Tuba1a	Tubulin alp	K.VGINYQPPTVVPGGDLAK#.V	105.76	90.33	1.17	0.85
P68369_TE	Tuba1a	Tubulin alp	R.AFVHWYVGEGM*EEGEFSEAR.E	18.96	50.14	0.38	2.64
P68369_TE	Tuba1a	Tubulin alp	R.AFVHWYVGEGM*EEGEFSEAR.E	3.93	5.35	0.73	1.36
P68369_TE	Tuba1a	Tubulin alp	R.AFVHWYVGEGMEEGEFSEAR.E	12.97	35.20	0.37	2.71
P68369_TE	Tuba1a	Tubulin alp	R.AVFVDLEPTVIDEVR.T	131.00	342.80	0.38	2.62
P68369_TE	Tuba1a	Tubulin alp	K.DVNAAIATIK#.T	463.42	376.11	1.23	0.81
P68369_TE	Tuba1a	Tubulin alp	K.DYEEVGVDSVEGEGEEEGEEY.-	21.22	21.22	1.00	1.00
P68369_TE	Tuba1a	Tubulin alp	R.EDMAALEK#.D	40.97	19.57	2.09	0.48
P68369_TE	Tuba1a	Tubulin alp	K.EIIDLVLDR.I	103.33	255.61	0.40	2.47
P68369_TE	Tuba1a	Tubulin alp	R.FDGALNVDLTEFQTNLVPYPR.I	56.31	129.80	0.43	2.31
P68369_TE	Tuba1a	Tubulin alp	K.FDLM*YAK#.R	83.68	43.81	1.91	0.52
P68369_TE	Tuba1a	Tubulin alp	K.FDLMYAK#.R	47.62	24.02	1.98	0.50
P68369_TE	Tuba1a	Tubulin alp	R.IHFPLATYAPVISAEK#.A	327.96	201.15	1.63	0.61
P68369_TE	Tuba1a	Tubulin alp	R.LDHK#FDLM*YAK#.R	81.54	38.76	2.10	0.48
P68369_TE	Tuba1a	Tubulin alp	R.LDHK#FDLMYAK#.R	70.43	27.75	2.54	0.39
P68369_TE	Tuba1a	Tubulin alp	R.LIGQIVSSITASLR.F	9.29	21.04	0.44	2.26
P68369_TE	Tuba1a	Tubulin alp	R.LSVDYGK#.K	162.27	99.87	1.62	0.62
P68369_TE	Tuba1a	Tubulin alp	R.LSVDYGK#K#.S	174.69	82.11	2.13	0.47
P68369_TE	Tuba1a	Tubulin alp	R.QLFHPEQLITGK#.E	43.55	31.94	1.36	0.73
P68369_TE	Tuba1a	Tubulin alp	K.TIGGGDDSFNTFFSETGAGK#.H	270.18	154.49	1.75	0.57
P68369_TE	Tuba1a	Tubulin alp	K.VGINYQPPTVVPGGDLAK#.V	284.25	173.07	1.64	0.61
P68369_TE	Tuba1a	Tubulin alp	R.AFVHWYVGEGM*EEGEFSEAR.E	41.93	102.13	0.41	2.44
P68369_TE	Tuba1a	Tubulin alp	R.AFVHWYVGEGMEEGEFSEAR.E	8.07	13.90	0.58	1.72
P68369_TE	Tuba1a	Tubulin alp	R.AVFVDLEPTVIDEVR.T	268.05	675.75	0.40	2.52
P68369_TE	Tuba1a	Tubulin alp	K.DVNAAIATIK#.T	871.92	532.74	1.64	0.61
P68369_TE	Tuba1a	Tubulin alp	K.DYEEVGVDSVEGEGEEEGEEY.-	58.06	58.06	1.00	1.00
P68369_TE	Tuba1a	Tubulin alp	K.EDAANNYAR.G	21.73	58.02	0.37	2.67
P68369_TE	Tuba1a	Tubulin alp	R.EDM*AALEK#DYEEVGVDSVEGEGEEEGEEY.-	44.31	26.68	1.66	0.60
P68369_TE	Tuba1a	Tubulin alp	K.EIIDLVLDR.I	206.14	572.32	0.36	2.78
P68369_TE	Tuba1a	Tubulin alp	R.FDGALNVDLTEFQTNLVPYPR.I	81.07	196.85	0.41	2.43
P68369_TE	Tuba1a	Tubulin alp	K.FDLM*YAK#.R	179.79	95.46	1.88	0.53
P68369_TE	Tuba1a	Tubulin alp	K.FDLMYAK#.R	66.45	40.62	1.64	0.61
P68369_TE	Tuba1a	Tubulin alp	R.GHYTIGK#.E	285.65	164.20	1.74	0.57
P68369_TE	Tuba1a	Tubulin alp	R.IHFPLATYAPVISAEK#.A	685.69	402.99	1.70	0.59
P68369_TE	Tuba1a	Tubulin alp	R.IHFPLATYAPVISAEK.A	81.10	52.22	1.55	0.64
P68369_TE	Tuba1a	Tubulin alp	R.LDHK#FDLMYAK#.R	77.86	37.01	2.10	0.48
P68369_TE	Tuba1a	Tubulin alp	R.LIGQIVSSITASLR.F	15.30	32.99	0.46	2.16
P68369_TE	Tuba1a	Tubulin alp	R.LSVDYGK#.K	497.16	279.93	1.78	0.56
P68369_TE	Tuba1a	Tubulin alp	R.LSVDYGK#K#.S	336.81	151.54	2.22	0.45
P68369_TE	Tuba1a	Tubulin alp	R.QLFHPEQLITGK.E	90.27	50.67	1.78	0.56
P68369_TE	Tuba1a	Tubulin alp	R.RNLDIERPTYTNLNR.L	1.19	32.95	0.04	27.79
P68369_TE	Tuba1a	Tubulin alp	K.TIGGGDDSFNTFFSETGAGK#.H	741.97	384.11	1.93	0.52
P68369_TE	Tuba1a	Tubulin alp	K.VGINYQPPTVVPGGDLAK#.V	667.33	369.39	1.81	0.55
P68373_TE	Tuba1c	Tubulin alp	K.DYEEVGADSAEGDDEGEEY.-	15.67	15.67	1.00	1.00
P68373_TE	Tuba1c	Tubulin alp	R.LISQIVSSITASLR.F	59.47	203.63	0.29	3.42
P68373_TE	Tuba1c	Tubulin alp	K.DYEEVGADSAEGDDEGEEY.-	6.79	6.79	1.00	1.00
P68373_TE	Tuba1c	Tubulin alp	R.LISQIVSSITASLR.F	24.08	62.06	0.39	2.58
P68373_TE	Tuba1c	Tubulin alp	K.DYEEVGADSAEGDDEGEEY.-	14.81	14.81	1.00	1.00
P68373_TE	Tuba1c	Tubulin alp	R.EDM*AALEK#DYEEVGADSAEGDDEGEEY.-	12.45	5.89	2.11	0.47
P68373_TE	Tuba1c	Tubulin alp	R.LISQIVSSITASLR.F	42.82	108.25	0.40	2.53
P68368_TE	Tuba4a	Tubulin alp	R.AVFVDLEPTVIDEIR.N	8.96	16.77	0.53	1.87
P68368_TE	Tuba4a	Tubulin alp	K.DVNAAIAAIK#.T	29.60	25.71	1.15	0.87
P68368_TE	Tuba4a	Tubulin alp	K.EIIDPVLDR.I	7.22	16.19	0.45	2.24
P68368_TE	Tuba4a	Tubulin alp	R.AVFVDLEPTVIDEIR.N	3.64	8.70	0.42	2.39
Q3UX10_TI	Tubal3	Tubulin alp	R.SFGGGTGSGFTSLLM*ER.L	3.18	9.98	0.32	3.14
Q3UX10_TI	Tubal3	Tubulin alp	R.SFGGGTGSGFTSLLM*ER.L	4.27	6.42	0.66	1.50
Q7TMM9_1	Tubb2a	Tubulin bet	R.AILVDLEPGTM*DSVR.S	102.18	316.81	0.32	3.10
Q7TMM9_1	Tubb2a	Tubulin bet	R.AILVDLEPGTMDSVR.S	66.57	225.76	0.29	3.39
Q7TMM9_1	Tubb2a	Tubulin bet	R.ALTVPELTQQM*FDSK#.N	47.45	42.57	1.11	0.90
Q7TMM9_1	Tubb2a	Tubulin bet	R.ALTVPELTQQMFDSK#.N	43.04	35.85	1.20	0.83
Q7TMM9_1	Tubb2a	Tubulin bet	K.EVDEQM*LNVQNK#.N	455.30	335.27	1.36	0.74
Q7TMM9_1	Tubb2a	Tubulin bet	K.EVDEQMLNVQNK#.N	383.94	292.50	1.31	0.76
Q7TMM9_1	Tubb2a	Tubulin bet	R.FPGQLNADLR.K	51.67	168.83	0.31	3.27
Q7TMM9_1	Tubb2a	Tubulin bet	R.FPGQLNADLRK.L	7.90	22.65	0.35	2.87
Q7TMM9_1	Tubb2a	Tubulin bet	K.FWEVISDEHGIDPTGSYHGDSDLQLER.I	7.16	20.98	0.34	2.93
Q7TMM9_1	Tubb2a	Tubulin bet	K.GHYTEGAELVDSVLDVVR.K	149.10	437.18	0.34	2.93
Q7TMM9_1	Tubb2a	Tubulin bet	K.GHYTEGAELVDSVLDVVR.K	26.43	64.44	0.41	2.44
Q7TMM9_1	Tubb2a	Tubulin bet	K.GHYTEGAELVDSVLDVVRK.E	33.93	82.31	0.41	2.43
Q7TMM9_1	Tubb2a	Tubulin bet	R.IM*NTFSVM*PSPK#.V	79.24	47.74	1.66	0.60
Q7TMM9_1	Tubb2a	Tubulin bet	R.IMNTFSVM*PSPK#.V	35.50	27.17	1.31	0.77
Q7TMM9_1	Tubb2a	Tubulin bet	R.IM*NTFSVMPSPK#.V	29.85	23.83	1.25	0.80
Q7TMM9_1	Tubb2a	Tubulin bet	R.IMNTFSVMPSPK#.V	31.72	31.77	1.00	1.00
Q7TMM9_1	Tubb2a	Tubulin bet	R.INVYYNEAAGNK#.Y	134.26	113.47	1.18	0.85
Q7TMM9_1	Tubb2a	Tubulin bet	K.IREEYPDR.I	27.16	270.10	0.10	9.94
Q7TMM9_1	Tubb2a	Tubulin bet	R.ISEQFTAM*FR.R	136.67	409.87	0.33	3.00
Q7TMM9_1	Tubb2a	Tubulin bet	R.ISEQFTAMFR.R	68.61	243.32	0.28	3.55
Q7TMM9_1	Tubb2a	Tubulin bet	K.LAVNM*VPFPR.L	64.80	207.38	0.31	3.20
Q7TMM9_1	Tubb2a	Tubulin bet	K.LAVNMVPFPR.L	105.35	358.34	0.29	3.40
Q7TMM9_1	Tubb2a	Tubulin bet	R.LHFFM*PGFAPLTSR.G	59.44	149.83	0.40	2.52
Q7TMM9_1	Tubb2a	Tubulin bet	R.LHFFMPGFAPLTSR.G	72.78	247.58	0.29	3.40
Q7TMM9_1	Tubb2a	Tubulin bet	K.MSATFIGNSTAIQELFKR.I	4.43	3.99	1.11	0.90
Q7TMM9_1	Tubb2a	Tubulin bet	R.M*SM*KEVDEQM*LNVQNK.N	25.71	18.93	1.36	0.74
Q7TMM9_1	Tubb2a	Tubulin bet	R.M*SM*KEVDEQMLNVQNK.N	28.22	17.63	1.60	0.62
Q7TMM9_1	Tubb2a	Tubulin bet	K.NSSYFVEWIPNNVK#.T	295.22	232.83	1.27	0.79
Q7TMM9_1	Tubb2a	Tubulin bet	K.RISEQFTAMFR.R	5.19	8.27	0.63	1.59

Q7TMM9_1	Tubb2a	Tubulin bet	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	91.34	245.63	0.37	2.69
Q7TMM9_1	Tubb2a	Tubulin bet	R.YLTVAAIFR.G	21.45	78.99	0.27	3.68
Q7TMM9_1	Tubb2a	Tubulin bet	R.AILVDLEPGTM*DSVR.S	44.08	171.45	0.26	3.89
Q7TMM9_1	Tubb2a	Tubulin bet	R.AILVDLEPGTMDSVR.S	5.72	28.85	0.20	5.05
Q7TMM9_1	Tubb2a	Tubulin bet	K.EVDEQM*LNVQNK#.N	5.37	4.97	1.08	0.93
Q7TMM9_1	Tubb2a	Tubulin bet	K.EVDEQMLNVQNK#.N	4.56	2.18	2.10	0.48
Q7TMM9_1	Tubb2a	Tubulin bet	K.GHYTEGAELVDSVLDVVR.K	13.31	63.86	0.21	4.80
Q7TMM9_1	Tubb2a	Tubulin bet	K.GHYTEGAELVDSVLDVVRK.E	8.58	23.18	0.37	2.70
Q7TMM9_1	Tubb2a	Tubulin bet	R.INVYYNEAAGNK.Y	15.88	15.23	1.04	0.96
Q7TMM9_1	Tubb2a	Tubulin bet	K.IREEYPDR.I	3.28	10.21	0.32	3.11
Q7TMM9_1	Tubb2a	Tubulin bet	R.ISEQFTAM*FR.R	8.63	16.71	0.52	1.94
Q7TMM9_1	Tubb2a	Tubulin bet	K.LAVNM*VPFPR.L	11.87	5.47	2.17	0.46
Q7TMM9_1	Tubb2a	Tubulin bet	K.LAVNMVPFPR.L	9.56	6.33	1.51	0.66
Q7TMM9_1	Tubb2a	Tubulin bet	R.LHFFM*PGFAPLTSR.G	4.64	9.84	0.47	2.12
Q7TMM9_1	Tubb2a	Tubulin bet	K.MSATFIGNSTAIQELFK#.R	4.41	3.08	1.43	0.70
Q7TMM9_1	Tubb2a	Tubulin bet	K.NSSYFVEWIPNNVK#.T	33.09	24.63	1.34	0.74
Q7TMM9_1	Tubb2a	Tubulin bet	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	10.77	30.27	0.36	2.81
Q7TMM9_1	Tubb2a	Tubulin bet	R.AILVDLEPGTM*DSVR.S	73.07	166.51	0.44	2.28
Q7TMM9_1	Tubb2a	Tubulin bet	R.AILVDLEPGTMDSVR.S	38.07	90.00	0.42	2.36
Q7TMM9_1	Tubb2a	Tubulin bet	R.ALTVPELTQQM*FDSK#.N	16.36	11.30	1.45	0.69
Q7TMM9_1	Tubb2a	Tubulin bet	R.ALTVPELTQQMFDSK#.N	17.03	13.35	1.28	0.78
Q7TMM9_1	Tubb2a	Tubulin bet	K.EVDEQM*LNVQNK#.N	167.42	108.59	1.54	0.65
Q7TMM9_1	Tubb2a	Tubulin bet	K.EVDEQMLNVQNK#.N	91.57	65.62	1.40	0.72
Q7TMM9_1	Tubb2a	Tubulin bet	R.FPGQLNADLRK.L	12.32	36.82	0.33	2.99
Q7TMM9_1	Tubb2a	Tubulin bet	K.GHYTEGAELVDSVLDVVR.K	86.09	248.73	0.35	2.89
Q7TMM9_1	Tubb2a	Tubulin bet	K.GHYTEGAELVDSVLDVVRK.E	28.11	89.37	0.31	3.18
Q7TMM9_1	Tubb2a	Tubulin bet	R.IMNTFSVM*PSPK#.V	11.05	6.55	1.69	0.59
Q7TMM9_1	Tubb2a	Tubulin bet	R.IM*NTFSVMPSPK#.V	8.98	6.55	1.37	0.73
Q7TMM9_1	Tubb2a	Tubulin bet	R.INVYYNEAAGNK#.Y	42.16	34.85	1.21	0.83
Q7TMM9_1	Tubb2a	Tubulin bet	K.IREEYPDR.I	32.28	319.58	0.10	9.90
Q7TMM9_1	Tubb2a	Tubulin bet	R.ISEQFTAM*FR.R	71.04	209.36	0.34	2.95
Q7TMM9_1	Tubb2a	Tubulin bet	R.ISEQFTAMFR.R	26.95	80.19	0.34	2.98
Q7TMM9_1	Tubb2a	Tubulin bet	K.LAVNM*VPFPR.L	37.72	110.65	0.34	2.93
Q7TMM9_1	Tubb2a	Tubulin bet	K.LAVNMVPFPR.L	40.09	132.59	0.30	3.31
Q7TMM9_1	Tubb2a	Tubulin bet	R.LHFFM*PGFAPLTSR.G	43.86	108.51	0.40	2.47
Q7TMM9_1	Tubb2a	Tubulin bet	K.M*SATFIGNSTAIQELFK#.R	29.34	21.38	1.37	0.73
Q7TMM9_1	Tubb2a	Tubulin bet	R.M*SM*KEVDEQM*LNVQNK.N	60.27	48.15	1.25	0.80
Q7TMM9_1	Tubb2a	Tubulin bet	R.M*SM*KEVDEQMLNVQNK.N	21.73	14.02	1.55	0.65
Q7TMM9_1	Tubb2a	Tubulin bet	K.NSSYFVEWIPNNVK#.T	199.57	131.34	1.52	0.66
Q7TMM9_1	Tubb2a	Tubulin bet	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	28.75	90.49	0.32	3.15
Q7TMM9_1	Tubb2a	Tubulin bet	R.YLTVAAIFR.G	9.59	31.70	0.30	3.31
Q7TMM9_1	Tubb2a	Tubulin bet	R.AILVDLEPGTM*DSVR.S	130.31	304.15	0.43	2.33
Q7TMM9_1	Tubb2a	Tubulin bet	R.AILVDLEPGTMDSVR.S	42.55	93.08	0.46	2.19
Q7TMM9_1	Tubb2a	Tubulin bet	R.ALTVPELTQQM*FDSK#.N	29.11	22.76	1.28	0.78
Q7TMM9_1	Tubb2a	Tubulin bet	R.ALTVPELTQQMFDSK#.N	33.80	16.25	2.08	0.48
Q7TMM9_1	Tubb2a	Tubulin bet	K.EVDEQM*LNVQNK#.N	372.25	245.85	1.51	0.66
Q7TMM9_1	Tubb2a	Tubulin bet	K.EVDEQMLNVQNK#.N	147.02	81.33	1.81	0.55
Q7TMM9_1	Tubb2a	Tubulin bet	R.FPGQLNADLR.K	30.92	99.76	0.31	3.23
Q7TMM9_1	Tubb2a	Tubulin bet	R.FPGQLNADLRK.L	22.48	57.49	0.39	2.56
Q7TMM9_1	Tubb2a	Tubulin bet	K.GHYTEGAELVDSVLDVVR.K	148.88	352.19	0.42	2.37
Q7TMM9_1	Tubb2a	Tubulin bet	K.GHYTEGAELVDSVLDVVRK.E	34.50	66.74	0.52	1.93
Q7TMM9_1	Tubb2a	Tubulin bet	R.IM*NTFSVM*PSPK#.V	34.53	25.16	1.37	0.73
Q7TMM9_1	Tubb2a	Tubulin bet	R.IMNTFSVM*PSPK#.V	14.67	7.68	1.91	0.52
Q7TMM9_1	Tubb2a	Tubulin bet	R.IM*NTFSVMPSPK#.V	9.53	7.09	1.34	0.74
Q7TMM9_1	Tubb2a	Tubulin bet	R.INVYYNEAAGNK#.Y	54.19	39.34	1.38	0.73
Q7TMM9_1	Tubb2a	Tubulin bet	R.ISEQFTAM*FR.R	92.05	242.64	0.38	2.64
Q7TMM9_1	Tubb2a	Tubulin bet	R.ISEQFTAMFR.R	35.75	110.25	0.32	3.08
Q7TMM9_1	Tubb2a	Tubulin bet	K.LAVNM*VPFPR.L	75.81	203.09	0.37	2.68
Q7TMM9_1	Tubb2a	Tubulin bet	K.LAVNMVPFPR.L	62.13	201.29	0.31	3.24
Q7TMM9_1	Tubb2a	Tubulin bet	R.LHFFM*PGFAPLTSR.G	69.73	195.53	0.36	2.80
Q7TMM9_1	Tubb2a	Tubulin bet	R.LHFFMPGFAPLTSR.G	36.47	80.71	0.45	2.21
Q7TMM9_1	Tubb2a	Tubulin bet	R.M*SM*KEVDEQM*LNVQNK.N	144.00	95.11	1.51	0.66
Q7TMM9_1	Tubb2a	Tubulin bet	R.MSM*KEVDEQM*LNVQNK.N	22.16	11.70	1.89	0.53
Q7TMM9_1	Tubb2a	Tubulin bet	R.M*SM*KEVDEQMLNVQNK.N	36.61	19.05	1.92	0.52
Q7TMM9_1	Tubb2a	Tubulin bet	R.MSM*K#EVDEQMLNVQNK#.N	5.58	3.44	1.62	0.62
Q7TMM9_1	Tubb2a	Tubulin bet	K.NSSYFVEWIPNNVK#.T	316.66	190.27	1.66	0.60
Q7TMM9_1	Tubb2a	Tubulin bet	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	45.98	115.26	0.40	2.51
Q7TMM9_1	Tubb2a	Tubulin bet	R.YLTVAAIFR.G	9.22	32.95	0.28	3.57
Q9CWF2_T	Tubb2b	Tubulin bet	R.INVYYNEATGNK#.Y	153.57	118.16	1.30	0.77
Q9CWF2_T	Tubb2b	Tubulin bet	R.INVYYNEATGNK#.Y	18.43	13.71	1.34	0.74
Q9CWF2_T	Tubb2b	Tubulin bet	R.INVYYNEATGNK#.Y	48.84	36.31	1.34	0.74
Q9CWF2_T	Tubb2b	Tubulin bet	R.INVYYNEATGNK#.Y	96.67	63.97	1.51	0.66
Q9ERD7_TE	Tubb3	Tubulin bet	R.ALTVPELTQQM*FDAK#.N	85.20	47.33	1.80	0.56
Q9ERD7_TE	Tubb3	Tubulin bet	R.ALTVPELTQQMFDAK#.N	77.12	49.79	1.55	0.65
Q9ERD7_TE	Tubb3	Tubulin bet	K.EVDEQMLAIQSK#.N	9.29	2.45	3.79	0.26
Q9ERD7_TE	Tubb3	Tubulin bet	K.FWEVISDEHGIDPSGNYVGDSDLQLER.I	2.59	4.37	0.59	1.69
Q9ERD7_TE	Tubb3	Tubulin bet	R.IM*NTFSVVPSPK#.V	399.56	300.89	1.33	0.75
Q9ERD7_TE	Tubb3	Tubulin bet	R.IMNTFSVVPSPK#.V	260.95	185.32	1.41	0.71
Q9ERD7_TE	Tubb3	Tubulin bet	K.LATPTYGDLNHLVSATMSGVTTSLR.F	2.70	4.58	0.59	1.70
Q9ERD7_TE	Tubb3	Tubulin bet	R.LHFFMPGFAPLTAR.G	9.78	21.51	0.45	2.20
Q9ERD7_TE	Tubb3	Tubulin bet	K.M*SSTFIGNSTAIQELFK#.R	9.23	6.06	1.52	0.66
Q9ERD7_TE	Tubb3	Tubulin bet	R.YLTVATVFR.G	28.43	75.72	0.38	2.66
Q9ERD7_TE	Tubb3	Tubulin bet	R.ALTVPELTQQM*FDAK#.N	20.68	11.34	1.82	0.55
Q9ERD7_TE	Tubb3	Tubulin bet	R.ALTVPELTQQMFDAK#.N	20.47	12.88	1.59	0.63
Q9ERD7_TE	Tubb3	Tubulin bet	R.IM*NTFSVVPSPK#.V	179.45	119.09	1.51	0.66
Q9ERD7_TE	Tubb3	Tubulin bet	R.IMNTFSVVPSPK#.V	99.75	70.16	1.42	0.70
Q9ERD7_TE	Tubb3	Tubulin bet	R.YLTVATVFR.G	5.47	11.27	0.49	2.06
Q9ERD7_TE	Tubb3	Tubulin bet	R.ALTVPELTQQM*FDAK#.N	39.24	24.38	1.61	0.62
Q9ERD7_TE	Tubb3	Tubulin bet	R.ALTVPELTQQMFDAK#.N	33.04	19.14	1.73	0.58
Q9ERD7_TE	Tubb3	Tubulin bet	R.ALTVPELTQQMFDAK#.N	21.35	6.69	3.19	0.31
Q9ERD7_TE	Tubb3	Tubulin bet	R.IM*NTFSVVPSPK#.V	293.95	190.02	1.55	0.65
Q9ERD7_TE	Tubb3	Tubulin bet	R.IMNTFSVVPSPK#.V	123.60	78.55	1.57	0.64
Q9ERD7_TE	Tubb3	Tubulin bet	R.LHFFM*PGFAPLTAR.G	5.56	9.54	0.58	1.72
Q9ERD7_TE	Tubb3	Tubulin bet	K.MSSTFIGNSTAIQELFK#.R	69.47	49.87	1.39	0.72
Q9ERD7_TE	Tubb3	Tubulin bet	K.M*SSTFIGNSTAIQELFK.R	7.49	7.99	0.94	1.07
Q9ERD7_TE	Tubb3	Tubulin bet	R.YLTVATVFR.G	9.70	18.41	0.53	1.90
Q9D6F9_TE	Tubb4a	Tubulin bet	R.AVLVDLEPGTM*DSVR.S	25.47	78.55	0.32	3.08
Q9D6F9_TE	Tubb4a	Tubulin bet	R.AVLVDLEPGTMDSVR.S	47.59	44.28	1.07	0.93
Q9D6F9_TE	Tubb4a	Tubulin bet	R.YLTVAAVFR.G	115.54	297.12	0.39	2.57
Q9D6F9_TE	Tubb4a	Tubulin bet	R.AVLVDLEPGTM*DSVR.S	6.83	25.52	0.27	3.74
Q9D6F9_TE	Tubb4a	Tubulin bet	R.AVLVDLEPGTM*DSVR.S	13.17	30.69	0.43	2.33
Q9D6F9_TE	Tubb4a	Tubulin bet	K.M*AATFIGNSTAIQELFK#.R	37.98	26.90	1.41	0.71
Q9D6F9_TE	Tubb4a	Tubulin bet	R.YLTVAAVFR.G	38.30	121.61	0.31	3.18

