Accession Number	Sequence	Observed Mass (Da)	Theoretical Mass (Da)	Mass Diff (Da)	Mass Diff (ppm)	Expectation Value
P26599	TDSSPNQARAQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLRIIVENLFYPVTLDVLHQIFSK	7105.67	7105.68	-0.01	-2.02	2.E-89
P22626	LFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGK	4480.22	4480.22	-0.01	-1.11	2.E-89
P06748	VKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4472.61	4472.71	-0.10	-22.30	9.E-89
P06748	VKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4472.72	4472.71	0.01	2.61	9.E-89
P06748	VKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4472.72	4472.71	0.01	2.16	1.E-82
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-3.85	1.E-76
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-1.76	2.E-76
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.03	4108.11	-0.08	-18.32	3.E-75
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-1.70	3.E-75
O75531	HRDFVAEPMGEKPVGSLAGIGEVLGK	2692.40	2692.40	0.00	-1.63	1.E-73
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-3.99	5.E-72
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3450.71	3449.79	0.92	267.75	5.E-72
P0C0S8	GNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	4090.14	4090.15	-0.01	-1.80	5.E-71
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-1.67	6.E-71

P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-3.30	9.E-71
P0C0S8	GNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	4090.15	4090.15	0.00	0.40	7.E-70
P06748	KVKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4600.81	4600.80	0.01	1.31	9.E-70
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-2.51	1.E-69
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-2.53	1.E-68
P05783	VIDDTNITRLQLETEIEALKEELLFMK	3203.69	3203.70	-0.01	-2.33	2.E-68
P80723	AQGPAASAEEPKPVEAPAANSDQTVTVKE	2891.42	2891.41	0.01	2.04	3.E-66
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK	3722.09	3722.19	-0.10	-25.97	5.E-66
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK	3722.18	3722.19	-0.01	-3.86	5.E-66
P22626	LFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGKK	4608.30	4608.31	-0.01	-2.05	5.E-66
P02545	AGQVVTIWAAGAGATHSPPTDLVWK	2532.26	2532.31	-0.05	-19.45	5.E-66
P02545	AGQVVTIWAAGAGATHSPPTDLVWK	2532.31	2532.31	-0.01	-1.99	5.E-66
Q92841	APILIATDVASRGLDVEDVK	2081.11	2081.14	-0.03	-14.55	6.E-66
Q92841	APILIATDVASRGLDVEDVK	2081.14	2081.14	0.00	0.64	6.E-66
P02545	AGQVVTIWAAGAGATHSPPTDLVWK	2532.26	2532.31	-0.05	-18.66	2.E-64

P02545	AGQVVTIWAAGAGATHSPPTDLVWK	2532.31	2532.31	0.00	-1.91	2.E-64
P09651	IFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGK	4438.18	4438.19	-0.01	-1.52	7.E-64
P04908	GNYSERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	4106.13	4106.14	-0.01	-1.43	1.E-63
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK	3722.10	3722.19	-0.09	-24.82	2.E-63
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-1.82	3.E-63
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.70	3449.79	-0.09	-25.91	3.E-63
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK	3722.18	3722.19	-0.01	-2.06	3.E-63
P07910	GFAFVQYVNERNARAAVAGEDGRMIAGQVLDINLAAEPK	4157.19	4160.12	-2.93	-704.38	2.E-62
P07910	GFAFVQYVNERNARAAVAGEDGRMIAGQVLDINLAAEPK	4159.03	4160.12	-1.10	-263.27	2.E-62
P07910	GFAFVQYVNERNARAAVAGEDGRMIAGQVLDINLAAEPK	4160.12	4160.12	0.00	0.28	2.E-62
P07910	GFAFVQYVNERNARAAVAGEDGRMIAGQVLDINLAAEPK	4163.05	4160.12	2.93	704.88	2.E-62
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.33	2270.37	-0.04	-16.88	1.E-61
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.37	2270.37	0.00	-1.24	1.E-61
P69905	VGAHAGEYGAEALERMFLSFPTTK	2581.25	2581.26	-0.01	-2.11	3.E-61
P06748	KVKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4600.80	4600.80	0.00	-0.43	5.E-61

P06748	VDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIK	4478.16	4478.17	-0.01	-3.28	6.E-61
P06748	VDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIK	4481.07	4478.17	2.90	647.41	1.E-60
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.88	9098.88	0.00	-0.46	6.E-60
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-2.92	2.E-59
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.45	2369.45	0.00	-2.06	3.E-59
P69905	VGAHAGEYGAEALERMFLSFPTTK	2581.21	2581.26	-0.05	-18.27	4.E-59
P69905	VGAHAGEYGAEALERMFLSFPTTK	2581.26	2581.26	0.00	-1.84	4.E-59
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.92	9082.91	0.01	1.55	7.E-59
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.79	3449.79	0.00	-0.63	1.E-58
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.70	9098.88	-0.18	-19.55	1.E-57
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.86	9098.88	-0.02	-2.55	2.E-57
P62841	TFNQVEIKPEMIGHYLGEFSITYKPVK	3167.63	3167.64	-0.01	-2.40	4.E-57
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.44	3357.44	0.00	-0.89	7.E-57
P05787	LLEGEESRLESGMQNMSIHTK	2388.14	2388.14	0.00	-0.76	9.E-57
P43243	NLRYQLLQLVEPFGVISNHLILNK	2820.59	2820.60	-0.01	-2.19	2.E-56

P14866	MAAAGGGGGGGRYYGGGSEGGRAPK	2197.01	2197.01	0.00	0.44	3.E-56
P05787	LLEGEESRLESGMQNMSIHTK	2388.14	2388.14	0.00	-1.73	8.E-56
P14866	SERSSSGLLEWESKSDALETLGFLNHYQMK	3441.64	3441.65	-0.01	-2.74	2.E-55
P0C0S8	GNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	4090.14	4090.15	-0.01	-2.16	2.E-55
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.03	4108.11	-0.08	-19.57	3.E-55
P14866	NRIQHPSNVLHFFNAPLEVTEENFFEICDELGVK	3984.94	3984.95	-0.01	-1.43	3.E-55
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-2.53	4.E-55
P25205	(41)AGTVVLDDVELREAQRDYLDFLDDEEDQGIYQSK	3985.76	3985.87	-0.11	-27.32	9.E-55
P25205	(41)AGTVVLDDVELREAQRDYLDFLDDEEDQGIYQSK	3985.85	3985.87	-0.02	-5.71	2.E-54
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.92	2019.92	0.00	-2.37	2.E-54
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2368.28	2369.45	-1.17	-494.95	4.E-54
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.38	2369.45	-0.07	-28.82	6.E-54
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-2.86	6.E-54
Q7L4M3	GQRASLEAAIADAEQRGELAIK	2296.17	2296.21	-0.04	-17.62	1.E-53
P20700	SLEGDLEDLKDQIAQLEASLAAAKK	2655.40	2655.40	0.00	-1.52	1.E-53

P20700	SLEGDLEDLKDQIAQLEASLAAAKK	2659.53	2655.40	4.13	1553.27	1.E-53
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.19	3153.55	-0.36	-113.21	1.E-53
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-4.62	1.E-53
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.92	2019.92	0.00	-0.84	1.E-53
Q7L4M3	GQRASLEAAIADAEQRGELAIK	2296.21	2296.21	0.00	-1.81	1.E-53
P09651	IFVGGIKEDTEEHHLRDYFEQYGK	2909.39	2909.40	-0.01	-1.74	2.E-53
P09651	IFVGGIKEDTEEHHLRDYFEQYGK	2913.35	2909.40	3.95	1354.26	3.E-53
P46777	HIMGQNVADYMRYLMEEDEDAYKK	2948.30	2948.31	-0.01	-2.33	7.E-53
P07910	GFAFVQYVNERNARAAVAGEDGRMIAGQVLDINLAAEPK	4160.12	4160.12	0.00	-1.07	1.E-52
P43243	NLRYQLLQLVEPFGVISNHLILNK	2820.59	2820.60	-0.01	-1.98	1.E-52
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.88	2019.92	-0.04	-22.23	1.E-52
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4107.04	4108.11	-1.07	-261.72	1.E-52
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-1.77	1.E-52
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-3.95	2.E-52
P09651	KIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGK	4566.29	4566.29	0.00	-0.82	2.E-52

P09651	GGNFGGRSSGPYGGGGQYFAK	2019.92	2019.92	0.00	-2.23	2.E-52
Q7L4M3	GQRASLEAAIADAEQRGELAIK	2296.17	2296.21	-0.04	-16.58	3.E-52
Q7L4M3	GQRASLEAAIADAEQRGELAIK	2296.21	2296.21	0.00	-1.51	3.E-52
P22626	LFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGKK	4608.30	4608.31	-0.01	-2.38	3.E-52
P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.88	3777.88	0.00	-0.21	6.E-52
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.02	4108.11	-0.09	-21.80	7.E-52
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-2.84	7.E-52
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.94	9082.91	0.03	3.13	1.E-51
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9083.73	9082.91	0.82	90.75	1.E-51
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.91	2019.92	-0.01	-2.52	2.E-51
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-3.91	2.E-51
P08670	TVETRDGQVINETSQHHDDLE	2422.10	2422.10	0.00	-1.96	3.E-51
P08670	TVETRDGQVINETSQHHDDLE	2422.05	2422.10	-0.05	-18.64	3.E-51
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-1.60	4.E-51
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.90	9082.91	-0.01	-1.08	9.E-51

A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.72	9082.91	-0.19	-21.24	2.E-50
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.92	9082.91	0.01	0.94	2.E-50
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.35	2369.45	-0.10	-41.52	3.E-50
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.38	2369.45	-0.07	-29.91	3.E-50
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-3.15	3.E-50
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.50	2369.45	0.05	20.31	3.E-50
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-3.50	3.E-50
P60903	PSQMEHAMETMMFTFHK	2081.88	2081.88	0.00	-1.41	5.E-50
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.79	3449.79	0.00	-1.38	6.E-50
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.47	3138.52	-0.05	-15.52	7.E-50
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.52	3138.52	0.00	-0.16	7.E-50
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.92	9098.88	0.04	4.34	9.E-50
P05787	AQYEDIANRSRAEAESMYQIKYEELQSLAGK	3590.72	3590.73	-0.01	-3.31	1.E-49
P60709	RGILTLKYPIE(317)HGIVTNWDDMEK	2741.36	2741.42	-0.06	-20.42	1.E-49
P60709	RGILTLKYPIE(317)HGIVTNWDDMEK	2741.42	2741.42	0.00	-1.71	1.E-49

A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.88	9098.88	0.00	0.16	3.E-49
P04908	GNYSERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	4106.13	4106.14	-0.01	-1.43	3.E-49
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.02	4108.11	-0.09	-22.58	3.E-49
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-3.11	3.E-49
P08670	TVETRDGQVINETSQHHDDLE	2422.10	2422.10	0.00	-1.75	4.E-49
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-2.04	5.E-49
P08758	YMTISGFQIEETIDRETSGNLEQLLLAVVK	3396.74	3396.75	-0.01	-2.86	5.E-49
P08670	TVETRDGQVINETSQHHDDLE	2422.06	2422.10	-0.04	-17.32	8.E-49
P60903	PSQMEHAMETMMFTFHK	2081.88	2081.88	0.00	-1.17	2.E-48
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-2.10	2.E-48
P60903	PSQMEHAMETMMFTFHK	2081.85	2081.88	-0.03	-14.91	2.E-48
P62241	TRIIDVVYNASNNELVRTK	2204.19	2204.19	0.00	-0.96	3.E-48
P62805	VFLENVIRDAVTYTEHAK	2104.09	2104.10	-0.01	-2.74	4.E-48
P22626	KLFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGK	4608.30	4608.31	-0.01	-2.87	4.E-48
Q7L4M3	GQRASLEAAIADAEQRGELAIK	2296.21	2296.21	0.00	-1.25	6.E-48

P61978	ALRTDYNASVSVPDSSGPERILSISADIETIGEILKK	3944.06	3944.07	-0.01	-2.40	7.E-48
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.88	2019.92	-0.04	-19.80	9.E-48
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.92	2019.92	-0.01	-2.47	9.E-48
P05783	VIDDTNITRLQLETEIEALKEELLFMKK	3331.78	3331.79	-0.01	-2.26	2.E-47
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.41	3138.52	-0.11	-35.02	4.E-47
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.51	3138.52	-0.01	-3.16	4.E-47
P60709	DLYANTVLSGGTTMYPGIADRMQK	2597.38	2601.26	-3.88	-1494.27	6.E-47
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.43	3357.44	-0.01	-1.93	9.E-47
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.26	2601.26	-0.01	-1.92	1.E-46
Q13813	IAALQAFADQLIAAGHYAK	1971.06	1971.06	0.00	-1.95	1.E-46
Q13813	IAALQAFADQLIAAGHYAK	1973.17	1971.06	2.11	1067.50	1.E-46
P22626	LFIGGLSFETTEESLRNYYEQWGK	2866.37	2866.38	-0.01	-2.70	2.E-46
P60709	DLYANTVLSGGTTMYPGIADRMQK	2599.17	2601.26	-2.09	-802.56	2.E-46
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.16	1930.16	0.00	-0.87	2.E-46
A6NMY7	SSGPPPPSGSSGSEAAAGAGAAAPASQHPATGTGAVQTEAMK	3702.72	3702.72	0.00	0.73	3.E-46

P08670	TVETRDGQVINETSQHHDDLE	2422.10	2422.10	0.00	-1.79	3.E-46
P62805	VFLENVIRDAVTYTEHAK	2104.05	2104.10	-0.05	-26.03	4.E-46
P62805	VFLENVIRDAVTYTEHAK	2104.09	2104.10	-0.01	-2.55	4.E-46
P08670	TVETRDGQVINETSQHHDDLE	2422.06	2422.10	-0.04	-17.85	4.E-46
P05783	YWSQQIEESTTVVTTQSAEVGAAETTLTELRRTVQSLEIDLDSMRNLK	5426.71	5426.72	-0.01	-1.33	4.E-46
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.26	2601.26	0.00	-1.84	5.E-46
P22626	KLFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGKK	4736.41	4736.41	0.00	-0.42	5.E-46
P05787	AQYEDIANRSRAEAESMYQIKYEELQSLAGK	3590.72	3590.73	-0.01	-1.89	6.E-46
P06748	TPKTPKGPSSVEDIKAKMQASIEK	2569.38	2569.38	0.00	1.09	7.E-46
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-2.07	7.E-46
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3567.85	3566.92	0.93	261.00	7.E-46
P08670	TVETRDGQVINETSQHHDDLE	2422.10	2422.10	0.00	0.89	1.E-45
P09651	RSRGFGFVTYATVEEVDAAMNARPHK	2908.39	2908.44	-0.05	-16.02	1.E-45
P09651	RSRGFGFVTYATVEEVDAAMNARPHK	2908.44	2908.44	0.00	-1.68	1.E-45
P09651	RSRGFGFVTYATVEEVDAAMNARPHK	2908.58	2908.44	0.14	48.69	1.E-45

P60709	RGILTLKYPIE(317)HGIVTNWDDMEK	2741.41	2741.42	-0.01	-2.33	2.E-45
P06748	NCFRMTDQEAIQDLWQWRK	2467.15	2467.15	0.00	-1.10	2.E-45
P22626	LFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGK	4480.23	4480.22	0.01	2.35	2.E-45
P07910	GFAFVQYVNERNARAAVAGEDGRMIAGQVLDINLAAEPK	4160.12	4160.12	0.00	-1.07	3.E-45
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.13	1930.16	-0.03	-14.03	4.E-45
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.16	1930.16	0.00	-0.46	4.E-45
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.92	2019.92	0.00	-1.98	4.E-45
P22626	KLFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGK	4608.32	4608.31	0.01	1.14	6.E-45
P06748	KVKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4600.81	4600.80	0.01	2.48	6.E-45
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.02	4108.11	-0.09	-21.42	1.E-44
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-1.75	1.E-44
P62316	SEMTPEELQKREEEEFNTGPLSVLTQSVK	3335.66	3334.62	1.04	311.00	2.E-44
P07910	GFAFVQYVNERNARAAVAGEDGRMIAGQVLDINLAAEPK	4160.11	4160.12	-0.01	-2.13	2.E-44
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.87	9098.88	-0.01	-0.75	3.E-44
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.43	3357.44	-0.01	-1.85	3.E-44

A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.88	9098.88	0.00	-0.09	3.E-44
P20674	EIYPYVIQELRPTLNELGISTPEELGLDKV	3427.81	3427.81	0.00	-0.32	3.E-44
Q53HU8	LLEGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSK	4133.15	4133.16	-0.01	-2.49	4.E-44
P22626	LFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGK	4480.20	4480.22	-0.02	-3.86	4.E-44
P80723	AQGPAASAEEPKPVEAPAANSDQTVTVKE	2891.42	2891.41	0.01	1.90	4.E-44
P07910	GFAFVQYVNERNARAAVAGEDGRMIAGQVLDINLAAEPK	4160.11	4160.12	-0.01	-1.31	4.E-44
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.43	3357.44	-0.01	-2.65	6.E-44
P22626	KLFVGGIKEDTEEHHLRDYFEEYGK	3038.48	3038.48	0.00	-0.80	9.E-44
P09651	RSRGFGFVTYATVEEVDAAMNARPHK	2908.44	2908.44	0.00	-1.10	9.E-44
P09651	RSRGFGFVTYATVEEVDAAMNARPHK	2909.39	2908.44	0.95	328.04	9.E-44
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.12	2256.13	-0.01	-2.37	1.E-43
P22626	KLFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGK	4608.30	4608.31	-0.02	-3.26	2.E-43
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-2.43	2.E-43
P17096	KLEKEEEEGISQESSEEEQ	2235.98	2235.99	-0.01	-2.38	2.E-43
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.08	2256.13	-0.05	-21.61	2.E-43

P60709	SYELPDGQVITIGNERFRCPEALFQPSFLGMESCGIHETTFNSIMK	5191.45	5191.46	-0.01	-1.54	2.E-43
Q7L4M3	GQRASLEAAIADAEQRGELAIK	2296.20	2296.21	-0.01	-2.29	2.E-43
P22626	RGFGFVTFDDHDPVDKIVLQK	2431.15	2432.25	-1.10	-453.28	2.E-43
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.36	2270.37	-0.01	-4.42	2.E-43
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.43	2270.37	0.06	27.30	2.E-43
P22626	RGFGFVTFDDHDPVDKIVLQK	2432.25	2432.25	0.00	-1.60	2.E-43
P02533	TEELNREVATNSELVQSGK	2103.04	2103.04	0.00	-1.51	3.E-43
P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.88	3777.88	0.00	-0.93	3.E-43
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.86	9098.88	-0.02	-2.14	3.E-43
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.09	1930.16	-0.07	-36.10	3.E-43
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.12	1930.16	-0.04	-23.10	3.E-43
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.57	3.E-43
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.20	1930.16	0.04	21.97	3.E-43
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.89	9098.88	0.01	1.25	4.E-43
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.93	9082.91	0.02	2.51	6.E-43

A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.92	9098.88	0.04	4.22	6.E-43
P51991	IFVGGIKEDTEEYNLRDYFEK	2564.24	2564.24	0.00	-0.79	8.E-43
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.38	3357.44	-0.06	-17.66	8.E-43
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.44	3357.44	0.00	0.78	8.E-43
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-2.40	1.E-42
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-2.40	1.E-42
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.88	9098.88	0.00	-0.08	1.E-42
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.43	3357.44	-0.01	-3.48	2.E-42
P22626	LFIGGLSFETTEESLRNYYEQWGK	2866.37	2866.38	-0.01	-3.01	2.E-42
P60709	YPIE(317)HGIVTNWDDMEK	1959.90	1959.90	0.00	-1.83	2.E-42
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.80	9098.88	-0.08	-8.61	3.E-42
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-2.01	3.E-42
P62316	MFLRGDSVIVVLRNPLIAGK	2197.28	2197.28	0.00	-2.21	4.E-42
Q7L4M3	GQRASLEAAIADAEQRGELAIK	2296.21	2296.21	0.00	-0.81	4.E-42
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.33	2467.39	-0.07	-26.35	5.E-42

P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-3.49	5.E-42
P09651	RGFAFVTFDDHDSVDK	1854.82	1854.85	-0.03	-13.77	7.E-42
P09651	RGFAFVTFDDHDSVDK	1854.85	1854.85	0.00	-0.13	7.E-42
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3149.55	3153.55	-4.00	-1269.41	7.E-42
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3150.88	3153.55	-2.67	-846.67	7.E-42
P63244	DVLSVAFSSDNRQIVSGSRDK	2279.15	2279.15	0.00	-0.51	1.E-41
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3152.21	3153.55	-1.34	-424.29	1.E-41
P08758	(41)AQVLRGTVTDFPGFDERADAETLRK	2833.44	2833.44	0.00	-1.25	1.E-41
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-1.96	1.E-41
Q09028	NTPFLYDLVMTHALEWPSLTAQWLPDVTRPEGK	3824.91	3824.92	-0.01	-3.07	2.E-41
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.48	3153.55	-0.07	-23.33	2.E-41
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-1.67	2.E-41
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.88	3153.55	1.33	421.26	2.E-41
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3156.21	3153.55	2.66	844.03	2.E-41
P04083	ALTGHLEEVVLALLK	1604.95	1604.95	0.00	-1.62	2.E-41

P43243	NLRYQLLQLVEPFGVISNHLILNK	2820.59	2820.60	-0.01	-2.47	2.E-41
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.13	1930.16	-0.03	-13.57	3.E-41
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.16	1930.16	0.00	-0.67	3.E-41
P60709	YPIE(317)HGIVTNWDDMEK	1959.86	1959.90	-0.04	-20.56	3.E-41
P60709	YPIE(317)HGIVTNWDDMEK	1959.89	1959.90	-0.01	-2.90	3.E-41
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.92	2019.92	0.00	-1.28	3.E-41
P0C0S8	GNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNK	3962.07	3962.05	0.02	4.29	3.E-41
P60709	YPIE(317)HGIVTNWDDMEK	1959.90	1959.90	-0.01	-2.54	4.E-41
P20700	SLEGDLEDLKDQIAQLEASLAAAKK	2655.40	2655.40	0.00	-1.78	4.E-41
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.64	9098.88	-0.24	-26.59	5.E-41
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.86	9098.88	-0.02	-1.81	6.E-41
P31949	TEFLSFMNTELAAFTK	1848.90	1848.90	0.00	-2.42	6.E-41
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.00	4108.11	-0.11	-27.53	7.E-41
P63220	(49)MQNDAGEFVDLYVPRK	1922.92	1922.92	0.00	0.80	8.E-41
P33778	RSTITSREIQTAVRLLLPGELAK	2551.44	2551.48	-0.04	-13.88	9.E-41

P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-0.95	9.E-41
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.41	2572.44	-0.03	-13.09	1.E-40
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.44	2572.44	0.00	-0.80	1.E-40
P51991	IFVGGIKEDTEEYNLRDYFEK	2564.24	2564.24	0.00	-1.85	1.E-40
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.08	4108.11	-0.03	-6.76	1.E-40
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.90	9098.88	0.02	2.33	1.E-40
P0C0S8	VTIAQGGVLPNIQAVLLPKK	2058.26	2058.26	0.00	-1.33	1.E-40
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.88	9098.88	0.00	0.48	1.E-40
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.93	9082.91	0.02	1.66	2.E-40
P0C0S8	VTIAQGGVLPNIQAVLLPK	1929.49	1930.16	-0.67	-346.25	2.E-40
P09651	RGFAFVTFDDHDSVDKIVIQK	2436.24	2436.24	0.00	-1.15	3.E-40
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.16	1930.16	0.00	-0.35	3.E-40
P0C0S8	VTIAQGGVLPNIQAVLLPK	1928.82	1930.16	-1.34	-692.49	3.E-40
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.86	9098.88	-0.02	-1.90	8.E-40
P22087	VLYLGAASGTTVSHVSDIVGPDGLVYAVEFSHRSGRDLINLAK	4483.34	4483.35	-0.01	-2.31	9.E-40

Q15427	VSEPLLWELFLQAGPVVNTHMPK	2604.38	2604.38	0.00	-1.68	2.E-39
P17096	KLEKEEEEGISQESSEEEQ	2231.07	2235.99	-4.92	-2205.01	2.E-39
P17096	KLEKEEEEGISQESSEEEQ	2235.98	2235.99	-0.01	-2.34	2.E-39
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.33	2467.39	-0.06	-23.91	3.E-39
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-5.31	3.E-39
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.87	9098.88	-0.01	-1.31	3.E-39
Q3BDU5	LDNARQSAERNSNLVGAAHEELQQSRIRIDSLSAQLSQLQK	4573.28	4573.37	-0.09	-19.50	4.E-39
Q3BDU5	LDNARQSAERNSNLVGAAHEELQQSRIRIDSLSAQLSQLQK	4573.36	4573.37	-0.01	-1.28	4.E-39
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.51	3138.52	-0.01	-1.85	5.E-39
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3139.46	3138.52	0.94	297.88	5.E-39
P09651	PRNQGGYGGSSSSSSYGSGRRF	2249.98	2250.02	-0.04	-16.09	5.E-39
P09651	PRNQGGYGGSSSSSSYGSGRRF	2250.02	2250.02	0.00	-1.96	5.E-39
P60709	YPIE(317)HGIVTNWDDMEK	1959.89	1959.90	-0.01	-2.70	6.E-39
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.90	9098.88	0.02	1.68	7.E-39
Q9NWH9	(41)AAATGAVAASAASGQAEGK	1629.77	1629.80	-0.03	-16.76	8.E-39

Q9NWH9	(41)AAATGAVAASAASGQAEGK	1629.80	1629.80	0.00	-1.85	8.E-39
P07355	SLYYYIQQDTKGDYQK	2011.95	2011.95	0.00	-2.00	8.E-39
P07355	SLYYYIQQDTKGDYQK	2015.98	2011.95	4.03	1996.64	8.E-39
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.36	2270.37	-0.01	-3.93	1.E-38
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2271.32	2270.37	0.95	417.10	1.E-38
P08758	(41)AQVLRGTVTDFPGFDERADAETLRK	2833.44	2833.44	0.00	-1.18	1.E-38
P09651	RGFAFVTFDDHDSVDK	1854.85	1854.85	0.00	-1.15	1.E-38
P22626	RGFGFVTFDDHDPVDK	1854.85	1850.86	3.99	2152.67	2.E-38
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKKSIRDTPAK	5114.03	5114.02	0.01	2.42	2.E-38
P09651	GGNFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSSYGSGRRF	4251.92	4251.92	0.00	-1.04	2.E-38
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.83	3566.92	-0.09	-24.44	2.E-38
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.90	3566.92	-0.02	-4.28	2.E-38
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.62	3307.68	-0.06	-18.72	2.E-38
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.68	3307.68	0.00	-0.46	2.E-38
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.89	2019.92	-0.03	-13.36	2.E-38

P09651	GGNFGGRSSGPYGGGGQYFAK	2019.92	2019.92	0.00	-0.99	2.E-38
P26599	LPIDVTEGEVISLGLPFGK	1983.09	1983.09	0.00	-2.21	2.E-38
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.09	1930.16	-0.07	-36.10	2.E-38
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.12	1930.16	-0.04	-23.10	2.E-38
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.57	2.E-38
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.20	1930.16	0.04	21.97	2.E-38
P06748	NCFRMTDQEAIQDLWQWRK	2467.15	2467.15	0.00	-0.61	3.E-38
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3356.36	3357.44	-1.08	-322.13	3.E-38
P22626	RGFGFVTFDDHDPVDK	1850.84	1850.86	-0.02	-12.65	4.E-38
P22626	RGFGFVTFDDHDPVDK	1850.86	1850.86	0.00	-0.98	4.E-38
P06748	NCFRMTDQEAIQDLWQWRK	2467.11	2467.15	-0.04	-16.13	5.E-38
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.43	3357.44	-0.01	-2.59	5.E-38
P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-1.98	5.E-38
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.44	3357.44	0.00	1.07	6.E-38
P62805	VFLENVIRDAVTYTEHAK	2104.05	2104.10	-0.05	-23.03	7.E-38

P0C0S5	SRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASK	3776.96	3776.97	-0.01	-3.19	8.E-38
P39023	LDWARERLEQQVPVNQVFGQDEMIDVIGVTK	3611.83	3611.84	-0.01	-3.14	1.E-37
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3179.56	3183.56	-4.00	-1258.77	1.E-37
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.55	3153.55	0.00	-1.00	1.E-37
P05387	MRYVASYLLAALGGNSSPSAK	2155.11	2155.11	0.00	-2.11	1.E-37
P05386	KVEAKKEESEESDDDMGFGLFD	2504.10	2504.09	0.01	2.11	1.E-37
P46777	HIMGQNVADYMRYLMEEDEDAYKK	2951.31	2948.31	3.00	1016.74	1.E-37
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.49	3183.56	-0.07	-22.78	1.E-37
P07355	AYTNFDAERDALNIETAIK	2151.05	2154.06	-3.01	-1397.44	2.E-37
P07355	AYTNFDAERDALNIETAIK	2154.01	2154.06	-0.05	-23.71	2.E-37
P07355	AYTNFDAERDALNIETAIK	2154.05	2154.06	-0.01	-2.73	2.E-37
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.55	3183.56	-0.01	-2.34	2.E-37
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.43	3357.44	-0.01	-3.45	2.E-37
P60709	YPIE(317)HGIVTNWDDMEK	1959.87	1959.90	-0.03	-14.48	2.E-37
P60709	YPIE(317)HGIVTNWDDMEK	1959.90	1959.90	0.00	-1.42	2.E-37

P09651	GGNFGGRSSGPYGGGGQYFAK	2019.92	2019.92	0.00	-1.88	3.E-37
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-3.85	3.E-37
P22626	LFIGGLSFETTEESLRNYYEQWGK	2866.38	2866.38	0.00	-0.61	4.E-37
Q8NC51	DRAKVEFNIRKPNEGADGQWKK	2588.28	2585.35	2.93	1133.45	4.E-37
Q08211	DAQSNAARDFVNYLVRINEIK	2436.22	2435.26	0.96	394.59	4.E-37
P22626	LFVGGIKEDTEEHHLRDYFEEYGK	2910.38	2910.38	0.00	-0.06	5.E-37
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.21	1930.16	0.05	23.58	5.E-37
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.87	9098.88	-0.01	-1.11	5.E-37
P07355	AYTNFDAERDALNIETAIK	2151.05	2154.06	-3.01	-1398.56	6.E-37
P09651	RGFAFVTFDDHDSVDKIVIQK	2436.24	2436.24	0.00	-1.81	6.E-37
P0C0S8	GNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	4090.15	4090.15	0.00	-1.06	7.E-37
Q08211	DAQSNAARDFVNYLVRINEIK	2435.25	2435.26	-0.01	-2.17	7.E-37
P60709	YPIE(317)HGIVTNWDDMEK	1959.89	1959.90	-0.01	-2.90	8.E-37
Q8NC51	DRAKVEFNIRKPNEGADGQWKK	2585.31	2585.35	-0.04	-16.21	8.E-37
Q8NC51	DRAKVEFNIRKPNEGADGQWKK	2585.35	2585.35	0.00	1.08	8.E-37

P22626	RGFGFVTFDDHDPVDK	1854.85	1850.86	3.99	2153.59	8.E-37
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.72	8.E-37
P07355	AYTNFDAERDALNIETAIK	2154.05	2154.06	-0.01	-2.96	8.E-37
P05787	AQYEDIANRSRAEAESMYQIK	2472.17	2472.17	0.00	0.40	8.E-37
Q8NC51	PGHLQEGFGCVVTNRFDQLFDDESDPFEVLK	3537.65	3537.65	0.00	-0.88	9.E-37
Q9Y2X3	FQDTAEALAAFTALMEGK	1912.92	1912.92	0.00	-1.42	1.E-36
P09651	PRNQGGYGGSSSSSSYGSGRRF	2250.02	2250.02	0.00	-1.74	1.E-36
P33778	RSTITSREIQTAVRLLLPGELAK	2551.45	2551.48	-0.03	-12.87	1.E-36
P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-0.01	1.E-36
P62241	TRIIDVVYNASNNELVRTK	2204.15	2204.19	-0.04	-16.83	1.E-36
P62241	TRIIDVVYNASNNELVRTK	2204.19	2204.19	0.00	-1.86	1.E-36
Q13727	FSMPGFKGEGPDVDVNLPKADLDVSGPKVDIDVPDVNIEGPDAK	4592.27	4592.26	0.01	1.59	2.E-36
Q86U42	(41)AAAAAAAAAAGAAGGRGSGPGRRRHLVPGAGGEAGEGAPGGAGDYGNGLESEELEPEELLLEPEPEPEPEEEPPRPRAPPGAPGPGPGSGAPGSQEEEEEPGLVEGDPGDGAIEDPELEAIK	11816.57	11816.60	-0.03	-2.69	2.E-36
P22626	RGFGFVTFDDHDPVDK	1850.86	1850.86	0.00	-0.17	2.E-36
Q3BDU5	LDNARQSAERNSNLVGAAHEELQQSRIRIDSLSAQLSQLQK	4573.35	4573.37	-0.02	-4.02	2.E-36

P22087	VLYLGAASGTTVSHVSDIVGPDGLVYAVEFSHRSGRDLINLAK	4483.34	4483.35	-0.01	-1.38	2.E-36
P02545	AGQVVTIWAAGAGATHSPPTDLVWK	2532.31	2532.31	0.00	-1.91	2.E-36
P51991	IFVGGIKEDTEEYNLRDYFEK	2565.24	2564.24	1.00	390.40	2.E-36
P09651	PRNQGGYGGSSSSSSYGSGRRF	2250.01	2250.02	-0.01	-2.80	2.E-36
P16401	(51)SETAPAETATPAPVEK	1639.79	1639.79	0.00	-1.83	3.E-36
P06748	VKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4344.62	4344.61	0.01	2.17	3.E-36
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-2.57	3.E-36
O43390	VLFVRNLATTVTEEILEK	2074.16	2074.17	-0.01	-2.97	3.E-36
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-2.90	3.E-36
P60709	YPIE(317)HGIVTNWDDMEK	1959.89	1959.90	-0.01	-2.90	3.E-36
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.45	2369.45	0.00	-1.34	4.E-36
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.38	2369.45	-0.07	-28.98	4.E-36
P22626	EDTEEHHLRDYFEEYGKIDTIEIITDRQSGK	3771.92	3765.78	6.14	1628.25	5.E-36
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.41	2369.45	-0.04	-17.34	5.E-36
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.19	3153.55	-0.36	-113.21	5.E-36

