

AC	sequence	pI	zscore	pvalue	deltaMass	modif	misscleav	Fraction
P0A005	EHWGFDDPAGKEWSEFQR	4.326	10.7	9E-26	0.22		1	2
P0A096	RVESMNMTEQIFR	5.719	7.277	0	0.069		1	6
P0A0D4	ADALIEEGNNCIAEAHR	4.325	9	2E-17	0.13		0	2
P0A0D8	IAITFSEEENVDRIVQAK	4.396	8.7	2E-16	0.18		1	2
P0A0F2	MQDLNAADEEAAMR	3.814	7.4	7E-12	0.09		0	1
P0A0F2	TQDQAGLIIPVEISVYEDR	3.826	10.8	3E-25	0.18		0	1
P0A0F2	EIANSKMQDLNAADEEAAMR	4.032	10.4	2E-23	0.13		1	1
P0A0F6	SGGGVRPGFEGGQLPLFR	8.818	9.819	0	-0.339		1	10
P0A0H7	MQSKEDFIEMR	4.567	7.8	3E-13	0.01		1	3
P0A0H7	IGPYDKDENIDFLR	4.143	7.9	1E-13	0.15		1	1
P0A0N1	ITGAQAWVGTLLK	8.889	6.8	6E-10	0		0	10
P0A0N1	KVLDIVKDFEEVTLF	4.289	6.8	7E-10	0.13		-1	2
P60076	SNSDLNIERINELAK	4.555	8	5E-14	0		-2	3
P60076	EVGLTQEEAKEQTALR	4.323	9.5	9E-20	0.1		1	2
P60088	LGVDLGPTAIR	5.702	7.3	1E-11	0.03		0	6
P60088	KLGVDLGPTAIR	8.424	7.307	0	0.062		1	10
P60088	AIDIIGAPSTFGQR	5.791	7.8	4E-13	-0.01		0	7
P60088	NYDEIIDVNQKLNK	4.437	9.097	0	0.09		1	3
P60088	AIDIIGAPSTFGQRK	8.935	8.5	5E-16	0.01		1	10
P60088	LGVDLGPTAIRYAGLISR	8.623	6.696	0	0.111		1	10
P60088	ILTGEGPKELLELSNVIKPENIVLIGMR	4.863	7.4	5E-12	0.09		2	4
P60120	SIVFPTVPR	8.83	7.9	2E-13	0.01		0	10
P60120	VNHSDMDDLRL	4.371	8.5	9E-16	0.09		0	2
P60120	HFGLQDKIDFQIGTLSK	6.119	10	1E-21	-0.27		1	8
P60120	DMLDEAIAAYEKVGKEMK	4.347	10.7	4E-25	0.09		2	2
P60120	LGYDTGESETPITPVIIGDEK	3.781	8	8E-14	0.21		0	1
P60120	NMPTAAHTKDMLDEAIAAYEK	4.719	7.1	9E-11	0.03		1	4
P60120	SYINLSSNNYLGLATNEDLKSAAK	5.709	10.9	5E-26	0.06		1	5
P60120	LGYDTGESETPITPVIIGDEKTTQEFSKR	4.251	12	3E-31	0.27		2	2
P60278	SYEWFLR	5.6	6.258	0	0.028		0	6
P60278	DTKLGPEEITR	4.496	7.2	2E-11	0.08		1	4
P60278	VNEFGFIETPYR	4.434	10.261	0	0.136		0	3
P60278	LRPGEPTVENAK	6.076	6.9	2E-10	0.1		1	8
P60278	LGEPKYDLEESKNR	4.779	9.7	9E-21	0.04		2	4
P60278	STGPYSLVTQQPLGGK	8.283	7.007	0	0.082		0	9
P60278	GVTELTAERLLHAIFGEK	4.834	9.241	0	0.131		1	4
P60278	LVEENGVEHEGELDRYPLAK	4.321	8.7	1E-16	0.16		1	2
P60278	VFNREEGDDTLSPGVNQLVR	4.193	7.9	5E-14	0.19		1	2

P60278	TYEAIVKGENISRPSVPESFR	5.941	7.9	4E-14	0.03		2	7
P60278	RLVEENGVEHEGELDRYPLAK	4.613	12.1	2E-32	-0		2	3
P60278	GIVYIGAEVKDGDILVGKVTPK	6.047	7.2	3E-12	-0.32		2	7
P60285	IQEIFEAR	4.442	6.9	3E-10	0.07		0	3
P60285	MIDVNNFHMYK	6.533	7.3	2E-11	0.09		0	8
P60285	IIVEIGQPVQR	5.924	6.3	1E-08	0.02		0	7
P60285	ITDAGIEQMYIR	4.208	9	1E-17	0.11		0	1
P60285	KITDAGIEQMYIR	5.598	6.112	0	0.075		1	6
P60285	LGIQAFEPTLVEGR	4.489	6.6	2E-09	-0.02		0	3
P60285	RDDLLGLKENVIIGK	5.664	7.7	1E-13	-0.3		2	6
P60285	EGLTVLEYFISTHGAR	5.35	6.4	1E-08	0.05		0	5
P60285	LLDLGAPGIIVQNEKR	5.97	9.6	3E-20	0.06		1	7
P60285	SWSFGEVKKPETINYR	8.083	10.511	0	0.097		2	9
P60285	TFHTGGVAGSDITQGLPR	6.553	12.9	2E-36	0.02		0	8
P60285	ILATSVGKIIFNEIIPDSFAYINEPTQENLER	4.231	7	1E-10	0.28		1	2
P60285	LHPLVTTAYNADFDGDQMAVHVPLSKEAQAEAR	4.74	7.4	8E-12	0.04		1	4
P60298	GYGPLLDGFR	5.786	6.6	3E-09	-0.03		0	7
P60298	ELCDEHNVLF	3.957	6.5	5E-09	0.11		-1	1
P60298	IADEIQAGLGR	4.2	8.6	4E-16	0.08		-2	2
P60298	KVDFGDVDALK	4.302	6.9	4E-10	0.09		1	2
P60298	QIDHPSIKEVR	6.415	9.5	5E-20	-0.38		1	8
P60298	AFHSDNLGEWYEK	4.605	8.7	2E-16	0		0	3
P60298	AIRELCDEHNVLF	4.463	8.2	2E-14	0	:Cys_CAM:.....	-1	3
P60298	SLELGDFKEQLK	4.519	7.7	9E-13	-0.01		1	3
P60298	LFATDWDNVKPDVY	3.904	11.4	3E-28	0.21		-1	1
P60298	TMAPVSLSSEAEYQR	4.496	9.9	2E-21	-0.03		0	3
P60298	ALPMNTGAEAVETALK	4.507	6.4	1E-08	-0.01		0	3
P60298	AFHSDNLGEWYEKICK	5.459	10.8	3E-25	0.08	:Cys_CAM::.....	1	5
P60298	IIQALKDQADKVTLVSR	8.467	8.5	2E-15	0.01		2	10
P60298	GRGLFIGVELNESARPY	6.136	7.3	2E-11	-0.26		-1	8
P60298	SGKLFATDWDNVKPDVY	4.39	15.1	7E-50	0.18		-1	3
P60298	GIEPNKAEIIAFNGNFHGR	6.799	7.8	5E-13	-0.23		1	9
P60298	IITKEELDLALEKIRHVFQ	5.531	7.5	4E-12	0.06		-2	5
P60298	ALPMNTGAEAVETALKAAAR	6.175	7.8	4E-13	0.14		1	8
P60298	CEALKEEGLLCKETHDTVIR	4.806	11.4	3E-28	0.04	:Cys_CAM:.....:Cys_CAM:.....	-2	4
P60298	FAPPLIITKEELDLALEKIR	4.791	15.1	2E-49	0.06		2	4
P60298	ALPMNTGAEAVETALKAAARR	8.665	6.659	0	0.108		2	10
P60298	SLELGDFKEQLKQIDHPSIK	5.403	9.5	2E-19	0.07		2	5
P60298	SGKLFATDWDNVKPDVYILGK	5.683	9.2	4E-18	0.06		2	6

P60298	LAGKDKALPMNTGAEAVETALK	6.138	13.5	4E-40	-0.39		2	8
P60298	AIRELCDEHNVLFIADEIQAGLGR	4.313	11.6	2E-29	0.14		1	2
P60298	SLELGDFYFKEQLKQIDHPSIKEVR	5.468	12.7	7E-35	0.05		3	5
P60298	GGNPLACAASIAALDVIVDEDLPGR	3.805	11.3	9E-28	0.17	Cys_CAM:.....	-2	1
P60298	TMAPVSLSSEAEYQRGYGPLLDGFR	4.642	10.219	0	0.206		1	4
P60298	LAGKDKALPMNTGAEAVETALKAAR	8.366	12.976	0	0.131		3	9
P60298	WAYDVKGIEPNKAEIIAFNGNFHGR	6.61	14.6	1E-46	-0.27		2	9
P60298	RWAYDVKGIEPNKAEIIAFNGNFHGR	8.071	17.356	0	0.128		3	9
P60298	AIRELCDEHNVLFIADEIQAGLGRSGK	4.726	6.1	6E-08	0.06		2	4
P60298	ELCDEHNVLFIADEIQAGLGR	3.957	11.1	2E-26	0.15	...Cys_CAM:.....	0	1
P60359	DVLNNVYR	5.632	8.801	0	0.067		0	6
P60392	GLPVIPEAYTPK	6.008	7.3	9E-12	-0.14		0	7
P60392	QVFQEYEKGPEVPR	4.714	7.7	1E-12	0.01		1	4
P60432	ATIGQVGNLQHELVNVGKAGR	8.674	7.727	0	0.114		1	10
P60798	IGEGAAMLR	5.885	6.2	4E-08	0.02		0	7
P60798	DQFTVPFVCGCR	5.519	8.4	3E-15	0.05	Cys_CAM::Cys_CAM::	0	5
P60798	GLDINQLSLEER	4.041	8.3	1E-14	0.11		0	1
P60798	GGVIMDVVNAEQAR	4.292	7.5	7E-12	0.15		0	2
P60798	TKGEPGTGNIVEAVR	5.859	9	2E-17	0.04		1	7
P60798	GLDINQLSLEERMQER	4.289	7.2	4E-11	0.19		1	2
P60798	AIVQATTHYQDYELIGR	5.348	11.7	1E-29	0.05		0	5
P60798	IVEEVMNAVSIPVMAKAR	6.078	8.2	8E-15	0.15		1	8
P60798	LASELGTAMKGLDINQLSLEER	4.321	8	1E-13	0.16		1	2
P60857	FNLEFINNNAK	5.678	9	2E-17	0.05		0	6
P60857	MMGEGFGINPTEGEVVSPIAGR	4.135	9.9	2E-21	0.28		0	1
P60876	YQERVNQAPNIEY	4.497	7.5	2E-12	0.11		1	3
P60876	KYQERVNQAPNIEY	5.709	7.9	8E-14	0.03		2	6
P60910	TPIFESTDLFAR	4.308	7.7	1E-12	0.11		0	2
P60910	HFEPVIHEFCSDCQSR	4.89	12.2	2E-32	0.04	Cys_CAM::Cys_CAM::	0	4
P63334	NLAWNIESR	5.822	6.6	3E-09	0.02	...:Oxidation_HW:...	0	7
P63334	GYSVSFNR	8.645	7.817	0	0.053		0	10
P63334	EGVFHTQWIEE	4.184	6.9	3E-10	0.13		0	1
P63334	AADLPANLIQAQR	5.769	9.2	1E-18	0.03		0	7
P63334	DKEGVFHTQWIEE	4.275	9.4	2E-19	0.17		1	2
P63334	TQQIGVIGLAVMGK	8.66	10.506	0	0.101		-2	10
P63334	KDKEGVFHTQWIEE	4.752	8.7	2E-16	0.04		2	4
P63334	SSEKTDLMVEESKGK	4.748	6.8	5E-10	0.03		2	4
P63334	ERKDKEGVFHTQWIEE	4.839	7.7	5E-13	0.04		-2	4
P63334	NLAWNIESRGYSVSFNR	8.505	6	6E-08	-0.38		1	10

P63334	NIHPTYSLEEFVNSLEKPR	5.507	10.8	2E-25	0.06		1	5
P63334	NIHPTYSLEEFVNSLEKPRK	6.669	9.3	1E-18	0		2	8
P63334	AADLPANLIQAQRDYFGAHTY	5.188	6.827	0	0.223		-1	4
P63334	TQQIGVIGLAVMGKNLAWNIESR	8.388	9.46	0	0.087		-2	10
P63334	AADLPANLIQAQRDYFGAHTYERK	6.835	8.9	6E-17	-0.11		2	9
P63489	FGLVAFASSLDQIGPLTR	5.49	9.8	7E-21	0.05		0	5
P63489	SIRYESVENLLTLIKDKK	8.067	10.298	0	0.139		-2	9
P63489	TFALSSGYYDAYYKKSQK	9.1	6.1	6E-08	0.01		-2	10
P63489	LFGIPMGIKDNIITNGLETTCAK	5.964	6.3	2E-08	0.03		1	7
P63489	AVPGGSSGGSAAAVAAGLVPLSLGSDTGGSIR	5.789	7.6	2E-12	0.03		0	6
P63554	CMSQPLFREDI	4.294	6.8	4E-10	0.14	:Cys_CAM:.....	1	2
P63554	LAAESIENPQVR	4.466	8.4	3E-15	0.09		0	3
P63554	GIKVIEISGSELVR	6.081	7.5	2E-12	0.09		1	8
P63585	NHTETMFR	6.656	8.6	6E-16	0.01		0	8
P63665	AESHLNDDDDNTDIHRAER	4.268	10.2	2E-22	0.16		1	2
P63665	ARAESHLNDDDDNTDIHRAER	4.533	7.2	5E-11	-0.05		2	3
P63740	APVFSFNK	8.941	6.4	1E-08	0		0	10
P63740	FPFDFEKGGER	5.866	8.9	6E-17	0.03		2	7
P63740	ITDIPMAQLAMR	5.712	6.704	0	0.036		0	6
P63740	AEDRKEFEALLR	4.665	7.2	6E-11	0.01		2	3
P63740	GKEVERDGFQIRR	8.624	6.8	7E-10	0		3	10
P63740	SIAGFKEIEYEVMR	4.718	8.6	6E-16	0.03		1	4
P63740	TVPFLSKITDIPMAQLAMR	8.388	9.852	0	0.081		1	9
P63740	SLEYGVHHLGLPNGESFDLDYIKER	4.813	11.4	3E-28	0.01		1	4
P63797	SLLDEESKQEISPK	4.336	8.9	3E-17	0.1		1	2
P63797	RSLLDEESKQEISPK	4.818	8.4	3E-15	0.04		2	4
P63797	NILMIGPTGVGKTEIAR	8.488	8.6	2E-16	-0.28		1	10
P63797	LAEIAYQVNQDTDNIGAR	3.911	9.8	1E-20	0.13		0	1
P63806	GIESNFEDLKR	4.555	7.2	4E-11	0.01		1	3
P63806	DQYDMNREISPLR	4.169	8.4	4E-15	0.11		1	2
P63806	NNDVTQHVSYSVASKEPVR	6.657	8.3	6E-15	0.01		1	8
P63844	IIQMLEER	4.506	6.752	0	0.047		0	3
P63844	HIPSEYTER	4.94	6.1	9E-08	0.02		0	4
P63844	TTIFPILGGGER	5.704	7.9	3E-13	0.04		0	6
P63871	AQKPDVNITQIIGGTPVVK	8.623	9.3	1E-18	0.06		-2	10
P63871	NLLKAYGAELVLTGPSEAMKGAIK	8.242	6.122	0	0.176		2	9
P63871	VAKEEGILAGISSGAAIYAAIQKAK	8.348	6.087	0	0.116		2	10
P64173	MPIEVVYGFQQLKR	8.231	10.502	0	0.098		1	9
P64173	ERMPIEVVYGFQQLKR	8.334	6.699	0	0.114		2	9

P64173	THLQDATPIKLGQEISGWR	6.56	6.4	1E-08	0.1		1	8
P64173	IEHDTFGEIEVPADKYWGAQTER	4.232	9.9	2E-21	0.24		1	2
P64214	VVEVNEELEDSPFEVNESPYEK	3.721	12.6	7E-35	0.23		0	1
P64218	NHMLIAVTELR	6.657	9	9E-18	-0.36		0	9
P64218	DLNIAEGEAETTLR	3.745	8.2	2E-14	0.18		0	1
P64218	GLHYQALQVLHTYAK	8.489	9.163	0	0.104		0	10
P64218	SIGELFGDVPSDILLNR	3.875	10.9	1E-25	0.12		0	1
P64218	TKDEIDTFVEKAGELND	3.986	12	2E-31	0.19		2	1
P64218	YIPLTEKDKQEMLTIGAK	5.801	10.6	3E-24	0.04		2	8
P64218	SHRYIPLTEKDKQEMLTIGAK	8.103	8	1E-13	0.04		-2	9
P64218	QGIYDIAVQNIEHANYAKQFIK	6.416	11.6	2E-29	0.17		1	8
P64218	QGIYDIAVQNIEHANYAKQFIKK	7.996	9.626	0	0.168		2	9
P64218	SIGELFGDVPSDILLNRDLNIAEGEAETTLR	3.829	9.9	3E-21	0.27		1	1
P64218	SIGELFGDVPSDILLNRDLNIAEGEAETTLRR	4.084	7.2	6E-11	0.22		2	1
P64225	QTPLYQNYVDR	5.4	7.2	1E-11	0.04		0	5
P64225	TVGLELLEKGIAR	5.888	7.9	6E-14	0.04		1	7
P64225	QTPLYQNYVDRGAK	8.095	9.286	0	0.102		1	9
P64225	RTVGLELLEKGIAR	8.24	10.33	0	0.096		2	9
P64225	SSDLKQTPLYQNYVDR	5.541	10.6	5E-25	0.05		-2	5
P64225	SSDLKQTPLYQNYVDRGAK	8.072	7.6	5E-13	0.2		-2	9
P64225	HKEKFDVEVQNVSNQYGLAIQGP	6.177	11.1	6E-28	-0.37		2	8
P64228	NAFFIGR	9.011	6.4	4E-09	0.01		0	10
P64228	ELLLKGLEKLEYR	5.958	8	4E-14	-0.15		2	7
P64228	SLTITNVAGSTLSR	8.83	6.6	1E-09	0.01		0	10
P64228	KVADSSDFDGPVGIGHTR	5.239	11.1	2E-26	0.05		1	5
P64228	EADHTLLLHAGPEIAVASTK	5.177	9.073	0	0.122		0	4
P64228	GYDSAGIAVVNDNTTVFKEK	4.108	8.6	9E-16	0.15		1	1
P64228	AYTAQIAVLSILSQIVAKEHGR	8.534	6.8	1E-09	0.02		1	10
P64228	GYDSAGIAVVNDNTTVFKEKGR	4.528	12.9	3E-36	-0.01		2	3
P64230	HQLFLEPEGR	4.942	9.8	2E-21	0.02		0	4
P64230	YCPSIEDKFVR	5.675	7.9	6E-14	0.04		1	5
P64230	LKDGIIDLLR	5.854	8.2	9E-16	-0.29		1	6
P64230	TIDYSKTEIQPGDDVGR	4.09	9.1	2E-18	0.13		1	1
P64230	KIPEDLDYSKIDSLATEAR	4.335	8.6	2E-16	0.25		2	2
P64230	NTNEVYVQGLSTSLPEHVQR	5.367	10.1	2E-22	0.05		0	5
P64230	ISGVNPADISILLIYLEQGKLQR	5.991	6.1	3E-08	-0.03		1	7
P64235	ALDYLENFKK	6.063	7.8	2E-13	0.09		1	8
P64270	NFDAPTYATAK	5.586	7.332	0	0.092		0	6
P64270	AAQLSEIFANR	6.035	9.4	2E-19	0.03		0	8

P64270	IAETEKYPHVTYF	5.43	9.5	4E-20	0.04		-1	5
P64270	MSGGRNEEFKGER	5.916	9.6	1E-20	-0.36		-2	7
P64270	FMSGGRNEEFKGER	5.905	7.5	2E-12	0.04		-2	7
P64270	FNELGIGQFASVSGR	5.649	9.31	0	0.046		0	6
P64270	AKKPTALIILDGFANRESEHGNVAVK	8.5	10.066	0	0.152		-2	10
P64270	LGDLAPTLLDLLNVEQPEDMTGESLIKH	3.878	7.8	1E-13	0.18		1	1
P64270	ETGRLGDLAPTLLDLLNVEQPEDMTGESLIKH	4.026	7.1	2E-11	0.17		2	1
P64334	YASSFFGPFR	8.312	8.023	0	0.07		0	9
P64334	AGADMIITYFAKDICR	5.847	9.6	5E-20	0.04		1	6
P64334	RGLDEAGYYNIPIMSYGVK	5.659	8.6	4E-16	0.06		1	6
P64334	AGADMIITYFAKDICRYLDK	5.941	9.7	3E-20	-0.02		2	7
P64334	QISLNLLESELKEAYDLGIR	4.36	9.7	1E-20	0.11		-2	2
P64334	YASSFFGPFRDAADSAPSFGRK	5.625	6.6	5E-10	-0.35		2	6
P64334	TAISQVEAGADIIAPSNMMDGFVAEIR	3.832	7.8	3E-13	0.15		0	1
P64334	AIMFFGVPNSKDDIGTGAYIHDGVIQQATR	5.256	8.3	1E-14	0.07		1	5
P64360	MIELWPAIDLIGSTSVR	4.278	10	2E-21	0.1		0	2
P64418	YLGKEDYADAR	4.422	7.7	9E-13	0.1		-2	3
P64418	MNDLIINHIAELILPK	5.3	8.2	1E-14	0.04		0	5
P64418	SYLEILEMGGGILSTVNATR	4.429	7.3	1E-11	0.13		0	3
P65119	ILPGDKVTVEMSPYDLTR	4.43	9.757	0	0.134		1	3
P65177	YAGILAGGIGSR	8.312	7.476	0	0.058		-2	9
P65177	MIYAGILAGGIGSR	8.385	8.219	0	0.085		0	9
P65237	LVANLIETAGATR	5.977	7.8	6E-13	0.02		0	7
P65237	ELSVAGLIAQAIIR	5.625	9.2	2E-18	0.03		0	6
P65237	HFKDDPNINPEECVVVSPDHGGVTR	4.569	9.7	4E-20	-0.01		1	3
P65256	AQIEQIFVQTR	5.986	8.5	2E-15	0.03		0	7
P65256	HATPYSPTTVR	8.488	6.2	2E-08	-0.31		0	10
P65256	LLLSEAFDVAPR	4.333	6.3	2E-08	0.1		0	2
P65256	GATYYGVAMGLAR	8.496	7.8	4E-13	-0.15		0	10
P65256	FRLLLSEAFDVAPR	5.805	6.1	9E-08	0.04		1	7
P65256	TLLEQRPEGKAQIEQIFVQTR	5.931	6.3	2E-09	-0.23		2	7
P65286	ATYDRTLEFLR	5.998	7.7	7E-13	-0.29		1	8
P65286	YYTPLEFGKLR	8.074	7.778	0	0.093		1	9
P65286	ATYDRTLEFLRR	8.681	6.919	0	0.083		2	10
P65286	ATKNEEILRKPDWLK	8.491	8.973	0	0.094		-2	10
P65286	SSYHADEQVNEAAKEKQR	5.483	6.8	6E-10	0.06		2	5
P65330	MNVESFNLDTKVVAPFIR	6.539	6.2	5E-08	0.17		1	8
P65330	TKMNVESFNLDTKVVAPFIR	8.269	9.921	0	0.131		-2	9
P65422	SLLFGPFAGFSPK	8.58	8.274	0	0.075		0	10