Q9D6F9_TE	Tubb4a	Tubulin bet	R.AVLVDLEPGTM*DSVR.S	25.00	68.56	0.36	2.74
Q9D6F9_TE	Tubb4a	Tubulin bet	K.M*AATFIGNSTAIQELFK#.R	59.18	24.15	2.45	0.41
Q9D6F9_TE	Tubb4a	Tubulin bet	R.YLTVAAVFR.G	63.34	169.51	0.37	2.68
P68372_TE	Tubb4b	Tubulin bet	R.INVYYNEATGGK#.Y	183.13	105.33	1.74	0.58
P68372_TE	Tubb4b	Tubulin bet	R.INVYYNEATGGK#.Y	32.64	27.95	1.17	0.86
P68372_TE	Tubb4b	Tubulin bet	R.INVYYNEATGGK#.Y	93.99	51.84	1.81	0.55
P68372_TE	Tubb4b	Tubulin bet	R.INVYYNEATGGK#.Y	164.50	88.64	1.86	0.54
P68372_TE	Tubb4b	Tubulin bet	K.YVPRAVLVDLEPGTMDSVR@.S	2.88	1.43	2.01	0.50
P99024_TE	Tubb5	Tubulin bet	R.ALTVPELTQQVFDAK#.N	188.55	120.64	1.56	0.64
P99024_TE	Tubb5	Tubulin bet	R.ALTVPELTQQVFDAK#.N	382.34	247.87	1.54	0.65
P99024_TE	Tubb5	Tubulin bet	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	17.80	35.79	0.50	2.01
P99024_TE	Tubb5	Tubulin bet	R.ISVYYNEATGGK#.Y	637.09	397.06	1.60	0.62
P99024_TE	Tubb5	Tubulin bet	K.M*AVTFIGNSTAIQELFK#.R	129.86	101.24	1.28	0.78
P99024_TE	Tubb5	Tubulin bet	K.MAVTFIGNSTAIQELFK.R	98.82	58.37	1.69	0.59
P99024_TE	Tubb5	Tubulin bet	K.MAVTFIGNSTAIQELFK#.R	172.94	110.62	1.56	0.64
P99024_TE	Tubb5	Tubulin bet	R.ALTVPELTQQVFDAK#.N	4.91	4.77	1.03	0.97
P99024_TE	Tubb5	Tubulin bet	K.FWEVISDEHGIDPTGTYHGDSDLQLDR@.I	13.27	8.72	1.52	0.66
P99024_TE	Tubb5	Tubulin bet	R.ISVYYNEATGGK#.Y	147.31	127.29	1.16	0.86
P99024_TE	Tubb5	Tubulin bet	R.ALTVPELTQQVFDAK#.N	234.28	157.79	1.48	0.67
P99024_TE	Tubb5	Tubulin bet	R.ALTVPELTQQVFDAK#.N	119.16	83.75	1.42	0.70
P99024_TE	Tubb5	Tubulin bet	R.ISVYYNEATGGK#.Y	490.00	377.60	1.30	0.77
P99024_TE	Tubb5	Tubulin bet	K.M*AVTFIGNSTAIQELFK#.R	83.33	49.94	1.67	0.60
P99024_TE	Tubb5	Tubulin bet	K.MAVTFIGNSTAIQELFK#.R	92.05	55.38	1.66	0.60
P99024_TE	Tubb5	Tubulin bet	R.ALTVPELTQQVFDAK#.N	460.53	280.39	1.64	0.61
P99024_TE	Tubb5	Tubulin bet	R.ISVYYNEATGGK#.Y	883.94	514.80	1.72	0.58
P99024_TE	Tubb5	Tubulin bet	K.M*AVTFIGNSTAIQELFK#.R	93.16	53.58	1.74	0.58
P99024_TE	Tubb5	Tubulin bet	K.M*AVTFIGNSTAIQELFK#.R	182.95	92.17	1.98	0.50
P99024_TE	Tubb5	Tubulin bet	K.MAVTFIGNSTAIQELFK#.R	77.22	47.06	1.64	0.61
P99024_TE	Tubb5	Tubulin bet	K.MAVTFIGNSTAIQELFKR.I	2.77	11.28	0.25	4.07
Q922F4_TE	Tubb6	Tubulin bet	R.AALVDLEPGTM*DSVR.S	13.91	42.54	0.33	3.06
Q922F4_TE	Tubb6	Tubulin bet	R.AALVDLEPGTMDSVR.S	6.69	19.96	0.34	2.98
Q922F4_TE	Tubb6	Tubulin bet	K.EVDEQM*LAIQNK#.N	33.53	27.66	1.21	0.83
Q922F4_TE	Tubb6	Tubulin bet	K.FWEVISDEHGIDQAGGYVGDSALQLER.I	10.35	30.24	0.34	2.92
Q922F4_TE	Tubb6	Tubulin bet	R.ISEQFSAMFR.R	7.63	20.77	0.37	2.72
Q922F4_TE	Tubb6	Tubulin bet	R.ISVYYNESSSK#.K	73.44	46.55	1.58	0.63
Q922F4_TE	Tubb6	Tubulin bet	K.LTTPTYGDLNHLVSATM*SGVTTSLR.F	4.43	12.33	0.36	2.78
Q922F4_TE	Tubb6	Tubulin bet	K.LTTPTYGDLNHLVSATMSGVTTSLR.F	9.23	23.78	0.39	2.57
Q922F4_TE	Tubb6	Tubulin bet	K.M*ASTFIGNSTAIQELFK#.R	28.75	20.64	1.39	0.72
Q922F4_TE	Tubb6	Tubulin bet	R.SGPFGQLFRPDNFIFGQTGAGNNWAK.G	21.65	36.61	0.59	1.69
Q922F4_TE	Tubb6	Tubulin bet	R.AALVDLEPGTM*DSVR.S	2.62	11.00	0.24	4.20
Q922F4_TE	Tubb6	Tubulin bet	R.AALVDLEPGTM*DSVR.S	3.29	6.95	0.47	2.11
Q922F4_TE	Tubb6	Tubulin bet	K.EVDEQM*LAIQNK#.N	7.76	4.63	1.68	0.60
Q922F4_TE	Tubb6	Tubulin bet	K.FWEVISDEHGIDQAGGYVGDSALQLER.I	2.03	5.62	0.36	2.77
Q922F4_TE	Tubb6	Tubulin bet	R.ISVYYNESSSK#.K	18.97	22.19	0.85	1.17
Q922F4_TE	Tubb6	Tubulin bet	K.M*ASTFIGNSTAIQELFK.R	29.34	21.38	1.37	0.73
Q922F4_TE	Tubb6	Tubulin bet	R.AALVDLEPGTM*DSVR.S	4.78	17.07	0.28	3.57
Q922F4_TE	Tubb6	Tubulin bet	K.EVDEQM*LAIQNK#.N	11.00	10.67	1.03	0.97
Q922F4_TE	Tubb6	Tubulin bet	K.EVDEQMLAIQNK#.N	10.25	6.25	1.64	0.61
Q922F4_TE	Tubb6	Tubulin bet	K.FWEVISDEHGIDQAGGYVGDSALQLER.I	3.30	7.33	0.45	2.22
Q922F4_TE	Tubb6	Tubulin bet	R.ISVYYNESSSK#.K	23.22	17.18	1.35	0.74
P83887_TE	Tubg1	Tubulin gar	R.AVLLDLEPR.V	7.41	18.20	0.41	2.46
P83887_TE	Tubg1	Tubulin gar	R.EIVQQLIDEYHAATRPDYISWGTQEQ.-	5.36	6.62	0.81	1.23
P83887_TE	Tubg1	Tubulin gar	K.IHEDIFDIIDR.E	4.48	8.69	0.52	1.94
P83887_TE	Tubg1	Tubulin gar	K.K#LVQTYSVFPNQDEMSDVVVQPYNSLLTLK#.R	4.85	3.66	1.32	0.76
P83887_TE	Tubg1	Tubulin gar	R.LHFLM*TGYTPLTTDQSVASVR.K	3.32	8.85	0.37	2.67
P83887_TE	Tubg1	Tubulin gar	R.LHIQNPSFSQINQLVSTIM*SASTTTLR.Y	4.66	4.91	0.95	1.05
P83887_TE	Tubg1	Tubulin gar	R.AVLLDLEPR.V	4.88	11.22	0.44	2.30
P83887_TE	Tubg1	Tubulin gar	R.LHFLM*TGYTPLTTDQSVASVR.K	15.79	9.49	1.66	0.60
P83887_TE	Tubg1	Tubulin gar	K.LYNPENIYLSEHGGGAGNNWASGFSQGEK#.I	3.96	3.21	1.23	0.81
Q921G8_G	Tubgcp2	Gamma-tul	R.ILPVAASYSTVTR.F	3.96	7.04	0.56	1.78
Q921G8_G	Tubgcp2	Gamma-tul	R.TFLVDPNLDLSIR.E	2.85	8.19	0.35	2.88
Q921G8_G	Tubgcp2	Gamma-tul	K.VLLDFLM*EEK#.E	7.18	4.91	1.46	0.68
Q921G8_G	Tubgcp2	Gamma-tul	R.YTVLPQQIPSFLQK#.V	9.42	5.94	1.59	0.63
Q921G8_G	Tubgcp2	Gamma-tul	K.AASAPYFEILEK.W	13.08	9.04	1.45	0.69
Q921G8_G	Tubgcp2	Gamma-tul	R.ILPVAASYSTVTR.F	4.80	11.05	0.43	2.30
Q921G8_G	Tubgcp2	Gamma-tul	K.LTEDK#ETLQFLQQNAK#.E	13.47	6.14	2.20	0.46
Q921G8_G	Tubgcp2	Gamma-tul	R.NLDPLVYLLSK#.L	22.15	12.23	1.81	0.55
Q921G8_G	Tubgcp2	Gamma-tul	R.TFLVDPNLDLSIR.E	3.11	8.68	0.36	2.79
Q921G8_G	Tubgcp2	Gamma-tul	K.VLLDFLM*EEK#.E	8.50	6.63	1.28	0.78
Q8BFR5_EF	Tufm	Elongation	R.AEAGDNLGALVR.G	28.44	14.13	2.01	0.50
Q8BFR5_EF	Tufm	Elongation	R.DLDKPFLLPVESVYSIPGR.G	9.40	10.23	0.92	1.09
Q8BFR5_EF	Tufm	Elongation	R.GTVVTGTLER.G	17.83	19.50	0.91	1.09
Q8BFR5_EF	Tufm	Elongation	K.LLDAVDTYIPVPTR.D	8.85	11.71	0.76	1.32
Q8BFR5_EF	Tufm	Elongation	K.TIGTGLVTDVPAM*TEEDK#NIK#.W	19.56	5.80	3.37	0.30
Q8BFR5_EF	Tufm	Elongation	K.VEAQVYILSK#.E	20.27	29.03	0.70	1.43
Q8BFR5_EF	Tufm	Elongation	R.ISLLLR.L	8.35	23.89	0.35	2.86
Q91YR1_TV	Twf1	Twinfilin-1	K.INEVQTDVSVDTK#.H	24.50	5.76	4.25	0.24
Q9Z0P5_TV	Twf2	Twinfilin-2	K.K#IEIGDGAELTAEFLYDEVHPK#.Q	5.46	2.92	1.87	0.53
A5D6P6_A	Twist2	Twist homo	K.GSPSAQSFEELQSQR.I	1.70	2.48	0.68	1.46
A5D6P6_A	Twist2	Twist homo	R.LSYAFSVWR.M	1.15	8.91	0.13	7.74
Q6PAM1_T	Txlna	Alpha-taxili	R.VQDLTAGGITDIGSER.R	2.65	5.83	0.46	2.20
P10639_TH	Txn	Thioredoxi	K.EAFQEALAAAGDK.L	13.23	18.48	0.72	1.40
P10639_TH	Txn	Thioredoxi	K.VGEFSGANK.E	8.01	4.31	1.86	0.54
Q9CQU0_T	Txndc12	Thioredoxi	R.DEDFSPDGGYIPR.I	2.24	12.01	0.19	5.37
Q9CQU0_T	Txndc12	Thioredoxi	R.ILFLDPSGK#.V	20.34	237.95	0.09	11.70
Q9CQU0_T	Txndc12	Thioredoxi	K.VRPEIINESGNPSYK.Y	8.29	24.53	0.34	2.96
Q9CQU0_T	Txndc12	Thioredoxi	K.YFYVSAEQVVQGM*K#.E	4.59	3.09	1.48	0.67
Q91W90_T	Txndc5	Thioredoxi	K.GTVLALTEK#.S	43.31	12.77	3.39	0.29
Q91W90_T	Txndc5	Thioredoxi	R.GYPTLLLFR.G	27.55	34.49	0.80	1.25
Q91W90_T	Txndc5	Thioredoxi	R.GYPTLLWFR.D	14.55	14.99	0.97	1.03
Q91W90_T	Txndc5	Thioredoxi	K.NLAPTWEELSK#.K	40.80	12.98	3.14	0.32
Q91W90_T	Txndc5	Thioredoxi	K.QGLYELSANNFELHVSQGNHFIK#.F	30.13	7.80	3.86	0.26
Q91W90_T	Txndc5	Thioredoxi	K.SFEDTIAQGITFVK#.F	86.27	26.61	3.24	0.31
Q9CQ79_T	Txndc9	Thioredoxi	K.LDQIGEDELELLK.E	4.39	5.69	0.77	1.30
Q9CQ79_T	Txndc9	Thioredoxi	K.VIPTLALLR.D	4.99	27.11	0.18	5.43
P07607_TY	Tyms	Thymidylat	R.HFGAEYK#DM*DSDYSGQGVDQLQK#.V	2.21	2.12	1.04	0.96
Q9D883_U	U2af1	Splicing fac	K.AVIDLNNR.W	48.78	185.07	0.26	3.79
Q9D883_U	U2af1	Splicing fac	R.NPQNSSQSADGLR.C	53.19	221.92	0.24	4.17
Q9D883_U	U2af1	Splicing fac	R.WFNGQPIHAELSPVTDFR.E	11.70	54.43	0.21	4.65
Q9D883_U	U2af1	Splicing fac	R.NPQNSSQSADGLR.C	1.56	15.76	0.10	10.08
Q9D883_U	U2af1	Splicing fac	R.NPQNSSQSADGLR.C	3.02	8.51	0.36	2.82
P26369_U	U2af2	Splicing fac	K.ELLTSFGPLK#.A	90.74	65.63	1.38	0.72
P26369_U	U2af2	Splicing fac	K.LFIGGLPNYLNDDQVK#.E	64.74	54.79	1.18	0.85

P26369_U	U2af2	Splicing fac	R.LGGLTQAPGNPVLAVQINQDK#.N	13.06	9.03	1.45	0.69
P26369_U	U2af2	Splicing fac	K.NFAFLEFR.S	14.11	30.25	0.47	2.14
P26369_U	U2af2	Splicing fac	R.RPHDYQPLPGM*SENPSVYVPGVVSTVVPDSAHK.L	8.19	24.27	0.34	2.96
P26369_U	U2af2	Splicing fac	R.RPHDYQPLPGMSENPSVYVPGVVSTVVPDSAHK.L	3.23	11.56	0.28	3.58
P26369_U	U2af2	Splicing fac	R.SVDETTQAM*AFDGIIFQGQSLK.I	4.81	3.22	1.50	0.67
P26369_U	U2af2	Splicing fac	R.SVDETTQAMAFDGIIFQGQSLK#.I	45.69	22.44	2.04	0.49
Q6NV83_S	U2surp	U2 snRNP-	R.AWEDWAIYPEPFLIK#.L	42.99	31.91	1.35	0.74
Q6NV83_S	U2surp	U2 snRNP-	R.DKLEEILR.G	25.03	66.81	0.37	2.67
Q6NV83_S	U2surp	U2 snRNP-	K.FQDELESGK#.R	63.50	38.71	1.64	0.61
Q6NV83_S	U2surp	U2 snRNP-	R.GGVVNAAKDEHETDEKR.G	3.44	10.27	0.33	2.99
Q6NV83_S	U2surp	U2 snRNP-	K.KPGQSFQEQVEHYR.D	10.77	54.89	0.20	5.10
Q6NV83_S	U2surp	U2 snRNP-	R.LK#NPNAPM*LPPPK#.N	19.27	20.80	0.93	1.08
Q6NV83_S	U2surp	U2 snRNP-	R.LYLVSDVLYNSSAK#.V	70.21	41.24	1.70	0.59
Q6NV83_S	U2surp	U2 snRNP-	K.LYSILQGDSPTK#.W	82.65	53.35	1.55	0.65
Q6NV83_S	U2surp	U2 snRNP-	R.MIEFVVR.E	5.49	23.69	0.23	4.32
Q6NV83_S	U2surp	U2 snRNP-	R.NLLALIHR.M	15.24	50.35	0.30	3.30
Q6NV83_S	U2surp	U2 snRNP-	K.SLDDDLDGVPLDATEDSK#.K	19.15	13.46	1.42	0.70
Q6NV83_S	U2surp	U2 snRNP-	K.SLDDDLDGVPLDATEDSK#K#.N	18.91	13.49	1.40	0.71
Q6NV83_S	U2surp	U2 snRNP-	K.SLDDDLDGVPLDATEDSKKNEPIFK.V	6.56	4.89	1.34	0.75
Q6NV83_S	U2surp	U2 snRNP-	K.SNLELFK#EELK#.Q	25.04	20.81	1.20	0.83
Q6NV83_S	U2surp	U2 snRNP-	K.TLSQAIVK#.V	81.66	48.75	1.68	0.60
Q6NV83_S	U2surp	U2 snRNP-	K.VANASYYR.K	11.78	34.17	0.34	2.90
Q6NV83_S	U2surp	U2 snRNP-	K.VAPSK#WEAVDESELEAQAVTTSK#.W	27.44	19.57	1.40	0.71
Q6NV83_S	U2surp	U2 snRNP-	K.WEAVDESELEAQAVTTSK.W	8.55	6.00	1.42	0.70
Q6NV83_S	U2surp	U2 snRNP-	R.FGPLASVK#.I	30.41	20.03	1.52	0.66
Q6NV83_S	U2surp	U2 snRNP-	K.FQDELESGK#.R	27.29	20.66	1.32	0.76
Q6NV83_S	U2surp	U2 snRNP-	R.GGVVNAAK#DEHETDEK#.R	16.59	12.78	1.30	0.77
Q6NV83_S	U2surp	U2 snRNP-	R.LK#NPNAPM*LPPPK#.N	9.04	11.59	0.78	1.28
Q6NV83_S	U2surp	U2 snRNP-	R.LYLVSDVLYNSSAK#.V	25.01	22.14	1.13	0.88
Q6NV83_S	U2surp	U2 snRNP-	K.LYSILQGDSPTK#.W	34.93	26.71	1.31	0.76
Q6NV83_S	U2surp	U2 snRNP-	R.NLLALIHR.M	4.54	24.32	0.19	5.36
Q6NV83_S	U2surp	U2 snRNP-	K.SLDDDLDGVPLDATEDSK#.K	11.79	8.64	1.37	0.73
Q6NV83_S	U2surp	U2 snRNP-	K.VAPSK#WEAVDESELEAQAVTTSK#.W	25.17	12.94	1.95	0.51
Q8CGB3_U	Uaca	Uveal auto	R.IGDNLDILNLLK#.T	11.97	8.09	1.48	0.68
Q02053_U	Uba1	Ubiquitin-	R.AAVASLLQSVQVPEFTPK#.S	65.31	17.97	3.63	0.28
Q02053_U	Uba1	Ubiquitin-	K.GNVQVVIPFLTESYSSSQDPPEK#.S	19.01	6.36	2.99	0.33
Q02053_U	Uba1	Ubiquitin-	R.K#LAYVAAGDLAPINAFIGGLAAQEVM*K#.A	9.52	2.68	3.56	0.28
Q02053_U	Uba1	Ubiquitin-	R.LAGTQPLEVLEAVQR.S	19.50	15.06	1.29	0.77
Q02053_U	Uba1	Ubiquitin-	R.NEEDATELVGLAQAVNAR.S	19.25	8.01	2.40	0.42
Q02053_U	Uba1	Ubiquitin-	K.QPAENVNQYLTDSK#.F	20.41	3.40	6.01	0.17
Q02053_U	Uba1	Ubiquitin-	K.SLPASLVEPDFVM*TDFAK#.Y	16.94	5.09	3.33	0.30
Q02053_U	Uba1	Ubiquitin-	R.YDGQVAVFGSDFQEK#.L	34.72	9.83	3.53	0.28
Q02053_U	Uba1	Ubiquitin-	R.AAVASLLQSVQVPEFTPK#.S	96.30	22.95	4.20	0.24
Q02053_U	Uba1	Ubiquitin-	R.AENYDISPADR.H	12.22	11.62	1.05	0.95
Q02053_U	Uba1	Ubiquitin-	R.DEFEGLFK#.Q	19.38	5.06	3.83	0.26
Q02053_U	Uba1	Ubiquitin-	R.DEFEGLFK#QPAENVNQYLTDSK#.F	5.14	1.66	3.10	0.32
Q02053_U	Uba1	Ubiquitin-	K.GNVQVVIPFLTESYSSSQDPPEK#.S	25.45	6.79	3.75	0.27
Q02053_U	Uba1	Ubiquitin-	R.K#LAYVAAGDLAPINAFIGGLAAQEVM*K#.A	8.64	4.26	2.03	0.49
Q02053_U	Uba1	Ubiquitin-	R.K#PLLESGTLGTK#.G	32.41	6.07	5.34	0.19
Q02053_U	Uba1	Ubiquitin-	R.LAGTQPLEVLEAVQR.S	20.10	18.71	1.07	0.93
Q02053_U	Uba1	Ubiquitin-	R.NEEDATELVGLAQAVNAR.S	6.68	5.95	1.12	0.89
Q02053_U	Uba1	Ubiquitin-	K.NIILGGVK#.A	39.45	10.98	3.59	0.28
Q02053_U	Uba1	Ubiquitin-	K.QPAENVNQYLTDSK#.F	20.36	2.94	6.93	0.14
Q02053_U	Uba1	Ubiquitin-	K.SLPASLVEPDFVM*TDFAK#.Y	21.57	4.68	4.60	0.22
Q02053_U	Uba1	Ubiquitin-	K.SLPASLVEPDFVMTDFAK#.Y	10.39	1.81	5.74	0.17
Q02053_U	Uba1	Ubiquitin-	R.YDGQVAVFGSDFQEK#.L	38.01	7.24	5.25	0.19
Q9Z1F9_SA	Uba2	SUMO-acti	K.SYASLFSK#.S	22.80	6.41	3.56	0.28
Q9Z1F9_SA	Uba2	SUMO-acti	K.VTVLTLQDK#.I	35.59	12.87	2.76	0.36
Q9Z1F9_SA	Uba2	SUMO-acti	K.VTVLTLQDK#.I	24.98	6.19	4.04	0.25
P62984_R	Uba52	Ubiquitin-	K.ESTLHLVLR.L	18.78	66.56	0.28	3.55
P62984_R	Uba52	Ubiquitin-	K.IQDKEGIPPDQQR.L	2.18	10.74	0.20	4.93
P62984_R	Uba52	Ubiquitin-	-.M*QIFVK#.T	74.14	67.01	1.11	0.90
P62984_R	Uba52	Ubiquitin-	-.MQIFVK#.T	149.06	134.85	1.11	0.90
P62984_R	Uba52	Ubiquitin-	K.TITLEVEPSDTIENVK.A	171.79	173.16	0.99	1.01
P62984_R	Uba52	Ubiquitin-	R.TLSDYNIQK#.E	292.57	224.93	1.30	0.77
P62984_R	Uba52	Ubiquitin-	K.EGIPPDQQR.L	67.32	497.91	0.14	7.40
P62984_R	Uba52	Ubiquitin-	K.ESTLHLVLR.L	133.17	857.06	0.16	6.44
P62984_R	Uba52	Ubiquitin-	K.IQDKEGIPPDQQR.L	58.81	448.63	0.13	7.63
P62984_R	Uba52	Ubiquitin-	K.IQDKEGIPPDQQR.L	17.99	132.34	0.14	7.36
P62984_R	Uba52	Ubiquitin-	-.MQIFVK#.T	567.79	793.80	0.72	1.40
P62984_R	Uba52	Ubiquitin-	K.TITLEVEPSDTIENVK#.A	1072.50	1660.28	0.65	1.55
P62984_R	Uba52	Ubiquitin-	K.TITLEVEPSDTIENVK#AK#.I	65.61	103.12	0.64	1.57
P62984_R	Uba52	Ubiquitin-	R.TLSDYNIQK#.E	1542.95	1987.69	0.78	1.29
P62984_R	Uba52	Ubiquitin-	K.TLTGK#TITLEVEPSDTIENVK#.A	18.56	27.82	0.67	1.50
P62984_R	Uba52	Ubiquitin-	-.M*QIFVK#.T	63.13	21.74	2.90	0.34
P62984_R	Uba52	Ubiquitin-	K.TITLEVEPSDTIENVK#.A	125.73	58.93	2.13	0.47
P62984_R	Uba52	Ubiquitin-	R.TLSDYNIQK#.E	232.59	101.80	2.28	0.44
P62984_R	Uba52	Ubiquitin-	-.M*QIFVK#.T	95.32	34.97	2.73	0.37
P62984_R	Uba52	Ubiquitin-	-.MQIFVK#.T	119.87	55.73	2.15	0.46
P62984_R	Uba52	Ubiquitin-	R.TLSDYNIQK#.E	317.29	142.65	2.22	0.45
Q8C7R4_U	Uba6	Ubiquitin-	K.FWQAYPSAEDVLQK#.I	8.39	4.11	2.04	0.49
Q8C7R4_U	Uba6	Ubiquitin-	R.NAVFQLEEALSSNK#.A	8.13	4.99	1.63	0.61
Q8C7R4_U	Uba6	Ubiquitin-	K.FWQAYPSAEDVLQK#.I	6.88	5.52	1.25	0.80
Q91VX2_U	Ubap2	Ubiquitin-	K.AINILLEGNSDTTSWETVGGK#.K	7.64	5.21	1.47	0.68
Q91VX2_U	Ubap2	Ubiquitin-	K.AINILLEGNSDTTSWETVGGK.K	6.14	5.42	1.13	0.88
Q91VX2_U	Ubap2	Ubiquitin-	R.ATALVTSGK.A	31.01	29.04	1.07	0.94
Q91VX2_U	Ubap2	Ubiquitin-	R.DGNLANNPYSGDVTK#.F	33.98	38.35	0.89	1.13
Q91VX2_U	Ubap2	Ubiquitin-	R.ESTAGDGPSTVSR.L	10.89	40.11	0.27	3.68
Q91VX2_U	Ubap2	Ubiquitin-	K.GGYGGSSQAPNK#.S	9.90	10.87	0.91	1.10
Q91VX2_U	Ubap2	Ubiquitin-	K.GVSVSSGTGLPDM*TGSVYNK#.T	12.08	9.51	1.27	0.79
Q91VX2_U	Ubap2	Ubiquitin-	K.GVSVSSGTGLPDMTGSVYNK#.T	6.52	5.62	1.16	0.86
Q91VX2_U	Ubap2	Ubiquitin-	R.LAQVIFDK#NDSDFEAK#.V	22.95	17.61	1.30	0.77
Q91VX2_U	Ubap2	Ubiquitin-	R.LPM*DYYGIPFAAPTALASR.D	3.36	12.02	0.28	3.58
Q91VX2_U	Ubap2	Ubiquitin-	R.LPMDYYGIPFAAPTALASR.D	3.32	10.26	0.32	3.09
Q91VX2_U	Ubap2	Ubiquitin-	K.NSVEEWTTEDWTEDLSETK#.V	9.47	7.17	1.32	0.76
Q91VX2_U	Ubap2	Ubiquitin-	K.QVVQATAEQM*R.L	3.73	14.48	0.26	3.88
Q91VX2_U	Ubap2	Ubiquitin-	K.SQASK#PTYGSAPYWTN.-	15.98	67.68	0.24	4.24
Q91VX2_U	Ubap2	Ubiquitin-	R.SQHTVDTTSSVPAPK#.K	10.87	11.71	0.93	1.08
Q91VX2_U	Ubap2	Ubiquitin-	K.SQPEPSPVLSQLSQR.Q	9.27	37.07	0.25	4.00
Q80X50_U	Ubap2l	Ubiquitin-	R.AINVLLEGNPDTHSWEM*VGK#.K	18.12	10.83	1.67	0.60
Q80X50_U	Ubap2l	Ubiquitin-	R.DGSLASNPYSGDLTK#.F	11.49	12.85	0.89	1.12
Q80X50_U	Ubap2l	Ubiquitin-	K.GFGDVGEAK#.G	16.83	17.09	0.98	1.02
Q80X50_U	Ubap2l	Ubiquitin-	K.GGSTTGSQFLEQFK#.T	41.33	17.72	2.33	0.43