P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-4.62	5.E-36
P07355	SALSGHLETVILGLLK	1649.94	1649.97	-0.03	-17.07	5.E-36
P07355	SALSGHLETVILGLLK	1649.97	1649.97	0.00	-2.04	5.E-36
P61978	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	3828.93	3828.94	-0.01	-3.19	5.E-36
P60709	YPIE(317)HGIVTNWDDMEK	1959.90	1959.90	0.00	-1.73	6.E-36
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.91	9082.91	0.00	-0.05	9.E-36
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.51	3138.52	-0.01	-2.55	9.E-36
P46776	TGAAPIIDVVRSGYYK	1708.88	1708.91	-0.03	-17.55	9.E-36
P46776	TGAAPIIDVVRSGYYK	1708.91	1708.91	0.00	-1.63	9.E-36
P05787	TEISEMNRNISRLQAEIEGLK	2427.10	2430.25	-3.15	-1297.12	1.E-35
P02533	TEELNREVATNSELVQSGK	2103.03	2103.04	-0.01	-2.84	1.E-35
P16401	(51)SETAPAETATPAPVEK	1639.79	1639.79	0.00	-0.97	1.E-35
P05787	TEISEMNRNISRLQAEIEGLK	2430.24	2430.25	-0.01	-2.82	1.E-35
P05387	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEKKEE(37)SEE(37)SDDDMGFGLFD	5364.34	5364.36	-0.02	-4.18	1.E-35
P07355	AYTNFDAERDALNIETAIK	2151.06	2154.06	-3.00	-1395.77	2.E-35

P07355	AYTNFDAERDALNIETAIK	2154.06	2154.06	0.00	-1.71	2.E-35
O75533	KLSSWDQAETPGHTPSLRWDETPGRAK	3049.50	3049.50	0.00	1.23	2.E-35
P62854	FVIRNIVEAAAVRDISEASVFDAYVLPK	3091.66	3091.67	-0.01	-2.70	2.E-35
P07355	AYTNFDAERDALNIETAIK	2154.01	2154.06	-0.05	-24.13	2.E-35
P07355	AYTNFDAERDALNIETAIK	2154.05	2154.06	-0.01	-2.82	2.E-35
P09651	GGNFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSSYGSGRRF	4251.92	4251.92	0.00	-0.93	3.E-35
P07355	AYTNFDAERDALNIETAIK	2151.02	2154.06	-3.04	-1415.32	3.E-35
P07355	AYTNFDAERDALNIETAIK	2151.05	2154.06	-3.01	-1397.91	3.E-35
P19338	FGYVDFESAEDLEK	1647.73	1647.73	0.00	-0.18	3.E-35
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.43	2572.44	-0.01	-2.01	3.E-35
P19338	FGYVDFESAEDLEK	1646.82	1647.73	-0.91	-553.55	3.E-35
P19338	FGYVDFESAEDLEK	1647.73	1647.73	0.00	-0.54	3.E-35
Q12906	EATDAIGHLDRQQREDITQSAQHALRLAAFGQLHK	3924.01	3924.01	0.00	-1.10	4.E-35
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.13	2256.13	0.00	-1.48	4.E-35
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2573.41	2572.44	0.97	375.62	4.E-35

P22626	RGFGFVTFDDHDPVDK	1854.83	1850.86	3.97	2140.51	5.E-35
P22626	RGFGFVTFDDHDPVDK	1854.85	1850.86	3.99	2153.16	5.E-35
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.52	3138.52	0.00	-0.87	5.E-35
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.89	9098.88	0.01	0.90	6.E-35
Q14839	GSSGASVAAAAAAAVAVVESMVTATEVAPPPPPVEVPIRK	3753.99	3754.00	-0.01	-2.88	7.E-35
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.45	3138.52	-0.07	-23.14	7.E-35
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-4.11	9.E-35
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYL VGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.91	9082.91	0.00	0.04	9.E-35
P19338	VEGTEPTTAFNLFVGNLNFNK	2311.14	2311.15	-0.01	-2.43	1.E-34
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3156.49	3153.55	2.94	931.27	1.E-34
P33778	RSTITSREIQTAVRLLLPGELAK	2551.44	2551.48	-0.04	-15.10	1.E-34
P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-1.07	1.E-34
P60709	YPIE(317)HGIVTNWDDMEK	1959.90	1959.90	0.00	-1.11	1.E-34
P05787	TEISEMNRNISRLQAEIEGLK	2427.10	2430.25	-3.15	-1296.01	1.E-34
P05787	TEISEMNRNISRLQAEIEGLK	2430.25	2430.25	0.00	-1.34	1.E-34

Q8IUE6	TRIIPRHLQLAVRNDEELNK	2414.35	2414.35	0.00	-1.82	1.E-34
P22626	RGFGFVTFDDHDPVDK	1850.84	1850.86	-0.02	-12.27	2.E-34
P22626	RGFGFVTFDDHDPVDK	1850.86	1850.86	0.00	-0.66	2.E-34
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYL VGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.99	9082.91	0.08	9.25	2.E-34
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYL VGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9083.69	9082.91	0.78	85.89	2.E-34
P60709	YPIE(317)HGIVTNWDDMEK	1959.86	1959.90	-0.04	-19.53	2.E-34
P0C0S8	LLGKVTIAQGGVLPNIQAVLLPK	2341.45	2341.45	0.00	-0.22	2.E-34
P07355	SALSGHLETVILGLLK	1649.94	1649.97	-0.03	-17.80	2.E-34
P07355	SALSGHLETVILGLLK	1649.96	1649.97	-0.01	-3.07	2.E-34
P06748	MSVQPTVSLGGFEITPPVVLRLK	2464.18	2467.39	-3.21	-1303.64	2.E-34
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-4.10	2.E-34
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYL VGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.91	9082.91	0.00	-0.17	2.E-34
P0C0S5	SRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASK	3776.96	3776.97	-0.01	-3.16	2.E-34
P07355	SLYYYIQQDTKGDYQK	2011.95	2011.95	0.00	-1.55	2.E-34
P07355	SLYYYIQQDTKGDYQK	2014.14	2011.95	2.19	1084.92	2.E-34

P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-3.16	3.E-34
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.88	2467.39	0.49	199.77	3.E-34
P26599	LPIDVTEGEVISLGLPFGK	1983.10	1983.09	0.01	3.03	3.E-34
O43390	VLFVRNLATTVTEEILEK	2074.17	2074.17	0.00	-1.96	4.E-34
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4117.46	4117.45	0.01	2.43	4.E-34
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4117.35	4117.45	-0.10	-25.41	4.E-34
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4117.46	4117.45	0.01	2.65	4.E-34
P09651	IEVIEIMTDRGSGK	1546.77	1546.80	-0.03	-16.53	4.E-34
P09651	IEVIEIMTDRGSGK	1546.80	1546.80	0.00	-1.27	4.E-34
Q7L4M3	GQRASLEAAIADAEQRGELAIK	2296.21	2296.21	0.00	-1.12	5.E-34
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.87	9098.88	-0.01	-1.44	6.E-34
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.68	3307.68	0.00	-1.00	7.E-34
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.42	2428.37	0.05	20.49	7.E-34
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.43	2428.37	0.06	24.73	7.E-34
P0C0S8	TRIIPRHLQLAIRNDEELNK	2429.31	2428.37	0.94	387.17	7.E-34

P08758	VLTEIIASRTPEELRAIK	2038.15	2038.18	-0.03	-15.55	8.E-34
P08758	VLTEIIASRTPEELRAIK	2038.18	2038.18	0.00	-1.42	8.E-34
P0C0S8	TRIIPRHLQLAIRNDEELNK	2431.34	2428.37	2.97	1221.45	9.E-34
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-4.05	1.E-33
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-2.98	1.E-33
P05204	VKDEPQRRSARLSAKPAPPKPEPKPK	2906.65	2906.66	-0.01	-2.02	1.E-33
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-2.37	1.E-33
P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.89	3777.88	0.01	2.65	1.E-33
P22626	LFIGGLSFETTEESLRNYYEQWGK	2866.37	2866.38	-0.01	-2.14	2.E-33
P08670	TVETRDGQVINETSQHHDDLE	2422.09	2422.10	-0.01	-3.65	2.E-33
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4117.44	4117.45	-0.01	-1.56	2.E-33
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.91	9082.91	0.00	-0.23	2.E-33
P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.81	3777.88	-0.07	-18.10	2.E-33
P08670	TVETRDGQVINETSQHHDDLE	2422.04	2422.10	-0.06	-25.04	2.E-33
P05387	ILDSVGIEADDDRLNK	1771.90	1771.90	0.00	-1.11	2.E-33

P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.41	2428.37	0.04	18.02	3.E-33
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.43	2428.37	0.06	25.68	3.E-33
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.45	2428.37	0.08	31.12	3.E-33
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.00	4108.11	-0.11	-27.96	3.E-33
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.09	4108.11	-0.02	-3.89	3.E-33
P06748	VDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIK	4478.08	4478.17	-0.09	-19.72	3.E-33
P06748	VDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIK	4478.17	4478.17	0.00	-1.07	3.E-33
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.30	2428.37	-0.07	-28.96	3.E-33
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.32	2428.37	-0.05	-18.88	3.E-33
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-1.95	3.E-33
P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-1.79	3.E-33
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.55	3153.55	0.00	-1.51	3.E-33
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.48	3153.55	0.93	294.99	3.E-33
P06748	GGSLPKVEAKFINYVK	1748.98	1748.98	0.00	1.11	4.E-33
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-1.46	4.E-33

P06748	VDNDENEHQLSLRTVSLGAGAKDELHIVEAEAMNYEGSPIK	4478.16	4478.17	-0.01	-1.45	6.E-33
P08729	LEAAIAEAEERGELALK	1811.96	1811.96	0.00	-2.28	6.E-33
P16403	(51)SETAPAAPAAAPPAEKAPVK	1915.01	1915.01	0.00	0.33	7.E-33
P22626	LFIGGLSFETTEESLRNYYEQWGK	2866.37	2866.38	-0.01	-2.98	7.E-33
P22626	RGFGFVTFDDHDPVDKIVLQK	2432.25	2432.25	0.00	-1.97	7.E-33
P05787	TEISEMNRNISRLQAEIEGLK	2430.25	2430.25	0.00	-1.99	8.E-33
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYL VGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.92	9082.91	0.01	1.25	8.E-33
Q04695	SEISELRRTMQALEIELQSQLSMK	2819.44	2819.45	-0.01	-1.95	8.E-33
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.12	2256.13	-0.01	-2.50	8.E-33
P07355	AYTNFDAERDALNIETAIK	2154.05	2154.06	-0.01	-2.91	9.E-33
P09651	RSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPK	3887.99	3887.99	0.00	-0.99	9.E-33
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.08	2256.13	-0.05	-21.61	1.E-32
P08670	TVETRDGQVINETSQHHDDLE	2422.09	2422.10	-0.01	-2.45	1.E-32
P0C0S8	GNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNK	3962.05	3962.05	0.00	0.05	1.E-32
P07355	AYTNFDAERDALNIETAIK	2151.05	2154.06	-3.01	-1397.40	1.E-32

P05783	YETELAMRQSVENDIHGLRK	2388.14	2388.19	-0.05	-19.54	1.E-32
P62081	IVKPNGEKPDEFESGISQALLELEMNSDLK	3330.65	3329.67	0.98	292.79	1.E-32
P16403	(51)SETAPAAPAAAPPAEKAPVK	1915.01	1915.01	0.00	1.06	1.E-32
P05787	TEISEMNRNISRLQAEIEGLK	2427.10	2430.25	-3.15	-1296.71	1.E-32
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-2.63	1.E-32
P05204	VKDEPQRRSARLSAKPAPPKPEPKPK	2906.65	2906.66	-0.01	-2.95	1.E-32
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4245.55	4245.54	0.01	1.61	2.E-32
Q13185	KVEEAEPEEFVVEK	1660.82	1660.82	0.00	-2.01	2.E-32
O14979	MFIGGLSWDTSKK	1468.72	1468.74	-0.02	-16.42	2.E-32
O14979	MFIGGLSWDTSKK	1468.74	1468.74	0.00	-1.58	2.E-32
O14979	MFIGGLSWDTSKK	1470.73	1468.74	1.99	1351.50	2.E-32
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-2.03	2.E-32
O60506	ALLERTGYTLDVTTGQRK	2021.09	2021.09	0.00	-1.00	2.E-32
O60506	ALLERTGYTLDVTTGQRK	2025.07	2021.09	3.98	1967.72	2.E-32
P22626	RGFGFVTFDDHDPVDK	1850.84	1850.86	-0.02	-13.03	2.E-32

P22626	RGFGFVTFDDHDPVDK	1850.86	1850.86	0.00	-1.41	2.E-32
P62304	VMVQPINLIFRYLQNRSRIQVWLYEQVNMRIEGCIIGFDEYMN LVLDDAEEIHSKTK	6869.49	6869.50	-0.01	-0.88	2.E-32
P22626	KRGFGFVTFDDHDPVDK	1978.95	1978.95	0.00	-1.20	2.E-32
P18077	IEGVYARDETEFYLGK	1892.96	1888.92	4.04	2133.51	2.E-32
P16403	(51)SETAPAAPAAAPPAEKAPVK	1915.01	1915.01	0.00	-2.28	2.E-32
P22626	KRGFGFVTFDDHDPVDK	1976.01	1978.95	-2.94	-1485.80	3.E-32
P22626	KRGFGFVTFDDHDPVDK	1982.94	1978.95	3.99	2013.73	3.E-32
P05386	KVEAKKEESEESDDDMGFGLFD	2504.05	2504.09	-0.04	-17.46	3.E-32
P05386	KVEAKKEESEESDDDMGFGLFD	2504.09	2504.09	0.00	0.87	3.E-32
P22626	IDTIEIITDRQSGKK	1715.91	1715.94	-0.03	-17.68	3.E-32
P22626	IDTIEIITDRQSGKK	1715.94	1715.94	0.00	-1.83	3.E-32
P18077	IEGVYARDETEFYLGK	1888.92	1888.92	0.00	-1.72	3.E-32
Q04695	VRALEEANTELEVK	1596.86	1599.85	-2.99	-1872.91	3.E-32
Q04695	VRALEEANTELEVK	1599.82	1599.85	-0.03	-17.29	3.E-32
Q04695	VRALEEANTELEVK	1599.85	1599.85	0.00	-1.35	3.E-32

Q04695	(52)TTSIRQFTSSSSIK	1583.82	1583.82	0.00	-1.22	3.E-32
P62805	VFLENVIRDAVTYTEHAK	2147.08	2104.10	42.98	20016.30	3.E-32
P62805	VFLENVIRDAVTYTEHAK	2147.10	2104.10	43.00	20027.80	3.E-32
P62805	VFLENVIRDAVTYTEHAK	2104.09	2104.10	-0.01	-2.45	4.E-32
P33778	RSTITSREIQTAVRLLLPGELAK	2551.45	2551.48	-0.03	-13.34	4.E-32
Q04695	(52)TTSIRQFTSSSSIK	1585.86	1583.82	2.04	1286.92	4.E-32
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQKDSYVGDEAQSK	4487.20	4487.19	0.01	1.58	5.E-32
P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-1.98	5.E-32
Q15233	TFTQRSRLFVGNLPPDITEEEMRK	2863.47	2863.47	0.00	-0.43	5.E-32
Q12905	GTMTTGHNVADLVVILK	1770.86	1767.96	2.90	1637.36	5.E-32
P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-1.15	5.E-32
O43390	YGGPPPDSVYSGVQPGIGTEVFVGKIPRDLYEDELVPLFEK	4463.26	4463.26	0.00	-0.17	5.E-32
P62805	VFLENVIRDAVTYTEHAK	2104.09	2104.10	-0.01	-3.22	6.E-32
P33778	RSTITSREIQTAVRLLLPGELAK	2553.45	2551.48	1.97	770.01	6.E-32
P08758	(41)AQVLRGTVTDFPGFDERADAETLRK	2833.44	2833.44	0.00	-1.29	7.E-32

P51991	IFVGGIKEDTEEYNLRDYFEK	2564.24	2564.24	0.00	-1.22	8.E-32
P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-0.64	8.E-32
P36578	APIRPDIVNFVHTNLRK	1989.13	1989.13	0.00	0.31	8.E-32
P62805	VFLENVIRDAVTYTEHAK	2104.05	2104.10	-0.05	-23.03	1.E-31
P60709	RGILTLKYPIE(317)HGIVTNWDDMEK	2741.41	2741.42	-0.01	-2.76	1.E-31
P51991	IFVGGIKEDTEEYNLRDYFEK	2560.34	2564.24	-3.90	-1523.99	1.E-31
P51991	RGFAFVTFDDHDTVDK	1870.87	1868.87	2.00	1070.90	1.E-31
P51991	RGFAFVTFDDHDTVDK	1871.10	1868.87	2.23	1190.22	1.E-31
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3179.56	3183.56	-4.00	-1259.15	1.E-31
O75367	AASADSTTEGTPADGFTVLSTK	2126.00	2126.00	0.00	-2.30	2.E-31
P22626	KRGFGFVTFDDHDPVDKIVLQK	2560.34	2560.34	0.00	-1.58	2.E-31
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.55	3183.56	-0.01	-2.93	2.E-31
P07355	DIISDTSGDFRK	1352.66	1352.66	0.00	-2.28	2.E-31
P19338	GYAFIEFASFEDAK	1593.71	1593.74	-0.03	-17.00	2.E-31
P19338	GYAFIEFASFEDAK	1593.74	1593.74	0.00	-2.19	2.E-31

P16403	(51)SETAPAAPAAAPPAEKAPVK	1915.01	1915.01	0.00	0.96	2.E-31
P51991	IFVGGIKEDTEEYNLRDYFEK	2565.24	2564.24	1.00	389.38	2.E-31
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-2.88	2.E-31
P51991	GGSFGGRSSGSPYGGGYGSGGGSGGYGSRRF	2831.23	2831.24	-0.01	-2.11	2.E-31
P07355	DIISDTSGDFRK	1351.73	1352.66	-0.93	-688.00	2.E-31
P05388	RVLALSVETDYTFPLAEK	2051.09	2051.09	0.00	-1.59	3.E-31
P04083	QAWFIENEEQEYVQTVK	2139.96	2140.01	-0.05	-21.25	3.E-31
Q548L2	LQEEMLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEIAFLK	5560.80	5560.81	-0.01	-0.99	3.E-31
Q7L4M3	TTSGYAGGLSSAYGGLTSPGLSYSLGSSFGSGAGSSSFSRTSSSRAVVVK	4739.31	4739.30	0.01	1.91	3.E-31
P14136	LALDIEIATYRK	1408.86	1404.80	4.06	2879.12	3.E-31
P20700	SLEGDLEDLKDQIAQLEASLAAAKK	2655.40	2655.40	0.00	-0.61	3.E-31
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.51	3153.55	-0.04	-13.85	3.E-31
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.55	3153.55	0.00	-0.65	3.E-31
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.14	3153.55	0.59	187.73	3.E-31
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.34	3153.55	0.79	251.19	3.E-31

P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.74	3153.55	1.19	378.14	3.E-31
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.94	3153.55	1.39	441.73	3.E-31
P07355	DIISDTSGDFRK	1354.65	1352.66	1.99	1465.42	3.E-31
P04083	QAWFIENEEQEYVQTVK	2140.01	2140.01	0.00	0.85	3.E-31
P05388	RVLALSVETDYTFPLAEK	2048.11	2051.09	-2.98	-1454.30	3.E-31
P14136	LALDIEIATYRK	1403.78	1404.80	-1.02	-727.92	3.E-31
P14136	LALDIEIATYRK	1404.80	1404.80	0.00	-1.59	3.E-31
P60903	EFPGFLENQKDPLAVDK	1945.98	1945.98	0.00	-1.80	4.E-31
P05387	ILDSVGIEADDDRLNK	1771.90	1771.90	0.00	-1.17	4.E-31
P08729	DARAKQEELEAALQRAK	1926.03	1926.03	0.00	-1.22	5.E-31
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.66	9098.88	-0.22	-24.32	5.E-31
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.86	9098.88	-0.02	-1.85	5.E-31
P02545	EGDLIAAQARLK	1285.67	1283.72	1.95	1513.76	5.E-31
P07355	AYTNFDAERDALNIETAIK	2154.05	2154.06	-0.01	-3.66	5.E-31
P51991	IFVGGIKEDTEEYNLRDYFEK	2565.24	2564.24	1.00	390.83	5.E-31

P05387	ILDSVGIEADDDRLNK	1766.97	1771.90	-4.93	-2791.27	6.E-31
P07355	AYTNFDAERDALNIETAIK	2151.05	2154.06	-3.01	-1398.98	6.E-31
P07355	AYTNFDAERDALNIETAIK	2154.01	2154.06	-0.05	-22.09	6.E-31
P02545	EGDLIAAQARLK	1283.72	1283.72	0.00	-0.79	6.E-31
P08670	FADLSEAANRNNDALRQAK	2103.05	2103.05	0.00	-1.23	6.E-31
P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-1.08	7.E-31
P08670	TVETRDGQVINETSQHHDDLE	2422.10	2422.10	0.00	1.14	7.E-31
P63220	(49)MQNDAGEFVDLYVPRK	1922.92	1922.92	0.00	-1.69	7.E-31
P25705	RTGAIVDVPVGEELLGRVVDALGNAIDGK	2932.59	2932.60	-0.01	-2.08	7.E-31
P02545	EGDLIAAQARLK	1287.62	1283.72	3.90	3031.54	8.E-31
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-2.61	1.E-30
Q04695	(52)TTSIRQFTSSSSIK	1583.82	1583.82	0.00	-0.09	1.E-30
Q04695	(52)TTSIRQFTSSSSIK	1584.79	1583.82	0.97	611.10	1.E-30
P62913	VLEQLTGQTPVFSK	1545.84	1545.84	0.00	-2.03	1.E-30
P0C0S8	TRIIPRHLQLAIRNDEELNK	2429.33	2428.37	0.96	396.02	1.E-30

P05787	KIETRDGKLVSESSDVLPK	2100.14	2100.14	0.00	-1.57	1.E-30
P05787	KIETRDGKLVSESSDVLPK	2103.04	2100.14	2.90	1379.05	1.E-30
O43390	VLFVRNLATTVTEEILEK	2077.12	2074.17	2.95	1418.96	1.E-30
P16403	AGGTPRKASGPPVSELITK	1865.04	1865.04	0.00	1.06	1.E-30
P62913	VLEQLTGQTPVFSK	1545.82	1545.84	-0.02	-15.42	1.E-30
O14979	VFVGGLSPDTSEEQIK	1704.86	1704.86	0.00	-1.82	1.E-30
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-1.64	2.E-30
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-3.72	2.E-30
P16403	KAGGTPRKASGPPVSELITK	1993.13	1993.13	0.00	0.77	2.E-30
P60709	RGILTLKYPIE(317)HGIVTNWDDMEK	2741.41	2741.42	-0.01	-2.76	2.E-30
P62913	VLEQLTGQTPVFSK	1543.89	1545.84	-1.95	-1261.51	2.E-30
O75934	(41)AGTGLVAGEVVVDALPYFDQGYEAPGVREAAAALVEEETRRYRPTK	4962.51	4962.52	-0.01	-1.49	2.E-30
P22626	RGFGFVTFDDHDPVDK	1854.85	1850.86	3.99	2152.35	2.E-30
P09651	PRNQGGYGGSSSSSSYGSGRRF	2250.02	2250.02	0.00	-2.00	2.E-30
P07355	SALSGHLETVILGLLK	1649.96	1649.97	-0.01	-3.19	2.E-30

P02545	EGDLIAAQARLK	1288.61	1283.72	4.89	3791.14	3.E-30
O14979	VFVGGLSPDTSEEQIK	1704.86	1704.86	0.00	-1.82	3.E-30
P33778	RSTITSREIQTAVRLLLPGELAK	2548.47	2551.48	-3.01	-1180.09	3.E-30
P16403	(51)SETAPAAPAAAPPAEKAPVK	1915.01	1915.01	0.00	-2.23	3.E-30
P16403	(51)SETAPAAPAAAPPAEKAPVK	1914.97	1915.01	-0.04	-18.94	3.E-30
P16403	(51)SETAPAAPAAAPPAEKAPVK	1915.01	1915.01	0.00	0.80	3.E-30
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.85	9098.88	-0.03	-3.69	3.E-30
P61978	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	3828.83	3828.94	-0.11	-27.97	3.E-30
P61978	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	3828.93	3828.94	-0.01	-2.14	3.E-30
P02545	EGDLIAAQARLK	1284.72	1283.72	1.00	779.77	3.E-30
P02545	EGDLIAAQARLK	1287.62	1283.72	3.90	3032.32	3.E-30
P08865	(51)SGALDVLQMKEEDVLK	1815.89	1815.93	-0.04	-21.27	3.E-30
P08865	(51)SGALDVLQMKEEDVLK	1815.93	1815.93	0.00	-2.16	3.E-30
P07355	SALSGHLETVILGLLK	1649.97	1649.97	0.00	-2.65	4.E-30
P33778	RSTITSREIQTAVRLLLPGELAK	2553.35	2551.48	1.87	731.38	4.E-30

P05787	KIETRDGKLVSESSDVLPK	2100.14	2100.14	0.00	0.62	4.E-30
Q15046	(41)AAVQAAEVKVDGSEPK	1639.84	1639.84	0.00	0.91	4.E-30
P22626	RGFGFVTFDDHDPVDK	1850.86	1850.86	0.00	-1.74	4.E-30
P0C0S8	TRIIPRHLQLAIRNDEELNK	2431.35	2428.37	2.98	1226.38	5.E-30
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-3.11	5.E-30
P33778	RSTITSREIQTAVRLLLPGELAK	2551.55	2551.48	0.07	25.58	5.E-30
P33778	RSTITSREIQTAVRLLLPGELAK	2552.43	2551.48	0.95	372.07	5.E-30
Q00839	NQSQGYNQWQQGQFWGQK	2210.99	2210.99	-0.01	-2.27	5.E-30
P08670	TVETRDGQVINETSQHHDDLE	2422.09	2422.10	-0.01	-2.21	5.E-30
P33778	RSTITSREIQTAVRLLLPGELAK	2551.37	2551.48	-0.11	-43.79	6.E-30
P33778	RSTITSREIQTAVRLLLPGELAK	2551.40	2551.48	-0.08	-31.76	6.E-30
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.34	2428.37	-0.03	-13.81	6.E-30
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-2.11	6.E-30
P05387	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEKKEESEESDDDMGFGLFD	5204.43	5204.43	0.00	0.94	6.E-30
P07355	WISIMTERSVPHLQK	1823.93	1823.97	-0.04	-21.22	7.E-30

P07355	WISIMTERSVPHLQK	1823.97	1823.97	0.00	-2.47	7.E-30
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-1.41	7.E-30
P07355	SLYYYIQQDTKGDYQK	2016.02	2011.95	4.07	2017.53	7.E-30
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-4.63	8.E-30
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.94	2369.45	0.49	208.62	8.E-30
P05787	LKLEAELGNMQGLVEDFK	2033.05	2033.05	0.00	-2.40	8.E-30
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3191.49	3153.55	37.94	11887.90	8.E-30
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3198.50	3153.55	44.95	14054.20	8.E-30
Q9H307	(41)AVAVRTLQEQLEK	1525.85	1525.85	0.00	-0.60	8.E-30
P08670	TVETRDGQVINETSQHHDDLE	2422.05	2422.10	-0.05	-22.48	9.E-30
P60709	DLYANTVLSGGTTMYPGIADRMQK	2603.21	2601.26	1.95	749.97	9.E-30
P07355	SLYYYIQQDTKGDYQK	2011.94	2011.95	-0.01	-2.74	1.E-29
P07355	SLYYYIQQDTKGDYQK	2012.91	2011.95	0.96	476.91	1.E-29
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.30	2428.37	-0.07	-29.99	1.E-29
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.42	2428.37	0.05	18.93	1.E-29

P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.43	2428.37	0.06	25.56	1.E-29
P07355	SLYYYIQQDTKGDYQK	2014.13	2011.95	2.18	1084.18	1.E-29
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.25	2601.26	-0.01	-2.65	1.E-29
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-4.01	1.E-29
P0C0S8	TRIIPRHLQLAIRNDEELNK	2429.33	2428.37	0.96	395.57	1.E-29
P04083	ALTGHLEEVVLALLK	1604.95	1604.95	0.00	-2.12	1.E-29
P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-1.27	1.E-29
P09651	GGNFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSSYGSGRRF	4251.93	4251.92	0.01	1.61	1.E-29
P60709	DLYANTVLSGGTTMYPGIADRMQK	2597.38	2601.26	-3.88	-1493.92	1.E-29
P05787	KIETRDGKLVSESSDVLPK	2100.14	2100.14	0.00	-1.57	1.E-29
P04083	ALTGHLEEVVLALLK	1604.85	1604.95	-0.10	-64.93	1.E-29
P04083	ALTGHLEEVVLALLK	1604.92	1604.95	-0.03	-17.13	1.E-29
P05388	ISRGTIEILSDVQLIK	1784.04	1784.04	0.00	-1.41	2.E-29
P07355	DIISDTSGDFRK	1352.64	1352.66	-0.02	-15.29	2.E-29
P07355	DIISDTSGDFRK	1352.66	1352.66	0.00	-1.02	2.E-29

P07355	DIISDTSGDFRK	1352.68	1352.66	0.02	18.20	2.E-29
P07355	DIISDTSGDFRK	1352.69	1352.66	0.03	25.66	2.E-29
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.80	3449.79	0.01	1.57	2.E-29
Q00839	HAAENPGKYNILGTNTIMDK	2186.07	2186.08	-0.01	-2.32	2.E-29
P07355	DIISDTSGDFRK	1352.62	1352.66	-0.04	-28.67	2.E-29
Q04695	(52)TTSIRQFTSSSSIK	1583.82	1583.82	0.00	-2.04	2.E-29
P19338	KMAPPPKEVEEDSEDEEMSEDEEDDSSGEEVVIPQK	4061.74	4061.73	0.01	1.52	2.E-29
Q04695	(52)TTSIRQFTSSSSIK	1584.78	1583.82	0.96	607.63	3.E-29
Q8NC51	DRKNPLPPSVGVVDKKEETQPPVALKK	2968.66	2968.67	-0.01	-2.08	3.E-29
Q04695	VRALEEANTELEVK	1596.86	1599.85	-2.99	-1872.66	3.E-29
Q04695	VRALEEANTELEVK	1599.85	1599.85	0.00	-1.60	3.E-29
Q04695	VRALEEANTELEVK	1600.82	1599.85	0.97	608.65	3.E-29
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.43	3357.44	-0.01	-1.58	3.E-29
Q53HU8	LLEGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSK	4133.04	4133.16	-0.12	-28.96	3.E-29
Q53HU8	LLEGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSK	4133.14	4133.16	-0.02	-6.02	3.E-29

P46776	LWTLVSEQTRVNAAK	1714.94	1714.94	0.00	-0.35	3.E-29
P22626	IDTIEIITDRQSGKK	1715.91	1715.94	-0.03	-19.14	3.E-29
P22626	IDTIEIITDRQSGKK	1715.94	1715.94	0.00	-2.47	3.E-29
O60506	ALLERTGYTLDVTTGQRK	2021.09	2021.09	0.00	-0.16	4.E-29
P69905	TYFPHFDLSHGSAQVK	1832.88	1832.88	0.00	-1.50	4.E-29
P55081	(51)SVPSALMKQPPIQSTAGAVPVRNEKGEISMEK	3420.78	3420.77	0.01	2.40	4.E-29
P46776	LWTLVSEQTRVNAAK	1710.91	1714.94	-4.03	-2356.29	4.E-29
P05787	TEISEMNRNISRLQAEIEGLK	2430.24	2430.25	-0.01	-2.36	4.E-29
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-0.18	5.E-29
Q99729	MFVGGLSWDTSKK	1456.71	1454.72	1.99	1363.30	5.E-29
O76021	SAALPIFSSFVSNWDEATK	2069.00	2069.01	-0.01	-2.58	5.E-29
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.88	9098.88	0.00	0.21	5.E-29
P51991	LFIGGLSFETTDDSLREHFEK	2440.19	2440.19	0.00	-1.89	5.E-29
P51991	LFIGGLSFETTDDSLREHFEK	2441.15	2440.19	0.96	393.09	5.E-29
Q7L4M3	TTSGYAGGLSSAYGGLTSPGLSYSLGSSFGSGAGSSSFSRTSSSRAVVVK	4739.29	4739.30	-0.01	-2.79	5.E-29

Q9H307	(41)AVAVRTLQEQLEK	1525.83	1525.85	-0.02	-15.94	5.E-29
Q9H307	(41)AVAVRTLQEQLEK	1525.85	1525.85	0.00	-1.12	5.E-29
P08729	LEAAIAEAEERGELALK	1809.93	1811.96	-2.03	-1120.61	5.E-29
P08729	LEAAIAEAEERGELALK	1811.79	1811.96	-0.17	-92.41	5.E-29
P08729	LEAAIAEAEERGELALK	1811.96	1811.96	0.00	-2.12	5.E-29
P05787	TEISEMNRNISRLQAEIEGLK	2427.10	2430.25	-3.15	-1297.82	6.E-29
Q99729	MFVGGLSWDTSKK	1454.70	1454.72	-0.02	-15.24	7.E-29
Q99729	MFVGGLSWDTSKK	1454.72	1454.72	0.00	-0.80	7.E-29
P31949	TEFLSFMNTELAAFTK	1848.89	1848.90	-0.01	-2.90	8.E-29
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.12	2256.13	-0.01	-3.21	8.E-29
Q86V81	LLVSNLDFGVSDADIQELFAEFGTLKK	2968.53	2968.54	-0.01	-1.71	9.E-29
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-3.41	9.E-29
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2260.18	2256.13	4.05	1791.74	1.E-28
O75533	IWDPTPSHTPAGAATPGRGDTPGHATPGHGGATSSARK	3673.78	3673.77	0.01	1.79	1.E-28
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4245.55	4245.54	0.01	1.45	1.E-28

P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.38	2369.45	-0.07	-29.96	1.E-28
P22626	IDTIEIITDRQSGK	1583.82	1587.85	-4.03	-2547.26	2.E-28
P22626	IDTIEIITDRQSGK	1584.78	1587.85	-3.07	-1936.60	2.E-28
P62805	RKTVTAMDVVYALK	1593.89	1593.89	0.00	-1.33	2.E-28
P09651	GGNFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSSYGSGRRF	4251.93	4251.92	0.01	1.40	2.E-28
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.89	9098.88	0.01	0.92	2.E-28
P02545	LALDMEIHAYRK	1458.73	1458.77	-0.04	-24.88	2.E-28
P02545	LALDMEIHAYRK	1458.77	1458.77	0.00	-1.23	2.E-28
P62280	(41)ADIQTERAYQKQPTIFQNK	2320.18	2320.18	0.00	1.52	2.E-28
P22626	IDTIEIITDRQSGK	1587.85	1587.85	0.00	-1.37	2.E-28
P67809	GAEAANVTGPGGVPVQGSK	1694.86	1694.86	0.00	-2.19	2.E-28
P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-1.74	2.E-28
P16403	ASGPPVSELITK	1198.65	1197.66	0.99	824.87	2.E-28
P16403	ASGPPVSELITK	1198.66	1197.66	1.00	836.29	2.E-28
P09651	GGNFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSSYGSGRRF	4251.83	4251.92	-0.09	-21.18	2.E-28