P65602	TEIQKPYDLKGR	8.161	6.813	0	0.114		-2	9
P65636	HYWNIGIAADTDR	4.716	8.827	0	0.091		0	4
P65636	IAADTDRLVVPVK	5.878	6.3	1E-08	0.03		-2	7
P65636	SIFQISDEINELAVKAR	4.649	7.8	4E-13	0.06		1	4
P65636	AFEFRLPDIGEGIHGEIVK	4.439	6.3	2E-08	0.04		-2	3
P65636	AFEFRLPDIGEGIHGEIVKW	4.434	6.4	1E-08	0.13		-1	3
P65636	AFEFRLPDIGEGIHGEIVKWFVK	4.846	9.9	3E-21	0.07		-2	4
P65636	IAQKPIVKDGEIVAAPVLALSLSFDHR	6.786	10.8	3E-25	-0.04		2	9
P65636	GATCTISNIGSAGGQWFTPVINHPEVAILGIGR	6.75	11.6	3E-29	-0.06	::::Cys_CAM:.....	0	9
P65636	GHDDSSSKEEPAKEEAPAEQAPVATQTEEV DENR	3.959	9.2	1E-18	0.22		2	1
P65753	SFTMGDYVTR	5.444	9.4	4E-19	0.03		0	5
P65753	QIVPQITEALTK	5.617	10.117	0	0.075		0	6
P65753	IANFETAGPLCYR	5.957	9.3	6E-19	-0.34		0	7
P65753	AIISDSLLFKSPTCTQQDVK	5.909	9.6	2E-20	0.05		-2	7
P65753	IFGHKNPDTDAISSAIIAEFEQLRGNSGAK	5.512	6.5	6E-09	0.07		-2	5
P65753	ILVVGAEKDKVGEAFNVQLEDDMAFLSGV VSR	4.217	7.6	3E-12	0.19		2	2
P65896	FGDPEAQVLLSR	4.207	8.1	3E-14	0.1		0	2
P65896	GVIIADTIEAAR	4.301	8.5	2E-15	0.11		0	2
P65896	YNIPTADYKEVER	4.54	9.2	2E-18	0.01		1	3
P65896	KYNIPTADYKEVER	5.711	10.1	6E-22	0.04		2	6
P65896	MNVLVIGAGGREHALAY	6.534	9.1	3E-18	0.11		-1	8
P65896	QQNVDWVVIGPEQPLIDGLADILR	3.726	8.6	8E-16	0.31		0	1
P65896	AFDHDEGPNTGGMGAYCPVPHISDDVLK	4.234	8.6	5E-16	0.21		0	2
P65901	MVVAEAYR	5.734	6.6	1E-09	0.03		0	6
P65901	YVYNNPYEGGK	5.639	7.6	2E-12	0.04		0	6
P65901	EIYQQLIDSTK	4.092	8.3	5E-15	0.11		0	1
P65901	AIASTIDGEAR	4.265	6.3	1E-08	0.07		0	2
P65901	FGELDNKQNQR	5.695	8.8	7E-17	0.03		1	6
P65901	SKFIEPSVEEIKLEK	4.873	11.4	2E-28	0.05		-2	4
P65901	HYLYDQYDQQVGANTIIPGLQASVV R	6.124	7.9	4E-13	-0.14		1	8
P65901	HYLYDQYDQQVGANTIIPGLQASVV RVEGTNK	6.165	11.4	3E-28	-0.21		2	8
P65906	VLPYASITTR	8.614	8	1E-14	-0.39		0	10
P65906	QIAPAIEPSNGVDIIDAK	4	8.1	1E-14	0.17		0	1
P65906	VYGNPILTMVEGEVKFEGDK	4.345	6.8	4E-10	0.12		1	2
P65906	APFGIVGSETAFPLLYTHFVK	6.835	7.3	4E-12	-0.38		0	9
P65906	AIVAHCEDNSLIYGGAMHEGKR	6.081	12.1	2E-32	0.01	::::Cys_CAM:.....	1	5
P65906	GGFTTVCPMPNTRPVPDSVEHFEALQK	5.447	6.6	1E-09	0.11	::::Cys_CAM:.....	1	5
P66019	TYNYPQSR	8.26	7.561	0	0.081		0	9
P66019	KYSKEQADLQKTVDVYR	7.914	8.588	0	0.121		3	9

P66133	RADGQFVTGGSILYR	8.255	8.627	0	0.086		1	9
P66173	FQLATGQLEETAR	4.504	8.48	0	0.066		0	3
P66334	SGADVSGPIPLPTEKSVYTIIR	5.678	9.008	0	0.085		1	6
P66388	LMEISSYR	5.892	6.2	3E-08	0.03		0	7
P66388	ILEEANVSADTR	4	7.1	1E-10	0.09		0	1
P66388	VKDLTDDELGRIR	4.605	7.5	5E-12	0		2	3
P66440	WLNDGAKPTDTVHNILSK	6.599	11	4E-26	0.12		1	8
P66468	HMALLPYVKEEQ	4.935	8.4	3E-15	0.04		1	4
P66468	SRHMALLPYVKEEQ	6.486	8.4	3E-15	0.02		2	8
P66494	LGEFAPTR	5.878	6.8	5E-10	0.03		0	7
P66494	LGEFAPTRTF	5.902	6	3E-08	-0.36		-1	7
P66494	KGPFVDEHLMK	6.387	6.8	8E-10	0.09		1	8
P66494	LGEFAPTRTFK	8.876	6.8	6E-10	0.01		1	10
P66494	STIFPNFIGHTF	6.474	10.8	1E-25	0.01		-1	8
P66494	STIFPNFIGHTFAVY	6.471	11.7	8E-30	0.02		-1	8
P66494	RSTIFPNFIGHTFAVY	8.527	11.93	0	0.097		-1	10
P66494	STIFPNFIGHTFAVYDGR	6.473	11.3	6E-28	0.01		0	8
P66494	STIFPNFIGHTFAVYDGRK	8.317	11.655	0	0.108		1	9
P66494	HVPVYVTEDMVGHLGEFAPTR	5.644	13.3	4E-39	-0.09		1	6
P66544	KVDEAYNFLK	5.552	8.2	8E-15	0.02		1	6
P66544	SMPQALFVVDPR	5.435	8.2	1E-14	0.04		0	5
P66544	QLLEAGVHFGHQTR	6.632	11.7	9E-30	0.11		0	8
P66544	QVSEDGGQVLFVGTCK	5.627	8.3	6E-15	0.03		1	6
P66544	AVISMKQLLEAGVHFGHQTR	8.682	7.144	0	0.111		-2	10
P66544	QAQESVKSEAERAGQFYINQR	5.815	6.1	4E-08	0.02		2	7
P66544	KLNIPIVGIVDTNCDPDEIDYVIPANDDAIR	3.766	10.1	3E-22	0.22		1	1
P66563	YLYGMTER	5.646	6.3	6E-09	0.03		0	6
P66563	LSEYGLQLR	5.924	7.4	5E-12	0.02		0	6
P66579	SLGSNTPINMVR	8.83	8.7	2E-16	0		0	10
P66579	ARREEETKEFEER	4.612	7.8	3E-13	-0.03		-2	3
P66579	AVLELAGITDILSK	4.229	9.2	1E-18	0.09		0	2
P66579	ATIDGLQNLKNAEDVAK	4.442	7	2E-10	0.16		1	3
P66579	ATIDGLQNLKNAEDVAKLR	6.098	10.8	3E-25	-0.02		2	8
P66579	ATIDGLQNLKNAEDVAKLRGK	8.491	8.866	0	0.114		3	10
P66579	AVLELAGITDILSKSLGSNTPINMVR	6.046	9.8	1E-20	-0.03		1	7
P66616	ILYSAFDLVEQR	4.302	9.2	2E-18	0.11		0	2
P66616	MAEANKAFAHYRW	8.271	9.936	0	0.075		2	9
P66616	VGGSNYQVPVEVRPER	6.056	6.8	4E-10	0.13		1	8
P66616	VGGSNYQVPVEVRPERR	8.612	8.277	0	0.109		2	10

P66630	TMTDPIADMLTR	4.007	9.5	2E-19	0.18		-2	1
P66630	KRNVGGEIIAYVW	8.189	8.571	0	0.086		2	9
P66630	NVEYVEDDKQGVLR	4.239	9	3E-17	0.11		1	2
P66630	TMTDPIADMLTRVR	5.623	8.698	0	0.079		-2	6
P66646	LVPGEGNITVNNR	5.943	6.2	3E-08	0.03		0	7
P66646	ALLEADPEYRGSLKR	6.175	7.8	3E-13	0.02		2	8
P66646	GNYDVLVNVHGGGFTGQAQAIR	6.791	10.8	2E-25	-0.14		0	9
P66706	FVVEPLER	4.499	6.1	5E-08	0		0	3
P66706	FGKFVVEPLER	5.892	8.1	5E-14	0.03		1	7
P66706	YKLEDLGLGLRKED	4.724	9.8	7E-21	0.04		3	4
P66706	KSLEEVKYKLEDLGLGLR	5.777	9.3	9E-19	0.05		3	7
P66706	AGINSVQELADKSEADMMKVR	4.704	10.7	6E-25	0.03		2	4
P66706	GYALAEQNNTSDLPIGVIPVDSLYSPVER	3.851	7.5	4E-12	0.22		0	1
P66726	EIDEQPETELLSEYHSFKPVGR	4.306	8.1	3E-14	0.19		1	2
P66726	AREIDEQPETELLSEYHSFKPVGR	4.615	7.2	3E-11	0.05		2	4
P66767	KIIVDTYGGYAR	8.055	6.987	0	0.08		1	9
P66919	TVNRFKDFFNN	8.409	8.198	0	0.066		2	10
P67011	SLSFIKDYIK	8.149	6.767	0	0.094		1	9
P67011	TNDIENVGFTAR	4.249	7.7	5E-13	0.09		0	2
P67011	SLSFIKDYIKNL	8.09	10.189	0	0.106		2	9
P67011	LTQLQDEEKALLKQLEQR	4.788	8.1	6E-14	0.05		2	4
P67011	FDFSHFGPMTNDEIDQVER	4.041	8.7	1E-16	0.25		0	1
P67011	TNYETDLFMPIMNEIEKVS GK	4.354	10.2	1E-22	0.18		1	2
P67011	SDDQVVEKLTQLQDEEKALLKQLEQR	4.333	8.7	3E-16	0.16		3	2
P67015	QLEELSLR	4.408	6.5	3E-09	0.07		0	3
P67015	GVEINGAFPR	5.9	7	8E-11	-0.37		0	7
P67015	YVAAHHPFTSPK	8.337	7.1	2E-11	-0.34		0	9
P67015	EVKGVEINGAFPR	5.834	7.3	9E-12	0.03		1	7
P67015	QLLMISGFDKYYQIVK	8.009	7.98	0	0.131		1	9
P67015	TASATCLLTNAPGEVSDKQLEELSLR	4.333	10.4	7E-24	0.19		1	2
P67015	LGTAPEEAEANAYDIVLNGYELGGGSIR	3.872	7.2	1E-11	0.18		0	1
P67047	ALSDPEFNEQYKEQMK	4.302	7.8	3E-13	0.13		1	2
P67047	ALSDPEFNEQYKEQMKQFK	4.786	9.5	1E-19	0.03		2	4
P67047	ALSDPEFNEQYKEQMKQFKQR	6.252	7.9	2E-13	0.01		3	8
P67182	SGEPNPESNQALR	4.432	8.349	0	0.03		0	3
P67396	AVEYFAKLPQDITER	4.601	7.5	0	0.114		1	4
P67396	AGLGMTDGILSLVPAAR	5.798	8	4E-14	0.03		0	6
P67396	QIIVVDPMLATGASAIEAITSLLKR	8.1	7.306	0	0.081		2	9
P67417	IAWLGYGER	5.931	8	7E-14	0.02		0	7

P67417	HVELMLEFQKR	6.164	9.4	2E-19	0.02		1	8
P67420	MIKGEETSHTPVWFMR	6.543	8.9	5E-17	0.1		1	8
P67420	TLQGNLDPSILLAPWNVIEER	4.068	9.4	1E-19	0.16		0	1
P67509	ATPQWFASISK	8.941	8.1	2E-14	0.02		0	10
P67509	VVEVDQALLDKWR	4.439	9.592	0	0.113		1	3
P67509	CWNYSEDLGAVDELTHLCPR	4.222	10.9	4E-26	0.14	:Cys_CAM:.....Cys_CAM::	0	2
P67509	GDFNDPYITLKPEYEAQIR	4.214	10.8	7E-26	0.24		1	2
P67509	TDFPMRGGLPNKEPQIQEKWDAEDQYHK	4.907	6.3	2E-09	0.03		3	4
P67509	YKTMQGFYAPYVPGWDTHGLPIEQALTKK	7.99	6.889	0	0.141		2	9
P67513	HINSGELDGLENEAAITK	4.285	9.7	8E-21	0.15		0	2
P67513	WQDYWDENKTFKTNDNLGQK	4.566	6.9	3E-10	-0		2	3
P67513	SKGNVINPDDIVQSHGADTLR	5.264	9.7	2E-20	0.04		1	5
P67513	ITEYADQLLADLDDLDWPESLKDMQR	3.709	6	6E-08	0.21		1	1
P67513	FYALDMFPYPSGAGLHVGHPEGYTATDIISR	5.186	6.11	0	0.232		0	4
P67572	NHGTEFLMDHR	6.047	7.5	4E-12	-0.39		0	5
P67572	TVAWISGVEHVR	6.556	7.7	1E-12	0.08		0	8
P67572	VKEHGLDEEAYSYY	4.321	7.6	1E-12	0.12		-1	2
P67572	YGSVPHCGFGLGLER	6.449	6.4	7E-09	0.02	Cys_CAM:.....	0	8
P67572	TVAWISGVEHVRETAPFPR	6.56	8.3	7E-15	-0.19		1	9
P67572	QAKDHLNQDVTIGAWLTNKR	8.146	10.901	0	0.106		2	9
P67579	HVVEQVFER	4.911	8.4	2E-15	0.02		0	4
P67579	HKHVVEQVFER	6.668	8.9	1E-17	0.01		1	8
P67579	NEMINNFIKPGLADLAVSR	5.832	6.9	1E-10	0.07		1	7
P67579	KNEMINNFIKPGLADLAVSR	8.158	11.219	0	0.109		2	9
P67610	FTDRFELF	4.39	8.4	1E-15	0.08		-1	2
P67610	DVLLFPYMR	5.627	6.8	2E-10	0.03		0	6
P67610	SEEMNDQMLVR	3.996	8.9	1E-17	0.09		-2	1
P67610	LQELYDLGIDPFGSKFDR	4.114	8.6	2E-16	0.18		1	1
P67610	SLRPLPDKFHGLQDIEQR	6.485	6.4	2E-09	0.03		2	8
P67725	MKEQLNQLSAYQPGLSPR	8.231	10.19	0	0.084		1	9
P68789	AREFSLEKTR	8.665	6	8E-08	-0		2	10
P68789	KCDPVILEPMMK	5.635	6.7	1E-09	0.03		1	6
P68789	SNTQGRGTYTMY	8.286	6.2	0	0.093		-1	9
P68789	PLSEMFGYATSLR	6.375	7.5	3E-12	-0.09		-2	7
P68789	VMTDPYVGKLTFFR	8.457	8.366	0	0.1		1	10
P68789	GTYTMYFDHYAEVPK	5.287	8.8	9E-17	0.07		0	5
P68789	LYDGSYHDVDSSEMAFK	4.07	10.5	5E-24	0.12		0	1
P68789	YLGDEEISVSELKEAIR	4.172	11	4E-26	0.22		1	1
P68789	NIGIMAHIDAGKTTTTER	6.659	11	3E-26	0.02		1	8

P68789	AKLYDGSYHDVDSSEMAFK	4.545	6.9	2E-10	0		1	3
P68789	VTIEMPEEYMGDIMGDVTSR	3.702	10.7	3E-25	0.14		0	1
P68789	QATTNVEFYPVLCGTAFKNK	7.488	7.4	7E-12	-0.2	Cys_CAM:.....	1	9
P68789	VTIEMPEEYMGDIMGDVTSRR	4.08	8.4	2E-15	0.16		1	1
P68789	GNAQVVNAYVPLSEMFGYATSLR	5.998	12	2E-31	0.03		0	7
P68789	VLDGAVTVLDAQSGVEPQTETVWR	3.8	9.6	3E-20	0.27		0	1
P68789	GTYTMYFDHYAEVPKSIAEDIIKK	5.483	6.2	3E-08	0.06		2	5
P68789	YTNDLGTEIEEIEIPEDHLDRAEEAR	3.911	7	6E-11	0.31		1	1
P68789	GVQLMLDAVIDYLPSPLDVKPIIGHR	5.294	8.5	6E-16	0.07		1	5
P68789	GNAQVVNAYVPLSEMFGYATSLRSNTQGR	8.496	8.9	0	0.086		1	10
P68789	KNKGVQLMLDAVIDYLPSPLDVKPIIGHR	8.019	9.2	5E-19	-0.21		-2	9
P68789	QATTNVEFYPVLCGTAFK	5.608	6.8	6E-10	0.06	Cys_CAM:.....	0	5
P68789	EFNVECNVGAPMVSYSR	4.326	9.8	6E-21	0.21	Cys_CAM:.....	0	2
P99062	GFLLDGFPR	5.784	6.4	9E-09	0.03		0	7
P99062	KGFLLDGFPR	8.424	6.217	0	0.074		1	10
P99062	FPIPHISTGDMFR	6.524	9.4	3E-19	0.12		0	8
P99062	KFPIPHISTGDMFR	8.476	9.661	0	0.099		1	10
P99062	KAIKEETELGKEAK	5.854	8.8	5E-17	-0.34		3	7
P99062	QSKPILDFYDQKGVLK	8.004	9.232	0	0.105		2	9
P99062	ISEDDAKKGFLLDGFPR	4.564	8.8	9E-17	-0		2	3
P99062	SYMDRGELVPDEVTVGIVKER	4.398	8.2	3E-14	0.27		2	2
P99063	AKETLEF	4.552	6.454	0	0.044		1	3
P99063	AILSLEAPIGR	6.011	7.5	5E-12	0.03		0	8
P99063	VVIPSGPYDAK	5.75	7.5	2E-12	0.02		0	6
P99063	SNDPVVYLEHMK	5.241	10.159	0	0.103		0	4
P99063	VTEGLQKEFGEDR	4.297	8.7	2E-16	0.09		1	2
P99063	AQMTMVQAINDALK	5.827	9.9	2E-21	0.03		-2	7
P99063	QAGVGAAVVAELSER	4.524	10.2	1E-22	0		0	3
P99063	FVFEVFDAIAGQIAR	4.282	11.1	2E-27	0.12		-2	2
P99063	SNDPVVYLEHMKLYR	6.478	9.2	1E-18	-0.16		1	9
P99063	SFREEVPEEEYTIDIGK	4.053	9	1E-17	0.15		1	1
P99063	TVQPIDVDTIVASVEKTGR	4.497	9.6	6E-20	0.03		1	3
P99063	VVIPSGPYDAKGLLISSIR	8.457	8.189	0	0.11		1	10
P99063	SFREEVPEEEYTIDIGKANVK	4.354	11.5	5E-29	0.22		2	2
P99063	SFREEVPEEEYTIDIGKANVKK	4.651	14.4	3E-45	0.04		3	4
P99063	AVVVQEAQRQAGVGAAVVAELSER	4.783	7.7	1E-12	0.05		1	4
P99063	QAGVGAAVVAELSERAILSLEAPIGR	4.754	6.7	3E-09	0.09		1	4
P99063	VAAADTIYPFTQAENVWLPNKNDIIEK	4.278	6.7	2E-09	0.17		1	2
P99063	SPFGGGVHTPELHADNLEGILAQSPGLK	5.249	12.855	0	0.293		0	4

P99063	VAAADTIYPFTQAENVWLPNKNNDIEKAKETLEF	4.355	7.8	5E-13	0.11		3	2
P99064	IIPLEVVVR	5.962	7	5E-11	-0.04		0	7
P99064	IWDKATNANFDKDVYR	5.952	11.9	2E-31	0.03		2	7
P99064	NNTGSLIETYQIFLNKLEDLK	4.613	11.551	0	0.138		1	4
P99064	QLSETEQLVKPVKIIPLEVVVR	5.832	10.9	3E-26	0.34		2	7
P99064	LNNQITSIIFKYLQENGIESHFIK	6.779	6.5	1E-09	0.01		1	9
P99064	IFSTNQENELRVEYKDEVTAGNGAK	4.501	8.5	6E-16	-0.02		2	3
P99064	RIFSTNQENELRVEYKDEVTAGNGAK	4.918	6.4	4E-09	0.04		3	4
P99065	ALDDDEIIELVDKSFGMVR	3.921	11.9	9E-31	0.15		1	1
P99065	SEESNSHLGHVFNDGPKESGGLR	5.312	11.7	8E-30	0.06		1	5
P99065	TEVRSEESNSHLGHVFNDGPKESGGLR	5.382	6.9	3E-10	0.06		2	5
P99065	GIYVDKISGKPLFTSEEKFHSECGWPSFSK	6.76	7	1E-10	-0.37	Cys_CAM:.....	3	9
P99066	AGEKVEPAMIENR	4.677	8.6	6E-16	-0.01		1	4
P99066	AGEKVEPAMIENRR	6.21	6.4	1E-08	0.01		2	8
P99066	TFRAGEKVEPAMIENR	5.948	6.8	1E-09	0.04		2	7
P99066	TVELTVTETEPGIKGDTATGATK	4.309	8.3	2E-14	0.17		1	2
P99067	VLNNQFGIVNGLMTTVHAITNDQK	6.763	8.9	1E-17	-0.34		0	9
P99069	IVIALGGNAIQTK	8.889	7.1	2E-11	0.01		0	10
P99069	AMQNLKPLFDSPAR	8.667	7.964	0	0.07		1	10
P99069	VVASPLPQSILEHQLIR	6.767	6.6	2E-10	-0.33		0	9
P99069	KVVASPLPQSILEHQLIR	8.476	8.297	0	0.118		1	10
P99069	IVISHGNGPQIGSLLIQQAQ	8.9	10	2E-22	0.04		0	10
P99069	VIITNLEQAYEALIGNKGTIHM	6.085	7.5	8E-13	0		1	5
P99070	VMVQGITGSTALFHTK	8.881	10.2	1E-22	0.02		0	10
P99070	LVGPNCPGVITADECKIGIMPGYIHKK	7.662	8.1	2E-14	-0.21	Cys_CAM:.....Cys_CAM:.....	2	9
P99070	AFNEDDETKAVVMIGEIGGTAEAAAAEWIK	3.884	6.9	1E-10	0.29		1	1
P99070	TAATPSEIGSTLIEAAKEAGIYESLLTVNK	4.456	13.1	1E-37	0.21		1	3
P99070	LVGPNCPGVITADECK	4.294	11.3	4E-28	0.1	Cys_CAM:.....Cys_CAM::	0	2
P99071	HKDVVELR	6.141	6.7	6E-10	0.01		1	8
P99071	IAFNINIPK	8.889	6	4E-08	0.03		0	10
P99071	NFDDNALFR	4.024	8.8	2E-17	0.09		-2	1
P99071	INFDDNALFR	4.08	7.1	2E-11	0.08		0	1
P99071	SLSEVETYAK	4.484	8.4	8E-16	0.07		0	3
P99071	EYYVGFVIDR	4.162	8.8	5E-17	0.12		0	1
P99071	SMGVAVPEGR	5.62	7.4	3E-12	0.03		0	6
P99071	LYIEEGCAIQK	4.456	7.1	2E-11	0.09		0	3
P99071	VAFTAEEAVEK	4.256	7.4	2E-12	0.08		0	2
P99071	TLVTHQTGPEGK	6.556	7.9	4E-14	0.01		0	8
P99071	RLYIEEGCAIQK	5.77	7.2	1E-11	0.03		1	7