Q80X50_U	Ubap2l	Ubiquitin-a	R.IDLAVLLGK#.T	38.32	22.73	1.69	0.59
Q80X50_U	Ubap2l	Ubiquitin-a	K.IFTASNVSSVPLPAENVTITAGQR.I	6.43	22.45	0.29	3.49
Q80X50_U	Ubap2l	Ubiquitin-a	R.LAQMISDHNDADFEEK#.V	15.50	11.03	1.41	0.71
Q80X50_U	Ubap2l	Ubiquitin-a	R.LDFIGVEGSNYPR.K	6.59	23.10	0.29	3.50
Q80X50_U	Ubap2l	Ubiquitin-a	R.TATEEWGTEDWNEDLSETK#.I	15.97	9.83	1.63	0.62
Q80X50_U	Ubap2l	Ubiquitin-a	K.TPSSM*ENDSSNLDPSQAPSLAQPLVFSNSK.Q	7.16	3.51	2.04	0.49
Q80X50_U	Ubap2l	Ubiquitin-a	R.AINVLLEGNPDTHSWEM*VGK#.K	26.17	24.45	1.07	0.93
Q80X50_U	Ubap2l	Ubiquitin-a	R.AINVLLEGNPDTHSWEMVGK#.K	19.45	16.49	1.18	0.85
Q80X50_U	Ubap2l	Ubiquitin-a	R.DGSLASNPYSGDLTK#.F	58.74	48.82	1.20	0.83
Q80X50_U	Ubap2l	Ubiquitin-a	R.FPLDYYSIPFPTPTTPLTGR.D	10.90	34.75	0.31	3.19
Q80X50_U	Ubap2l	Ubiquitin-a	K.GFGDVGEAK#.G	45.02	43.04	1.05	0.96
Q80X50_U	Ubap2l	Ubiquitin-a	K.GGSTTGSQFLEQFK#.T	56.51	33.67	1.68	0.60
Q80X50_U	Ubap2l	Ubiquitin-a	R.IDLAVLLGK#.T	84.00	62.10	1.35	0.74
Q80X50_U	Ubap2l	Ubiquitin-a	K.IFTASNVSSVPLPAENVTITAGQR.I	13.01	47.61	0.27	3.66
Q80X50_U	Ubap2l	Ubiquitin-a	K.IFTASNVSSVPLPAENVTITAGQR.I	2.86	4.85	0.59	1.70
Q80X50_U	Ubap2l	Ubiquitin-a	R.LAQM*ISDHNDADFEEK#.V	41.29	35.06	1.18	0.85
Q80X50_U	Ubap2l	Ubiquitin-a	R.LAQMISDHNDADFEEK#.V	23.35	21.45	1.09	0.92
Q80X50_U	Ubap2l	Ubiquitin-a	R.LDFIGVEGSNYPR.K	8.40	37.69	0.22	4.49
Q80X50_U	Ubap2l	Ubiquitin-a	R.RYPSSISSSPQK.D	7.49	21.79	0.34	2.91
Q80X50_U	Ubap2l	Ubiquitin-a	K.SANDSTVHSPFTK.R	11.69	14.16	0.83	1.21
Q80X50_U	Ubap2l	Ubiquitin-a	R.SQTSSIPQKPQTNK.S	8.09	6.65	1.22	0.82
Q80X50_U	Ubap2l	Ubiquitin-a	K.STSAPQM*SPGSSDNQSSSPQPAQQK#.L	7.45	4.50	1.65	0.60
Q80X50_U	Ubap2l	Ubiquitin-a	R.TATEEWGTEDWNEDLSETK#.I	20.52	16.13	1.27	0.79
Q80X50_U	Ubap2l	Ubiquitin-a	R.DGSLASNPYSGDLTK#.F	14.39	10.66	1.35	0.74
Q80X50_U	Ubap2l	Ubiquitin-a	R.FPLDYYSIPFPTPTTPLTGR.D	3.24	4.68	0.69	1.44
Q80X50_U	Ubap2l	Ubiquitin-a	R.IDLAVLLGK.T	13.42	11.20	1.20	0.83
Q80X50_U	Ubap2l	Ubiquitin-a	K.IFTASNVSSVPLPAENVTITAGQR.I	4.51	10.95	0.41	2.43
Q9D1C1_U	Ube2c	Ubiquitin-c	R.DPAAASVAAVR.K	2.21	5.95	0.37	2.69
Q9D1C1_U	Ube2c	Ubiquitin-c	K.GISAFPESDNLFK.W	5.25	13.23	0.40	2.52
Q9D1C1_U	Ube2c	Ubiquitin-c	K.LSLEFPSGYPYNAPTVK.F	6.55	13.26	0.49	2.03
Q6ZWY6_U	Ube2d2b	Ubiquitin-c	R.SQWSPALTISK.V	26.96	18.36	1.47	0.68
P60605_U	Ube2g2	Ubiquitin-c	K.ILLSVVSM*LAEPNDESGANVDASK#.M	12.96	7.68	1.69	0.59
P62257_U	Ube2h	Ubiquitin-c	K.FYGPQGTPYEGGVWK#.V	22.06	10.33	2.14	0.47
P62257_U	Ube2h	Ubiquitin-c	K.HEVTILGGLNEFVVK#.F	89.88	45.98	1.95	0.51
P62257_U	Ube2h	Ubiquitin-c	K.SPSIGFM*NK#.I	23.67	10.91	2.17	0.46
P62257_U	Ube2h	Ubiquitin-c	K.SPSIGFMNK#.I	12.52	3.78	3.31	0.30
P62257_U	Ube2h	Ubiquitin-c	R.VDLPDK#YPFK#.S	39.19	14.94	2.62	0.38
P61087_U	Ube2k	Ubiquitin-c	K.IPETYPFNPPK#.V	9.30	10.48	0.89	1.13
P61087_U	Ube2k	Ubiquitin-c	R.NAVIVALSSK#.S	58.61	33.95	1.73	0.58
P61087_U	Ube2k	Ubiquitin-c	K.SWDVETATELLLSN.-	30.58	30.58	1.00	1.00
P61089_U	Ube2n	Ubiquitin-c	K.LELFLPEEYPM*AAPK#.V	92.01	45.14	2.04	0.49
P61089_U	Ube2n	Ubiquitin-c	K.LELFLPEEYPM*AAPK#.V	10.41	4.97	2.10	0.48
P61089_U	Ube2n	Ubiquitin-c	R.LLAEPVPGIK#.A	188.61	103.23	1.83	0.55
P61089_U	Ube2n	Ubiquitin-c	K.TNEAQAIETAR.A	50.43	98.23	0.51	1.95
P61089_U	Ube2n	Ubiquitin-c	R.YFHVVIAGPQDSPFEGGTFK#.L	87.75	48.84	1.80	0.56
Q921J4_U	Ube2s	Ubiquitin-c	R.LLLENYEEYAAR.A	3.91	7.41	0.53	1.89
Q921J4_U	Ube2s	Ubiquitin-c	K.EVTTLTADPPDGIK.V	4.41	6.37	0.69	1.44
Q921J4_U	Ube2s	Ubiquitin-c	R.LLLENYEEYAAR.A	8.32	18.13	0.46	2.18
Q9CZY3_U	Ube2v1	Ubiquitin-c	R.LLEELEEGQK#.G	54.89	9.92	5.53	0.18
Q9CZY3_U	Ube2v1	Ubiquitin-c	K.VILQELR.R	8.73	12.31	0.71	1.41
Q9CZY3_U	Ube2v1	Ubiquitin-c	K.YPEAPPSVR.F	5.21	4.79	1.09	0.92
O08759_U	Ube3a	Ubiquitin-p	K.GASSAYLENSK#.G	7.77	3.08	2.52	0.40
O08759_U	Ube3a	Ubiquitin-p	R.NLVNDDDAIVAASK#.C	15.04	5.00	3.01	0.33
O08759_U	Ube3a	Ubiquitin-p	R.VDPLETELGVK#.T	13.62	5.07	2.69	0.37
Q9ES00_U	Ube4b	Ubiquitin c	K.ELFEEVISK#.M	29.29	4.54	6.45	0.15
Q9ES00_U	Ube4b	Ubiquitin c	R.LTELYGDQPPFSEPK#.F	12.92	3.37	3.83	0.26
P21126_U	Ubl4a	Ubiquitin-l	R.HFSVADASR.V	8.60	10.59	0.81	1.23
P21126_U	Ubl4a	Ubiquitin-l	R.LSDYNIGPNSK#.L	35.44	14.17	2.50	0.40
P21126_U	Ubl4a	Ubiquitin-l	R.LVDSPATPIWQLISK#.V	10.96	3.69	2.97	0.34
Q8BGR9_U	Ublcp1	Ubiquitin-l	K.FSEFYSK#.K	21.95	3.53	6.21	0.16
Q8BGR9_U	Ublcp1	Ubiquitin-l	R.GLIDVK#PLGVIWGK#.F	20.31	2.34	8.67	0.12
Q8BGR9_U	Ublcp1	Ubiquitin-l	K.M*K#ELGVSTNANYK#.I	2.17	4.31	0.50	1.99
Q811S7_U	Ubp1	Upstream-b	R.LFSNFSGADLLK.L	14.12	19.18	0.74	1.36
Q6WKZ8_U	Ubr2	E3 ubiquiti	R.FELYQLFSTPDYGK#.R	5.97	2.83	2.11	0.47
Q6WKZ8_U	Ubr2	E3 ubiquiti	R.YAVDILTWEK#ESELPEDLEVAEK#.S	3.98	3.83	1.04	0.96
A2AN08_U	Ubr4	E3 ubiquiti	K.ELPQLVASVIESESEILHHEK#.Q	8.59	6.54	1.31	0.76
A2AN08_U	Ubr4	E3 ubiquiti	K.SVFIAQNVASLQELGGSEK#.L	8.81	2.18	4.04	0.25
A2AN08_U	Ubr4	E3 ubiquiti	K.SVFIAQNVASLQELGGSEK#.L	5.09	1.57	3.25	0.31
A2AN08_U	Ubr4	E3 ubiquiti	R.TGSTSSK#EDDYESDAATIVQK#.C	12.24	2.45	4.99	0.20
A2AN08_U	Ubr4	E3 ubiquiti	R.AYLLQNLNEEGSTEK#PSQEK#.L	16.02	4.21	3.80	0.26
A2AN08_U	Ubr4	E3 ubiquiti	K.HAAQELATLLLSLPAPASVQQQSK#.S	72.32	132.93	0.54	1.84
A2AN08_U	Ubr4	E3 ubiquiti	R.LLALEEATLSTDLQQGYALK#.S	10.37	5.44	1.91	0.52
A2AN08_U	Ubr4	E3 ubiquiti	R.LLQTLPQLR.N	14.26	12.28	1.16	0.86
A2AN08_U	Ubr4	E3 ubiquiti	K.SVFIAQNVASLQELGGSEK#.L	7.25	2.40	3.02	0.33
A2AN08_U	Ubr4	E3 ubiquiti	R.TLLPLLLESSTESAAEISSNSLER.I	10.86	13.04	0.83	1.20
A2AN08_U	Ubr4	E3 ubiquiti	R.TVPSPPISPQALVEGENDEQSSPDQVSAAK#.T	11.49	6.39	1.80	0.56
A2AN08_U	Ubr4	E3 ubiquiti	K.VNEAAPEKPQEDSGTAGGISSTSASVNR.Y	3.94	6.17	0.64	1.57
A2AN08_U	Ubr4	E3 ubiquiti	R.YTTTQQVVK#.L	15.36	5.71	2.69	0.37
E9Q2H1_E	Ubr5	E3 ubiquiti	R.AASTAPSSTSTPAASSAGLIYIDPSNLR.R	3.76	7.55	0.50	2.01
E9Q2H1_E	Ubr5	E3 ubiquiti	R.AYPAAITILETAQK#.I	8.90	5.52	1.61	0.62
E9Q2H1_E	Ubr5	E3 ubiquiti	K.EGEEQSLLAEEADSSKPGPSAPDVAAQLK.S	7.25	8.41	0.86	1.16
E9Q2H1_E	Ubr5	E3 ubiquiti	R.IDELQVVK#.T	15.68	8.83	1.78	0.56
E9Q2H1_E	Ubr5	E3 ubiquiti	K.IVLLSANSIR.A	15.20	11.69	1.30	0.77
E9Q2H1_E	Ubr5	E3 ubiquiti	K.LEHTAQTYSELQGER.I	5.02	16.86	0.30	3.36
E9Q2H1_E	Ubr5	E3 ubiquiti	K.LTYQDAVNLQNYVEEK#.L	6.72	5.41	1.24	0.80
E9Q2H1_E	Ubr5	E3 ubiquiti	R.SVAIFTAGQESPIVLR.D	7.46	7.95	0.94	1.07
E9Q2H1_E	Ubr5	E3 ubiquiti	K.VATWVDETLSSVASK#.L	12.65	6.29	2.01	0.50
P25976_U	Ubtf	Nucleolar t	R.FLESLPEEEQQR.V	4.18	9.23	0.45	2.21
P25976_U	Ubtf	Nucleolar t	K.HPELNISEEGITK#.S	11.90	4.62	2.58	0.39
Q99PL6_U	Ubxn6	UBX domai	K.ELQAEATSSNNPGAPGTNSVPEPK#.E	3.04	1.25	2.43	0.41
Q99PL6_U	Ubxn6	UBX domai	K.LGVDTIAK#.Y	25.67	13.98	1.84	0.54
Q99PL6_U	Ubxn6	UBX domai	K.SVLRPELLAAIEQLS.-	7.48	12.52	0.60	1.67
Q6P5G6_U	Ubxn7	UBX domai	R.DVWSNEAVK#.N	13.77	4.68	2.95	0.34
Q6P5G6_U	Ubxn7	UBX domai	R.EQITLPEQAK#.L	21.10	6.21	3.40	0.29
Q6P5G6_U	Ubxn7	UBX domai	K.GLIQQFTAITGASESVGK#.H	11.21	3.82	2.94	0.34
Q6P5G6_U	Ubxn7	UBX domai	K.LGDFPYVSILDPR.T	4.42	7.67	0.58	1.74
Q9JKB1_U	Uchl3	Ubiquitin c	K.FLENYDAIR.V	4.49	11.10	0.40	2.47
Q9JKB1_U	Uchl3	Ubiquitin c	K.SQGQDVTSSVYFM*K#.Q	5.02	3.96	1.27	0.79
Q9JKB1_U	Uchl3	Ubiquitin c	R.VTHETSAHEGQTEAPSIDEK#.V	3.49	1.95	1.79	0.56
Q9WUP7_	Uchl5	Ubiquitin c	K.EFSQSFDAAM*K#.G	14.05	4.28	3.28	0.30
Q9WUP7_	Uchl5	Ubiquitin c	R.GAQVEEIWSLEPESFEK#.L	24.34	8.19	2.97	0.34
Q9WUP7_	Uchl5	Ubiquitin c	R.GAQVEEIWSLEPESFEK#.L	17.04	3.45	4.94	0.20
Q9WUP7_	Uchl5	Ubiquitin c	R.LETIFFAK#.Q	54.00	12.63	4.28	0.23

Q9WUP7_l	Uchl5	Ubiquitin c	R.NQM*LIEEEVQK#.L	31.75	7.24	4.38	0.23
Q9WUP7_l	Uchl5	Ubiquitin c	R.NQMLIEEEVQK#.L	20.09	4.51	4.45	0.22
Q9WUP7_l	Uchl5	Ubiquitin c	K.WQPGEEPAGSVVQDSR.L	6.20	7.21	0.86	1.16
Q9WUP7_l	Uchl5	Ubiquitin c	R.GAQVEEIWSLEPESFEK#.L	9.51	2.49	3.82	0.26
Q9WUP7_l	Uchl5	Ubiquitin c	R.NQM*LIEEEVQK#.L	9.22	3.06	3.02	0.33
P70362_UI	Ufd1l	Ubiquitin fı	K.AVLENALR.N	9.06	20.48	0.44	2.26
P70362_UI	Ufd1l	Ubiquitin fı	R.FIAFSGEGQSLR.K	11.62	30.06	0.39	2.59
P70362_UI	Ufd1l	Ubiquitin fı	K.FQPQSPDFLDITNPK#.A	30.60	18.16	1.68	0.59
P70362_UI	Ufd1l	Ubiquitin fı	R.LNITYPMLFK#.L	12.72	5.32	2.39	0.42
P70362_UI	Ufd1l	Ubiquitin fı	R.SDVEK#GGK#.I	34.10	2.34	14.58	0.07
P61961_UI	Ufm1	Ubiquitin-f	K.VLSVPESTPFTAVLK#.F	15.24	8.06	1.89	0.53
Q6P5E4_U(	Uggt1	UDP-glucos	R.AIWAALQTQASSSAK#.N	14.82	15.75	0.94	1.06
Q6P5E4_U(	Uggt1	UDP-glucos	R.AVYLGELSHDQDVVEYIM*NQPNVVPR.I	3.20	7.26	0.44	2.27
Q6P5E4_U(	Uggt1	UDP-glucos	R.AYNYVAQEVDGYHAFQTLTQIYNK#.V	41.71	26.15	1.60	0.63
Q6P5E4_U(	Uggt1	UDP-glucos	K.DISQNFPTK#.A	36.85	32.04	1.15	0.87
Q6P5E4_U(	Uggt1	UDP-glucos	K.EGETYYDVVAVVDPVTR.E	3.91	18.68	0.21	4.77
Q6P5E4_U(	Uggt1	UDP-glucos	K.ELGTLHTEETQEGSQK#HEEL.-	14.32	13.63	1.05	0.95
Q6P5E4_U(	Uggt1	UDP-glucos	R.ELYPALEGQLK#.E	24.34	24.84	0.98	1.02
Q6P5E4_U(	Uggt1	UDP-glucos	R.EYLDLTASNNFYVDDFAR.F	1.88	7.90	0.24	4.20
Q6P5E4_U(	Uggt1	UDP-glucos	K.FLFVDADQIVR.T	6.81	34.79	0.20	5.11
Q6P5E4_U(	Uggt1	UDP-glucos	R.FLSPLQQNLLK.F	31.80	40.14	0.79	1.26
Q6P5E4_U(	Uggt1	UDP-glucos	R.GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK#.S	3.90	1.99	1.96	0.51
Q6P5E4_U(	Uggt1	UDP-glucos	R.HYISNPSK#EPVYLSGYGVELAIK#.S	8.57	3.10	2.77	0.36
Q6P5E4_U(	Uggt1	UDP-glucos	R.HYISNPSKEPVYLSGYGVELAIK.S	4.97	5.49	0.91	1.10
Q6P5E4_U(	Uggt1	UDP-glucos	K.ILETTTFFQR.A	12.52	46.50	0.27	3.71
Q6P5E4_U(	Uggt1	UDP-glucos	K.INYVFR.H	6.00	30.52	0.20	5.08
Q6P5E4_U(	Uggt1	UDP-glucos	R.ISM*INNPSQEISDSSTPIFR.A	2.43	6.25	0.39	2.57
Q6P5E4_U(	Uggt1	UDP-glucos	R.ISMINNPSQEISDSSTPIFR.A	2.11	4.64	0.45	2.20
Q6P5E4_U(	Uggt1	UDP-glucos	R.IVPEWQDYDQEIK#.Q	26.39	29.34	0.90	1.11
Q6P5E4_U(	Uggt1	UDP-glucos	R.IYSHDGTDSPPDANDVVVILNNFK#.S	29.54	28.93	1.02	0.98
Q6P5E4_U(	Uggt1	UDP-glucos	K.KADM*ANEDLLSDGTNENESGFWDSFK.W	5.41	8.16	0.66	1.51
Q6P5E4_U(	Uggt1	UDP-glucos	K.K#YNFQYELVQYK#.W	16.86	13.71	1.23	0.81
Q6P5E4_U(	Uggt1	UDP-glucos	K.KYNFQYELVQYK.W	5.16	6.67	0.77	1.29
Q6P5E4_U(	Uggt1	UDP-glucos	R.LGIEGLSLHNILK#.L	40.64	36.15	1.12	0.89
Q6P5E4_U(	Uggt1	UDP-glucos	R.LGIEGLSLHNILK#.L	14.37	11.03	1.30	0.77
Q6P5E4_U(	Uggt1	UDP-glucos	K.LNIQPSETDYAVDIR.S	9.61	37.13	0.26	3.87
Q6P5E4_U(	Uggt1	UDP-glucos	K.NYLSPTFK#.E	30.77	30.07	1.02	0.98
Q6P5E4_U(	Uggt1	UDP-glucos	R.QLLYDAIK.H	16.49	17.91	0.92	1.09
Q6P5E4_U(	Uggt1	UDP-glucos	K.QLQTLFQEEK.E	12.01	12.17	0.99	1.01
Q6P5E4_U(	Uggt1	UDP-glucos	R.SPAISWVNNLEVDSR.Y	4.08	15.66	0.26	3.84
Q6P5E4_U(	Uggt1	UDP-glucos	K.TAAIANSM*NYLTK#.K	26.31	23.20	1.13	0.88
Q6P5E4_U(	Uggt1	UDP-glucos	K.TAVSAQLR.A	8.60	38.53	0.22	4.48
Q6P5E4_U(	Uggt1	UDP-glucos	R.TGETVK#VEHVVSVLEK#.K	24.35	18.55	1.31	0.76
Q6P5E4_U(	Uggt1	UDP-glucos	K.VDALLSAQPK#.G	35.55	40.90	0.87	1.15
Q6P5E4_U(	Uggt1	UDP-glucos	K.VWQLQDLSFQTAAR.I	8.60	13.26	0.65	1.54
Q6P5E4_U(	Uggt1	UDP-glucos	K.YNFQYELVQYK#.W	11.11	9.77	1.14	0.88
Q6P5E4_U(	Uggt1	UDP-glucos	R.YVLEPEISFTADSSFAK#.G	40.80	33.73	1.21	0.83
Q6P5E4_U(	Uggt1	UDP-glucos	K.AEEVKQDKDDIINIFSVASGHLYER.F	4.53	6.79	0.67	1.50
Q6P5E4_U(	Uggt1	UDP-glucos	K.AITTSLTTK#.W	95.31	72.13	1.32	0.76
Q6P5E4_U(	Uggt1	UDP-glucos	R.AIWAALQTQASSSAK#.N	33.19	29.74	1.12	0.90
Q6P5E4_U(	Uggt1	UDP-glucos	R.AVYLGELSHDQDVVEYIMNQPNVVPR.I	1.20	10.45	0.11	8.70
Q6P5E4_U(	Uggt1	UDP-glucos	R.AYNYVAQEVDGYHAFQTLTQIYNK#.V	68.90	46.03	1.50	0.67
Q6P5E4_U(	Uggt1	UDP-glucos	K.DISQNFPTK#.A	56.77	50.87	1.12	0.90
Q6P5E4_U(	Uggt1	UDP-glucos	K.EGETYYDVVAVVDPVTR.E	8.58	29.54	0.29	3.44
Q6P5E4_U(	Uggt1	UDP-glucos	R.EYLDLTASNNFYVDDFAR.F	5.73	14.28	0.40	2.49
Q6P5E4_U(	Uggt1	UDP-glucos	K.FLFVDADQIVR.T	12.77	49.58	0.26	3.88
Q6P5E4_U(	Uggt1	UDP-glucos	R.FLSPLQQNLLK#.F	71.20	68.36	1.04	0.96
Q6P5E4_U(	Uggt1	UDP-glucos	R.GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK#.S	10.06	7.13	1.41	0.71
Q6P5E4_U(	Uggt1	UDP-glucos	R.GYYEQTGVGPLPVVLFNGM*PFEK.E	17.76	15.92	1.12	0.90
Q6P5E4_U(	Uggt1	UDP-glucos	R.HYISNPSK#.E	12.88	14.38	0.90	1.12
Q6P5E4_U(	Uggt1	UDP-glucos	R.IEYQFFEDK#.H	35.85	30.57	1.17	0.85
Q6P5E4_U(	Uggt1	UDP-glucos	R.IGFIFVVNDSEDVDGM*QDAGVAVLR.A	2.59	5.78	0.45	2.23
Q6P5E4_U(	Uggt1	UDP-glucos	R.ILAASGALSLVVM*K#.D	8.91	7.89	1.13	0.89
Q6P5E4_U(	Uggt1	UDP-glucos	K.ILETTTFFQR.A	24.34	93.51	0.26	3.84
Q6P5E4_U(	Uggt1	UDP-glucos	R.ISMINNPSQEISDSSTPIFR.A	6.82	7.69	0.89	1.13
Q6P5E4_U(	Uggt1	UDP-glucos	R.IVPEWQDYDQEIK#.Q	70.87	58.03	1.22	0.82
Q6P5E4_U(	Uggt1	UDP-glucos	R.IYSHDGTDSPPDANDVVVILNNFK#.S	76.74	61.25	1.25	0.80
Q6P5E4_U(	Uggt1	UDP-glucos	K.K#ADM*ANEDLLSDGTNENESGFWDSFK#.W	14.33	12.62	1.14	0.88
Q6P5E4_U(	Uggt1	UDP-glucos	K.K#ADMANEDLLSDGTNENESGFWDSFK#.W	5.80	4.51	1.28	0.78
Q6P5E4_U(	Uggt1	UDP-glucos	K.KYNFQYELVQYK.W	17.19	15.26	1.13	0.89
Q6P5E4_U(	Uggt1	UDP-glucos	K.KYPYVEVNSILGIDSAYDQNR.K	2.40	6.84	0.35	2.84
Q6P5E4_U(	Uggt1	UDP-glucos	R.LGIEGLSLHNILK#.L	95.71	62.40	1.53	0.65
Q6P5E4_U(	Uggt1	UDP-glucos	K.LNIQPSETDYAVDIR.S	50.66	80.60	0.63	1.59
Q6P5E4_U(	Uggt1	UDP-glucos	K.LRELYPALEGQLK.E	1.11	4.65	0.24	4.18
Q6P5E4_U(	Uggt1	UDP-glucos	K.LSDM*PLK#.S	34.90	28.79	1.21	0.82
Q6P5E4_U(	Uggt1	UDP-glucos	K.NYLSPTFK#.E	75.47	65.09	1.16	0.86
Q6P5E4_U(	Uggt1	UDP-glucos	R.QLLYDAIK#.H	45.35	39.61	1.14	0.87
Q6P5E4_U(	Uggt1	UDP-glucos	K.QLQTLFQEEK#.E	25.51	25.88	0.99	1.01
Q6P5E4_U(	Uggt1	UDP-glucos	K.QLQTLFQEEK#ELGTLHTEETQEGSQK#HEEL.-	7.14	5.94	1.20	0.83
Q6P5E4_U(	Uggt1	UDP-glucos	R.SPAISWVNNLEVDSR.Y	7.07	24.52	0.29	3.47
Q6P5E4_U(	Uggt1	UDP-glucos	K.TAAIANSM*NYLTK#.K	51.78	43.65	1.19	0.84
Q6P5E4_U(	Uggt1	UDP-glucos	K.TAVSAQLR.A	19.35	74.48	0.26	3.85
Q6P5E4_U(	Uggt1	UDP-glucos	R.TGETVK#VEHVVSVLEK#.K	66.73	60.13	1.11	0.90
Q6P5E4_U(	Uggt1	UDP-glucos	K.VDALLSAQPK.G	57.67	55.20	1.04	0.96
Q6P5E4_U(	Uggt1	UDP-glucos	R.VEEDVASDLVM*K#.V	51.00	39.89	1.28	0.78
Q6P5E4_U(	Uggt1	UDP-glucos	R.VEEDVASDLVMK#.V	14.42	10.94	1.32	0.76
Q6P5E4_U(	Uggt1	UDP-glucos	K.VEHVVSVLEK#.K	16.69	17.74	0.94	1.06
Q6P5E4_U(	Uggt1	UDP-glucos	K.VWQLQDLSFQTAAR.I	11.09	30.48	0.36	2.75
Q6P5E4_U(	Uggt1	UDP-glucos	K.YNFQYELVQYK#.W	23.19	18.25	1.27	0.79
Q6P5E4_U(	Uggt1	UDP-glucos	R.YVLEPEISFTADSSFAK#.G	80.10	63.92	1.25	0.80
Q6P5E4_U(	Uggt1	UDP-glucos	R.YVLEPEISFTADSSFAK.G	10.60	12.95	0.82	1.22
Q91ZJ5_UC	Ugp2	UTP--glucos	R.LVEIAQVPK#.A	36.49	7.22	5.05	0.20
Q91ZJ5_UC	Ugp2	UTP--glucos	R.NENTFLDLTVQQIEHLNK#.T	33.56	5.95	5.64	0.18
Q91ZJ5_UC	Ugp2	UTP--glucos	K.TLDGGLNVIQLETAVGAAIK#.S	8.12	2.71	2.99	0.33
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.SGFLVWR.Y	3.82	12.97	0.29	3.40
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.SKLEPYTLSEQQANLIK.E	3.35	7.27	0.46	2.17
Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.TDSSEVVQAGEK.L	19.94	39.19	0.51	1.97
Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.DDTEPEPWTR.E	1.73	11.53	0.15	6.68
Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.DNIFGAWFEAQVVQVQK.R	9.38	17.81	0.53	1.90
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.LEPYTLSEQQANLIK.E	5.93	8.41	0.71	1.42
Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.LNDTIQLLVR.Q	9.35	56.62	0.17	6.06
Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.QLGLTM*QYPEGYLEALANK.E	2.63	3.64	0.72	1.38
Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.QLGLTM*QYPEGYLEALANK.E	5.18	10.73	0.48	2.07

Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.RDDTEPEPWTR.E	1.81	14.67	0.12	8.09
Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.RPLIASPSQPPPALR.N	1.48	44.64	0.03	30.18
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.SGFLVWR.Y	7.90	43.38	0.18	5.49
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.SKLEPYTLSEQQANLIK.E	13.57	26.36	0.51	1.94
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.SKLEPYTLSEQQANLIKEDK.G	8.16	15.25	0.54	1.87
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.SSTHGEGAAEADDK#TVWEDTDLGLYK#.V	7.21	7.32	0.99	1.02
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.STGPTLSSPR.A	12.36	78.31	0.16	6.34
Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.TDSSEVVQAGEK#.L	40.51	70.37	0.58	1.74
Q8VDF2_UI	Uhrf1	E3 ubiquiti	R.TM*DGKETHTVNSLSR.L	3.04	22.98	0.13	7.56
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.VNEYVDVR.D	7.55	66.88	0.11	8.86
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.YDDYPEHGVDIVK.A	37.29	68.55	0.54	1.84
Q8VDF2_UI	Uhrf1	E3 ubiquiti	K.YDDYPEHGVDIVK#.A	8.67	16.78	0.52	1.94
Q7TMI3_UI	Uhrf2	E3 ubiquiti	K.ASDSTDAVEAFQLTPQQQR.L	1.72	3.12	0.55	1.82
Q7TMI3_UI	Uhrf2	E3 ubiquiti	R.GFWYDAEITTLK#.T	11.32	9.31	1.22	0.82
P13439_UI	Umps	Uridine 5'-r	K.FGSFVLK#.S	17.15	5.93	2.89	0.35
P13439_UI	Umps	Uridine 5'-r	K.IASWADIVNAHVVPGSGVVK#.G	29.78	13.07	2.28	0.44
P13439_UI	Umps	Uridine 5'-r	R.K#FADIGNTVK#.K	19.68	8.55	2.30	0.43
P13439_UI	Umps	Uridine 5'-r	K.SGLSSPVYIDLR.G	4.83	9.44	0.51	1.96
P13439_UI	Umps	Uridine 5'-r	K.VTDAIVLLDR.E	6.45	11.07	0.58	1.72
Q8C4B4_U	Unc119b	Protein unc	R.SDSFYFVDNK#.L	9.12	4.53	2.01	0.50
Q99KD5_U	Unc45a	Protein unc	K.ALLPLALEGTDVGQTK#.A	12.05	4.14	2.91	0.34
Q99KD5_U	Unc45a	Protein unc	R.ALVGLCKLGSAGGTDFSMK#.Q	25.08	2.71	9.26	0.11
Q99KD5_U	Unc45a	Protein unc	K.DPNNSLTLWVIDQGLK#K#.I	8.65	2.67	3.24	0.31
Q99KD5_U	Unc45a	Protein unc	K.ALLPLALEGTDVGQTK#.A	18.65	5.13	3.63	0.28
Q99KD5_U	Unc45a	Protein unc	R.GTVVVLNM*M*QSSK#.E	6.51	2.43	2.68	0.37
Q9EPU0_RI	Upf1	Regulator c	K.AGAKPDQIGIITPYEGQR.S	17.55	54.65	0.32	3.11
Q9EPU0_RI	Upf1	Regulator c	K.AGLSQSLFER.L	23.63	70.79	0.33	3.00
Q9EPU0_RI	Upf1	Regulator c	K.ALVEGPLNNLR.E	19.55	66.15	0.30	3.38
Q9EPU0_RI	Upf1	Regulator c	R.AYQHGGVTGLSQY.-	75.02	75.02	1.00	1.00
Q9EPU0_RI	Upf1	Regulator c	K.DINWDSSQWQPLIQDR.C	5.19	12.62	0.41	2.43
Q9EPU0_RI	Upf1	Regulator c	R.EAIIPGSVYDR.S	25.44	72.94	0.35	2.87
Q9EPU0_RI	Upf1	Regulator c	K.ENPSATLEDLEKPGVDEEPQHVLLR.Y	6.18	25.19	0.25	4.07
Q9EPU0_RI	Upf1	Regulator c	K.ESQTQDNITVR.W	9.89	33.73	0.29	3.41
Q9EPU0_RI	Upf1	Regulator c	R.FM*TTAM*YDAR.E	5.35	22.45	0.24	4.20
Q9EPU0_RI	Upf1	Regulator c	K.GIGHVIK#.V	38.70	19.05	2.03	0.49
Q9EPU0_RI	Upf1	Regulator c	R.IAFFTLPK#.T	115.79	72.17	1.60	0.62
Q9EPU0_RI	Upf1	Regulator c	K.IPSEQEQLR.A	20.57	67.45	0.30	3.28
Q9EPU0_RI	Upf1	Regulator c	R.KLVNTVNPGAR.F	11.73	35.11	0.33	2.99
Q9EPU0_RI	Upf1	Regulator c	K.LEADYDK#K#.L	34.64	18.14	1.91	0.52
Q9EPU0_RI	Upf1	Regulator c	K.LEELWK#.E	46.93	11.36	4.13	0.24
Q9EPU0_RI	Upf1	Regulator c	K.LKESQTQDNITVR.W	18.24	44.33	0.41	2.43
Q9EPU0_RI	Upf1	Regulator c	K.LLGHEVEDVVIK#.C	37.30	21.52	1.73	0.58
Q9EPU0_RI	Upf1	Regulator c	K.LQQLKDETGELSSADEK.R	22.15	12.45	1.78	0.56
Q9EPU0_RI	Upf1	Regulator c	K.LYQEVEIASVDAFQGR.E	9.91	28.76	0.34	2.90
Q9EPU0_RI	Upf1	Regulator c	R.NM*DSMPELQK#.L	11.38	6.26	1.82	0.55
Q9EPU0_RI	Upf1	Regulator c	R.NM*DSM*PELQK#.L	70.54	50.08	1.41	0.71
Q9EPU0_RI	Upf1	Regulator c	R.NVFLLGFIPAK#.A	135.09	67.56	2.00	0.50
Q9EPU0_RI	Upf1	Regulator c	R.QITAQQINK#.L	41.40	23.01	1.80	0.56
Q9EPU0_RI	Upf1	Regulator c	K.RFTAQGLPDLNHSQVYAVK.T	5.29	14.81	0.36	2.80
Q9EPU0_RI	Upf1	Regulator c	K.SQIDVALSQDSTYQGER.A	4.20	9.73	0.43	2.32
Q9EPU0_RI	Upf1	Regulator c	R.SSVGAPVEVTHNFQVDFVWK.S	4.94	4.50	1.10	0.91
Q9EPU0_RI	Upf1	Regulator c	R.SYLVQYM*QFSGSLHTK#.L	9.43	7.75	1.22	0.82
Q9EPU0_RI	Upf1	Regulator c	K.TFAVDETSVSGYIYHK#.L	14.92	10.10	1.48	0.68
Q9EPU0_RI	Upf1	Regulator c	K.TSQLLAELNFEEDEEDTYYTK#.D	11.66	3.43	3.39	0.29
Q9EPU0_RI	Upf1	Regulator c	K.TSQLLAELNFEEDEEDTYYTK#.D	12.14	8.73	1.39	0.72
Q9EPU0_RI	Upf1	Regulator c	K.TVLQRPLSLIQGPPGTGK.T	20.01	70.74	0.28	3.54
Q9EPU0_RI	Upf1	Regulator c	K.VPDNYGDEIAIELR.S	22.41	24.33	0.92	1.09
Q9EPU0_RI	Upf1	Regulator c	R.YEDAYQYQNIFGPLVK#.L	28.35	20.31	1.40	0.72
Q9EPU0_RI	Upf1	Regulator c	R.YGVIIVGNPK#.A	78.94	53.67	1.47	0.68
Q9EPU0_RI	Upf1	Regulator c	R.AYQHGGVTGLSQY.-	25.94	25.94	1.00	1.00
Q9EPU0_RI	Upf1	Regulator c	R.FM*TTAM*YDAR.E	3.23	8.33	0.39	2.58
Q9EPU0_RI	Upf1	Regulator c	R.IAFFTLPK#.T	35.62	19.50	1.83	0.55
Q9EPU0_RI	Upf1	Regulator c	R.KLVNTVNPGAR.F	2.31	12.38	0.19	5.35
Q9EPU0_RI	Upf1	Regulator c	K.LQQLKDETGELSSADEKR.Y	3.91	11.41	0.34	2.92
Q9EPU0_RI	Upf1	Regulator c	R.NM*DSM*PELQK#.L	21.91	16.58	1.32	0.76
Q9EPU0_RI	Upf1	Regulator c	R.NVFLLGFIPAK#.A	32.35	27.59	1.17	0.85
Q9EPU0_RI	Upf1	Regulator c	K.TVLQRPLSLIQGPPGTGK.T	6.98	17.34	0.40	2.48
Q9EPU0_RI	Upf1	Regulator c	K.VPDNYGDEIAIELR.S	7.31	7.54	0.97	1.03
Q9EPU0_RI	Upf1	Regulator c	R.YEDAYQYQNIFGPLVK#.L	13.41	8.21	1.63	0.61
Q9EPU0_RI	Upf1	Regulator c	R.YGVIIVGNPK#.A	29.02	17.66	1.64	0.61
A2AT37_A2	Upf2	Protein Upf	K.AFVPAILFK#.D	38.89	14.28	2.72	0.37
A2AT37_A2	Upf2	Protein Upf	K.FNLSFPPSEIISPEK#.Q	7.80	2.92	2.67	0.37
A2AT37_A2	Upf2	Protein Upf	K.YIAEAVASIVEAK#.L	18.63	9.18	2.03	0.49
A2AT37_A2	Upf2	Protein Upf	R.YSDFAPSLLQVWK#.K	17.81	5.82	3.06	0.33
Q3ULL6_Q	Upf3b	Protein Upf	K.FLESYATDNEK#.M	11.13	5.13	2.17	0.46
Q3ULL6_Q	Upf3b	Protein Upf	K.M*TSTPETLLEEIEAK#.N	8.43	7.33	1.15	0.87
Q3ULL6_Q	Upf3b	Protein Upf	R.TTPLLSFLK#.N	11.75	5.33	2.21	0.45
Q9CQY6_U	Uqcc2	Ubiquinol-	K.LILSTDTLEEFQEM*NK#.S	8.35	2.34	3.56	0.28
Q9DB77_Q	Uqcrc2	Cytochrom	K.AVAQGNLSSADVQAAK#.N	7.01	7.18	0.98	1.02
Q9Z1Z0_US	Uso1	General ves	R.LSALLQETK#.E	18.51	7.80	2.37	0.42
Q9Z1Z0_US	Uso1	General ves	R.ASQKPQPNFPSPEYM*IFDHEFTK.L	13.34	6.59	2.02	0.49
Q9Z1Z0_US	Uso1	General ves	R.ASQK#PQPNFPSPEYMIFDHEFTK#.L	12.02	5.69	2.11	0.47
Q9Z1Z0_US	Uso1	General ves	K.DSLIENLK#.S	17.19	7.59	2.26	0.44
Q9Z1Z0_US	Uso1	General ves	R.EIIRNDGVLLLQALTR.S	3.61	29.91	0.12	8.29
Q9Z1Z0_US	Uso1	General ves	K.ELEGVITK#.A	137.74	54.25	2.54	0.39
Q9Z1Z0_US	Uso1	General ves	K.EQDDLLVLLADQDQK#.I	26.50	11.99	2.21	0.45
Q9Z1Z0_US	Uso1	General ves	R.EQDLQLEELK#.Q	63.05	26.97	2.34	0.43
Q9Z1Z0_US	Uso1	General ves	K.IVAFENAFER.L	57.41	96.52	0.59	1.68
Q9Z1Z0_US	Uso1	General ves	K.K#EQDDLLVLLADQDQK#.I	13.75	3.02	4.56	0.22
Q9Z1Z0_US	Uso1	General ves	R.LLTSLLK#.Q	149.27	63.16	2.36	0.42
Q9Z1Z0_US	Uso1	General ves	R.LM*DLLADSR.E	16.33	32.31	0.51	1.98
Q9Z1Z0_US	Uso1	General ves	R.LMDLLADSR.E	11.57	15.01	0.77	1.30
Q9Z1Z0_US	Uso1	General ves	R.LREEIEELK.S	8.88	26.21	0.34	2.95
Q9Z1Z0_US	Uso1	General ves	R.LSALLQETK#.E	194.74	68.85	2.83	0.35
Q9Z1Z0_US	Uso1	General ves	R.M*K#PWFEVGEENSGWSAQK#.V	38.54	12.60	3.06	0.33
Q9Z1Z0_US	Uso1	General ves	R.NDGVLLLQALTR.S	37.65	59.65	0.63	1.58
Q9Z1Z0_US	Uso1	General ves	K.QLGPPVQQIILVSPM*GVSR.L	3.13	5.13	0.61	1.64
Q9Z1Z0_US	Uso1	General ves	R.QSEDLGSQFTEIFIK#.Q	71.98	35.38	2.03	0.49
Q9Z1Z0_US	Uso1	General ves	K.SQQALLQGQLAEK#.D	13.59	4.82	2.82	0.35
Q9Z1Z0_US	Uso1	General ves	K.SQQALLQGQLAEK#DSLIENLK#.S	62.92	25.84	2.43	0.41
Q9Z1Z0_US	Uso1	General ves	K.TLEQHDNIVTHYK#.N	121.58	50.19	2.42	0.41
Q9Z1Z0_US	Uso1	General ves	R.ASQK#PQPNFPSPEYMIFDHEFTK#.L	4.19	4.48	0.94	1.07
Q9Z1Z0_US	Uso1	General ves	K.DSLIENLK#.S	13.54	5.35	2.53	0.40