P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-1.65	2.E-28
Q04695	ATMQNLNDRLASYLDK	1848.88	1851.91	-3.03	-1639.20	3.E-28
P07355	SALSGHLETVILGLLK	1649.94	1649.97	-0.03	-17.98	3.E-28
P07355	SALSGHLETVILGLLK	1649.97	1649.97	0.00	-1.98	3.E-28
P62805	VFLENVIRDAVTYTEHAK	2099.60	2104.10	-4.50	-2142.44	3.E-28
P62805	VFLENVIRDAVTYTEHAK	2101.10	2104.10	-3.00	-1428.62	3.E-28
P62805	VFLENVIRDAVTYTEHAK	2102.60	2104.10	-1.50	-715.15	3.E-28
P62805	VFLENVIRDAVTYTEHAK	2104.05	2104.10	-0.05	-23.89	3.E-28
P14866	SKPGAAMVEMADGYAVDRAITHLNNNFMFGQK	3482.65	3482.65	0.00	-0.89	3.E-28
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-5.05	3.E-28
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.95	2369.45	0.50	210.90	3.E-28
P62913	VLEQLTGQTPVFSK	1543.89	1545.84	-1.95	-1261.70	4.E-28
P62913	VLEQLTGQTPVFSK	1545.84	1545.84	0.00	-1.77	4.E-28
Q04695	ATMQNLNDRLASYLDK	1851.91	1851.91	0.00	-0.96	4.E-28
P41219	MALDIEIATYRK	1423.75	1422.75	1.00	704.01	4.E-28

P62805	TVTAMDVVYALK	1310.67	1309.70	0.97	741.11	4.E-28
P62318	IRFLILPDMLK	1357.82	1357.82	0.00	-0.69	4.E-28
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.39	2369.45	-0.06	-24.93	4.E-28
P60709	YPIE(317)HGIVTNWDDMEK	1956.08	1959.90	-3.82	-1950.88	4.E-28
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	6898.52	6722.54	175.98	25509.60	4.E-28
P62805	TVTAMDVVYALK	1312.70	1309.70	3.00	2281.99	5.E-28
P60709	YPIE(317)HGIVTNWDDMEK	1959.87	1959.90	-0.03	-13.36	5.E-28
P02545	EGDLIAAQARLK	1283.70	1283.72	-0.02	-13.18	6.E-28
P02545	EGDLIAAQARLK	1283.72	1283.72	0.00	-1.49	6.E-28
P02545	EGDLIAAQARLK	1285.67	1283.72	1.95	1514.38	6.E-28
P0C0S8	TRIIPRHLQLAIRNDEELNK	2429.34	2428.37	0.97	400.59	6.E-28
P04083	ALTGHLEEVVLALLK	1604.95	1604.95	0.00	-1.24	6.E-28
O00148	GLAITFVSDENDAK	1478.73	1478.73	0.00	-1.46	6.E-28
P05387	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEKKEE(37)SEE(37)SDDDMGFGLFD	5364.34	5364.36	-0.02	-3.28	7.E-28
P60709	YPIE(317)HGIVTNWDDMEK	1959.90	1959.90	0.00	-1.57	7.E-28

P0C0S8	TRIIPRHLQLAIRNDEELNK	2429.34	2428.37	0.97	400.88	7.E-28
P33778	RSTITSREIQTAVRLLLPGELAK	2551.40	2551.48	-0.08	-31.84	7.E-28
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-3.15	7.E-28
P02545	EGDLIAAQARLK	1287.62	1283.72	3.90	3032.32	7.E-28
P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3778.72	7.E-28
P05787	LSELEAALQRAK	1327.63	1327.75	-0.12	-91.47	8.E-28
P05787	LSELEAALQRAK	1327.71	1327.75	-0.04	-28.80	8.E-28
P05787	LSELEAALQRAK	1327.72	1327.75	-0.03	-24.28	8.E-28
P05787	LSELEAALQRAK	1327.75	1327.75	0.00	-2.36	8.E-28
P05787	LSELEAALQRAK	1327.77	1327.75	0.02	17.52	8.E-28
P16403	ASGPPVSELITK	1198.66	1197.66	1.00	837.95	8.E-28
P62805	TVTAMDVVYALK	1312.70	1309.70	3.00	2281.99	9.E-28
P07355	AYTNFDAERDALNIETAIK	2154.02	2154.06	-0.04	-16.93	9.E-28
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-2.41	9.E-28
P62805	TVTAMDVVYALK	1309.74	1309.70	0.04	31.87	9.E-28

P62805	TVTAMDVVYALK	1309.75	1309.70	0.05	38.44	9.E-28
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-0.39	9.E-28
P62805	TVTAMDVVYALK	1310.67	1309.70	0.97	740.96	1.E-27
P07355	AYTNFDAERDALNIETAIK	2154.06	2154.06	0.00	-1.61	1.E-27
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-1.74	1.E-27
P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3779.33	1.E-27
P62805	TVTAMDVVYALK	1309.65	1309.70	-0.05	-41.66	1.E-27
P62805	TVTAMDVVYALK	1309.65	1309.70	-0.05	-37.46	1.E-27
P62805	TVTAMDVVYALK	1309.67	1309.70	-0.03	-23.41	1.E-27
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.93	9098.88	0.05	6.03	1.E-27
Q15149	AVTGYRDPYTGQSVSLFQALKK	2437.21	2428.28	8.93	3664.64	2.E-27
P07355	WISIMTERSVPHLQK	1823.93	1823.97	-0.04	-19.52	2.E-27
P07355	WISIMTERSVPHLQK	1823.97	1823.97	0.00	-1.81	2.E-27
P62805	TVTAMDVVYALK	1309.68	1309.70	-0.02	-15.54	2.E-27
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-2.33	2.E-27

Q15046	(41)AAVQAAEVKVDGSEPK	1639.84	1639.84	0.00	0.91	2.E-27
P05204	VKDEPQRRSARLSAKPAPPKPEPKPK	2906.65	2906.66	-0.01	-1.75	2.E-27
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.44	2572.44	0.00	-1.77	2.E-27
P08758	(41)AQVLRGTVTDFPGFDERADAETLRK	2833.43	2833.44	-0.01	-2.27	2.E-27
P62805	TVTAMDVVYALK	1309.68	1309.70	-0.02	-15.16	2.E-27
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-0.73	2.E-27
P62805	TVTAMDVVYALK	1309.66	1309.70	-0.04	-33.87	2.E-27
P62805	TVTAMDVVYALK	1309.67	1309.70	-0.03	-24.40	2.E-27
P62906	KYDAFLASESLIK	1483.79	1483.79	0.00	-1.29	2.E-27
P16403	(51)SETAPAAPAAAPPAEK	1517.84	1519.75	-1.91	-1259.31	2.E-27
P16403	(51)SETAPAAPAAAPPAEK	1519.73	1519.75	-0.02	-16.34	2.E-27
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	-2.52	2.E-27
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.39	2572.44	-0.05	-17.99	2.E-27
O14979	EYFGAFGEIENIELPMDTK	2202.01	2202.02	-0.01	-2.65	2.E-27
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.89	9098.88	0.01	1.05	2.E-27

P07355	DIISDTSGDFRK	1355.77	1352.66	3.11	2293.92	2.E-27
P06748	TPKTPKGPSSVEDIKAKMQASIEK	2569.38	2569.38	0.00	1.40	2.E-27
P0C0S5	SRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASK	3776.96	3776.97	-0.01	-3.80	3.E-27
P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3779.78	3.E-27
P06748	VKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4344.50	4344.61	-0.11	-26.33	3.E-27
P06748	VKLAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4344.62	4344.61	0.01	1.41	3.E-27
P36578	AFRNIPGITLLNVSK	1641.96	1641.96	0.00	-1.64	3.E-27
P36578	AFRNIPGITLLNVSK	1645.87	1641.96	3.91	2377.95	3.E-27
P07355	SYSPYDMLESIRK	1587.76	1587.76	0.00	-2.32	4.E-27
P07355	SYSPYDMLESIRK	1588.74	1587.76	0.98	613.89	4.E-27
P61978	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	3828.84	3828.94	-0.10	-27.00	4.E-27
P61978	IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK	3828.92	3828.94	-0.02	-4.49	4.E-27
P07355	DIISDTSGDFRK	1352.66	1352.66	0.00	-0.21	4.E-27
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.87	9082.91	-0.04	-4.73	4.E-27
P08670	ILLAELEQLKGQGK	1535.88	1538.90	-3.02	-1968.61	5.E-27

P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.47	3138.52	-0.05	-16.22	5.E-27
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.52	3138.52	0.00	0.06	5.E-27
O95777	(52)TSALENYINRTVAVITSDGRMIVGTLK	2963.58	2963.58	0.00	-1.66	5.E-27
P26599	HQNVQLPREGQEDQGLTK	2076.03	2076.03	0.00	-1.64	6.E-27
P08670	ILLAELEQLKGQGK	1538.88	1538.90	-0.02	-15.11	6.E-27
P08670	ILLAELEQLKGQGK	1538.90	1538.90	0.00	0.35	6.E-27
P08670	ILLAELEQLKGQGK	1543.83	1538.90	4.93	3190.99	6.E-27
Q12906	YELISETGGSHDK	1431.71	1434.66	-2.95	-2063.03	7.E-27
Q12906	YELISETGGSHDK	1434.64	1434.66	-0.02	-16.43	7.E-27
Q12906	YELISETGGSHDK	1434.66	1434.66	0.00	-1.23	7.E-27
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-3.58	7.E-27
Q13185	WKDSDEADLVLAK	1488.75	1488.75	0.00	-0.73	7.E-27
P62805	TVTAMDVVYALK	1309.68	1309.70	-0.02	-14.55	7.E-27
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-0.58	7.E-27
P62805	TVTAMDVVYALK	1312.70	1309.70	3.00	2283.43	7.E-27

P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKKSIRDTPAK	5114.03	5114.02	0.01	1.35	8.E-27
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9096.92	9098.88	-1.96	-215.25	9.E-27
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.45	3138.52	-0.07	-23.30	9.E-27
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.52	3138.52	0.00	-1.28	9.E-27
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3142.60	3138.52	4.08	1299.78	9.E-27
Q12906	YELISETGGSHDK	1438.77	1434.66	4.11	2860.02	1.E-26
P62805	TVTAMDVVYALK	1309.67	1309.70	-0.03	-26.38	1.E-26
P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3780.39	1.E-26
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.44	3357.44	0.00	-0.15	1.E-26
Q04695	EPVTTRQVRTIVEEVQDGK	2183.12	2183.15	-0.03	-13.68	1.E-26
Q04695	EPVTTRQVRTIVEEVQDGK	2183.15	2183.15	0.00	-0.72	1.E-26
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.87	9098.88	-0.01	-0.96	1.E-26
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9099.65	9098.88	0.77	84.15	1.E-26
Q71UI9	ATIAGGGVIPHIHK	1369.76	1369.78	-0.02	-15.24	1.E-26
Q71UI9	ATIAGGGVIPHIHK	1369.78	1369.78	0.00	-0.71	1.E-26

Q04695	(52)TTSIRQFTSSSSIK	1583.82	1583.82	0.00	-2.04	1.E-26
Q04695	EPVTTRQVRTIVEEVQDGK	2183.15	2183.15	0.00	-0.58	1.E-26
Q04695	EPVTTRQVRTIVEEVQDGK	2184.12	2183.15	0.97	443.99	1.E-26
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-3.58	1.E-26
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.37	3357.44	-0.07	-21.74	1.E-26
P02545	SNEDQSMGNWQIK	1535.67	1535.67	0.00	-1.27	1.E-26
P07355	SALSGHLETVILGLLK	1649.94	1649.97	-0.03	-17.98	2.E-26
P07355	SALSGHLETVILGLLK	1649.97	1649.97	0.00	-1.98	2.E-26
Q04695	VRALEEANTELEVK	1604.85	1599.85	5.00	3113.47	2.E-26
P09651	RGFAFVTFDDHDSVDK	1854.85	1854.85	0.00	-1.42	2.E-26
P46777	HIMGQNVADYMRYLMEEDEDAYKK	2948.30	2948.31	-0.01	-2.03	2.E-26
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.31	3357.44	-0.13	-37.92	2.E-26
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.34	2428.37	-0.03	-12.49	2.E-26
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-0.34	2.E-26
Q86V81	LLVSNLDFGVSDADIQELFAEFGTLKK	2968.54	2968.54	0.00	-1.11	2.E-26

P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-3.76	2.E-26
P16403	KAGGTPRKASGPPVSELITK	1993.13	1993.13	0.00	1.57	2.E-26
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.21	1930.16	0.05	24.82	2.E-26
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.33	2428.37	-0.04	-18.26	2.E-26
P09651	RGFAFVTFDDHDSVDK	1854.81	1854.85	-0.04	-20.07	2.E-26
P09651	RGFAFVTFDDHDSVDK	1854.85	1854.85	0.00	-2.01	2.E-26
P52272	(41)AAGVEAAAEVAATEIKMEEESGAPGVPSGNGAPGPKGEGERPAQNEK	4585.16	4586.18	-1.02	-223.03	2.E-26
P52272	(41)AAGVEAAAEVAATEIKMEEESGAPGVPSGNGAPGPKGEGERPAQNEK	4587.16	4586.18	0.98	213.77	2.E-26
Q04695	VRALEEANTELEVK	1599.82	1599.85	-0.03	-17.79	2.E-26
Q04695	VRALEEANTELEVK	1599.85	1599.85	0.00	-1.10	2.E-26
Q04695	VRALEEANTELEVK	1603.86	1599.85	4.01	2500.12	2.E-26
Q04695	VRALEEANTELEVK	1603.86	1599.85	4.01	2500.12	2.E-26
P42766	SIARVLTVINQTQK	1569.92	1569.92	0.00	-1.35	2.E-26
O14979	EYFGAFGEIENIELPMDTK	2201.97	2202.02	-0.05	-22.86	2.E-26
O14979	EYFGAFGEIENIELPMDTK	2202.01	2202.02	-0.01	-3.15	2.E-26

P22626	LFIGGLSFETTEESLRNYYEQWGK	2866.37	2866.38	-0.01	-2.25	2.E-26
Q96A72	IGSLIDVNQSKDPEGLRVFYYLVQDLK	3108.65	3108.65	0.00	-1.38	2.E-26
P02545	SNEDQSMGNWQIK	1531.75	1535.67	-3.92	-2557.90	2.E-26
Q12905	RNQDLAPNSAEQASILSLVTK	2257.17	2254.19	2.98	1322.23	2.E-26
P26373	STESLQANVQRLK	1472.79	1472.79	0.00	-1.35	3.E-26
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.12	1930.16	-0.04	-22.69	3.E-26
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.62	3.E-26
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.60	3307.68	-0.08	-24.77	3.E-26
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.68	3307.68	0.00	-0.88	3.E-26
Q12905	RNQDLAPNSAEQASILSLVTK	2254.15	2254.19	-0.04	-16.94	3.E-26
Q12905	RNQDLAPNSAEQASILSLVTK	2254.19	2254.19	0.00	1.20	3.E-26
P05388	AIRGHLENNPALEK	1559.80	1560.84	-1.04	-666.37	3.E-26
P05388	AIRGHLENNPALEK	1560.84	1560.84	0.00	0.12	3.E-26
Q8WVK2	KVDGSVNAYAINVSQK	1691.87	1691.88	-0.01	-7.76	3.E-26
P10412	(51)SETAPAAPAAPAPAEKTPVK	1945.02	1945.02	0.00	0.91	3.E-26

P42766	SIARVLTVINQTQK	1569.92	1569.92	0.00	-2.56	3.E-26
P09651	RGFAFVTFDDHDSVDK	1850.85	1854.85	-4.00	-2160.16	4.E-26
P39019	DVNQQEFVRALAAFLK	1847.99	1847.99	0.00	-2.41	4.E-26
P31949	TEFLSFMNTELAAFTK	1847.99	1848.90	-0.91	-492.03	4.E-26
P31949	TEFLSFMNTELAAFTK	1848.90	1848.90	0.00	-1.28	4.E-26
P30050	EILGTAQSVGCNVDGRHPHDIIDDINSGAVECPAS	3588.66	3588.66	0.00	-0.96	4.E-26
P25705	AVDSLVPIGRGQRELIIGDRQTGK	2577.44	2577.44	0.00	-1.68	5.E-26
P16403	KAGGTPRKASGPPVSELITK	1993.13	1993.13	0.00	1.42	5.E-26
Q00839	LNTLLQRAPQCLGK	1553.87	1553.87	0.00	-1.20	5.E-26
P84090	(51)SHTILLVQPTK	1277.71	1277.73	-0.02	-13.90	5.E-26
P62750	AYVRLAPDYDALDVANKIGII	2289.23	2289.24	-0.01	-3.20	5.E-26
P0C0S5	SRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASK	3776.96	3776.97	-0.01	-1.57	5.E-26
P22626	IDTIEIITDRQSGK	1587.85	1587.85	0.00	-1.12	5.E-26
P02545	EGDLIAAQARLK	1283.72	1283.72	0.00	-1.18	5.E-26
P02545	EGDLIAAQARLK	1285.67	1283.72	1.95	1513.76	5.E-26

P07910	LKGDDLQAIKK	1231.73	1227.72	4.01	3256.68	5.E-26
P08708	LLDFGSLSNLQVTQPTVGMNFK	2408.23	2408.24	-0.01	-3.88	6.E-26
P84090	(51)SHTILLVQPTK	1277.73	1277.73	0.00	-1.61	6.E-26
P22626	IDTIEIITDRQSGK	1587.82	1587.85	-0.03	-16.67	6.E-26
Q00839	LNTLLQRAPQCLGK	1554.85	1553.87	0.98	628.25	6.E-26
P10412	(51)SETAPAAPAAPAPAEK(38)TPVK	2024.98	2024.98	0.00	-2.04	6.E-26
P04083	ALTGHLEEVVLALLK	1604.95	1604.95	0.00	-2.12	6.E-26
Q04695	(52)TTSIRQFTSSSSIK	1583.82	1583.82	0.00	-1.66	7.E-26
P84090	(51)SHTILLVQPTK	1277.70	1277.73	-0.03	-23.21	7.E-26
P60709	YPIE(317)HGIVTNWDDMEK	1959.90	1959.90	0.00	-1.83	8.E-26
Q04695	(52)TTSIRQFTSSSSIK	1584.80	1583.82	0.98	615.33	8.E-26
Q04695	VRALEEANTELEVK	1602.82	1599.85	2.97	1850.27	8.E-26
P08729	LLETKWTLLQEQK	1628.91	1628.91	0.00	-0.82	8.E-26
P08729	LLETKWTLLQEQK	1631.86	1628.91	2.95	1810.11	8.E-26
O14979	LLESRYHQIGSGK	1486.79	1486.79	0.00	-0.27	9.E-26

Q71UI9	ATIAGGGVIPHIHK	1369.75	1369.78	-0.03	-25.24	9.E-26
Q71UI9	ATIAGGGVIPHIHK	1369.76	1369.78	-0.02	-15.24	9.E-26
Q71UI9	ATIAGGGVIPHIHK	1369.78	1369.78	0.00	-2.54	9.E-26
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-2.12	1.E-25
P62910	AIVERAAQLAIRVTNPNARLRSEENE	2919.55	2919.56	-0.01	-1.75	1.E-25
Q04695	VRALEEANTELEVK	1599.82	1599.85	-0.03	-17.92	1.E-25
Q04695	VRALEEANTELEVK	1599.85	1599.85	0.00	-1.48	1.E-25
Q04695	VRALEEANTELEVK	1600.70	1599.85	0.85	531.92	1.E-25
P16403	ASGPPVSELITK	1198.66	1197.66	1.00	836.12	1.E-25
Q15233	GIVEFSGKPAARK	1358.77	1358.77	0.00	-1.54	1.E-25
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-2.74	1.E-25
P22626	IDTIEIITDRQSGK	1583.82	1587.85	-4.03	-2546.81	1.E-25
P51991	GGSFGGRSSGSPYGGGYGSGGGSGGYGSRRF	2831.24	2831.24	0.00	1.35	1.E-25
P61513	TVAGGAWTYNTTSAVTVK	1825.92	1825.92	0.00	-1.92	1.E-25
P60903	PSQMEHAMETMMFTFHK	2081.88	2081.88	0.00	-2.09	2.E-25

P22626	IDTIEIITDRQSGK	1587.85	1587.85	0.00	-2.19	2.E-25
P22626	IDTIEIITDRQSGK	1589.83	1587.85	1.98	1243.49	2.E-25
P62851	IRGSLARAALQELLSK	1725.03	1725.03	0.00	-1.26	2.E-25
P07910	LKGDDLQAIKK	1228.71	1227.72	0.99	803.16	2.E-25
P21796	SRVTQSNFAVGYK	1455.75	1455.75	0.00	0.81	2.E-25
P21796	SRVTQSNFAVGYK	1455.83	1455.75	0.08	57.48	2.E-25
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9096.92	9098.88	-1.96	-215.04	2.E-25
Q13185	WKDSDEADLVLAK	1488.75	1488.75	0.00	-1.13	2.E-25
P38159	LFIGGLNTETNEK	1432.62	1434.74	-2.12	-1477.95	2.E-25
P38159	LFIGGLNTETNEK	1434.74	1434.74	0.00	-0.72	2.E-25
P38159	LFIGGLNTETNEK	1435.72	1434.74	0.98	680.54	2.E-25
P62805	TVTAMDVVYALK	1311.68	1309.70	1.98	1508.03	2.E-25
P62805	TVTAMDVVYALK	1312.69	1309.70	2.99	2281.46	2.E-25
P07910	LKGDDLQAIKK	1227.72	1227.72	0.00	-0.78	2.E-25
P05386	KVEAKKEESEESDDDMGFGLFD	2504.08	2504.09	-0.01	-2.97	2.E-25

P17096	RGRGRPRKQPPVSPGTALVGSQKEPSEVPTPK	3392.88	3392.88	0.00	-1.04	3.E-25
O75367	AASADSTTEGTPADGFTVLSTK	2126.00	2126.00	0.00	-0.75	3.E-25
P62805	TVTAMDVVYALK	1310.75	1309.70	1.05	797.45	3.E-25
P38159	LFIGGLNTETNEK	1434.74	1434.74	0.00	-1.35	3.E-25
P38159	LFIGGLNTETNEK	1435.72	1434.74	0.98	680.89	3.E-25
P38159	LFIGGLNTETNEK	1437.75	1434.74	3.01	2092.14	3.E-25
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-2.94	3.E-25
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-3.20	3.E-25
P62805	TVTAMDVVYALK	1309.68	1309.70	-0.02	-16.46	3.E-25
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-2.94	3.E-25
P62805	TVTAMDVVYALK	1309.74	1309.70	0.04	33.48	3.E-25
P62805	TVTAMDVVYALK	1309.76	1309.70	0.06	42.56	3.E-25
P05787	KIETRDGKLVSESSDVLPK	2100.14	2100.14	0.00	-0.53	3.E-25
P05787	KIETRDGKLVSESSDVLPK	2101.11	2100.14	0.97	462.28	3.E-25
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-3.26	4.E-25

P63220	(49)MQNDAGEFVDLYVPRK	1922.92	1922.92	0.00	-2.47	4.E-25
P38919	EQIYDVYRYLPPATQVVLISATLPHEILEMTNK	3844.00	3844.01	-0.01	-3.00	4.E-25
P62805	TVTAMDVVYALK	1309.64	1309.70	-0.06	-42.65	4.E-25
P62805	TVTAMDVVYALK	1309.66	1309.70	-0.04	-33.49	4.E-25
P62805	TVTAMDVVYALK	1309.67	1309.70	-0.03	-25.01	4.E-25
P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3778.80	4.E-25
P61247	VERADGYEPPVQESV	1673.79	1673.79	0.00	0.57	4.E-25
P61247	VERADGYEPPVQESV	1677.82	1673.79	4.03	2403.03	4.E-25
P26599	HQNVQLPREGQEDQGLTK	2076.03	2076.03	0.00	-0.77	4.E-25
P08865	LLLAARAIVAIENPADVSVISSRNTGQRAVLK	3344.92	3344.93	-0.01	-1.80	4.E-25
Q14103	IFVGGLSPDTPEEK	1487.75	1487.75	0.00	-1.37	4.E-25
P07355	DIISDTSGDFRK	1352.64	1352.66	-0.02	-14.63	4.E-25
P07355	DIISDTSGDFRK	1352.66	1352.66	0.00	0.38	4.E-25
P42766	SIARVLTVINQTQK	1565.86	1569.92	-4.06	-2593.67	5.E-25
Q71UI9	ATIAGGGVIPHIHK	1373.70	1369.78	3.92	2854.42	5.E-25

P62910	AIVERAAQLAIRVTNPNARLRSEENE	2919.55	2919.56	-0.01	-1.99	5.E-25
P69905	TYFPHFDLSHGSAQVK	1829.92	1832.88	-2.96	-1619.23	5.E-25
P69905	TYFPHFDLSHGSAQVK	1832.88	1832.88	0.00	-2.16	5.E-25
P69905	TYFPHFDLSHGSAQVK	1836.95	1832.88	4.07	2215.00	5.E-25
Q71UI9	ATIAGGGVIPHIHK	1365.70	1369.78	-4.08	-2986.28	6.E-25
Q71UI9	ATIAGGGVIPHIHK	1369.78	1369.78	0.00	-1.59	6.E-25
P41219	NLQEAEEWYK	1308.60	1308.60	0.00	-1.69	6.E-25
P20674	EIYPYVIQELRPTLNELGISTPEELGLDKV	3427.80	3427.81	-0.01	-2.71	7.E-25
P39019	DVNQQEFVRALAAFLK	1847.99	1847.99	0.00	-1.32	7.E-25
P39019	DVNQQEFVRALAAFLK	1848.89	1847.99	0.90	488.92	7.E-25
P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.87	3777.88	-0.01	-1.85	8.E-25
Q16695	QLAT(55)KVARKSAPATGGVK	1824.06	1824.06	0.00	-0.84	8.E-25
P05204	VKDEPQRRSARLSAKPAPPKPEPKPK	2906.65	2906.66	-0.01	-1.78	8.E-25
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-2.53	8.E-25
P42766	SIARVLTVINQTQK	1569.92	1569.92	0.00	-1.16	9.E-25

Q8IUE6	TRIIPRHLQLAVRNDEELNK	2414.35	2414.35	0.00	-0.91	9.E-25
Q00839	EKPYFPIPEEYTFIQNVPLEDRVRGPK	3260.68	3260.69	-0.01	-2.46	9.E-25
P07355	SALSGHLETVILGLLK	1646.58	1649.97	-3.39	-2057.63	1.E-24
P07355	SALSGHLETVILGLLK	1649.97	1649.97	0.00	-2.22	1.E-24
P07355	SALSGHLETVILGLLK	1650.94	1649.97	0.97	588.78	1.E-24
P16401	(51)SETAPAETATPAPVEK	1639.79	1639.79	0.00	-1.89	1.E-24
Q9Y3U8	ALRYPMAVGLNK	1336.69	1331.74	4.95	3701.58	1.E-24
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.31	2270.37	-0.06	-26.35	1.E-24
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.36	2270.37	-0.01	-4.55	1.E-24
O75367	AASADSTTEGTPADGFTVLSTK	2125.99	2126.00	-0.01	-2.39	1.E-24
Q8IUE6	TRIIPRHLQLAVRNDEELNK	2418.26	2414.35	3.91	1616.13	1.E-24
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.55	3153.55	0.00	-0.91	1.E-24
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.51	3138.52	-0.01	-2.14	1.E-24
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3142.60	3138.52	4.08	1299.81	1.E-24
P62304	VMVQPINLIFRYLQNRSRIQVWLYEQVNMRIEGCIIGFDEYMNLVLDDAEEIHSKTK	6869.51	6869.50	0.01	1.12	1.E-24

Q16695	QLAT(55)KVARKSAPATGGVK	1824.02	1824.06	-0.04	-20.79	1.E-24
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-0.14	1.E-24
P07355	LSLEGDHSTPPSAYGSVK	1843.89	1843.90	-0.01	-3.46	1.E-24
P20674	EIYPYVIQELRPTLNELGISTPEELGLDKV	3427.80	3427.81	-0.01	-3.67	1.E-24
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.42	2428.37	0.05	21.69	1.E-24
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.44	2428.37	0.07	27.49	1.E-24
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.28	2428.37	-0.09	-38.03	1.E-24
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.29	2428.37	-0.08	-32.38	1.E-24
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.33	2428.37	-0.04	-17.89	1.E-24
Q9Y3U8	ALRYPMAVGLNK	1331.72	1331.74	-0.02	-14.76	1.E-24
Q9Y3U8	ALRYPMAVGLNK	1331.74	1331.74	0.00	-1.17	1.E-24
Q9Y3U8	ALRYPMAVGLNK	1331.83	1331.74	0.09	67.01	1.E-24
O14979	LLESRYHQIGSGK	1486.79	1486.79	0.00	-0.61	1.E-24
P62805	RISGLIYEETRGVLK	1732.98	1732.98	0.00	-1.64	1.E-24
Q00839	LNTLLQRAPQCLGK	1553.87	1553.87	0.00	-0.69	1.E-24

O75367	NGPLEVAGAAVSAGHGLPAK	1814.96	1814.96	0.00	-1.78	2.E-24
Q02539	SLVSKGTLVQTK	1256.63	1259.74	-3.11	-2474.05	2.E-24
Q02539	SLVSKGTLVQTK	1259.74	1259.74	0.00	-1.34	2.E-24
Q71UI9	ATIAGGGVIPHIHK	1368.69	1369.78	-1.10	-800.02	2.E-24
Q71UI9	ATIAGGGVIPHIHK	1369.76	1369.78	-0.02	-14.87	2.E-24
Q71UI9	ATIAGGGVIPHIHK	1369.78	1369.78	0.00	-1.59	2.E-24
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9096.92	9098.88	-1.96	-215.41	2.E-24
P07355	LSLEGDHSTPPSAYGSVK	1847.85	1843.90	3.95	2135.42	2.E-24
P16403	(51)SETAPAAPAAAPPAEK	1517.84	1519.75	-1.91	-1258.38	2.E-24
P16403	(51)SETAPAAPAAAPPAEK	1519.73	1519.75	-0.02	-16.14	2.E-24
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	-2.52	2.E-24
P0C0S5	SRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASK	3776.96	3776.97	-0.01	-1.92	2.E-24
P98179	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	3493.73	3493.74	-0.01	-2.97	2.E-24
O75526	SRGFAFVTFESPADAK	1725.81	1728.85	-3.04	-1760.85	2.E-24
O75526	SRGFAFVTFESPADAK	1728.85	1728.85	0.00	-1.44	2.E-24

O75526	SRGFAFVTFESPADAK	1732.98	1728.85	4.13	2384.85	2.E-24
Q71UI9	ATIAGGGVIPHIHK	1369.76	1369.78	-0.02	-14.58	2.E-24
Q71UI9	ATIAGGGVIPHIHK	1369.78	1369.78	0.00	-0.64	2.E-24
P35659	KKVERLTMQVSSLQREPFTIAQGK	2773.52	2773.53	-0.01	-2.28	2.E-24
P26373	STESLQANVQRLK	1472.79	1472.79	0.00	-1.29	2.E-24
Q6FI13	SRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	6509.50	6509.51	-0.01	-0.89	3.E-24
Q04695	ATMQNLNDRLASYLDK	1854.85	1851.91	2.94	1584.07	3.E-24
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.44	3357.44	0.00	-0.80	3.E-24
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.61	3307.68	-0.07	-22.17	3.E-24
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-3.42	3.E-24
P14866	RQRQPPLLGDHPAEYGGPHGGYHSHYHDEGYGPPPPHYEGRRMGPPVGGHRRGPSRYGPQYGHPPPPPPPPEYGPHADSPVLMVYGLDQSK	9977.75	9977.75	0.00	-0.40	3.E-24
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9097.93	9098.88	-0.95	-104.64	4.E-24
O60506	ALLERTGYTLDVTTGQRK	2021.09	2021.09	0.00	-1.55	4.E-24
P38159	LFIGGLNTETNEK	1434.74	1434.74	0.00	-1.42	4.E-24
Q08211	LAQFEPSQRQNQVGVVPWSPPQSNWNPWTSSNIDEGPLAFATPEQISMDLKNELMYQLEQDHDLQAILQERELLPVK	8867.36	8867.37	-0.01	-1.34	5.E-24

Q04695	ATMQNLNDRLASYLDK	1850.85	1851.91	-1.06	-571.13	5.E-24
Q04695	ATMQNLNDRLASYLDK	1851.91	1851.91	0.00	-1.07	5.E-24
P61978	IILDLISESPIK	1339.80	1339.80	0.00	-1.07	5.E-24
P07355	LSLEGDHSTPPSAYGSVK	1843.89	1843.90	-0.01	-3.02	5.E-24
Q548L2	LQEEMLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEIAFLK	5560.80	5560.81	-0.01	-2.30	5.E-24
P26447	ELLTRELPSFLGK	1501.83	1501.85	-0.02	-15.91	5.E-24
P26447	ELLTRELPSFLGK	1501.85	1501.85	0.00	-0.33	5.E-24
P04083	GVDEATIIDILTK	1384.69	1386.76	-2.07	-1498.08	6.E-24
P04083	GVDEATIIDILTK	1386.76	1386.76	0.00	-1.50	6.E-24
Q15233	LEMEMEAARHEHQVMLMRQDLMRRQEELRRMEELHNQEVQK	5216.50	5216.51	-0.01	-1.18	6.E-24
Q548L2	LQEEMLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEIAFLK	5560.81	5560.81	0.00	-0.39	6.E-24
P17096	RGRGRPRKQPPVSPGTALVGSQKEPSEVPTPK	3392.88	3392.88	0.00	-1.25	6.E-24
Q71UI9	ATIAGGGVIPHIHK	1369.75	1369.78	-0.03	-25.24	7.E-24
Q71UI9	ATIAGGGVIPHIHK	1369.76	1369.78	-0.02	-15.24	7.E-24
Q71UI9	ATIAGGGVIPHIHK	1369.78	1369.78	0.00	-2.54	7.E-24