P99071	GIFVNIFGGIMK	8.9	7.4	3E-12	0.01		0	10
P99071	NIHEYQGKEIFR	6.661	8.3	1E-15	0.01		-2	8
P99071	VAFTAEEAVEKAK	4.767	8.5	5E-16	0.03		1	4
P99071	MNIHEYQGKEIFR	6.545	6.7	1E-10	0.39	:Oxidation_M:.....	1	9
P99071	EIFRSMGVAVPEGR	5.858	7.3	4E-12	0.02		1	7
P99071	ETIDPVIGLSPFQAR	4.073	10.2	5E-23	0.19		0	1
P99071	SLSEVETYAKELLGK	4.711	9.6	2E-20	0.03		1	4
P99071	TLVTHQGTGPEGKEIK	6.562	7.2	9E-12	0.01		1	8
P99071	ETIDPVIGLSPFQARR	5.743	7.7	2E-13	-0.16		1	6
P99071	TLVTHQGTGPEGKEIKR	8.269	10.685	0	0.113		2	9
P99071	ELNSDVYVVKAIHAGGR	6.638	7.4	2E-12	0.29		1	9
P99071	DSGLAIEPAATMAEGAQK	3.878	10.1	1E-22	0.14		0	1
P99071	IFKETIDPVIGLSPFQAR	5.974	10.2	2E-23	0.03		1	7
P99071	IFKETIDPVIGLSPFQARR	8.616	8.438	0	0.114		2	10
P99071	VAFTAEEAVEKAKELNSDVY	4.203	9.9	3E-22	0.28		-1	2
P99071	ELNSDVYVVKAIHAGGRGK	8.329	11.332	0	0.115		2	9
P99071	AKELNSDVYVVKAIHAGGR	8.44	8.718	0	0.115		2	10
P99071	ILKDSEGLAIEPAATMAEGAQK	4.62	11.6	8E-30	-0		1	4
P99071	TPEKIFKETIDPVIGLSPFQAR	5.866	14.5	9E-47	0.04		2	6
P99071	KILKDSEGLAIEPAATMAEGAQK	5.77	7.2	7E-12	0.03		2	7
P99071	VAFTAEEAVEKAKELNSDVYVVK	4.514	8.8	8E-18	-0.03		2	3
P99071	AGGVKIAKSLSEVETYAKELLGK	8.351	6.515	0	0.143		3	9
P99071	TPEKIFKETIDPVIGLSPFQARR	8.242	8.078	0	0.127		3	9
P99071	ILKDSEGLAIEPAATMAEGAQKIVK	6.16	11.8	3E-31	-0.24		2	8
P99071	VAFTAEEAVEKAKELNSDVYVVKAIHAGGR	5.601	6.9	3E-11	0.06		3	5
P99072	GLGIQPDIVVR	5.788	8.2	8E-15	0.04		0	6
P99072	SFIEASLKYQQNK	8.149	6.472	0	0.104		1	9
P99072	SDLGRENVMYVHCTLLPYIK	6.459	7.8	8E-14	0.01		1	8
P99072	RGDYLGGTVQVIPHITNEIKER	6.439	7.2	1E-11	0		2	9
P99072	LGLYPCSIKEGTLAQDVYGKAEIEERHR	5.576	7.3	5E-12	0.12		3	5
P99074	TLQPGLDLVGKI	5.565	7.2	2E-11	0.04		1	5
P99074	KDQFKEVTQEDLK	4.641	9.9	2E-21	-0		2	3
P99074	NFDVLDEATGLAQR	3.938	9.4	3E-19	0.16		0	1
P99074	AWHDHSDAISKITY	6.066	9.8	3E-21	0.02		-1	5
P99074	ITYTMIGDPSQTITR	5.69	10.129	0	0.087		0	6
P99074	NPGEVCPAKWEEGAK	4.654	6.6	2E-09	-0		1	3
P99074	KNPGEVCPAKWEEGAK	5.776	7.9	5E-14	0.05	Cys_CAM:.....	2	7
P99074	LGVNVFSVSTDTHFVHK	6.953	10.4	5E-24	-0.1		0	9
P99074	SLINKEILPFTAQAFDPK	5.688	9.158	0	0.104		-2	6

P99074	EILPFTAQAFDPKKDQFK	5.793	10.4	1E-23	0.05		2	7
P99074	TAQAFDPKKDQFKEVTQEDLK	4.73	7.2	2E-11	0.04		-2	4
P99074	AAQYVRKNPGEVCPAKWEEGAK	7.891	6.3	1E-08	0.19		3	9
P99074	GTFIIDPDGVVQASEINADGIGR	3.737	6.3	8E-09	0.18		0	1
P99074	SLINKEILPFTAQAFDPKKDQFK	8.06	14.416	0	0.134		-2	9
P99074	AWHDHSDAISKITMTMIGDPSQTITR	6.07	9.6	3E-20	0.11		1	5
P99075	AIPFGTAK	8.941	6.8	4E-10	0		0	10
P99075	IKEFGTSNR	8.618	6.4	5E-09	-0.22		1	9
P99075	YMSGFYTIVK	8.144	6.747	0	0.077		0	9
P99075	INVNTENQIASAK	5.976	9	1E-17	0.04		0	7
P99075	DVLNNDKEVYDPR	3.984	10	1E-21	0.12		1	1
P99075	PLVSMKEMLIDAK	6.43	9.4	4E-19	0.05		-2	8
P99075	DVLNNDKEVYDPRK	4.441	10.4	1E-23	0.11		2	3
P99075	AVRDVLNNDKEVYDPR	4.53	11.2	4E-27	-0.01		2	3
P99075	AIPFGTAKINVNTENQIASAK	8.623	6.1	4E-08	0.01		1	10
P99075	TGIDALAPALGSHVHPYKGEPK	6.558	11.7	2E-30	-0.35		1	9
P99075	EMEEIGLSTGLPLVLHGGTGIPTKDIQK	4.672	6.511	0	0.282		1	4
P99075	LGFKEMEEIGLSTGLPLVLHGGTGIPTK	5.518	11.9	6E-31	0.06		1	5
P99075	CKEIDAGFTSVMIDASHSPFEENVATTKK	4.822	8.5	2E-15	0.02		2	4
P99075	LGFKEMEEIGLSTGLPLVLHGGTGIPTKDIQK	5.541	8.5	9E-16	0.05		2	5
P99075	NINNLEFTQAILEASQEENAPVILGVSEGAAR	3.925	7.9	2E-13	0.18		-2	1
P99075	ADPKECQELVEKTGIDALAPALGSHVHPYKGEPK	4.911	6.3	2E-08	0.01		-2	4
P99076	DTHFVTF	4.996	6.362	0	0.062		-1	4
P99076	GVVNFVPGDPK	5.753	6.6	2E-09	0.02		0	7
P99076	ATKQDVEDAFK	4.516	10.4	3E-23	-0		1	3
P99076	SAVVQEGQNFLK	5.673	8.091	0	0.069		0	6
P99076	LMEILEEAGLPK	4.212	7.9	3E-13	0.18		0	2
P99076	GYFVEPTIISGLK	5.999	9.5	6E-20	-0.36		0	7
P99076	SAVVQEGQNFLKR	8.308	8.996	0	0.061		1	9
P99076	TWSANDRAELMLR	5.791	6.4	1E-08	0.04		1	7
P99076	TGSPDYLLHFLEQK	5.264	8.1	4E-14	0.04		0	5
P99076	SMMDLAQGKPVLDLDR	5.588	8.842	0	0.074		1	6
P99076	AIVHKDVYDEVLEK	4.726	9.2	3E-18	0.02		1	4
P99076	AVNEFDVGNLYLNR	4.268	8.6	4E-16	0.17		0	2
P99076	IMQEEIFGPVVGFBK	4.482	8.8	1E-16	0.03		0	3
P99076	SINPADTSQVIANASK	5.418	11	5E-26	0.05		0	5
P99076	DRIMQEEIFGPVVGFBK	4.557	7.9	4E-13	0.03		1	3
P99076	AIVHKDVYDEVLEKSIK	5.507	9.3	1E-18	0.04		2	5
P99076	IYERSAVVQEGQNFLKR	8.476	10.842	0	0.078		2	10

P99076	SKDRIMQEEIFGPVVGVFK	5.852	10.4	3E-23	0.04		2	7
P99076	SINPADTSQVIANASKATK	8.267	10.737	0	0.103		1	9
P99076	ELTLGNTVDNTYMGPVINKK	5.731	11.6	7E-29	0.04		1	6
P99076	TGSPDYLLHFLEQKVVSEMF	4.63	9.1	1E-17	0.05		1	4
P99076	AIVHKDVYDEVLEKSIKLTk	6.84	12.9	9E-37	-0.28		3	9
P99076	ALKDVEKELGQDIPLVINGEK	4.391	10	3E-21	0.03		2	3
P99076	EIGDYLVDHKDTHFVTFTGSR	5.123	9.5	3E-19	0.07		1	4
P99076	ATKQDVEDAFKAANEAYKSWK	6.239	15.2	4E-50	-0.23		3	8
P99076	NYIEIGKEEGKLEQGGGTDDSK	4.217	11.1	1E-26	0.14		2	2
P99076	KALKDVEKELGQDIPLVINGEK	4.824	11.6	4E-29	0.04		3	4
P99076	VVEFKNEPGYDFSVQENVDMFK	4.072	9.9	2E-21	0.29		-2	1
P99076	VVEFKNEPGYDFSVQENVDMFKK	4.405	14.8	1E-47	0.21		-2	3
P99076	LTkELTLGNTVDNTYMGPVINKK	8.356	12.691	0	0.127		2	9
P99076	SMMDLAQGKPVLDREGEHNKYFYK	6.483	11.1	1E-26	0.06		3	8
P99076	EAGKPWDEAVGDAAEGIDFIEYYAR	3.836	10.6	2E-24	0.17		-2	1
P99076	VYEAGKPWDEAVGDAAEGIDFIEYYAR	3.884	6.7	7E-10	0.19		-2	1
P99076	GVVNFVPGDPKEIGDYLVDHKDTHFVTFTGSR	5.249	6.8	2E-09	0.04		2	4
P99076	NYIEIGKEEGKLEQGGGTDDSKGYFVEPTIISGLK	4.364	8.5	2E-15	0.25		3	3
P99077	AKDIEGNDIQLR	4.417	7.2	2E-11	0.09		1	3
P99077	EFLVNSQDEEIAKR	4.26	7.2	2E-11	0.12		1	2
P99079	TLSILVAHDLQR	6.553	10.1	2E-22	0.01		0	8
P99079	NTIPHTFLHLIR	9.04	8.343	0	-0.13		0	10
P99080	QINVPGFR	8.764	6.6	1E-09	0		0	10
P99080	MVSEFAQR	5.656	6.178	0	0.023		0	6
P99080	QFNISVEDIK	4.313	8.3	5E-15	0.12		0	2
P99080	VIDLLRDNak	5.83	7	8E-11	0.02		1	7
P99080	IQKVIDLLRDNak	8.573	8.651	0	0.079		2	10
P99080	NTLGNTDIIKNDVRIQK	8.445	7.755	0	0.115		2	10
P99080	VIDLLRDNakFVEGTKED	4.388	8.6	2E-16	0.19		3	2
P99080	EGNEGLLTVTVPAEKVNK	4.59	8.6	2E-16	0.01		1	3
P99080	ATDNTTIDIPEAMVNTELDK	3.672	9.4	1E-19	0.24		0	1
P99080	LAEQKATDAENVEKEEAITK	4.338	12.6	7E-35	0.14		2	2
P99080	QFNISVEDIKNTLGNTDIIKNDVR	4.552	9	7E-18	0.07		2	3
P99080	TATWEKKEGNEGLLTVTVPAEKVNK	6.015	14.7	2E-47	0.01		-2	8
P99080	QFNISVEDIKNTLGNTDIIKNDVRIQK	5.716	9	5E-18	0.03		3	6
P99080	EVPELTDEIANELDAEANTVDEYKENLR	3.711	10.7	3E-25	0.17		1	1
P99080	FKEVPELTDEIANELDAEANTVDEYKENLR	3.944	9.9	1E-21	0.2		2	1
P99080	TNLTlTAIAEAekIEATDEDIDKELEKMSK	4.22	9.6	1E-20	0.13		3	2
P99082	ALAFDGEIR	4.265	6.1	4E-08	0.07		0	2

P99082	HYTWPTASAAMGR	8.488	6.124	0	0.073		0	10
P99082	AYAALTTETVQEAQTR	4.48	8.3	5E-15	0.01		0	3
P99082	AYVDHPQTHFPLNEQGKLDVR	6.083	7.1	7E-11	0.01		1	8
P99083	YISEAMEK	4.484	6.5	3E-09	-0.01		0	3
P99083	LRIEDALNSTR	5.952	7.2	3E-11	0.02		1	7
P99083	NVTSGANPVGLR	9.011	7.5	2E-12	-0.01		0	10
P99083	VGAASETELKER	4.723	7	1E-10	-0.02		1	4
P99083	KLRIEDALNSTR	8.423	7.325	0	0.079		2	10
P99083	SQIEETESDFDREK	3.986	6	6E-08	0.12		1	1
P99083	QIAENAGLEGSVIVER	4.191	7	8E-11	0.13		0	2
P99083	GTFTAVAVKAPGFGDR	8.626	7.713	0	0.08		1	10
P99083	GVDQLANAVKVTIGPK	8.583	9.2	2E-18	0.04		1	10
P99083	SQIEETESDFDREKLQER	4.171	8.2	8E-15	0.14		2	1
P99083	QIAENAGLEGSVIVERLK	4.695	8.797	0	0.124		1	4
P99083	LAGGVAVIKVGAASETELKER	6.177	6.2	2E-08	-0.01		2	8
P99083	VENKNEIAQVGAISAADEEIGR	4.149	7.7	7E-13	0.16		1	1
P99083	VSQLKSQIEETESDFDREKLQER	4.43	7.9	1E-13	-0.01		3	3
P99083	ALTAPVRQIAENAGLEGSVIVER	4.76	6.7	1E-09	0.04		1	4
P99083	LAKLAGGVAVIKVGAASETELKER	8.368	9.801	0	0.093		3	10
P99083	ALTAPVRQIAENAGLEGSVIVERLK	6.247	9.1	3E-18	0.06		2	8
P99083	NAEPGVGFNAATNEWVNMLEAGIVDPTKVTR	4.323	8.8	6E-17	0.16		1	2
P99083	LKNAEPGVGFNAATNEWVNMLEAGIVDPTKVTR	4.82	7.1	9E-11	0.07		2	4
P99083	VAVEALHENSQKVENKNEIAQVGAISAADEEIGR	4.463	10.2	8E-23	-0.03		2	3
P99084	GVEIVTEAMAK	4.405	7.8	1E-13	0.09		0	3
P99084	ALSLDDTNGFVK	4.116	9.6	1E-20	0.09		0	1
P99084	GEAYFVDNNSLR	4.166	7.8	1E-13	0.08		0	1
P99084	TIEADYVLVTVGR	4.237	9.3	2E-19	0.13		0	2
P99084	EKGVEIVTEAMAK	4.572	8.7	6E-17	0.01		1	3
P99084	FADRGILLEVDKQSR	5.796	9.5	7E-20	0.03		2	6
P99084	RPNTDELGLEELGVK	4.378	9	6E-18	0.16		1	2
P99084	GNLGGVCLNVGCIPSK	7.676	10.9	2E-26	0.02	:::::Cys_CAM::::Cys_CAM::::	0	9
P99084	SAEETDNGVKVTYEAK	4.313	8.7	5E-17	0.14		1	2
P99084	NAIIATGSRPIEIPNFK	8.756	10.945	0	0.11		1	10
P99084	VNIVKGEAYFVDNNSLR	5.981	10.6	3E-25	-0.35		1	7
P99084	SAEETDNGVKVTYEAKGEEK	4.316	12.9	9E-37	0.16		2	2
P99084	GNKVNIVKGEAYFVDNNSLR	8.392	13.492	0	0.085		2	10
P99084	TSISNIYAIGDIVPGLPLAHK	6.553	11.8	1E-30	0.14		0	8
P99084	ANFGSEVTILEGAKDILGGFEK	4.325	8.8	1E-17	0.13		-2	2
P99084	GNKVNIVKGEAYFVDNNSLRVMDEK	6.17	6.8	2E-10	-0.05		3	8

P99084	VVGDFPIETDTIVIGAGPGGYVAAIR	3.93	11.3	2E-28	0.17		-2	1
P99084	TSISNIYAIGDIVPGLPLAHKASYEAK	6.558	11.1	4E-27	-0.02		1	8
P99084	TIEADYVLVTVGRRPNTDELGLEELGVK	4.309	6.1	1E-08	0.18		2	2
P99084	LTGGVEGLLKGNKVNIVKGEAYFVDNNSLR	8.306	6.012	0	0.148		3	9
P99084	VMDEKSAQTYNFKNAIIATGSRPIEIPNFK	8.348	10.591	0	0.124		3	9
P99086	VLTDILPAIDNIER	3.952	9.1	8E-18	0.15		0	1
P99086	IQKENEINKTYQAQR	8.383	7.505	0	0.124		2	9
P99086	ALQIEGDDETFKSLQK	4.306	8.3	1E-14	0.15		1	2
P99086	INELQQLADENEEKYLR	4.2	10.7	1E-24	0.24		1	1
P99087	STVDVNFEGLK	4.246	8.7	9E-17	0.11		0	2
P99087	IISTPGVAYLTR	8.635	7.265	0	0.072		-2	10
P99087	GVANQELTPELAFK	4.477	6.9	0	0.091		0	3
P99087	LGIISTPGVAYLTR	8.624	9.9	1E-21	-0.19		0	10
P99087	GVANQELTPELAFKLGR	6.117	8.8	4E-17	-0.17		1	8
P99087	NQELNNDMIVSTVMSNLGFYK	4.246	11.1	4E-27	0.15		0	2
P99087	GKYFGTDGVRGVANQELTPELAFK	6.152	9.5	8E-20	-0.25		-2	8
P99087	GKYFGTDGVRGVANQELTPELAFKLGR	8.392	12.147	0	0.126		-2	9
P99087	VMVEAATDEDAERFAQQIADVVDKMGDLK	3.984	7	1E-10	0.18		2	1
P99088	PIITDVYAR	6.203	8.8	7E-17	0.01		-2	8
P99088	WGTEIFHNLK	6.601	7.2	3E-11	-0.3		0	9
P99088	AAADLLGQPLYK	5.781	10.4	4E-24	-0.32		0	6
P99088	GIENGIGNSILIK	5.914	8.4	2E-15	-0.15		0	7
P99088	IEDELFTAKYDGIK	4.077	8.6	2E-16	0.15		1	1
P99088	PIITDVYAREVLDSR	4.355	6.1	5E-08	0.16		-2	2
P99088	GNPTVEVEVLTESGAFGR	4.226	11.7	6E-30	0.21		0	2
P99088	ALVPSGASTGEHEAVELR	4.672	9.398	0	0.072		0	4
P99088	AAADLLGQPLYKYLGGFNGK	8.419	7.3	5E-12	0.25		1	10
P99088	SGETEDTTIADIAVATNAGQIK	3.815	7	9E-11	0.22		0	1
P99088	IGDRVQLVGDDLFTNTEILAK	4.113	6.2	2E-08	0.22		1	1
P99088	EVLDSRGNPTVEVEVLTESGAFGR	4.087	9.6	3E-20	0.25		1	1
P99088	ALVPSGASTGEHEAVELRDGDKSR	4.779	10.2	1E-22	0.03		2	4
P99088	SGETEDTTIADIAVATNAGQIKTGSLSR	4.196	9.7	2E-20	0.24		1	1
P99088	ALVPSGASTGEHEAVELRDGDKSRYLGK	5.54	8.1	5E-14	0.05		3	5
P99088	VNQIGTLTETFDAIEMAQKAGYTAVVSHR	5.485	7.5	2E-12	0.05		1	5
P99089	MNLIPTVIETTNRGER	5.849	7.9	2E-13	0.07		1	7
P99089	RFALPNAEVMIHQPLGGAQGQATEIEIAANHILK	6.018	6.8	9E-11	-0.37		1	7
P99089	FALPNAEVMIHQPLGGAQGQATEIEIAANHILKTR	6.051	14.2	9E-44	-0.16		1	5
P99090	QLQEGFEK	4.482	6.182	0	0.066		0	3
P99090	YNAVEAIQHR	6.464	8.3	5E-15	0.08		0	8

P99090	QLQEGFEKYIESHSI	4.666	10.832	0	0.187		1	4
P99090	LDGEPINDGKVGPIR	4.374	9.9	1E-21	0.1		1	2
P99090	KLVDNMNIETGAIYIQATR	5.623	8.3	8E-16	-0.29		1	6
P99090	SYDRPYDHLENGVNGVTVEDIR	4.285	8.9	4E-17	0.22		1	2
P99090	GVAERNHSFPTPEVEPAIVAYTK	5.528	7.2	5E-11	0.07		1	5
P99090	SLNLLGNVLAKEYAVKYNAVEAIQHR	8.06	8.993	0	0.145		2	9
P99091	INYDEVR	4.248	6.6	2E-09	0.06		0	2
P99091	TNKYAEGYPGR	8.166	8.41	0	0.097		-2	9
P99091	VLAELINEGFR	4.478	7.4	4E-12	-0.02		0	3
P99091	GFDEKAFEEVAK	4.266	7.7	7E-13	0.11		1	2
P99091	VIAEAIEREFQR	4.644	6.7	1E-09	0.04		1	4
P99091	VAKLTAEYPLYQ	5.972	7.1	5E-11	0.03		1	7
P99091	SYITKQDKVIAEAIER	5.864	12.9	3E-36	0.03		-2	7
P99091	NTIPFDQEKPFVTSGIR	5.902	7.4	8E-12	0.06		1	6
P99091	TIDFKKFKEIADEVNAK	5.919	10.8	1E-25	0.09		3	7
P99091	YYGGCEFVDVOTESIAIDRAK	4.215	7.3	2E-11	0.16	Cys_CAM:.....	1	2
P99091	SYITKQDKVIAEAIEREFQR	5.893	11.7	4E-30	0.05		-2	7
P99091	LGTPAATTRGFDEKAFEEVAK	4.772	6.7	7E-10	0.05		2	4
P99091	AVAFGEALENNFKTYQQQVVK	6.175	6.6	1E-09	0.3		1	8
P99091	AVAFGEALENNFKTYQQQVVKNAK	8.414	15.835	0	0.133		2	10
P99091	LMVDMAHIAGLVAAGLHPNPVEYADFVTTTTHK	5.811	7.7	5E-13	-0.07		0	5
P99092	VAMLSFSTK	8.87	6	8E-08	0		0	10
P99092	IVLPEGEDER	4	6.1	3E-08	0.08		0	1
P99092	SALSFGMDPK	5.446	8.7	2E-16	0.03		0	5
P99092	AELVQSFVER	4.39	7.1	6E-11	0.1		0	2
P99092	ADLLNVLKDKLSGK	8.493	10.515	0	0.096		-2	10
P99092	LGGYDAVGPNLQGLNSPVNDLSR	4.058	9.8	7E-21	0.2		0	1
P99092	LQGDANVFVFPVSLEAGNIGYKIAQR	6.004	10.6	3E-24	0.01		1	7
P99092	KAPGAKLQGDANVFVFPVSLEAGNIGYK	8.028	14.653	0	0.131		2	9
P99092	AGKADGLVSGAAHSTGDTVVRPALQIIK	8.63	11.868	0	0.108		-2	10
P99093	YITGQTIHVNGGMYM	6.456	9.2	2E-18	0.11		0	8
P99093	SGAIINLSSVVGAVGNPGQANYVATK	8.283	7.588	0	0.167		0	9
P99094	NAINLLQAFLEGEKNV	4.499	10.8	2E-25	0.03		1	3
P99094	RNAINLLQAFLEGEKNV	5.76	9.7	1E-20	0.02		2	6
P99095	SIEWDYR	4.256	6.5	7E-09	0.09		0	2
P99095	TQVSEWER	4.516	6.9	4E-10	-0		0	3
P99095	KFAEEENVR	4.747	6.7	2E-09	-0.02		1	4
P99095	NVEVPVSQLEK	4.439	8.2	2E-14	0.09		0	3
P99095	KTDGTPFEGDPR	4.384	7.7	1E-12	0.1		-2	2