Q9Z1Z0_U	Uso1	General ves	K.ELEGVITK#.A	58.62	24.63	2.38	0.42
Q9Z1Z0_U	Uso1	General ves	R.EQDLQLEELK#.Q	33.19	11.32	2.93	0.34
Q9Z1Z0_U	Uso1	General ves	R.LSALLQETK#.E	75.54	25.67	2.94	0.34
Q9Z1Z0_U	Uso1	General ves	R.M*K#PWFEVGEENSGWSAQK#.V	14.07	4.48	3.14	0.32
Q9Z1Z0_U	Uso1	General ves	R.NDGVLLLQALTR.S	16.30	27.43	0.59	1.68
Q9Z1Z0_U	Uso1	General ves	K.QLGPPVQQIILVSPM*GVSR.L	5.74	7.42	0.77	1.29
Q9Z1Z0_U	Uso1	General ves	K.SQQALLQGQLAEK#.D	13.54	5.33	2.54	0.39
Q9Z1Z0_U	Uso1	General ves	K.SVPVEGESEHVSAAK#.T	33.98	12.48	2.72	0.37
Q9Z1Z0_U	Uso1	General ves	K.TNNSNQNFFK#.E	37.06	17.80	2.08	0.48
P52479_U	Usp10	Ubiquitin c	K.EGLVPVSEDPVAIK#.I	26.41	14.46	1.83	0.55
P52479_U	Usp10	Ubiquitin c	R.ELLSPGIK#.N	19.43	8.70	2.23	0.45
P52479_U	Usp10	Ubiquitin c	R.ESVQGYTTK#.T	18.10	9.47	1.91	0.52
P52479_U	Usp10	Ubiquitin c	K.IAELLETVTLIHKPVSLQPR.G	10.66	23.29	0.46	2.18
P52479_U	Usp10	Ubiquitin c	K.NIDYPVDLEISR.E	6.19	11.71	0.53	1.89
P52479_U	Usp10	Ubiquitin c	R.QADFVQTPITGIFGGHIR.S	4.86	10.10	0.48	2.08
P52479_U	Usp10	Ubiquitin c	R.SDLIEDEELEDTGK#GSEDEWEQVGPK#.N	5.41	2.29	2.37	0.42
P52479_U	Usp10	Ubiquitin c	R.TVQDALESLVAR.E	9.10	22.16	0.41	2.44
P52479_U	Usp10	Ubiquitin c	R.DIRPGAAFEPTYIYR.L	14.31	18.07	0.79	1.26
P52479_U	Usp10	Ubiquitin c	K.EGLVPVSEDPVAIK#.I	28.57	12.85	2.22	0.45
P52479_U	Usp10	Ubiquitin c	R.ESVQGYTTK#.T	28.96	11.89	2.44	0.41
P52479_U	Usp10	Ubiquitin c	K.NIDYPVDLEISR.E	8.57	14.60	0.59	1.70
P52479_U	Usp10	Ubiquitin c	R.SDLIEDEELEDTGK#GSEDEWEQVGPK#.N	9.50	2.49	3.82	0.26
P52479_U	Usp10	Ubiquitin c	R.TVQDALESLVAR.E	7.71	17.47	0.44	2.26
Q9JMA1_U	Usp14	Ubiquitin c	K.AQLFALTGVQPAR.Q	11.48	13.75	0.83	1.20
Q9JMA1_U	Usp14	Ubiquitin c	K.EK#FEGVELNTDEPPMVFK#.A	14.04	3.06	4.59	0.22
Q9JMA1_U	Usp14	Ubiquitin c	K.GGTLK#DDDWGNIK#.M	15.05	2.62	5.74	0.17
Q9JMA1_U	Usp14	Ubiquitin c	K.K#VNQQPNANDK#NSPPK#.E	7.09	2.25	3.15	0.32
Q9JMA1_U	Usp14	Ubiquitin c	R.RVEIMEEESEQ.-	7.83	7.99	0.98	1.02
Q9JMA1_U	Usp14	Ubiquitin c	R.RVEIM*EEESEQ.-	2.11	4.30	0.49	2.04
Q9JMA1_U	Usp14	Ubiquitin c	K.EK#FEGVELNTDEPPM*VFK#.A	13.53	2.68	5.05	0.20
Q9JMA1_U	Usp14	Ubiquitin c	R.ETDSSSAPAVTPSK#.K	12.90	2.26	5.72	0.17
Q9JMA1_U	Usp14	Ubiquitin c	K.LEAIEDDSGRETDSSSAPAVTPSK.K	7.40	7.23	1.02	0.98
Q8R5H1_U	Usp15	Ubiquitin c	R.SFLALDWDPDLK#.K	11.88	3.58	3.31	0.30
Q99LG0_U	Usp16	Ubiquitin c	R.TPDVQESPEDLGVK#.S	9.48	5.66	1.68	0.60
Q9WTV6_U	Usp18	Ubl carbox	K.DQITDTDLTER.L	3.96	11.12	0.36	2.81
Q3UJD6_U	Usp19	Ubiquitin c	R.GEVGSGAGPGTQAGPSAK#.R	9.16	4.80	1.91	0.52
B1AY13_U	Usp24	Ubiquitin c	K.GIIELLGSK#.L	10.92	3.05	3.59	0.28
B1AY13_U	Usp24	Ubiquitin c	K.GQHDLESDVQQQLFK#.E	14.80	6.00	2.47	0.41
B1AY13_U	Usp24	Ubiquitin c	K.IQSGQSSTVIENIHTIIAAAAVK#.F	11.62	6.43	1.81	0.55
B1AY13_U	Usp24	Ubiquitin c	K.LIEDSTLSK#.S	20.44	6.21	3.29	0.30
B1AY13_U	Usp24	Ubiquitin c	K.LQYYVPENFWK#.I	9.48	3.07	3.09	0.32
B1AY13_U	Usp24	Ubiquitin c	K.NTFQGIYSDQK#.I	12.17	6.14	1.98	0.50
B1AY13_U	Usp24	Ubiquitin c	K.TLLSETSSQSSK#.S	19.57	5.26	3.72	0.27
B1AY13_U	Usp24	Ubiquitin c	R.VAVATILEK#.T	16.29	7.18	2.27	0.44
B1AY13_U	Usp24	Ubiquitin c	R.VLYNLEVLSSK#.L	11.64	4.78	2.43	0.41
Q91W36_U	Usp3	Ubiquitin c	R.SAILQENSTLSASNK#.C	7.48	3.34	2.24	0.45
Q3TIX9_SN	Usp39	U4/U6.U5 t	R.AYDGTTYLPGIVGLNNIK#.A	6.75	3.98	1.70	0.59
Q3TIX9_SN	Usp39	U4/U6.U5 t	K.NPTIVNFPITNVDLR.E	5.55	7.60	0.73	1.37
Q3TIX9_SN	Usp39	U4/U6.U5 t	R.AYDGTTYLPGIVGLNNIK#.A	10.61	3.47	3.05	0.33
Q3TIX9_SN	Usp39	U4/U6.U5 t	K.NPTIVNFPITNVDLR.E	5.91	4.82	1.23	0.82
Q3TIX9_SN	Usp39	U4/U6.U5 t	R.NYFLEEDNYK#.N	14.85	2.97	4.99	0.20
Q3TIX9_SN	Usp39	U4/U6.U5 t	R.AYDGTTYLPGIVGLNNIK#.A	25.03	6.13	4.08	0.25
Q3TIX9_SN	Usp39	U4/U6.U5 t	R.EVPAPALPVVR.V	8.82	10.53	0.84	1.19
Q3TIX9_SN	Usp39	U4/U6.U5 t	K.NPTIVNFPITNVDLR.E	7.77	9.59	0.81	1.23
Q3TIX9_SN	Usp39	U4/U6.U5 t	R.NYFLEEDNYK#.N	21.34	5.77	3.70	0.27
P35123_U	Usp4	Ubiquitin c	K.ADTIATIEK#.E	17.21	12.50	1.38	0.73
P35123_U	Usp4	Ubiquitin c	K.EHLIDELDYVLVPAEAWNK#.L	13.70	4.92	2.79	0.36
P35123_U	Usp4	Ubiquitin c	K.GEIAEAYAELIK#.Q	15.98	8.32	1.92	0.52
P35123_U	Usp4	Ubiquitin c	R.LRNDSVIVDTFHGLFK.S	8.67	8.77	0.99	1.01
P35123_U	Usp4	Ubiquitin c	K.YMSNTYEQLSK#.L	7.54	3.11	2.42	0.41
P35123_U	Usp4	Ubiquitin c	K.YM*SNTYEQLSK#.L	11.74	4.15	2.83	0.35
Q8BY87_U	Usp47	Ubiquitin c	R.LFVLLPEQSPGSYSK#.R	12.52	5.38	2.33	0.43
Q8BY87_U	Usp47	Ubiquitin c	K.LSEISGIPLEDIEFAK#.G	20.17	3.46	5.83	0.17
Q3V0C5_U	Usp48	Ubiquitin c	K.ALGLDTGQQQDAQEFSK#.L	10.37	7.22	1.44	0.70
Q3V0C5_U	Usp48	Ubiquitin c	R.ISEYAANIFYSR.Y	4.53	8.85	0.51	1.95
Q3V0C5_U	Usp48	Ubiquitin c	R.LPAGAEPYEFVSLEWLQK#.W	5.68	5.93	0.96	1.04
Q3V0C5_U	Usp48	Ubiquitin c	K.ALGLDTGQQQDAQEFSK#.L	18.00	8.25	2.18	0.46
Q3V0C5_U	Usp48	Ubiquitin c	K.LFM*SLLEDTLSK#.Q	10.22	3.23	3.16	0.32
Q3V0C5_U	Usp48	Ubiquitin c	R.LPAGAEPYEFVSLEWLQK.W	7.96	11.64	0.68	1.46
P56399_U	Usp5	Ubiquitin c	R.DGLGGLPDIVR.D	6.84	17.84	0.38	2.61
P56399_U	Usp5	Ubiquitin c	R.FASFPDYLVIQIK#.K	21.97	13.14	1.67	0.60
P56399_U	Usp5	Ubiquitin c	K.IFQNAPTDPTQDFSTQVAK#.L	8.64	7.26	1.19	0.84
P56399_U	Usp5	Ubiquitin c	R.IGEWELIQESGVPLKPLFGPGYTGIR.N	7.27	19.85	0.37	2.73
P56399_U	Usp5	Ubiquitin c	K.IVILPDYLEIAR.D	8.25	20.76	0.40	2.52
P56399_U	Usp5	Ubiquitin c	K.LGTITPDGADVYSYDEDDM*VLDPSLAEHLSHFGIDM*LK#.M	9.20	2.62	3.52	0.28
P56399_U	Usp5	Ubiquitin c	R.VDYIMQLPVPMDAALNK#EELLEYEEK#.K	3.07	4.51	0.68	1.47
Q6A4J8_U	Usp7	Ubiquitin c	R.AGFIQDTSLILYEEVKPNLTER.I	6.70	4.65	1.44	0.69
Q6A4J8_U	Usp7	Ubiquitin c	K.INDRFEFPEQLPLDEFLQK.T	4.29	9.58	0.45	2.23
Q6A4J8_U	Usp7	Ubiquitin c	R.LNTDPM*LLQFFK#.S	6.84	2.82	2.43	0.41
Q6A4J8_U	Usp7	Ubiquitin c	K.LSEVLQAVTDHDIPQQLVER.L	7.24	10.39	0.70	1.44
Q6A4J8_U	Usp7	Ubiquitin c	R.VLLDNVENK#.M	27.64	12.13	2.28	0.44
Q6A4J8_U	Usp7	Ubiquitin c	R.LLEIVSYK#.I	13.20	5.43	2.43	0.41
Q6A4J8_U	Usp7	Ubiquitin c	R.VLLDNVENK#.M	14.28	9.83	1.45	0.69
P70398_U	Usp9x	Probable u	K.K#EAK#NEAK#.N	4.99	1.72	2.91	0.34
P70398_U	Usp9x	Probable u	K.ALTLQDLDNIWAAQAGK#.H	12.36	6.57	1.88	0.53
P70398_U	Usp9x	Probable u	R.AQENYEGGEEVSPPQTK#.G	11.04	3.38	3.27	0.31
P70398_U	Usp9x	Probable u	R.DDVFGYPQQFEDK#PPLSK#.T	17.49	4.95	3.53	0.28
P70398_U	Usp9x	Probable u	R.ELDM*EPYTVAGVAK#.L	14.76	5.81	2.54	0.39
P70398_U	Usp9x	Probable u	K.K#EAK#NEAK#.N	2.33	1.46	1.59	0.63
P70398_U	Usp9x	Probable u	R.LAQQISDEASR.Y	13.46	16.38	0.82	1.22
P70398_U	Usp9x	Probable u	K.LEGDNVNPESQLIQQNEQSESEK#.A	16.98	6.04	2.81	0.36
P70398_U	Usp9x	Probable u	K.LIGQLNLK#.D	23.01	4.29	5.36	0.19
P70398_U	Usp9x	Probable u	K.LM*PPDSTTIEK#.L	19.08	7.24	2.63	0.38
P70398_U	Usp9x	Probable u	K.LPPVLAIQLK#.R	14.86	6.01	2.47	0.40
P70398_U	Usp9x	Probable u	K.LSVPATFM*LVSLDEGPGPPIK#.Y	14.01	10.96	1.28	0.78
P70398_U	Usp9x	Probable u	K.M*NALNEVNK#.V	21.80	4.20	5.19	0.19
P70398_U	Usp9x	Probable u	R.NHQNLLDSLEQYVK#.G	17.81	5.46	3.26	0.31
P70398_U	Usp9x	Probable u	K.VLGGSFADQK#.I	31.90	12.99	2.46	0.41
P70398_U	Usp9x	Probable u	R.VPGQEETVK#.N	31.52	9.94	3.17	0.32
P70398_U	Usp9x	Probable u	R.WVVPVLPK#.G	16.84	7.76	2.17	0.46
Q640M1_U	Utp14a	U3 small n	K.LALSDLLGPLK#PSSSLAAVK#.K	8.84	11.25	0.79	1.27
Q640M1_U	Utp14a	U3 small n	R.TPLEQEVFNLLHK#.N	14.81	10.52	1.41	0.71
Q8C7V3_U	Utp15	U3 small n	K.FIVLQELVEK#.E	12.62	15.05	0.84	1.19

Q5SSI6_UT	Utp18	U3 small n	R.IAASTFSSDSK#.R	3.89	1.86	2.09	0.48
Q9CX11_U	Utp23	rRNA-proc	K.AVEAGQLVSVHEK#.Q	7.20	1.36	5.30	0.19
E9Q6R7_E	Utrn	Protein Utr	R.ELGQTLIDGGILDDIISEK.L	10.39	14.38	0.72	1.38
E9Q6R7_E	Utrn	Protein Utr	R.EVETSLQR.C	1.38	10.37	0.13	7.50
E9Q6R7_E	Utrn	Protein Utr	R.IDAFQLPQEAQK.I	4.00	7.88	0.51	1.97
E9Q6R7_E	Utrn	Protein Utr	R.LDELNQTGQTLR.E	23.26	17.22	1.35	0.74
E9Q6R7_E	Utrn	Protein Utr	R.LEDSSNQVTQAVAK.L	15.71	17.37	0.90	1.11
E9Q6R7_E	Utrn	Protein Utr	K.LLDLLEGLTGTSLPK.E	16.39	18.23	0.90	1.11
E9Q6R7_E	Utrn	Protein Utr	R.LLSELDDASLQVENVR.E	1.81	7.61	0.24	4.20
E9Q6R7_E	Utrn	Protein Utr	R.LVDYQSQLEK.F	12.39	19.69	0.63	1.59
E9Q6R7_E	Utrn	Protein Utr	K.M*ESLPLGDDLPSLQK#.L	7.48	6.88	1.09	0.92
E9Q6R7_E	Utrn	Protein Utr	K.SLQNDLEAEQVK#.V	11.11	9.31	1.19	0.84
E9Q6R7_E	Utrn	Protein Utr	R.STPDPEESPQELTDLAQETEVQAENIK.W	9.19	9.26	0.99	1.01
E9Q6R7_E	Utrn	Protein Utr	R.VLQVLHQNNVDLVNIGGTDIVDGNPK.L	3.96	5.08	0.78	1.28
E9Q6R7_E	Utrn	Protein Utr	K.VLYNDLGAQVTEGK.Q	5.91	11.93	0.50	2.02
E9Q6R7_E	Utrn	Protein Utr	K.YGDLEARPDDGQNEFSDIIK.S	2.18	9.28	0.23	4.26
Q8CEJ2_Q	Uxt	MCG1177	R.ELQGLQNFPEPSPH.-	10.99	10.99	1.00	1.00
Q8CEJ2_Q	Uxt	MCG1177	K.SSLLTELSDSLTK#.D	18.40	6.70	2.74	0.36
Q8CEJ2_Q	Uxt	MCG1177	R.YETFISDVLQR.D	6.98	16.93	0.41	2.43
Q80WQ2_	Vac14	Protein VA	R.GAVLPHFNVLFDGLSK#.L	16.78	10.87	1.54	0.65
Q80WQ2_	Vac14	Protein VA	K.LAADPDPNVK#.S	74.32	30.21	2.46	0.41
Q80WQ2_	Vac14	Protein VA	K.LVTPEDDEPDEPK.S	12.67	13.38	0.95	1.06
Q80WQ2_	Vac14	Protein VA	R.HAYDLIQK#.F	11.63	39.23	0.30	3.37
Q80WQ2_	Vac14	Protein VA	K.LAADPDPNVK#.S	141.43	48.94	2.89	0.35
P63044_V	Vamp2	Vesicle-ass	K.LSELDDRADALQAGASQFETSAAK.L	10.22	43.69	0.23	4.28
O70404_V	Vamp8	Vesicle-ass	R.NK#TEDLEATSEHFK#.T	8.61	6.50	1.32	0.76
Q9Z1Q9_S	Vars	Valine--tRN	R.DPGVITYDLPTPPGEK#.K	7.22	3.23	2.24	0.45
Q9Z1Q9_S	Vars	Valine--tRN	K.GALINVPPPFLGLPR.F	5.13	6.90	0.74	1.34
Q9Z1Q9_S	Vars	Valine--tRN	R.GPGQDPQAALGALGK#.A	62.99	13.71	4.60	0.22
Q9Z1Q9_S	Vars	Valine--tRN	R.IETM*LGDVAVAVHPK#.D	15.38	4.20	3.66	0.27
Q9Z1Q9_S	Vars	Valine--tRN	R.SLPIVFDDFVDM*EFGTGAVK#.I	27.29	7.33	3.72	0.27
Q9Z1Q9_S	Vars	Valine--tRN	R.SVTQQPGSEVIAPQK#.T	63.40	13.75	4.61	0.22
Q9Z1Q9_S	Vars	Valine--tRN	R.TLLPVPGYK#.E	21.73	4.35	4.99	0.20
Q9Z1Q9_S	Vars	Valine--tRN	K.VPLEVQEADEAK#.L	51.99	15.81	3.29	0.30
Q9Z1Q9_S	Vars	Valine--tRN	K.VQGSDSDEEVVVATTR.I	9.18	10.23	0.90	1.11
Q9Z1Q9_S	Vars	Valine--tRN	K.ALNPLEDWLR.L	34.58	21.28	1.63	0.62
Q9Z1Q9_S	Vars	Valine--tRN	R.DPGVITYDLPTPPGEK#.K	42.93	8.44	5.09	0.20
Q9Z1Q9_S	Vars	Valine--tRN	R.EAFLEEVWK#.W	110.94	19.98	5.55	0.18
Q9Z1Q9_S	Vars	Valine--tRN	R.EFGVSPDK#.I	74.76	14.21	5.26	0.19
Q9Z1Q9_S	Vars	Valine--tRN	K.GALINVPPPFLGLPR.F	26.06	24.32	1.07	0.93
Q9Z1Q9_S	Vars	Valine--tRN	R.GPGQDPQAALGALGK#.A	194.25	33.01	5.88	0.17
Q9Z1Q9_S	Vars	Valine--tRN	R.IETM*LGDVAVAVHPK#.D	74.90	13.47	5.56	0.18
Q9Z1Q9_S	Vars	Valine--tRN	R.IETMLGDVAVAVHPK#.D	26.25	5.94	4.42	0.23
Q9Z1Q9_S	Vars	Valine--tRN	R.K#AVLAALK#.E	79.56	18.64	4.27	0.23
Q9Z1Q9_S	Vars	Valine--tRN	R.K#VDEAIALFQK#.M	58.88	11.58	5.08	0.20
Q9Z1Q9_S	Vars	Valine--tRN	K.LGSSLDWDR.A	11.66	11.82	0.99	1.01
Q9Z1Q9_S	Vars	Valine--tRN	R.M*VM*LGLK#.L	28.14	2.01	14.02	0.07
Q9Z1Q9_S	Vars	Valine--tRN	R.SLPIVFDDFVDM*EFGTGAVK#.I	36.83	21.40	1.72	0.58
Q9Z1Q9_S	Vars	Valine--tRN	R.SVTQQPGSEVIAPQK#.T	197.80	35.56	5.56	0.18
Q9Z1Q9_S	Vars	Valine--tRN	K.VPLEVQEADEAK#.L	185.41	31.66	5.86	0.17
Q9Z1Q9_S	Vars	Valine--tRN	K.VQGSDSDEEVVVATTR.I	31.16	19.99	1.56	0.64
Q62465_V	Vat1	Synaptic ve	K.GVDIVM*DPLGGSDTAK#.G	57.18	13.68	4.18	0.24
Q62465_V	Vat1	Synaptic ve	K.GVDIVMDPLGGSDTAK#.G	32.94	8.95	3.68	0.27
Q62465_V	Vat1	Synaptic ve	R.IDSVWPFEK#.V	104.74	19.11	5.48	0.18
Q62465_V	Vat1	Synaptic ve	R.LPPLPVTPGM*EGAGVVVAVGEGVGDR.K	7.69	7.95	0.97	1.03
Q62465_V	Vat1	Synaptic ve	R.LPPLPVTPGMEGAGVVVAVGEGVGDR.K	4.74	7.86	0.60	1.66
Q62465_V	Vat1	Synaptic ve	R.TVENVTVFGTASASK#.H	84.79	19.57	4.33	0.23
Q62465_V	Vat1	Synaptic ve	K.VLLVPGPEK#.E	40.77	9.54	4.28	0.23
Q62465_V	Vat1	Synaptic ve	K.VLLVPGPEK#ET.-	112.86	27.22	4.15	0.24
Q62465_V	Vat1	Synaptic ve	K.VVTYGM*ANLLTGPK#.R	74.04	16.91	4.38	0.23
Q62465_V	Vat1	Synaptic ve	K.VVTYGMANLLTGPK#.R	39.09	8.41	4.65	0.22
Q62465_V	Vat1	Synaptic ve	K.GVDIVM*DPLGGSDTAK#.G	5.45	1.83	2.97	0.34
Q62465_V	Vat1	Synaptic ve	R.IDSVWPFEK#.V	17.30	15.96	1.08	0.92
Q62465_V	Vat1	Synaptic ve	K.GVDIVM*DPLGGSDTAK#.G	31.45	6.89	4.57	0.22
Q62465_V	Vat1	Synaptic ve	R.IDSVWPFEK#.V	43.23	10.84	3.99	0.25
Q62465_V	Vat1	Synaptic ve	R.TVENVTVFGTASASK#.H	34.21	7.30	4.69	0.21
Q62465_V	Vat1	Synaptic ve	K.VLLVPGPEK#ET.-	80.07	19.28	4.15	0.24
Q62465_V	Vat1	Synaptic ve	K.VVTYGM*ANLLTGPK#.R	49.27	8.47	5.82	0.17
Q62465_V	Vat1	Synaptic ve	K.VVTYGMANLLTGPK#.R	18.95	2.22	8.53	0.12
Q62465_V	Vat1	Synaptic ve	K.ENGVTHPIDYHTTDYVDEIK#K#.I	17.55	4.68	3.75	0.27
Q62465_V	Vat1	Synaptic ve	K.GVDIVM*DPLGGSDTAK#.G	64.57	13.59	4.75	0.21
Q62465_V	Vat1	Synaptic ve	K.GVDIVMDPLGGSDTAK#.G	18.63	5.95	3.13	0.32
Q62465_V	Vat1	Synaptic ve	R.IDSVWPFEK#.V	95.73	20.05	4.77	0.21
Q62465_V	Vat1	Synaptic ve	R.LPPLPVTPGM*EGAGVVVAVGEGVGDR.K	9.88	11.76	0.84	1.19
Q62465_V	Vat1	Synaptic ve	R.TVENVTVFGTASASK#.H	84.97	15.28	5.56	0.18
Q62465_V	Vat1	Synaptic ve	K.VLLVPGPEK#.E	39.53	8.22	4.81	0.21
Q62465_V	Vat1	Synaptic ve	K.VLLVPGPEK#ET.-	143.58	28.64	5.01	0.20
Q62465_V	Vat1	Synaptic ve	K.VVTYGM*ANLLTGPK#.R	92.16	19.23	4.79	0.21
Q62465_V	Vat1	Synaptic ve	K.VVTYGMANLLTGPK#.R	28.96	7.27	3.99	0.25
P61759_P	Vbp1	Prefoldin s	K.FM*ELNLAQK#.K	23.23	11.57	2.01	0.50
P61759_P	Vbp1	Prefoldin s	K.FMELNLAQK#.K	16.25	4.94	3.29	0.30
P61759_P	Vbp1	Prefoldin s	K.K#LDEQYQK#.Y	15.79	6.42	2.46	0.41
P61759_P	Vbp1	Prefoldin s	R.LHLGIPEAVFVEDVDSFM*K#.Q	16.22	3.39	4.78	0.21
P61759_P	Vbp1	Prefoldin s	R.LHLGIPEAVFVEDVDSFMK#QPGNETADTVLK#.K	9.41	3.08	3.06	0.33
P61759_P	Vbp1	Prefoldin s	K.NLDSLEEDLDFLRDQFTTTEVNM*AR.V	6.67	11.72	0.57	1.76
P61759_P	Vbp1	Prefoldin s	R.VYNWDVK#.R	19.45	5.48	3.55	0.28
Q64727_V	Vcl	Vinculin O	K.AAVHLEGK#.I	43.82	17.65	2.48	0.40
Q64727_V	Vcl	Vinculin O	K.AGEVINQPM*M*M*AAR.Q	9.79	17.26	0.57	1.76
Q64727_V	Vcl	Vinculin O	R.ALASIDSK#.L	97.18	44.54	2.18	0.46
Q64727_V	Vcl	Vinculin O	R.ALASQLQDSLK#.D	157.33	43.85	3.59	0.28
Q64727_V	Vcl	Vinculin O	K.AQM*QEAM*TQEVSDVFSDTTTPIK#.L	11.34	4.64	2.44	0.41
Q64727_V	Vcl	Vinculin O	K.AQMQEAMTQEVSDVFSDTTTPIK#.L	3.80	2.10	1.81	0.55
Q64727_V	Vcl	Vinculin O	K.AQQVSQGLDVLTAK#.V	111.68	58.42	1.91	0.52
Q64727_V	Vcl	Vinculin O	K.AVAGNISDPGLQK#.S	158.52	55.77	2.84	0.35
Q64727_V	Vcl	Vinculin O	R.EAEAASIK#.I	85.43	69.83	1.22	0.82
Q64727_V	Vcl	Vinculin O	K.ELLPVLISAM*K#.I	93.39	32.20	2.90	0.34
Q64727_V	Vcl	Vinculin O	K.ELLPVLISAMK#.I	123.55	54.67	2.26	0.44
Q64727_V	Vcl	Vinculin O	R.GILSGTSDLLLTFDEAEVR.K	16.53	28.38	0.58	1.72
Q64727_V	Vcl	Vinculin O	K.GNDIIAAAK#.R	129.68	48.26	2.69	0.37
Q64727_V	Vcl	Vinculin O	R.GQGASPVAMQK#.A	46.98	15.22	3.09	0.32
Q64727_V	Vcl	Vinculin O	R.GQGASPVAM*QK#.A	41.22	1.44	28.71	0.03
Q64727_V	Vcl	Vinculin O	R.IPTISTQLK#.I	133.85	54.87	2.44	0.41
Q64727_V	Vcl	Vinculin O	K.KIDAAQNWLADPNGGPEGEEQIR.G	3.42	6.49	0.53	1.90