P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3150.74	3153.55	-2.81	-891.40	8.E-24
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3150.95	3153.55	-2.60	-825.07	8.E-24
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3151.34	3153.55	-2.21	-701.56	8.E-24
Q09666	ISMPDVDLHLK	1266.64	1266.66	-0.02	-12.70	8.E-24
Q09666	ISMPDVDLHLK	1266.66	1266.66	0.00	-0.46	8.E-24
Q09666	ISMPDVDLHLK	1269.62	1266.66	2.96	2330.78	8.E-24
P10412	(51)SETAPAAPAAPAPAEKTPVK	1945.02	1945.02	0.00	1.06	8.E-24
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK	3739.21	3722.19	17.02	4550.81	8.E-24
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK	3742.12	3722.19	19.93	5326.98	8.E-24
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK	3745.16	3722.19	22.97	6134.50	8.E-24
P62304	VMVQPINLIFRYLQNRSRIQVWLYEQVNMRIEGCIIGFDEYMN LVLDDAEEIHSKTKSRKQLGRIMLKGDNITLLQSVSN	9421.92	9421.92	0.00	-0.03	8.E-24
P25705	RTGAIVDVPVGEELLGRVVDALGNAIDGK	2932.54	2932.60	-0.06	-20.02	8.E-24
P25705	RTGAIVDVPVGEELLGRVVDALGNAIDGK	2932.59	2932.60	-0.01	-2.25	8.E-24
O75526	SRGFAFVTFESPADAK	1728.82	1728.85	-0.03	-17.06	9.E-24
O75526	SRGFAFVTFESPADAK	1728.85	1728.85	0.00	-1.96	9.E-24

P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.82	3777.88	-0.06	-14.77	9.E-24
P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.89	3777.88	0.01	2.04	9.E-24
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.55	3183.56	-0.01	-3.03	1.E-23
P51991	LFIGGLSFETTDDSLREHFEK	2440.19	2440.19	0.00	-1.48	1.E-23
P62805	TVTAMDVVYALK	1310.68	1309.70	0.98	751.32	1.E-23
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.14	3153.55	-0.41	-128.97	1.E-23
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.51	3153.55	-0.04	-12.86	1.E-23
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.55	3153.55	0.00	0.04	1.E-23
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.74	3153.55	0.19	60.99	1.E-23
P26447	ELLTRELPSFLGK	1503.75	1501.85	1.90	1263.91	1.E-23
P05787	AQYEDIANRSRAEAESMYQIK	2472.17	2472.17	0.00	0.36	1.E-23
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.95	3153.55	0.40	125.32	1.E-23
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.35	3153.55	0.80	252.04	1.E-23
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.43	2572.44	-0.01	-2.44	1.E-23
P39023	SFPKDDPSKPVHLTAFLGYK	2246.17	2246.17	0.00	-0.94	2.E-23

P05783	YWSQQIEESTTVVTTQSAEVGAAETTLTELRRTVQSLEIDLDSMRNLK	5426.71	5426.72	-0.01	-2.62	2.E-23
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.21	1930.16	0.05	24.88	2.E-23
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.40	2467.39	0.01	2.96	2.E-23
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-1.49	2.E-23
P62805	TVTAMDVVYALK	1314.65	1309.70	4.95	3766.75	2.E-23
P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3778.72	2.E-23
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.30	2428.37	-0.07	-30.41	2.E-23
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.42	2428.37	0.05	19.42	2.E-23
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.39	2572.44	-0.05	-18.92	2.E-23
P62906	AVDIPHMDIEALKK	1578.84	1578.84	0.00	-1.98	2.E-23
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.33	2428.37	-0.04	-17.80	2.E-23
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-3.47	2.E-23
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.12	1930.16	-0.05	-23.31	2.E-23
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.36	2.E-23
P62277	GLAPDLPEDLYHLIK	1688.87	1692.91	-4.04	-2393.22	2.E-23

P62277	GLAPDLPEDLYHLIK	1692.91	1692.91	0.00	-1.55	2.E-23
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.43	2572.44	-0.01	-2.59	2.E-23
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.69	3307.68	0.01	1.75	2.E-23
P05787	KIETRDGKLVSESSDVLPK	2103.04	2100.14	2.90	1378.05	3.E-23
P07355	SALSGHLETVILGLLK	1649.94	1649.97	-0.03	-17.07	3.E-23
P07355	SALSGHLETVILGLLK	1649.97	1649.97	0.00	-2.04	3.E-23
O95232	(49)MISAAQLLDELMGRDRNLAPDEK	2627.29	2627.30	-0.01	-2.02	3.E-23
P40429	YQAVTATLEEK	1251.61	1251.63	-0.02	-13.31	3.E-23
P40429	YQAVTATLEEK	1251.63	1251.63	0.00	-1.01	3.E-23
P19338	TLVLSNLSYSATEETLQEVFEK	2500.25	2500.26	-0.01	-4.33	3.E-23
P98179	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	3493.73	3493.74	-0.01	-3.51	3.E-23
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	0.77	3.E-23
P05787	KIETRDGKLVSESSDVLPK	2100.14	2100.14	-0.01	-2.38	3.E-23
Q9UMS4	TVPEELVKPEELSK	1593.76	1596.86	-3.10	-1944.72	4.E-23
Q9UMS4	TVPEELVKPEELSK	1596.86	1596.86	0.00	-1.51	4.E-23

Q9UMS4	TVPEELVKPEELSK	1598.71	1596.86	1.85	1157.36	4.E-23
P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-2.03	4.E-23
P23246	ERETPPRFAQHGTFEYEYSQRWK	2941.39	2941.39	0.00	-1.34	4.E-23
P33778	RSTITSREIQTAVRLLLPGELAK	2552.81	2551.48	1.33	521.81	4.E-23
Q9UKM9	SNIDALLSRLEQIAAEQK	1995.14	1998.07	-2.93	-1468.73	5.E-23
Q9UKM9	SNIDALLSRLEQIAAEQK	1998.03	1998.07	-0.04	-21.04	5.E-23
Q9UKM9	SNIDALLSRLEQIAAEQK	1998.07	1998.07	0.00	-2.22	5.E-23
P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-0.79	5.E-23
P07355	LSLEGDHSTPPSAYGSVK	1843.90	1843.90	0.00	0.07	5.E-23
P07355	LSLEGDHSTPPSAYGSVK	1847.85	1843.90	3.95	2139.91	5.E-23
P26447	ELLTRELPSFLGK	1501.85	1501.85	0.00	-1.86	5.E-23
P63220	(49)MQNDAGEFVDLYVPRK	1922.92	1922.92	0.00	-2.32	6.E-23
Q00839	HAAENPGKYNILGTNTIMDK	2186.08	2186.08	0.00	-1.91	6.E-23
P07355	LSLEGDHSTPPSAYGSVK	1843.87	1843.90	-0.03	-18.64	6.E-23
P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-0.79	6.E-23

P33778	RSTITSREIQTAVRLLLPGELAK	2555.15	2551.48	3.67	1437.05	6.E-23
Q71UI9	ATIAGGGVIPHIHK	1373.70	1369.78	3.92	2854.49	7.E-23
P33778	RSTITSREIQTAVRLLLPGELAK	2551.14	2551.48	-0.34	-131.48	7.E-23
Q9NWH9	(41)AAATGAVAASAASGQAEGK	1629.80	1629.80	0.00	-1.67	7.E-23
P09651	GGNFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSSYGSGRRF	4251.93	4251.92	0.01	2.44	8.E-23
P38159	LFIGGLNTETNEK	1434.74	1434.74	0.00	-1.07	8.E-23
P05204	VKDEPQRRSARLSAKPAPPKPEPKPK	2906.66	2906.66	0.00	-1.23	9.E-23
P22626	KRGFGFVTFDDHDPVDK	1978.95	1978.95	0.00	-0.04	9.E-23
P05787	MLETKWSLLQQQK	1628.91	1631.87	-2.96	-1816.31	1.E-22
P05787	MLETKWSLLQQQK	1631.87	1631.87	0.00	-1.04	1.E-22
P62158	(41)ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMARK	8353.94	8353.95	-0.01	-0.95	1.E-22
Q9UKM9	LFARSTAVTTSSAK	1438.78	1438.78	0.00	-0.68	1.E-22
Q71UI9	ATIAGGGVIPHIHK	1369.78	1369.78	0.00	-1.37	1.E-22
Q71UI9	ATIAGGGVIPHIHK	1370.76	1369.78	0.98	716.33	1.E-22
P07355	SYSPYDMLESIRK	1587.76	1587.76	0.00	-2.89	1.E-22

Q9UKM9	LFARSTAVTTSSAK	1438.76	1438.78	-0.02	-14.72	1.E-22
Q9H307	(41)AVAVRTLQEQLEK	1525.85	1525.85	0.00	-2.04	1.E-22
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.12	1930.16	-0.04	-22.69	1.E-22
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.62	1.E-22
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.21	1930.16	0.05	24.82	1.E-22
Q7L4M3	GQRASLEAAIADAEQRGELAIK	2296.21	2296.21	0.00	-1.25	1.E-22
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-1.25	2.E-22
Q00839	KRNFILDQTNVSAAAQRRK	2215.23	2215.23	0.00	-1.06	2.E-22
P22626	KRGFGFVTFDDHDPVDK	1982.94	1978.95	3.99	2014.24	2.E-22
P26447	ELLTRELPSFLGK	1501.85	1501.85	0.00	-0.73	2.E-22
P17844	LIRLMEEIMSEK	1488.32	1490.78	-2.46	-1650.55	2.E-22
P17844	LIRLMEEIMSEK	1490.75	1490.78	-0.03	-17.68	2.E-22
P17844	LIRLMEEIMSEK	1490.78	1490.78	0.00	-1.71	2.E-22
P39023	SINPLGGFVHYGEVTNDFVMLK	2436.20	2436.21	-0.01	-2.19	2.E-22
P19338	EVFEDAAEIRLVSK	1604.84	1604.84	0.00	-0.40	2.E-22

P38919	MLVLDEADEMLNK	1520.73	1519.73	1.00	658.70	2.E-22
P22626	KRGFGFVTFDDHDPVDKIVLQK	2560.30	2560.34	-0.04	-16.70	3.E-22
P22626	KRGFGFVTFDDHDPVDKIVLQK	2560.34	2560.34	0.00	1.19	3.E-22
P16402	RKASGPPVSELITK	1481.86	1481.86	0.00	-2.39	3.E-22
P17844	LIRLMEEIMSEK	1492.77	1490.78	1.99	1331.85	3.E-22
Q9H307	(41)AVAVRTLQEQLEK	1525.83	1525.85	-0.02	-15.87	3.E-22
Q9H307	(41)AVAVRTLQEQLEK	1525.85	1525.85	0.00	-1.58	3.E-22
Q13185	WKDSDEADLVLAK	1483.82	1488.75	-4.93	-3325.21	3.E-22
Q13185	WKDSDEADLVLAK	1488.75	1488.75	0.00	-0.86	3.E-22
Q13185	WKDSDEADLVLAK	1488.81	1488.75	0.06	41.32	3.E-22
O14979	MFIGGLSWDTSKK	1468.74	1468.74	0.00	-0.42	3.E-22
O60506	ALLERTGYTLDVTTGQRK	2021.09	2021.09	0.00	-1.99	4.E-22
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.39	2467.39	0.00	-1.54	4.E-22
Q13185	WKDSDEADLVLAK	1488.75	1488.75	0.00	-0.80	4.E-22
P19338	EVFEDAAEIRLVSK	1601.81	1604.84	-3.03	-1888.63	4.E-22

P07355	WISIMTERSVPHLQK	1823.97	1823.97	0.00	-2.47	5.E-22
P22626	KRGFGFVTFDDHDPVDKIVLQK	2560.33	2560.34	-0.01	-2.36	5.E-22
P46777	HIMGQNVADYMRYLMEEDEDAYKK	2948.30	2948.31	-0.01	-1.86	5.E-22
P11387	(51)SGDHLHNDSQIEADFRLNDSHK	2576.16	2576.16	0.00	1.59	5.E-22
P10412	(51)SETAPAAPAAPAPAEKTPVK	1945.02	1945.02	0.00	-2.28	6.E-22
O14979	VFVGGLSPDTSEEQIK	1704.86	1704.86	0.00	-1.29	6.E-22
Q12906	RFVMEVEVDGQK	1438.67	1435.71	2.96	2056.26	6.E-22
Q12906	RFVMEVEVDGQK	1438.79	1435.71	3.08	2141.84	6.E-22
P19338	MAPPPKEVEEDSEDEEMSEDEEDD(37)S(37)SGEEVVIPQKK	4221.67	4221.66	0.01	1.47	6.E-22
P22626	IDTIEIITDRQSGK	1587.85	1587.85	0.00	-0.74	7.E-22
P19338	GYAFIEFASFEDAK	1593.74	1593.74	0.00	-0.12	7.E-22
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.26	2601.26	0.00	-0.61	7.E-22
Q04695	ATMQNLNDRLASYLDK	1851.91	1851.91	0.00	-1.40	7.E-22
Q53F64	KIFVGGLNPEATEEK	1630.86	1630.86	0.00	-0.43	7.E-22
Q53F64	KIFVGGLNPEATEEK	1634.82	1630.86	3.96	2423.94	7.E-22

P51991	GGSFGGRSSGSPYGGGYGSGGGSGGYGSRRF	2831.19	2831.24	-0.05	-19.10	8.E-22
P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.88	3777.88	0.00	-0.87	8.E-22
P52272	GIGMGNIGPAGMGMEGIGFGINK	2177.04	2177.04	0.00	-1.79	8.E-22
P62318	IRFLILPDMLK	1357.80	1357.82	-0.02	-16.60	9.E-22
P62318	IRFLILPDMLK	1357.82	1357.82	0.00	-1.57	9.E-22
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9080.87	9082.91	-2.04	-225.12	9.E-22
P09651	RGFAFVTFDDHDSVDK	1854.85	1854.85	0.00	0.47	9.E-22
P51991	KIFVGGIKEDTEEYNLRDYFEK	2702.27	2692.34	9.93	3674.99	9.E-22
P51991	KIFVGGIKEDTEEYNLRDYFEK	2710.16	2692.34	17.82	6576.07	9.E-22
P26599	TDSSPNQARAQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLRIIVENLFYPVTLDVLHQIFSK	7105.70	7105.68	0.02	2.58	9.E-22
P51991	GGSFGGRSSGSPYGGGYGSGGGSGGYGSRRF	2831.24	2831.24	0.00	-1.69	1.E-21
P02545	QREFESRLADALQELRAQHEDQVEQYKK	3443.72	3443.72	0.00	0.25	1.E-21
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.25	2601.26	-0.01	-4.61	1.E-21
Q13185	WKDSDEADLVLAK	1488.75	1488.75	0.00	-1.00	1.E-21
P39023	LDWARERLEQQVPVNQVFGQDEMIDVIGVTK	3611.84	3611.84	0.00	-0.98	1.E-21

P07355	SYSPYDMLESIRK	1587.73	1587.76	-0.03	-18.13	1.E-21
P07355	SYSPYDMLESIRK	1587.76	1587.76	0.00	-0.37	1.E-21
P26599	HQNVQLPREGQEDQGLTK	2076.03	2076.03	0.00	-1.98	1.E-21
P07355	LSLEGDHSTPPSAYGSVK	1843.90	1843.90	0.00	-2.43	1.E-21
P02545	AAYEAELGDARK	1292.64	1292.64	0.00	-0.34	1.E-21
P04083	DITSDTSGDFRNALLSLAK	2023.02	2023.02	0.00	-1.96	2.E-21
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-2.85	2.E-21
Q00839	YNILGTNTIMDK	1381.69	1381.69	0.00	-0.83	2.E-21
P19338	NLPYKVTQDELKEVFEDAAEIRLVSK	3033.59	3033.60	-0.01	-2.05	2.E-21
P23246	AFERCSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK	4042.01	4042.02	-0.01	-1.76	2.E-21
P16403	(51)SETAPAAPAAAPPAEK	1516.76	1519.75	-2.99	-1974.16	2.E-21
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	0.44	2.E-21
P63220	(49)MQNDAGEFVDLYVPRK	1924.93	1922.92	2.01	1043.96	2.E-21
P05387	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEKKEESEESDDDMGFGLFD	5204.44	5204.43	0.01	2.09	2.E-21
P46778	RQPAPPREAHFVRTNGKEPELLEPIPYEFMA	3619.83	3618.84	0.99	274.00	2.E-21

O14979	VFVGGLSPDTSEEQIK	1704.83	1704.86	-0.03	-18.42	2.E-21
O14979	VFVGGLSPDTSEEQIK	1704.86	1704.86	0.00	-1.70	2.E-21
P16402	RKASGPPVSELITK	1481.86	1481.86	0.00	-2.05	2.E-21
P19338	GIAYIEFKTEADAEK	1683.84	1683.84	0.00	-1.02	2.E-21
A6NI71	PLLGGSLMEYAILSAIAAMNEPK	2388.23	2388.24	-0.01	-2.32	2.E-21
Q3BDU5	LDNARQSAERNSNLVGAAHEELQQSRIRIDSLSAQLSQLQK	4573.36	4573.37	-0.01	-1.90	2.E-21
Q3BDU5	LDNARQSAERNSNLVGAAHEELQQSRIRIDSLSAQLSQLQK	4574.25	4573.37	0.88	192.80	2.E-21
P04083	QAWFIENEEQEYVQTVK	2140.01	2140.01	-0.01	-2.32	2.E-21
P19338	TLVLSNLSYSATEETLQEVFEK	2501.20	2500.26	0.94	374.77	2.E-21
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.43	3357.44	-0.01	-2.56	2.E-21
P0C0S8	TRIIPRHLQLAIRNDEELNK	2432.35	2428.37	3.98	1636.47	2.E-21
P05386	KVEAKKEESEESDDDMGFGLFD	2504.08	2504.09	-0.01	-2.21	3.E-21
P19338	GIAYIEFKTEADAEK	1685.93	1683.84	2.09	1237.11	3.E-21
Q16695	KPHRYRPGTVALREIRRYQK	2523.44	2523.44	0.00	-1.06	3.E-21
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.33	2428.37	-0.04	-17.06	3.E-21

P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-1.83	3.E-21
Q53F64	IFVGGLNPEATEEK	1500.78	1502.76	-1.98	-1322.40	3.E-21
Q53F64	IFVGGLNPEATEEK	1505.83	1502.76	3.07	2039.45	3.E-21
Q53F64	IFVGGLNPEATEEK	1505.85	1502.76	3.09	2053.89	3.E-21
P05787	KIETRDGKLVSESSDVLPK	2103.04	2100.14	2.90	1377.67	3.E-21
P41219	NLQEAEEWYK	1308.60	1308.60	0.00	-1.16	3.E-21
P22626	SGNFGGSRNMGGPYGGGNYGPGGSGGSGGYGGRSRY	3357.37	3357.44	-0.07	-21.30	3.E-21
Q16695	KPHRYRPGTVALREIRRYQK	2523.41	2523.44	-0.03	-12.99	3.E-21
P19338	TLVLSNLSYSATEETLQEVFEK	2500.25	2500.26	-0.01	-2.85	3.E-21
Q12905	RNQDLAPNSAEQASILSLVTK	2254.19	2254.19	0.00	-1.24	4.E-21
P16401	(51)SETAPAETATPAPVEK	1639.79	1639.79	0.00	-0.97	4.E-21
Q53F64	IFVGGLNPEATEEK	1502.76	1502.76	0.00	-1.55	4.E-21
Q53F64	IFVGGLNPEATEEK	1503.74	1502.76	0.98	649.62	4.E-21
Q53F64	IFVGGLNPEATEEK	1506.80	1502.76	4.04	2682.21	4.E-21
P62805	TVTAMDVVYALK	1310.67	1309.70	0.97	741.41	4.E-21

P62805	TVTAMDVVYALK	1310.69	1309.70	0.99	751.86	4.E-21
P63220	(49)MQNDAGEFVDLYVPRK	1922.92	1922.92	0.00	1.79	4.E-21
P05787	LKLEAELGNMQGLVEDFK	2033.04	2033.05	-0.01	-2.65	4.E-21
P62805	TVTAMDVVYALK	1312.70	1309.70	3.00	2282.75	5.E-21
P05787	KIETRDGKLVSESSDVLPK	2100.14	2100.14	-0.01	-2.38	5.E-21
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-2.79	6.E-21
P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3778.49	6.E-21
P05787	KIETRDGKLVSESSDVLPK	2100.14	2100.14	0.00	1.52	6.E-21
P14136	LALDIEIATYRK	1404.80	1404.80	0.00	-0.45	6.E-21
P35268	FTLDCTHPVEDGIMDAANFEQFLQERIK	3400.52	3266.54	133.98	39398.60	6.E-21
Q99848	WNTRESYDDVSSFRAK	1957.02	1959.91	-2.89	-1477.39	6.E-21
P18621	EQIVPKPEEEVAQK	1622.85	1622.85	0.00	-1.43	6.E-21
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	1.43	8.E-21
P04083	TPAQFDADELRAAMK	1662.80	1662.80	0.00	-0.92	8.E-21
Q16695	QLAT(55)KVARKSAPATGGVK	1824.01	1824.06	-0.05	-25.12	9.E-21

P04083	TPAQFDADELRAAMK	1662.80	1662.80	0.00	-2.54	9.E-21
Q16695	QLAT(55)KVARKSAPATGGVK	1824.04	1824.06	-0.02	-12.95	1.E-20
Q16695	QLAT(55)KVARKSAPATGGVK	1824.06	1824.06	0.00	-1.11	1.E-20
Q16695	QLAT(55)KVARKSAPATGGVK	1824.09	1824.06	0.03	15.50	1.E-20
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK	3739.21	3722.19	17.02	4551.74	1.E-20
Q04695	ATMQNLNDRLASYLDK	1851.91	1851.91	0.00	-2.04	1.E-20
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK	3745.17	3722.19	22.98	6135.19	1.E-20
P84090	(51)SHTILLVQPTK	1277.73	1277.73	0.00	-0.51	1.E-20
P09651	RAVSREDSQRPGAHLTVK	2010.92	2006.08	4.84	2408.83	1.E-20
P09651	RAVSREDSQRPGAHLTVK	2010.92	2006.08	4.84	2408.83	1.E-20
Q04695	ATMQNLNDRLASYLDK	1850.85	1851.91	-1.06	-572.27	1.E-20
P14866	SDALETLGFLNHYQMK	1865.90	1865.90	0.00	-1.05	1.E-20
Q9Y3U8	ALRYPMAVGLNK	1331.74	1331.74	0.00	-1.32	1.E-20
Q9Y3U8	ALRYPMAVGLNK	1331.83	1331.74	0.09	67.08	1.E-20
Q9Y3U8	ALRYPMAVGLNK	1332.73	1331.74	0.99	739.65	1.E-20

P10412	(51)SETAPAAPAAPAPAEK(38)TPVK	2024.97	2024.98	-0.01	-3.72	2.E-20
Q8IUE6	TRIIPRHLQLAVRNDEELNK	2414.35	2414.35	0.00	-1.65	2.E-20
P09651	RAVSREDSQRPGAHLTVK	2006.08	2006.08	0.00	-1.01	2.E-20
P62805	VFLENVIRDAVTYTEHAK	2147.10	2104.10	43.00	20028.30	2.E-20
P62805	RQGRTLYGFGG	1213.60	1210.62	2.98	2452.72	2.E-20
P09651	PRNQGGYGGSSSSSSYGSGRRF	2250.01	2250.02	-0.01	-2.71	2.E-20
P21796	WNTDNTLGTEITVEDQLARGLK	2473.24	2473.24	0.00	-0.46	2.E-20
P07355	LSLEGDHSTPPSAYGSVK	1843.90	1843.90	0.00	0.39	2.E-20
P08670	TVETRDGQVINETSQHHDDLE	2422.10	2422.10	0.00	1.59	3.E-20
Q13573	GWIPRLLEDFGDGGAFPEIHVAQYPLDMGRK	3493.73	3483.74	9.99	2860.07	3.E-20
P62805	RQGRTLYGFGG	1213.60	1210.62	2.98	2452.47	3.E-20
P62805	RQGRTLYGFGG	1210.60	1210.62	-0.02	-12.54	3.E-20
P08758	TLFGRDLLDDLK	1408.83	1404.76	4.07	2886.27	3.E-20
P62805	RQGRTLYGFGG	1210.62	1210.62	0.00	-0.90	3.E-20
P16403	ASGPPVSELITK	1198.66	1197.66	1.00	835.04	3.E-20

P23246	DKLESEMEDAYHEHQANLLRQDLMRRQEELRRMEELHNQEMQK	5435.54	5435.56	-0.02	-4.17	3.E-20
O14979	EYFGAFGEIENIELPMDTK	2202.01	2202.02	-0.01	-2.70	3.E-20
P08758	TLFGRDLLDDLK	1404.76	1404.76	0.00	-1.31	3.E-20
A6NI71	PLLGGSLMEYAILSAIAAMNEPK	2388.24	2388.24	0.00	-1.15	4.E-20
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-2.17	4.E-20
P19338	KMAPPPKEVEEDSEDEEMSEDEEDD(37)SSGEEVVIPQK	4141.70	4141.69	0.01	1.40	4.E-20
P62805	RQGRTLYGFGG	1209.75	1210.62	-0.87	-715.26	4.E-20
P62805	RQGRTLYGFGG	1210.62	1210.62	0.00	-0.15	4.E-20
P62805	RQGRTLYGFGG	1206.71	1210.62	-3.91	-3242.53	4.E-20
P55769	AYPLADAHLTKK	1322.77	1326.73	-3.97	-2997.48	5.E-20
P55769	AYPLADAHLTKK	1326.73	1326.73	0.00	-1.25	5.E-20
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-2.85	5.E-20
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-2.62	5.E-20
P07910	LKGDDLQAIKK	1228.72	1227.72	1.00	815.76	6.E-20
P14136	LALDIEIATYRK	1404.80	1404.80	0.00	-0.81	6.E-20

P62805	RQGRTLYGFGG	1206.71	1210.62	-3.91	-3242.20	6.E-20
P62917	DIIHDPGRGAPLAK	1458.79	1458.79	0.00	-1.69	6.E-20
P0C0S8	GNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	4133.15	4090.15	43.00	10403.60	6.E-20
P26447	ELLTRELPSFLGK	1501.85	1501.85	0.00	-1.26	6.E-20
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-3.11	6.E-20
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.60	3307.68	-0.08	-24.37	7.E-20
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-2.18	7.E-20
P18621	EQIVPKPEEEVAQK	1622.85	1622.85	0.00	-1.80	7.E-20
P51991	WGTLTDCVVMRDPQTK	1848.89	1848.89	0.00	-0.82	7.E-20
P14136	LALDIEIATYRK	1408.84	1404.80	4.04	2869.14	7.E-20
P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-1.73	8.E-20
P33778	RSTITSREIQTAVRLLLPGELAK	2552.45	2551.48	0.97	378.76	8.E-20
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	6856.49	6722.54	133.95	19536.50	8.E-20
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	6871.52	6722.54	148.98	21681.40	8.E-20
P35637	GEATVSFDDPPSAK	1419.65	1419.65	0.00	3.41	8.E-20

P35637	GEATVSFDDPPSAK	1419.63	1419.65	-0.02	-13.85	8.E-20
P35637	GEATVSFDDPPSAK	1419.65	1419.65	0.00	1.58	8.E-20
		2104.05				8.E-20
P60709	DLYANTVLSGGTTMYPGIADRMQK	2597.38	2601.26	-3.88	-1493.73	8.E-20
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-2.15	8.E-20
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.65	3566.92	-0.27	-76.93	9.E-20
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-3.16	9.E-20
P40429	YQAVTATLEEK	1251.63	1251.63	0.00	-0.93	9.E-20
P40429	YQAVTATLEEK	1253.64	1251.63	2.01	1600.72	9.E-20
P62244	VRMNVLADALK	1228.70	1228.70	0.00	-0.94	9.E-20
P35659	KKVERLTMQVSSLQREPFTIAQGK	2773.53	2773.53	0.00	-1.35	9.E-20
P62805	VFLENVIRDAVTYTEHAK	2147.10	2104.10	43.00	20027.00	9.E-20
Q15233	(49)MQSNKTFNLEK	1380.67	1380.67	0.00	1.10	9.E-20
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.21	2601.26	-0.05	-20.33	9.E-20
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.68	3307.68	0.00	-1.09	1.E-19

P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.25	2601.26	-0.01	-1.99	1.E-19
O14979	LLESRYHQIGSGK	1486.79	1486.79	0.00	-1.42	1.E-19
Q71UI9	AVSRSQRAGLQFPVGRIHRHLK	2512.44	2512.44	0.00	-1.20	1.E-19
P38159	LFIGGLNTETNEK	1434.74	1434.74	0.00	-0.37	1.E-19
P38159	LFIGGLNTETNEK	1435.72	1434.74	0.98	680.40	1.E-19
P62805	RKTVTAMDVVYALK	1593.89	1593.89	0.00	-2.02	1.E-19
P98179	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	3493.74	3493.74	0.00	-1.31	1.E-19
P60903	GYLTKEDLRVLMEK	1693.91	1693.91	0.00	-1.40	1.E-19
P11142	NQVAMNPTNTVFDAK	1648.79	1648.79	0.00	-1.82	1.E-19
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-2.40	1.E-19
P19338	TLVLSNLSYSATEETLQEVFEK	2500.25	2500.26	-0.01	-3.85	1.E-19
P07355	SYSPYDMLESIRK	1587.73	1587.76	-0.03	-17.75	1.E-19
P07355	SYSPYDMLESIRK	1587.76	1587.76	0.00	-1.00	1.E-19
P09651	LFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTK	4229.02	4229.02	0.00	-0.76	2.E-19
P09651	LFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTK	4230.15	4229.02	1.13	267.74	2.E-19

P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.33	2428.37	-0.04	-17.19	2.E-19
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.09	1930.16	-0.07	-35.90	2.E-19
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.36	2.E-19
P19338	VFGNEIKLEKPK	1400.80	1400.80	0.00	-0.51	2.E-19
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.36	2270.37	-0.01	-3.09	2.E-19
O75526	YGRIVEVLLMK	1319.76	1319.76	0.00	-0.91	2.E-19
P05787	KIETRDGKLVSESSDVLPK	2100.14	2100.14	0.00	2.14	3.E-19
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.11	4108.11	0.00	-0.63	3.E-19
P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-1.93	3.E-19
P62851	LITPAVVSERLK	1324.81	1324.81	0.00	-0.38	3.E-19
P62851	LITPAVVSERLK	1325.69	1324.81	0.88	664.86	3.E-19
P09651	RSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPK	3887.99	3887.99	0.00	-1.04	3.E-19
Q16695	KPHRYRPGTVALREIRRYQK	2523.43	2523.44	-0.01	-2.45	3.E-19
Q08211	ILTTEGRNALIHK	1464.84	1464.84	0.00	-1.53	4.E-19
P62805	RQGRTLYGFGG	1210.62	1210.62	0.00	-0.98	4.E-19

Q16695	KPHRYRPGTVALREIRRYQK	2524.40	2523.44	0.96	378.87	4.E-19
P0C0S8	VTIAQGGVLPNIQAVLLPK	1927.15	1930.16	-3.01	-1559.54	4.E-19
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.12	1930.16	-0.05	-23.31	4.E-19
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.36	4.E-19
P16104	GHYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	4115.16	4113.16	2.00	485.61	4.E-19
P62805	RQGRTLYGFGG	1210.60	1210.62	-0.02	-13.78	4.E-19
P60709	SYELPDGQVITIGNERFRCPEALFQPSFLGMESCGIHETTFNSIMK	5192.45	5191.46	0.99	189.93	5.E-19
Q92522	ALVQNDTLLQVK	1341.77	1340.77	1.00	747.19	5.E-19
Q92522	ALVQNDTLLQVK	1344.72	1340.77	3.95	2936.57	5.E-19
P09651	PRNQGGYGGSSSSSSYGSGRRF	2250.02	2250.02	0.00	-1.91	5.E-19
P19338	VFGNEIKLEKPK	1400.80	1400.80	0.00	-0.44	5.E-19
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQKDSYVGDEAQSK	4487.20	4487.19	0.01	1.58	5.E-19
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.40	2467.39	0.01	2.71	6.E-19
A2BDF6	STELLIRKLPFQRLVREIAQDFK	2799.56	2799.61	-0.05	-18.92	6.E-19
A2BDF6	STELLIRKLPFQRLVREIAQDFK	2799.61	2799.61	0.00	0.48	6.E-19

P84090	(51)SHTILLVQPTK	1277.73	1277.73	0.00	-0.59	6.E-19
P26599	ELKTDSSPNQARAQAALQAVNSVQSGNLALAASAAAVDAGM AMAGQSPVLRIIVENLFYPVTLDVLHQIFSK	7475.90	7475.90	0.00	-0.51	6.E-19
P14136	LALDIEIATYRK	1404.80	1404.80	0.00	-0.10	6.E-19
Q04695	(52)TTSIRQFTSSSSIK	1583.82	1583.82	0.00	1.05	7.E-19
P62241	LLACIASRPGQCGRADGYVLEGK	2388.14	2376.20	11.94	4998.13	7.E-19
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3452.80	3449.79	3.01	870.43	7.E-19
P07355	TPAQYDASELK	1222.58	1221.59	0.99	807.63	7.E-19
P07355	TPAQYDASELK	1222.62	1221.59	1.03	843.01	7.E-19
Q99729	MFVGGLSWDTSKK	1454.72	1454.72	0.00	-1.49	7.E-19
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.55	3183.56	-0.01	-2.68	7.E-19
P13645	NQILNLTTDNANILLQIDNARLAADDFRLK	3395.81	3395.82	-0.01	-3.85	8.E-19
P0C0S8	TRIIPRHLQLAIRNDEELNK	2430.71	2428.37	2.34	961.19	8.E-19
P62805	RQGRTLYGFGG	1210.62	1210.62	0.00	-1.14	8.E-19
P07355	TPAQYDASELK	1217.56	1221.59	-4.03	-3307.44	9.E-19
Q9NW13	(41)AGLTLFVGRLPPSARSEQLEELFSQVGPVK	3266.76	3266.77	-0.01	-2.23	9.E-19

P62805	RQGRTLYGFGG	1210.60	1210.62	-0.02	-14.20	9.E-19
P46777	ASFLRAQERAAES	1434.72	1434.72	0.00	-1.61	9.E-19
Q14103	IFVGGLSPDTPEEK	1487.75	1487.75	0.00	-1.17	9.E-19
P62805	TVTAMDVVYALK	1310.67	1309.70	0.97	740.96	9.E-19
P07355	LSLEGDHSTPPSAYGSVK	1843.86	1843.90	-0.04	-19.67	9.E-19
P07355	LSLEGDHSTPPSAYGSVK	1843.89	1843.90	-0.01	-2.75	9.E-19
P0C0S8	TRIIPRHLQLAIRNDEELNK	2427.04	2428.37	-1.33	-547.47	1.E-18
P0C0S8	TRIIPRHLQLAIRNDEELNK	2429.76	2428.37	1.39	570.62	1.E-18
Q08211	GMTLVTPLQLLLFASK	1731.00	1731.00	0.00	-2.10	1.E-18
Q9NW13	(41)AGLTLFVGRLPPSARSEQLEELFSQVGPVK	3266.76	3266.77	-0.01	-1.86	1.E-18
P07355	TPAQYDASELK	1221.59	1221.59	0.00	-0.91	1.E-18
P07355	TPAQYDASELK	1225.61	1221.59	4.02	3280.97	1.E-18
P07355	TPAQYDASELK	1225.66	1221.59	4.07	3322.69	1.E-18
P07355	TPAQYDASELK	1225.68	1221.59	4.09	3336.92	1.E-18
P53999	EQISDIDDAVRKL	1500.78	1500.78	0.00	2.10	1.E-18