P99095	TQVSEWERDQYMK	4.605	7.852	0	0.072		1	4
P99095	ALGNHIYNQFINSK	8.647	10.519	0	0.078		0	10
P99095	YLRLQFTDILGTIK	8.267	6.667	0	0.092		1	9
P99095	TQVSEWERDQYMKQY	4.62	8.2	8E-16	0.33		2	4
P99095	LVPGYEAPCYIAWSGK	5.948	10.5	5E-24	0.04	Cys_CAM:.....	0	7
P99095	TFTKEDIRKFAEEENVR	4.94	7.5	8E-12	0.04		3	4
P99095	VPEPVNQNIYEMNREER	4.343	6.2	6E-08	0.14		1	2
P99095	LICDVYKTDGTPFEGDPR	4.061	10.7	2E-24	0.13		1	1
P99095	LVPGYEAPCYIAWSGKNR	7.836	9.1	1E-17	-0.24		1	9
P99095	LKVPEPVNQNIYEMNREER	4.81	9.9	7E-21	0.04		2	4
P99095	EAVGIQDLPSTLYTALKAMR	5.764	7.3	5E-12	-0.15		1	6
P99095	SVDPAANPYMALAAILEAGLDGIKNK	4.437	7.2	8E-12	-0.04		1	4
P99095	EAVGIQDLPSTLYTALKAMRENEVIKK	5.981	9.4	9E-19	0.31		3	7
P99095	KLDEKGPTLELNDDGGYFDLAPTDLGENCRR	4.036	7.8	2E-13	0.37		-2	1
P99096	LFAEMYR	5.907	6.8	3E-10	0.02		0	7
P99096	TIQAFDTALSR	5.536	7.4	8E-12	0.03		0	5
P99096	LAQLVIDRVPSIEK	6.022	8.1	2E-14	-0.11		1	7
P99096	MVSSGTEATLDTLR	4.251	7.1	9E-11	0.1		0	2
P99096	VAETLMPGGVNSPVR	5.897	8.4	6E-16	0.02		0	7
P99096	LAQLVIDRVPSIEKVR	8.606	8.4	2E-16	-0.29		2	10
P99096	YTKSEEAMKVAETLMPGGVNSPVR	5.852	11.5	1E-29	0.06		2	7
P99096	MRYTKSEEAMKVAETLMPGGVNSPVR	8.142	10.302	0	0.196		3	9
P99098	SIEEIVANLDSVPANIQTAVR	4.012	10.4	3E-23	0.13		0	1
P99098	LNAAVEGTDLESKSIEEIVANLDSVPANIQTAVR	4.005	9.9	6E-21	0.22		1	1
P99099	VGWFDSVVLRL	5.74	7.7	8E-13	0.03		0	5
P99099	TLEELPENAR	4.154	8.3	9E-15	0.08		0	1
P99099	RVGWFDVSVLR	8.628	8.261	0	-0.299		1	10
P99099	TLEELPENARK	4.697	7.1	1E-10	-0		1	3
P99099	MADLLEKETFER	4.35	8.4	3E-15	0.12		1	2
P99099	ITDFLAEQSDVIAR	3.894	9	2E-17	0.14		0	1
P99099	EVGREYGTGTTGRPR	8.488	6.203	0	0.096		2	10
P99099	EITEYPANLDQLKR	4.458	7.4	2E-11	0.12		1	3
P99099	MADLLEKETFERLLK	4.82	10	2E-21	0.04		2	4
P99099	AQVILPYHLAQDEYEER	4.415	10.1	8E-22	0		0	3
P99099	SSIVVVGTVQWGDEGKGK	5.678	8.2	2E-14	0.05		-2	5
P99099	VGDGPFPTLFDGDGHHR	4.357	8.8	1E-16	0.21		0	2
P99099	AQVILPYHLAQDEYEERLR	4.834	7	2E-10	0.06		1	4
P99099	RCKPIFEELPGWTEDEVTSVR	4.846	7.2	5E-11	0.04		2	4
P99099	ISNRAQVILPYHLAQDEYEER	4.86	8.402	0	0.171		1	4

P99099	GMFNETCPSFDDIFEEYYAAGQR	3.793	8.7	1E-16	0.16	:::::Cys_CAM::::::	0	1
P99099	SSIVVVGQTQWGDEGKGKITDFLAEQSDVIAR	4.336	9.2	5E-18	0.17	::::::	-2	2
P99100	EYIPVIMYSPK	5.654	6.562	0	0.049	::::::	0	6
P99100	IIARPYVGEPGNFTR	8.633	8.625	0	0.083	::::::	1	10
P99100	INDIYDGEGVTEAVRTK	4.222	9.1	4E-18	0.14	::::::	1	2
P99100	KVYPNGFPEELIQQIEEMTGR	4.487	8.4	4E-15	0.04	::::::	-2	3
P99100	IVKKDFTGISFLNLVDFDALYGHRR	8.392	9.072	0	0.11	::::::	3	9
P99100	SNLKEDDLVIITADHGNDPTAPGTDHTR	4.285	9.7	3E-20	0.19	::::::	-2	2
P99101	IGVPGEQELGGR	4.477	6.4	9E-09	0.08	::::::	0	3
P99101	KFGAVYQYGDIK	8.035	8.089	0	0.092	::::::	1	9
P99101	KIGVPGEQELGGR	5.722	7.8	5E-13	0.03	::::::	1	6
P99101	NDKIDFIWSHTLK	6.654	8.2	2E-14	0.05	::::::	1	8
P99101	GVSYCAVCDGAFFK	5.707	8.7	9E-17	-0.13	:::::Cys_CAM:::Cys_CAM:::::	0	6
P99101	FADKVTIVHRRDELRL	8.385	7.042	0	0.105	::::::	3	9
P99101	AFKNDKIDFIWSHTLK	8.5	11.8	4E-30	0.01	::::::	2	10
P99101	SVEDKGEYKVINFGNKELTAK	5.846	11.9	7E-31	0.03	::::::	3	7
P99101	KFGAVYQYGDIKSVEDKGEYK	5.721	6.6	8E-10	0.09	::::::	3	6
P99101	AVIATGAEYKKIGVPGEQELGGR	6.237	14.7	2E-47	-0.31	::::::	2	8
P99101	QIVTATGDGSIAAQSAAEYIEHLNDQA	3.856	9.1	8E-18	0.24	::::::	0	1
P99103	LLEGHYPDTRR	5.212	6.211	0	0.099	::::::	0	4
P99103	GDDSVTQLILPARTY	3.928	9	1E-17	0.15	::::::	1	1
P99103	DYFITQLNDTLKAISPR	5.916	10.5	5E-24	0.05	::::::	1	7
P99103	ILKPKGDDSVTQLILPIR	8.467	9.7	2E-20	0.02	::::::	-2	10
P99103	LLEGHYPDTRRLFPENYEIK	4.723	7.751	0	0.182	::::::	1	4
P99103	ILKPKGDDSVTQLILPARTY	8.447	12.126	0	0.116	::::::	-2	10
P99105	IDWEVLQK	4.214	6.4	3E-09	0.09	:::::	0	1
P99105	QVIREEGLER	4.642	7.7	3E-13	0.02	:::::	1	4
P99105	QPFPGPGLGIR	8.764	8.52	0	-0.307	:::::	0	10
P99105	IDWEVLQKISSR	5.987	8.3	2E-15	-0.2	:::::	1	7
P99105	RIYGVQFHPEVR	8.298	10.14	0	0.082	:::::	1	9
P99105	HTEYGNDLLNNFVR	4.764	11.6	7E-30	0.05	:::::	0	4
P99105	AVTSIDGMTSDFAR	4.056	8.2	3E-15	0.11	:::::	0	1
P99105	HTEYGNDLLNNFVRR	6.133	8.5	4E-16	0.03	:::::	1	8
P99105	VVYDITSKPPSTIEWE	4.142	8.6	1E-16	0.19	:::::	1	1
P99105	QVIREEGLEREIWQYF	4.364	8	2E-14	0.12	:::::	-1	2
P99105	TVLPNIQSVGVMGDYR	5.519	9.7	2E-21	0.05	:::::	-2	5
P99105	AIGDQLTCIFVDHGLLR	5.133	9.9	6E-22	0.05	:::::	0	4
P99105	KIIGNEFVYVFDDEASKLK	4.752	9.2	8E-19	0.06	:::::	2	4
P99105	KGEGDMVMEQFGEGFNMNIIR	4.277	7.9	6E-14	0.14	:::::	1	2

P99105	VLGEITEDKLEIVRESDAILR	4.19	7.1	2E-11	0.21		2	2
P99105	EIWQYFTVLPNIQSVGVMGDYR	4.077	7.1	2E-11	0.18		0	1
P99105	KGEGDMVMEQFGEGFNMNIIRVNAK	4.745	8.1	6E-15	0.07		2	4
P99105	KLGIELGIPEHLVWRQPFPGPLGIR	8.474	12.196	0	0.111		2	10
P99105	SHHNVGGLPEDMEFELIEPINTLFKDEV	4.463	8.7	4E-17	0.02		1	3
P99106	FVPEGIEGR	4.41	6.4	9E-09	-0		0	3
P99106	NLVGILTNR	9.011	7.188	0	-0.138		0	10
P99106	KFVPEGIEGR	5.705	6.8	8E-10	0.02		1	6
P99106	NLVGILTNRDLR	8.997	6.3	2E-08	0.03		1	10
P99106	ISGVPIVDNKEDR	4.417	6.8	9E-10	-0.01		1	3
P99106	TAYKGALQDTIYQLMGGVR	8.166	6.5	8E-09	0.24		1	9
P99106	GMGSLGAMEKGSNDRYFQEDKAPK	6.158	7.2	5E-11	0.01		3	8
P99106	IVDVMTQENLITAPVNTTLEEAEKILQK	4.196	7.8	7E-13	0.24		1	1
P99107	LPEYMIPR	5.917	6.5	3E-09	-0.33		0	7
P99107	TAEVFNFDGIR	3.935	9.7	1E-20	0.12		0	1
P99107	NDLKSRLPEYMIPR	8.349	7.726	0	0.091		2	9
P99107	LQAFADANPQSI AVR	5.734	10.7	7E-25	0.04		0	6
P99107	AGCGYVPVDT SIPEDRIK	4.422	8.8	5E-17	0		1	3
P99107	KFEWMEQLPLTSNGKIDR	5.717	10.9	2E-26	-0.3		2	6
P99107	KFEWMEQLPLTSNGKIDRK	8.125	10.997	0	0.122		3	9
P99107	HTTDELTYQQLMDESSKLAHR	4.972	9.796	0	0.234		1	4
P99107	TDIINKLQAFADANPQSI AVR	5.608	11.849	0	0.099		-2	6
P99107	MTDIINKLQAFADANPQSI AVR	5.612	10.014	0	0.118		1	6
P99107	MIGAIAKAGCGYVPVDT SIPEDRIK	5.788	6.4	2E-09	-0.37	Cys_CAM:.....	-2	6
P99108	TIMSNQGSALMGIGVSSGENR	5.661	9.522	0	0.079		0	6
P99108	IAKEMGALT VGVVTRPFSFEGR	8.616	9.196	0	0.128		2	10
P99110	SLGIEILGGR	5.652	6.299	0	0.036		-2	6
P99110	FQLTDIPPAER	4.318	7.7	4E-13	0.11		0	2
P99110	SKFEELSDSLIR	4.557	8.6	1E-16	0		1	3
P99110	DAGKIAGLEVER	4.524	6.8	2E-10	0		1	3
P99110	HMGTDYKVDIEGK	4.87	10	3E-22	0.03		1	4
P99110	NTAESYLGEKV DK	4.571	6.2	9E-09	0		1	3
P99110	SKFEELSDSLIRR	5.805	9.2	9E-19	-0		2	7
P99110	AVITVPAYFNDAER	4.323	8.1	2E-14	0.16		0	2
P99110	RHMGTDYKVDIEGK	6.434	6.3	8E-09	0.02		2	8
P99110	TLGRFQLTDIPPAER	5.813	6.9	1E-10	0.06		1	7
P99110	SYTPQEISAMILQNLK	5.656	8.8	3E-17	0.02		0	6
P99110	QATKDAGKIAGLEVER	5.776	10.7	2E-25	0.04		2	7
P99110	AVITVPAYFNDAERQATK	6.081	6.4	3E-09	-0.07		1	7

P99110	IINEPTAAALAYGLDKTDKDEK	4.34	10.2	3E-23	0.22		2	2
P99110	QAMKDAGLTNSDIDEVILVGGSTR	4.162	7.3	4E-12	0.28		1	1
P99110	SQIYSTAVDNQPSVDVHVLQGERPMAADNK	4.53	7.377	0	0.11		1	3
P99110	AVITVPAYFNDAERQATKDAGKIAGLEVER	4.88	7.3	2E-12	0.05		3	4
P99110	AKKDLSGVSQTQISLPFISAGENGPLHLEVNLTR	6.838	12	3E-32	-0.39		2	9
P99111	AIDALVPIGR	5.765	7.3	8E-12	0.02		0	6
P99111	SVDEPLQTGIK	4.26	8.9	2E-17	0.08		0	2
P99111	IMEVPVGEELIGR	4.157	9.6	4E-20	0.15		0	1
P99111	EAYPGDVFYLHSR	5.203	10	6E-22	0.04		0	4
P99111	VVNPLGQPIDGQGPINTTK	5.76	10.2	7E-23	0.05		0	7
P99111	SVDEPLQTGIKAIDALVPIGR	4.419	7.588	0	0.1		1	3
P99111	ELESFAQFGSDLDEFTASKLER	3.967	7.2	1E-11	0.16		1	1
P99111	VVNPLGQPIDGQGPINTTKTRPVEK	8.553	6.986	0	0.1		2	10
P99112	IGLFGGAGVGK	8.889	8.3	3E-15	0.01		0	10
P99112	VTQVMGPVIDVR	5.769	7.5	2E-12	0.03		0	5
P99112	FTQAGSEVSALLGR	5.697	7.114	0	0.06		0	6
P99112	TAMVFGQMNEPPGAR	5.798	10.3	2E-23	0.04		0	5
P99112	ALEPSIVGQEHYEVAR	4.646	10.5	4E-24	0.01		0	3
P99112	DILDGKYDHIPEDAFR	4.106	8.3	3E-15	0.18		1	1
P99112	LTEMGIYPAVDPLASTSR	4.186	8.9	3E-17	0.24		0	1
P99112	KLTEMGIYPAVDPLASTSR	5.557	8.2	1E-14	0.04		1	6
P99112	TREGNDLYFEMSDSGVIKK	4.593	7	6E-11	-0.01		2	3
P99112	MPSAVGYQPTLATEMGQLQER	4.494	9.25	0	0.22		0	3
P99112	TVLIQELINNIAQEHGGISVF	4.545	7.9	1E-13	0.26		-1	4
P99112	GMDVKDTGKEISVPVGDETLGR	4.273	14	7E-43	0.17		2	2
P99112	ALEPSIVGQEHYEVARDVQSTLQK	4.719	6.459	0	0.158		1	4
P99112	TVLIQELINNIAQEHGGISVFAGVGER	4.695	6.308	0	0.148		0	4
P99113	AILFNQK	8.941	6.569	0	-0.318		0	10
P99113	WILDNVEGAR	4.261	6.6	3E-09	0.11		0	2
P99113	GQACFECGDVK	4.272	7.4	9E-12	0.1		-2	2
P99113	AAHITDYSNASR	6.83	7	9E-11	-0.34		0	9
P99113	WILDNVEGAREK	4.48	6.5	5E-09	0.03		1	3
P99113	ADQIAGIGITNQR	5.721	7.4	7E-12	0.02		0	6
P99113	MINSAPQSESYATR	5.745	8	6E-14	0.04		0	7
P99113	NMLPEVKPSSEIYGK	5.965	8.6	7E-16	0.05		1	7
P99113	MEKYILSIDQGTSSR	5.697	6.2	6E-08	0.02		1	6
P99113	AILFNQKGEIAGVAQR	8.667	9.6	3E-20	0.01		1	10
P99113	LEEKFDPKMDEGEREK	4.29	8.8	1E-16	0.12		3	2
P99113	GAIFGLTRGTEKEHFIR	8.635	7.928	0	0.089		2	10

P99113	QTQSICSELKQQGYEQTFR	5.687	9	1E-17	0.06	:::::Cys_CAM:::::	1	6
P99113	NTYGTGGFMLMNTGDKAVK	8.325	8.357	0	0.102	:::::	1	9
P99113	AILFNQKGEIAGVAQREFK	8.623	11.2	5E-28	-0.34	:::::	2	10
P99113	VDSTEGVYVVPAFVGLGTPYWDSEAR	3.764	10.5	6E-24	0.16	:::::	0	1
P99115	FLKDRYEAMK	8.199	6.493	0	0.102	:::::	2	9
P99115	NEDWQLYTAGK	4.167	9.1	2E-18	0.09	:::::	0	1
P99115	LDRPAIESSNER	4.595	6.3	8E-09	-0.01	:::::	1	3
P99115	NEDWQLYTAGKR	5.816	8.5	4E-16	0.04	:::::	1	7
P99115	NFPEYKTEWAPK	5.928	8.9	7E-18	0.04	:::::	1	7
P99115	HLGGFPISGQFL	6.08	12.2	4E-33	-0.35	:::::	-1	8
P99115	EFINPLPHISYVR	6.637	9.3	3E-19	-0.05	:::::	0	9
P99115	TLLFGPFANVGPK	8.66	7.794	0	0.085	:::::	0	10
P99115	EIEPDWNIHVYER	4.256	10.4	4E-24	0.17	:::::	0	2
P99115	TYNITTLAAAVK	8.361	10.325	0	0.093	:::::	0	9
P99115	IDEGTDVNFGELTR	3.726	8.1	2E-14	0.12	:::::	0	1
P99115	KQTSKDLELGYYEN	4.59	10.4	4E-24	0.01	:::::	2	3
P99115	TFYPEARNEDWQLY	4.043	6.7	4E-10	0.19	:::::	-1	1
P99115	NFPEYKTEWAPKIK	8.242	7.399	0	0.104	:::::	2	9
P99115	IDEGTDVNFGELTRK	4.132	6.1	2E-08	0.12	:::::	1	1
P99115	NLPLIKYSFDQVIMTK	8.325	6.353	0	0.137	:::::	1	9
P99115	MIPSYGESLIEDEKLMR	4.331	9.3	4E-19	0.15	:::::	1	2
P99115	KMIPSYGESLIEDEKLMR	4.793	12.5	3E-34	0.06	:::::	2	4
P99115	TFYPEARNEDWQLYTAGK	4.547	6.085	0	0.097	:::::	1	3
P99115	VINEEFEISKQFWGHLVK	5.545	9.6	1E-20	0.06	:::::	1	5
P99115	SGSIENPREFINPLPHISY	5.311	6.1	2E-08	0.06	:::::	-1	5
P99115	KMIPSYGESLIEDEKLMRK	5.82	10.9	4E-26	-0.17	:::::	3	7
P99115	TFYPEARNEDWQLYTAGKR	5.878	8.3	4E-15	0.03	:::::	2	7
P99115	YIDGQRTLLFGPFANVGPK	8.267	9.404	0	0.107	:::::	1	9
P99115	SGSIENPREFINPLPHISYVR	6.483	10.8	9E-26	-0.22	:::::	1	8
P99115	FKQVTDYVFIGAGGGAIPLLQK	8.199	10.248	0	0.134	:::::	1	9
P99115	GREDNPGIMAASKIDEGTDVNFGELTR	4.089	8.6	1E-16	0.28	:::::	2	1
P99115	HLGGFPISGQFLACTNPQVIEQHDAK	5.586	10.3	2E-23	0.05	:::::Cys_CAM:::::	0	5
P99116	RFPDIER	5.67	6.9	3E-10	0.02	:::::	1	6
P99116	NMTVAIIGTGR	9.011	6.8	7E-10	0	:::::	0	10
P99116	ESYHLFDKAMFDHVK	6.044	7.8	2E-13	0.03	:::::	1	9
P99116	SDEAVQNLVEGGLNAALSVINTGTCETR	3.824	6.1	8E-08	0.29	:::::	-2	1
P99117	VVVLSGGYSR	8.614	7.9	1E-13	-0.32	:::::	0	10
P99117	ANERHIFGTK	8.942	7.358	0	-0.386	:::::	1	10
P99117	GLVPIIEPEVNINAK	4.566	7.389	0	0.18	:::::	0	3

P99117	GFIAALDQSGGSTPK	5.75	8.1	5E-14	0.03		0	6
P99117	ANELLKDNDELIASFSR	4.208	10.3	8E-23	0.25		1	2
P99117	NGKGFIAALDQSGGSTPK	8.445	11.7	5E-30	-0.37		1	10
P99117	EKANELLKDNDELIASFSR	4.34	13.5	1E-39	0.18		2	2
P99117	LTIPTEPNLYKELAEHPNVVR	5.506	11.4	3E-28	0.06		1	5
P99117	SNILELNEQGIKDVVEQQFEVAK	4.215	7.4	2E-11	0.13		1	2
P99117	EYGVNEDQYSNEDEMFQLVHDMR	3.831	7.3	1E-11	0.24		0	1
P99117	ALKEYGVNEDQYSNEDEMFQLVHDMR	4.121	11.7	3E-30	0.29		1	1
P99117	VVVLSSGGYSREKANELLKDNDELIASFSR	4.781	10.1	7E-22	0.03		3	4
P99118	LNGEEFGNGR	4.442	9.4	2E-19	0.08		-2	3
P99118	TVIIATGAGWR	8.91	7.6	1E-12	0.01		0	10
P99118	ELLTEISDMSPR	3.913	8.6	3E-16	0.13		0	1
P99118	KLNIPGEEQLINK	5.719	7.9	2E-13	0.03		1	6
P99118	TPSFVSVNRPGEETGVTF	4.523	8	7E-14	0.21		-1	4
P99118	LGSTADASEFENKEPYDVLIVGGGPASGSAAIYTAR	4.101	8.1	2E-14	0.32		1	1
P99118	GVAFCPHCDGPLFENK	5.316	7.6	3E-12	0.05	Cys_CAM::Cys_CAM:.....	0	5
P99119	AEEIYVNTR	4.347	6.4	2E-08	0.07		0	2
P99119	FVKEYTGLPAER	5.823	8.1	3E-14	0.04		1	7
P99119	GSTYYGIALALMR	8.496	10.27	0	0.077		0	10
P99119	ILEDTFDSIKYLLD	3.808	8.9	5E-17	0.12		1	1
P99119	ADVQDLNHGTVHSPSPVDVK	5.119	10.6	2E-24	0.06		0	4
P99119	DTLKEQTGSEAKAEEIYVNTR	4.405	9.9	2E-21	0.14		-2	3
P99119	SVMDSGFDGYFLIAANPVDILTR	3.752	8.5	3E-15	0.2		0	1
P99119	AGEYEDCKDADLVVITAGAPQKPGETR	4.155	10.5	7E-24	0.17	Cys_CAM:.....	2	1
P99120	VALVTGGAQGIGFK	8.87	9.8	7E-21	0.01		0	10
P99120	ADVSNRDDVFNAVR	4.226	9.2	2E-18	0.1		1	2
P99120	TVYGVNVAGVLWGIQAAHEQFK	6.556	7.9	3E-13	0.13		0	8
P99120	TVYGVNVAGVLWGIQAAHEQFKK	8.254	9.099	0	0.113		1	9
P99120	VSQPEDVSNVVSFLAGKDSYITGQTIIVDGGMR	3.909	6.9	2E-10	0.19		1	1
P99122	VTDAFDSDKVESGVQLVDFWATWCGPCK	3.926	8.1	5E-14	0.18		1	1
P99122	AIVKVTDAFDSDKVESGVQLVDFWATWCGPCK	4.27	14.5	1E-45	0.14	Cys_CAM::Cys_CAM::	-2	2
P99126	HTQGLNIPGM	6.08	7.6	9E-13	0.08		0	8
P99126	GGNMQQMMK	8.9	7	5E-11	-0		0	10
P99126	MAQEKEKLKEER	4.813	10.7	3E-25	0.02		2	4
P99126	KMAQEKEKLKEER	5.835	9.3	1E-19	-0.37		3	7
P99126	LGKHTQGLNIPGM	8.64	7.756	0	0.081		1	10
P99127	AIIVATNDNEAVAIDKMLAGKKR	8.424	8.274	0	0.116		3	10
P99128	DKFFVSEPSYR	6.112	9.2	2E-18	0.03		1	8
P99128	LIGDDEHGWNK	4.422	7.2	5E-11	0.08		0	2