Q64727_VI	Vcl	Vinculin OS	R.LANVM*M*GPYR.Q	8.42	17.37	0.48	2.06
Q64727_VI	Vcl	Vinculin OS	K.LLAVAATAPPDAPNREEVFDER.A	5.55	29.45	0.19	5.31
Q64727_VI	Vcl	Vinculin OS	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4.64	6.75	0.69	1.46
Q64727_VI	Vcl	Vinculin OS	K.LVQAAQMLQSDPYSVPAR.D	3.24	7.01	0.46	2.16
Q64727_VI	Vcl	Vinculin OS	K.M*LGQM*TDQVADLR.A	9.99	18.23	0.55	1.83
Q64727_VI	Vcl	Vinculin OS	K.M*SAEINEIIR.V	16.16	20.63	0.78	1.28
Q64727_VI	Vcl	Vinculin OS	K.MSAEINEIIR.V	16.29	21.60	0.75	1.33
Q64727_VI	Vcl	Vinculin OS	K.M*TGLVDEAIDTK#.S	22.96	12.81	1.79	0.56
Q64727_VI	Vcl	Vinculin OS	K.MTGLVDEAIDTK#.S	27.34	6.06	4.51	0.22
Q64727_VI	Vcl	Vinculin OS	K.NQGIEEALK#.N	124.70	55.67	2.24	0.45
Q64727_VI	Vcl	Vinculin OS	K.QVATALQNLQTK#.T	49.56	21.05	2.35	0.42
Q64727_VI	Vcl	Vinculin OS	R.SLGEIAALTSK#.L	72.10	26.29	2.74	0.36
Q64727_VI	Vcl	Vinculin OS	K.STVEGIQASVK#.T	107.32	51.70	2.08	0.48
Q64727_VI	Vcl	Vinculin OS	R.TDAGFTLR.W	21.46	31.00	0.69	1.44
Q64727_VI	Vcl	Vinculin OS	K.TISPM*VM*DAK#.A	28.33	9.17	3.09	0.32
Q64727_VI	Vcl	Vinculin OS	R.TNISDEESEQATEM*LVHNAQNLM*QSVK#.E	11.90	3.11	3.83	0.26
Q64727_VI	Vcl	Vinculin OS	R.TNISDEESEQATEM*LVHNAQNLMQSVK#.E	15.32	6.36	2.41	0.42
Q64727_VI	Vcl	Vinculin OS	R.VLQLTSWDEDAWASK#.D	72.62	26.97	2.69	0.37
Q64727_VI	Vcl	Vinculin OS	R.VM*LVNSMNTVK#.E	14.13	40.19	0.35	2.84
Q64727_VI	Vcl	Vinculin OS	R.VMLVNSMNTVK#.E	20.58	7.62	2.70	0.37
Q64727_VI	Vcl	Vinculin OS	R.GQGASPVAM*QK#.A	7.42	2.96	2.51	0.40
Q64727_VI	Vcl	Vinculin OS	R.IPTISTQLK#.I	16.45	6.01	2.74	0.37
Q64727_VI	Vcl	Vinculin OS	R.VLQLTSWDEDAWASK#.D	8.86	2.60	3.40	0.29
Q01853_TE	Vcp	Transitiona	K.DVDLEFLAK#.M	28.32	10.01	2.83	0.35
Q01853_TE	Vcp	Transitiona	R.IVSQLLTLM*DGLK#.Q	9.65	5.25	1.84	0.54
Q01853_TE	Vcp	Transitiona	R.IVSQLLTLMDGLK#.Q	25.68	8.55	3.00	0.33
Q01853_TE	Vcp	Transitiona	R.LDQLIYIPLPDEK#.S	38.50	13.46	2.86	0.35
Q01853_TE	Vcp	Transitiona	R.LIVDEAINEDNSVVSLSQPK#.M	40.26	15.97	2.52	0.40
Q01853_TE	Vcp	Transitiona	R.LIVDEAINEDNSVVSLSQPK#.M	16.69	4.46	3.74	0.27
Q8CDG3_V	Vcpip1	Deubiquiti	K.APYSPTTSK#.E	8.96	5.97	1.50	0.67
Q8CDG3_V	Vcpip1	Deubiquiti	R.TGVIGVQPEEVTAAAK#.K	9.66	6.19	1.56	0.64
Q8CDG3_V	Vcpip1	Deubiquiti	R.VGDVQGQELESQLPTK#.I	13.63	7.11	1.92	0.52
Q8CDG3_V	Vcpip1	Deubiquiti	R.SSGDYSATFLPGLIPAEK#.C	7.13	2.79	2.55	0.39
Q8CDG3_V	Vcpip1	Deubiquiti	R.TGVIGVQPEEVTAAAK#.K	9.03	4.95	1.83	0.55
Q60932_VI	Vdac1	Voltage-de	K.TDEFQLHTNVNDGTEFGGSIYQK#.V	7.34	4.85	1.51	0.66
Q60932_VI	Vdac1	Voltage-de	R.VTQSNFAVGYK#.T	25.13	19.83	1.27	0.79
Q60932_VI	Vdac1	Voltage-de	R.WTEYGLTFTEK#.W	14.14	8.62	1.64	0.61
Q60930_VI	Vdac2	Voltage-de	K.YQLDPTASISAK.V	9.84	7.91	1.24	0.80
P40338_VH	Vhl	Von Hippel	R.SLYEDLEDYPSVR.K	2.34	7.01	0.33	2.99
P20152_VI	Vim	Vimentin O	K.FADLSEAANR.N	4.21	33.78	0.12	8.02
P20152_VI	Vim	Vimentin O	K.ILLAELEQLK.G	21.33	33.61	0.63	1.58
P20152_VI	Vim	Vimentin O	R.KVESLQEEIAFLK.K	6.89	22.70	0.30	3.30
P20152_VI	Vim	Vimentin O	R.KVESLQEEIAFLKK.L	10.15	11.59	0.88	1.14
P20152_VI	Vim	Vimentin O	R.LGDLYEEEM*R.E	1.73	12.47	0.14	7.19
P20152_VI	Vim	Vimentin O	R.LLQDSVDFSLADAINTEFK.N	4.80	8.53	0.56	1.78
P20152_VI	Vim	Vimentin O	R.SLYSSSPGGAYVTR.S	4.14	31.39	0.13	7.58
Q920Q4_VI	Vps16	Vacuolar pr	K.ALLLVGDVAQAAEVAIEHR.N	1.88	15.31	0.12	8.15
Q920Q4_VI	Vps16	Vacuolar pr	K.LAALADLEDWEELEK.F	8.18	4.83	1.69	0.59
Q920Q4_VI	Vps16	Vacuolar pr	K.LGDTPGVSYSDIAAR.A	2.03	7.28	0.28	3.59
Q9CQ80_VI	Vps25	Vacuolar pr	R.SGQNNSVFTLYELTSGEDTEDEEFHGLDEATLLR.A	1.69	3.35	0.51	1.98
P40336_VP	Vps26a	Vacuolar pr	K.EITGIGPSTTTETETIAK#.Y	123.30	67.51	1.83	0.55
P40336_VP	Vps26a	Vacuolar pr	K.ELALPGELTQSR.S	42.58	111.63	0.38	2.62
P40336_VP	Vps26a	Vacuolar pr	K.EYDLIVHQLATYPDVNNSIK#.M	110.89	53.78	2.06	0.48
P40336_VP	Vps26a	Vacuolar pr	R.FESPDSQASAEQPEM*.-	81.94	81.94	1.00	1.00
P40336_VP	Vps26a	Vacuolar pr	R.FESPDSQASAEQPEM.-	10.12	10.12	1.00	1.00
P40336_VP	Vps26a	Vacuolar pr	K.HYLFYDGESVSGK#.V	47.10	17.34	2.72	0.37
P40336_VP	Vps26a	Vacuolar pr	R.IEFVGQIELFNDK#.S	44.69	20.98	2.13	0.47
P40336_VP	Vps26a	Vacuolar pr	K.IQHMELQLIK#.K	35.93	18.82	1.91	0.52
P40336_VP	Vps26a	Vacuolar pr	K.IYFLLVR.I	27.85	60.34	0.46	2.17
P40336_VP	Vps26a	Vacuolar pr	R.LFLAGYDPTPTM*R.D	18.18	51.93	0.35	2.86
P40336_VP	Vps26a	Vacuolar pr	R.LFLAGYDPTPTMR.D	14.09	32.14	0.44	2.28
P40336_VP	Vps26a	Vacuolar pr	K.QQEIILWR.K	23.58	45.46	0.52	1.93
P40336_VP	Vps26a	Vacuolar pr	K.SNTHEFVNLVK#.E	38.35	22.53	1.70	0.59
P40336_VP	Vps26a	Vacuolar pr	R.SYDFEFM*QVEKPYESYIGANVR.L	7.57	13.70	0.55	1.81
P40336_VP	Vps26a	Vacuolar pr	K.EITGIGPSTTTETETIAK#.Y	23.46	10.68	2.20	0.46
P40336_VP	Vps26a	Vacuolar pr	K.EYDLIVHQLATYPDVNNSIK#.M	14.53	6.28	2.31	0.43
P40336_VP	Vps26a	Vacuolar pr	R.FESPDSQASAEQPEM*.-	11.96	11.96	1.00	1.00
P40336_VP	Vps26a	Vacuolar pr	K.HYLFYDGESVSGK#.V	9.80	3.84	2.55	0.39
P40336_VP	Vps26a	Vacuolar pr	R.LFLAGYDPTPTM*R.D	8.08	9.05	0.89	1.12
P40336_VP	Vps26a	Vacuolar pr	K.EITGIGPSTTTETETIAK#.Y	12.22	6.51	1.88	0.53
Q8C0E2_VP	Vps26b	Vacuolar pr	K.DLARPGEITQSQAFDFEFTHVEKPYESYTGQNVK.L	3.93	6.04	0.65	1.53
Q8C0E2_VP	Vps26b	Vacuolar pr	K.EMDIVVHTLSTYPELNSSIK#.M	14.33	7.64	1.87	0.53
Q8C0E2_VP	Vps26b	Vacuolar pr	R.FEGTTSLGEVR.T	23.02	39.99	0.58	1.74
Q8C0E2_VP	Vps26b	Vacuolar pr	R.GNHHEFVSLVK#.D	23.37	11.38	2.05	0.49
Q8C0E2_VP	Vps26b	Vacuolar pr	K.SM*SHQAAIASQR.F	1.52	4.45	0.34	2.93
Q8C0E2_VP	Vps26b	Vacuolar pr	R.TPGQLSDNNSR.Q	3.72	8.67	0.43	2.33
Q8C0E2_VP	Vps26b	Vacuolar pr	K.YFLFYDGETVSGK#.V	37.32	18.20	2.05	0.49
Q9D1C8_VI	Vps28	Vacuolar pr	R.EK#YDNM*AELFAVVK#.T	13.54	7.03	1.92	0.52
Q9D1C8_VI	Vps28	Vacuolar pr	R.LLVQYK#.A	47.77	16.80	2.84	0.35
Q9D1C8_VI	Vps28	Vacuolar pr	R.QM*LFDLESAYNAFNR.F	7.63	16.75	0.46	2.20
Q9D1C8_VI	Vps28	Vacuolar pr	K.YDNM*AELFAVVK#.T	28.97	15.64	1.85	0.54
Q9D1C8_VI	Vps28	Vacuolar pr	K.YDNMAELFAVVK#.T	17.10	9.99	1.71	0.58
Q9QZ88_VI	Vps29	Vacuolar pr	R.GDFDENLNYPEQK#.V	203.46	89.56	2.27	0.44
Q9QZ88_VI	Vps29	Vacuolar pr	K.IGLIHGHQVIPWGDM*ASLALLQR.Q	16.72	36.96	0.45	2.21
Q9QZ88_VI	Vps29	Vacuolar pr	K.IGLIHGHQVIPWGDMASLALLQR.Q	6.27	8.95	0.70	1.43
Q9QZ88_VI	Vps29	Vacuolar pr	K.K#LLVPGK#.I	44.73	22.48	1.99	0.50
Q9QZ88_VI	Vps29	Vacuolar pr	R.GDFDENLNYPEQK#.V	8.79	4.49	1.96	0.51
Q9QZ88_VI	Vps29	Vacuolar pr	R.GDFDENLNYPEQK#.V	14.84	6.15	2.41	0.41
Q9EQH3_VI	Vps35	Vacuolar pr	K.AELAELPLR.L	8.60	15.77	0.55	1.83
Q9EQH3_VI	Vps35	Vacuolar pr	R.ILVGTNLVR.L	11.64	21.13	0.55	1.82
Q9EQH3_VI	Vps35	Vacuolar pr	K.IPVDTYNNILTVLK#.L	40.74	20.55	1.98	0.50
Q9EQH3_VI	Vps35	Vacuolar pr	K.LFDIFSQQVATVIQSR.Q	8.41	11.73	0.72	1.40
Q9EQH3_VI	Vps35	Vacuolar pr	K.LLDEAIQAVK#.V	24.76	10.19	2.43	0.41
Q9EQH3_VI	Vps35	Vacuolar pr	K.NIIIALIDR.L	4.02	10.10	0.40	2.51
Q9EQH3_VI	Vps35	Vacuolar pr	R.SDDPDQQYLILNTAR.K	4.08	9.92	0.41	2.43
Q9EQH3_VI	Vps35	Vacuolar pr	K.VLETTVEIFNK#.L	28.23	10.84	2.61	0.38
Q9EQH3_VI	Vps35	Vacuolar pr	K.IREDLPNLESSEETEQINK.H	8.33	18.42	0.45	2.21
Q9EQH3_VI	Vps35	Vacuolar pr	K.AELAELPLR.L	20.34	45.30	0.45	2.23
Q9EQH3_VI	Vps35	Vacuolar pr	R.EDGPGIPAEIK#.L	36.58	13.99	2.61	0.38
Q9EQH3_VI	Vps35	Vacuolar pr	R.ESPESEGPIYEGLIL.-	61.99	61.99	1.00	1.00
Q9EQH3_VI	Vps35	Vacuolar pr	K.HASNM*LGELR.T	10.59	14.46	0.73	1.37
Q9EQH3_VI	Vps35	Vacuolar pr	R.ILVGTNLVR.L	39.06	73.24	0.53	1.88
Q9EQH3_VI	Vps35	Vacuolar pr	K.IPVDTYNNILTVLK#.L	149.34	58.16	2.57	0.39

Q9EQH3_V	Vps35	Vacuolar pr	K.IREDLPNLESSEETEQINK.H	20.06	34.23	0.59	1.71
Q9EQH3_V	Vps35	Vacuolar pr	R.KVADLYELVQYAGNIIPR.L	15.69	32.03	0.49	2.04
Q9EQH3_V	Vps35	Vacuolar pr	K.LFDIFSQQVATVIQSR.Q	34.88	52.02	0.67	1.49
Q9EQH3_V	Vps35	Vacuolar pr	K.LLDEAIQAVK#.V	72.41	26.93	2.69	0.37
Q9EQH3_V	Vps35	Vacuolar pr	R.LLK#IPVDTYNNILTVLK#.L	9.70	3.55	2.73	0.37
Q9EQH3_V	Vps35	Vacuolar pr	K.LNLEHIATSSAVSK#.E	116.52	44.62	2.61	0.38
Q9EQH3_V	Vps35	Vacuolar pr	R.LSQLEGVNVER.Y	33.37	70.71	0.47	2.12
Q9EQH3_V	Vps35	Vacuolar pr	K.NIIIALIDR.L	17.97	23.99	0.75	1.34
Q9EQH3_V	Vps35	Vacuolar pr	R.NILPDEGEPTDEETTGDISDSM*DFVLLNFAEM*NK#.L	6.11	4.72	1.29	0.77
Q9EQH3_V	Vps35	Vacuolar pr	R.SDDPDQQYLILNTAR.K	14.34	26.65	0.54	1.86
Q9EQH3_V	Vps35	Vacuolar pr	K.VLETTVEIFNK#.L	77.42	37.03	2.09	0.48
Q9EQH3_V	Vps35	Vacuolar pr	K.VQSFQM*K#.R	28.06	10.31	2.72	0.37
Q9EQH3_V	Vps35	Vacuolar pr	R.YIYFYEK#ENDAVTIQVLNQLIQK#.I	7.52	4.95	1.52	0.66
Q9EQH3_V	Vps35	Vacuolar pr	K.AELAELPLR.L	38.19	72.01	0.53	1.89
Q9EQH3_V	Vps35	Vacuolar pr	R.EDGPGIPAEIK#.L	81.95	33.48	2.45	0.41
Q9EQH3_V	Vps35	Vacuolar pr	R.EDLPNLESSEETEQINK#.H	11.96	4.25	2.81	0.36
Q9EQH3_V	Vps35	Vacuolar pr	K.ENDAVTIQVLNQLIQK#.I	15.79	8.40	1.88	0.53
Q9EQH3_V	Vps35	Vacuolar pr	R.ESPESEGPIYEGLIL.-	156.05	156.05	1.00	1.00
Q9EQH3_V	Vps35	Vacuolar pr	K.HASNM*LGELR.T	13.80	25.33	0.54	1.84
Q9EQH3_V	Vps35	Vacuolar pr	K.HASNMLGELR.T	8.90	13.34	0.67	1.50
Q9EQH3_V	Vps35	Vacuolar pr	R.ILVGTNLVR.L	63.32	110.06	0.58	1.74
Q9EQH3_V	Vps35	Vacuolar pr	K.IPVDTYNNILTVLK#.L	207.53	97.96	2.12	0.47
Q9EQH3_V	Vps35	Vacuolar pr	K.IREDLPNLESSEETEQINK.H	30.97	60.50	0.51	1.95
Q9EQH3_V	Vps35	Vacuolar pr	R.LALFAHREDGPGIPAEIK.L	9.67	23.00	0.42	2.38
Q9EQH3_V	Vps35	Vacuolar pr	K.LFDIFSQQVATVIQSR.Q	49.64	88.70	0.56	1.79
Q9EQH3_V	Vps35	Vacuolar pr	K.LLDEAIQAVK#.V	76.36	30.92	2.47	0.40
Q9EQH3_V	Vps35	Vacuolar pr	K.LNLEHIATSSAVSK#.E	225.31	89.77	2.51	0.40
Q9EQH3_V	Vps35	Vacuolar pr	R.LSQLEGVNVER.Y	50.91	89.76	0.57	1.76
Q9EQH3_V	Vps35	Vacuolar pr	K.NIIIALIDR.L	20.73	29.31	0.71	1.41
Q9EQH3_V	Vps35	Vacuolar pr	R.NILPDEGEPTDEETTGDISDSM*DFVLLNFAEM*NK#.L	21.75	7.66	2.84	0.35
Q9EQH3_V	Vps35	Vacuolar pr	R.QDM*PSEDVVSLQVSLINLAM*K#.C	16.67	6.89	2.42	0.41
Q9EQH3_V	Vps35	Vacuolar pr	R.SDDPDQQYLILNTAR.K	25.83	45.95	0.56	1.78
Q9EQH3_V	Vps35	Vacuolar pr	R.TSM*LSPK#.S	57.72	36.10	1.60	0.63
Q9EQH3_V	Vps35	Vacuolar pr	K.VLETTVEIFNK#.L	81.13	34.90	2.32	0.43
Q9EQH3_V	Vps35	Vacuolar pr	K.VQSFQM*K#.R	34.20	15.00	2.28	0.44
Q8CHS8_V	Vps37a	Vacuolar pr	K.SASSSAAGSPAGLTSLQQQK#.Q	5.29	3.46	1.53	0.65
Q8R0J7_VP	Vps37b	Vacuolar pr	R.GM*EEAQTVQLNK#.E	18.65	11.79	1.58	0.63
Q8R0J7_VP	Vps37b	Vacuolar pr	K.IEEDTENM*AEK#.F	7.83	4.25	1.84	0.54
Q8R0J7_VP	Vps37b	Vacuolar pr	R.SLAEGNLLYQPQLDAQK#.A	9.61	3.79	2.54	0.39
P46467_V	Vps4b	Vacuolar pr	K.AVATEANNSTFFSISSSDLVSK#.W	13.46	7.58	1.78	0.56
P46467_V	Vps4b	Vacuolar pr	K.AVATEANNSTFFSISSSDLVSK#.W	6.07	2.71	2.24	0.45
P46467_V	Vps4b	Vacuolar pr	K.GILLFGPPGTGK#.T	52.86	28.63	1.85	0.54
P46467_V	Vps4b	Vacuolar pr	R.LHLGSTQNSLTEADFQELGR.K	8.35	16.40	0.51	1.96
Q3UVL4_V	Vps51	Vacuolar pr	R.IDVFSPVEFNK#.V	11.90	7.33	1.62	0.62
Q62481_V	Vps72	Vacuolar pr	K.AYK#EPLK#.S	9.05	14.80	0.61	1.64
Q62481_V	Vps72	Vacuolar pr	R.DPVTDIPYATAR.A	4.92	10.34	0.48	2.10
Q62481_V	Vps72	Vacuolar pr	K.YITAHGLPPTASALGPGPPPPEPLPGSGPR.A	1.63	4.94	0.33	3.03
Q9CR26_V	Vta1	Vacuolar pr	K.YAGSALQYEDVGTAVQNLQK#.A	8.62	2.55	3.38	0.30
Q99KC8_V	Vwa5a	von Willebr	K.LSVNPAVFGV.-	10.09	10.09	1.00	1.00
Q99KC8_V	Vwa5a	von Willebr	R.VSGGTAVFITGK#.D	26.56	9.97	2.66	0.38
Q99KC8_V	Vwa5a	von Willebr	R.VTFSLQPK#.A	11.26	3.11	3.62	0.28
Q99KC8_V	Vwa5a	von Willebr	R.VSGGTAVFITGK#.D	19.91	9.89	2.01	0.50
Q65Z40_W	Wapal	Wings apar	K.DSQLIISSAK.A	10.80	21.20	0.51	1.96
Q65Z40_W	Wapal	Wings apar	K.LEFFGFEDHDETGGDEGGSGSSNYK#.I	7.50	4.43	1.69	0.59
Q65Z40_W	Wapal	Wings apar	R.LLELEQDASSAK#.L	12.25	10.42	1.18	0.85
Q65Z40_W	Wapal	Wings apar	R.LLELEQDASSAK#.L	27.20	17.45	1.56	0.64
Q65Z40_W	Wapal	Wings apar	K.RPNFKPDIQEIPK.K	3.15	8.79	0.36	2.80
Q65Z40_W	Wapal	Wings apar	R.SM*DEFTASTPADLGEAGR.L	3.79	5.62	0.67	1.48
Q65Z40_W	Wapal	Wings apar	R.VLESVTVHNPENQSYLIAYK#.D	15.71	10.18	1.54	0.65
P32921_SY	Wars	Tryptopha	K.ISFPAVQAAPSFSNSFPK#.I	5.10	1.75	2.91	0.34
Q8BH43_W	Wasf2	Wiskott-Al	K.MGQEFVESK#.E	10.97	2.16	5.07	0.20
Q8BH43_W	Wasf2	Wiskott-Al	R.TNITLANVIR.Q	10.05	11.68	0.86	1.16
Q8BH43_W	Wasf2	Wiskott-Al	K.VTQLDPKEEEVSLQGINTR.K	4.89	7.83	0.62	1.60
Q923D5_W	Wbp11	WW domai	R.SEDDSAVPVAK#.A	29.01	16.58	1.75	0.57
Q61048_W	Wbp4	WW domai	R.LGLPLPSDISEPTVSPVISTVQPTPTSNQQK#.E	12.27	7.70	1.59	0.63
Q61048_W	Wbp4	WW domai	K.TVSSLGVAADGVAPVFK#.K	16.73	15.47	1.08	0.92
Q61048_W	Wbp4	WW domai	K.TVSSLGVAADGVAPVFK#.K	5.48	4.06	1.35	0.74
P59328_W	Wdhd1	WD repeat	K.ADLSHKEEGDDDQAR.S	6.03	11.65	0.52	1.93
P59328_W	Wdhd1	WD repeat	K.LLAVPVEK.S	20.71	21.76	0.95	1.05
P59328_W	Wdhd1	WD repeat	K.SGAVFSSSQGWVNPFK#.V	7.22	11.06	0.65	1.53
P59328_W	Wdhd1	WD repeat	R.SQILSDNPDISDETDIIK.E	5.72	5.01	1.14	0.88
P59328_W	Wdhd1	WD repeat	R.VEKDYNDLFDGDDTSSAGDFLNDNAVEIPSFSK.G	3.26	3.58	0.91	1.10
P59328_W	Wdhd1	WD repeat	K.ADLSHKEEGDDDQAR.S	3.66	8.29	0.44	2.27
P59328_W	Wdhd1	WD repeat	K.SGAVFSSSQGWVNPFK.V	8.70	12.11	0.72	1.39
P59328_W	Wdhd1	WD repeat	R.SQILSDNPDISDETDIIK#.E	4.94	5.87	0.84	1.19
P59328_W	Wdhd1	WD repeat	R.VEK#DYNDLFDGDDTSSAGDFLNDNAVEIPSFSK#.G	4.18	4.89	0.85	1.17
P59328_W	Wdhd1	WD repeat	K.VVDVM*DNSQQQTFR.G	2.95	6.90	0.43	2.34
O88342_W	Wdr1	WD repeat-	R.DYSGQGVVK#.L	83.96	9.13	9.20	0.11
O88342_W	Wdr1	WD repeat-	R.FATASADGQIFIYDGK#.T	66.30	9.25	7.17	0.14
O88342_W	Wdr1	WD repeat-	K.FGAVFLWDTGSSVGEITGHNK#.V	93.28	14.02	6.66	0.15
O88342_W	Wdr1	WD repeat-	R.IAVVGEGR.E	47.48	26.40	1.80	0.56
O88342_W	Wdr1	WD repeat-	R.LHHVSSLAWLDEHTLVTTSHDASVK#.E	41.90	6.09	6.88	0.15
O88342_W	Wdr1	WD repeat-	K.SYIYSGSHDGHINYWDSETGENDSFSGK#.G	14.71	2.93	5.02	0.20
O88342_W	Wdr1	WD repeat-	K.VFASLPQVER.G	38.44	24.83	1.55	0.65
O88342_W	Wdr1	WD repeat-	K.VINSVDIK#.Q	113.55	12.86	8.83	0.11
O88342_W	Wdr1	WD repeat-	K.VVTVFSVADGYSENNVFYGHHAK#.I	24.38	3.91	6.24	0.16
O88342_W	Wdr1	WD repeat-	K.YAPSGFYIASGDISGK#.L	61.51	7.71	7.98	0.13
O88342_W	Wdr1	WD repeat-	K.YEYQPFAGK#.I	66.79	11.81	5.66	0.18
O88342_W	Wdr1	WD repeat-	K.YAPSGFYIASGDISGK#.L	4.32	1.73	2.49	0.40
O88342_W	Wdr1	WD repeat-	R.DYSGQGVVK#.L	73.48	8.62	8.52	0.12
O88342_W	Wdr1	WD repeat-	R.FATASADGQIFIYDGK#.T	37.19	4.13	9.01	0.11
O88342_W	Wdr1	WD repeat-	K.FGAVFLWDTGSSVGEITGHNK#.V	64.66	8.06	8.02	0.12
O88342_W	Wdr1	WD repeat-	R.LHHVSSLAWLDEHTLVTTSHDASVK#.E	37.57	3.64	10.32	0.10
O88342_W	Wdr1	WD repeat-	K.VVTVFSVADGYSENNVFYGHHAK#.I	73.18	8.76	8.35	0.12
O88342_W	Wdr1	WD repeat-	K.YAPSGFYIASGDISGK#.L	67.43	8.02	8.40	0.12
O88342_W	Wdr1	WD repeat-	K.YEYQPFAGK#.I	90.26	10.11	8.93	0.11
O88342_W	Wdr1	WD repeat-	R.DYSGQGVVK#.L	83.34	9.28	8.98	0.11
O88342_W	Wdr1	WD repeat-	R.FATASADGQIFIYDGK#.T	58.13	8.47	6.86	0.15
O88342_W	Wdr1	WD repeat-	K.FGAVFLWDTGSSVGEITGHNK#.V	57.31	13.86	4.14	0.24
O88342_W	Wdr1	WD repeat-	R.IAVVGEGR.E	35.52	18.64	1.91	0.52
O88342_W	Wdr1	WD repeat-	K.VFASLPQVER.G	24.87	15.86	1.57	0.64
O88342_W	Wdr1	WD repeat-	K.VINSVDIK#.Q	90.30	11.20	8.07	0.12
O88342_W	Wdr1	WD repeat-	K.VVTVFSVADGYSENNVFYGHHAK#.I	43.14	4.14	10.42	0.10