Q53F64	IFVGGLNPEATEEK	1502.76	1502.76	0.00	1.51	1.E-18
Q6FI13	SRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYMAAVLE YLTAEILELAGNAARDNKK	6509.50	6509.51	-0.01	-1.88	1.E-18
P0C0S8	TRIIPRHLQLAIRNDEELNK	2427.32	2428.37	-1.05	-433.42	1.E-18
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	1.10	1.E-18
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.43	2428.37	0.06	24.53	1.E-18
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.44	2428.37	0.07	29.80	1.E-18
P0C0S8	TRIIPRHLQLAIRNDEELNK	2432.04	2428.37	3.67	1509.99	1.E-18
P0C0S8	TRIIPRHLQLAIRNDEELNK	2432.10	2428.37	3.73	1535.41	1.E-18
P19338	EVFEDAAEIRLVSK	1604.84	1604.84	0.00	-0.90	1.E-18
P62805	TVTAMDVVYALK	1309.68	1309.70	-0.02	-15.54	1.E-18
P62805	TVTAMDVVYALK	1312.70	1309.70	3.00	2281.99	1.E-18
Q9H307	(41)AVAVRTLQEQLEK	1525.85	1525.85	0.00	-2.30	1.E-18
P16402	RKASGPPVSELITK	1481.86	1481.86	0.00	1.12	1.E-18
P16402	RKASGPPVSELITK	1484.84	1481.86	2.98	2007.40	1.E-18
P07355	LSLEGDHSTPPSAYGSVK	1843.90	1843.90	0.00	-2.37	1.E-18

P62805	TVTAMDVVYALK	1309.65	1309.70	-0.05	-36.46	2.E-18
P62805	TVTAMDVVYALK	1309.66	1309.70	-0.04	-33.87	2.E-18
P62805	TVTAMDVVYALK	1309.67	1309.70	-0.03	-24.40	2.E-18
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-2.33	2.E-18
P26373	LATQLTGPVMPVRNVYK	1887.04	1886.04	1.00	529.47	2.E-18
P26373	LATQLTGPVMPVRNVYK	1888.91	1886.04	2.87	1521.37	2.E-18
P62280	(41)ADIQTERAYQK	1362.68	1363.67	-0.99	-724.17	2.E-18
P62280	(41)ADIQTERAYQK	1363.67	1363.67	0.00	-1.18	2.E-18
P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3779.33	2.E-18
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9096.92	9098.88	-1.96	-215.26	2.E-18
P02545	NIYSEELRETK	1380.69	1380.69	0.00	-1.52	2.E-18
P06576	GFQQILAGEYDHLPEQAFYMVGPIEEAVAK	3349.62	3349.63	-0.01	-2.28	2.E-18
P07355	LSLEGDHSTPPSAYGSVK	1843.90	1843.90	0.00	-1.88	2.E-18
P07355	SYSPYDMLESIRK	1587.73	1587.76	-0.03	-16.43	2.E-18
P07355	SYSPYDMLESIRK	1587.76	1587.76	0.00	-1.50	2.E-18

P07355	SYSPYDMLESIRK	1590.75	1587.76	2.99	1880.06	2.E-18
Q9Y277	VNNASLIGLGYTQTLRPGVK	2102.17	2100.17	2.00	951.97	2.E-18
Q00839	EKPYFPIPEEYTFIQNVPLEDRVRGPK	3260.68	3260.69	-0.01	-3.08	3.E-18
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.13	1930.16	-0.03	-15.07	3.E-18
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.16	1930.16	0.00	-0.61	3.E-18
P22626	KRGFGFVTFDDHDPVDK	1978.95	1978.95	0.00	-1.15	3.E-18
P22626	KRGFGFVTFDDHDPVDK	1982.94	1978.95	3.99	2013.08	3.E-18
Q16695	KPHRYRPGTVALREIRRYQK	2523.41	2523.44	-0.03	-13.46	3.E-18
Q16695	KPHRYRPGTVALREIRRYQK	2523.44	2523.44	0.00	-0.94	3.E-18
P47914	AQAAAPASVPAQAPK	1376.74	1376.74	0.00	-0.35	3.E-18
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.09	1930.16	-0.07	-35.90	3.E-18
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.36	3.E-18
P19338	GLSEDTTEETLK	1324.69	1321.62	3.07	2320.54	3.E-18
Q09666	ISMPDVDLHLKGPK	1548.83	1548.83	0.00	1.38	3.E-18
P26373	LILFPRKPSAPK	1370.77	1365.85	4.92	3585.88	3.E-18

P22626	LFIGGLSFETTEESLRNYYEQWGKLTDCVVMRDPASK	4282.07	4282.07	0.00	-1.15	3.E-18
Q00839	YNILGTNTIMDK	1381.69	1381.69	0.00	1.13	3.E-18
P19338	GLSEDTTEETLK	1321.60	1321.62	-0.02	-14.44	3.E-18
P19338	GLSEDTTEETLK	1321.62	1321.62	0.00	-0.37	3.E-18
P09651	KRGFAFVTFDDHDSVDK	1982.95	1982.95	0.00	-1.36	4.E-18
P60709	RGILTLKYPIE(317)HGIVTNWDDMEK	2741.42	2741.42	0.00	1.65	4.E-18
Q02539	SLVSKGTLVQTK	1257.73	1259.74	-2.01	-1594.75	4.E-18
Q02539	SLVSKGTLVQTK	1259.74	1259.74	0.00	-1.02	4.E-18
P07355	LSLEGDHSTPPSAYGSVK	1843.90	1843.90	0.00	-2.43	4.E-18
O43390	VLFVRNLATTVTEEILEK	2074.16	2074.17	-0.01	-2.83	4.E-18
O43390	VLFVRNLATTVTEEILEK	2077.11	2074.17	2.94	1417.32	4.E-18
P05386	KVEAKKEESEESDDDMGFGLFD	2504.09	2504.09	0.00	1.47	4.E-18
P12270	(41)AAVLQQVLERTELNK	1752.97	1752.97	0.00	-1.89	5.E-18
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-2.31	5.E-18
P06748	MSVQPTVSLGGFEITPPVVLRLK	2469.35	2467.39	1.96	793.24	5.E-18

P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-1.34	5.E-18
P33778	RSTITSREIQTAVRLLLPGELAK	2553.45	2551.48	1.97	771.10	5.E-18
P26373	STESLQANVQRLK	1472.79	1472.79	0.00	-1.56	5.E-18
P63220	DHASIQMNVAEVDKVTGRFNGQFK	2690.32	2690.32	0.00	1.14	5.E-18
P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-1.38	5.E-18
P33778	RSTITSREIQTAVRLLLPGELAK	2552.41	2551.48	0.93	365.25	5.E-18
P26373	LILFPRKPSAPK	1365.83	1365.85	-0.02	-14.28	6.E-18
P26373	LILFPRKPSAPK	1365.85	1365.85	0.00	-1.03	6.E-18
P26373	LILFPRKPSAPK	1368.76	1365.85	2.91	2126.37	6.E-18
P23396	GGKPEPPAMPQPVPTA	1569.79	1572.80	-3.01	-1918.97	6.E-18
P23396	GGKPEPPAMPQPVPTA	1572.80	1572.80	0.00	-1.64	6.E-18
P23396	GGKPEPPAMPQPVPTA	1575.02	1572.80	2.22	1410.54	6.E-18
Q14103	IFVGGLSPDTPEEK	1487.75	1487.75	0.00	-0.83	6.E-18
O00567	MSQVAPSLSALIGEAVGARLIAHAGSLTNLAK	3147.73	3145.73	2.00	636.37	6.E-18
Q53F64	IFVGGLNPEATEEK	1505.85	1502.76	3.09	2054.09	6.E-18

A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9096.93	9098.88	-1.95	-214.51	6.E-18
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-4.04	7.E-18
P07355	GLGTDEDSLIEIICSRTNQELQEINRVYK	3335.66	3335.67	-0.01	-2.52	7.E-18
P60903	EFPGFLENQKDPLAVDK	1945.98	1945.98	0.00	-0.51	7.E-18
P35268	AGNLGGGVVTIERSK	1456.80	1456.80	0.00	-1.62	7.E-18
P35268	AGNLGGGVVTIERSK	1457.78	1456.80	0.98	671.74	7.E-18
P35268	AGNLGGGVVTIERSK	1458.79	1456.80	1.99	1365.41	7.E-18
Q08211	GMTLVTPLQLLLFASK	1731.00	1731.00	0.00	-2.16	7.E-18
P16403	ERSGVSLAALKK	1257.71	1257.74	-0.03	-22.78	7.E-18
P16403	ERSGVSLAALKK	1257.72	1257.74	-0.02	-13.56	7.E-18
P16403	ERSGVSLAALKK	1257.74	1257.74	0.00	-2.27	7.E-18
P16403	ERSGVSLAALKK	1257.76	1257.74	0.02	14.82	7.E-18
O75475	GYPHWPARVDEVPDGAVKPPTNKLPIFFFGTHETAFLGPK	4431.28	4432.28	-1.00	-226.18	7.E-18
Q00839	YNILGTNTIMDK	1381.69	1381.69	0.00	-0.61	7.E-18
Q00839	YNILGTNTIMDK	1381.67	1381.69	-0.02	-14.44	8.E-18

Q00839	YNILGTNTIMDK	1381.69	1381.69	0.00	-1.05	8.E-18
Q16695	KPHRYRPGTVALREIRRYQK	2523.36	2523.44	-0.08	-29.99	8.E-18
Q16695	KPHRYRPGTVALREIRRYQK	2523.43	2523.44	-0.01	-2.57	8.E-18
Q16695	KPHRYRPGTVALREIRRYQK	2524.40	2523.44	0.96	379.07	8.E-18
Q53F64	IFVGGLNPEATEEK	1502.76	1502.76	0.00	-1.02	9.E-18
P20700	LLEGEEERLK	1214.65	1214.65	0.00	-0.93	9.E-18
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.36	2270.37	-0.01	-3.05	9.E-18
P22626	KRGFGFVTFDDHDPVDK	1978.92	1978.95	-0.03	-13.63	9.E-18
P22626	KRGFGFVTFDDHDPVDK	1978.95	1978.95	0.00	-1.10	9.E-18
Q6FG99	(49)MASVSELARIYSALILHDDEVTVTEDKINALIK	3690.71	3698.94	-8.23	-2230.56	1.E-17
Q6FG99	(49)MASVSELARIYSALILHDDEVTVTEDKINALIK	3690.79	3698.94	-8.15	-2207.75	1.E-17
Q04695	(52)TTSIRQFTSSSSIK	1583.82	1583.82	0.00	-1.35	1.E-17
Q04695	(52)TTSIRQFTSSSSIK	1584.78	1583.82	0.96	607.45	1.E-17
P62805	VFLENVIRDAVTYTEHAK	2107.78	2104.10	3.68	1745.79	1.E-17
P62805	VFLENVIRDAVTYTEHAK	2108.45	2104.10	4.35	2062.49	1.E-17

P08670	KLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALRDVRQQYESVAAK	5424.80	5424.79	0.01	2.11	1.E-17
O60812	QKVDSLLENLEK	1411.77	1414.77	-3.00	-2125.16	1.E-17
Q53F64	IFVGGLNPEATEEK	1502.76	1502.76	0.00	-0.89	1.E-17
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.51	3138.52	-0.01	-2.84	1.E-17
P07355	DIISDTSGDFRK	1352.66	1352.66	0.00	-2.28	1.E-17
P22626	KRGFGFVTFDDHDPVDK	1975.03	1978.95	-3.92	-1983.75	1.E-17
P22626	KRGFGFVTFDDHDPVDK	1982.94	1978.95	3.99	2013.98	1.E-17
P62805	VFLENVIRDAVTYTEHAK	2100.10	2104.10	-4.00	-1906.85	1.E-17
P62805	VFLENVIRDAVTYTEHAK	2104.06	2104.10	-0.04	-16.76	1.E-17
P62805	VFLENVIRDAVTYTEHAK	2104.10	2104.10	0.00	-1.88	1.E-17
P35268	ITVTSEVPFSK	1206.65	1206.65	0.00	-0.65	1.E-17
P35268	ITVTSEVPFSK	1207.67	1206.65	1.02	845.03	1.E-17
P35268	ITVTSEVPFSK	1210.62	1206.65	3.97	3279.74	1.E-17
P26373	LATQLTGPVMPVRNVYKK	2014.14	2014.14	0.00	-1.10	1.E-17
O00148	FMQDPMEVFVDDETK	1829.79	1829.79	0.00	-2.22	1.E-17

P62314	NREPVQLETLSIRGNNIRYFILPDSLPLDTLLVDVEPK	4376.36	4376.37	-0.01	-3.02	1.E-17
P05783	GLQAQIASSGLTVEVDAPK	1883.00	1883.00	0.00	-1.42	2.E-17
P19338	QGTEIDGRSISLYYTGEK	2015.98	2015.98	0.00	-1.38	2.E-17
O14979	VFVGGLSPDTSEEQIKEYFGAFGEIENIELPMDTK	3888.88	3888.87	0.01	2.86	2.E-17
P02545	NIYSEELRETK	1380.69	1380.69	0.00	-1.01	2.E-17
P02545	NIYSEELRETK	1383.70	1380.69	3.01	2174.32	2.E-17
Q92522	ALVQNDTLLQVK	1340.77	1340.77	0.00	-0.70	2.E-17
O60812	QKVDSLLENLEK	1414.75	1414.77	-0.02	-14.59	2.E-17
O60812	QKVDSLLENLEK	1414.77	1414.77	0.00	-0.31	2.E-17
P02545	SNEDQSMGNWQIK	1535.67	1535.67	0.00	-1.86	2.E-17
P61978	RPAEDMEEEQAFK	1578.70	1578.70	0.00	-1.71	2.E-17
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.36	2270.37	-0.01	-3.27	2.E-17
P32969	TILSNQTVDIPENVDITLK	2112.13	2112.13	0.00	-1.51	2.E-17
P62917	KVISSANRAVVGVVAGGGRIDKPILK	2603.56	2603.56	0.00	-0.35	2.E-17
P05787	NKYEDEINKRTEMENEFVLIKK	2769.40	2769.40	0.00	-1.08	2.E-17

P36578	MINTDLSRILK	1302.73	1302.73	0.00	-0.50	2.E-17
O00567	YPASTVQILGAEK	1376.73	1375.73	1.00	728.17	2.E-17
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	0.51	2.E-17
P02545	QREFESRLADALQELRAQHEDQVEQYKK	3443.72	3443.72	0.00	0.65	2.E-17
P05386	KVEAKKEESEESDDDMGFGLFD	2504.09	2504.09	0.00	1.15	3.E-17
Q14103	MFIGGLSWDTTKK	1482.75	1482.75	0.00	-0.92	3.E-17
P19338	GFGFVDFNSEEDAK	1559.78	1560.67	-0.89	-569.51	3.E-17
P19338	GFGFVDFNSEEDAK	1560.65	1560.67	-0.02	-15.84	3.E-17
P19338	GFGFVDFNSEEDAK	1560.67	1560.67	0.00	-1.23	3.E-17
Q96I25	(51)SLYDDLGVETSDSKTEGWSK	2258.02	2258.02	0.00	1.44	3.E-17
P02545	LRDLEDSLARERDTSRRLLAEK	2641.43	2641.43	0.00	0.37	3.E-17
P41219	NLQEAEEWYK	1308.60	1308.60	0.00	-0.55	3.E-17
Q9BUQ0	SRDYTRPDLPSGDSQPSLDQTMAAAFGAPGIISASPYAGAGFPPTFAIPQAAGLSVPNVHGALAPLAIPSAAAAAAAAGRIAIPGLAGAGNSVLLVSNLNPERVTPQSLFILFGVYGDVQRVK	12213.38	12214.40	-1.02	-83.24	4.E-17
Q15233	ALDRCSEGSFLLTTFPRPVTVEPMDQLDDEEGLPEK	4033.92	4033.93	-0.01	-1.74	4.E-17
P62805	VFLENVIRDAVTYTEHAK	2147.10	2104.10	43.00	20027.30	4.E-17

P62805	VFLENVIRDAVTYTEHAK	2148.08	2104.10	43.98	20472.90	4.E-17
P62277	GLSQSALPYRRSVPTWLK	2058.11	2058.14	-0.03	-14.88	4.E-17
P62277	GLSQSALPYRRSVPTWLK	2058.14	2058.14	0.00	-1.66	4.E-17
P26599	LPIDVTEGEVISLGLPFGK	1983.09	1983.09	0.00	-1.86	4.E-17
P16403	ERSGVSLAALKK	1255.72	1257.74	-2.02	-1606.53	4.E-17
P07355	TPAQYDASELK	1221.59	1221.59	0.00	-0.59	5.E-17
P07355	TPAQYDASELK	1222.62	1221.59	1.03	844.08	5.E-17
Q00839	RNFILDQTNVSAAAQRRK	2087.13	2087.13	0.00	-1.10	5.E-17
Q9UMS4	VAHPIRPKPPSATSIPAILK	2092.25	2092.25	0.00	-1.16	5.E-17
P16403	ERSGVSLAALKK	1257.72	1257.74	-0.02	-13.88	6.E-17
P16403	ERSGVSLAALKK	1257.74	1257.74	0.00	-1.00	6.E-17
P14866	SDALETLGFLNHYQMK	1865.90	1865.90	0.00	-1.70	6.E-17
O43390	YGGPPPDSVYSGVQPGIGTEVFVGK	2506.17	2506.24	-0.07	-25.99	6.E-17
O43390	YGGPPPDSVYSGVQPGIGTEVFVGK	2506.23	2506.24	-0.01	-2.73	6.E-17
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-2.92	6.E-17

P06748	MSVQPTVSLGGFEITPPVVLRLK	2469.35	2467.39	1.96	793.57	6.E-17
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-3.15	6.E-17
P07355	TPAQYDASELK	1221.58	1221.59	-0.02	-12.29	7.E-17
P07355	TPAQYDASELK	1225.61	1221.59	4.02	3281.21	7.E-17
P07355	TPAQYDASELK	1225.68	1221.59	4.09	3337.00	7.E-17
P18621	EQIVPKPEEEVAQK	1622.85	1622.85	0.00	-2.29	7.E-17
Q02539	KALAAAGYDVEK	1234.66	1234.66	0.00	-0.58	7.E-17
Q02539	KALAAAGYDVEK	1235.65	1234.66	0.99	799.49	7.E-17
Q8NC51	PGHLQEGFGCVVTNRFDQLFDDESDPFEVLK	3537.65	3537.65	0.00	-1.05	7.E-17
P33778	RSTITSREIQTAVRLLLPGELAK	2551.40	2551.48	-0.08	-31.84	7.E-17
P61978	ALRTDYNASVSVPDSSGPERILSISADIETIGEILKK	3944.06	3944.07	-0.01	-1.33	7.E-17
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.92	3566.92	0.00	-1.06	7.E-17
Q09666	AGLRVSAPEVSVGHK	1513.65	1505.83	7.82	5169.09	7.E-17
P41219	MALDIEIATYRK	1422.75	1422.75	0.00	-1.38	8.E-17
P33778	RSTITSREIQTAVRLLLPGELAK	2547.47	2551.48	-4.01	-1572.86	8.E-17

P46783	NRIAIYELLFK	1378.80	1378.80	0.00	-1.70	8.E-17
P41219	NLQEAEEWYK	1308.58	1308.60	-0.02	-12.16	8.E-17
P41219	NLQEAEEWYK	1308.60	1308.60	0.00	0.98	8.E-17
Q14103	IFVGGLSPDTPEEK	1487.75	1487.75	0.00	-1.84	9.E-17
P46777	HIMGQNVADYMRYLMEEDEDAYKK	2962.56	2948.31	14.25	4810.50	9.E-17
P46777	HIMGQNVADYMRYLMEEDEDAYKK	2965.44	2948.31	17.13	5776.31	9.E-17
P62987	IIEPSLRQLAQK	1394.82	1394.82	0.00	-1.17	1.E-16
P20700	NSQGEEVAQRSTVFK	1676.71	1678.83	-2.12	-1263.75	1.E-16
P33778	RSTITSREIQTAVRLLLPGELAK	2551.48	2551.48	0.00	-1.42	1.E-16
P62841	EAPPMEKPEVVK	1352.70	1352.70	0.00	-1.08	1.E-16
P62841	EAPPMEKPEVVK	1355.70	1352.70	3.00	2216.52	1.E-16
P05787	LLEGEESRLESGMQNMSIHTK	2388.14	2388.14	0.00	-1.35	1.E-16
Q09666	FSMPGFKGEGPEVDVKLPKADVDVSGPKMDAEVPDVNIEGPDAK	4610.26	4610.26	0.00	0.80	1.E-16
P46783	NRIAIYELLFK	1375.59	1378.80	-3.21	-2332.93	1.E-16
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.55	3183.56	-0.01	-2.90	1.E-16

P33778	RSTITSREIQTAVRLLLPGELAK	2552.41	2551.48	0.93	364.59	1.E-16
P26447	ALDVMVSTFHK	1246.64	1246.64	0.00	-0.86	2.E-16
P26447	ALDVMVSTFHK	1247.63	1246.64	0.99	790.64	2.E-16
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.77	2.E-16
P20700	NSQGEEVAQRSTVFK	1678.80	1678.83	-0.03	-17.72	2.E-16
P63244	(52)TEQMTLRGTLK	1318.69	1318.69	0.00	-0.92	2.E-16
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.12	2256.13	-0.01	-2.90	2.E-16
P16401	RKATGPPVSELITK	1495.87	1495.87	0.00	-1.07	2.E-16
Q92522	ALVQNDTLLQVK	1340.77	1340.77	0.00	-0.41	2.E-16
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.35	2467.39	-0.04	-17.88	2.E-16
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-2.19	2.E-16
P43243	FDSEYERMGRGPGPLQERSLFEK	2727.31	2727.31	0.00	-1.63	2.E-16
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-2.60	2.E-16
P0C0S8	GNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKK	4133.16	4090.15	43.01	10404.90	2.E-16
P20700	NSQGEEVAQRSTVFK	1678.83	1678.83	0.00	-1.64	2.E-16

P20700	NSQGEEVAQRSTVFK	1683.79	1678.83	4.96	2945.00	2.E-16
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.87	9082.91	-0.04	-4.43	2.E-16
P05787	MLETKWSLLQQQK	1631.87	1631.87	0.00	1.47	2.E-16
P35659	KKVERLTMQVSSLQREPFTIAQGK	2773.53	2773.53	0.00	-1.53	2.E-16
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-3.69	2.E-16
P33778	RSTITSREIQTAVRLLLPGELAK	2551.53	2551.48	0.05	20.45	2.E-16
P33778	RSTITSREIQTAVRLLLPGELAK	2552.41	2551.48	0.93	362.59	2.E-16
P14866	NRIQHPSNVLHFFNAPLEVTEENFFEICDELGVK	3984.94	3984.95	-0.01	-1.33	2.E-16
P19338	GIAYIEFKTEADAEK	1683.84	1683.84	0.00	-1.38	3.E-16
P62277	GLAPDLPEDLYHLIK	1688.87	1692.91	-4.04	-2393.22	3.E-16
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.26	2601.26	0.00	-1.69	3.E-16
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3192.46	3183.56	8.90	2789.09	3.E-16
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3196.54	3183.56	12.98	4062.13	3.E-16
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.68	3307.68	0.00	-1.43	3.E-16
Q15149	LLSAERAVTGYK	1304.67	1306.72	-2.05	-1570.95	3.E-16

P60709	ILTERGYSFTTTAEREIVRDIK	2597.38	2597.38	0.00	-1.26	3.E-16
Q02539	KALAAAGYDVEK	1234.66	1234.66	0.00	-0.50	3.E-16
P19338	TLVLSNLSYSATEETLQEVFEK	2500.25	2500.26	-0.01	-4.29	3.E-16
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-2.76	4.E-16
P62277	GLAPDLPEDLYHLIK	1692.91	1692.91	0.00	-1.55	4.E-16
P09651	GGNFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSSYGSGRRF	4251.91	4251.92	-0.01	-2.36	4.E-16
Q15149	LLSAERAVTGYK	1306.62	1306.72	-0.10	-79.04	4.E-16
Q15149	LLSAERAVTGYK	1306.70	1306.72	-0.02	-15.21	4.E-16
Q15149	LLSAERAVTGYK	1306.72	1306.72	0.00	-1.21	4.E-16
P62280	(41)ADIQTERAYQK	1362.69	1363.67	-0.98	-722.77	4.E-16
P62280	(41)ADIQTERAYQK	1363.67	1363.67	0.00	-1.11	4.E-16
P36578	GHRIEEVPELPLVVEDKVEGYKK	2662.43	2662.43	0.00	-1.41	5.E-16
P20700	LREYEAALNSK	1293.67	1292.67	1.00	774.81	5.E-16
P14866	RQRQPPLLGDHPAEYGGPHGGYHSHYHDEGYGPPPPHYEGRRMGPPVGGHRRGPSRYGPQYGHPPPPPPPPEYGPHADSPVLMVYGLDQSK	9977.74	9977.75	-0.01	-0.65	5.E-16
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3196.55	3153.55	43.00	13452.10	5.E-16

P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3198.50	3153.55	44.95	14054.30	5.E-16
Q07955	FRSHEGETAYIRVK	1688.85	1691.87	-3.02	-1785.48	5.E-16
Q92804	TGKPMINLYTDKDTGKPKGEATVSFDDPPSAK	3407.69	3407.69	0.00	1.14	5.E-16
P22626	KRGFGFVTFDDHDPVDK	1978.95	1978.95	0.00	-2.01	6.E-16
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.12	1930.16	-0.04	-20.15	6.E-16
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-3.15	6.E-16
P15880	SPYQEFTDHLVK	1462.71	1462.71	0.00	-2.20	6.E-16
P61978	RPAEDMEEEQAFK	1578.70	1578.70	0.00	-1.77	6.E-16
P16403	(51)SETAPAAPAAAPPAEK	1519.71	1519.75	-0.04	-28.05	7.E-16
P16403	(51)SETAPAAPAAAPPAEK	1519.72	1519.75	-0.03	-17.32	7.E-16
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	-2.52	7.E-16
P16403	(51)SETAPAAPAAAPPAEK	1519.78	1519.75	0.03	18.74	7.E-16
Q07955	FRSHEGETAYIRVK	1691.84	1691.87	-0.03	-18.81	8.E-16
Q07955	FRSHEGETAYIRVK	1691.87	1691.87	0.00	-1.61	8.E-16
P62318	IRFLILPDMLK	1357.82	1357.82	0.00	-1.13	8.E-16

P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.60	3307.68	-0.08	-24.04	8.E-16
Q53F64	KIFVGGLNPEATEEK	1630.86	1630.86	0.00	-0.92	8.E-16
P08758	(41)AQVLRGTVTDFPGFDERADAETLRK	2833.44	2833.44	0.00	-1.53	8.E-16
P62081	IVKPNGEKPDEFESGISQALLELEMNSDLK	3330.65	3329.67	0.98	294.47	9.E-16
P09651	LFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTK	4229.01	4229.02	-0.01	-2.44	9.E-16
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.68	3307.68	0.00	0.18	9.E-16
P18621	EQIVPKPEEEVAQK	1623.85	1622.85	1.00	616.06	9.E-16
P18621	EQIVPKPEEEVAQK	1626.76	1622.85	3.91	2402.99	9.E-16
P41219	NLQEAEEWYK	1308.60	1308.60	0.00	-1.54	9.E-16
P16403	ALAAAGYDVEKNNSRIKLGLK	2230.24	2230.24	0.00	1.38	1.E-15
Q71UI9	ATIAGGGVIPHIHK	1369.78	1369.78	0.00	1.41	1.E-15
Q71UI9	ATIAGGGVIPHIHK	1373.70	1369.78	3.92	2855.07	1.E-15
Q71UI9	ATIAGGGVIPHIHK	1373.72	1369.78	3.94	2869.81	1.E-15
P36578	MINTDLSRILK	1302.73	1302.73	0.00	-0.73	1.E-15
P06748	CGSGPVHISGQHLVAVEEDAESEDEEEEDVK	3334.45	3322.44	12.01	3600.37	1.E-15

P16403	KAGGTPRKASGPPVSELITK	1993.13	1993.13	0.00	0.41	1.E-15
P02545	AGQVVTIWAAGAGATHSPPTDLVWK	2532.30	2532.31	-0.01	-3.45	1.E-15
P68104	IGGIGTVPVGRVETGVLKPGMVVTFAPVNVTTEVK	3520.96	3520.97	-0.01	-1.91	1.E-15
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-3.30	1.E-15
P19338	GFGFVDFNSEEDAK	1560.67	1560.67	0.00	-1.55	1.E-15
P19338	GFGFVDFNSEEDAK	1560.79	1560.67	0.12	75.14	1.E-15
P19338	GFGFVDFNSEEDAK	1564.77	1560.67	4.10	2617.82	1.E-15
Q92499	(41)AAFSEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAETGSGK	5329.56	5329.58	-0.02	-3.86	1.E-15
P46778	RQPAPPREAHFVRTNGKEPELLEPIPYEFMA	3619.84	3618.84	1.00	276.18	2.E-15
Q9UKM9	SNIDALLSRLEQIAAEQK	1998.07	1998.07	0.00	2.33	2.E-15
Q53F64	KIFVGGLNPEATEEK	1631.86	1630.86	1.00	614.27	2.E-15
P0C0S8	VTIAQGGVLPNIQAVLLPKK	2058.26	2058.26	0.00	-0.80	2.E-15
P08758	(41)AQVLRGTVTDFPGFDERADAETLRK	2833.43	2833.44	-0.01	-1.92	2.E-15
P05787	AQYEDIANRSRAEAESMYQIKYEELQSLAGK	3590.72	3590.73	-0.01	-2.31	2.E-15
P19338	TLVLSNLSYSATEETLQEVFEK	2500.19	2500.26	-0.07	-27.09	2.E-15

P19338	TLVLSNLSYSATEETLQEVFEK	2500.25	2500.26	-0.01	-5.01	2.E-15
Q13151	SGGGGGGGGSSWGGRSNSGPYRGGYGGGGGYGGSSF	3141.34	3113.30	28.04	8925.03	2.E-15
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9006.92	9082.91	-75.99	-8436.67	2.E-15
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9020.94	9082.91	-61.97	-6869.47	2.E-15
P11142	NQVAMNPTNTVFDAK	1648.79	1648.79	0.00	-1.70	2.E-15
Q8IUE6	TRIIPRHLQLAVRNDEELNK	2414.35	2414.35	0.00	-1.69	2.E-15
P52272	(41)AAGVEAAAEVAATEIKMEEESGAPGVPSGNGAPGPKGEGERPAQNEK	4585.15	4586.18	-1.03	-223.59	2.E-15
P52272	(41)AAGVEAAAEVAATEIKMEEESGAPGVPSGNGAPGPKGEGERPAQNEK	4587.16	4586.18	0.98	213.27	2.E-15
P20700	SLEGDLEDLKDQIAQLEASLAAAKK	2655.39	2655.40	-0.01	-1.97	2.E-15
P47914	AQAAAPASVPAQAPK	1372.72	1376.74	-4.02	-2928.54	2.E-15
P47914	AQAAAPASVPAQAPK	1376.74	1376.74	0.00	0.45	2.E-15
P20700	LREYEAALNSK	1293.67	1292.67	1.00	774.81	3.E-15
Q15149	ADSMIRLLFNDVQTLK	1862.99	1862.99	0.00	-1.98	3.E-15
Q9Y5B9	YTEGVQSLNWTK	1424.69	1424.69	0.00	-1.32	3.E-15
P62906	AVDIPHMDIEALKK	1578.84	1578.84	0.00	-1.54	3.E-15

P62805	VFLENVIRDAVTYTEHAK	2107.11	2104.10	3.01	1427.05	3.E-15
P22626	RGFGFVTFDDHDPVDK	1850.86	1850.86	0.00	-2.12	3.E-15
P62841	HGRPGIGATHSSRFIPLK	1930.06	1930.06	0.00	-2.39	3.E-15
P11142	SQIHDIVLVGGSTRIPK	1815.95	1819.03	-3.08	-1697.54	3.E-15
P11142	SQIHDIVLVGGSTRIPK	1819.03	1819.03	0.00	1.24	3.E-15
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-2.72	3.E-15
P46777	NSVTPDMMEEMYKK	1704.86	1701.74	3.12	1828.59	3.E-15
P26599	MALIQMGSVEEAVQALIDLHNHDLGENHHLRVSFSK	4038.01	4038.02	-0.01	-2.90	3.E-15
Q02878	PRHQEGEIFDTEK	1579.84	1584.75	-4.91	-3107.46	4.E-15
Q02878	PRHQEGEIFDTEK	1584.75	1584.75	0.00	-1.71	4.E-15
O75526	YGRIVEVLLMK	1319.74	1319.76	-0.02	-12.96	4.E-15
O75526	YGRIVEVLLMK	1319.76	1319.76	0.00	-1.06	4.E-15
P19338	FGYVDFESAEDLEKALELTGLK	2473.23	2473.23	0.00	-1.73	4.E-15
P33778	RSTITSREIQTAVRLLLPGELAK	2594.48	2551.48	43.00	16573.60	4.E-15
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-2.44	4.E-15

P62081	AQLRELNITAAK	1326.76	1326.76	0.00	-1.07	4.E-15
P62081	AQLRELNITAAK	1328.70	1326.76	1.94	1462.53	4.E-15
O75526	YGRIVEVLLMK	1319.76	1319.76	0.00	-0.31	5.E-15
P62805	TVTAMDVVYALK	1310.75	1309.70	1.05	797.45	5.E-15
P62805	TVTAMDVVYALK	1311.68	1309.70	1.98	1508.03	5.E-15
P20700	LREYEAALNSK	1292.67	1292.67	0.00	-0.03	5.E-15
Q53F64	IFVGGLNPEATEEK	1500.78	1502.76	-1.98	-1322.61	5.E-15
Q53F64	IFVGGLNPEATEEK	1502.76	1502.76	0.00	-1.55	5.E-15
Q53F64	IFVGGLNPEATEEK	1504.76	1502.76	2.00	1332.01	5.E-15
Q53F64	IFVGGLNPEATEEK	1505.85	1502.76	3.09	2054.03	5.E-15
P62988	ESTLHLVLRLRGG	1449.84	1449.84	0.00	-1.56	5.E-15
P0C0S8	TRIIPRHLQLAIRNDEELNK	2430.33	2428.37	1.96	806.96	5.E-15
P62805	TVTAMDVVYALK	1309.68	1309.70	-0.02	-16.46	6.E-15
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-2.94	6.E-15
P62805	TVTAMDVVYALK	1309.74	1309.70	0.04	33.48	6.E-15