P99128	AQAEDLIQRFEK	4.613	6.5	5E-09	0.01		1	3
P99128	NGVFNIEGGCYAK	5.849	9.1	4E-18	0.04	Cys_CAM:...	0	7
P99128	TILNPINAWSDKEK	5.757	9	3E-18	-0.28		1	6
P99128	YKAQAEDLIQRFEK	5.834	11.4	2E-28	0.03		2	7
P99128	AQAEDLIQRFEKNFEK	4.786	6.8	5E-10	0.04		2	4
P99128	NFEKFGEKVEHIAEKGSFNK	6.669	11.2	2E-27	0.01		3	8
P99128	AAHPNTIIFLTADAFGVIPPISK	6.832	8.3	3E-15	-0.27		0	9
P99128	TILNPINAWSDKEKYKAQAEDLIQR	5.936	10.5	7E-25	-0.3		3	7
P99128	ILDNNEGVLTTELGAVNASTGKYTGRSPK	6.16	10.7	5E-25	-0.14		2	8
P99130	IAPALTEER	4.499	7.7	7E-13	0		0	3
P99130	SIESLSRELANISAGR	5.687	9.059	0	0.071		1	6
P99130	APTPVQQLASINVPEAR	5.981	9.2	2E-18	-0.06		-2	7
P99130	AIIAANLGVNPTSDGEVIR	4.263	10.5	5E-24	0.19		0	2
P99130	ANSNLLNGVTVDYYGAPTPVQQLASINVPEAR	4.266	11.7	7E-30	0.16		0	2
P99130	LLVISPYDKTSVADIEKAIIAANLGVNPTSDGEVIR	4.343	7.8	6E-13	0.14		2	2
P99132	PIVNVKLLEGR	9.052	7.612	0	-0.286		1	10
P99133	TPIIAGNWK	8.66	7	8E-11	-0.34		0	10
P99133	AVAGLSEDQLK	4.309	6.9	2E-10	0.08		0	2
P99133	ELFHETDEEINK	4.123	6.7	6E-10	0.1		0	1
P99133	ELFHETDEEINKK	4.463	9.2	1E-18	-0		1	3
P99133	RELFHETDEEINKK	4.856	6.2	4E-08	0.04		2	4
P99133	SSTSEDANEMCAFVR	4.046	11.3	8E-28	0.12		0	1
P99133	SVVIAYEPIWAIGTGK	5.717	10.9	3E-26	0.05		0	6
P99133	QTIADLSSKEVSEATR	4.555	9.9	2E-21	0.01		1	3
P99133	ELFHETDEEINKKAHAIFK	5.412	8.7	1E-16	0.07		2	5
P99133	QTIADLSSKEVSEATRIQYGGSVKPNNIK	8.004	9.361	0	0.136		3	9
P99133	HGMTPIICVGETDEERESGKANDVVGEQVK	4.366	8.6	4E-16	-0.04		2	3
P99133	SVVIAYEPIWAIGTGKSSTSEDANEMCAFVR	4.369	10.9	5E-26	0.03	Cys_CAM:...	1	3
P99133	HGMTPIICVGETDEERESGKANDVVGEQVKK	4.596	6.4	1E-08	0.02	Cys_CAM:.....	3	4
P99134	NMPNLNADQR	5.603	8.6	2E-16	0.03	::Oxidation_M:.....	-2	6
P99134	HLPNLNEEQR	4.947	6.9	1E-10	0.03		-2	4
P99134	NGFIQSLKDD	4.343	9.9	2E-21	0.09		-1	2
P99134	NMPNLNEAQR	5.851	8.2	6E-15	0.03		-2	7
P99134	LNMPNLNADQR	5.722	10.1	1E-22	0.04		-2	7
P99134	AQHDEAQQNAFY	4.244	11.8	8E-31	0.12		-1	2
P99134	PSQSTNVLGAEK	6.374	7.9	6E-14	0.02		-2	8
P99134	EILNMPNLNEEQR	4.07	8.2	5E-15	0.12		-2	1
P99134	EILNMPNLNEAQR	4.296	9	7E-18	0.12	Oxidation_M:.....	-2	2
P99134	QVLNMPNLNADQR	5.358	9.7	9E-21	-0		-2	5

P99134	EILHLPNLNEEQR	4.598	7.5	2E-12	0.01		-2	3
P99134	YEILNMPNLNEAQR	4.403	8.2	8E-15	0.16		-2	3
P99134	NMIKPGQELVVDDK	8.318	6.637	0	0.117		2	9
P99134	AQHDEAQQNAFYQVL	4.246	11.9	2E-31	0.16		-1	2
P99134	KDDPSQSTNVLGEAK	4.325	6.9	2E-10	0.11		-2	2
P99134	KDDPSQSANVLGEAQK	4.333	6.2	2E-08	0.12		-2	2
P99134	LADKNMIKPGQELVVDDK	8.351	9.6	0	0.113		3	9
P99134	DQQSAFYEILNMPNLNEAQR	3.855	7.6	5E-13	0.16		0	1
P99134	PSQSANVLGEAQKLNDSQAPK	6.447	7.2	6E-12	0.02		-2	9
P99134	NGFIQSLKDDPSQSTNVLGEAK	4.415	7.7	3E-13	-0.01		1	3
P99134	NGFIQSLKDDPSVSKEILAEAK	4.648	7.7	3E-13	-0.02		2	3
P99134	NGFIQSLKDDPSQSANVLGEAQK	4.427	8.3	3E-15	0.27	:DEAM_N:.....	1	3
P99134	NGFIQSLKDDPSQSTNVLGEAKK	5.899	12	8E-32	0.05	:DEAM_N:.....	2	7
P99134	KLNESQAPKADNNFNKEQQNAFY	5.704	7.5	8E-13	0.05		-1	6
P99134	KDDPSQSANVLGEAQKLNDSQAPK	4.487	8.4	6E-16	0.16		-2	3
P99134	AQHDEAQQNAFYQVLNMPNLNADQR	4.381	11.6	8E-30	0.09		0	3
P99134	ADNNFNKEQQNAFYEILNMPNLNEEQR	4.142	8.8	1E-17	0.23		1	1
P99134	ADNKFNKEQQNAFYEILHLPNLNEEQR	4.887	8.2	5E-15	0.05		2	4
P99134	ADAQQNNFNKDQQSAFYEILNMPNLNEAQR	4.174	9.2	2E-19	0.26		1	1
P99134	NGFIQSLKDDPSQSANVLGEAQKLNDSQAPK	4.555	9.9	6E-22	0.37		2	3
P99134	NGFIQSLKDDPSQSTNVLGEAKKLNESQAPK	6.011	8.6	5E-17	0.07		3	8
P99135	IVLFSHLGK	8.9	6.744	0	-0.342		0	10
P99135	LTLRPVAEDLSK	6.032	8.4	2E-15	0.01		1	8
P99135	KLDKEVVFPETR	5.705	8.6	2E-16	0.01		2	6
P99135	IVQALPTIQYIIIEQGGK	5.986	9	1E-17	0.04		0	6
P99135	EGDVLLVENTRYEDLDGKKESK	4.261	7.9	1E-13	0.16		3	2
P99136	TLAYLAELSK	5.731	7.6	2E-12	0.04		0	5
P99136	GSLFDATQTR	5.743	8.1	3E-14	0.02		-2	6
P99136	VLISAPATGDLK	5.745	7.5	3E-12	0.03		0	5
P99136	FTGEVEVVDGGFR	4.034	9.7	3E-20	0.11		0	1
P99136	SFSEPDASKLPWK	5.699	7.5	3E-12	0.04		1	6
P99136	KVLISAPATGDLK	8.332	7.767	0	0.087		1	9
P99136	AYTGDQNTQDAPHR	5.177	7.2	3E-11	0.05		-2	4
P99136	VIPEIDGKLDGGAQR	4.403	7.9	1E-13	0.01		1	3
P99136	FTGEVEVVDGGFRVNGK	4.598	10.762	0	0.076		1	4
P99136	VAAWYDNEMSYTAQLVR	4.302	11.6	4E-29	0.13		0	2
P99136	ARAAAENIIPNSTGAAK	8.935	8.2	1E-14	-0.01		1	10
P99136	VLNDDFGLVEGLMTTIHAY	4.022	9.2	3E-18	0.2		-1	1
P99136	FTGEVEVVDGGFRVNGKEVK	4.757	12	4E-31	0.04		2	4

P99136	IQEVEGLEVVAVNDLTDDDMLAHLLK	3.862	6.8	1E-09	0.2		0	1
P99136	VMSVGDRQLVKVAAWYDNEMSYTAQLVR	6.051	7.3	1E-11	-0.02		2	8
P99136	VLNDDFGLVEGLMTTIHAYTGDQNTQDAPHR	4.251	11.8	5E-30	0.15		0	2
P99136	TIVFNTNHQELDGSETVVSGASCTTNSLAPVAK	4.569	9.7	3E-20	-0.07		0	3
P99136	IQEVEGLEVVAVNDLTDDDMLAHLLKYDTMQGR	3.969	9.5	1E-19	0.22		1	1
P99136	NASNESFGYTEDEIVSSDVVGMTYGSFLDATQTR	3.615	7.7	1E-12	0.18		0	1
P99137	YLSYVEDVGTR	4.278	8.8	1E-16	0.09		0	2
P99138	IYVEDEYVR	4.084	7.5	2E-12	0.08		0	1
P99138	NLGYEVEER	4.251	8.3	4E-15	0.07		0	2
P99138	DGEVALFRPEENFK	4.172	8.7	2E-16	0.13		1	1
P99138	DGEVALFRPEENFKR	4.668	8.9	4E-17	-0		2	4
P99138	VITPELNGSILPGITR	5.934	7.5	5E-13	-0.3		0	7
P99138	VITPELNGSILPGITRK	8.865	6.4	7E-09	0.05		1	10
P99138	LYDVYTGIQNGTLEDKNGWR	4.412	10.4	1E-23	0.22		1	3
P99138	LYDVYTGIQNGTLEDKNGWRVVVPKY	6.027	7.2	4E-12	0.2		3	8
P99138	IVPYGPIEISPAAQGVHYGQSVFEGLKAYKR	8.283	12.297	0	0.114		2	9
P99139	FDKSPYDGFAIR	5.577	7.4	1E-11	0.03		1	5
P99139	SVDSQGASGQNRIEFK	5.659	9.5	2E-19	0.06		1	6
P99139	DIPRFDKSPYDGFAIR	5.999	10.9	2E-25	0.07		-2	8
P99139	IVNQSSMPAITVALEK	5.969	6.6	4E-09	0.06		0	7
P99139	VIDHIGAGSVSDKLVGDHEAVR	5.224	11.4	7E-28	0.06		1	4
P99139	KGQVINPGAIAVLATYGYAEVK	8.035	8.206	0	0.129		1	9
P99141	FNDFITGR	5.459	6	4E-08	0.03		0	5
P99141	GVSKVNDQTNVPVIFGILTTESIEQAVER	4.342	7.4	1E-12	0.18		1	2
P99142	ISDDIIRY	4.06	7.7	1E-12	0.07		-1	1
P99142	YMVIREDEDK	4.234	7.1	5E-11	0.08		1	2
P99142	SDNNKATDEFQR	4.379	9	2E-17	0.1		1	2
P99142	LAYEINDFKDGFYNIVR	4.436	9.6	9E-20	0.03		1	3
P99142	TYEVMYIVRPNIEEDAK	4.371	6.6	3E-09	0.2		1	2
P99142	ISDDIIRYMVIREDEDK	4.138	7.7	9E-13	0.22		2	1
P99142	TYEVMYIVRPNIEEDAKK	4.808	8.3	7E-15	0.06		2	4
P99142	RLAYEINDFKDGFYNIVR	5.733	12	2E-31	0.05		2	6
P99142	RRLAYEINDFKDGFYNIVR	8.033	7.526	0	0.17		3	9
P99142	FNGILATEGAEVLEAKDWGKR	4.805	8.3	7E-15	0.06		2	4
P99142	FNGILATEGAEVLEAKDWGKRR	5.967	6.2	5E-08	0.06		3	7
P99145	GASQDDQHRITTPPEAR	4.675	6.359	0	0.121		1	4
P99145	LANAAGLDGVVCSPLSR	4.234	8.4	2E-15	0.19	Cys_CAM:.....	0	2
P99145	GHDVFLDLKLHDIPNTVGK	6.066	8	4E-14	0.06		1	8
P99145	QLGSTHIVVGRPITQSDNPVESYHK	6.633	6.2	3E-08	-0.02		1	9

P99146	TISADLPFAQKR	8.388	6.652	0	0.051		-2	9
P99146	DLSFGENYGVVMEELR	3.735	11.1	2E-26	0.14		0	1
P99146	LISVVPSIDTGVCDQQTR	4.068	8	6E-14	0.15		0	1
P99146	LISVVPSIDTGVCDQQTRK	5.847	8.3	5E-15	0.03		1	7
P99146	KFNSEASKEEGIVLTISADLPFAQKR	5.815	10.6	2E-24	0.03		3	7
P99146	KLISVVPSIDTGVCDQQTR	5.485	7.9	1E-13	0.05	Cys_CAM:.....	1	5
P99146	WCASAGLDNVITLSDHR	5.148	8.6	4E-16	0.05	::Cys_CAM:.....	0	4
P99148	VSNLPYSIR	8.614	8.143	0	0.058		0	10
P99148	YLQDHQVPIR	6.457	9.3	5E-19	0.09		0	8
P99148	HGGILQMVLRL	8.992	6.1	3E-08	0.02		0	10
P99148	FDSLVEMDYYR	3.884	9.6	2E-20	0.13		0	1
P99148	NFEGRIHPLVK	8.771	6.226	0	0.075		1	10
P99148	RPQDLIFLSDMK	5.5	7	3E-11	0.07		1	5
P99148	EPGTIVPLNGLR	5.661	9.2	1E-18	0.03		0	6
P99148	HFDLNGQSYTTY	4.489	8.1	1E-14	0.01		-1	3
P99148	YLQDHQVPIREF	5.212	7.6	5E-13	0.03		-1	4
P99148	DGNEGEVPFKPSR	4.477	9	3E-18	0.09		1	3
P99148	NYERYQFLNWATK	8.334	7.844	0	0.15		1	9
P99148	KHFDLNGQSYTTY	6.377	6.6	1E-09	-0		-1	8
P99148	SNLVMMGVLPLEFK	5.627	9.198	0	0.114		0	6
P99148	KQDGDLEFEDAMVR	4.135	10.1	2E-22	0.14		1	1
P99148	HFDLNGQSYTTYDLK	4.663	11.1	3E-27	0.05		0	4
P99148	YLQDHQVPIREFNSY	5.181	11.6	1E-29	0.05		-1	4
P99148	AVEEQGITKVSNLPLY	4.449	7.1	3E-11	0.16		-1	3
P99148	KHFDLNGQSYTTYDLK	6.38	9.6	1E-20	0.02		1	8
P99148	FVEFFGPGVQHLPLADR	5.273	8.9	2E-17	0.05		0	5
P99148	LVNSLPQGATATDLALR	5.741	8.1	1E-14	0.06		0	7
P99148	QGLSKEPGTIVPLNGLR	8.245	12.894	0	0.096		-2	9
P99148	AVEEQGITKVSNLPSIR	6.128	10.4	2E-24	-0.35		1	8
P99148	VILQDFTGVPVAVDLASLR	4.078	8.7	6E-17	0.12		0	1
P99148	YLQDHQVPIREFNSYGSRR	8.204	9.277	0	0.112		2	9
P99148	VILQDFTGVPVAVDLASLRK	5.871	8.6	2E-16	0.25		1	7
P99148	ALSQFGKDGNEGEVPFKPSR	6.191	11.3	3E-28	0.02		2	8
P99148	AIADEDLLVTSVLSGNRNFEGR	4.237	6.4	2E-09	0.15		1	2
P99148	GVVGKFVEFFGPGVQHLPLADR	6.798	6.7	3E-10	0.16		1	9
P99148	YKEDGTGLVVLAGNDYGMGSSR	4.301	10.2	3E-23	0.2		1	2
P99148	LVNSLPQGATATDLALRVLTQELR	5.987	9.4	1E-19	0.13		1	7
P99148	KGVVGKFVEFFGPGVQHLPLADR	8.209	9.623	0	0.115		2	9
P99148	FGDSVTTDHISPAGAIGKDTFAGK	5.198	9.7	9E-21	0.06		1	4

P99148	ANFKEQSKKHFDLNGQSYTTYDLK	8.272	12.038	0	0.102		-2	9
P99148	IQNPSFFQGLSKEPGTIVPLNGLR	8.618	8.657	0	0.126		-2	10
P99148	LVNSLPQGATATDLALRVQTQLRK	8.87	6.732	0	0.116		2	10
P99148	AANFKEQSKKHFDLNGQSYTTYDLK	8.272	9.201	0	0.11		-2	9
P99148	AFDNYNAVPPATGIVHQVNLEYLASVVHVR	6.081	13.5	2E-40	-0.16		0	5
P99152	EHILLSR	6.637	7.4	7E-12	-0.24		0	9
P99152	DNIGALLR	5.634	6.3	1E-08	0.02		-2	6
P99152	TTVTGVEMFR	5.714	8.7	1E-16	0.03		0	6
P99152	TVGSGVVTEIIK	5.729	7.5	5E-12	0.04		0	6
P99152	NVGVPALVVFLNK	8.759	9.037	0	0.093		0	10
P99152	TTLTAAIATVLAK	8.66	7.458	0	0.09		0	10
P99152	HTPFFSNYRPQFY	8.447	9.126	0	0.144		-1	10
P99152	VGEEVEIIGLHDTSK	4.273	7.9	2E-13	0.12		0	1
P99152	HYAHVDCPGHADYVK	6.083	11.1	8E-27	0.02		0	6
P99152	LLDYAEAGDNIGALLR	3.901	10.2	3E-22	0.15		0	1
P99152	GITINTSHIEYQTDKR	6.796	6.5	6E-09	0.36		1	9
P99152	EGGRTVGSGVVTEIIK	5.878	9	2E-17	0.01		1	7
P99152	ILELMEAVDTYIPTPER	3.954	7.3	3E-11	0.13		0	1
P99152	KLLDYAEAGDNIGALLR	4.454	10.7	1E-24	0.13		1	3
P99152	DSDKPFMMPVEDVFSITGR	3.976	9.5	1E-19	0.15		1	1
P99152	NGDSVAQSYDMIDNAPEEKER	3.923	11.7	7E-30	0.14	:DEAM_N:.....	1	1
P99152	GQVLAAPGSITPHTEFKAENVY	5.393	9.7	4E-20	0.08		-1	5
P99152	DLLSEYDFPGDDVPVIAGSALK	3.511	10.4	2E-23	0.16		0	1
P99152	VGEEVEIIGLHDTSKTTVTGVEMFR	4.47	10	2E-21	0.2		1	2
P99152	VGEEVEIIGLHDTSKTTVTGVEMFRK	4.88	11.8	5E-30	0.06		2	4
P99152	NMITGAAQMDGGILVVSADGPMPTQR	4.053	6.2	5E-08	0.23		0	1
P99152	ALEGDAQYEEKILELMEAVDTYIPTPER	3.878	9.4	4E-19	0.29		1	1
P99152	GQVLAAPGSITPHTEFKAENVVLSKDEGGR	5.494	7.6	5E-12	0.12		2	5
P99152	SKEHANIGTIGHVDHGKTTTLTAAIATVLAK	8.235	14.347	0	0.133		2	9
P99153	QQWIPVYK	8.218	6.969	0	0.057		0	9
P99153	HGQSEWNAK	6.14	8.2	1E-14	0.01		0	8
P99153	EFGEEQVHIWR	4.56	6.479	0	0.043		0	3
P99153	EFGEEQVHIWRR	5.425	8.7	2E-16	0.04		1	5
P99153	KEFGEEQVHIWR	5.422	9.7	2E-20	0.03		1	5
P99153	ALDTTHYILTESK	5.29	9.5	1E-19	0.05		0	5
P99153	MMPYSESLKDTLVR	5.762	7.7	7E-13	0.04		1	7
P99153	SYDVKPPAETEEQR	4.328	9.8	1E-20	0.1		1	2
P99153	RSYDVKPPAETEEQR	4.812	8.2	2E-14	0.03		2	4
P99153	ENNI AIDVAFTSLLTR	4.113	7.8	4E-13	0.1		0	1

P99153	SYDVKPPAETEEQREAY	4.145	6.5	5E-09	0.14		-1	1
P99153	NLFTGWEDVNLSEQGINEATR	3.925	11.1	8E-27	0.18		0	1
P99153	SYDVKPPAETEEQREAYLADR	4.236	8.8	1E-16	0.15		2	2
P99153	ALDTTHYILTESKQQWIPVYK	6.832	7.1	4E-11	-0.35		1	9
P99153	SYDVKPPAETEEQREAYLADRR	4.528	7.7	8E-13	-0.02		3	3
P99153	ALDTTHYILTESKQQWIPVYKSWR	8.377	16.77	0	0.125		2	10
P99153	HYGGLQGLNKDDARKEFGEEQVHIWR	5.694	8.4	5E-15	0.02		3	5
P99153	VIPFWTDHISQYLLDGQTVLVSAHGNSIR	6.059	10.6	3E-24	0.39		0	5
P99154	EATGLGLKDAKELVDGAPK	4.554	10.6	6E-25	0		2	3
P99154	AVKEATGLGLKDAKELVDGAPK	6.17	9.8	2E-21	0.01		3	8
P99154	ANHEQIIIEAIKEMSVLELNDLVK	4.516	10.6	6E-25	0.04		-2	3
P99154	EALPKEEAELKEQLEEVGATVELK	4.372	6.8	2E-10	0.17		3	2
P99156	ELEELKTVKRPEVVEK	4.904	6.9	3E-10	0.03		3	4
P99156	GLDDEVVRVPLPNGGEMNVK	4.22	10.8	1E-25	0.19		1	2
P99156	MENQKQYPMTQEGFEKLER	4.842	11.1	6E-27	0.04		2	4
P99156	ALIGKGLDDEVVRVPLPNGGEMNVK	4.716	11.2	2E-27	0.03		2	4
P99156	SFGDLSENSEYDAAKDEQGFIQDIQR	3.759	9.7	8E-21	0.35		1	1
P99156	SFGDLSENSEYDAAKDEQGFIQDIQRIEHMLR	4.13	7.7	8E-13	0.19		2	1
P99157	QQEQNQEPQFK	4.466	9.5	1E-19	0.11		0	3
P99157	VILEYGESAPK	4.468	8.6	6E-16	-0		0	3
P99157	KVTELVKEQVK	8.125	6.801	0	0.102		2	9
P99157	QAYDNQTGVNEK	4.299	8.2	2E-14	0.12		0	2
P99157	NKLTFSDEVVEK	4.649	8.749	0	0.07		1	4
P99157	QKQQEQNQEPQFK	5.753	10.2	5E-23	-0.4		1	6
P99157	NNENNNQERQGLQ	4.446	9	1E-17	0.12		1	3
P99157	QAYDNQTGVNEKER	4.564	9.1	5E-18	-0.04		1	3
P99157	VILEYGESAPKIFR	6.085	7.2	4E-11	0.04		1	8
P99157	QKQQEQNQEPQFKNK	8.079	8	1E-13	-0.34		2	9
P99157	VILEYGESAPKIFRK	8.433	7.025	0	0.076		2	10
P99157	HEKNNNNNNQERQGLQ	5.008	8.8	1E-16	0.02		2	4
P99157	QAYDNQTGVNEKEREER	4.419	12.2	4E-32	-0.06		2	3
P99157	LTFSDEVVEKIAGIAAR	4.629	9.186	0	0.107		1	4
P99157	QKHEKNNNNNNQERQGLQ	6.428	10.1	5E-22	0.03		3	8
P99157	NKLTFSDEVVEKIAGIAAR	6.022	14.5	2E-45	0.05		2	8
P99157	QAYDNQTGVNEKEREERQK	4.806	8.6	7E-16	0.03		3	4
P99157	AKQAYDNQTGVNEKEREER	4.854	9.2	2E-18	0.04		3	4
P99157	QAAVDLKVILEYGESAPKIFR	5.794	8.5	1E-15	0.03		2	6
P99157	NKLTFSDEVVEKIAGIAAREVK	6.058	9.6	5E-20	0.07		3	8
P99157	QKQQEQNQEPQFKNKLTFSDEVVEK	4.972	10.5	8E-24	0.03		3	4