O88342_W	Wdr1	WD repeat-	K.YAPSGFYIASGDISGK#.L	68.45	9.38	7.30	0.14
O88342_W	Wdr1	WD repeat-	K.YEYQPFAGK#.I	85.38	11.20	7.63	0.13
Q8K1X1_W	Wdr11	WD repeat-	R.DLLNELGSTK#EELTES.-	5.10	2.58	1.98	0.50
Q8K1X1_W	Wdr11	WD repeat-	K.LLLDPDFSLLQR.C	5.55	7.05	0.79	1.27
Q8K1X1_W	Wdr11	WD repeat-	R.VNLQEVK#.R	10.93	7.71	1.42	0.71
Q8K1X1_W	Wdr11	WD repeat-	R.DLLLAIHPPNYIVLWNADTGTK#.L	3.73	8.66	0.43	2.32
Q8K1X1_W	Wdr11	WD repeat-	K.LLLDPDFSLLQR.C	5.74	15.76	0.36	2.75
Q8K1X1_W	Wdr11	WD repeat-	K.LPDLSLDNM*IGQSAIAGEEHPK#.G	6.12	4.62	1.32	0.76
Q8K1X1_W	Wdr11	WD repeat-	K.LPDLSLDNMIGQSAIAGEEHPK#.G	7.06	5.94	1.19	0.84
Q8K1X1_W	Wdr11	WD repeat-	R.YSLDISHIDYPENEEIK#.T	9.90	5.77	1.71	0.58
Q8K1X1_W	Wdr11	WD repeat-	K.GDTLVLGDM*DGNLNFWDLK.A	6.04	3.19	1.89	0.53
Q8K1X1_W	Wdr11	WD repeat-	K.LLLDPDFSLLQR.C	5.86	18.39	0.32	3.14
Q8K1X1_W	Wdr11	WD repeat-	K.LPDLSLDNM*IGQSAIAGEEHPK#.G	10.06	4.11	2.45	0.41
Q8K1X1_W	Wdr11	WD repeat-	R.YSLDISHIDYPENEEIK#.T	9.40	5.07	1.85	0.54
Q9JJA4_W	Wdr12	Ribosome	K.LYSYSYSPTTSHVGA.-	18.70	18.70	1.00	1.00
Q4VBE8_W	Wdr18	WD repeat-	K.HLLGAEHGDEAQGGGLR.L	7.54	20.19	0.37	2.68
Q4VBE8_W	Wdr18	WD repeat-	R.LEQLQAVLSSYLEK.N	6.63	5.23	1.27	0.79
Q4VBE8_W	Wdr18	WD repeat-	R.VATASLDQTVK#.L	43.00	51.39	0.84	1.20
Q4VBE8_W	Wdr18	WD repeat-	R.VFDLEDEVR.S	8.22	30.62	0.27	3.72
Q4VBE8_W	Wdr18	WD repeat-	R.EHSFQPEQNTGK#.V	2.65	2.94	0.90	1.11
Q4VBE8_W	Wdr18	WD repeat-	R.VATASLDQTVK#.L	25.13	17.09	1.47	0.68
Q4VBE8_W	Wdr18	WD repeat-	R.VFDLEDEVR.S	1.69	13.61	0.12	8.06
Q4VBE8_W	Wdr18	WD repeat-	R.VATASLDQTVK#.L	31.59	24.42	1.29	0.77
Q4VBE8_W	Wdr18	WD repeat-	R.VFDLEDEVR.S	6.35	13.06	0.49	2.06
Q8C6G8_W	Wdr26	WD repeat-	R.GYNFEDLTDR.N	2.50	8.98	0.28	3.59
Q8C6G8_W	Wdr26	WD repeat-	R.LALLNVATQGVHLWDLQDR.V	5.06	14.91	0.34	2.95
Q8C6G8_W	Wdr26	WD repeat-	K.YLEYLEDGKVLEALQVLR.C	2.18	4.48	0.49	2.06
Q3TAQ9_Q	Wdr36	Protein Wd	K.LEEGLLNNQYEAALNLLK#.E	5.42	3.73	1.45	0.69
Q3TAQ9_Q	Wdr36	Protein Wd	R.TLPSEPALLEELVK#.L	13.75	9.43	1.46	0.69
Q8CBE3_W	Wdr37	WD repeat-	R.LAGEGQAIDGAELSK#.G	18.55	12.53	1.48	0.68
Q6ZQL4_W	Wdr43	WD repeat-	K.LGSTEATIEER.L	3.02	16.04	0.19	5.32
Q6ZQL4_W	Wdr43	WD repeat-	K.LILLVTQVTASEK#.S	7.13	6.59	1.08	0.92
Q6ZQL4_W	Wdr43	WD repeat-	R.VVIPLLQELTK#.R	9.08	6.62	1.37	0.73
P61965_W	Wdr5	WD repeat-	K.FSPNGEWLASSSADK#.L	8.20	9.64	0.85	1.18
P61965_W	Wdr5	WD repeat-	K.LGISDVAWSSDSNLLVSASDDK#.T	7.90	5.80	1.36	0.73
P61965_W	Wdr5	WD repeat-	K.TLIDDDNPPVSFVK.F	26.19	34.08	0.77	1.30
P61965_W	Wdr5	WD repeat-	K.WIVSGSEDNLVYIWNLQTK.E	5.84	6.13	0.95	1.05
P61965_W	Wdr5	WD repeat-	K.YILAATLDNTLK#.L	120.41	50.61	2.38	0.42
Q99ME2_W	Wdr6	WD repeat-	R.GYPGLGVSSLSFK#.S	8.39	5.40	1.55	0.64
Q99ME2_W	Wdr6	WD repeat-	R.LLAGEGPDLLVYNLDLGGHLR.M	4.13	8.22	0.50	1.99
Q99ME2_W	Wdr6	WD repeat-	K.VVPINTPTAAVEQK#.L	10.76	6.26	1.72	0.58
Q99ME2_W	Wdr6	WD repeat-	R.VLAVTDVGSLYLYDLEVK#.S	14.06	6.41	2.19	0.46
Q99ME2_W	Wdr6	WD repeat-	K.VVPINTPTAAVEQK#.L	22.86	11.67	1.96	0.51
Q9ERF3_W	Wdr61	WD repeat-	K.ENIETVVTGSLDDLVK#.V	49.22	18.48	2.66	0.38
Q9ERF3_W	Wdr61	WD repeat-	K.FILSIAYSPDGK#.Y	19.61	8.04	2.44	0.41
Q9ERF3_W	Wdr61	WD repeat-	K.QEQAHDDAIWSVAWETNK#K#.E	12.53	3.84	3.26	0.31
Q9ERF3_W	Wdr61	WD repeat-	K.SIDAGPVDAWTLAFSPDSQYLATGTHMGK#.V	17.10	5.38	3.18	0.31
Q9ERF3_W	Wdr61	WD repeat-	R.SLTFSPDSQLLVTASDDGYIK#.I	27.76	11.28	2.46	0.41
Q9ERF3_W	Wdr61	WD repeat-	K.VNIFGVESGK#.K	44.64	8.32	5.36	0.19
Q9ERF3_W	Wdr61	WD repeat-	K.VNIFGVESGK#K#.E	25.68	9.90	2.59	0.39
Q3TWF6_W	Wdr70	WD repeat-	R.LVTGGYDYDVK#.F	20.72	9.62	2.15	0.46
A6PWY4_W	Wdr76	WD repeat-	R.ENANFFASLQLAESAAR.L	1.57	5.74	0.27	3.67
A6PWY4_W	Wdr76	WD repeat-	K.GAISSVALHPSEVR.T	2.73	11.43	0.24	4.18
A6PWY4_W	Wdr76	WD repeat-	K.SGQIGLWDLTQQSEDAM*YVFYAHSR.Y	2.14	4.11	0.52	1.92
A6PWY4_W	Wdr76	WD repeat-	K.SIASAYFSPVTGNR.V	4.44	8.80	0.50	1.98
A6PWY4_W	Wdr76	WD repeat-	K.SSVDAYTESTR.L	2.25	15.82	0.14	7.02
A6PWY4_W	Wdr76	WD repeat-	K.TWAEM*SQTSNEK.T	4.33	8.02	0.54	1.85
A6PWY4_W	Wdr76	WD repeat-	R.VFDSSSISSQLPLLSTIR.H	1.25	8.44	0.15	6.75
Q99J09_M	Wdr77	Methyloso	K.YEHDDIVSTVTVLSSGTQAVSGSK#.D	19.86	4.14	4.79	0.21
Q8BFQ4_W	Wdr82	WD repeat-	R.VVALSM*SPVDDTFISGSLDK.T	11.05	11.52	0.96	1.04
Q8BFQ4_W	Wdr82	WD repeat-	R.VVALSMSPVDDTFISGSLDK#.T	10.67	9.92	1.08	0.93
Q8BFQ4_W	Wdr82	WD repeat-	K.YGVDLIR.Y	4.20	18.98	0.22	4.52
Q8BFQ4_W	Wdr82	WD repeat-	R.YTHAANTVVYSSNK#.I	166.58	48.02	3.47	0.29
Q8BVE8_N	Whsc1	Histone-lys	K.AIEAASSLK.S	15.84	17.62	0.90	1.11
Q8BVE8_N	Whsc1	Histone-lys	K.FTFLYVGDQLHLNPQVAK.E	15.67	13.02	1.20	0.83
Q8BVE8_N	Whsc1	Histone-lys	R.SIKYDSLLEQGLVEAALVSK.I	12.93	10.16	1.27	0.79
Q8BVE8_N	Whsc1	Histone-lys	K.VQIYTADISEIPK#.C	9.19	10.47	0.88	1.14
Q8BVE8_N	Whsc1	Histone-lys	K.YNVGDLVWSK#.V	12.94	8.37	1.55	0.65
Q8BVE8_N	Whsc1	Histone-lys	K.VQIYTADISEIPK#.C	7.64	8.33	0.92	1.09
Q6P2L6_N	Whsc1l1	Histone-lys	K.EAIPVQPILSSVPTTETSTGVK#.F	11.54	8.18	1.41	0.71
Q6P2L6_N	Whsc1l1	Histone-lys	K.EAIPVQPILSSVPTTETSTGVK#.F	4.51	2.83	1.59	0.63
Q6P2L6_N	Whsc1l1	Histone-lys	K.FIDQFVYSTK#.G	15.02	9.97	1.51	0.66
Q6P2L6_N	Whsc1l1	Histone-lys	K.FQVGDLVWSK#.V	11.17	8.78	1.27	0.79
Q6P2L6_N	Whsc1l1	Histone-lys	R.SVLNSQPEQTNAGEVASSQSSTDLRR.Q	1.96	19.02	0.10	9.70
Q6P2L6_N	Whsc1l1	Histone-lys	R.VEQYTFIYIDK#QPEEASSQAK#.K	5.84	6.03	0.97	1.03
F6ZBR8_F6	Wiz	Protein Wi	R.AADSGERPLATSPPGTVK.S	5.01	30.76	0.16	6.14
F6ZBR8_F6	Wiz	Protein Wi	R.EDM*APLNLSAR.A	3.71	11.04	0.34	2.97
F6ZBR8_F6	Wiz	Protein Wi	R.ELSLSPITGSK#PSAASYLGPVATK#.R	19.14	24.33	0.79	1.27
F6ZBR8_F6	Wiz	Protein Wi	R.GGEEVNDLQQK.L	37.68	25.70	1.47	0.68
F6ZBR8_F6	Wiz	Protein Wi	K.GLPDAPLGLTPSLTK#.K	20.91	28.31	0.74	1.35
F6ZBR8_F6	Wiz	Protein Wi	K.GSPIDVLHGLIR.R	1.36	8.13	0.17	5.98
F6ZBR8_F6	Wiz	Protein Wi	K.KAPLTLAGSPTPK.N	14.76	16.70	0.88	1.13
F6ZBR8_F6	Wiz	Protein Wi	R.SAGGEPGLEAGR.A	5.41	25.79	0.21	4.77
F6ZBR8_F6	Wiz	Protein Wi	K.SLPVSGTLEQVASR.L	3.05	12.91	0.24	4.24
F6ZBR8_F6	Wiz	Protein Wi	R.SPSDLHISPLTK.K	9.05	15.31	0.59	1.69
F6ZBR8_F6	Wiz	Protein Wi	K.TYIQTELPFK#.A	21.14	22.34	0.95	1.06
F6ZBR8_F6	Wiz	Protein Wi	K.VLSTGGPGSSLEAR.S	13.48	48.16	0.28	3.57
P83741_W	Wnk1	Serine/thre	R.FQVTTTANK#.V	12.42	4.91	2.53	0.40
P83741_W	Wnk1	Serine/thre	R.SQQQDDIEELETK#.A	27.79	10.51	2.64	0.38
Q91XU0_W	Wrnip1	ATPase WR	K.AVDTLAYLSDGDAR.T	6.14	22.60	0.27	3.68
Q91XU0_W	Wrnip1	ATPase WR	R.FVTLSATNAK#.T	25.09	17.74	1.41	0.71
Q91XU0_W	Wrnip1	ATPase WR	K.SIEVYSAYNNVK#.A	13.79	20.22	0.68	1.47
Q91XU0_W	Wrnip1	ATPase WR	K.TTLAHIIANNSK#.K	12.61	5.72	2.20	0.45
Q91XU0_W	Wrnip1	ATPase WR	K.SIEVYSAYNNVK#.A	11.42	5.79	1.97	0.51
Q9ER69_FL	Wtap	Pre-mRNA-	R.M*LIQENQELGR.Q	3.53	7.40	0.48	2.09
Q9ER69_FL	Wtap	Pre-mRNA-	R.STM*VDPAINLFFLK#.M	12.50	7.76	1.61	0.62
Q9ER69_FL	Wtap	Pre-mRNA-	R.TTSSEPVDQAEVTSK.D	11.33	15.27	0.74	1.35
Q9ER69_FL	Wtap	Pre-mRNA-	K.YTDLNSNDVTGLR.E	3.72	13.47	0.28	3.62
Q9DCD2_S	Xab2	Pre-mRNA-	R.EIINTYTEAVQTVDPFK#.A	5.21	7.51	0.69	1.44
Q9DCD2_S	Xab2	Pre-mRNA-	R.HENYDEALK#.L	14.46	13.41	1.08	0.93
Q9DCD2_S	Xab2	Pre-mRNA-	K.LSPESAEEYIEYLK.S	8.55	9.39	0.91	1.10
Q9DCD2_S	Xab2	Pre-mRNA-	K.SSDRLDEAAQR.L	1.33	5.76	0.23	4.32
Q9DCD2_S	Xab2	Pre-mRNA-	R.AEQLAAEAERDQPPR.A	1.44	22.96	0.06	15.90

Q9DCD2_S	Xab2	Pre-mRNA-	R.DFTQVFDSYAQFEESM*IAAK#.M	9.12	7.40	1.23	0.81
Q9DCD2_S	Xab2	Pre-mRNA-	R.EIINTYTEAVQTVDPFK.A	17.32	15.15	1.14	0.87
Q9DCD2_S	Xab2	Pre-mRNA-	R.HENYDEALK#.L	22.27	16.64	1.34	0.75
Q9DCD2_S	Xab2	Pre-mRNA-	R.LATVVNDER.F	7.21	22.37	0.32	3.10
Q9DCD2_S	Xab2	Pre-mRNA-	K.LSPESAEEYIEYLK#.S	19.80	18.02	1.10	0.91
Q9DCD2_S	Xab2	Pre-mRNA-	K.M*ETASELGREEEDDVDLELR.L	3.69	13.04	0.28	3.53
Q9DCD2_S	Xab2	Pre-mRNA-	R.SERPDLVFEEEDLPYEEEIM*R.N	2.82	14.04	0.20	4.97
Q9DCD2_S	Xab2	Pre-mRNA-	R.SERPDLVFEEEDLPYEEEIMR.N	1.75	4.32	0.40	2.47
Q9DCD2_S	Xab2	Pre-mRNA-	K.VWSM*LADLEESLGTFQSTK#.A	11.07	4.24	2.61	0.38
Q6P1B1_X	Xpnpep1	Xaa-Pro am	R.GSLTFEPLTLVPIQTK#.M	20.30	2.93	6.94	0.14
Q6P1B1_X	Xpnpep1	Xaa-Pro am	R.TLSLDEVYLIDSGAQYK#.D	5.38	4.80	1.12	0.89
Q6P1B1_X	Xpnpep1	Xaa-Pro am	R.VGVDPLIIPTDYWK#.K	14.86	2.64	5.64	0.18
Q6P5F9_X	Xpo1	Exportin-1	K.EFAGEDTSDLFLEER.E	2.89	4.86	0.59	1.68
Q6P5F9_X	Xpo1	Exportin-1	K.AVGHPFVIQLGR.I	7.61	12.99	0.59	1.71
Q6P5F9_X	Xpo1	Exportin-1	R.ETLVYLTHLDYVDTEIIM*TK#.K	8.64	4.51	1.91	0.52
Q6P5F9_X	Xpo1	Exportin-1	K.LLSEEVFDFSSGQITQVK#.A	35.06	16.51	2.12	0.47
Q6P5F9_X	Xpo1	Exportin-1	R.VDTILEFSQNM*NTK#.Y	10.19	3.66	2.79	0.36
Q6P5F9_X	Xpo1	Exportin-1	K.YYGLQILENVIK#.T	65.71	19.50	3.37	0.30
Q6P5F9_X	Xpo1	Exportin-1	K.AIIASNIM*YIVGQYPR.F	3.72	7.44	0.50	2.00
Q6P5F9_X	Xpo1	Exportin-1	K.AIIASNIMYIVGQYPR.F	5.68	9.88	0.58	1.74
Q6P5F9_X	Xpo1	Exportin-1	K.AVGHPFVIQLGR.I	18.13	37.53	0.48	2.07
Q6P5F9_X	Xpo1	Exportin-1	K.DTDSINLYK#.N	32.57	15.42	2.11	0.47
Q6P5F9_X	Xpo1	Exportin-1	K.EFAGEDTSDLFLEER.E	11.16	18.96	0.59	1.70
Q6P5F9_X	Xpo1	Exportin-1	R.EPEVLSTM*AIIVNK#.L	18.07	11.25	1.61	0.62
Q6P5F9_X	Xpo1	Exportin-1	R.EPEVLSTMAIIVNK#.L	18.84	9.88	1.91	0.52
Q6P5F9_X	Xpo1	Exportin-1	R.FLVTVIK#.D	16.18	7.84	2.06	0.48
Q6P5F9_X	Xpo1	Exportin-1	R.IYLDMLNVYK#.C	29.00	16.30	1.78	0.56
Q6P5F9_X	Xpo1	Exportin-1	K.LISTLIYK#.F	63.50	31.29	2.03	0.49
Q6P5F9_X	Xpo1	Exportin-1	K.LLSEEVFDFSSGQITQVK#.A	105.46	42.36	2.49	0.40
Q6P5F9_X	Xpo1	Exportin-1	R.M*AQEVLTHLK#.E	39.51	17.75	2.23	0.45
Q6P5F9_X	Xpo1	Exportin-1	R.QLYLTVLSK#.V	37.28	15.26	2.44	0.41
Q6P5F9_X	Xpo1	Exportin-1	R.VDTILEFSQNM*NTK#.Y	33.05	14.25	2.32	0.43
Q6P5F9_X	Xpo1	Exportin-1	R.VDTILEFSQNMNTK#.Y	10.63	5.17	2.06	0.49
Q6P5F9_X	Xpo1	Exportin-1	K.YVVGLIIK#.T	32.53	10.22	3.18	0.31
Q6P5F9_X	Xpo1	Exportin-1	K.YYGLQILENVIK#.T	134.31	59.69	2.25	0.44
Q924C1_X	Xpo5	Exportin-5	K.ALDIVESEK#.T	28.38	14.44	1.97	0.51
Q924C1_X	Xpo5	Exportin-5	R.AVM*EQIPEINK#.E	8.40	3.43	2.45	0.41
Q924C1_X	Xpo5	Exportin-5	K.AVTVM*M*DPSSTQR.Y	3.90	8.05	0.48	2.06
Q924C1_X	Xpo5	Exportin-5	R.DPALLAVIPK#.Y	29.07	12.73	2.28	0.44
Q924C1_X	Xpo5	Exportin-5	K.LFSFVTFESVGESK#.A	40.08	12.17	3.29	0.30
Q924C1_X	Xpo5	Exportin-5	R.LLDNLLALVR.T	7.99	14.90	0.54	1.87
Q924C1_X	Xpo5	Exportin-5	K.TADHTAAPTADGDDEEM*M*ATEVAPSSVVELTDLGK#.C	3.48	2.36	1.47	0.68
Q924C1_X	Xpo5	Exportin-5	K.TAILGLPQPLLEFNDHPVYR.T	14.32	34.72	0.41	2.43
Q9EPK7_X	Xpo7	Exportin-7	R.LAASVPYVK#.A	13.96	4.40	3.17	0.32
Q9EPK7_X	Xpo7	Exportin-7	R.LYGDDALENALQTFIK#.L	14.22	4.45	3.19	0.31
Q9EPK7_X	Xpo7	Exportin-7	K.ATEPHM*LETYTPEVTK#.A	15.76	3.92	4.02	0.25
Q9EPK7_X	Xpo7	Exportin-7	R.LAASVPYVK#.A	45.84	10.59	4.33	0.23
Q9EPK7_X	Xpo7	Exportin-7	R.LYGDDALENALQTFIK#.L	29.19	5.14	5.67	0.18
Q9EPK7_X	Xpo7	Exportin-7	R.NSIVNSQPPEK#.Q	30.04	7.98	3.77	0.27
Q9EPK7_X	Xpo7	Exportin-7	K.SNYQLGELVK#.V	25.31	7.71	3.28	0.30
Q9CRT8_X	Xpot	Exportin-T	K.NAQEALEAIETK#.V	11.51	0.99	11.58	0.09
Q9CRT8_X	Xpot	Exportin-T	K.ANVEAIMLAVMK#.K	11.97	3.06	3.91	0.26
Q9CRT8_X	Xpot	Exportin-T	K.QLPVLSDQQK#.A	16.87	1.45	11.63	0.09
Q60596_X	Xrcc1	DNA repair	K.LLPHQLYGVVPQA.-	20.95	20.95	1.00	1.00
Q60596_X	Xrcc1	DNA repair	R.TPAAAPASTPAQR.A	4.34	14.42	0.30	3.33
Q60596_X	Xrcc1	DNA repair	K.DSPYGLSFVK#.F	12.49	9.44	1.32	0.76
Q60596_X	Xrcc1	DNA repair	K.LLPHQLYGVVPQA.-	29.57	29.57	1.00	1.00
Q60596_X	Xrcc1	DNA repair	R.TPAAAPASTPAQR.A	10.05	30.80	0.33	3.06
P27641_X	Xrcc5	X-ray repair	K.DEGPGSSITAEEATK#.F	23.08	6.93	3.33	0.30
P27641_X	Xrcc5	X-ray repair	R.FNSFLEALR.E	10.55	15.64	0.67	1.48
P27641_X	Xrcc5	X-ray repair	R.HLM*LPDFDLLEDIGNK#.I	45.00	15.79	2.85	0.35
P27641_X	Xrcc5	X-ray repair	K.K#NEEEDIVEDLFPTSK#.I	21.23	7.19	2.95	0.34
P27641_X	Xrcc5	X-ray repair	R.QVFSESK#DEIALVLYGTDGTDNALAGK#.D	5.65	2.27	2.49	0.40
P27641_X	Xrcc5	X-ray repair	R.SNPQVGVAFPYIK#.D	24.68	8.65	2.85	0.35
P27641_X	Xrcc5	X-ray repair	K.TLFPLTEVIK#.K	67.21	18.46	3.64	0.27
P27641_X	Xrcc5	X-ray repair	K.VGSVNPVENFR.F	17.42	22.89	0.76	1.31
P27641_X	Xrcc5	X-ray repair	K.K#NEEEDIVEDLFPTSK#.I	11.26	4.06	2.77	0.36
P27641_X	Xrcc5	X-ray repair	K.TLFPLTEVIK#.K	30.29	8.45	3.58	0.28
P23475_X	Xrcc6	X-ray repair	R.DTGIFLDLMHLK#.K	22.08	5.47	4.03	0.25
P23475_X	Xrcc6	X-ray repair	K.ELVYPPGYNPEGK#.V	13.96	4.94	2.82	0.35
P23475_X	Xrcc6	X-ray repair	R.LGSLADEFK#.E	30.35	9.33	3.25	0.31
P23475_X	Xrcc6	X-ray repair	K.NIYVLQDLDNPGAK#.R	31.10	12.75	2.44	0.41
P23475_X	Xrcc6	X-ray repair	K.VELSEEELK#.A	85.99	22.31	3.86	0.26
P23475_X	Xrcc6	X-ray repair	R.VLELDQFK#.G	51.43	14.94	3.44	0.29
P23475_X	Xrcc6	X-ray repair	K.VTANQEQIDK#.M	79.77	30.59	2.61	0.38
P97789_X	Xrn1	5'-3' exorib	R.APELFSYIAK#.N	46.05	20.44	2.25	0.44
P97789_X	Xrn1	5'-3' exorib	K.EAQSSQATPLQTNK#PGSSEATK#.M	19.49	10.03	1.94	0.51
P97789_X	Xrn1	5'-3' exorib	R.EYIDYEFSALK#.E	9.92	3.24	3.06	0.33
P97789_X	Xrn1	5'-3' exorib	K.FYIEEPPGTQK#.V	24.59	10.38	2.37	0.42
P97789_X	Xrn1	5'-3' exorib	K.QILPFVYQTIVK#.D	18.52	9.64	1.92	0.52
P97789_X	Xrn1	5'-3' exorib	K.VQEIITWLK#.G	25.30	10.17	2.49	0.40
P97789_X	Xrn1	5'-3' exorib	K.YLNEAAGAAAEEAK#.N	25.85	14.72	1.76	0.57
P97789_X	Xrn1	5'-3' exorib	K.YNPGYVLAGR.L	7.07	14.33	0.49	2.03
Q9DBR1_X	Xrn2	5'-3' exorib	R.DLTQNTAVSINFK#DPQFAEDYVFK#.A	19.20	7.65	2.51	0.40
Q9DBR1_X	Xrn2	5'-3' exorib	R.ELTM*ASLPFPFDVER.S	3.76	7.85	0.48	2.09
Q9DBR1_X	Xrn2	5'-3' exorib	K.NK#FDVDAADEK#.F	19.20	5.41	3.55	0.28
Q9DBR1_X	Xrn2	5'-3' exorib	K.NLTVILSDASAPGEGEHK#.I	17.50	12.56	1.39	0.72
Q9DBR1_X	Xrn2	5'-3' exorib	R.NSLGGDVLFVGK#.L	44.36	14.90	2.98	0.34
Q9DBR1_X	Xrn2	5'-3' exorib	K.TGGYLTESGYVNLQR.V	3.88	6.28	0.62	1.62
Q9DBR1_X	Xrn2	5'-3' exorib	K.YAWQGVALLPFVDER.R	7.62	10.56	0.72	1.38
Q9DBR1_X	Xrn2	5'-3' exorib	R.DLTQNTAVSINFK#DPQFAEDYVFK#.A	7.77	3.04	2.56	0.39
Q9DBR1_X	Xrn2	5'-3' exorib	R.ELTM*ASLPFPFDVER.S	4.20	5.99	0.70	1.42
Q9DBR1_X	Xrn2	5'-3' exorib	R.K#PATVLK#PGDWEK#.S	11.16	1.68	6.63	0.15
Q9DBR1_X	Xrn2	5'-3' exorib	K.NLTVILSDASAPGEGEHK#.I	14.37	6.72	2.14	0.47
Q9DBR1_X	Xrn2	5'-3' exorib	R.NSLGGDVLFVGK#.L	17.57	5.30	3.32	0.30
P62960_Y	Ybx1	Nuclease-s	K.AADPPAENSSAPEAEQGGAE.-	134.16	134.16	1.00	1.00
P62960_Y	Ybx1	Nuclease-s	R.EDGNEEDKENQGDETQGQQPPQR.R	43.91	140.72	0.31	3.20
P62960_Y	Ybx1	Nuclease-s	K.ENQGDETQGQQPPQR.R	1.36	9.15	0.15	6.71
P62960_Y	Ybx1	Nuclease-s	K.GAEAANVTGPGGVPVQGSK#.Y	607.17	367.87	1.65	0.61
P62960_Y	Ybx1	Nuclease-s	R.NDTK#EDVFVHQTAIK#.K	268.60	190.53	1.41	0.71
P62960_Y	Ybx1	Nuclease-s	R.NDTK#EDVFVHQTAIK#K#.N	314.83	191.13	1.65	0.61
P62960_Y	Ybx1	Nuclease-s	K.NEGSESAPEGQAQQR.R	8.66	25.78	0.34	2.98
P62960_Y	Ybx1	Nuclease-s	R.NYQQNYQNSESGEK#.N	19.28	11.65	1.65	0.60