P62805	TVTAMDVVYALK	1309.76	1309.70	0.06	42.56	6.E-15
P62805	TVTAMDVVYALK	1312.69	1309.70	2.99	2281.46	6.E-15
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-2.68	6.E-15
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-2.61	6.E-15
O75526	YGRIVEVLLMK	1323.65	1319.76	3.89	2941.62	6.E-15
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.33	2428.37	-0.04	-17.43	6.E-15
P62805	TVTAMDVVYALK	1309.64	1309.70	-0.06	-42.65	6.E-15
P62805	TVTAMDVVYALK	1309.66	1309.70	-0.04	-33.49	6.E-15
P62805	TVTAMDVVYALK	1309.67	1309.70	-0.03	-25.01	6.E-15
P14866	RQRQPPLLGDHPAEYGGPHGGYHSHYHDEGYGPPPPHYEGRRMGPPVGGHRRGPSRYGPQYGHPPPPPPPPEYGPHADSPVLMVYGLDQSK	9977.74	9977.75	-0.01	-0.95	7.E-15
P07355	GLGTDEDSLIEIICSRTNQELQEINRVYK	3335.67	3335.67	0.00	-1.32	7.E-15
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.21	1930.16	0.05	24.10	7.E-15
P62805	TVTAMDVVYALKRQGRTLYGFGG	2497.55	2502.31	-4.76	-1905.86	7.E-15
P62805	TVTAMDVVYALKRQGRTLYGFGG	2502.31	2502.31	0.00	-1.55	7.E-15
P08758	SIRSIPAYLAETLYYAMK	2089.09	2089.09	0.00	-2.24	7.E-15

P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3778.80	7.E-15
P16403	(51)SETAPAAPAAAPPAEK	1519.71	1519.75	-0.04	-27.78	7.E-15
P16403	(51)SETAPAAPAAAPPAEK	1519.72	1519.75	-0.03	-17.98	7.E-15
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	-1.86	7.E-15
P16403	(51)SETAPAAPAAAPPAEK	1519.79	1519.75	0.04	28.74	7.E-15
P05787	TARSNMDNMFESYINNLRRQLETLGQEK	3357.61	3357.62	-0.01	-2.41	8.E-15
Q01130	(51)SYGRPPPDVEGMTSLKVDNLTYRTSPDTLRRVFEK	4066.05	4066.06	-0.01	-2.73	8.E-15
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.15	1930.16	-0.01	-4.19	8.E-15
Q08211	ETPFELIEALLKYIETLNVPGAVLVFLPGWNLIYTMQK	4362.37	4362.36	0.01	2.37	8.E-15
Q12906	QGGYSQSNYNSPGSGQNYSGPPSSYQSSQGGYGRNADHSMNYQYR	4882.04	4882.04	0.00	0.32	8.E-15
Q7L4M3	TTSGYAGGLSSAYGGLTSPGLSYSLGSSFGSGAGSSSFSRTSSSRAVVVK	4739.29	4739.30	-0.01	-3.11	9.E-15
P16403	ASGPPVSELITK	1201.64	1197.66	3.98	3309.17	9.E-15
P35268	ITVTSEVPFSK	1208.67	1206.65	2.02	1675.24	9.E-15
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3306.58	3307.68	-1.10	-332.40	9.E-15
A2BDF6	STELLIRKLPFQRLVREIAQDFK	2799.60	2799.61	-0.01	-2.99	9.E-15

P33778	RSTITSREIQTAVRLLLPGELAK	2551.37	2551.48	-0.11	-43.99	9.E-15
P33778	RSTITSREIQTAVRLLLPGELAK	2551.40	2551.48	-0.08	-30.74	9.E-15
P05787	TARSNMDNMFESYINNLRRQLETLGQEK	3357.61	3357.62	-0.01	-2.26	1.E-14
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.67	3307.68	-0.01	-2.12	1.E-14
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3308.62	3307.68	0.94	284.80	1.E-14
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-3.93	1.E-14
P33778	RSTITSREIQTAVRLLLPGELAK	2551.53	2551.48	0.05	19.98	1.E-14
P33778	RSTITSREIQTAVRLLLPGELAK	2551.56	2551.48	0.08	31.54	1.E-14
P07355	SALSGHLETVILGLLK	1649.97	1649.97	0.00	-2.22	1.E-14
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9097.92	9098.88	-0.96	-104.98	1.E-14
P98179	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	3493.74	3493.74	0.00	-1.37	1.E-14
P07910	LKGDDLQAIKK	1228.71	1227.72	0.99	803.16	1.E-14
P05787	TEISEMNRNISRLQAEIEGLK	2427.10	2430.25	-3.15	-1298.73	1.E-14
P05787	TEISEMNRNISRLQAEIEGLK	2430.24	2430.25	-0.01	-4.30	1.E-14
P05787	TEISEMNRNISRLQAEIEGLK	2431.19	2430.25	0.94	387.61	1.E-14

P05787	LSELEAALQRAK	1327.75	1327.75	0.00	-0.93	1.E-14
P16403	ASGPPVSELITK	1198.66	1197.66	1.00	835.70	1.E-14
P46087	GADSELSTVPSVTK	1389.70	1389.70	0.00	-0.95	1.E-14
P26373	STESLQANVQRLK	1472.79	1472.79	0.00	-1.35	1.E-14
P60709	ILTERGYSFTTTAEREIVRDIK	2597.34	2597.38	-0.04	-14.35	2.E-14
P60709	ILTERGYSFTTTAEREIVRDIK	2597.38	2597.38	0.00	-0.95	2.E-14
O00422	(41)AVESRVTQEEIK	1429.74	1429.74	0.00	-1.11	2.E-14
Q00839	YNILGTNTIMDK	1381.69	1381.69	0.00	-0.39	2.E-14
Q00839	YNILGTNTIMDK	1382.67	1381.69	0.98	710.55	2.E-14
A5PLR1	TDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	6435.04	6317.28	117.76	18299.70	2.E-14
P06748	NCFRMTDQEAIQDLWQWRK	2467.15	2467.15	0.00	1.30	2.E-14
P06748	NCFRMTDQEAIQDLWQWRK	2467.14	2467.15	-0.01	-2.56	2.E-14
P11387	WWEEERYPEGIK	1620.76	1620.76	0.00	-0.20	2.E-14
P62857	(49)MDTSRVQPIK	1215.63	1215.63	0.00	-1.06	2.E-14
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3179.56	3183.56	-4.00	-1259.24	2.E-14

P05387	NIEDVIAQGIGK	1255.68	1255.68	0.00	-0.31	2.E-14
P07910	LKGDDLQAIKK	1227.72	1227.72	0.00	-0.78	2.E-14
P04083	QAWFIENEEQEYVQTVK	2140.00	2140.01	-0.01	-2.70	2.E-14
P08865	RKSDGIYIINLK	1417.74	1418.82	-1.08	-759.39	2.E-14
P08865	RKSDGIYIINLK	1418.82	1418.82	0.00	-0.58	2.E-14
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.55	3183.56	-0.01	-2.08	3.E-14
O75526	YGRIVEVLLMK	1324.68	1319.76	4.92	3714.24	3.E-14
P06748	GGSLPKVEAKFINYVK	1748.98	1748.98	0.00	0.76	3.E-14
P15880	SPYQEFTDHLVK	1462.71	1462.71	0.00	-2.20	3.E-14
Q53HU8	NTRTNEKVELQELNDRFANYIDK	2809.40	2809.40	0.00	-1.44	3.E-14
P46777	GAVDGGLSIPHSTK	1337.69	1337.69	0.00	-0.52	3.E-14
Q9H307	(41)AVAVRTLQEQLEK	1525.85	1525.85	0.00	-1.39	3.E-14
P26599	DYGNSPLHRFK	1332.66	1332.66	0.00	-0.57	3.E-14
P26599	DYGNSPLHRFK	1336.70	1332.66	4.04	3023.82	3.E-14
P62805	VFLENVIRDAVTYTEHAK	2107.11	2104.10	3.01	1426.53	3.E-14

P14866	SERSSSGLLEWESK	1591.57	1593.76	-2.19	-1374.45	3.E-14
P08865	RKSDGIYIINLK	1414.76	1418.82	-4.06	-2869.12	3.E-14
O75526	YGRIVEVLLMK	1319.74	1319.76	-0.02	-14.55	4.E-14
O75526	YGRIVEVLLMK	1319.76	1319.76	0.00	-0.99	4.E-14
O75526	YGRIVEVLLMK	1320.75	1319.76	0.99	746.92	4.E-14
P24928	LLQFHVATMVDNELPGLPRAMQK	2616.27	2607.37	8.90	3400.58	4.E-14
P46777	AHAAIRENPVYEK	1495.80	1496.77	-0.97	-647.71	4.E-14
P46777	AHAAIRENPVYEK	1496.74	1496.77	-0.03	-21.01	4.E-14
P46777	AHAAIRENPVYEK	1496.74	1496.77	-0.03	-21.01	4.E-14
P46777	AHAAIRENPVYEK	1496.77	1496.77	0.00	-0.50	4.E-14
P46777	AHAAIRENPVYEK	1499.78	1496.77	3.01	2006.39	4.E-14
P07355	LSLEGDHSTPPSAYGSVK	1843.90	1843.90	-0.01	-2.70	4.E-14
P11142	EDIERMVQEAEK	1475.69	1475.69	0.00	-1.28	4.E-14
Q13435	AAPPPMSAQLPGIPMPPPPLGLPPLQPPPPPPPPPPGLGLGF PMAHPPNLGPPPPLRVGEPVALSEEERLK	7206.84	7206.88	-0.04	-5.74	4.E-14
P16403	(51)SETAPAAPAAAPPAEK	1519.72	1519.75	-0.03	-17.12	4.E-14

P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	-2.65	4.E-14
P16403	(51)SETAPAAPAAAPPAEK	1519.78	1519.75	0.03	19.07	4.E-14
Q7L4M3	TTSGYAGGLSSAYGGLTSPGLSYSLGSSFGSGAGSSSFSRTSSSRAVVVK	4739.31	4739.30	0.01	1.66	4.E-14
Q6ZQN2	FSMPGFKGEGPEVDVNLPKADIDVSGPKVDIDTPDIDIHGPEGK	4638.32	4631.27	7.05	1520.33	4.E-14
P49755	LKPLEVELRRLEDLSESIVNDFAYMK	3106.63	3106.64	-0.01	-2.58	5.E-14
P16403	ASGPPVSELITK	1198.66	1197.66	1.00	836.70	5.E-14
P16403	(51)SETAPAAPAAAPPAEK	1519.69	1519.75	-0.06	-37.92	5.E-14
P16403	(51)SETAPAAPAAAPPAEK	1519.71	1519.75	-0.04	-28.18	5.E-14
P16403	(51)SETAPAAPAAAPPAEKAPVKK	2043.10	2043.10	0.00	1.60	5.E-14
P26599	ELKTDSSPNQARAQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLRIIVENLFYPVTLDVLHQIFSK	7475.89	7475.90	-0.01	-1.26	5.E-14
P23396	GGKPEPPAMPQPVPTA	1572.80	1572.80	0.00	-2.15	5.E-14
P16403	ASGPPVSELITK	1201.69	1197.66	4.03	3356.20	6.E-14
P16403	ASGPPVSELITK	1202.57	1197.66	4.91	4086.34	6.E-14
P84090	IYVLLRRQAQQAGK	1640.78	1642.96	-2.18	-1326.00	6.E-14
P84090	IYVLLRRQAQQAGK	1642.96	1642.96	0.00	-1.63	6.E-14

P26599	DYGNSPLHRFK	1332.66	1332.66	0.00	-0.57	6.E-14
P50995	TPVLFDIYEIK	1335.78	1336.73	-0.95	-713.16	6.E-14
P21796	SRVTQSNFAVGYK	1455.75	1455.75	0.00	0.88	6.E-14
P05787	LSELEAALQRAK	1327.75	1327.75	0.00	-0.70	6.E-14
P09651	LFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTK	4229.02	4229.02	0.00	-1.09	7.E-14
P09651	LFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTK	4229.16	4229.02	0.14	33.41	7.E-14
P16403	ASGPPVSELITK	1198.66	1197.66	1.00	838.37	7.E-14
Q04695	EPVTTRQVRTIVEEVQDGK	2183.15	2183.15	0.00	-0.54	7.E-14
Q16891	TDHPEIGEGKPTPALSEEASSSSIRERPPEEVAARLAQQEK	4426.19	4426.20	-0.01	-1.19	7.E-14
O95926	(41)AAIAASEVLVDSAEEGSLAAAAELAAQK	2697.36	2697.37	-0.01	-2.05	8.E-14
Q16695	KPHRYRPGTVALREIRRYQK	2523.44	2523.44	0.00	-1.22	8.E-14
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9006.88	9082.91	-76.03	-8441.42	8.E-14
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9020.93	9082.91	-61.98	-6870.70	8.E-14
P51991	RAVSREDSVKPGAHLTVK	1949.09	1949.08	0.01	7.53	8.E-14
Q13247	DFMRQAGEVTYADAHK	1843.87	1837.84	6.03	3268.72	8.E-14

Q13247	DFMRQAGEVTYADAHK	1843.89	1837.84	6.05	3282.13	8.E-14
P05204	VKDEPQRRSARLSAKPAPPKPEPKPK	2906.66	2906.66	0.00	-0.54	8.E-14
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.55	3183.56	-0.01	-1.80	9.E-14
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3187.57	3183.56	4.01	1257.56	9.E-14
P69905	TYFPHFDLSHGSAQVK	1832.88	1832.88	0.00	-1.61	9.E-14
Q09666	ISMPDIDLNLK	1257.66	1257.66	0.00	-1.16	1.E-13
P06748	CGSGPVHISGQHLVAVEEDAE(37)SEDEEEEDVK	3536.39	3402.41	133.98	37886.80	1.E-13
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPK	7564.00	7564.00	0.00	-0.07	1.E-13
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4244.55	4245.54	-0.99	-233.40	1.E-13
P08621	(52)TQFLPPNLLALFAPRDPIPYLPPLEKLPHEK	3605.99	3606.00	-0.01	-2.51	1.E-13
P62854	KFVIRNIVEAAAVRDISEASVFDAYVLPK	3219.76	3219.77	-0.01	-3.42	1.E-13
P46777	GAVDGGLSIPHSTK	1337.69	1337.69	0.00	-0.74	1.E-13
P62750	AYVRLAPDYDALDVANK	1892.96	1892.96	0.00	-0.10	1.E-13
P15880	SLEEIYLFSLPIKESEIIDFFLGASLKDEVLK	3684.97	3684.98	-0.01	-2.98	1.E-13
O43390	VAERLDEIFQTGLVAYVDLDERAIDALREFNEEGALSVLQQFK	4909.51	4909.51	0.00	0.78	1.E-13

A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	6898.52	6722.54	175.98	25510.10	2.E-13
P07910	LKGDDLQAIKK	1228.72	1227.72	1.00	815.60	2.E-13
P46087	ELLLSAIDSVNATSK	1560.67	1559.84	0.83	531.87	2.E-13
P20700	LREYEAALNSK	1292.67	1292.67	0.00	-0.19	2.E-13
P04083	VLDLELKGDIEK	1370.77	1370.77	0.00	-1.06	2.E-13
P22626	KRGFGFVTFDDHDPVDK	1978.95	1978.95	0.00	-1.60	2.E-13
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9006.91	9082.91	-76.00	-8438.11	2.E-13
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9019.92	9082.91	-62.99	-6983.09	2.E-13
P19338	KMAPPPKEVEEDSEDEEMSEDEEDDSSGEEVVIPQK	4061.71	4061.73	-0.02	-3.99	2.E-13
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3179.56	3183.56	-4.00	-1258.58	2.E-13
P62854	FVIRNIVEAAAVRDISEASVFDAYVLPK	3091.66	3091.67	-0.01	-2.57	2.E-13
P25815	MTELETAMGMIIDVFSRYSGSEGSTQTLTK	3282.54	3282.55	-0.01	-3.01	2.E-13
P04083	VLDLELKGDIEK	1370.77	1370.77	0.00	-1.50	2.E-13
P62304	GDNITLLQSVSN	1259.64	1259.64	0.00	-0.82	3.E-13
Q00839	EKPYFPIPEEYTFIQNVPLEDRVRGPK	3260.68	3260.69	-0.01	-2.13	3.E-13

P18077	IEGVYARDETEFYLGK	1888.92	1888.92	0.00	-1.99	3.E-13
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9006.93	9082.91	-75.98	-8436.27	3.E-13
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9020.94	9082.91	-61.97	-6870.04	3.E-13
P84090	(51)SHTILLVQPTK	1277.73	1277.73	0.00	-0.90	3.E-13
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.14	2256.13	0.01	2.91	3.E-13
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3169.54	3153.55	15.99	5043.65	3.E-13
P61978	(49)METEQPEETFPNTETNGEFGKRPAEDMEEEQAFK	4017.71	4016.72	0.99	246.21	3.E-13
P07910	(41)ASNVTNKTDPRSMNSRVFIGNLNTLVVK	3116.63	3116.64	-0.01	-2.08	3.E-13
P07910	(41)ASNVTNKTDPRSMNSRVFIGNLNTLVVK	3117.57	3116.64	0.93	299.15	3.E-13
P52272	(41)AAGVEAAAEVAATEIKMEEESGAPGVPSGNGAPGPKGEGERPAQNEK	4587.17	4586.18	0.99	216.34	3.E-13
Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.55	3183.56	-0.01	-1.99	4.E-13
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.13	2256.13	0.00	-1.75	4.E-13
P60709	DLYANTVLSGGTTMYPGIADRMQK	2597.38	2601.26	-3.88	-1494.08	4.E-13
P62857	(49)MDTSRVQPIK	1214.65	1215.63	-0.98	-805.49	4.E-13
P62857	(49)MDTSRVQPIK	1215.63	1215.63	0.00	-0.97	4.E-13

P22626	KRGFGFVTFDDHDPVDK	1982.94	1978.95	3.99	2011.67	4.E-13
P08729	QEELEAALQRAK	1384.73	1384.73	0.00	-1.02	4.E-13
P0C0S8	VTIAQGGVLPNIQAVLLPK	1930.16	1930.16	0.00	1.10	4.E-13
P16403	ERSGVSLAALKK	1257.72	1257.74	-0.02	-14.28	4.E-13
Q92879	EGPEGANLFIYHLPQEFGDQDLLQMFMPFGNVVSAK	4037.91	4037.93	-0.02	-5.97	4.E-13
P39019	SVARRVLQALEGLK	1538.93	1538.93	0.00	-0.93	5.E-13
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3169.54	3153.55	15.99	5044.38	5.E-13
P07355	AYTNFDAERDALNIETAIK	2154.06	2154.06	0.00	-0.96	5.E-13
P16403	ERSGVSLAALKK	1257.74	1257.74	0.00	-1.40	5.E-13
P08729	QEELEAALQRAK	1384.71	1384.73	-0.02	-15.61	5.E-13
P08729	QEELEAALQRAK	1388.64	1384.73	3.91	2812.75	5.E-13
Q00839	EVLAGRPLFPHVLCHNCAVEFNFGQK	2922.44	2924.46	-2.02	-692.25	5.E-13
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.13	2256.13	0.00	1.04	5.E-13
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2257.86	2256.13	1.73	765.88	5.E-13
P62750	AYVRLAPDYDALDVANK	1892.96	1892.96	0.00	-2.00	6.E-13

P02545	NIYSEELRETK	1380.69	1380.69	0.00	-1.37	6.E-13
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.25	2601.26	-0.01	-3.61	6.E-13
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2259.59	2256.13	3.46	1530.79	7.E-13
Q04695	ATMQNLNDRLASYLDK	1850.85	1851.91	-1.06	-571.94	7.E-13
Q04695	ATMQNLNDRLASYLDK	1851.91	1851.91	0.00	-1.83	7.E-13
Q04695	ATMQNLNDRLASYLDK	1854.84	1851.91	2.93	1579.92	7.E-13
Q9Y277	AADFQLHTHVNDGTEFGGSIYQK	2533.35	2534.18	-0.83	-327.74	7.E-13
Q9Y277	AADFQLHTHVNDGTEFGGSIYQK	2533.40	2534.18	-0.78	-307.40	7.E-13
Q9Y277	AADFQLHTHVNDGTEFGGSIYQK	2534.18	2534.18	0.00	-1.17	7.E-13
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.19	2601.26	-0.07	-28.60	7.E-13
Q09666	GSEVGFHGAAPDISVK	1569.78	1569.78	0.00	-1.77	7.E-13
Q09666	GSEVGFHGAAPDISVK	1572.79	1569.78	3.01	1916.86	7.E-13
P39019	SVARRVLQALEGLK	1541.80	1538.93	2.87	1858.99	7.E-13
P62701	GIPHLVTHDARTIRYPDPLIK	2411.34	2411.34	0.00	-1.53	7.E-13
P62701	GIPHLVTHDARTIRYPDPLIK	2412.30	2411.34	0.96	396.06	7.E-13

Q04695	ATMQNLNDRLASYLDK	1854.05	1851.91	2.14	1154.07	8.E-13
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2252.69	2256.13	-3.44	-1528.77	8.E-13
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2254.41	2256.13	-1.72	-763.50	8.E-13
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3176.51	3153.55	22.96	7226.70	9.E-13
P05783	YWSQQIEESTTVVTTQSAEVGAAETTLTELRRTVQSLEIDLDSMRNLK	5426.57	5426.72	-0.15	-28.01	9.E-13
P05783	YWSQQIEESTTVVTTQSAEVGAAETTLTELRRTVQSLEIDLDSMRNLK	5426.73	5426.72	0.01	2.45	9.E-13
P16403	ASGPPVSELITK	1198.64	1197.66	0.98	814.78	1.E-12
P16403	ASGPPVSELITK	1198.65	1197.66	0.99	822.53	1.E-12
P16403	ASGPPVSELITK	1198.66	1197.66	1.00	834.79	1.E-12
P39019	DVNQQEFVRALAAFLK	1847.98	1847.99	-0.01	-2.84	1.E-12
P39019	DVNQQEFVRALAAFLK	1851.00	1847.99	3.01	1627.58	1.E-12
P20700	HETRLVEVDSGRQIEYEYK	2350.16	2350.16	0.00	-0.81	1.E-12
P69905	VGAHAGEYGAEALERMFLSFPTTK	2581.26	2581.26	0.00	-1.30	2.E-12
P16403	(51)SETAPAAPAAAPPAEK	1519.69	1519.75	-0.06	-37.92	2.E-12
P16403	(51)SETAPAAPAAAPPAEK	1519.71	1519.75	-0.04	-28.18	2.E-12

P16403	(51)SETAPAAPAAAPPAEK	1519.72	1519.75	-0.03	-17.12	2.E-12
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	-2.65	2.E-12
P16403	(51)SETAPAAPAAAPPAEK	1519.78	1519.75	0.03	19.07	2.E-12
P02545	NIYSEELRETK	1380.69	1380.69	0.00	-1.23	2.E-12
P39019	DVNQQEFVRALAAFLK	1847.99	1847.99	0.00	-2.30	2.E-12
P39019	DVNQQEFVRALAAFLK	1848.89	1847.99	0.90	489.30	2.E-12
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.38	2467.39	-0.01	-3.12	2.E-12
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3449.78	3449.79	-0.01	-2.69	2.E-12
P60709	IWHHTFYNELRVAPEEHPVLLTEAPLNPK	3450.73	3449.79	0.94	273.49	2.E-12
Q15427	LLYDTFSAFGVILQTPK	1912.03	1912.03	0.00	-0.45	2.E-12
P05783	VKLEAEIATYRRLLEDGEDFNLGDALDSSNSMQTIQK	4169.05	4169.06	-0.02	-3.60	2.E-12
P43243	KRGAPPSSNIEDFHGLLPK	2062.10	2062.10	0.00	0.04	2.E-12
Q12905	RNQDLAPNSAEQASILSLVTK	2254.19	2254.19	0.00	-0.80	2.E-12
Q16695	KPHRYRPGTVALREIRRYQK	2523.44	2523.44	0.00	-0.90	3.E-12
Q9Y5B9	YTEGVQSLNWTK	1424.69	1424.69	0.00	-1.46	3.E-12

P11387	AVQRLEEQLMK	1341.65	1343.72	-2.07	-1540.34	3.E-12
P11387	AVQRLEEQLMK	1343.70	1343.72	-0.02	-14.89	3.E-12
P07355	SALSGHLETVILGLLK	1649.97	1649.97	0.00	-2.77	3.E-12
Q16695	KPHRYRPGTVALREIRRYQK	2523.44	2523.44	0.00	-1.34	3.E-12
Q16695	KPHRYRPGTVALREIRRYQK	2524.40	2523.44	0.96	379.94	3.E-12
P08758	TLFGRDLLDDLK	1404.74	1404.76	-0.02	-14.41	4.E-12
P08758	TLFGRDLLDDLK	1404.76	1404.76	0.00	-1.46	4.E-12
P08758	TLFGRDLLDDLK	1408.83	1404.76	4.07	2886.20	4.E-12
P02545	NIYSEELRETK	1380.69	1380.69	0.00	-0.58	4.E-12
P11387	AVQRLEEQLMK	1343.72	1343.72	0.00	-0.52	4.E-12
P11387	AVQRLEEQLMK	1346.67	1343.72	2.95	2190.73	4.E-12
P25205	(41)AGTVVLDDVELREAQRDYLDFLDDEEDQGIYQSK	3985.86	3985.87	-0.01	-1.90	4.E-12
P16402	RKASGPPVSELITK	1481.86	1481.86	0.00	1.05	4.E-12
P16402	RKASGPPVSELITK	1484.84	1481.86	2.98	2007.13	4.E-12
Q00839	GNFTLPEVAECFDEITYVELQK	2544.21	2544.21	0.00	-1.76	4.E-12

P62158	(41)ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMARK	8353.95	8353.95	0.00	0.06	4.E-12
P62273	GHQQLYWSHPRK	1535.77	1535.77	0.00	-1.74	5.E-12
P52272	(41)AAGVEAAAEVAATEIKMEEESGAPGVPSGNGAPGPKGEGERPAQNEK	4587.18	4586.18	1.00	217.89	5.E-12
Q00839	GNFTLPEVAECFDEITYVELQK	2544.20	2544.21	-0.01	-2.58	5.E-12
P20700	LLEGEEERLK	1214.63	1214.65	-0.02	-13.78	5.E-12
P20700	LLEGEEERLK	1214.65	1214.65	0.00	-0.93	5.E-12
P20700	LLEGEEERLK	1216.60	1214.65	1.95	1605.51	5.E-12
Q00839	YNILGTNTIMDK	1381.67	1381.69	-0.02	-14.07	5.E-12
Q00839	YNILGTNTIMDK	1381.69	1381.69	0.00	-0.39	5.E-12
Q562M3	IWHHTFYNELRVAPEEHPVLLTQAPLNPK	3444.71	3448.80	-4.09	-1187.72	6.E-12
P60709	RGILTLKYPIE(317)HGIVTNWDDMEK	2741.42	2741.42	0.00	-1.23	6.E-12
P07355	GVDEVTIVNILTNRSNAQRQDIAFAYQRRTK	3575.82	3575.89	-0.07	-18.75	6.E-12
P07355	GVDEVTIVNILTNRSNAQRQDIAFAYQRRTK	3575.89	3575.89	0.00	0.16	6.E-12
Q12906	AEPPQAMNALMRLNQLKPGLQYK	2610.38	2610.38	0.00	-1.80	6.E-12
P62072	KLTELSMQDEELMK	1701.74	1693.83	7.91	4649.04	6.E-12

P62072	KLTELSMQDEELMK	1704.85	1693.83	11.02	6465.18	6.E-12
P05386	(41)ASVSELACIYSALILHDDEVTVTEDK	2862.37	2862.38	-0.01	-2.05	6.E-12
P24928	LLQFHVATMVDNELPGLPRAMQK	2616.27	2607.37	8.90	3400.04	7.E-12
O76021	SAALPIFSSFVSNWDEATK	2069.01	2069.01	-0.01	-2.43	7.E-12
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-2.98	7.E-12
P07355	WISIMTERSVPHLQK	1823.97	1823.97	0.00	-1.98	7.E-12
P15880	SPYQEFTDHLVK	1457.88	1462.71	-4.83	-3312.98	8.E-12
P15880	SPYQEFTDHLVK	1462.71	1462.71	0.00	-1.73	8.E-12
P0C0S8	TRIIPRHLQLAIRNDEELNK	2429.31	2428.37	0.94	386.60	8.E-12
A2BDF6	STELLIRKLPFQRLVREIAQDFK	2799.60	2799.61	-0.01	-2.06	8.E-12
P84090	(51)SHTILLVQPTK	1277.73	1277.73	0.00	-0.20	8.E-12
Q16695	KPHRYRPGTVALREIRRYQK	2523.44	2523.44	0.00	-0.90	9.E-12
Q16695	KPHRYRPGTVALREIRRYQK	2524.41	2523.44	0.97	382.48	9.E-12
P35268	FTLDCTHPVEDGIMDAANFEQFLQERIK	3266.54	3266.54	0.00	-1.22	9.E-12
P12956	IQVTPPGFQLVFLPFADDK	2131.14	2131.14	0.00	1.82	9.E-12

P63244	(52)TEQMTLRGTLK	1318.69	1318.69	0.00	1.05	1.E-11
P16403	ASGPPVSELITK	1198.66	1197.66	1.00	836.79	1.E-11
Q12906	RFVMEVEVDGQK	1433.74	1435.71	-1.97	-1374.11	1.E-11
Q12906	RFVMEVEVDGQK	1435.71	1435.71	0.00	-1.13	1.E-11
Q12906	RFVMEVEVDGQK	1438.67	1435.71	2.96	2056.81	1.E-11
Q00839	LKVSELKEELK	1314.78	1314.78	0.00	0.81	1.E-11
P26447	ALDVMVSTFHK	1246.62	1246.64	-0.02	-12.33	1.E-11
P26447	ALDVMVSTFHK	1246.62	1246.64	-0.02	-12.33	1.E-11
P26447	ALDVMVSTFHK	1246.64	1246.64	0.00	-0.94	1.E-11
P19338	VFGNEIKLEKPK	1400.80	1400.80	0.00	-1.51	1.E-11
P05387	MRYVASYLLAALGGNSSPSAKDIKK	2639.41	2639.41	0.00	1.57	1.E-11
Q14980	LADDLSTLQEK	1231.63	1231.63	0.00	-0.47	1.E-11
P08729	VDALNDEINFLRTLNETELTELQSQISDTSVVLSMDNSRSLDLDGIIAEVK	5662.83	5662.84	-0.01	-1.39	2.E-11
Q99848	GFSDKLDFLEGDQK	1599.81	1597.76	2.05	1279.11	2.E-11
P47914	GVSRKLDRLAYIAHPK	1822.88	1823.05	-0.17	-92.13	2.E-11

P47914	GVSRKLDRLAYIAHPK	1823.05	1823.05	0.00	-2.11	2.E-11
P19338	KMAPPPKEVEEDSEDEEMSEDEEDD(37)S(37)SGEEVVIPQK	4221.66	4221.66	0.00	0.26	2.E-11
P62805	VFLENVIRDAVTYTEHAK	2147.10	2104.10	43.00	20027.80	2.E-11
P98179	LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	3493.74	3493.74	0.00	0.44	2.E-11
P62244	HGYIGEFEIIDDHRAGK	1955.95	1955.95	0.00	-0.42	2.E-11
P62750	AYVRLAPDYDALDVANKIGII	2289.24	2289.24	0.00	1.87	2.E-11
P68431	DIQLARRIRGERA	1548.61	1552.89	-4.28	-2760.97	2.E-11
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.44	2572.44	0.00	-0.57	2.E-11
P20700	EELRELNDRLAVYIDK	1978.95	1975.04	3.91	1977.96	2.E-11
Q92841	KWDLSELPKFEK	1526.81	1518.81	8.00	5236.43	2.E-11
P05783	YWSQQIEESTTVVTTQSAEVGAAETTLTELRRTVQSLEIDLDSMRNLK	5426.73	5426.72	0.01	2.71	2.E-11
P61254	FNPFVTSDRSK	1299.68	1296.65	3.03	2330.40	2.E-11
P61254	FNPFVTSDRSK	1299.74	1296.65	3.09	2374.46	2.E-11
P68431	DIQLARRIRGERA	1553.87	1552.89	0.98	627.61	2.E-11
P62805	RISGLIYEETRGVLK	1732.97	1732.98	-0.01	-3.48	2.E-11

Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.40	2572.44	-0.04	-17.40	2.E-11
P19338	FGYVDFESAEDLEKALELTGLK	2471.41	2473.23	-1.82	-737.67	2.E-11
P68431	DIQLARRIRGERA	1552.89	1552.89	0.00	-2.30	2.E-11
P10412	(51)SETAPAAPAAPAPAEKTPVKK	2073.11	2073.11	0.00	1.11	2.E-11
P20700	EELRELNDRLAVYIDK	1975.04	1975.04	0.00	-1.02	2.E-11
P18621	VRYSLDPENPTK	1421.76	1417.72	4.04	2840.69	2.E-11
P61254	FNPFVTSDRSK	1296.63	1296.65	-0.02	-14.22	2.E-11
P61254	FNPFVTSDRSK	1296.65	1296.65	0.00	-0.41	2.E-11
P08729	QDMARQLREYQELMSVK	2124.05	2124.05	0.00	-0.04	3.E-11
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	6856.51	6722.54	133.97	19539.50	3.E-11
P60903	EFPGFLENQKDPLAVDK	1945.98	1945.98	0.00	-0.82	3.E-11
P60903	EFPGFLENQKDPLAVDK	1946.44	1945.98	0.46	238.85	3.E-11
P11387	WWEEERYPEGIK	1620.76	1620.76	0.00	-0.26	3.E-11
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3157.48	3153.55	3.93	1245.31	3.E-11
P19338	FGYVDFESAEDLEKALELTGLK	2474.18	2473.23	0.95	385.59	3.E-11