P99158	LVANLVHHFLK	8.898	8.3	3E-15	0.02		0	10
P99158	AEQQSTSGTSFR	5.924	8.5	4E-16	-0.32		0	7
P99158	QTFLGSGGHDIAYAQYLATR	6.408	10.6	4E-24	0.16		0	8
P99158	QGEPNLWTGRLDSEDPKKFR	5.791	6.9	2E-10	0.02		3	7
P99160	AYKAQGLGAWGF	8.537	9.8	9E-21	-0.16		1	10
P99160	TGVSASTWAAIAR	8.91	9.2	2E-18	-0.01		0	10
P99160	LSNGNTAGATGSSAAQIMAQR	9.13	11.1	7E-27	0.05		0	10
P99160	NAQSSNSNVEAVSAPTYHNYSTTTSSSVR	6.657	6.4	7E-09	-0.01		-2	8
P99160	SYNAQSSNSNVEAVSAPTYHNYSTTTSSSVR	6.48	7.2	3E-11	-0.03		-2	8
P99161	ALSIDTIEK	4.342	6.9	4E-10	0.07		0	2
P99161	VFSDYLKPALR	8.457	6.986	0	0.067		-2	10
P99161	VAIEMASPLGWHK	6.765	6.2	9E-09	-0.19		0	9
P99161	LTFENYGLDPEKR	4.543	10.4	2E-23	0		1	3
P99161	QWGSKTPGHPEYR	8.156	8.4	3E-15	-0.39		1	9
P99161	MFNEKDQLAVDTLR	4.388	9.6	5E-20	0.12		1	2
P99161	KLTFENYGLDPEKR	5.733	12	4E-31	0.01		2	6
P99161	YGFTKENILNQVMSL	5.601	9.313	0	0.131		1	6
P99161	AGTNGVHGAPLGEVER	5.434	9.5	1E-19	0.05		0	5
P99161	GATFFVFSDYLKPALR	8.486	6.501	0	0.089		-2	10
P99161	FNVSEEVYEIFQNTMLK	4.241	11	4E-26	0.21		0	2
P99161	QNLPLVDVPEDVVEEGVR	3.807	9.7	1E-20	0.17		0	1
P99161	FNVSEEVYEIFQNTMLKR	4.781	10.5	1E-23	0.09		1	4
P99161	NYKDELPRFELGHNGASR	6.662	12	4E-31	0.02		2	8
P99161	QNLPLVDVPEDVVEEGVRK	4.155	8.3	7E-15	0.22		1	1
P99161	VAWEVALESESTPTSLVLTR	4.195	9.8	8E-21	0.18		0	1
P99161	VAIEMASPLGWHKYVGTAGK	8.443	6.519	0	0.123		1	10
P99161	ANSGHPGLPMGAAPMAYTLWTR	8.693	8.565	0	0.113		0	10
P99161	TTIGFGSPNKAGTNGVHGAPLGEVER	6.567	12.4	2E-33	0.01		1	8
P99161	TTIGFGSPNKAGTNGVHGAPLGEVERK	8.372	7.3	4E-11	0		2	9
P99161	VVSMNPWNAFEQQSEYKESVIPSSVTKR	4.897	10.8	2E-25	0.04		2	4
P99162	KHDIPVYINEPK	6.389	7.1	7E-11	0.01		1	8
P99162	KLEYELYPVIAK	5.716	9.3	3E-19	-0.27		1	6
P99162	QCDIRPDDSKEQLEEKVK	4.451	9.4	2E-19	-0.02		3	3
P99163	ALPAGYAAR	8.684	6.1	3E-08	-0.25		0	10
P99163	AYEQSGVNIHAGYEAVR	4.709	8.1	1E-14	0.01		0	4
P99163	ALPAGYAARIDTTSFPTPK	8.636	8.4	4E-16	-0.32		1	10
P99163	SKAYEQSGVNIHAGYEAVR	5.487	11.8	4E-31	0.05		-2	5
P99163	EVSİKAMNHITGGGFYENIPR	6.645	9.9	7E-22	0		1	9
P99163	EGQVVIGLASSGIHSNGYSLVR	6.637	7.5	7E-13	0.05		0	9

P99164	TFIQPTQELR	5.702	6.15	0	0.053		0	6
P99164	GYQHAIGHVR	8.662	7.3	1E-11	0.03		0	10
P99164	NKHFFDSEGNLNV	5.348	8.1	4E-14	0.04		1	5
P99164	SKAPTFEELKESLR	5.905	9.3	6E-19	0.05		2	7
P99164	TFIQPTQELREQGVR	5.805	7.5	5E-12	0.05		1	5
P99164	GLGLLTEAINDDQMER	3.899	8.2	8E-15	0.2		0	1
P99164	TFIQPTQELREQGVRVK	8.652	7.2	4E-11	0.27		2	10
P99164	QYISKNKHFFDSEGNLNV	6.42	10.3	5E-23	0.02		2	8
P99164	GQEGAGIVVSDQNELKGER	4.277	11	3E-26	0.11		1	2
P99164	QKQYISKNKHFFDSEGNLNV	8.007	8.84	0	0.119		3	9
P99164	CGVFGIWNHPEAAQLTYMGLHSLQHR	7.165	6.7	2E-09	-0.04		0	9
P99164	GLGLLTEAINDDQMERLKGYQHAIGHVR	6.1	6.9	3E-10	0.36		2	6
P99165	GGTFLYSAR	8.645	6.5	3E-09	-0.32		0	10
P99165	CPEFKEQEV	4.583	6.9	3E-10	0.03		1	4
P99165	IAVLTSGGDSPGMNAAVR	5.741	6.5	4E-09	0.05		0	7
P99165	GIEGLVVIGGDGSYRGAQR	5.962	6.4	6E-09	-0.33		1	7
P99165	IVATSFDEIFDGKDHKFDYSLYELANKLSI	4.4	6.8	9E-10	0.12		3	2
P99166	SGVEAEYVDYR	4.053	9.8	9E-21	0.09		0	1
P99166	SGAMASVAPISEVKR	8.308	7.97	0	0.117		1	9
P99166	YVNNPNGSYDDIAGIVNEK	4.008	10	6E-22	0.17		0	1
P99166	FAVLVFPGSNCDRDMFNAAIK	5.603	7.3	2E-11	0.07	Cys_CAM.....	1	5
P99166	ETSLSGFDGVLIPGGFSFGDYLR	3.798	10.6	8E-25	0.16		0	1
P99166	ALETLLGTDSGVKLFEAMVKSWREQHV	5.471	7	1E-10	0.03		3	5
P99167	VVTYDFAR	5.753	7.3	2E-11	0.02		0	7
P99167	AAIQYAIDNNR	5.811	8.6	3E-16	0.03		0	6
P99167	IEWKEVLAGQK	6.03	7.6	3E-13	-0.4		1	7
P99167	RIEWKEVLAGQK	8.202	7.492	0	0.072		2	9
P99167	YAGLNKVNPSVILSSVL	8.17	9.873	0	0.124		-1	9
P99167	GVPSPVKRPQDQDMVIFR	8.626	7.158	0	0.117		2	10
P99167	VIDFLQNEMGATNIRFPETSGIGIKPVSK	6.107	8.4	2E-15	-0.11		2	7
P99167	ITQGTEGLNVPNEPIIPFIIGDGIGPDIWK	3.832	6.7	1E-09	0.24		0	1
P99167	KVIDFLQNEMGATNIRFPETSGIGIKPVSK	8.127	10.718	0	0.11		3	9
P99167	TAEKITQGTEGLNVPNEPIIPFIIGDGIGPDIWK	4.082	6.7	1E-09	0.19		-2	1
P99167	ITQGTEGLNVPNEPIIPFIIGDGIGPDIWKAASR	4.237	7.3	2E-11	0.21		1	2
P99168	SSPLIFER	5.682	6.2	9E-09	0.02		0	6
P99168	HEFVLGVR	6.11	7.6	9E-13	0.01		0	8
P99168	YAYSLPKSDIK	8.057	7.433	0	0.094		1	9
P99168	TSKSSPLIFER	8.388	8.756	0	0.071		-2	9
P99168	AEFPEVAELDLVR	3.935	9	2E-18	0.14		0	1

P99168	SNERGEVDIDDLKR	4.366	10.5	2E-24	0.1		2	2
P99168	TNSVESLLDDKFIR	4.472	7	6E-11	-0.02		1	3
P99168	NKAEFPEVAELDLVR	4.36	9.8	2E-21	0.13		1	2
P99168	TNSVESLLDDKFIRK	5.846	6.5	2E-09	0.07		2	7
P99168	KNKAEFPEVAELDLVR	4.842	11.5	4E-29	0.05		2	4
P99168	SDIKTNSVESLLDDKFIRK	5.788	9.7	7E-21	0.09		3	6
P99168	TFTGPHGGGGPGSGPVGVVK	8.684	10.71	0	0.106		0	10
P99168	LSEHFEIPYKQYCKHEFVLSGVR	6.91	10.3	5E-24	-0.01	Cys_CAM:.....	2	9
P99168	HYTELSNKNFGVDNGFYPLGSCTMK	6.112	10.4	7E-24	-0.14	Cys_CAM:...	1	8
P99168	YAYSLPKSDIKTNSVESLLDDKFIR	5.784	12.4	3E-34	0.04		3	6
P99168	VVNENTAAIMLTNPNTLGIFEKNIMEIR	4.709	8.634	0	0.116		1	4
P99168	HYTELSNKNFGVDNGFYPLGSCTMKYNPK	7.684	7.9	3E-14	0.03		2	9
P99169	AVDWAMR	5.757	6.5	3E-09	0.02		0	6
P99169	NLNSFNYVR	8.505	7.235	0	0.067		0	10
P99169	YIDDAWKER	4.424	6.8	2E-10	0.08		-2	3
P99169	EAYAYLEKLR	5.859	7.9	9E-14	0.02		1	7
P99169	CDANISLRPY	5.782	6.7	5E-10	0.03		-1	6
P99169	AMGFLVGQIMK	8.941	7.5	2E-12	-0		0	10
P99169	VRQTIPELPDER	4.646	8.3	3E-15	0.02		1	4
P99169	RFDESTGKTILMR	8.24	6.872	0	0.087		2	9
P99169	QTIPELPDERKAK	5.757	7.8	2E-13	0.04		2	6
P99169	STHKGEYSLVDLNR	6.48	10.9	1E-26	0.02		1	8
P99169	QGTPLIEIVSEPDIR	4.102	9.9	1E-21	0.22		0	1
P99169	QGTPLIEIVSEPDIRSPK	4.634	6.272	0	0.143		1	4
P99169	YFPEPDIVPLYIDDAWKER	4.053	9.3	4E-19	0.15		1	1
P99169	GQANPQLVNQLLKQELDKR	8.477	7.1	4E-11	0.11		2	9
P99169	LHMEEDAGKSTHKGEYSLVDLNR	5.37	13.9	1E-42	0.06		2	5
P99169	GLEYYEKRQEEELLNGGEIGQETR	4.162	10.1	8E-23	0.18		2	1
P99169	KGLEYYEKRQEEELLNGGEIGQETR	4.367	14.7	5E-48	0.2		3	2
P99170	HYNGDFVIR	6.097	8.6	4E-16	-0.35		0	8
P99170	TALFNLYAK	8.236	8.184	0	0.114		0	9
P99170	YGGQHAHLTEEQR	6.008	10.4	2E-23	-0.34		0	6
P99170	QQFEAEGRQPSIR	5.728	7.9	2E-13	0.04		1	6
P99170	DTETVFQLALPHLIK	5.23	7.14	0	0.142		0	4
P99170	YAPSPTGYLHIGNAR	8.206	8.567	0	0.082		0	9
P99170	FRVPQNQTYSFDDMVK	5.671	7.997	0	0.067		1	6
P99170	HYNGDFVIRIEDTDKK	4.943	7.3	2E-11	0.04		2	4
P99170	ANLIPEVPSEEDLSWGR	3.955	8	8E-14	0.19		0	1
P99170	HYNGDFVIRIEDTDKKR	6.17	6.4	1E-08	0.21		3	8

P99170	QHIIYQPLIDQLLAEDKAYK	5.338	6.9	3E-10	0.05		1	5
P99170	WLGLDWDESVDKDNGYGPYR	3.95	9.2	2E-18	0.23		1	1
P99170	YGGQHAHLTEEQRQQFEAEGR	5.398	6.3	2E-08	0.07		1	5
P99170	CYMTEEELEAEREAQIARGEMPR	4.294	7.3	1E-11	0.25		2	2
P99170	YGGQHAHLTEEQRQQFEAEGRQPSIR	6.039	10.9	9E-26	0.06		2	6
P99171	EENFADEVKGQMK	4.217	9.4	1E-19	0.11		1	2
P99171	QQALNEGKPENIVEK	4.716	8.8	3E-17	0.04		1	4
P99171	TDNDAFGAYLHMGGR	5.119	7.9	2E-13	0.06		0	4
P99171	IKEAISTIGEKL SVR	8.467	8.608	0	0.084		2	10
P99171	YVSSEQVSEEEINHER	4.311	12.2	2E-32	0.11		0	2
P99171	LVDFVRYEVGEGMEKR	4.774	7.2	3E-11	0.05		2	4
P99171	ALTETDGDIDKAIDYLR	3.952	10.2	5E-23	0.22		1	1
P99171	TKTDNDAFGAYLHMGGR	6.555	12.2	1E-32	0.01		1	8
P99171	ALTETDGDIDKAIDYLREK	4.099	12.4	9E-34	0.24		2	1
P99171	GGKLVDVRYEVGEGMEKR	6.213	7.5	2E-12	-0.3		3	8
P99171	YVSSEQVSEEEINHEREVLK	4.383	11.9	7E-31	0.17		1	2
P99171	KALTETDGDIDKAIDYLREK	4.407	11.5	1E-28	-0		3	3
P99171	SVDERIKEAISTIGEKL SVR	5.851	9.6	3E-20	0.03		3	7
P99171	FAIRTKTDNDAFGAYLHMGGR	8.25	11.838	0	0.146		2	9
P99171	EVLKQQALNEGKPENIVEKMVEGR	4.9	8.3	5E-15	0.06		3	4
P99172	QIVFSPEIMSWIEQR	4.419	9.1	8E-18	0.09		0	3
P99174	TQIDQIIDEAK	3.961	7.2	3E-11	0.16		0	1
P99174	NLEDFNKMVEAGATR	4.538	8.4	3E-15	0		1	3
P99174	TSTGFAGGGATAEDVK	4.318	8.3	4E-15	0.1		0	2
P99174	TQIDQIIDEAKAYHFK	5.372	8.7	2E-16	0.05		1	5
P99174	ASGGVRNLEDFNKMVEAGATR	6.169	9.5	1E-19	-0.28		2	8
P99174	LIDHTLLKPESTRTQIDQIIDEAKAYHFK	6.095	8.4	3E-15	-0.04		3	8
P99177	FINAKYFEEIIFTR	5.844	6	2E-08	0.03		1	7
P99177	NLQDVHPPHDVATAVDTEGVAVR	4.506	10.1	6E-22	-0		-2	3
P99177	AEHSFDVNEVIKDFPILDQKVNGKR	5.482	10	1E-21	0.06		-2	5
P99177	LAYLDSTATSQTPMQVLNVLEDYYKR	4.478	7	2E-10	0.14		1	3
P99177	AGVITFNLQDVHPPHDVATAVDTEGVAVR	4.523	7.34	0	0.264		0	3
P99178	AHWDIVEELK	4.601	6.1	3E-08	0		0	3
P99178	FVYLTNEGAQLER	4.489	9.8	5E-21	-0.01		0	3
P99178	VVDEILELDEQRR	4.102	6.1	2E-08	0.11		1	1
P99178	NKENADDVIAEMR	4.214	9.8	5E-21	0.09		1	2
P99178	AHWDIVEELKMADFDR	4.357	11.6	2E-29	0.12		1	2
P99178	EGLYTIPTAEVPLTNFYR	4.287	7.5	4E-12	0.12		0	2
P99178	GDDPKVVDEILELDEQRR	4.022	6.3	7E-09	0.25		2	1

P99178	AAKPELAHTLNGSGLAVGR	8.674	9.8	3E-21	0.01		1	10
P99178	AHWDIVEELKMADFDR	4.771	12.1	5E-32	0.05		2	4
P99178	NEIIQPGVLPEKFTGQSACFR	5.921	9.9	1E-21	0.07		1	7
P99178	DKAAKPELAHTLNGSGLAVGR	8.58	10.944	0	0.104		2	10
P99178	TLGDDIKEKDSQLNEIDNKM	4.4	8.3	3E-15	0.21		3	2
P99178	IPNLISDDVPQGESDEDNVEV	4.12	12.5	2E-34	0.22		2	1
Q49VA2	IYVEDQYVR	4.249	7.4	6E-12	0.08	DEAM_Q::	0	2
Q49VA2	LVTPELNGSILPGITR	5.955	6.3	2E-08	0.05		0	7
Q49VA2	LVTPELNGSILPGITRK	8.876	6.5	4E-09	0.05		1	10
Q49W00	IVQALPTIKYIIIEQGGK	8.452	9	9E-18	0.08		1	10
Q49W01	EIFHETDEEINK	4.12	6.8	4E-10	0.1		0	1
Q49W01	EIFHETDEEINKK	4.46	9.3	8E-19	-0		1	3
Q49W01	REIFHETDEEINKK	4.853	6.2	3E-08	0.04		2	4
Q49W96	IIQALKEQADKVTLVSR	8.467	6.524	0	0.122		2	10
Q49W96	NIQPDKAEIIAFNGNFHGR	6.659	6.6	1E-09	0.32		1	9
Q49W96	RWAYDVKNIQPDKAEIIAFNG	8.071	6.887	0	0.202		3	9
Q49XE4	YKENGTLVLVLAGNDYGMGSSR	5.615	10.3	7E-23	0.2		1	4
Q49XM5	SGLTLFLPHSFEGQGPEHSSARLER	6.023	8.6	9E-16	-0.05		1	5
Q49XR0	TVAWLSGVEHVR	6.556	7.7	8E-13	0.08		0	8
Q49XR0	INDLELLEERLS	3.894	6.5	6E-09	0.14		-1	1
Q49XR0	TVAWLSGVEHVRETAPFPR	6.56	8.3	8E-15	-0.19		1	9
Q49XV6	DYFGAHTYER	5.268	8.3	5E-15	0.04		0	5
Q49XV6	NIHPTYSIEEFVNSLEKPR	5.511	10.8	2E-25	0.06		1	5
Q49XV6	NIHPTYSIEEFVNSLEKPRK	6.671	9.2	2E-18	0		2	8
Q49Y61	NVPIYILGSSTDSAHLAAR	6.652	8	2E-14	0.06		0	8
Q49YC4	VIDAAVEQAYNGEK	4.051	8.5	1E-15	-0.04		0	3
Q49YC4	IIGDGIGPDIWKAASR	5.861	10	5E-22	0.04		-2	7
Q49YI8	ETNTMPQWAGSCWYYLR	5.625	7.7	7E-13	0.06		0	6
Q49YI8	SKGNVINPDDIVKSHGADTLR	6.48	9.7	4E-20	0.08		2	8
Q49YL7	AAHPNTIIFLTADAFGLVPPISK	6.832	8.3	6E-15	-0.27		0	9
Q49YV3	HDVVAFTTR	6.086	7.4	6E-12	0.01		0	8
Q49YV3	HHLNQVDTIFQR	6.657	10.8	2E-25	0.04	DEAM_Q::	0	9
Q49YV3	AQEIEQETRHDVVAFTTR	4.736	8.2	2E-14	0.04		1	4
Q49ZC7	QRREQQNQQPEFTNKLFSDEVIEKIAGIAAR	4.933	7	2E-10	-0.16		-2	4
Q4L3N6	LFVDQIVSFVNNSPYHLK	5.294	9.6	4E-20	0.06		0	5
Q4L4X3	GYGPLLDGFRK	8.597	6.3	6E-09	-0.39		1	10
Q4L4X3	LFATDWDNVKPDVYILGK	4.336	7.4	1E-11	0.14		1	2
Q4L4X3	GLEPDKAEIIAFNGNFHGR	5.43	7.9	1E-13	0.37		1	5
Q4L5A8	VVIPSGPYDAKGLLLSSIR	8.457	8.214	0	0.11		1	10

Q4L5C8	SFGNSEVYIER	4.497	8.4	3E-15	0.08		0	3
Q4L5C8	FIGPHIEHLDMFGDKVK	6.02	7.6	4E-13	0.05		1	5
Q4L5W5	AGVKFNDADLIGLPIR	5.958	9.8	9E-21	0.05		1	7
Q4L5W5	AGVKFNDADLIGLPIRIVVGK	8.623	10.797	0	0.102		2	10
Q4L658	SNLVMMGVLPQFK	8.58	8.4	3E-15	0.05		0	10
Q4L6T0	IINEPTAAALAYGLDKTDQDQK	4.116	10.3	4E-23	0.19	DEAM_Q::	1	2
Q4L7C9	LTVINELAWHNLFAQ	5.302	6.3	2E-08	0.36		-1	5
Q4L848	VADIKIPTSEIKNISQDQEIHAVPDLDSKNISR	4.767	6.8	5E-10	0.04		3	4
Q4L860	QAYNNQTGVNEKEREE	4.355	7.3	7E-12	-0.04		-1	3
Q4L881	YGGAEHPhAAQQPENYELRG	6.02	12.2	2E-32	0.07		-2	5
Q4L881	LFVYGGAEHPHAAQQPENYELRG	6.092	10.7	5E-25	0.05		1	5
Q4L881	KLFVYGGAEHPHAAQQPENYELRG	6.613	6.1	5E-08	-0.02		2	8
Q4L8E9	AGLHNPPMEDAAYTNIAK	5.347	8.1	3E-14	0.05		0	5
Q4L8T0	SYDVKPPAQTEEQR	4.562	9.8	8E-21	0.1	DEAM_Q::	1	3
Q4L8T0	RSYDVKPPAQTEEQR	5.776	8.2	3E-14	0.03	DEAM_Q::	2	7
Q5HK07	AHWDLVEELK	4.608	6.1	9E-08	0		0	3
Q5HL19	HLGGFPISGQFI	6.081	9.7	2E-20	0.11		-1	8
Q5HL19	HLGGFPISGQFIActNPQVIEQHDAK	5.586	10.3	2E-23	0.05	Cys_CAM::	0	5
Q5HL59	LMEILEEAGLPQ	3.614	8.2	7E-15	0.15		-1	1
Q5HLP4	MVHDFPIYPIR	6.533	8.4	2E-15	0.08		0	8
Q5HM47	QAYDNQTGVNEQ	3.639	8.4	3E-15	0.09		-1	2
Q5HM47	QAYDNQTGVNEQER	4.063	9.1	6E-18	-0.07		0	3
Q5HN81	SLNLSNTAALLIYEALR	5.683	6.5	4E-09	0.06		0	5
Q5HN81	TNHIVLYQPEIPANTGNIAR	6.558	10.3	6E-23	0.03		-2	8
Q5HNJ5	RNDAQLTIVNVIDSR	5.507	8.298	0	0.048		1	5
Q5HNS2	QLQELSLR	5.56	6.5	3E-09	0.07		0	6
Q5HP16	FYTWNPATLSIGYFQR	8.231	6.37	0	0.083	Oxidation_HW::	0	9
Q5HRD1	GNDILIDLMGADHHGYINRLK	6.066	7.5	7E-12	-0.03	Oxidation_M::	1	5
Q5HRF7	IQGDANVFVFPsLEAGNIGYKIAQR	6.015	10.6	3E-24	0.01		1	7
Q5HRF7	KAPGAKIQGDANVFVFPsLEAGNIGYK	8.028	14.652	0	0.131		2	9
Q5HRM3	NSYKLIEER	5.976	6.7	1E-09	0.03		1	7
Q6GHQ0	LGGFDWFKR	8.607	6.4	7E-09	0.03		1	10
Q6GHQ0	NGLIDDFDIAR	3.908	8.1	6E-14	0.14		0	1
Q6GHQ0	FIVDKENEVSDPKELIAR	4.376	7.7	6E-13	0		2	3
Q6GHQ0	VNGGFIVTGGSANLLGVKELLSDMVSEKVR	6.086	6	9E-08	-0.24		2	7
Q7A3C4	TMFWSEFEIR	4.466	8.9	3E-17	0.01		0	3
Q7A3C4	METLELQGAKLR	5.83	7.5	4E-12	0.02		1	7
Q7A3C4	MMSQPADTEEGRIEQYKR	4.803	9.6	7E-20	0.04		2	4
Q7A3C4	DYGESELTEPLPDSASNPDSDYR	3.395	10.3	5E-23	0.15		0	1