P62960_YE	Ybx1	Nuclease-se	R.NYQQNYQNSESGEKNEGSESAPEGQAQQR.R	49.37	101.41	0.49	2.05
P62960_YE	Ybx1	Nuclease-se	R.RPQYSNPPVQGEVM*EGADNQGAGEQGRPVR.Q	4.96	41.71	0.12	8.40
P62960_YE	Ybx1	Nuclease-se	R.RPQYSNPPVQGEVM*EGADNQGAGEQGRPVR.Q	9.63	174.02	0.06	18.07
P62960_YE	Ybx1	Nuclease-se	R.RPQYSNPPVQGEVMEGADNQGAGEQGRPVR.Q	3.82	73.59	0.05	19.27
P62960_YE	Ybx1	Nuclease-se	R.SVGDGETVEFDVVEGEK#.G	788.97	300.88	2.62	0.38
P62960_YE	Ybx1	Nuclease-se	R.SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK.Y	34.10	17.25	1.98	0.51
P62960_YE	Ybx1	Nuclease-se	K.GAEAANVTGPGGVPVQGSK#.Y	40.64	29.84	1.36	0.73
P62960_YE	Ybx1	Nuclease-se	R.NDTK#EDVFVHQTAIK#K#.N	9.04	4.13	2.19	0.46
P62960_YE	Ybx1	Nuclease-se	R.SVGDGETVEFDVVEGEKGAEAANVTGPGGVPVQGSK.Y	2.84	2.43	1.17	0.86
Q9JKB3_YB	Ybx3	Y-box-bindi	K.AGEAPTENPAPATEQSSAE.-	31.62	31.62	1.00	1.00
Q9JKB3_YB	Ybx3	Y-box-bindi	K.DGVPEGTQLQAHR.N	2.43	12.76	0.19	5.26
Q9JKB3_YB	Ybx3	Y-box-bindi	K.GAEAANVTGPDGVPVEGSR.Y	19.95	98.76	0.20	4.95
Q9JKB3_YB	Ybx3	Y-box-bindi	R.SRPLNAVSQDGK.E	4.89	21.63	0.23	4.42
Q3TUF7_YE	Yeats2	YEATS doma	K.LLLIPQGAILR.A	2.47	15.36	0.16	6.23
Q3TUF7_YE	Yeats2	YEATS doma	K.TTLFTQAATAGQASLLK.L	2.69	5.75	0.47	2.14
Q9CR11_YE	Yeats4	YEATS doma	R.K#LEEDDQTK#DI.-	5.44	4.37	1.25	0.80
Q9CR11_YE	Yeats4	YEATS doma	K.LFQSDTNAM*LGK#.K	3.87	2.87	1.35	0.74
Q9CR11_YE	Yeats4	YEATS doma	R.K#LEEDDQTK#DI.-	21.04	15.72	1.34	0.75
Q9CR11_YE	Yeats4	YEATS doma	K.TSFEIAELK#.E	20.42	12.07	1.69	0.59
Q9CR11_YE	Yeats4	YEATS doma	R.VKGVTIVKPIVYGNVAR.Y	2.72	10.32	0.26	3.79
Q9CR11_YE	Yeats4	YEATS doma	R.VVTK#PPYEITETGWGEFEIIIK#.I	6.81	7.35	0.93	1.08
Q9CQW1_Y	Ykt6	Synaptobre	K.AAYDVSSFSFFQR.S	4.95	19.07	0.26	3.86
Q9CQW1_Y	Ykt6	Synaptobre	R.SDSLAGVVIADSEYPSR.V	1.85	6.24	0.30	3.37
Q9CQW1_Y	Ykt6	Synaptobre	R.VAFTLLEK#.V	8.70	8.08	1.08	0.93
D3YWX2_D	Ylpm1	YLP motif-c	K.AAQSNENLSDSQQEPTK#.S	4.17	5.51	0.76	1.32
D3YWX2_D	Ylpm1	YLP motif-c	R.AIGFVVGQTDWEK#.I	5.89	4.37	1.35	0.74
D3YWX2_D	Ylpm1	YLP motif-c	R.AIGFVVGQTDWEK#.I	14.59	20.62	0.71	1.41
D3YWX2_D	Ylpm1	YLP motif-c	K.ATVGQQHQQQPK.Q	1.69	3.24	0.52	1.92
D3YWX2_D	Ylpm1	YLP motif-c	R.DKEVEFGGPAPR.V	5.97	18.70	0.32	3.13
D3YWX2_D	Ylpm1	YLP motif-c	R.GPASQFYITPNTSLSPR.Q	1.57	7.67	0.20	4.90
D3YWX2_D	Ylpm1	YLP motif-c	K.IQSAAFSISADVK#.D	11.25	16.64	0.68	1.48
D3YWX2_D	Ylpm1	YLP motif-c	R.M*EDYLQLPDDYETR.A	1.53	7.97	0.19	5.20
D3YWX2_D	Ylpm1	YLP motif-c	R.M*PLPAPALGHQPPPVPR.V	3.79	19.72	0.19	5.20
D3YWX2_D	Ylpm1	YLP motif-c	R.MPLPAPALGHQPPPVPR.V	2.94	8.39	0.35	2.85
D3YWX2_D	Ylpm1	YLP motif-c	R.SLLQDAAIEEVEM*EDFDANIEDQK#EEK#.K	1.95	4.47	0.44	2.29
D3YWX2_D	Ylpm1	YLP motif-c	K.SQAEPLSGNKEPLADTSNNQQK.N	24.68	28.88	0.85	1.17
D3YWX2_D	Ylpm1	YLP motif-c	R.SSQGPSK#PQLPPPPSIPSGNK#.T	16.69	18.53	0.90	1.11
D3YWX2_D	Ylpm1	YLP motif-c	K.TAIQQEPLESGAK#.N	37.51	42.66	0.88	1.14
D3YWX2_D	Ylpm1	YLP motif-c	K.VFSSEQGLGESSALSQSIIAAK#.D	24.87	22.57	1.10	0.91
D3YWX2_D	Ylpm1	YLP motif-c	K.VFSSEQGLGESSALSQSIIAAK.D	10.06	7.36	1.37	0.73
D3YWX2_D	Ylpm1	YLP motif-c	K.VGSM*EGGAAAAALTADDFKPLGVGLSHSENHQEKDLPQPDSR.E	3.29	1.96	1.67	0.60
D3YWX2_D	Ylpm1	YLP motif-c	K.VNSFQTVK#.S	29.46	19.31	1.53	0.66
P62700_YP	Ypel5	Protein yip	R.ESEGFEEHVPSDNS.-	45.65	45.65	1.00	1.00
P62700_YP	Ypel5	Protein yip	K.LGWIYEFATEDSQR.Y	2.21	8.80	0.25	3.99
P62700_YP	Ypel5	Protein yip	K.VVNLQYSEVQDR.V	6.37	15.78	0.40	2.48
Q3U5F4_YF	Yrdc	YrdC domai	R.LPESEPVEAASPER.S	1.38	5.27	0.26	3.80
B2RR83_YT	Ythdc2	Probable A	K.VVLIVGETGSGK#.T	10.12	3.58	2.83	0.35
P59326_YT	Ythdf1	YTH domai	R.DTQEVPLEK#.A	63.77	56.93	1.12	0.89
P59326_YT	Ythdf1	YTH domai	R.LENNDNKPVTNSR.D	5.91	7.99	0.74	1.35
P59326_YT	Ythdf1	YTH domai	K.SGPIVGGALPPPPIK.H	5.22	4.99	1.04	0.96
P59326_YT	Ythdf1	YTH domai	K.SYSEDDIHR.S	6.50	23.97	0.27	3.69
P59326_YT	Ythdf1	YTH domai	K.HTTSIFDDFSHYEK#.R	19.79	18.71	1.06	0.95
P59326_YT	Ythdf1	YTH domai	R.LENNDNKPVTNSR.D	5.68	3.93	1.44	0.69
P59326_YT	Ythdf1	YTH domai	K.SGPIVGGALPPPPIK.H	3.76	5.87	0.64	1.56
P59326_YT	Ythdf1	YTH domai	K.SYSEDDIHR.S	3.95	18.40	0.21	4.65
Q91YT7_YT	Ythdf2	YTH domai	K.APGM*NTIDQGM*AALK.L	5.84	7.47	0.78	1.28
Q91YT7_YT	Ythdf2	YTH domai	K.LGSTEVASSVPK#.V	26.06	33.48	0.78	1.28
Q91YT7_YT	Ythdf2	YTH domai	K.LGSTEVASSVPK#.V	30.25	28.99	1.04	0.96
Q8BYK6_YT	Ythdf3	YTH domai	K.AINNYNPK#.D	11.16	9.52	1.17	0.85
Q8BYK6_YT	Ythdf3	YTH domai	R.AITDGQAGFGNDTLSK.V	21.65	22.96	0.94	1.06
Q8BYK6_YT	Ythdf3	YTH domai	K.GNVGIGGSAVPPPPIK.H	12.15	16.06	0.76	1.32
Q8BYK6_YT	Ythdf3	YTH domai	K.HTTSIFDDFAHYEK#.R	24.36	21.49	1.13	0.88
Q8BYK6_YT	Ythdf3	YTH domai	K.IGGDLTAAVTK#.T	17.63	23.26	0.76	1.32
Q8BYK6_YT	Ythdf3	YTH domai	K.VPGISSIEQGM*TGLK.I	14.02	14.01	1.00	1.00
Q8BYK6_YT	Ythdf3	YTH domai	K.VPGISSIEQGMTGLK.I	6.85	8.85	0.77	1.29
Q8BYK6_YT	Ythdf3	YTH domai	R.AITDGQAGFGNDTLSK.V	4.16	7.63	0.55	1.83
Q8BYK6_YT	Ythdf3	YTH domai	R.AITDGQAGFGNDTLSK#.V	28.52	19.93	1.43	0.70
Q8BYK6_YT	Ythdf3	YTH domai	K.GNVGIGGSAVPPPPIK#.H	10.33	10.88	0.95	1.05
Q8BYK6_YT	Ythdf3	YTH domai	K.HTTSIFDDFAHYEK#.R	23.20	19.27	1.20	0.83
Q8BYK6_YT	Ythdf3	YTH domai	K.IGGDLTAAVTK.T	17.33	20.48	0.85	1.18
Q8BYK6_YT	Ythdf3	YTH domai	K.VPGISSIEQGM*TGLK#.I	13.73	8.86	1.55	0.64
Q9CQV8_1	Ywhab	14-3-3 prot	K.DSTLIM*QLLR.D	28.45	37.67	0.76	1.32
Q9CQV8_1	Ywhab	14-3-3 prot	K.DSTLIMQLLR.D	69.17	78.32	0.88	1.13
Q9CQV8_1	Ywhab	14-3-3 prot	K.LAEQAER.Y	54.92	65.35	0.84	1.19
Q9CQV8_1	Ywhab	14-3-3 prot	R.NLLSVAYK#.N	494.89	155.24	3.19	0.31
Q9CQV8_1	Ywhab	14-3-3 prot	K.QTTVSNSQQAYQEAFEISK#.K	12.96	2.43	5.33	0.19
Q9CQV8_1	Ywhab	14-3-3 prot	K.TAFDEAIAELDTLNEESYK#.D	13.67	7.99	1.71	0.58
Q9CQV8_1	Ywhab	14-3-3 prot	R.YDDMAAAMK#.A	22.79	8.12	2.81	0.36
Q9CQV8_1	Ywhab	14-3-3 prot	R.YDDM*AAAM*K#.A	33.39	10.86	3.07	0.33
Q9CQV8_1	Ywhab	14-3-3 prot	R.YDDMAAAM*K#.A	38.41	13.56	2.83	0.35
Q9CQV8_1	Ywhab	14-3-3 prot	K.YLILNATQAESK#.V	29.55	7.44	3.97	0.25
Q9CQV8_1	Ywhab	14-3-3 prot	R.YLSEVASGENK#.Q	79.45	21.24	3.74	0.27
Q9CQV8_1	Ywhab	14-3-3 prot	K.AVTEQGHELSNEER.N	12.55	22.01	0.57	1.75
Q9CQV8_1	Ywhab	14-3-3 prot	R.DNLTLWTSENQGDEGDAGEGEN.-	3.55	3.55	1.00	1.00
Q9CQV8_1	Ywhab	14-3-3 prot	K.LAEQAER.Y	17.06	20.64	0.83	1.21
Q9CQV8_1	Ywhab	14-3-3 prot	K.M*KGDYFR.Y	10.87	8.63	1.26	0.79
Q9CQV8_1	Ywhab	14-3-3 prot	R.NLLSVAYK#.N	684.71	162.46	4.21	0.24
Q9CQV8_1	Ywhab	14-3-3 prot	K.QTTVSNSQQAYQEAFEISK#.K	24.89	7.83	3.18	0.31
Q9CQV8_1	Ywhab	14-3-3 prot	K.QTTVSNSQQAYQEAFEISK#K#.E	16.08	5.28	3.04	0.33
Q9CQV8_1	Ywhab	14-3-3 prot	R.VISSIEQK#.T	511.48	198.37	2.58	0.39
Q9CQV8_1	Ywhab	14-3-3 prot	R.YDDM*AAAM*K#.A	13.90	5.62	2.47	0.40
Q9CQV8_1	Ywhab	14-3-3 prot	K.YLILNATQAESK#.V	17.84	6.11	2.92	0.34
Q9CQV8_1	Ywhab	14-3-3 prot	R.YLSEVASGENK#.Q	96.62	45.55	2.12	0.47
Q9CQV8_1	Ywhab	14-3-3 prot	R.NLLSVAYK#.N	78.76	20.92	3.76	0.27
Q9CQV8_1	Ywhab	14-3-3 prot	R.VISSIEQK#.T	58.22	22.93	2.54	0.39
Q9CQV8_1	Ywhab	14-3-3 prot	R.YLSEVASGENK#.Q	21.82	3.78	5.78	0.17
Q9CQV8_1	Ywhab	14-3-3 prot	-.MTM*DKSELVQKAK.L	2.02	10.94	0.18	5.43
Q9CQV8_1	Ywhab	14-3-3 prot	R.NLLSVAYK#.N	99.30	30.97	3.21	0.31
Q9CQV8_1	Ywhab	14-3-3 prot	R.VISSIEQK#.T	81.17	44.48	1.82	0.55
P62259_14	Ywhae	14-3-3 prot	K.AAFDDAIAELDTLSEESYK#.D	181.50	42.52	4.27	0.23
P62259_14	Ywhae	14-3-3 prot	K.AAFDDAIAELDTLSEESYK#.D	89.76	24.35	3.69	0.27
P62259_14	Ywhae	14-3-3 prot	K.AASDIAM*TELPPTHPIR.L	22.20	24.89	0.89	1.12
P62259_14	Ywhae	14-3-3 prot	R.DNLTLWTSDM*QGDGEEQNK#.E	12.79	4.83	2.65	0.38

P62259_14	Ywhae	14-3-3 prot	R.DNLTLWTSDMQGDGEEQNK#.E	6.07	2.07	2.94	0.34
P62259_14	Ywhae	14-3-3 prot	R.DNLTLWTSDMQGDGEEQNK#EALQDVEDENQ.-	16.63	4.36	3.81	0.26
P62259_14	Ywhae	14-3-3 prot	K.EAAENSLVAYK#.A	430.51	104.60	4.12	0.24
P62259_14	Ywhae	14-3-3 prot	K.EALQDVEDENQ.-	71.80	71.80	1.00	1.00
P62259_14	Ywhae	14-3-3 prot	R.EDLVYQAK#.L	47.90	8.95	5.35	0.19
P62259_14	Ywhae	14-3-3 prot	K.EENK#GGEDK#LK#.M	3.20	2.59	1.23	0.81
P62259_14	Ywhae	14-3-3 prot	K.HLIPAANTGESK#.V	188.59	60.23	3.13	0.32
P62259_14	Ywhae	14-3-3 prot	R.IISSIEQK#.E	347.07	79.35	4.37	0.23
P62259_14	Ywhae	14-3-3 prot	R.K#EAAENSLVAYK#.A	17.10	7.56	2.26	0.44
P62259_14	Ywhae	14-3-3 prot	K.LAEQAERYDEM*VESM*KK.V	8.48	10.95	0.77	1.29
P62259_14	Ywhae	14-3-3 prot	R.QM*VETELK#.L	106.70	23.84	4.47	0.22
P62259_14	Ywhae	14-3-3 prot	K.VAGMDVELTVEER.N	8.69	11.23	0.77	1.29
P62259_14	Ywhae	14-3-3 prot	K.VFYYK#.M	285.61	62.58	4.56	0.22
P62259_14	Ywhae	14-3-3 prot	R.YDEMVESM*K#.K	16.94	2.38	7.12	0.14
P62259_14	Ywhae	14-3-3 prot	R.YLAEFATGNDR.K	88.40	30.80	2.87	0.35
P62259_14	Ywhae	14-3-3 prot	K.AAFDDAIAELDTLSEESYK#.D	2.54	2.69	0.95	1.06
P62259_14	Ywhae	14-3-3 prot	K.EAAENSLVAYK#.A	59.03	20.06	2.94	0.34
P62259_14	Ywhae	14-3-3 prot	K.EALQDVEDENQ.-	3.78	3.78	1.00	1.00
P62259_14	Ywhae	14-3-3 prot	R.IISSIEQK#.E	15.99	4.71	3.39	0.29
P62259_14	Ywhae	14-3-3 prot	K.VAGM*DVELTVEER.N	6.63	6.71	0.99	1.01
P62259_14	Ywhae	14-3-3 prot	K.EAAENSLVAYK#.A	24.85	6.49	3.83	0.26
P61982_14	Ywhag	14-3-3 prot	R.ATVVESSEK#.A	60.59	22.48	2.70	0.37
P61982_14	Ywhag	14-3-3 prot	K.AYSEAHEISK#.E	96.54	35.08	2.75	0.36
P61982_14	Ywhag	14-3-3 prot	R.DNLTLWTSDQQDDDGGEGNN.-	18.65	18.65	1.00	1.00
P61982_14	Ywhag	14-3-3 prot	K.NVTELNEPLSNEER.N	45.05	69.92	0.64	1.55
P61982_14	Ywhag	14-3-3 prot	K.TAFDDAIAELDTLNEDSYK#.D	51.84	14.49	3.58	0.28
P61982_14	Ywhag	14-3-3 prot	R.YLAEVATGEK#.R	214.46	73.89	2.90	0.34
P61982_14	Ywhag	14-3-3 prot	R.ATVVESSEK#.A	33.92	23.58	1.44	0.70
P61982_14	Ywhag	14-3-3 prot	K.AYSEAHEISK#.E	31.02	9.88	3.14	0.32
P61982_14	Ywhag	14-3-3 prot	R.DNLTLWTSDQQDDDGGEGNN.-	21.93	21.93	1.00	1.00
P61982_14	Ywhag	14-3-3 prot	K.NVTELNEPLSNEER.N	27.84	44.64	0.62	1.60
P61982_14	Ywhag	14-3-3 prot	K.TAFDDAIAELDTLNEDSYK#.D	14.31	4.64	3.08	0.32
P61982_14	Ywhag	14-3-3 prot	R.YLAEVATGEK#.R	113.17	43.36	2.61	0.38
P61982_14	Ywhag	14-3-3 prot	R.YLAEVATGEKR.A	7.23	11.29	0.64	1.56
P68510_14	Ywhah	14-3-3 prot	R.YLAEVASGEK#.K	57.68	21.39	2.70	0.37
P68510_14	Ywhah	14-3-3 prot	K.AVTELNEPLSNEDR.N	14.20	20.99	0.68	1.48
P68510_14	Ywhah	14-3-3 prot	R.DNLTLWTSDQQDEEAGEGN.-	17.13	17.13	1.00	1.00
P68510_14	Ywhah	14-3-3 prot	K.K#NSVVEASEAAYK#.E	11.82	4.29	2.76	0.36
P68510_14	Ywhah	14-3-3 prot	K.K#NSVVEASEAAYK#EAFEISK#.E	9.86	2.36	4.17	0.24
P68510_14	Ywhah	14-3-3 prot	K.NSVVEASEAAYK#.E	94.36	32.49	2.90	0.34
P68510_14	Ywhah	14-3-3 prot	K.NSVVEASEAAYK#EAFEISK#.E	73.97	19.82	3.73	0.27
P68510_14	Ywhah	14-3-3 prot	K.QAFDDAIAELDTLNEDSYK#.D	9.23	2.14	4.32	0.23
P68510_14	Ywhah	14-3-3 prot	K.QAFDDAIAELDTLNEDSYK#.D	6.25	2.26	2.77	0.36
P68510_14	Ywhah	14-3-3 prot	R.YDDM*ASAM*K#.A	5.02	1.34	3.76	0.27
P68510_14	Ywhah	14-3-3 prot	R.YLAEVASGEK#.K	114.55	44.13	2.60	0.39
P68510_14	Ywhah	14-3-3 prot	R.YLAEVASGEK#K#.N	43.48	2.54	17.09	0.06
P68510_14	Ywhah	14-3-3 prot	K.AVTELNEPLSNEDR.N	4.72	7.10	0.66	1.51
P68254_14	Ywhaq	14-3-3 prot	K.AVTEQGAELSNEER.N	15.55	20.82	0.75	1.34
P68254_14	Ywhaq	14-3-3 prot	R.K#QTIENSQGAYQEAFDISK#K#.E	5.68	13.02	0.44	2.29
P68254_14	Ywhaq	14-3-3 prot	K.YLIANATNPESK#.V	15.09	4.65	3.25	0.31
P68254_14	Ywhaq	14-3-3 prot	K.AVTEQGAELSNEER.N	18.47	32.67	0.57	1.77
P68254_14	Ywhaq	14-3-3 prot	R.K#QTIENSQGAYQEAFDISK#.K	4.37	1.76	2.48	0.40
P68254_14	Ywhaq	14-3-3 prot	R.K#QTIENSQGAYQEAFDISK#K#.E	10.57	2.72	3.88	0.26
P68254_14	Ywhaq	14-3-3 prot	K.QTIENSQGAYQEAFDISK#K#.E	13.59	3.68	3.69	0.27
P68254_14	Ywhaq	14-3-3 prot	K.AVTEQGAELSNEER.N	7.32	10.34	0.71	1.41
P63101_14	Ywhaz	14-3-3 prot	R.DNLTLWTSDTQGDEAEAGEGGEN.-	8.08	8.08	1.00	1.00
P63101_14	Ywhaz	14-3-3 prot	K.FLIPNASQPESK#.V	289.54	82.80	3.50	0.29
P63101_14	Ywhaz	14-3-3 prot	K.GIVDQSQQAYQEAFEISK#.K	132.92	38.63	3.44	0.29
P63101_14	Ywhaz	14-3-3 prot	K.K#GIVDQSQQAYQEAFEISK#.K	13.93	2.27	6.13	0.16
P63101_14	Ywhaz	14-3-3 prot	K.SVTEQGAELSNEER.N	70.37	85.14	0.83	1.21
P63101_14	Ywhaz	14-3-3 prot	K.TAFDEAIAELDTLSEESYK#.D	98.79	30.64	3.22	0.31
P63101_14	Ywhaz	14-3-3 prot	R.VVSSIEQK#.T	258.18	63.17	4.09	0.24
P63101_14	Ywhaz	14-3-3 prot	R.YLAEVAAGDDK#K#.G	157.71	35.03	4.50	0.22
P63101_14	Ywhaz	14-3-3 prot	R.DNLTLWTSDTQGDEAEAGEGGEN.-	7.88	7.88	1.00	1.00
P63101_14	Ywhaz	14-3-3 prot	K.FLIPNASQPESK#.V	428.27	116.84	3.67	0.27
P63101_14	Ywhaz	14-3-3 prot	K.GIVDQSQQAYQEAFEISK#.K	138.19	39.31	3.52	0.28
P63101_14	Ywhaz	14-3-3 prot	K.GIVDQSQQAYQEAFEISK#.K	65.54	16.22	4.04	0.25
P63101_14	Ywhaz	14-3-3 prot	K.K#GIVDQSQQAYQEAFEISK#.K	18.55	5.37	3.46	0.29
P63101_14	Ywhaz	14-3-3 prot	K.SVTEQGAELSNEER.N	111.92	145.15	0.77	1.30
P63101_14	Ywhaz	14-3-3 prot	K.TAFDEAIAELDTLSEESYK#.D	96.51	27.56	3.50	0.29
P63101_14	Ywhaz	14-3-3 prot	R.VVSSIEQK#.T	314.39	87.87	3.58	0.28
P63101_14	Ywhaz	14-3-3 prot	R.YLAEVAAGDDK#K#.G	113.34	28.70	3.95	0.25
P63101_14	Ywhaz	14-3-3 prot	K.FLIPNASQPESK#.V	34.53	9.10	3.79	0.26
P63101_14	Ywhaz	14-3-3 prot	K.GIVDQSQQAYQEAFEISK#.K	16.38	5.70	2.87	0.35
P63101_14	Ywhaz	14-3-3 prot	K.GIVDQSQQAYQEAFEISK#K#.E	16.81	2.72	6.18	0.16
P63101_14	Ywhaz	14-3-3 prot	K.SVTEQGAELSNEER.N	13.03	12.17	1.07	0.93
P63101_14	Ywhaz	14-3-3 prot	K.TAFDEAIAELDTLSEESYK#.D	21.30	5.84	3.65	0.27
P63101_14	Ywhaz	14-3-3 prot	R.VVSSIEQK#.T	37.02	9.66	3.83	0.26
P63101_14	Ywhaz	14-3-3 prot	R.YLAEVAAGDDK#K#.G	16.55	3.58	4.63	0.22
P63101_14	Ywhaz	14-3-3 prot	K.GIVDQSQQAYQEAFEISK#.K	16.21	6.34	2.56	0.39
P63101_14	Ywhaz	14-3-3 prot	K.SVTEQGAELSNEER.N	11.95	17.03	0.70	1.43
P63101_14	Ywhaz	14-3-3 prot	K.TAFDEAIAELDTLSEESYK#.D	20.28	3.18	6.38	0.16
P63101_14	Ywhaz	14-3-3 prot	R.YLAEVAAGDDK#K#.G	17.63	4.85	3.64	0.27
Q00899_TY	Yy1	Transcripti	R.FSLDFNLR.T	1.69	13.24	0.13	7.86
Q00899_TY	Yy1	Transcripti	K.SYLGGGAGAAGGGGADPGNK#.K	21.64	17.91	1.21	0.83
Q00899_TY	Yy1	Transcripti	K.SYLGGGAGAAGGGGADPGNK#K#.W	5.04	2.45	2.05	0.49
Q9QY24_ZB	Zbp1	Z-DNA-bind	K.ILQVLSDDGGPVK#.I	20.94	8.08	2.59	0.39
Q8K0L9_ZB	Zbtb20	Zinc finger	K.LLLGYSDIEIPSVVSVQSVQK#.L	12.06	11.57	1.04	0.96
Q8K0L9_ZB	Zbtb20	Zinc finger	K.LLLGYSDIEIPSVVSVQSVQK#.L	3.77	2.80	1.35	0.74
Q8BJH1_ZC	Zc2hc1a	Zinc finger	R.AIAAPQAGANTK#.A	29.32	24.58	1.19	0.84
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.LK#AEEPSGADDSPSGTK#.S	9.74	14.94	0.65	1.53
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.DSSVLSSAQAASEPLLPEGSGPSSSQTATKPR.R	1.49	3.20	0.47	2.14
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.GEVETSGIGDSILNVK#.C	12.36	11.72	1.05	0.95
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.K#VESPETNIDK#APK#.K	25.34	21.11	1.20	0.83
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.LK#AEEPSGADDSPSGTK#.S	49.75	39.29	1.27	0.79
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.LSVQSNPSPQLR.S	8.94	29.62	0.30	3.31
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.M*EANETSDETISDPTK#.L	11.71	13.91	0.84	1.19
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.MEANETSDETISDPTK#.L	5.75	6.14	0.94	1.07
Q6NZF1_ZC	Zc3h11a	Zinc finger	R.RLSSASTGKPPLSVEDDFEK.L	1.84	6.11	0.30	3.32
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.TLEEILLER.A	29.51	31.36	0.94	1.06
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.TVLPTVPESQEEEVK#.T	10.39	12.78	0.81	1.23
Q6NZF1_ZC	Zc3h11a	Zinc finger	K.TVSLPTVAVSK#.G	27.75	22.57	1.23	0.81
Q6NZF1_ZC	Zc3h11a	Zinc finger	R.VAGKPVLTAVSGVTR.H	10.77	23.48	0.46	2.18