P20700	ALYETELADARRALDDTARERAK	2633.34	2633.35	-0.01	-2.16	3.E-11
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.43	3153.55	-0.12	-38.01	3.E-11
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-3.92	3.E-11
Q13123	FAGSAGWEGTESLK	1440.80	1438.67	2.13	1478.67	3.E-11
P63244	(52)TEQMTLRGTLK	1318.69	1318.69	0.00	0.90	4.E-11
P11387	WWEEERYPEGIK	1624.81	1620.76	4.05	2494.61	4.E-11
Q9NWH9	(41)AAATGAVAASAASGQAEGK	1629.80	1629.80	0.00	-0.13	4.E-11
Q13123	FAGSAGWEGTESLK	1442.83	1438.67	4.16	2884.03	4.E-11
P62736	AGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK	3307.68	3307.68	0.00	0.72	4.E-11
O60812	QKVDSLLENLEK	1410.76	1414.77	-4.01	-2840.13	4.E-11
O43823	FRSFDDEEIQK	1411.82	1412.66	-0.84	-597.66	4.E-11
P63244	(52)TEQMTLRGTLK	1314.78	1318.69	-3.91	-2977.09	4.E-11
P13645	VRALEESNYELEGK	1635.81	1635.81	0.00	-0.48	5.E-11
P13645	VRALEESNYELEGK	1639.94	1635.81	4.13	2516.26	5.E-11
P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.88	3777.88	0.00	-0.79	5.E-11

P18621	VRYSLDPENPTK	1417.70	1417.72	-0.02	-16.45	6.E-11
P18621	VRYSLDPENPTK	1417.72	1417.72	0.00	-1.43	6.E-11
P52272	(41)AAGVEAAAEVAATEIKMEEESGAPGVPSGNGAPGPK	3391.61	3390.62	0.99	293.26	6.E-11
Q71DI3	TDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	4116.92	3940.93	175.99	42748.10	7.E-11
O60812	QKVDSLLENLEK	1414.75	1414.77	-0.02	-15.72	7.E-11
O60812	QKVDSLLENLEK	1414.77	1414.77	0.00	-1.44	7.E-11
Q00839	YNILGTNTIMDK	1381.69	1381.69	0.00	-1.19	7.E-11
O75526	YGRIVEVLLMK	1319.76	1319.76	0.00	0.00	7.E-11
Q86U42	(41)AAAAAAAAAAGAAGGRGSGPGRRRHLVPGAGGEAGEGAPGGAGDYGNGLESEELEPEELLLEPEPEPEPEEEPPRPRAPPGAPGPGPGSGAPGSQEEEEEPGLVEGDPGDGAIEDPELEAIK	11816.58	11816.60	-0.02	-1.93	8.E-11
P22626	LFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGKK	4608.30	4608.31	-0.01	-1.98	8.E-11
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3169.48	3153.55	15.93	5025.82	8.E-11
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3169.54	3153.55	15.99	5043.78	8.E-11
P46777	HIMGQNVADYMRYLMEEDEDAYKK	2948.30	2948.31	-0.01	-1.96	8.E-11
P62805	RISGLIYEETRGVLK	1732.98	1732.98	0.00	-2.39	8.E-11
P45973	WKDTDEADLVLAK	1505.85	1502.76	3.09	2054.23	9.E-11

Q92522	(51)SVELEEALPVTTAEGMAK	1916.95	1915.94	1.01	524.35	1.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-2.78	1.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.50	3153.55	0.95	301.26	1.E-10
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVKK	4245.55	4245.54	0.01	2.36	1.E-10
P16403	(51)SETAPAAPAAAPPAEKAPVKK	2043.10	2043.10	0.00	0.48	1.E-10
P09651	GGNFGGRSSGPYGGGGQYFAK	2019.92	2019.92	0.00	-0.39	1.E-10
P22626	RGFGFVTFDDHDPVDKIVLQK	2432.24	2432.25	-0.01	-3.08	1.E-10
P39019	DQDGGRKLTPQGQRDLDRIAGQVAAANK	2977.54	2977.54	0.00	-1.59	1.E-10
P08729	QEELEAALQRAK	1384.71	1384.73	-0.02	-15.83	1.E-10
P08729	QEELEAALQRAK	1384.73	1384.73	0.00	-1.24	1.E-10
P45973	WKDTDEADLVLAK	1502.76	1502.76	0.00	-1.15	1.E-10
P05204	VKDEPQRRSARLSAKPAPPKPEPKPK	2906.66	2906.66	0.00	-0.58	1.E-10
P62913	VLEQLTGQTPVFSK	1545.85	1545.84	0.01	5.80	1.E-10
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.45	2369.45	-0.01	-2.10	1.E-10
P84090	(51)SHTILLVQPTK	1278.73	1277.73	1.00	783.70	1.E-10

P62910	AIVERAAQLAIRVTNPNARLRSEENE	2919.56	2919.56	0.00	-1.51	1.E-10
P08670	TVETRDGQVINETSQHHDDLE	2422.10	2422.10	0.00	-1.79	1.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3169.53	3153.55	15.98	5040.39	1.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3175.46	3153.55	21.91	6899.18	1.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3175.52	3153.55	21.97	6919.19	1.E-10
A6NFF6	(49)MASVSKLACIYSALILHDDEVTVTEDKINALIK	3690.80	3644.90	45.90	12435.60	1.E-10
P62857	(49)MDTSRVQPIK	1215.63	1215.63	0.00	0.75	2.E-10
Q9Y3U8	ALRYPMAVGLNK	1331.72	1331.74	-0.02	-13.41	2.E-10
Q9Y3U8	ALRYPMAVGLNK	1331.74	1331.74	0.00	1.16	2.E-10
Q9Y3U8	ALRYPMAVGLNK	1331.83	1331.74	0.09	69.79	2.E-10
P17096	RGRGRPRKQPPVSPGTALVGSQKEPSEVPTPK	3392.87	3392.88	-0.01	-2.07	2.E-10
P17096	RGRGRPRKQPPVSPGTALVGSQKEPSEVPTPK	3395.74	3392.88	2.86	842.25	2.E-10
A6NFA7	(46)GIMNSFVNDIFERIAGEASRLAHYNK	3169.53	2993.48	176.05	55544.60	2.E-10
Q09666	GSRVDIETPNLEGTLTGPRLGSPSGK	2637.37	2637.37	0.00	-1.08	2.E-10
P39019	SVARRVLQALEGLK	1538.83	1538.93	-0.10	-67.99	2.E-10

P39019	SVARRVLQALEGLK	1538.90	1538.93	-0.03	-17.43	2.E-10
P39019	SVARRVLQALEGLK	1538.93	1538.93	0.00	-0.21	2.E-10
P39019	SVARRVLQALEGLK	1541.80	1538.93	2.87	1860.80	2.E-10
P61513	TVAGGAWTYNTTSAVTVK	1825.92	1825.92	0.00	-0.66	2.E-10
P62805	RISGLIYEETRGVLK	1732.98	1732.98	0.00	-2.27	2.E-10
P62841	EAPPMEKPEVVK	1352.70	1352.70	0.00	-1.37	2.E-10
P62841	EAPPMEKPEVVK	1353.68	1352.70	0.98	725.76	2.E-10
P62841	EAPPMEKPEVVK	1355.71	1352.70	3.01	2218.72	2.E-10
P17096	RGRGRPRKQPPVSPGTALVGSQKEPSEVPTPK	3391.80	3392.88	-1.08	-318.99	2.E-10
Q09666	GSRVDIETPNLEGTLTGPRLGSPSGK	2641.42	2637.37	4.05	1534.23	2.E-10
Q00839	YNILGTNTIMDK	1381.69	1381.69	0.00	-2.06	2.E-10
Q09666	ISMPDVDLHLK	1266.64	1266.66	-0.02	-13.41	2.E-10
Q09666	ISMPDVDLHLK	1266.66	1266.66	0.00	-0.94	2.E-10
Q09666	ISMPDVDLHLK	1268.64	1266.66	1.98	1556.88	2.E-10
Q09666	ISMPDVDLHLK	1268.65	1266.66	1.99	1569.31	2.E-10

Q09666	ISMPDVDLHLK	1269.62	1266.66	2.96	2330.62	2.E-10
P25705	AVDSLVPIGRGQRELIIGDRQTGK	2577.44	2577.44	0.00	-1.02	2.E-10
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.31	2428.37	-0.06	-24.23	2.E-10
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-1.74	2.E-10
Q16695	RVTIMPKDIQLARRIRGERA	2375.27	2378.38	-3.11	-1307.36	2.E-10
Q16695	RVTIMPKDIQLARRIRGERA	2378.37	2378.38	-0.01	-2.54	2.E-10
P04083	GVDEATIIDILTK	1386.26	1386.76	-0.50	-357.92	2.E-10
P04083	GVDEATIIDILTK	1386.76	1386.76	0.00	-0.13	2.E-10
P22626	KLFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGK	4608.29	4608.31	-0.02	-4.20	2.E-10
Q09666	MDIDAPDVEVQGPDWHLK	2063.95	2063.96	-0.01	-2.57	3.E-10
Q9BUV3	ATGATQQDANASSLLDIYSFWLNRSAK	2927.44	2927.44	0.00	-1.17	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3149.55	3153.55	-4.00	-1270.81	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3149.88	3153.55	-3.67	-1164.99	3.E-10
P09651	RSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPK	3887.98	3887.99	-0.01	-1.79	3.E-10
Q00839	YNILGTNTIMDK	1381.69	1381.69	0.00	-0.25	3.E-10

Q00839	YNILGTNTIMDK	1382.67	1381.69	0.98	710.62	3.E-10
P04083	GVDEATIIDILTK	1385.73	1386.76	-1.03	-744.50	3.E-10
P53999	EQISDIDDAVRKL	1500.78	1500.78	0.00	-0.37	3.E-10
P53999	EQISDIDDAVRKL	1505.77	1500.78	4.99	3315.81	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3152.21	3153.55	-1.34	-425.02	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3155.88	3153.55	2.33	738.22	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3156.21	3153.55	2.66	843.90	3.E-10
P07355	DIISDTSGDFRK	1351.73	1352.66	-0.93	-685.63	3.E-10
P07355	DIISDTSGDFRK	1352.66	1352.66	0.00	0.90	3.E-10
P35637	LKGEATVSFDDPPSAK	1656.95	1660.83	-3.88	-2339.09	3.E-10
P35637	LKGEATVSFDDPPSAK	1660.83	1660.83	0.00	1.34	3.E-10
P62304	GDNITLLQSVSN	1259.64	1259.64	0.00	-0.66	3.E-10
Q09666	LKGPQITGPSLEGDLGLK	1822.02	1822.02	0.00	2.05	3.E-10
Q09666	ISMPDVDLHLK	1266.65	1266.66	-0.02	-11.83	3.E-10
Q09666	ISMPDVDLHLK	1266.66	1266.66	0.00	1.35	3.E-10

Q09666	ISMPDVDLHLK	1268.66	1266.66	2.00	1574.27	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3152.88	3153.55	-0.67	-212.87	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.41	3153.55	-0.14	-45.78	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.48	3153.55	-0.07	-22.63	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-2.46	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.65	3153.55	0.10	31.59	3.E-10
P05783	KGPQVRDWSHYFK	1646.83	1646.83	0.00	-1.42	3.E-10
P08758	GLGTDEESILTLLTSRSNAQRQEISAAFK	3134.61	3134.62	-0.01	-1.89	3.E-10
P19338	EVFEDAAEIRLVSK	1604.84	1604.84	0.00	-0.65	3.E-10
P19338	EAMEDGEIDGNKVTLDWAKPK	2345.12	2345.12	0.00	-0.63	3.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3156.50	3153.55	2.95	934.43	4.E-10
P22626	LFVGGIKEDTEEHHLRDYFEEYGK	2913.34	2910.38	2.96	1016.50	4.E-10
P22626	LFVGGIKEDTEEHHLRDYFEEYGK	2913.40	2910.38	3.02	1037.45	4.E-10
P60709	YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHRK	4118.19	4227.11	-108.93	-26449.90	4.E-10
P62805	RISGLIYEETRGVLK	1732.98	1732.98	0.00	-2.27	4.E-10

O14979	VFVGGLSPDTSEEQIK	1704.86	1704.86	0.00	-2.05	4.E-10
P62857	(49)MDTSRVQPIK	1216.62	1215.63	0.99	812.18	4.E-10
P22626	RGFGFVTFDDHDPVDKIVLQK	2432.24	2432.25	-0.01	-3.04	5.E-10
P13010	KKDQVTAQEIFQDNHEDGPTAK	2508.08	2498.20	9.88	3938.23	5.E-10
P23246	DKLESEMEDAYHEHQANLLRQDLMRRQEELRRMEELHNQEMQK	5435.55	5435.56	-0.01	-1.10	5.E-10
Q9Y6M9	(41)AFLASGPYLTHQQK	1602.82	1601.82	1.00	626.45	5.E-10
Q6P2Q9	QNPFWWTHQRHDGKLWNLNNYRTDMIQALGGVEGILEHTLFK	4885.49	5062.52	-177.03	-36236.60	5.E-10
P05783	VKLEAEIATYRRLLEDGEDFNLGDALDSSNSMQTIQK	4168.93	4169.06	-0.13	-31.47	5.E-10
P05783	VKLEAEIATYRRLLEDGEDFNLGDALDSSNSMQTIQK	4169.05	4169.06	-0.01	-3.53	5.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-3.06	5.E-10
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-2.10	5.E-10
P62081	IVKPNGEKPDEFESGISQALLELEMNSDLK	3330.65	3329.67	0.98	293.30	5.E-10
O14979	MFIGGLSWDTSKK	1468.74	1468.74	0.00	-1.92	5.E-10
P60709	LCYVALDFEQEMATAASSSSLEK	2492.15	2492.15	0.00	-1.79	5.E-10
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3169.54	3153.55	15.99	5043.75	5.E-10

Q7Z4V5	PHAFKPGDLVFAK	1426.79	1425.78	1.01	705.00	6.E-10
P08758	GLGTDEESILTLLTSRSNAQRQEISAAFK	3134.61	3134.62	-0.01	-1.83	6.E-10
P62857	(49)MDTSRVQPIK	1215.63	1215.63	0.00	0.84	6.E-10
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4117.34	4117.45	-0.11	-26.55	6.E-10
P06748	LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK	4117.44	4117.45	-0.01	-2.75	6.E-10
P19338	KQKVEGTEPTTAFNLFVGNLNFNK	2695.40	2695.40	0.00	1.55	6.E-10
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.31	2428.37	-0.06	-24.72	7.E-10
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-3.76	7.E-10
Q14980	EVARLETLVRK	1312.78	1312.78	0.00	-0.50	7.E-10
P04083	QAWFIENEEQEYVQTVK	2140.01	2140.01	0.00	-0.22	7.E-10
P60866	RLIDLHSPSEIVK	1509.73	1505.86	3.88	2566.65	8.E-10
P62805	VFLENVIRDAVTYTEHAKRKTVTAMDVVYALKRQGRTLYGFGG	4922.77	4872.59	50.18	10193.10	8.E-10
P62805	VFLENVIRDAVTYTEHAKRKTVTAMDVVYALKRQGRTLYGFGG	4924.28	4872.59	51.69	10496.90	8.E-10
Q14980	EVARLETLVRK	1315.67	1312.78	2.89	2194.43	9.E-10
P62987	IIEPSLRQLAQK	1394.82	1394.82	0.00	-0.38	9.E-10

P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.87	3777.88	-0.01	-1.98	9.E-10
P07910	ELTQIKQKVDSLLENLEK	2129.04	2127.18	1.86	872.38	9.E-10
Q00839	KRNFILDQTNVSAAAQRRK	2215.23	2215.23	0.00	-0.52	1.E-09
P62829	GRLNRLPAAGVGDMVMATVKK	2183.20	2183.20	0.00	-1.12	1.E-09
Q08211	SEEVPAFGVASPPPLTDTPDTTANAEGDLPTTMGGPLPPHLALK	4408.16	4408.18	-0.02	-3.84	1.E-09
P23396	GGKPEPPAMPQPVPTA	1572.80	1572.80	0.00	-1.89	1.E-09
P14866	DFSESRNNRFSTPEQAAK	2082.97	2082.97	0.00	-0.52	1.E-09
Q13813	VNSLGETAERLIQSHPESAEDLQEK	2779.36	2779.36	0.00	-0.35	1.E-09
P83731	FQRAITGASLADIMAK	1691.90	1691.90	0.00	-0.74	1.E-09
P83731	FQRAITGASLADIMAK	1692.90	1691.90	1.00	592.62	1.E-09
P39019	SVARRVLQALEGLK	1538.93	1538.93	0.00	-1.19	1.E-09
P31943	DRETMGHRYVEVFK	1765.86	1765.86	0.00	-1.00	2.E-09
P47914	GVSRKLDRLAYIAHPK	1822.88	1823.05	-0.17	-92.13	2.E-09
P47914	GVSRKLDRLAYIAHPK	1823.05	1823.05	0.00	-2.05	2.E-09
P15880	SLEEIYLFSLPIKESEIIDFFLGASLKDEVLK	3684.97	3684.98	-0.01	-3.66	2.E-09

P05387	NIEDVIAQGIGK	1255.68	1255.68	0.00	-0.94	2.E-09
P62805	RISGLIYEETRGVLK	1734.95	1732.98	1.97	1135.80	2.E-09
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4107.99	4108.11	-0.12	-28.18	2.E-09
P08708	LLDFGSLSNLQVTQPTVGMNFK	2408.23	2408.24	-0.01	-3.43	2.E-09
P33240	(41)AGLTVRDPAVDRSLRSVFVGNIPYEATEEQLK	3571.86	3571.86	0.00	-0.71	2.E-09
P62805	RISGLIYEETRGVLK	1732.97	1732.98	-0.01	-4.06	2.E-09
P62805	RISGLIYEETRGVLK	1736.68	1732.98	3.70	2132.89	2.E-09
P02751	TYHVGEQWQK	1279.70	1274.60	5.10	3985.31	2.E-09
P02751	TYHVGEQWQK	1279.72	1274.60	5.12	3998.39	2.E-09
P39019	SVARRVLQALEGLK	1535.79	1538.93	-3.14	-2042.16	2.E-09
Q92900	LLGHEVEDVIIK	1365.85	1363.77	2.08	1520.98	2.E-09
Q92841	KWDLSELPKFEK	1525.85	1518.81	7.04	4611.29	2.E-09
P28370	APRPPKQPNVQDFQFFPPRLFELLEK	3145.72	3137.68	8.04	2556.55	2.E-09
P40429	YQAVTATLEEK	1251.63	1251.63	0.00	-0.77	2.E-09
Q86V81	LLVSNLDFGVSDADIQELFAEFGTLKK	2968.54	2968.54	0.00	-0.60	3.E-09

Q86V81	LLVSNLDFGVSDADIQELFAEFGTLKK	2969.63	2968.54	1.09	366.95	3.E-09
Q86V81	LLVSNLDFGVSDADIQELFAEFGTLKK	2969.92	2968.54	1.38	464.19	3.E-09
Q86V81	LLVSNLDFGVSDADIQELFAEFGTLKK	2971.22	2968.54	2.68	901.82	3.E-09
P11021	KSDIDEIVLVGGSTRIPK	1925.04	1926.08	-1.04	-541.42	3.E-09
P43243	RGAPPSSNIEDFHGLLPK	1934.00	1934.00	0.00	-1.38	3.E-09
P05783	IMADIRAQYDELARK	1791.93	1791.93	0.00	-1.86	3.E-09
P62701	GIPHLVTHDARTIRYPDPLIK	2411.33	2411.34	-0.01	-2.36	3.E-09
Q16695	RVTIMPKDIQLARRIRGERA	2380.38	2378.38	2.00	840.56	3.E-09
P05787	TEISEMNRNISRLQAEIEGLK	2435.25	2430.25	5.00	2053.69	3.E-09
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.09	4108.11	-0.02	-4.38	3.E-09
P68431	DIQLARRIRGERA	1553.86	1552.89	0.97	627.36	3.E-09
P06748	TPKGPSSVEDIK	1258.67	1256.66	2.01	1593.51	3.E-09
P22626	RSRGFGFVTFSSMAEVDAAMAARPHSIDGRVVEPK	3777.87	3777.88	-0.01	-1.75	3.E-09
Q00839	AVVVCPKDEDYK	1360.80	1364.66	-3.86	-2835.06	3.E-09
Q00839	AVVVCPKDEDYK	1364.66	1364.66	0.00	-0.42	3.E-09

P62805	VLRDNIQGITKPAIRRLARRGGVK	2686.63	2686.63	0.00	-0.91	3.E-09
P22626	LTDCVVMRDPASK	1432.69	1433.70	-1.02	-708.43	3.E-09
P22626	LTDCVVMRDPASK	1433.70	1433.70	0.00	-0.18	3.E-09
P22626	LTDCVVMRDPASK	1435.69	1433.70	1.99	1384.94	3.E-09
P68431	DIQLARRIRGERA	1552.89	1552.89	0.00	-2.24	4.E-09
Q9UKM9	LFARSTAVTTSSAK	1435.64	1438.78	-3.15	-2190.65	4.E-09
Q9UKM9	LFARSTAVTTSSAK	1438.78	1438.78	0.00	0.09	4.E-09
Q99623	MLGEALSKNPGYIK	1523.73	1519.81	3.92	2573.28	4.E-09
P06748	TPKGPSSVEDIK	1256.66	1256.66	0.00	-0.88	4.E-09
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	0.64	4.E-09
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAY LVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9096.91	9098.88	-1.97	-216.17	4.E-09
A2BDF6	STELLIRKLPFQRLVREIAQDFK	2799.60	2799.61	-0.01	-1.84	4.E-09
P62244	VRMNVLADALK	1228.70	1228.70	0.00	-1.67	4.E-09
P06748	TPKGPSSVEDIK	1254.62	1256.66	-2.04	-1627.11	4.E-09
P06748	TPKGPSSVEDIK	1256.64	1256.66	-0.02	-18.39	4.E-09

P39019	SVARRVLQALEGLK	1535.79	1538.93	-3.14	-2043.14	4.E-09
P39019	SVARRVLQALEGLK	1538.93	1538.93	0.00	-1.97	4.E-09
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3169.54	3153.55	15.99	5044.66	4.E-09
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3170.49	3153.55	16.94	5344.26	4.E-09
P06748	TPKGPSSVEDIK	1261.58	1256.66	4.92	3902.63	5.E-09
O00422	(41)AVESRVTQEEIK	1429.74	1429.74	0.00	-0.97	5.E-09
P22626	KRGFGFVTFDDHDPVDKIVLQK	2560.33	2560.34	-0.01	-3.57	5.E-09
Q15233	(49)MQSNKTFNLEK	1380.67	1380.67	0.00	1.39	6.E-09
Q8IY81	GSFAGIEDDADEALEISQAQLLFENRRK	3123.48	3121.53	1.95	624.25	6.E-09
O00422	(41)AVESRVTQEEIK	1433.60	1429.74	3.86	2690.58	7.E-09
P16403	ERSGVSLAALKK	1255.72	1257.74	-2.02	-1606.29	7.E-09
P35908	TLNNKFASFIDK	1392.75	1396.74	-3.99	-2867.83	7.E-09
P62987	IIEPSLRQLAQK	1394.82	1394.82	0.00	-0.88	7.E-09
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.11	4108.11	0.00	-0.80	8.E-09
P04083	GTDVNVFNTILTTRSYPQLRRVFQK	2952.58	2952.59	-0.01	-2.32	8.E-09

P16403	(51)SETAPAAPAAAPPAEK	1541.71	1519.75	21.96	14241.30	8.E-09
P16403	(51)SETAPAAPAAAPPAEK	1541.73	1519.75	21.98	14256.20	8.E-09
P36578	AFRNIPGITLLNVSK	1641.93	1641.96	-0.03	-18.63	8.E-09
P36578	AFRNIPGITLLNVSK	1641.96	1641.96	0.00	-1.89	8.E-09
P36578	AFRNIPGITLLNVSK	1645.88	1641.96	3.92	2378.68	8.E-09
O60506	NRGFCFLEYEDHK	1656.74	1656.74	0.00	-0.82	9.E-09
P02545	EREMAEMRARMQQQLDEYQELLDIK	3152.50	3152.51	-0.01	-1.77	9.E-09
O00422	(41)AVESRVTQEEIK	1434.60	1429.74	4.86	3389.80	9.E-09
Q15149	GLVGPELHDRLLSAERAVTGYRDPYTEQTISLFQAMK	4161.12	4161.13	-0.01	-1.72	9.E-09
P16403	ERSGVSLAALKK	1257.74	1257.74	0.00	-0.44	1.E-08
P46013	VDMKEEPLAVSK	1343.54	1344.70	-1.16	-860.02	1.E-08
P46013	VDMKEEPLAVSK	1344.70	1344.70	0.00	-0.95	1.E-08
P23246	ERETPPRFAQHGTFEYEYSQRWK	2941.38	2941.39	-0.01	-1.72	1.E-08
P05204	VKDEPQRRSARLSAKPAPPKPEPKPK	2908.66	2906.66	2.00	687.61	1.E-08
P16403	ERSGVSLAALKK	1257.72	1257.74	-0.02	-13.80	1.E-08

P16403	ERSGVSLAALKK	1257.74	1257.74	0.00	-1.32	1.E-08
P35908	TLNNKFASFIDK	1396.74	1396.74	0.00	1.40	1.E-08
P35908	TLNNKFASFIDK	1396.79	1396.74	0.05	35.76	1.E-08
P08621	(52)TQFLPPNLLALFAPRDPIPYLPPLEK	3001.66	3001.67	-0.01	-2.19	1.E-08
P22626	RAVAREESGKPGAHVTVK	1891.04	1891.04	0.00	-0.34	1.E-08
P22626	KRGFGFVTFDDHDPVDKIVLQK	2560.33	2560.34	-0.01	-2.01	1.E-08
P06748	MSVQPTVSLGGFEITPPVVLRLK	2467.39	2467.39	0.00	-1.95	1.E-08
Q2TA72	SFPPHLNRPPMGIPALPPGIPPPQFPGFPPPVPPGTPMIPVPMSIMAPAPTVLVPTVSMVGK	6431.42	6361.39	70.03	10889.40	1.E-08
P18077	IEGVYARDETEFYLGK	1892.96	1888.92	4.04	2133.46	1.E-08
Q01082	KHQILEQAVEDYAETVHQLSK	2473.25	2465.26	7.99	3229.00	1.E-08
P09651	RSRGFGFVTYATVEEVDAAMNARPHK	2908.44	2908.44	0.00	-0.51	1.E-08
P09651	RSRGFGFVTYATVEEVDAAMNARPHK	2908.58	2908.44	0.14	48.72	1.E-08
P09651	RAVSREDSQRPGAHLTVK	2006.05	2006.08	-0.03	-14.97	1.E-08
P09651	RAVSREDSQRPGAHLTVK	2006.08	2006.08	0.00	-0.67	1.E-08
P16403	(51)SETAPAAPAAAPPAEK	1519.75	1519.75	0.00	1.10	2.E-08

Q16695	RVTIMPKDIQLARRIRGERA	2380.38	2378.38	2.00	840.23	2.E-08
P25398	(41)AEEGIAAGGVMDVNTALQEVLK	2256.14	2256.13	0.01	2.46	2.E-08
P16403	ERSGVSLAALKK	1257.74	1257.74	0.00	-0.04	2.E-08
O75531	HRDFVAEPMGEKPVGSLAGIGEVLGK	2692.40	2692.40	0.00	-1.71	2.E-08
Q9Y3U8	ALRYPMAVGLNK	1330.58	1331.74	-1.16	-870.87	2.E-08
Q1KMD3	VVVVVPNEEDWKK	1539.83	1539.83	0.00	-1.72	2.E-08
Q1KMD3	VVVVVPNEEDWKK	1543.89	1539.83	4.06	2631.43	2.E-08
P33778	RSTITSREIQTAVRLLLPGELAK	2551.49	2551.48	0.01	2.11	2.E-08
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3175.52	3153.55	21.97	6919.19	2.E-08
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3176.46	3153.55	22.91	7213.32	2.E-08
P26373	LILFPRKPSAPK	1365.85	1365.85	0.00	-1.03	2.E-08
Q71DI3	TDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	4116.90	3940.93	175.97	42743.90	2.E-08
Q9Y3U8	ALRYPMAVGLNK	1327.62	1331.74	-4.12	-3100.32	2.E-08
Q9Y3U8	ALRYPMAVGLNK	1331.74	1331.74	0.00	-0.87	2.E-08
P05787	TEISEMNRNISRLQAEIEGLK	2432.24	2430.25	1.99	818.40	2.E-08

Q14103	KIFVGGLSPDTPEEK	1615.85	1615.85	0.00	-1.23	2.E-08
P14866	NPNGPYPYTLK	1262.63	1262.63	0.00	-0.73	2.E-08
P42677	RLVQSPNSYFMDVK	1679.85	1682.85	-3.00	-1788.63	3.E-08
P42677	RLVQSPNSYFMDVK	1682.85	1682.85	0.00	-1.61	3.E-08
P07355	AYTNFDAERDALNIETAIK	2154.06	2154.06	0.00	-1.52	3.E-08
P05783	KGPQVRDWSHYFK	1646.83	1646.83	0.00	-0.26	3.E-08
Q14978	(41)ADAGIRRVVPSDLYPLVLGFLRDNQLSEVANK	3566.91	3566.92	-0.01	-2.82	3.E-08
P62987	IIEPSLRQLAQK	1394.82	1394.82	0.00	-0.59	3.E-08
Q13727	ISMPDFDLHLK	1314.64	1314.66	-0.02	-12.69	3.E-08
Q13727	ISMPDFDLHLK	1314.66	1314.66	0.00	1.23	3.E-08
Q09666	ISMPDIDLNLKGPK	1537.82	1539.83	-2.01	-1308.37	3.E-08
P14866	NPNGPYPYTLK	1263.61	1262.63	0.98	778.15	3.E-08
Q9Y5J1	AIMNLVTGVTSLTFNPTTEILAIASEK	2842.61	2833.51	9.10	3200.00	3.E-08
P05783	GLQAQIASSGLTVEVDAPK	1883.00	1883.00	0.00	-2.42	4.E-08
P05783	GLQAQIASSGLTVEVDAPK	1883.00	1883.00	0.00	-2.42	4.E-08

P05783	YWSQQIEESTTVVTTQSAEVGAAETTLTELRRTVQSLEIDLDSMRNLK	5425.69	5426.72	-1.03	-189.65	4.E-08
Q3BDU5	LDNARQSAERNSNLVGAAHEELQQSRIRIDSLSAQLSQLQK	4573.36	4573.37	-0.01	-2.36	4.E-08
P02545	EDLQELNDRLAVYIDRVRSLETENAGLRLRITESEEVVSREVSGIK	5298.77	5298.78	-0.01	-2.34	4.E-08
Q09666	ISMPDIDLNLKGPK	1543.64	1539.83	3.81	2471.27	4.E-08
P14866	NPNGPYPYTLK	1265.62	1262.63	2.99	2361.59	4.E-08
P14866	NPNGPYPYTLK	1266.65	1262.63	4.02	3169.85	4.E-08
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAK	6736.48	6738.51	-2.03	-300.80	4.E-08
Q2TA72	(51)SFPPHLNRPPMGIPALPPGIPPPQFPGFPPPVPPGTPMIPVPMSIMAPAPTVLVPTVSMVGK	6431.42	6403.40	28.02	4356.38	4.E-08
P46778	RQPAPPREAHFVRTNGKEPELLEPIPYEFMA	3618.84	3618.84	0.00	0.61	4.E-08
P61978	RSRNTDEMVELRILLQSK	2187.18	2187.18	0.00	-0.12	5.E-08
Q9Y4Y9	(41)AANATTNPSQLLPLELVDKCIGSRIHIVMKSDKEIVGTLLGFDDFVNMVLEDVTEFEITPEGRRITKLDQILLNGNNITMLVPGGEGPEV	9842.10	9842.10	0.00	-0.47	5.E-08
Q53HU8	LLEGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSK	4133.15	4133.16	-0.01	-3.31	5.E-08
P11940	GFGFVSFERHEDAQK	1758.79	1752.82	5.97	3393.73	5.E-08
Q15149	ESYSALMRELELK	1568.79	1567.79	1.00	638.34	5.E-08
P07355	VLIRIMVSRSEVDMLK	1888.06	1888.06	0.00	-1.74	5.E-08

P46778	RQPAPPREAHFVRTNGKEPELLEPIPYEFMA	3619.82	3618.84	0.98	270.60	6.E-08
P62805	RISGLIYEETRGVLK	1732.98	1732.98	0.00	-0.89	6.E-08
P60866	RLIDLHSPSEIVK	1509.73	1505.86	3.87	2565.40	6.E-08
P62805	RISGLIYEETRGVLK	1732.97	1732.98	-0.01	-3.48	6.E-08
Q12905	RNQDLAPNSAEQASILSLVTK	2254.19	2254.19	0.00	-0.49	6.E-08
P16401	ATGPPVSELITK	1211.68	1211.68	0.00	-0.35	7.E-08
P62805	RISGLIYEETRGVLK	1732.95	1732.98	-0.03	-19.47	7.E-08
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.32	2270.37	-0.05	-23.31	8.E-08
Q96QV6	LLGGVTIAQGGVLPNIQAVLLPK	2270.36	2270.37	-0.01	-2.96	8.E-08
A6NJM3	RSIITSREIQTAVRLLLPGELAK	2560.52	2563.52	-3.00	-1172.23	8.E-08
P07355	GRRAEDGSVIDYELIDQDARDLYDAGVK	3138.52	3138.52	0.00	-1.41	8.E-08
P07355	VLIRIMVSRSEVDMLK	1888.04	1888.06	-0.02	-12.97	8.E-08
P07355	VLIRIMVSRSEVDMLK	1888.06	1888.06	0.00	-0.79	8.E-08
P69905	VGAHAGEYGAEALERMFLSFPTTK	2581.26	2581.26	0.00	-1.26	8.E-08
Q71UI9	ATIAGGGVIPHIHK	1369.78	1369.78	0.00	0.89	9.E-08

Q71UI9	ATIAGGGVIPHIHK	1373.70	1369.78	3.92	2855.51	9.E-08
Q71UI9	ATIAGGGVIPHIHK	1373.72	1369.78	3.94	2868.06	9.E-08
P62750	SAPRRNKLDHYAIIKFPLTTESAMK	2887.55	2886.55	1.00	344.90	9.E-08
P68431	DIQLARRIRGERA	1552.87	1552.89	-0.02	-15.50	9.E-08
P68431	DIQLARRIRGERA	1552.89	1552.89	0.00	-1.08	9.E-08
P36578	GHRIEEVPELPLVVEDKVEGYKK	2658.33	2662.43	-4.10	-1540.68	1.E-07
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3153.54	3153.55	-0.01	-2.75	1.E-07
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3155.50	3153.55	1.95	616.56	1.E-07
Q9Y3U8	ALRYPMAVGLNK	1331.74	1331.74	0.00	-0.87	1.E-07
A5PLR1	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9098.94	9098.88	0.06	6.08	1.E-07
P08865	(51)SGALDVLQMKEEDVLK	1815.93	1815.93	0.00	-1.61	1.E-07
Q16695	QLAT(55)KVARKSAPATGGVK	1807.00	1824.06	-17.06	-9442.71	1.E-07
Q16695	QLAT(55)KVARKSAPATGGVK	1807.03	1824.06	-17.03	-9424.38	1.E-07
P05787	LSELEAALQRAK	1327.75	1327.75	0.00	-1.08	1.E-07
P16401	ATGPPVSELITK	1211.67	1211.68	-0.01	-11.58	1.E-07