Q7A3F4	DGLLDPVIGR	3.795	7.2	4E-11	0.08		0	1
Q7A3F4	GLSDILKPALSR	8.626	7.2	4E-11	0.02		1	10
Q7A3F4	IIGQDQAVEMVSR	4.244	10.2	1E-22	0.1		0	2
Q7A3F4	MNNGFFNSDFDSIFR	4.128	9.3	7E-19	0.12		0	1
Q7A3F4	SKIIGQDQAVEMVSR	5.714	8.9	3E-17	0.06		1	6
Q7A3F4	MNNGFFNSDFDSIFRR	5.668	7	2E-10	0.05		1	6
Q7A3F4	QQGQQGGNGNYLEQIGR	5.57	11.1	2E-26	0.05		0	5
Q7A3F4	LTGIPVSQMDDNDIERLK	4.195	7.5	6E-12	0.23		1	2
Q7A3F4	AVSAEEYKKADDIQNEIK	4.43	9.2	4E-18	0.13		2	3
Q7A3F4	RFNEVLVNEPSAKDTVEILK	4.788	10	2E-21	0.06		2	4
Q7A3F4	FNEVLVNEPSAKDTVEILKGIR	4.806	6.2	4E-08	0.04		2	4
Q7A3F4	MIGTTAGYVGYYDDNSNTLTEKVR	4.453	9.4	6E-19	-0.01		1	3
Q7A3F4	RFNEVLVNEPSAKDTVEILKGIR	5.866	7.6	3E-12	0.06		3	7
Q7A3F4	LLPDKAIDVLDITAAHLSAQSPAVDKVETEKR	4.789	6.2	5E-08	0.04		3	4
Q7A3F6	DYLATRPNEK	6.046	6.8	3E-10	0.03		1	8
Q7A3F6	YLSNIENNVR	5.664	8.631	0	0.039		-2	6
Q7A3F6	SFQQSWNEYAK	5.656	8.178	0	0.074		0	6
Q7A3F6	SGYEDAVDYNR	3.921	6	4E-08	0.09		0	1
Q7A3F6	YYVDMAKLAEAR	5.646	7.095	0	0.059		1	6
Q7A3F6	SFQQSWNEYAKR	8.173	9.494	0	0.084		1	9
Q7A3F6	HIFYLSNIENNVR	6.141	10.5	4E-24	-0.19		0	8
Q7A3F6	TIGIDKINFYVPK	8.228	9.627	0	0.141		-2	9
Q7A3F6	TIGIDKINFYVPKYY	8.09	10.706	0	0.13		-1	9
Q7A3F6	ALESIIDNADETTQER	3.769	8.7	4E-17	0.12		0	1
Q7A3F6	KALESIIDNADETTQER	4.097	9.9	1E-21	0.12		1	1
Q7A3F6	ALESIIDNADETTQERLR	4.066	8.3	2E-15	0.17		1	1
Q7A3F6	HIFYLSNIENNVRREYHRPE	5.647	6.9	9E-11	0.05		2	5
Q7A3F6	DYLATRPNEKVLVIATDTAR	6.093	6.4	3E-09	0.03		2	8
Q7A3F6	EACYAATPAIQLAKDYLATRPNEK	5.873	9	4E-18	0.37	:::Cys_CAM:.....	2	7
Q7A3G6	QMNDSVNNDVDEHEYRK	4.328	8.9	1E-17	0.15		1	2
Q7A3H8	KYEAQTIPAVEQK	5.668	7.1	5E-11	0.04		1	6
Q7A3H8	QAYEDVIEWVGPKE	3.969	10.6	1E-24	0.2		1	1
Q7A3H8	SNMNQTIMDAFHFR	6.474	6.3	2E-08	0.03		-2	8
Q7A3H8	QLDTASHFVLIFAR	6.408	10.5	1E-24	0.12		0	8
Q7A3H8	KVSKEDFETILESGR	4.818	13.8	2E-41	0.04		2	4
Q7A3H8	TRQAYEDVIEWVGPKE	4.39	12	2E-31	0.16		2	2
Q7A3I0	HMLEKEDSYQDVYLG	4.489	9.9	3E-21	0.12		1	3
Q7A3I0	QGENKFYIGDDENNALAEITYR	4.087	11.7	6E-30	0.27		1	1
Q7A3I0	FVDNNEINIDHTGVSDDELGGQGVGK	3.974	9.1	8E-18	0.18		0	1

Q7A3I0	FVDNNEINIDHTGVSDDELGGQGVGKK	4.323	9	2E-17	0.21		1	2
Q7A3I0	SNLEIKQGENKFYIGDDENNALAEITYR	4.253	9.1	9E-18	0.23		-2	2
Q7A3I5	RPNFEMEER	4.796	6.5	1E-09	0.03		1	4
Q7A3I5	MLSDFGLNPDEGR	3.867	10	5E-22	0.11		0	1
Q7A3I5	ILSEGIDELSIKR	4.617	7.71	0	0.066		1	4
Q7A3I5	KMLSDFGLNPDEGR	4.425	8.6	2E-16	0.01		1	3
Q7A3I5	GTEHFVSDLHGEYEAFQHVLR	5.246	10.229	0	0.261		0	4
Q7A3L9	HVNVNEITVRPV	6.138	10.6	1E-24	0.02		1	8
Q7A3L9	KKLDPQDIAEAVLYALTQPK	5.7	9.7	2E-20	0.06		2	6
Q7A3L9	VTSISPGMVDTAITAAYNPSPDRK	5.856	6.6	5E-09	0.05		1	7
Q7A3L9	TVLTDKIAVVTGAGSGIGEAIATLLHEEGAKVVLGR	5.519	6.8	2E-09	0.09		-2	5
Q7A3Z5	SFSEELGPK	4.465	9	1E-17	0.07		0	3
Q7A3Z5	SFSEELGPKGIR	5.801	7	2E-10	0.02		1	7
Q7A3Z5	EGADVAINYLPSEEQDAQEVR	3.639	11.2	3E-27	0.17		0	1
Q7A3Z5	VNCVAPGPFWSPLQISGGQPQSK	7.855	7.5	2E-12	-0.01	:::Cys_CAM:.....	0	9
Q7A417	TTGFDGWAPLFFR	5.529	8.2	7E-15	0.03	Oxidation_HW.....	0	5
Q7A417	NADFITINAAYNPK	5.593	11.001	0	0.111		0	6
Q7A417	AFDMDVLYTGPNRKEEK	4.627	8.4	2E-15	-0		2	4
Q7A417	SLNNVVLTPHIGNATFEAR	6.48	12.6	4E-35	0.04		0	8
Q7A417	AFDMDVLYTGPNRKEEKER	4.783	11.1	5E-27	0.04		3	4
Q7A417	IVANAAISAVQGEKPQFVVN	5.94	11.6	2E-29	0.09		1	7
Q7A417	IIANYGAGFNNIDIEYAREK	4.524	7.7	4E-13	0.06		1	4
Q7A465	MYEFLDKLISVSLPR	5.753	9.4	3E-19	0.04		1	7
Q7A467	ALAEAARESGLF	4.226	8.3	7E-15	0.1		1	2
Q7A467	VKALAEAARESGLF	4.743	9.7	2E-20	0.05		2	4
Q7A469	RGDGAESVIELV	4.118	7	2E-10	0.12		1	1
Q7A469	ILKQGPRRGDGAESVIELV	6.169	6.5	4E-09	-0.2		3	7
Q7A469	NVEILNEDETTQTALQKLFGEIAER	4.101	8.1	3E-14	0.15		1	1
Q7A492	NLFTGDNFGK	5.622	8.057	0	0.071		0	6
Q7A492	IQSQVTIEDGFENAPHAFK	4.634	6.685	0	0.129		0	3
Q7A492	VPVCGAISSYNHPEADIGPR	5.299	12.6	1E-34	0.05	:::Cys_CAM:.....	0	5
Q7A492	ADSYVQPFEIGKPIVSHVAK	6.833	7.2	2E-11	0.06		1	9
Q7A492	VIDSTLADYKKGDVVVGMLPWR	5.888	13.6	1E-40	0.04		2	7
Q7A4A8	TVGIRFETLPPEEK	4.743	6.982	0	0.1		1	4
Q7A4A8	EIIVTTPHPTAAFVAAR	6.638	6.4	1E-08	0.09		0	8
Q7A4A8	TIEGLLSQNNPVEFIAIASGKGGVGK	5.852	8.3	7E-15	0.04		1	6
Q7A4B6	RQQIYYEVFPFEGNR	5.765	8.5	3E-16	-0.18		1	6
Q7A4B6	SQDPINGVSHSEWSSR	5.232	9.1	5E-18	0.05		0	4
Q7A4C4	HYADDYLR	4.687	6.6	8E-10	0.02		0	4

Q7A4C4	ENVPFTAGVR	5.63	6.3	2E-08	0.03		0	6
Q7A4C4	QAFDDSGDLKPYTIK	4.282	8.5	1E-15	0.13		1	2
Q7A4C4	MNILVIGANGGVGSLLVQQLAK	8.64	9.7	2E-20	-0.24		0	10
Q7A4C4	MNILVIGANGGVGSLLVQQLAKENVPFTAGVR	8.368	9.7	3E-20	-0		1	9
Q7A4C8	GysAEQMVEELSQDFTNISK	3.896	10	7E-22	0.17		0	1
Q7A4D0	TLEDAEALAHAMVR	4.571	9.6	3E-20	0		0	3
Q7A4D0	NTMAIISDMNQPLGR	5.61	7.7	1E-12	0.01		0	6
Q7A4D0	DVTGTVNSIPLIASSIMSK	5.618	8.031	0	0.153		0	6
Q7A4D0	TGSGAFMKTLEDALAHAMVR	5.444	8.6	8E-16	0.05		1	5
Q7A4D0	SGYVTELVSNDIGVASMMLGAGR	4.251	11.8	4E-30	0.15		0	2
Q7A4D0	KSGYVTELVSNDIGVASMMLGAGR	5.618	7.2	4E-11	0.02		1	6
Q7A4D0	LYALRDVTGTVNSIPLIASSIMSK	8.578	6.3	2E-09	-0.3		1	10
Q7A4D0	IGDKVEEGESLLTIHSNRQDVDDVVK	4.343	7.2	4E-11	0.25		2	2
Q7A4D0	VDKHSTGGVGDTTTLVLAPLVAAVDVPVAK	5.227	6.49	0	0.193		1	4
Q7A4D5	AKELCFEGITLK	6.035	8	2E-14	-0.09		-2	7
Q7A4D8	DALDNYEFEER	3.646	8.2	1E-14	0.1		0	1
Q7A4D8	VLVPNLIKDAFLAELKEQFSQVR	8.358	7.9	1E-13	0.07		3	9
Q7A4E8	NATDNATELIDDLISLEYNR	3.658	9.3	2E-18	0.17		0	1
Q7A4N7	TNLETYFK	5.717	7.3	1E-11	0.03		-2	5
Q7A4N7	HISEALNLEVR	4.895	8.2	1E-14	0.03		0	4
Q7A4N7	ANEVQKFVTDVR	6.028	6.6	2E-09	0.02		1	8
Q7A4N7	NDQFEQETVWGPR	4.032	11	2E-26	0.1		-2	1
Q7A4N7	TDASFWKAVYNSILNKLENK	8.144	10.2	8E-23	0.02		2	9
Q7A4N7	AIPIFVFLNDQFEQETVWGPR	4.113	8.1	3E-14	0.3		0	1
Q7A4N7	VFHRDDDTKLIDQYLTINGKSR	6.765	7.5	6E-12	0.09		3	9
Q7A4N7	SRAIPFVFLNDQFEQETVWGPR	4.692	7.92	0	0.186		1	4
Q7A4P6	NSLGAEVEQHV	4.484	11.3	3E-28	0.09		0	3
Q7A4Q3	MALWYTEMQR	5.683	6.177	0	0.041		0	6
Q7A4Q3	EVEEAFAGQK	4.618	7.98	0	0.087		1	4
Q7A4Q3	HHLNQVDTIFER	5.61	10.8	2E-25	0.04		0	5
Q7A4R2	IYNYINDR	5.786	7.9	7E-14	0.03		0	5
Q7A4R2	FYNLSEIAR	5.697	6.391	0	0.051		0	6
Q7A4R2	LYEKELGAR	6.056	6.5	2E-09	-0.27		-2	8
Q7A4R2	IGDDSNALYLYEKELGAR	4.164	10.3	6E-24	0.21		1	1
Q7A4R2	IDFSSILETFKDSLSQEVEVTR	4.024	9.6	8E-21	0.19		1	1
Q7A4R2	IGDDSNALYLYEKELGARTFDEE	3.916	13.5	1E-40	0.23		2	1
Q7A4R2	IDFSSILETFKDSLSQEVEVTRR	4.388	8.1	1E-14	0.13		2	2
Q7A4R2	AVSAPKIDFSSILETFKDSLSQEVEVTR	4.417	10.6	3E-25	0.04		2	3
Q7A4S2	LSPSEVTAIADALGQLRHD	4.571	10.4	2E-23	0.11		1	3

Q7A4S5	MNEQQTIEQIK	4.437	7.7	7E-13	0.09		0	3
Q7A4S5	MNEQQTIEQIKAR	5.839	8.7	2E-16	0.03		1	7
Q7A4T5	LQQLSNEYILGGVNSPSR	5.977	9	1E-18	-0.28		0	7
Q7A4T5	EGHGAYLYDVGDNKFIDYLGAYGPPIAGHAHPHITK	6.064	6.3	9E-09	0.36		1	5
Q7A4T8	IVDFQYPQLNEIER	4.065	9	3E-17	0.2		0	1
Q7A4U5	EIFLVVTGANKR	8.472	7.3	9E-12	0		1	10
Q7A4U5	LYQENGKTSFEPADLK	4.61	10.7	2E-25	0.02		1	4
Q7A4U5	VFDNSQLVAEYAADIIR	3.884	11	1E-26	0.14		0	1
Q7A4U5	VFDNSQLVAEYAADIIRK	4.446	8.4	1E-15	0.12		1	3
Q7A4U5	LYQENGKTSFEPADLKAHR	6.78	8.2	5E-15	0.29		2	9
Q7A4U5	AMNFKVFDNSQLVAEYAADIIR	4.47	7.4	3E-12	0.03		-2	3
Q7A4U5	AMNFKVFDNSQLVAEYAADIIRK	6.133	9.3	3E-19	0.21		-2	8
Q7A4U5	DVVEKLYQENGKTSFEPADLKAHR	5.543	12.5	2E-34	0.06		3	5
Q7A4U5	MVNVILDKEAAAGLPEDVKAYFTSR	4.675	6.8	2E-10	0.09		2	4
Q7A4U5	MVNVILDKEAAAGLPEDVKAYFTSRFA	4.687	7.2	2E-11	0.09		3	4
Q7A4U5	KQFNNNPTTIAGFHLDTDQAPVLDELKK	5.372	7.3	5E-12	0.05		2	5
Q7A4V3	ANEESSKKLFDEFR	4.736	11.3	2E-27	0.01		2	4
Q7A4V3	LFDEFRETQINFQQK	4.451	6.9	3E-10	-0		1	3
Q7A4V3	AVNLYDYANQLEQALR	4.287	10.8	2E-25	0.09		-2	2
Q7A4V3	KLFDEFRETQINFQQK	5.671	12.3	6E-33	0.06		2	6
Q7A4V3	EAFANVKANEESSKKLFDEFR	4.846	11.2	3E-27	0.07		3	4
Q7A4V3	AVNLYDYANQLEQALRESEY	3.892	9.3	2E-18	0.16		-1	1
Q7A4V3	MSQVFQEINQIIVKPLDEIYAD	3.971	11.1	1E-26	0.23		1	1
Q7A4V3	AVNLYDYANQLEQALRESEYK	4.147	12.3	1E-32	0.15		-2	1
Q7A4V3	ANEESSKKLFDEFRETQINFQQK	4.834	10	2E-21	0.06		3	4
Q7A4V9	LQSHIENLQNRGEDIGNEISK	4.702	8.8	4E-17	0.04		1	4
Q7A4W3	LISVDDNFRNFGGFK	5.914	8.5	1E-15	0.04		1	7
Q7A4W3	LISVDDNFRNFGGFKSY	5.914	8	2E-14	-0.35		-1	7
Q7A4W3	LISVDDNFRNFGGFKSYR	8.466	10	1E-21	-0.07		2	10
Q7A4W3	DALSHYFGSSGQHSSYFER	6.08	9.9	3E-21	-0.38		0	5
Q7A4W3	QSDAFNDHFSKDALSHYFGSSGQHSSYFER	5.765	6.8	1E-09	-0.37		1	5
Q7A4Z8	IGPDPKTFEG	5.941	6.9	2E-10	0.07		1	7
Q7A4Z8	VYGNEEQVGAGIR	4.507	10.4	6E-24	0.09		0	3
Q7A4Z8	SIDTAKVYGNEEQVGAGIR	4.62	11.1	3E-27	0.01		1	4
Q7A521	GKFDDEGGAAPNNNLR	4.472	9.4	3E-19	-0.01		1	3
Q7A521	ATQLGTIANETIKEVK	6.133	8.3	3E-15	-0.2		1	8
Q7A521	FTEYDNKTDESIEKGKFDDEGGAAPNNNLR	4.178	11.5	5E-29	0.21		3	1
Q7A522	ILED MNVDWK	3.904	7.9	9E-14	0.1		0	1
Q7A522	YNMVPDHAEAR	5.241	8.2	5E-15	0.04		0	4

Q7A522	ALDYMIEIAHR	5.311	8.3	2E-15	0.04		0	5
Q7A522	ASEDAPVGPGR	4.196	6.9	1E-10	0.09		0	1
Q7A522	DGFTTHDVDHIAGR	5.024	9.6	2E-20	0.03		0	4
Q7A522	GTLDDKGPTIAAAY	4.078	11.5	2E-29	0.12		-1	1
Q7A522	SGERYNMVPDHAEAR	5.348	10.1	9E-23	0.06		1	5
Q7A522	GTLDDKGPTIAAAYAIK	5.875	11	7E-27	-0.3		1	7
Q7A522	NQTNDMTEPYTIGGGTYAR	4.321	11.3	5E-28	0.14		0	2
Q7A522	RNQTNDMTEPYTIGGGTYAR	5.724	6.3	3E-09	0.14		-2	6
Q7A522	LVTAYRNQTNDMTEPYTIGGGTYAR	6.068	8.8	3E-17	0.14		1	8
Q7A522	GLLAIESVRDDAKASEDAPVGPGR	4.321	12.6	3E-35	0.23		2	2
Q7A522	VQQYEDQIINDLKGLLAIESVRDDAK	4.16	6.3	7E-09	0.17		2	1
Q7A522	KALDYMIEIAHRDGFTTHDVDHIAGR	5.764	9.9	5E-22	-0.15		2	5
Q7A526	GNQPLSGELGKGLIR	8.626	6.8	7E-10	0.01		1	10
Q7A526	YIHSTDSVFDIRDYFAAR	5.201	6.7	2E-09	0.06		1	4
Q7A526	GIDIGDTIVPHTPFTQLSEHR	5.188	9.81	0	0.271		0	4
Q7A526	NGMIQFTNLGGVANDIWQGR	5.663	6.6	3E-09	0.07		0	6
Q7A527	VIEPDLPELEAR	3.957	8.6	3E-16	0.12		0	1
Q7A527	NGELLGSYIGKER	5.904	7.2	3E-11	0.04		1	7
Q7A527	KSIEQIDAFLAQYV	4.309	9.2	2E-18	0.1		1	2
Q7A529	LTDELNVVFQKR	5.958	8.3	8E-15	-0.11		1	7
Q7A529	VGAVMPSGMVIKDAELR	5.943	7.5	3E-12	-0.13		1	7
Q7A530	VGIEVPNQNPPTVNLR	5.905	9.9	6E-21	0.03		0	7
Q7A535	ITIGYTR	8.635	6	3E-08	-0.25		0	9
Q7A535	IALTEVWEK	4.547	6.2	2E-08	0		0	3
Q7A535	IDINKITPR	8.616	6.9	9E-11	-0		1	10
Q7A535	ENGWDNYPVCMAC	4.116	8.2	4E-15	0.12		0	1
Q7A535	VVLVTAMSPTPAGEGK	5.9	8.3	2E-15	0.03		0	7
Q7A535	EAGFDLAHVVVVATIR	4.101	8.6	2E-16	0.16		0	1
Q7A535	EENVEAVKAGIVNLER	4.342	8.3	2E-15	0.16		1	2
Q7A535	QFKENGWDNYPVCMAC	5.601	10.4	1E-23	0.05	Cys_CAM:...	1	5
Q7A535	NVMVALREPALGPTFGIK	8.756	7.9	3E-14	-0.34		1	9
Q7A535	QLKQFKENGWDNYPVCMAC	7.479	10.6	3E-25	0.19	Cys_CAM:...	2	9
Q7A535	DNLKEENVEAVKAGIVNLER	4.477	12.3	1E-33	0.25		2	3
Q7A535	TQYSFSDDQTLGAPSGFEITIR	3.916	11	1E-26	0.18		0	1
Q7A535	FGVEPVVAINAFIHDTDAEVEYVK	4.113	11	5E-27	0.17		0	1
Q7A535	DLADIVVTEAGFGSDLGAEKFMIDIK	3.757	10.3	8E-24	0.15		1	1
Q7A535	KFGVEPVVAINAFIHDTDAEVEYVKS	4.976	6.7	4E-10	0.09		3	4
Q7A535	STVTVGLADAFHELKNVMVALREPALGPTFGIK	6.486	9.3	2E-19	-0.03		2	9
Q7A537	ISQALFSGDLK	5.758	7.4	7E-12	0.03		0	7

Q7A537	TNVLIEDLKWR	5.803	9.5	6E-20	0.05		-2	7
Q7A537	FIHGEDALNDAIR	4.398	8.4	2E-15	0.1		0	2
Q7A537	VLQTEEQVDKNIEGISK	4.335	10.6	1E-24	0.13		1	2
Q7A551	HAPCDVLVVR	6.08	7.7	7E-13	0.01	::::Cys_CAM::::	0	8
Q7A551	FIVGSVSESIVR	5.717	7.426	0	0.059		0	6
Q7A551	DVETRLEFGSPK	4.414	8.8	9E-17	0.09		1	3
Q7A551	SKHFAEELLNGYK	6.488	8.2	1E-14	0.02		1	8
Q7A551	TYSSYEVYDAQFTEK	4.106	6.4	6E-09	0.12		0	1
Q7A551	TEELPADFQPQVATTQLR	3.966	10.3	4E-23	0.16		0	1
Q7A551	TEELPADFQPQVATTQLREK	4.183	8.5	6E-16	0.21		1	2
Q7A551	KLAHEINADLIMSGTSGLNAVER	5.405	11.4	2E-28	0.11		1	5
Q7A551	MITYKNILIAVDGSHEAEWAFNR	5.43	7.8	3E-13	0.07		1	5
Q7A552	GYGEYFPHR	6.792	6.1	9E-08	-0.37		0	9
Q7A552	NIISEKGYGEYFPHR	6.662	9.5	2E-19	0.02		1	8
Q7A552	QKQLISGFNVNSFGDVLTIKQLR	8.1	8.3	1E-14	0.07		2	9
Q7A553	ALEDYGIDYDQIIVR	3.742	9.8	8E-21	0.23		0	1
Q7A553	KALEDYGIDYDQIIVR	4.145	11.2	4E-27	0.18		1	1
Q7A556	GALEVEATHINEEMKK	4.837	9.7	2E-20	0.03		1	4
Q7A556	LLEPNYGGINLEDISAPR	4.038	8.7	5E-17	0.22		0	1
Q7A556	SDYPNQINNVLAFPGIFR	5.369	11.7	7E-30	0.05		0	5
Q7A556	AMANPNPEIIPDDAKAAGAR	4.484	12	5E-31	0.14		-2	3
Q7A556	VVGTRSDYPNQINNVLAFPGIFR	8.614	8.1	4E-14	0.02		1	10
Q7A559	IHLVGDEIANGQGIGR	5.323	10.2	1E-22	0.04		0	5
Q7A559	YRPHSDIIAVTPSEETAR	5.432	7.9	2E-13	0.05		1	5
Q7A559	KSTDALLNNAVATAVETGR	5.601	8.2	2E-15	0.04		1	6
Q7A559	IENQEGIDNIAEILEVSDGLMVAR	3.679	6.9	4E-10	0.18		0	1
Q7A561	KYIPLEERK	8.137	6.7	1E-09	-0.3		2	9
Q7A561	GLEGVIAAETK	4.378	6.3	9E-09	0.08		0	2
Q7A561	DAGREELFEMSVK	4.166	8	9E-14	0.14		1	2
Q7A561	SAGWIAHILEQYKDNR	6.48	11.8	3E-30	0.01		1	8
Q7A561	DAGREELFEMSVKMEKR	4.81	7.3	2E-11	0.04		3	4
Q7A561	QITKDAGREELFEMSVK	4.724	11.6	2E-29	0.04		2	4
Q7A561	ALILHADHELNASAFTAR	6.078	11.1	1E-26	0.01		0	5
Q7A561	HCMEIPHDLFTPIFAVSR	5.562	10.6	3E-24	0.04		-2	5
Q7A561	VYTHFEEYVTDHVHPMTALR	5.822	11.8	5E-30	-0.1		0	5
Q7A561	VRQDKEPLKPNPDLSYAANFLY	6.03	10.1	5E-22	0.06		-1	8
Q7A561	SASVYHCMEIPHDLFTPIFAVSR	5.993	8.5	1E-15	0	::::Cys_CAM::::	-2	5
Q7A561	TLSYIAHFDPDAENESDENRYER	4.149	6.7	1E-09	0.19		1	1
Q7A569	SKFDEQIIVVPR	5.663	9.7	2E-20	0.03		-2	6