Q6NZF1_ZC	Zc3h11a	Zinc finger	R.YVDGLFLPPSK#.T	11.54	10.30	1.12	0.89
Q8BJ05_ZC	Zc3h14	Zinc finger	K.AISEAQESVTK#.T	52.93	55.85	0.95	1.06
Q8BJ05_ZC	Zc3h14	Zinc finger	R.FSHDGEEEEEDEDYGTR.I	3.01	16.15	0.19	5.37
Q8BJ05_ZC	Zc3h14	Zinc finger	R.KLPVVSSVVK.V	16.63	17.85	0.93	1.07
Q8BJ05_ZC	Zc3h14	Zinc finger	K.LSEEIVVTPNQDSGM*K#.T	7.38	9.44	0.78	1.28
Q8BJ05_ZC	Zc3h14	Zinc finger	K.QLDVQSSQVSEAGR.L	3.17	12.64	0.25	3.98
Q8BJ05_ZC	Zc3h14	Zinc finger	K.SPDASIFDSHVPSNK#.S	15.75	18.02	0.87	1.14
Q8BJ05_ZC	Zc3h14	Zinc finger	K.TTNYSAVPQK.Q	27.97	28.34	0.99	1.01
Q3TIV5_ZC	Zc3h15	Zinc finger	R.DVEETGITVASVER.F	11.88	36.84	0.32	3.10
Q3TIV5_ZC	Zc3h15	Zinc finger	R.EVFEFRPELVNDDDEEADDTR.Y	4.55	21.69	0.21	4.77
Q3TIV5_ZC	Zc3h15	Zinc finger	R.FSTYAPDK#DENK#.L	17.98	11.72	1.53	0.65
Q3TIV5_ZC	Zc3h15	Zinc finger	R.HFLEAIENNK#.Y	13.92	8.34	1.67	0.60
Q3TIV5_ZC	Zc3h15	Zinc finger	K.IDKLEQDM*ER.R	5.78	12.90	0.45	2.23
Q3TIV5_ZC	Zc3h15	Zinc finger	K.ITLESFLAWK#.K	60.76	33.90	1.79	0.56
Q3TIV5_ZC	Zc3h15	Zinc finger	R.SALGPNVTK#.I	62.38	42.05	1.48	0.67
Q3TIV5_ZC	Zc3h15	Zinc finger	R.DVEETGITVASVER.F	3.16	13.77	0.23	4.35
Q0P678_Z	Zc3h18	Zinc finger	K.AGAEEEEEK#GEGAPGEEGK#PDVQSVGEQEPTEAAK#.E	14.60	13.91	1.05	0.95
Q0P678_Z	Zc3h18	Zinc finger	R.ASDLEEEENATR.V	12.59	46.81	0.27	3.72
Q0P678_Z	Zc3h18	Zinc finger	K.ASQQAAAPQPAVPGQPQQGSFVAHK#.E	102.64	81.67	1.26	0.80
Q0P678_Z	Zc3h18	Zinc finger	K.AVEDAIAR.K	9.98	37.09	0.27	3.72
Q0P678_Z	Zc3h18	Zinc finger	R.DTTLEPYADPYYDYEIER.F	5.89	22.45	0.26	3.81
Q0P678_Z	Zc3h18	Zinc finger	R.ELDEHELDYDEEVPEEPAPAAQEEEAEK#.A	11.19	8.29	1.35	0.74
Q0P678_Z	Zc3h18	Zinc finger	K.ESTSVGPQVK#.R	54.89	52.71	1.04	0.96
Q0P678_Z	Zc3h18	Zinc finger	R.GGQYENFR.V	753.82	11.76	64.08	0.02
Q0P678_Z	Zc3h18	Zinc finger	K.GNYSLITK#.A	37.64	20.55	1.83	0.55
Q0P678_Z	Zc3h18	Zinc finger	R.KEQEPDFEEKR.F	4.92	17.48	0.28	3.55
Q0P678_Z	Zc3h18	Zinc finger	K.KPAPPPAPPQATK.T	23.37	29.83	0.78	1.28
Q0P678_Z	Zc3h18	Zinc finger	K.K#PAPPPAPPQATK#.T	42.75	54.81	0.78	1.28
Q0P678_Z	Zc3h18	Zinc finger	K.SQDQDSEAHELSR.G	2.95	7.87	0.38	2.66
Q0P678_Z	Zc3h18	Zinc finger	R.TK#GEPAPPPGK#.A	17.32	23.15	0.75	1.34
Q0P678_Z	Zc3h18	Zinc finger	K.AGAEEEEEK#GEGAPGEEGK#PDVQSVGEQEPTEAAK#.E	8.98	6.26	1.43	0.70
Q0P678_Z	Zc3h18	Zinc finger	K.ASQQAAAPQPAVPGQPQQGSFVAHK#.E	25.02	17.84	1.40	0.71
Q0P678_Z	Zc3h18	Zinc finger	R.DTTLEPYADPYYDYEIER.F	2.27	8.46	0.27	3.73
Q0P678_Z	Zc3h18	Zinc finger	K.ESTSVGPQVK#.R	31.66	17.58	1.80	0.56
Q6ZPZ3_ZC	Zc3h4	Zinc finger	K.GQPPAEEEEGER.A	3.55	9.36	0.38	2.64
Q6ZPZ3_ZC	Zc3h4	Zinc finger	R.HAETSGGSGPGDSGPSDPR.L	2.01	8.73	0.23	4.35
Q6ZPZ3_ZC	Zc3h4	Zinc finger	R.VLAAGGLGQGSSSGQSSVLSGISLYDPR.T	3.32	5.22	0.64	1.57
Q6ZPZ3_ZC	Zc3h4	Zinc finger	K.AEGSLHSSPAGPSSSK#.G	5.50	6.25	0.88	1.14
Q6ZPZ3_ZC	Zc3h4	Zinc finger	K.AGAGVPDFLPSAQR.A	4.08	11.61	0.35	2.84
Q6ZPZ3_ZC	Zc3h4	Zinc finger	K.IPSLFEIVVRPTGQLAEK.L	4.32	16.13	0.27	3.73
Q6ZPZ3_ZC	Zc3h4	Zinc finger	R.QRPGSTDPSTSGSNLPDFELLSR.I	2.14	11.39	0.19	5.32
Q6ZPZ3_ZC	Zc3h4	Zinc finger	K.TAEPASDTSAQPK#.G	18.39	21.93	0.84	1.19
Q6ZPZ3_ZC	Zc3h4	Zinc finger	R.VLAAGGLGQGSSSGQSSVLSGISLYDPR.T	4.60	15.48	0.30	3.37
F8VPP8_F8	Zc3h7b	Protein Zc3	R.DLLFDPLGGVK.R	10.10	34.09	0.30	3.37
F8VPP8_F8	Zc3h7b	Protein Zc3	K.GLQFIQSTLPLK#QEEYEAFLLK#.L	7.44	9.47	0.79	1.27
F8VPP8_F8	Zc3h7b	Protein Zc3	K.VFTSDSDASGWAYR.F	1.36	6.57	0.21	4.82
Q3UPF5_Z	Zc3hav1	Zinc finger	R.ASQEFLEDGDPDGLFSR.N	2.09	4.20	0.50	2.01
Q3UPF5_Z	Zc3hav1	Zinc finger	K.YSHDVLSEQNFQVLK#.N	8.80	6.30	1.40	0.72
Q3UPF5_Z	Zc3hav1	Zinc finger	R.FVLLETGDQAGITR.S	3.00	10.53	0.28	3.51
Q3UPF5_Z	Zc3hav1	Zinc finger	R.FVLLETGDQAGITR.S	2.00	10.97	0.18	5.49
Q3UPF5_Z	Zc3hav1	Zinc finger	R.TSAAGFPLVAAQR.N	5.50	12.11	0.45	2.20
Q3UPF5_Z	Zc3hav1	Zinc finger	R.ASQEFLEDGDPDGLFSR.N	2.86	7.45	0.38	2.61
Q3UPF5_Z	Zc3hav1	Zinc finger	R.TSAAGFPLVAAQR.N	1.88	13.99	0.13	7.46
Q80YV2_NI	Zc3hc1	Nuclear-int	R.ELIDEGIVPEEGGTEPK#.D	9.41	9.30	1.01	0.99
Q80YV2_NI	Zc3hc1	Nuclear-int	R.SNQPAETDSMSLSEK#.S	6.90	5.55	1.24	0.80
Q80YV2_NI	Zc3hc1	Nuclear-int	R.SNQPAETDSM*SLSEK#.S	10.45	7.86	1.33	0.75
Q80YV2_NI	Zc3hc1	Nuclear-int	R.SQDATVSPGSEQSEK#.S	8.09	4.07	1.99	0.50
B2RX14_TL	Zcchc11	Terminal ur	K.SALENSSLSQK#.Q	16.81	19.98	0.84	1.19
B2RX14_TL	Zcchc11	Terminal ur	R.SPLEPENVPSLLLK#.E	18.29	4.68	3.91	0.26
Q8VD24_Z	Zcchc18	Zinc finger	-.M*ASLLAR.M	22.10	39.12	0.56	1.77
B2RVL6_ZC	Zcchc24	Zinc finger	R.GEALSSSVYR.N	5.27	12.82	0.41	2.43
Q9CYA6_ZC	Zcchc8	Zinc finger	R.FK#PGVISEELQDALGVTDK#.S	21.29	11.55	1.84	0.54
Q9CYA6_ZC	Zcchc8	Zinc finger	K.YQQVFSHIVPLEGQEM*QVK#.A	11.07	4.73	2.34	0.43
Q9CYA6_ZC	Zcchc8	Zinc finger	K.EAELENSGLALYDGNDDADGETETGEIQNK#.N	7.96	3.34	2.38	0.42
Q9CYA6_ZC	Zcchc8	Zinc finger	R.FK#PGVISEELQDALGVTDK#.S	62.93	47.89	1.31	0.76
Q9CYA6_ZC	Zcchc8	Zinc finger	K.LGQPLLNENPQLTEGWEIPK#.Y	5.52	4.18	1.32	0.76
Q9CYA6_ZC	Zcchc8	Zinc finger	K.LGQPLLNENPQLTEGWEIPK#.Y	15.05	9.33	1.61	0.62
Q9CYA6_ZC	Zcchc8	Zinc finger	K.LVNYPGFNISTPR.G	11.01	24.90	0.44	2.26
Q9CYA6_ZC	Zcchc8	Zinc finger	R.QLGYPPGWLK#.E	9.04	6.06	1.49	0.67
Q9CYA6_ZC	Zcchc8	Zinc finger	K.QYHQEIEEFVSNLVK#.R	18.64	13.82	1.35	0.74
Q9CYA6_ZC	Zcchc8	Zinc finger	R.FK#PGVISEELQDALGVTDK#.S	21.51	15.42	1.40	0.72
Q8R1J3_ZC	Zcchc9	Zinc finger	R.ANVDPALGEFPFAK#.C	7.30	3.31	2.21	0.45
Q61329_ZF	Zfhx3	Zinc finger	K.GLPEEDEDLGQIFTIR.R	2.03	8.95	0.23	4.40
E9QML5_E	Zfml	Zinc finger	R.NK#ETLSNETVSSNVIDYGHASK#.Y	6.09	3.85	1.58	0.63
E9QML5_E	Zfml	Zinc finger	K.QSSVTQVTEQSPK.V	11.17	13.34	0.84	1.19
E9QML5_E	Zfml	Zinc finger	K.SENLEDDTLPEGK#.Q	14.95	10.38	1.44	0.69
E9QML5_E	Zfml	Zinc finger	K.SM*TSDVPGDLDFLVPK#.A	5.65	5.60	1.01	0.99
E9QML5_E	Zfml	Zinc finger	R.SPFGIVK#.A	19.98	15.00	1.33	0.75
E9QML5_E	Zfml	Zinc finger	K.SSVLTVSNVYSSK#.S	10.82	50.25	0.22	4.64
E9QML5_E	Zfml	Zinc finger	K.TMETVSSSSSAK#.S	6.02	7.17	0.84	1.19
E9QML5_E	Zfml	Zinc finger	K.DYQSEADLPIR.S	2.55	10.75	0.24	4.22
E9QML5_E	Zfml	Zinc finger	K.GVDQTSKPDETGK.S	3.37	3.28	1.03	0.97
E9QML5_E	Zfml	Zinc finger	K.LDSFSQVGPGSETVTQK#.D	8.27	6.93	1.19	0.84
E9QML5_E	Zfml	Zinc finger	K.M*SGLHISGQSVLEPVK.S	12.24	8.31	1.47	0.68
E9QML5_E	Zfml	Zinc finger	K.QSSVTQVTEQSPK#.V	16.11	19.81	0.81	1.23
E9QML5_E	Zfml	Zinc finger	K.SAEESPSGTLEATEK#EPVNK#.E	7.87	12.56	0.63	1.60
E9QML5_E	Zfml	Zinc finger	K.SAEESPSGTLEATEKEPVNKESEEM*SVVFISNLPNK.G	37.36	2.46	15.21	0.07
E9QML5_E	Zfml	Zinc finger	K.SENLEDDTLPEGK.Q	11.82	14.06	0.84	1.19
E9QML5_E	Zfml	Zinc finger	K.SM*TSDVPGDLDFLVPK.A	8.60	10.70	0.80	1.24
E9QML5_E	Zfml	Zinc finger	R.SPFGIVK.A	13.70	18.51	0.74	1.35
E9QML5_E	Zfml	Zinc finger	K.TM*ETVSSSSSAK#.S	6.49	5.21	1.25	0.80
E9QML5_E	Zfml	Zinc finger	R.WDDESHITPPVEVK.Q	8.92	12.43	0.72	1.39
E9QML5_E	Zfml	Zinc finger	K.YIETM*PLVIK.G	9.60	8.22	1.17	0.86
P23949_TI	Zfp36l2	Zinc finger	K.AVGTPVAAAPSSSFTPGFLR.R	5.64	6.72	0.84	1.19
E9Q1A5_E9	Zfp384	Protein Zfp	R.AYTSETYLM*K.H	10.52	13.00	0.81	1.23
Q923D1_Q	Zfp61	Protein Zfp	R.SNLIIHHR.I	3.70	15.98	0.23	4.31
I7HJS4_I7H	Zfp683	Protein Zfp	R.HQPPSLYK#ASTDSEK#.L	6.42	2.76	2.33	0.43
O88532_ZF	Zfr	Zinc finger	K.AGYSQGATQYTQAQQAR.Q	3.03	8.29	0.37	2.73
O88532_ZF	Zfr	Zinc finger	K.AISSASSPQSPGDALR.R	11.47	31.17	0.37	2.72
O88532_ZF	Zfr	Zinc finger	K.GLSTTGNSSLNSTSNTK#.V	37.93	16.41	2.31	0.43
O88532_ZF	Zfr	Zinc finger	K.HATIYPTEEELQAVQK#.I	32.37	20.51	1.58	0.63
O88532_ZF	Zfr	Zinc finger	R.IAENLPK#.Q	48.60	28.38	1.71	0.58
O88532_ZF	Zfr	Zinc finger	K.INFVGGNK#.L	40.06	17.02	2.35	0.42

O88532_ZF	Zfr	Zinc finger	K.LQSTGNKTEDLK.G	8.42	4.39	1.92	0.52
O88532_ZF	Zfr	Zinc finger	K.LVSDSLSEHEK#.S	28.38	16.38	1.73	0.58
O88532_ZF	Zfr	Zinc finger	K.NTPAASAVQIPEVK.Q	27.67	20.74	1.33	0.75
O88532_ZF	Zfr	Zinc finger	K.VLGM*DPLPQM*NQR.F	2.86	10.02	0.29	3.50
O88532_ZF	Zfr	Zinc finger	K.VSAIPTNM*AAK#.K	22.99	13.17	1.75	0.57
O88532_ZF	Zfr	Zinc finger	K.AISSASSPQSPGDALR.R	4.65	10.14	0.46	2.18
O88532_ZF	Zfr	Zinc finger	K.GLSTTGNSSLNSTSNTK#.V	17.67	11.42	1.55	0.65
Q9CPW7_Z	Zmat2	Zinc finger	R.RAEEDLTFEEDDEM*AAVM*GFSGFGSTK.K	1.90	13.44	0.14	7.07
Q9CU65_ZI	Zmym2	Zinc finger	K.GAGNNVLVVDGQQK#.R	9.01	7.09	1.27	0.79
Q9CU65_ZI	Zmym2	Zinc finger	K.QQGVDSLSPVASLPK.Q	6.10	6.74	0.90	1.11
A2A791_ZN	Zmym4	Zinc finger	K.DVISAQFENSTTSK#.D	8.58	7.63	1.12	0.89
A2A791_ZN	Zmym4	Zinc finger	K.ESIGSELGNSFASNIR.I	2.25	6.34	0.36	2.81
Q3UH28_Q	Zmynd8	Protein Zm	K.SSQGNSSNTQSAPSEPASAPK.E	6.17	15.23	0.41	2.47
Q3UH28_Q	Zmynd8	Protein Zm	R.VVWNASTVQQK#.E	161.53	77.56	2.08	0.48
Q61624_ZN	Znf148	Zinc finger	K.FLQQALDR.T	4.48	27.83	0.16	6.21
Q61624_ZN	Znf148	Zinc finger	K.GGLLTSEEDSGFSTSPK.D	13.10	10.26	1.28	0.78
Q61624_ZN	Znf148	Zinc finger	K.ILTINEDGSLGLK.T	17.84	20.75	0.86	1.16
Q61624_ZN	Znf148	Zinc finger	R.LPQGLQYALNVPISVK.Q	10.02	11.68	0.86	1.17
Q61624_ZN	Znf148	Zinc finger	R.SLK#QPLEQSQTISPLSSYEDSK#.V	8.57	8.51	1.01	0.99
Q61624_ZN	Znf148	Zinc finger	K.YAFELVDK#.Q	14.83	13.22	1.12	0.89
Q61624_ZN	Znf148	Zinc finger	R.YLQAASNNSR.E	4.17	9.97	0.42	2.39
Q9JMD0_ZI	Znf207	BUB3-inter	K.ILIQHQK#.A	22.44	4.78	4.69	0.21
Q6P3Y5_Z2	Znf280c	Zinc finger	R.ASSPPSSTIPSTSLQLSVPK#.S	4.51	2.60	1.74	0.58
Q99LI5_ZN	Znf281	Zinc finger	K.SLSGKPGGSLGIVSNNSVETISLLQSTSGK.Q	4.17	6.57	0.63	1.58
Q99LI5_ZN	Znf281	Zinc finger	K.SYLNFVSPLPDVVGQK.S	7.77	7.47	1.04	0.96
O88291_ZN	Znf326	DBIRD com	R.ESVLTATSILNNPIVK#.A	41.18	45.66	0.90	1.11
O88291_ZN	Znf326	DBIRD com	R.FGPYESYDSR.S	6.61	27.91	0.24	4.22
O88291_ZN	Znf326	DBIRD com	K.GENPFEIQDHPQDQQIEGDEEDEEK#.I	9.95	8.93	1.11	0.90
O88291_ZN	Znf326	DBIRD com	R.NQGGSSWEAPYSR.S	6.17	20.52	0.30	3.33
O88291_ZN	Znf326	DBIRD com	R.NSLDSFGGR.N	4.95	28.88	0.17	5.84
O88291_ZN	Znf326	DBIRD com	R.SGYGFNEPEQTR.F	11.24	44.63	0.25	3.97
O88291_ZN	Znf326	DBIRD com	R.SM*DSYLNQSYGM*DNHSGGGGGSR.F	3.95	11.48	0.34	2.91
O88291_ZN	Znf326	DBIRD com	R.TFEEK#DIELHLESSSHQETLDHIQK#.Q	22.56	19.15	1.18	0.85
Q922H9_ZI	Znf330	Zinc finger	R.QTGGEEDGASGYDAYWK#.N	7.50	4.50	1.67	0.60
Q922H9_ZI	Znf330	Zinc finger	R.TYASGYAHYEEQES.-	27.12	27.12	1.00	1.00
Q9R0B7_ZN	Znf346	Zinc finger	R.LADPAVSDLPAGK#.G	14.96	15.35	0.97	1.03
Q9R0B7_ZN	Znf346	Zinc finger	K.TLVTLGSQTPVQTQPTPK#.D	7.75	4.98	1.56	0.64
Q8VD12_Z3	Znf385a	Zinc finger	R.GAAELAGTLTFSK#.E	14.22	14.52	0.98	1.02
Q8VD12_Z3	Znf385a	Zinc finger	R.LGPPTPGEPEAPAQDR.T	4.84	6.91	0.70	1.43
Q8VD12_Z3	Znf385a	Zinc finger	R.TAHGPILFSPY.-	26.99	26.99	1.00	1.00
Q69Z99_ZN	Znf512	Zinc finger	K.AGDEVDEPSER.E	6.06	18.06	0.34	2.98
Q69Z99_ZN	Znf512	Zinc finger	K.IAVYHLQELASAELTK#.E	26.82	48.24	0.56	1.80
Q69Z99_ZN	Znf512	Zinc finger	R.IKPAATSQVEGAGEK.E	7.46	7.81	0.96	1.05
Q69Z99_ZN	Znf512	Zinc finger	R.KEPPVYAAGSM*EEK.W	3.91	5.39	0.73	1.38
Q69Z99_ZN	Znf512	Zinc finger	K.AGDEVDEPSER.E	5.03	11.90	0.42	2.37
Q69Z99_ZN	Znf512	Zinc finger	K.IAVYHLQELASAELTK.E	2.90	6.26	0.46	2.16
Q69Z99_ZN	Znf512	Zinc finger	R.LGAVTATPGPTSLK#.Q	27.65	25.21	1.10	0.91
Q69Z99_ZN	Znf512	Zinc finger	K.YTRPGLPTFSQEVLHK.W	1.11	7.59	0.15	6.83
B2RRF6_Z5	Znf518a	Zinc finger	K.ESSNSDNLFASINPLNGTLKIK.T	5.21	20.27	0.26	3.89
Q9DB42_ZI	Znf593	Zinc finger	R.AAGM*GSYVQPQR.L	7.15	11.18	0.64	1.56
Q91VY9_ZN	Znf622	Zinc finger	R.AVAEAAEASK#.G	12.85	7.57	1.70	0.59
Q91VY9_ZN	Znf622	Zinc finger	K.EGQDPAELEALSTDK#.I	5.67	2.51	2.26	0.44
Q91VY9_ZN	Znf622	Zinc finger	R.LQWFEQQAK#.K	18.80	10.39	1.81	0.55
Q91VY9_ZN	Znf622	Zinc finger	K.VHSFFIPDIEYLSDLK#.G	42.84	16.55	2.59	0.39
Q9D2D7_ZI	Znf687	Zinc finger	K.SATGPGTAGGSVISR.T	4.64	19.78	0.23	4.27
Q9D2D7_ZI	Znf687	Zinc finger	K.SVLGLVPQTLPK.A	16.00	20.06	0.80	1.25
Q9D2D7_ZI	Znf687	Zinc finger	K.VVSVQLGDGTR.L	4.71	24.60	0.19	5.22
Q9D2D7_ZI	Znf687	Zinc finger	K.SATGPGTAGGSVISR.T	3.39	10.02	0.34	2.96
Q8R151_ZN	Znfx1	NFX1-type	K.ELAIIQGPPGTGK.T	10.17	7.15	1.42	0.70
Q8R151_ZN	Znfx1	NFX1-type	R.INVFDFGQWPSK#.E	8.66	11.67	0.74	1.35
Q8R151_ZN	Znfx1	NFX1-type	K.IQGSAGEISTSQEQLK#.A	7.45	12.82	0.58	1.72
Q62384_ZF	Zpr1	Zinc finger	R.IPELDFEIPAFSQK#.G	12.25	3.86	3.17	0.32
Q9R020_ZF	Zranb2	Zinc finger	K.AGGTEIGK.T	19.22	33.13	0.58	1.72
Q9R020_ZF	Zranb2	Zinc finger	R.ENVEYIER.E	35.93	157.76	0.23	4.39
Q9R020_ZF	Zranb2	Zinc finger	K.ESEGEEEDEDEDLSK.Y	15.53	32.84	0.47	2.12
Q9R020_ZF	Zranb2	Zinc finger	K.EVEDKESEGEEEDEDEDLSK.Y	41.90	89.78	0.47	2.14
Q9R020_ZF	Zranb2	Zinc finger	K.LDEDEDEDDADLSK.Y	6.89	13.76	0.50	2.00
Q9R020_ZF	Zranb2	Zinc finger	R.TGYGGGFNER.E	24.13	144.81	0.17	6.00
Q9R020_ZF	Zranb2	Zinc finger	K.YKLDEDEDEDDADLSK.Y	36.01	53.93	0.67	1.50
Q9R020_ZF	Zranb2	Zinc finger	K.YNLDASEEEDSNK.K	8.38	6.62	1.27	0.79
Q9R020_ZF	Zranb2	Zinc finger	K.YNLDASEEEDSNKKK.S	5.17	3.64	1.42	0.70
Q9R020_ZF	Zranb2	Zinc finger	K.ESEGEEEDEDEDLSK.Y	2.70	5.48	0.49	2.03
Q9R020_ZF	Zranb2	Zinc finger	K.EVEDKESEGEEEDEDEDLSK.Y	6.22	15.58	0.40	2.51
Q9R020_ZF	Zranb2	Zinc finger	K.LDEDEDEDDADLSK#.Y	2.32	3.17	0.73	1.36
Q9R020_ZF	Zranb2	Zinc finger	K.YKLDEDEDEDDADLSK.Y	2.28	3.87	0.59	1.70
Q9R020_ZF	Zranb2	Zinc finger	K.YKLDEDEDEDDADLSK.Y	1.37	2.52	0.54	1.84
Q8R060_Z	Zwilch	Protein zwi	R.GFAQYELFK#.S	10.73	9.01	1.19	0.84
Q8R060_Z	Zwilch	Protein zwi	K.NLYQSEK#PQK#.W	4.04	4.00	1.01	0.99
Q8R060_Z	Zwilch	Protein zwi	K.TILNENDSVFLVEK#.V	7.92	6.36	1.25	0.80
Q9CQU5_Z	Zwint	ZW10 inter	K.EVLAEAAAILEPVGLQEEAELPAK#.I	7.98	5.01	1.59	0.63
Q62523_Z	Zyx	Zyxin OS=	K.FSPGAPSGPGPQPNQK#.M	19.54	18.82	1.04	0.96
Q62523_Z	Zyx	Zyxin OS=	R.GPLSQAPTPAPK.F	27.29	43.67	0.62	1.60
Q62523_Z	Zyx	Zyxin OS=	K.FSPGAPSGPGPQPNQK#.M	66.77	47.86	1.40	0.72
Q62523_Z	Zyx	Zyxin OS=	R.GPLSQAPTPAPK.F	84.03	65.21	1.29	0.78
Q62523_Z	Zyx	Zyxin OS=	K.MVPPDAPSSVSTGSPQPPSFTYAQQK#.E	6.62	4.10	1.61	0.62
Q62523_Z	Zyx	Zyxin OS=	K.QHPQPPPAQNQNQVR.S	3.65	11.72	0.31	3.21
Q62523_Z	Zyx	Zyxin OS=	K.VNPFRPGDSEPPVAAGAQR.A	4.43	48.59	0.09	10.97
Q8R3Y5_CS047_MOUS		Uncharacte	K.AAVVSEAQDSQVTSTK#.S	14.89	280.71	0.05	18.85
Q9CQE8_CN166_MOUS		UPF0568 p	R.HDDYLVMLK#.A	4.84	4.88	0.99	1.01
Q9CQE8_CN166_MOUS		UPF0568 p	R.NFIVWLEDQK#.I	13.94	10.84	1.29	0.78
Q8C3W1_CA198_MOU		Uncharacte	K.ATPTESPEKPPPPAVQRDEDDDALFSEPALAQISSSNVLLK.T	1.53	2.08	0.74	1.36
Q8C3W1_CA198_MOU		Uncharacte	R.FGDEDITWQDEHSAPFSWETR.S	2.41	2.96	0.81	1.23
Q9CXL3_CG050_MOUS		Uncharacte	K.LDEAEPEDSGGSPGK#.V	21.30	11.37	1.87	0.53
Q9CXL3_CG050_MOUS		Uncharacte	K.VQTLPAK#PSAATLALEYLQGWAQK#.Q	13.20	4.55	2.90	0.34
Q8VDP2_CX056_MOUS		UPF0428 p	K.NAPVTFIVDGAVVK#.F	13.25	8.68	1.53	0.65
Q80X32_CE024_MOUS		UPF0461 p	R.AADQFDLYSSQQNK#.Y	11.26	13.33	0.84	1.18
Q80X32_CE024_MOUS		UPF0461 p	R.VVHGLQETSGEVKPPSE.-	41.27	76.32	0.54	1.85
Q80X32_CE024_MOUS		UPF0461 p	R.VVHGLQETSGEVK#PPSE.-	6.61	11.22	0.59	1.70
Q9D937_CK098_MOUS		Uncharacte	K.AAM*EVEAPSK#.S	15.25	8.47	1.80	0.56
Q9D937_CK098_MOUS		Uncharacte	K.APQDVAM*EDLEDK#S.-	14.80	10.54	1.40	0.71
Q9D937_CK098_MOUS		Uncharacte	K.APQDVAMEDLEDK#S.-	5.93	1.94	3.05	0.33
Q9D937_CK098_MOUS		Uncharacte	R.QVVGAVIDEGLTTK#.H	71.62	32.00	2.24	0.45
Q9CQE8_CN166_MOUS		UPF0568 p	K.AGVM*ALANLLQIQR.H	25.31	69.43	0.36	2.74

Q9CQE8_CN166_MOUS	UPF0568 p	K.AGVM*ALANLLQIQR.H	6.38	25.41	0.25	3.98
Q9CQE8_CN166_MOUS	UPF0568 p	K.AGVMALANLLQIQR.H	20.51	47.76	0.43	2.33
Q9CQE8_CN166_MOUS	UPF0568 p	K.EGLPVALEK#.H	186.73	128.37	1.45	0.69
Q9CQE8_CN166_MOUS	UPF0568 p	R.HDDYLVM*LK#.A	52.74	162.97	0.32	3.09
Q9CQE8_CN166_MOUS	UPF0568 p	R.HDDYLVMLK#.A	71.31	44.65	1.60	0.63
Q9CQE8_CN166_MOUS	UPF0568 p	K.HILGFDTGDAVLNEAAQILR.L	56.57	141.20	0.40	2.50
Q9CQE8_CN166_MOUS	UPF0568 p	K.INEAIVAVQAIIADPK#.T	59.71	34.49	1.73	0.58
Q9CQE8_CN166_MOUS	UPF0568 p	R.LLHIEELR.E	22.49	57.90	0.39	2.57
Q9CQE8_CN166_MOUS	UPF0568 p	R.LTQDAVAK#.A	176.14	96.46	1.83	0.55
Q9CQE8_CN166_MOUS	UPF0568 p	K.NAEPLINLDVNNPDFK#.A	127.25	85.26	1.49	0.67
Q9CQE8_CN166_MOUS	UPF0568 p	R.NFIVWLEDQK#.I	113.31	71.15	1.59	0.63
Q9CXL3_CG050_MOUS	Uncharacte	R.EAGIAATQTAK#.V	157.78	73.86	2.14	0.47
Q9CXL3_CG050_MOUS	Uncharacte	K.LDEAEPEDSGGSPGK#.V	111.84	65.17	1.72	0.58
Q9CXL3_CG050_MOUS	Uncharacte	K.VQTLPAK#PSAATLALEYLQGWAQK#.Q	183.33	75.03	2.44	0.41
Q9CR55_CP087_MOUS	UPF0547 p	K.EIDIYANLSDEK#.A	5.52	2.36	2.34	0.43
P10404_ENV1_MOUSE	MLV-relate	R.GLDLLFLK#.E	14.08	9.90	1.42	0.70
P10404_ENV1_MOUSE	MLV-relate	R.ISVVQALVLTQQYHQLK#.S	14.57	14.86	0.98	1.02
P10404_ENV1_MOUSE	MLV-relate	K.SLTSLSEVVLQNR.R	3.27	11.16	0.29	3.41
Q5XFZ0_CR021_MOUS	UPF0711 p	R.SFLWALK#.S	11.11	5.95	1.87	0.54
Q8BZR9_CQ085_MOUS	Uncharacte	R.ADSISTSNIK#.N	30.00	16.43	1.83	0.55
Q8BZR9_CQ085_MOUS	Uncharacte	R.AEVNLAQR.N	8.74	17.00	0.51	1.95
Q8BZR9_CQ085_MOUS	Uncharacte	K.AGSFITGIDVTSK#.E	38.39	21.63	1.77	0.56
Q8BZR9_CQ085_MOUS	Uncharacte	R.ALIGDDVGLTSYK#.H	35.89	21.20	1.69	0.59
Q8BZR9_CQ085_MOUS	Uncharacte	R.ALINM*SSLPAQDK#.M	21.60	9.81	2.20	0.45
Q8BZR9_CQ085_MOUS	Uncharacte	R.ASGAEEDDSELQR.A	7.11	19.04	0.37	2.68
Q8BZR9_CQ085_MOUS	Uncharacte	K.M*TM*YADEVESQLK#.S	13.68	6.80	2.01	0.50
Q8BZR9_CQ085_MOUS	Uncharacte	K.YGNPNYGGM*K#.G	14.37	7.35	1.95	0.51
Q6PIU9_YJ005_MOUSE	Uncharacte	R.ASDDLGEPDVFATAPFR.S	4.67	10.88	0.43	2.33
Q6PIU9_YJ005_MOUSE	Uncharacte	R.SSLVPADDVDIFSK#.A	24.85	15.65	1.59	0.63
Q6PIU9_YJ005_MOUSE	Uncharacte	K.TQNTLASDSLAR.E	5.89	18.64	0.32	3.17
Q6PIU9_YJ005_MOUSE	Uncharacte	R.ASDDLGEPDVFATAPFR.S	6.08	14.73	0.41	2.42
Q6PIU9_YJ005_MOUSE	Uncharacte	R.HYSPEDELSAEAQPIAAYK#.I	9.39	6.72	1.40	0.72
Q6PIU9_YJ005_MOUSE	Uncharacte	K.TQNTLASDSLAR.E	8.01	18.73	0.43	2.34
Q8BWQ6_CP062_MOU	UPF0505 p	K.FLPFLDM*FQK#.E	8.45	8.31	1.02	0.98
Q8BWQ6_CP062_MOU	UPF0505 p	K.LLSDTSVIQFYPSK#.F	30.34	24.85	1.22	0.82
Q9CYI0_NJMU_MOUSE	Protein Njn	R.SGGINAETPSGDDFSLSLVDTNLPSEVEPELR.S	1.79	3.33	0.54	1.87