P05783	ETMQSLNDRLASYLDRVRSLETENRRLESK	3607.76	3608.83	-1.07	-295.36	1.E-07
P19338	GIAYIEFKTEADAEK	1683.84	1683.84	0.00	-0.37	1.E-07
Q53HU8	VELQELNDRFANYIDK	1965.98	1965.98	0.00	-1.92	1.E-07
P05783	ETMQSLNDRLASYLDRVRSLETENRRLESK	3608.82	3608.83	-0.01	-1.52	1.E-07
P04908	LLGRVTIAQGGVLPNIQAVLLPK	2369.44	2369.45	-0.01	-3.91	1.E-07
P08621	(52)TQFLPPNLLALFAPRDPIPYLPPLEKLPHEK	3606.99	3606.00	0.99	274.73	1.E-07
P68431	DIQLARRIRGERA	1548.62	1552.89	-4.27	-2759.93	1.E-07
Q15427	(41)AAGPISERNQDATVYVGGLDEK	2338.51	2331.13	7.38	3155.23	2.E-07
P68431	DIQLARRIRGERA	1552.86	1552.89	-0.03	-16.73	2.E-07
P68431	DIQLARRIRGERA	1552.89	1552.89	0.00	-0.31	2.E-07
O60506	ALLERTGYTLDVTTGQRK	2021.09	2021.09	0.00	-1.89	2.E-07
O60506	ALLERTGYTLDVTTGQRK	2021.93	2021.09	0.84	415.23	2.E-07
Q9P0L0	FKGPFTDVVTTNLK	1568.81	1565.85	2.96	1883.85	2.E-07
O60812	QKVDSLLENLEK	1397.72	1414.77	-17.05	-12197.30	2.E-07
O60812	QKVDSLLENLEK	1397.74	1414.77	-17.03	-12181.80	2.E-07

P23396	FVDGLMIHSGDPVNYYVDTAVRHVLLRQGVLGIK	3781.00	3781.01	-0.01	-2.54	2.E-07
P68104	NVSV(74)KDVRRGNVAGDSKNDPPMEAAGFTAQVIILNHPGQ ISAGYAPVLDCHTAHIACK	6092.04	6095.08	-3.04	-498.29	2.E-07
Q15233	EREQPPRFAQPGSFEYEYAMRWK	2901.37	2901.37	0.00	1.57	2.E-07
Q71DI3	TDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	4074.91	3940.93	133.98	32878.80	2.E-07
O95271	QVTELLLRKGANVNEKNK	2038.17	2053.16	-14.99	-7353.41	2.E-07
P22626	RGFGFVTFDDHDPVDK	1850.85	1850.86	-0.01	-2.87	2.E-07
P36578	MINTDLSRILK	1302.73	1302.73	0.00	-2.11	2.E-07
P51991	GGSFGGRSSGSPYGGGYGSGGGSGGYGSRRF	2831.24	2831.24	0.00	-0.59	2.E-07
P62805	TVTAMDVVYALK	1310.67	1309.70	0.97	741.11	2.E-07
Q9P0L0	FKGPFTDVVTTNLK	1565.85	1565.85	0.00	-1.67	2.E-07
Q9UMS4	TLQLDNNFEVK	1319.67	1319.67	0.00	-0.84	2.E-07
P26373	LILFPRKPSAPK	1365.85	1365.85	0.00	-1.39	3.E-07
P18859	LFVDKIREYK	1309.74	1309.74	0.00	2.22	3.E-07
P10412	(51)SETAPAAPAAPAPAEKTPVKK	2073.11	2073.11	0.00	0.73	3.E-07
P47914	LDRLAYIAHPK	1295.73	1295.73	0.00	-1.06	3.E-07

P47914	LDRLAYIAHPK	1299.75	1295.73	4.02	3089.07	3.E-07
P08865	RKSDGIYIINLK	1414.76	1418.82	-4.06	-2869.82	3.E-07
P08865	RKSDGIYIINLK	1417.74	1418.82	-1.08	-760.87	3.E-07
P08865	RKSDGIYIINLK	1418.82	1418.82	0.00	-1.43	3.E-07
P98179	(51)SSEEGKLFVGGLNFNTDEQALEDHFSSFGPISEVVVVK	4153.03	4153.02	0.01	1.41	3.E-07
O00422	(41)AVESRVTQEEIK	1429.74	1429.74	0.00	-0.90	3.E-07
O00422	(41)AVESRVTQEEIK	1434.61	1429.74	4.87	3391.53	3.E-07
P62805	TVTAMDVVYALK	1309.70	1309.70	0.00	-2.41	3.E-07
P62805	TVTAMDVVYALK	1312.70	1309.70	3.00	2281.99	3.E-07
P62805	TVTAMDVVYALK	1314.67	1309.70	4.97	3778.72	3.E-07
P39019	DQDGGRKLTPQGQRDLDRIAGQVAAANK	2977.53	2977.54	-0.01	-2.43	3.E-07
P22626	RGFGFVTFDDHDPVDK	1854.05	1850.86	3.19	1722.97	3.E-07
P62805	TVTAMDVVYALK	1309.65	1309.70	-0.05	-37.46	3.E-07
P62805	TVTAMDVVYALK	1309.66	1309.70	-0.04	-30.28	3.E-07
P62917	DIIHDPGRGAPLAK	1456.79	1458.79	-2.00	-1370.04	4.E-07

P62917	DIIHDPGRGAPLAK	1458.79	1458.79	0.00	-0.87	4.E-07
P18621	GLDVDSLVIEHIQVNK	1777.96	1777.96	0.00	-0.72	4.E-07
P09651	(51)SKSESPKEPEQLRK	1683.88	1683.88	0.00	-0.28	4.E-07
P60709	MTQIMFETFNTPAMYVAIQAVLSLYASGRTTGIVMDSGDGVTHTVPIYEGYALPHAILRLDLAGRDLTDYLMK	8022.00	8022.02	-0.02	-2.00	4.E-07
P60903	PSQMEHAMETMMFTFHK	2098.88	2081.88	17.00	8097.78	4.E-07
P61978	ALRTDYNASVSVPDSSGPERILSISADIETIGEILK	3815.96	3815.98	-0.02	-3.98	5.E-07
P62847	QMVIDVLHPGK	1240.67	1235.67	5.00	4026.63	5.E-07
P12956	IQVTPPGFQLVFLPFADDK	2133.15	2131.14	2.01	942.45	5.E-07
P52597	ATENDIYNFFSPLNPVRVHIEIGPDGRVTGEADVEFATHEEAVAAMSK	5241.52	5242.53	-1.01	-193.58	6.E-07
Q00839	EVLAGRPLFPHVLCHNCAVEFNFGQK	2922.44	2924.46	-2.02	-691.87	6.E-07
P61513	TVAGGAWTYNTTSAVTVK	1825.92	1825.92	0.00	-0.82	6.E-07
O60812	QKVDSLLENLEK	1410.76	1414.77	-4.01	-2839.98	6.E-07
O60812	QKVDSLLENLEK	1414.75	1414.77	-0.02	-15.72	6.E-07
O60812	QKVDSLLENLEK	1414.77	1414.77	0.00	-1.44	6.E-07
Q86V81	AAVHYDRSGRSLGTADVHFERKADALK	2969.52	2969.52	0.00	-0.85	6.E-07

P07910	RSAAEMYGSVTEHPSPSPLLSSSFDLDYDFQRDYYDRMYSYPARVPPPPPIARAVVPSKRQRVSGNTSRRGKSGFNSKSGQRGSSK	9567.60	9565.74	1.86	194.28	6.E-07
P06748	TPKGPSSVEDIK	1256.66	1256.66	0.00	-0.96	6.E-07
P02545	QREFESRLADALQELRAQHEDQVEQYKK	3443.71	3443.72	-0.01	-2.54	7.E-07
P06748	TPKGPSSVEDIK	1256.64	1256.66	-0.02	-18.70	7.E-07
P06748	TPKGPSSVEDIK	1261.58	1256.66	4.92	3903.18	7.E-07
P05204	VKDEPQRRSARLSAKPAPPKPEPKPK	2906.66	2906.66	0.00	-0.23	7.E-07
P05783	IMADIRAQYDELARK	1791.93	1791.93	0.00	-0.85	7.E-07
Q71UI9	ATIAGGGVIPHIHK	1412.78	1369.78	43.00	30439.30	7.E-07
Q71UI9	ATIAGGGVIPHIHK	1416.85	1369.78	47.07	33222.80	7.E-07
P49755	GTGRIPDQLVILDMK	1649.92	1654.91	-4.99	-3025.55	7.E-07
P49755	GTGRIPDQLVILDMK	1654.91	1654.91	0.00	-0.36	7.E-07
Q86V81	AAVHYDRSGRSLGTADVHFERKADALK	2969.52	2969.52	0.00	-1.09	7.E-07
P05783	VIDDTNITRLQLETEIEALKEELLFMK	3203.69	3203.70	-0.01	-2.77	7.E-07
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.52	3153.55	0.97	308.20	7.E-07
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	6898.53	6722.54	175.99	25510.50	8.E-07

P63261	(44)EEEIAALVIDNGSGMCK	1953.81	1819.83	133.98	68574.10	8.E-07
O43390	VLFVRNLATTVTEEILEK	2074.17	2074.17	0.00	-0.95	8.E-07
Q71DI3	TDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	4074.89	3940.93	133.96	32875.40	8.E-07
Q71DI3	TDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	4075.81	3940.93	134.88	33092.30	8.E-07
O75152	LSVQSNPSPQLRSVMK	1766.86	1769.95	-3.09	-1747.28	9.E-07
Q9Y6C9	EVSSSFDHVIK	1241.65	1246.62	-4.97	-4005.53	9.E-07
Q9Y6C9	EVSSSFDHVIK	1243.62	1246.62	-3.00	-2411.30	9.E-07
Q9Y6C9	EVSSSFDHVIK	1246.62	1246.62	0.00	1.01	9.E-07
P07355	LSLEGDHSTPPSAYGSVK	1843.90	1843.90	0.00	1.42	9.E-07
P07355	LSLEGDHSTPPSAYGSVK	1847.85	1843.90	3.95	2137.69	9.E-07
P33778	RSTITSREIQTAVRLLLPGELAK	2593.32	2551.48	41.84	16134.50	9.E-07
P33778	RSTITSREIQTAVRLLLPGELAK	2594.44	2551.48	42.96	16558.40	9.E-07
P33778	RSTITSREIQTAVRLLLPGELAK	2594.48	2551.48	43.00	16574.10	9.E-07
P60709	LCYVALDFEQEMATAASSSSLEK	2500.26	2492.15	8.11	3244.04	9.E-07
P60709	LCYVALDFEQEMATAASSSSLEK	2500.78	2492.15	8.63	3451.82	9.E-07

Q99880	AMGIMNSFVNDIFERIASEASRLAHYNK	3183.55	3183.56	-0.01	-2.05	1.E-06
P62750	AYVRLAPDYDALDVANKIGII	2289.23	2289.24	-0.01	-2.85	1.E-06
P62805	VFLENVIRDAVTYTEHAK	2147.10	2104.10	43.00	20027.50	1.E-06
P19338	TLVLSNLSYSATEETLQEVFEK	2500.25	2500.26	-0.01	-4.17	1.E-06
Q9Y6C9	EVSSSFDHVIK	1247.65	1246.62	1.03	828.40	1.E-06
Q9Y6C9	EVSSSFDHVIK	1249.60	1246.62	2.98	2381.61	1.E-06
P14866	DFSESRNNRFSTPEQAAK	2082.97	2082.97	0.00	-1.72	1.E-06
Q9UKV3	RRWGASTATTQKKPSISITTESLK	2646.45	2646.45	0.00	1.29	1.E-06
Q16891	SLEDALRQTASVTLQAIAAQNAAVQAVNAHSNILK	3615.92	3615.93	-0.01	-1.50	1.E-06
P08670	ARVEVERDNLAEDIMRLREK	2441.28	2441.28	0.00	-1.66	1.E-06
Q548L2	LQEEMLQREEAENTLQSFRQDVDNASLARLDLERKVESLQEEIAFLK	5560.79	5560.81	-0.02	-2.75	1.E-06
P31949	KLDTNSDGQLDFSEFLNLIGGLAMACHDSFLK	3632.66	3498.68	133.98	36881.40	2.E-06
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.38	2428.37	0.01	2.79	2.E-06
P62906	KYDAFLASESLIK	1483.79	1483.79	0.00	-2.37	2.E-06
P62851	IRGSLARAALQELLSK	1725.03	1725.03	0.00	-1.43	2.E-06

Q16695	QLATKVARKSAPATGGV(55)KKPHRYRPGTVALREIRRYQK	4343.50	4329.49	14.01	3225.80	2.E-06
P62841	HGRPGIGATHSSRFIPLK	1930.06	1930.06	0.00	1.09	2.E-06
Q9Y4Y9	AANATTNPSQLLPLELVDKCIGSRIHIVMKSDKEIVGTLLGFDDFVNMVLEDVTEFEITPEGRRITKLDQILLNGNNITMLVPGGEGPEV	9842.10	9800.09	42.01	4267.95	2.E-06
A6NCA2	PRNQGGYGGSSSSSSCVSGRRF	2250.01	2232.01	18.00	8000.71	2.E-06
P62857	GPVREGDVLTLLESEREARRLR	2552.40	2550.40	2.00	784.33	2.E-06
P33778	RSTITSREIQTAVRLLLPGELA(55)K	2594.48	2593.49	0.99	381.57	2.E-06
Q09666	ISMPDVDLHLK	1266.66	1266.66	0.00	-1.01	2.E-06
P09651	RSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPK	3887.98	3887.99	-0.01	-2.15	2.E-06
P60953	TPFLLVGTQIDLRDDPSTIEK	2357.25	2357.25	0.00	0.81	2.E-06
P33778	RSTITSREIQTAVRLLLPGELA(55)K	2594.44	2593.49	0.95	365.66	2.E-06
Q9Y230	TAIAMGMAQALGPDTPFTAIAGSEIFSLEMSK	3263.46	3255.59	7.87	2412.56	2.E-06
Q9Y230	TAIAMGMAQALGPDTPFTAIAGSEIFSLEMSK	3269.60	3255.59	14.01	4284.72	2.E-06
P07910	TDPRSMNSRVFIGNLNTLVVK	2360.26	2360.26	0.00	-1.58	2.E-06
P07910	TDPRSMNSRVFIGNLNTLVVK	2361.23	2360.26	0.97	411.55	2.E-06
Q9Y230	IAGRAVLIAGQPGTGK	1507.88	1507.88	0.00	-1.93	2.E-06

Q9Y230	IAGRAVLIAGQPGTGK	1509.88	1507.88	2.00	1326.98	2.E-06
P04908	LLGRVTIAQGGVLPNIQAVLLPKKTESHHK	3344.92	3216.88	128.04	38278.60	3.E-06
P05783	GLQAQIASSGLTVEVDAPK	1883.00	1883.00	0.00	-2.05	3.E-06
P61254	MKFNPFVTSDRSK	1555.78	1555.78	0.00	-1.66	3.E-06
P61254	MKFNPFVTSDRSK	1559.85	1555.78	4.07	2610.70	3.E-06
Q09028	TPSSDVLVFDYTK	1470.72	1470.72	0.00	-1.02	3.E-06
P61313	FFEVILIDPFHK	1502.76	1503.81	-1.05	-698.14	3.E-06
P61313	FFEVILIDPFHK	1503.81	1503.81	0.00	-1.43	3.E-06
Q969X6	IYKPLLFMDLLDERTLVAVERPLDDIIAQLPPPIK	4049.93	4044.27	5.66	1397.27	3.E-06
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3196.51	3153.55	42.96	13439.60	3.E-06
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3196.55	3153.55	43.00	13452.00	3.E-06
Q504R3	NFFWMTDQEAIQDLWQWRK	2539.19	2541.19	-2.00	-788.25	3.E-06
P09651	LFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTK	4229.01	4229.02	-0.01	-2.58	3.E-06
Q53HU8	LLEGEESRISLPLPNFSSLNLRETNLDSLPLVDTHSK	4133.15	4133.16	-0.01	-3.21	3.E-06
Q9P0L0	VAHSDKPGSTSTASFRDNVTSPLPSLLVVIAAIFIGFFLGKFIL	4632.44	4632.54	-0.10	-21.60	4.E-06

Q9P0L0	VAHSDKPGSTSTASFRDNVTSPLPSLLVVIAAIFIGFFLGKFIL	4632.54	4632.54	0.00	0.40	4.E-06
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.31	2428.37	-0.06	-25.59	4.E-06
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-0.88	4.E-06
Q09028	TPSSDVLVFDYTK	1474.62	1470.72	3.90	2645.96	4.E-06
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.33	2428.37	-0.04	-17.15	4.E-06
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-1.54	4.E-06
P69905	VGAHAGEYGAEALERMFLSFPTTK	2581.26	2581.26	0.00	-1.30	4.E-06
P62805	TVTAMDVVYALK	1352.70	1309.70	43.00	31791.60	4.E-06
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.52	3153.55	0.97	308.93	4.E-06
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3156.47	3153.55	2.92	924.08	4.E-06
P02545	RTLEGELHDLRGQVAKLEAALGEAKK	2832.56	2831.56	1.00	353.26	4.E-06
P61978	ALRTDYNASVSVPDSSGPERILSISADIETIGEILK	3815.97	3815.98	-0.01	-2.39	5.E-06
P05783	IMADIRAQYDELARK	1791.93	1791.93	0.00	-2.13	5.E-06
P39019	DQDGGRKLTPQGQRDLDRIAGQVAAANKKH	3242.71	3242.70	0.01	2.31	5.E-06
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3169.54	3153.55	15.99	5043.94	5.E-06

Q9NW13	TVFIRNLSFDSEEEELGELLQQFGELK	3170.52	3169.58	0.94	295.64	5.E-06
Q99729	NEEDAGKMFVGGLSWDTSKK	2196.18	2198.03	-1.85	-844.08	5.E-06
P68431	DIQLARRIRGERA	1552.89	1552.89	0.00	-1.08	5.E-06
P09651	RGFAFVTFDDHDSVDK	1854.85	1854.85	0.00	-2.23	5.E-06
Q00839	AVVVCPKDEDYK	1364.66	1364.66	0.00	-0.42	6.E-06
P61313	AIRRNPDTQWITKPVHK	2059.14	2059.14	0.00	0.05	6.E-06
P22626	KLFVGGIKEDTEEHHLRDYFEEYGKIDTIEIITDRQSGKK	4736.41	4736.41	0.00	-0.80	6.E-06
P05387	MRYVASYLLAALGGNSSPSAK	2155.10	2155.11	-0.01	-2.90	7.E-06
P09651	RGFAFVTFDDHDSVDK	1857.85	1854.85	3.00	1616.74	7.E-06
P09651	RGFAFVTFDDHDSVDK	1858.37	1854.85	3.52	1892.18	7.E-06
Q01082	AEHERELALRNELIRQEK	2234.19	2233.19	1.00	447.95	7.E-06
P05787	TEISEMNRNISRLQAEIEGLK	2430.24	2430.25	-0.01	-3.31	7.E-06
Q71UI9	RITPRHLQLAIRGDEELDSLIK	2572.44	2572.44	0.00	-0.57	7.E-06
Q01130	VDNLTYRTSPDTLRRVFEK	2309.21	2309.21	0.00	-0.63	7.E-06
P04083	GLGTDEDTLIEILASRTNK	2045.03	2045.06	-0.03	-14.83	7.E-06

Q09666	FKMPEMHFKAPK	1489.76	1489.76	0.00	1.29	7.E-06
P08729	VDALNDEINFLRTLNETELTELQSQISDTSVVLSMDNSRSLDLDGIIAEVK	5662.83	5662.84	-0.01	-1.35	8.E-06
P68431	DIQLARRIRGERA	1552.87	1552.89	-0.02	-15.89	8.E-06
P68431	DIQLARRIRGERA	1552.89	1552.89	0.00	1.63	8.E-06
P05787	TEISEMNRNISRLQAEIEGLK	2427.10	2430.25	-3.15	-1298.32	8.E-06
P07910	ELTQIKQKVDSLLENLEK	2123.17	2127.18	-4.01	-1889.52	8.E-06
Q9NR30	DAIRLLDSVPPTAISHFK	1979.08	1979.08	0.00	-0.74	9.E-06
Q9NR30	DAIRLLDSVPPTAISHFK	1982.87	1979.08	3.79	1909.67	9.E-06
P62807	RSRKESYSVYVYKVLKQVHPDTGISS(75)KAMGIMNSFVNDIFERIAGEASRLAHYNK	6323.22	6317.26	5.96	943.02	9.E-06
P05783	KGPQVRDWSHYFK	1646.83	1646.83	0.00	0.22	9.E-06
Q00839	AELMERLQAALDDEEAGGRPAMEPGNG(37)SLDLGGDSAGRSGAGLEQEAAAGGDEEEEEEEEEEEGISALDGDQMELGEENGAAGAADSGPMEEEEAASEDENGDDQGFQEGEDELGDEEEGAGDENGHGEQQPQPPATQQQQPQQQRGAAK	15572.41	15570.50	1.91	122.40	9.E-06
P46777	ASFLRAQERAAES	1434.72	1434.72	0.00	-1.47	9.E-06
A7E2U8	KKTISNTFKPSSPGKK	1793.01	1747.00	46.01	25662.50	9.E-06
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3196.55	3153.55	43.00	13452.10	9.E-06
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	-1.00	1.E-05

P0C0S8	TRIIPRHLQLAIRNDEELNK	2432.39	2428.37	4.02	1651.17	1.E-05
P04083	GLGTDEDTLIEILASRTNK	2045.06	2045.06	0.00	-1.48	1.E-05
P62805	RISGLIYEETRGVLK	1736.68	1732.98	3.70	2132.89	1.E-05
P0C0S8	TRIIPRHLQLAIRNDEELNK	2429.34	2428.37	0.97	401.00	1.E-05
Q15149	ELIPTEEALRLLDAQLATGGIVDPRLGFHLPLEVAYQRGYLNK	4788.60	4788.60	0.00	-0.47	1.E-05
P62805	RISGLIYEETRGVLK	1732.97	1732.98	-0.01	-4.06	1.E-05
P62805	RISGLIYEETRGVLK	1734.95	1732.98	1.97	1135.80	1.E-05
P14866	VFSGKSERSSSGLLEWESKSDALETLGFLNHYQMK	3959.92	3959.94	-0.02	-5.89	1.E-05
P62899	LYTLVTYVPVTTFK	1643.92	1643.92	0.00	-1.66	1.E-05
Q5XJ17	(49)MSIMAPAPTVLVPTVSMVGK	2145.14	2070.09	75.05	34986.90	1.E-05
Q14978	RGAAGDWGERANQVLK	1726.89	1726.89	0.00	-1.14	1.E-05
Q14978	RGAAGDWGERANQVLK	1727.96	1726.89	1.07	617.22	1.E-05
O60506	ALLERTGYTLDVTTGQRK	2021.09	2021.09	0.00	-1.74	1.E-05
O43390	VAERLDEIFQTGLVAYVDLDERAIDALREFNEEGALSVLQQFKESDLSHVQNK	6046.05	6047.06	-1.01	-166.28	1.E-05
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4109.11	4108.11	1.00	243.90	1.E-05

P33778	RSTITSREIQTAVRLLLPGELAK	2551.40	2551.48	-0.08	-29.68	1.E-05
O43933	NKLDCDINK	965.49	1061.52	-96.03	-99463.20	1.E-05
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.31	2428.37	-0.06	-25.26	1.E-05
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.36	2428.37	-0.01	-2.16	1.E-05
Q08211	LAQFEPSQRQNQVGVVPWSPPQSNWNPWTSSNIDEGPLAFATPEQISMDLKNELMYQLEQDHDLQAILQERELLPVK	8867.35	8867.37	-0.02	-2.69	1.E-05
P33778	RSTITSREIQTAVRLLLPGELAK	2551.47	2551.48	-0.01	-2.44	2.E-05
P33778	RSTITSREIQTAVRLLLPGELAK	2551.98	2551.48	0.50	194.15	2.E-05
P05388	AIRGHLENNPALEK	1560.85	1560.84	0.01	8.90	2.E-05
P05388	AIRGHLENNPALEK	1562.84	1560.84	2.00	1278.70	2.E-05
P05388	AIRGHLENNPALEK	1562.84	1560.84	2.00	1278.70	2.E-05
P09651	RGFAFVTFDDHDSVDK	1854.85	1854.85	0.00	-1.58	2.E-05
P46013	KADVEEEFLAFRK	1580.82	1580.82	0.00	1.51	2.E-05
P46013	KADVEEEFLAFRK	1584.77	1580.82	3.95	2492.34	2.E-05
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3169.54	3153.55	15.99	5045.66	2.E-05
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3173.55	3153.55	20.00	6303.29	2.E-05

Q8N257	RSTITSREVQTAVRLLLPGELAK	2537.47	2537.47	0.00	-1.68	2.E-05
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.34	2428.37	-0.03	-12.49	2.E-05
P0C0S8	TRIIPRHLQLAIRNDEELNK	2431.35	2428.37	2.98	1224.12	2.E-05
Q0VGL3	FAYLGRLAHEVGWKYQAVTATLEDKRKEK	3307.67	3406.81	-99.14	-29972.70	2.E-05
P0C0S8	TRIIPRHLQLAIRNDEELNK	2428.37	2428.37	0.00	0.40	2.E-05
P05388	AIRGHLENNPALEK	1558.66	1560.84	-2.18	-1396.07	2.E-05
P05388	AIRGHLENNPALEK	1559.82	1560.84	-1.03	-657.13	2.E-05
Q14978	NKPGPYSSVPPPSAPPPK	1815.95	1815.95	0.00	-0.77	2.E-05
Q14978	NKPGPYSSVPPPSAPPPK	1816.00	1815.95	0.05	25.11	2.E-05
Q6DKI1	(41)AEQEQRKIPLVPENLLKK	2174.00	2174.24	-0.24	-109.11	2.E-05
P22626	ALSRQEMQEVQSSRSGRGGNFGFGDSRGGGGNFGPGPGSNFRGGSDGYGSGRGFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGSGNYNDFGNYNQQPSNYGPMK	12761.44	12733.40	28.04	2197.37	2.E-05
Q16695	KPHRYRPGTVALREIRRYQK	2523.44	2523.44	0.00	-0.94	2.E-05
P62318	(51)SIGVPIKVLHEAEGHIVTCETNTGEVYRGKLIEAEDNMNCQMSNITVTYRDGRVAQLEQVYIRGSKIRFLILPDMLKNAPMLK	9397.83	9397.84	-0.01	-0.63	2.E-05
P60660	EGNGTVMGAEIRHVLVTLGEK	2210.13	2209.15	0.98	443.79	2.E-05
Q01130	(51)SYGRPPPDVEGMTSLK	1774.86	1774.86	0.00	-0.73	2.E-05

P51991	IFVGGIKEDTEEYNLRDYFEK	2564.23	2564.24	-0.01	-3.56	2.E-05
Q8NC51	PGHLQEGFGCVVTNRFDQLFDDESDPFEVLK	3537.66	3537.65	0.01	2.43	2.E-05
Q9Y5S9	GYTLVEYETYK	1364.84	1364.65	0.19	137.10	3.E-05
Q00839	RNFILDQTNVSAAAQRRK	2087.13	2087.13	0.00	-0.33	3.E-05
A2BDF6	STELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA	9082.92	9082.91	0.01	1.23	3.E-05
Q00839	EKPYFPIPEEYTFIQNVPLEDRVRGPKGPEEKK	3929.03	3929.04	-0.01	-1.87	3.E-05
P22626	LFIGGLSFETTEESLRNYYEQWGK	2866.37	2866.38	-0.01	-2.63	3.E-05
O43390	VTEGLVDVILYHQPDDK	1939.99	1939.99	0.00	-0.76	3.E-05
P68431	DIQLARRIRGERA	1553.87	1552.89	0.98	631.28	3.E-05
P62857	GPVREGDVLTLLESEREARRLR	2549.34	2550.40	-1.06	-416.88	3.E-05
P62857	GPVREGDVLTLLESEREARRLR	2550.40	2550.40	0.00	1.30	3.E-05
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.48	3153.55	0.93	294.77	3.E-05
P33778	AMGIMNSFVNDIFERIAGEASRLAHYNK	3154.53	3153.55	0.98	311.09	3.E-05
P23246	GGKMPGGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQGPPPGGPGGRSEEK	6292.09	6292.09	0.00	-0.70	3.E-05
P68431	DIQLARRIRGERA	1552.89	1552.89	0.00	3.17	4.E-05

A6NJM3	RSIITSREIQTAVRLLLPGELAK	2558.84	2563.52	-4.68	-1827.67	4.E-05
A6NJM3	RSIITSREIQTAVRLLLPGELAK	2559.17	2563.52	-4.35	-1700.32	4.E-05
A6NJM3	RSIITSREIQTAVRLLLPGELAK	2562.44	2563.52	-1.08	-420.23	4.E-05
A6NJM3	RSIITSREIQTAVRLLLPGELAK	2562.55	2563.52	-0.97	-378.84	4.E-05
P16403	ASGPPVSELITK	1197.66	1197.66	0.00	-2.32	4.E-05
P16403	ASGPPVSELITK	1198.16	1197.66	0.50	416.91	4.E-05
P09874	SLQELFLAHILSPWGAEVK	2137.16	2137.16	0.00	0.60	4.E-05
Q9P013	(52)TTAARPTFEPARGGRGKGEGDLSQLSK	2828.46	2828.45	0.01	1.77	4.E-05
P62424	KQEAKKVVNPLFEK	1656.96	1656.96	0.00	-1.00	4.E-05
P62424	KQEAKKVVNPLFEK	1660.84	1656.96	3.88	2334.46	4.E-05
P06748	(49)MEDSMDMDMSPLRPQNYLFGCELK	3025.21	2891.23	133.98	44287.40	4.E-05
A6NG44	(49)MGIMNSFVNDIFERIASEASRLAHYNK	3154.53	3154.53	0.00	-1.24	5.E-05
Q09666	FKMPEMHFKAPK	1489.76	1489.76	0.00	-1.53	5.E-05
Q6P2Q9	LWNLNNYRTDMIQALGGVEGILEHTLFK	3245.66	3244.67	0.99	305.84	5.E-05
P20700	NQNSWGTGEDVK	1332.63	1333.59	-0.96	-717.79	6.E-05

P20700	NQNSWGTGEDVK	1332.69	1333.59	-0.90	-671.68	6.E-05
P20700	NQNSWGTGEDVK	1333.59	1333.59	0.00	-0.26	6.E-05
P20700	NQNSWGTGEDVK	1334.58	1333.59	0.99	739.00	6.E-05
P22626	RGFGFVTFDDHDPVDKIVLQK	2432.25	2432.25	0.00	-1.52	6.E-05
P14866	DFSESRNNRFSTPEQAAK	2082.96	2082.97	-0.01	-2.44	6.E-05
Q00839	SSGPTSLFAVTVAPPGARQGQQQAGGK	2603.31	2596.34	6.97	2676.29	6.E-05
P09651	RSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPK	3887.98	3887.99	-0.01	-1.91	6.E-05
O76021	TVSQIISLQTLKK	1458.76	1457.88	0.88	605.02	6.E-05
P68431	DIQLARRIRGERA	1552.87	1552.89	-0.02	-15.63	6.E-05
P68431	DIQLARRIRGERA	1552.89	1552.89	0.00	0.66	6.E-05
P62314	NREPVQLETLSIRGNNIRYFILPDSLPLDTLLVDVEPK	4376.35	4376.37	-0.02	-4.02	6.E-05
Q09666	FGVSTGREGQTPK	1366.78	1362.69	4.09	2995.46	6.E-05
P09651	GGNFGGRSSGPYGGGGQYFAKPRNQGGYGGSSSSSSYGSGRRF	4251.93	4251.92	0.01	1.87	6.E-05
P08621	(52)TQFLPPNLLALFAPRDPIPYLPPLEK	3001.61	3001.67	-0.06	-19.98	7.E-05
P08621	(52)TQFLPPNLLALFAPRDPIPYLPPLEK	3001.67	3001.67	-0.01	-1.65	7.E-05

P68431	DIQLARRIRGERA	1552.86	1552.89	-0.03	-16.15	7.E-05
P68431	DIQLARRIRGERA	1552.89	1552.89	0.00	1.56	7.E-05
P42704	IPENIYRGIRNLLESYHVPELIK	2765.52	2765.52	0.00	-1.33	8.E-05
P33778	RSTITSREIQTAVRLLLPGELAKHAVSEGTK	3455.79	3360.88	94.91	27464.80	8.E-05
Q09666	FGVSTGREGQTPK	1365.69	1362.69	3.00	2196.87	8.E-05
Q8NC51	NPLPPSVGVVDKKEETQPPVALKK	2585.35	2569.45	15.90	6151.21	8.E-05
Q16695	KPHRYRPGTVALREIRRYQK	2523.44	2523.44	0.00	-1.65	8.E-05
P05386	(49)MASVSELACIYSALILHDDEVTVTEDKINALIK	3648.79	3645.85	2.94	804.89	8.E-05
P60709	DLYANTVLSGGTTMYPGIADRMQK	2601.25	2601.26	-0.01	-2.19	8.E-05
Q16695	VARKSAPATGGVKKPHRYRPGTVALREIRRYQK	3746.15	3746.16	-0.01	-1.93	8.E-05
Q6FI13	GNYAERVGAGAPVYMAAVLEYLTAEILELAGNAARDNKK	4108.10	4108.11	-0.01	-2.09	8.E-05
Q15149	ANEALRLRLQAEEVAQQK	2064.09	2066.12	-2.03	-985.87	9.E-05
Q15149	ANEALRLRLQAEEVAQQK	2066.12	2066.12	0.00	1.59	9.E-05
Q15149	QRALQALEELRLQAEEAERRLRQAEVERARQVQVALETAQRSAEAELQSK	5784.07	5784.09	-0.02	-3.58	9.E-05
Q09666	FGVSTGREGQTPK	1362.69	1362.69	0.00	1.21	9.E-05

Q09666	FGVSTGREGQTPK	1362.73	1362.69	0.04	31.15	9.E-05
Q9UKM9	SNIDALLSRLEQIAAEQK	1998.07	1998.07	0.00	-2.27	9.E-05
P0C0S8	VTIAQGGVLPNIQAVLLPK	1973.16	1930.16	43.00	21793.30	1.E-04