Q7A569	EIIFNNEKNTFNGFLNK	5.897	10.2	1E-22	-0.28		1	7
Q7A569	NKPEGQNIFDALSQYEVKR	5.964	7.8	5E-13	0.06		2	7
Q7A593	ADESKFDQFK	4.313	9.6	4E-20	0.08		-2	2
Q7A593	ETVGNVTDNKELEKEGQQDKATGK	4.46	7.2	1E-11	-0.04		3	3
Q7A598	TLFDEEGNEVLYR	3.955	11.4	4E-28	0.14		-2	1
Q7A598	TEHNHDSQLEINNEEELLTLFDEEGNEVLYR	3.972	11.9	1E-30	0.19		-2	1
Q7A598	TEHNHDSQLEINNEEELLTLFDEEGNEVLYRK	4.159	6.5	3E-09	0.22		-2	1
Q7A5C9	SYQPHYFQEV	6.478	9.2	2E-18	0.02		-2	8
Q7A5D1	LAQINDEIAVIERVL	4.09	8.2	1E-14	0.1		1	1
Q7A5G0	AREYFEGYAPSSPSFALVK	6.092	8.4	1E-15	-0.19		1	7
Q7A5G0	AREYFEGYAPSSPSFALVKDGG	6.124	9.2	2E-18	-0.03		2	7
Q7A5G0	HQIEGHDVMNVINQLQTLFNKYCEER	4.964	6.2	2E-08	0.05		1	4
Q7A5G2	SLNLLASQVLEIHK	5.654	8.261	0	0.1		0	6
Q7A5G5	EAVAYQVYPR	5.632	7.1	3E-11	0.03		0	6
Q7A5G5	QLENKGWNALFIENHDQPR	5.345	7.7	1E-12	0.07		1	5
Q7A5G5	TYAPAFDMDMNQPGIQTWLQEMKDR	4.142	6.5	8E-09	0.19		1	1
Q7A5G5	TINVAQQLEDEHVSVLQFYKDLIQLRK	5.446	6.3	4E-08	0.07		2	5
Q7A5G7	WAGVPFYIR	8.45	6.1	5E-08	-0.19		0	10
Q7A5G7	SAEALNNQIR	5.596	7	2E-10	0.03		0	5
Q7A5G7	LVIEKPFSGDLK	5.984	6.4	1E-08	0.02		1	7
Q7A5G7	DITNDDFRNQVK	4.164	6.2	5E-08	0.1		1	1
Q7A5G7	NFVRGQYGEYIDGK	5.885	7.9	2E-13	0.04		1	7
Q7A5G7	HFQSEDVKKNFVRGQYGEYIDGK	6.201	7.9	1E-13	-0.06		3	8
Q7A5G8	QQLECNPNVAR	5.564	7	1E-10	0.03		0	5
Q7A5G8	LGLEKEQVEESIR	4.427	7.4	4E-12	0.1		1	3
Q7A5G8	AGTKLGLKEQVEESIRNLIIGTSK	6.314	7.7	4E-13	-0.01		3	8
Q7A5G8	GGTTQAGLDTLSQYDLVSIFEDCLNAAVDR	3.643	7.5	2E-12	0.32		0	1
Q7A5G8	LGVNYSYDDATLLKDADYVFLGTPHDFDALATR	4.256	6.3	1E-08	0.18		2	2
Q7A5I3	IADESFDGDALKFE	3.709	8.8	6E-17	0.14		1	1
Q7A5J0	IKVEELDPENNR	4.325	6.4	1E-08	0.08		1	2
Q7A5J0	GQFHENDVIEGVVVR	4.615	11.3	7E-28	0		0	3
Q7A5J0	VTEVVKGGLVVDVGQR	5.95	8.3	8E-15	0.02		1	7
Q7A5J0	ILGIDEENERVSLSIK	4.425	7.7	7E-13	0.18		1	3
Q7A5J0	IKVEELDPENNRVILSR	4.786	10.6	2E-24	0.04		2	4
Q7A5J0	HIGTPGEVLEPGQQVNVK	4.964	11.2	1E-27	0.04		0	4
Q7A5J0	AYLENEEEDNPTIGDMIGDKLK	3.899	10.8	2E-25	0.25		1	1
Q7A5J0	GFVPASLISTDFIEDFSVFDGQTIR	3.744	8.6	6E-16	0.32		0	1
Q7A5J0	LANFGAFVEIAPGVQGLVHISEIAHK	6.08	6.8	7E-10	0		0	6
Q7A5J0	AVEQEENDAKKDQLLQSLNEGDVIHGK	4.379	7.7	2E-12	0.22		2	2

Q7A5J0	KAVEQEENDAKKDQLLQSLNEGDVIHGK	4.646	11	5E-26	-0.04		3	3
Q7A5J0	TEEFNESMINDIKEGDKVTGEVQQVEDK	3.966	8.3	4E-15	0.33		-2	1
Q7A5J0	AVEQEENDAKKDQLLQSLNEGDVIHGKVAR	4.649	10.6	2E-24	-0.03		3	3
Q7A5J0	ISLSIKDTLPTPFENIKGQFHENDVIEGVVVR	4.853	6.9	5E-10	0.06		2	4
Q7A5J1	VQLIGFGNFEVR	5.929	8.7	3E-17	-0.39		0	7
Q7A5J1	GEKVQLIGFGNFEVR	6.047	9.5	5E-20	-0.3		1	7
Q7A5M6	GQDLVYFMPR	5.719	8.1	2E-14	-0.04		0	6
Q7A5M6	EFIQQAPSSPSYALFKGQDLVYFMPR	5.736	8.4	1E-15	0.04		1	6
Q7A5N4	LGFMSFFTK	8.881	7.5	2E-12	-0.37	:::Oxidation_M:::	0	10
Q7A5N4	ENGVNLAEVSPK	4.314	9.1	3E-18	0.08		0	2
Q7A5N4	NFAEIEAEIANLAVK	4.212	11	2E-26	0.09		0	2
Q7A5N4	YARENGVNLAEVSPK	5.722	9.5	1E-19	0.03		1	6
Q7A5N4	NFAEIEAEIANLAVKAR	4.755	10.3	2E-23	0.05		1	4
Q7A5N4	ENGVNLAEVSPKTN DVVR	4.484	9.8	6E-21	0.13		1	3
Q7A5N4	PEVKVPELAESITEGTIAEWLK	4.222	8.5	8E-16	0.15		-2	2
Q7A5P8	GAALNAVQVLEQVMR	5.976	9.4	5E-19	-0.18		0	7
Q7A5Q0	QLEKIELDDIQSSR	4.256	6.1	8E-08	0.14		1	2
Q7A5Q0	ILSGELDSQTGHVSLGKNER	5.442	8.7	2E-16	0.06		1	5
Q7A5R6	CITAHVDTLGAMVK	6.903	8.1	3E-14	0.02		0	9
Q7A5R6	HGLFGAGIESSHAMER	5.625	10	6E-22	0.03		0	5
Q7A5R6	HLDDKASVAMILQLLK	6.104	9.5	2E-19	0.01		1	8
Q7A5T2	GVGIENICPFSR	5.948	8.2	1E-14	-0.01	:::Cys_CAM:::	0	7
Q7A5T2	LGVNHWWQIPVNPQK	8.889	8.4	3E-15	0.01		0	10
Q7A5T2	IFSEIGKQTEMFAR	6.052	9.8	1E-21	-0.3		1	8
Q7A5T2	QDDDN YFEQPGKLFR	4.099	6.9	4E-10	0.15		1	1
Q7A5T2	GVGIENICPFSRDGQMR	5.989	8.1	4E-14	-0.15	:::Cys_CAM:::	1	7
Q7A5U6	LVNITIKEIEER	4.733	8.9	2E-17	0.03		1	4
Q7A5V7	VVNAAGPWVDDVR	4.159	9	1E-17	0.1		0	1
Q7A5V7	EGLKGGGYVEYR	5.858	6.3	8E-09	0.03		1	7
Q7A5V7	HMAQDIVDLVSKR	6.124	10.3	2E-23	0.02		1	8
Q7A5V7	KVVNAAGPWVDDVR	5.533	7.4	8E-12	0.04		1	5
Q7A5V7	VALVEMQDFAQGTSSR	4.306	7.6	9E-13	0.2		0	2
Q7A5V7	GVHVVIDQSKFPLGQAVYFDTEKDGR	5.415	9.1	4E-18	0.06		2	5
Q7A5X7	KPDEIRPLDSEVGILPR	4.595	6.1	4E-08	0		2	3
Q7A5X7	ALKYIIPDTADFPYTIR	5.964	7.5	2E-12	0.03		1	7
Q7A5X8	KNEIKEYR	8.047	6.3	2E-08	-0.25		2	9
Q7A5X8	VHETDTGSPEVQIAVLTAEINAVNEHLR	4.468	7.5	2E-12	0.14		0	3
Q7A5Y2	AVLIDAIEAALITAYKK	6.114	9.7	6E-21	-0		1	8
Q7A5Y2	SSNELL LATEYLEKEKKIPR	5.928	13.1	5E-38	0.05		-2	7

Q7A5Y3	ASEGIVEVKER	4.668	6.4	5E-09	-0.01		1	4
Q7A5Y3	DVPSEAEQSHR	4.538	7.8	2E-13	0.09		0	3
Q7A5Y3	SVTPFDLHLISINPK	6.473	9.3	6E-19	0.14		0	8
Q7A5Y3	AGVKFNDADLIGLPLR	5.957	8.8	6E-18	-0.36		1	7
Q7A5Z1	AGAIQDLKVVWGER	6.059	8.1	2E-14	-0.31		1	7
Q7A5Z1	AVPDAPHEALLCLDATTGQNALSQAR	4.386	10.3	3E-23	0.2		0	2
Q7A5Z3	VIEEDFSSYINQFEWR	3.932	9.7	1E-20	0.14		0	1
Q7A5Z3	DAKFPVVQNVNAQGETDKEVIKSNMVK	6.223	8.1	4E-14	0.16		3	8
Q7A612	LAFQTEDMKR	5.996	7	1E-10	-0.39		1	7
Q7A612	PFTPNEIKNK	9.002	6.2	3E-08	0		-2	10
Q7A612	PFTPNEIKNKEFSR	8.886	12.7	4E-35	-0		-2	10
Q7A612	AEAQANQMVGDAVEKAR	4.535	8.1	4E-14	-0		1	3
Q7A612	NGLEPTEVANFLEQLSTEIER	3.925	7.8	6E-13	0.25		0	1
Q7A612	VKNGLEPTEVANFLEQLSTEIER	4.292	11.5	6E-29	0.2		1	2
Q7A615	RIIDFLSGTVY	5.381	6.5	5E-09	0.04		-1	5
Q7A615	VFSDTQDIADELKNR	4.126	7.7	9E-13	0.13		1	1
Q7A615	IIDFLSGTVYAIGGDIQR	4.036	7.6	2E-12	0.13		0	1
Q7A627	GFIFVEDAGR	4.285	8	5E-14	0.12		0	2
Q7A627	GFIFVEDAGRGYR	6.039	6.7	1E-09	-0.25		1	7
Q7A627	GSVLITSLNELDAALEGKVGTVIKK	6.145	8.1	3E-14	0.01		2	8
Q7A642	EIFDVCINQK	4.108	7.2	2E-11	0.11		0	1
Q7A642	QLWNMLVLAR	8.764	6.4	2E-09	-0		0	10
Q7A642	SYTDMDESIFEKR	4.22	11.4	4E-29	0.13		1	2
Q7A642	GAHVDLFSVVPVKR	8.636	11	6E-27	0.02		1	10
Q7A642	KAEEQERFDKLLAMR	5.803	6.4	2E-09	0.36		3	7
Q7A642	GAHYKPEFPERNDEEWLK	4.924	7.4	3E-12	0.04		2	4
Q7A642	AAEKGAHVDLFSVVPVKR	8.524	8.3	2E-15	0.01		2	10
Q7A642	TAYAGATTGQQLLYALDEQVR	4.318	6.1	2E-08	0.13		0	2
Q7A642	TTMASFQGAFEKPQFTYDDVDVSLIPPRKR	5.912	6.3	1E-09	-0.01		3	7
Q7A642	GLFAAGECDFSQHGGNR	5.318	9.5	4E-20	0.05	Cys_CAM:.....	0	5
Q7A666	IVREESELEDAFHR	4.484	10	6E-22	0.01		1	3
Q7A666	NGETVEIEIDKGKR	4.795	8	7E-14	0.04		2	4
Q7A666	VVEVAPSVGLSPTLR	5.885	8.6	3E-16	0.03		0	7
Q7A666	SEAEKSFGNSEVYIER	4.388	9.1	3E-18	0.12		1	2
Q7A666	IVREESELEDAFHRAK	4.882	7.8	3E-13	0.04		2	4
Q7A666	FIEETPELFDIQPSLDR	3.768	7.4	9E-12	0.19		0	1
Q7A666	FIGPHLEHLD MF GDKVK	6.02	7.6	2E-12	0.05		1	7
Q7A666	IASFSGTKQLLDEVGPK	6.058	8.6	3E-16	0.05		1	8
Q7A666	AKSEAEKSFGNSEVYIER	4.885	15.3	3E-51	0.03		2	4

Q7A666	NQYGNLSLLDTPFFFFGMR	5.652	9.315	0	0.166		0	6
Q7A666	FIEETPELFDIQPSLDRGTK	4.094	9	7E-18	0.26		1	1
Q7A666	HLRTDIEGMESLSHYWSTVR	5.661	6.9	2E-10	0.06		1	5
Q7A666	QANVDAIHPPGYGFLSENEQFAR	4.627	12.074	0	0.163		0	3
Q7A666	YKADESYLVGSDLGPAESYLNIER	4.065	9.6	4E-20	0.26		1	1
Q7A666	RCAEEGIKFIGPHLEHLD MF GDKVK	6.01	6.1	6E-08	0.09	:Cys_CAM:.....	3	6
Q7A666	TLEYIGNVTINGFPNVEKRPKPDYELASITVSSSK	5.977	6.3	2E-08	0.02		3	7
Q7A669	GVFDGSKPIDFEDNHEWNR	4.318	8.6	7E-16	0.21		1	2
Q7A669	GAVKFPITLDSTTWIFDDR	4.36	7.5	3E-12	0.12		1	2
Q7A669	LYSDNGVDSFIYNQEDGYSYR	3.697	10.1	1E-22	0.27		0	1
Q7A669	KVSIEDLEKGVFDGSKPIDFEDNHEWNR	4.444	8.2	2E-14	0.19		3	3
Q7A682	YFLPIHG EYR	6.461	8.5	2E-15	0.08		0	8
Q7A694	AVHDLGYAQVNDIR	5.17	10.6	2E-24	0.02		0	4
Q7A694	AVHDLGYAQVNDIRVGK	6.832	6.2	5E-08	0.33		1	9
Q7A694	AVHDLGYAQVNDIRVGKVLVY	6.83	9.5	2E-19	0.05		-1	9
Q7A694	TIELHITLQPQVLDTQGQTLTR	5.234	9.6	5E-20	0.06		0	4
Q7A694	MKTIELHITLQPQVLDTQGQTLTR	6.538	9.8	4E-21	-0.27		1	9
Q7A696	MMVQFASEAR	5.694	7.1	5E-11	0.03		0	6
Q7A696	GIDSLLSIVQMPGGIPVATTAIGAAGAK	5.733	8.4	3E-16	-0.31		0	6
Q7A696	SLKGIDSLLSIVQMPGGIPVATTAIGAAGAK	8.267	9.1	4E-18	-0.18		1	9
Q7A697	NASVTILHSR	9.026	7.7	5E-13	0		0	10
Q7A697	QGLQDQVEALKEK	4.612	10.4	6E-24	0.01		1	3
Q7A697	DYRQGLQDQVEALKEK	4.632	7.9	1E-13	0		2	4
Q7A697	HADIDLEAKNAV VIGR	4.894	9.2	9E-19	0.04		1	4
Q7A697	LSVILVGNDGASQSYVR	5.746	10.5	5E-24	0.06		0	5
Q7A697	QGLQDQVEALKEKGFTPK	5.772	11.8	3E-30	0.03		2	6
Q7A697	QIAKD YRQGLQDQVEALKEK	5.794	8.6	3E-16	0.02		3	6
Q7A697	DYRQGLQDQVEALKEKGFTPK	6.247	10.5	5E-24	0.04		3	8
Q7A697	GFTPKLSVILVGNDGASQSYVR	8.486	8	2E-14	-0.31		1	10
Q7A697	IGMISEIVHLEETATEEEVLNELNR	4.072	6.2	1E-08	0.19		0	1
Q7A6A9	EIWYLCR	5.588	7.1	6E-11	0.02		0	6
Q7A6A9	TVAEMIDAFSR	4.27	10.6	3E-24	0.16		0	2
Q7A6A9	DPDFDQFPKFP	3.812	9.8	9E-21	0.15		1	1
Q7A6A9	RDPDFDQFPKFP	4.347	10.2	1E-22	0.14		2	2
Q7A6A9	GHGGYVGEDQIPR	5.323	9.9	3E-21	0.04		0	5
Q7A6A9	EKRDPDFDQFPKFP	4.501	8.8	2E-16	0.18		3	4
Q7A6A9	RGHGGYVGEDQIPR	6.432	9.5	2E-19	0.02		1	8
Q7A6A9	VGSFDAGYGS GYLAR	5.711	6.4	1E-08	0.03		0	6
Q7A6A9	NAFTPKTVAEMIDAFSR	5.917	11.2	5E-27	0.05		1	7

Q7A6A9	GHGGYVGEDQIPRLNVLDLQR	5.386	8.6	1E-15	0.07		1	5
Q7A6A9	RGHGGYVGEDQIPRLNVLDLQR	6.437	6.3	4E-08	0.06		2	8
Q7A6C4	TVAEVGNIVEFMDGLR	4.051	8.6	4E-16	0.11		-2	1
Q7A6C4	MTVAEVGNIVEFMDGLR	4.078	9.3	5E-19	0.12		0	1
Q7A6D4	SFQEAVDSYR	4.26	9.4	2E-19	0.07		0	2
Q7A6D4	ARINGIPAVEVHATK	8.942	9.3	1E-18	0.01		1	10
Q7A6D4	LALIPSKSFQEAVDSYR	6.027	11.4	2E-28	0.05		-2	8
Q7A6D4	APFEIEDGDLDSVIEQVR	3.674	9.4	3E-19	0.16		0	1
Q7A6D4	LALIPSKSFQEAVDSYRK	8.442	10.6	1E-24	-0.07		-2	10
Q7A6D4	APFEIEDGDLDSVIEQVRAR	3.967	6.4	1E-08	0.19		1	1
Q7A6D4	MILGLALIPSKSFQEAVDSYR	5.791	7.8	4E-13	0.06		1	5
Q7A6D4	IKPHVTIKAPFEIEDGDLDSVIEQVR	4.584	9.8	7E-21	0.04		2	4
Q7A6D4	IKPHVTIKAPFEIEDGDLDSVIEQVRAR	4.957	8.9	2E-17	0.04		3	4
Q7A6D8	GVGGFNTILKEIEER	4.73	9.3	8E-19	0.04		1	4
Q7A6E5	WVDVYENK	4.258	6.9	2E-10	0.07		0	2
Q7A6E5	WVDVYENK GK R	8.204	6.5	5E-10	-0.4		2	9
Q7A6E5	LLLLNQELERFR	6.104	7.2	4E-12	-0.39		1	8
Q7A6E5	IHAIEEAGEPLTPTR	4.771	9.2	7E-19	0.03		0	4
Q7A6F8	AMQAAMDDAGIEPK	3.983	7.1	1E-10	0.09		0	1
Q7A6F8	NFNIEDHIDKKEAR	5.422	8.6	5E-16	0.05		2	5
Q7A6F8	IDTEPYSVHLAGELK	4.535	7.6	2E-12	0.01		0	3
Q7A6F8	AMSNSLGFGGHNVLVFK	8.947	6.8	7E-10	0.07		-2	10
Q7A6F8	ALSTNDDIETACRPFQEGR	4.29	8.7	3E-16	0.13		1	2
Q7A6F8	DVQYLNAHGTSTPVGDLNEVK	4.354	11.8	3E-30	0.19		0	2
Q7A6F8	VVITGMGALSPIGNDVKTTWENALK	6.006	8.3	8E-15	0.03		1	8
Q7A6F8	SMTGHLLGATGGIEAIFSALSISKDSK	6.481	11.6	5E-29	-0		1	8
Q7A6F8	GANIYAEIVGYGTTGDAYHITAPAPEGEGGSR	4.32	6.6	3E-09	0.19		0	2
Q7A6H1	HVDLPASVPLAWGAHR	6.657	11	3E-26	-0.19		0	9
Q7A6H1	GFIPVNDKFETNPNIYAIGDIATSHYR	5.403	8.7	2E-16	0.07		1	5
Q7A6H3	TLLAGLQQNHTLDFQEQR	5.314	10.7	5E-25	0.07		0	5
Q7A6H3	ALALDYVYGYTIINDITDR	3.843	7.2	2E-11	0.13		0	1
Q7A6H3	TLLAGLQQNHTLDFQEQRK	6.562	11.1	4E-27	-0.15		1	9
Q7A6H3	ALALDYVYGYTIINDITDRK	4.32	8.9	2E-17	0.11		1	2
Q7A6H3	NYKDHANELNHEVEKLYVFTK	6.075	14.6	3E-46	-0.04		2	6
Q7A6H3	ISFNDIEFLPPVTPPNNVIAFGR	4.316	10.4	2E-23	0.13		0	2
Q7A6H3	REDAVWDLTQVFADFAEGDFHPK	4.055	6.7	8E-10	0.23		1	1
Q7A6H3	VKREDAVWDLTQVFADFAEGDFHPK	4.36	7.2	2E-11	0.18		2	2
Q7A6H8	QMSIHEVER	5.365	6.5	4E-09	0.03		0	5
Q7A6H8	STALGVVIAIEQAAK	5.661	10.075	0	0.096		0	6

Q7A6H8	VVIQGFGNAGSFLAK	8.87	7.5	2E-12	0		0	10
Q7A6H8	LGFDEGMYDLIKEPLR	4.22	8.4	1E-15	0.12		1	2
Q7A6H8	ASIVVEAANGPTTPEATR	4.454	10	4E-22	0.11		0	3
Q7A6H9	EAYGNKDFIVGYR	5.741	10.4	1E-23	0.02		1	6
Q7A6H9	SKYEPLFDKVELPNGVELR	4.766	8	5E-14	0.04		2	4
Q7A6H9	AFPGQPSIAHDSIEGLKR	5.381	9.4	7E-19	0.05		1	5
Q7A6H9	MKSKYEPLFDKVELPNGVELR	5.967	6.8	1E-09	0.05		3	7
Q7A6H9	ALVQIHGGGAQALPELIPDGDVVPSPISLK	5.244	9.3	1E-18	0.06		0	4
Q7A6I1	TVENFVTHAK	6.556	7.4	7E-12	0.1		0	8
Q7A6I1	NGYYDGITFHR	6.652	7.3	2E-11	0.03		0	9
Q7A6I1	ANYPQLNKEVQQGEIK	6.116	6.2	5E-08	0.33		-2	8
Q7A6J4	HIEDKFANYAASK	6.119	7.4	7E-12	-0.01		1	8
Q7A6J4	ILNGESTEEFEYVDR	3.877	7.4	9E-12	0.13		0	1
Q7A6J4	DKVNFVQAEVTKIDRDAK	6.174	10.1	5E-22	0.05		3	8
Q7A6J4	MLPMFSEELVNHAVSYLEDR	4.347	8	8E-14	0.12		0	2
Q7A6J9	ALHEEVPGVIEVEQVF	4.126	9.2	4E-18	0.17		0	1
Q7A6J9	PTEDTTMFDQVAEVIER	3.74	10.4	2E-23	0.14		-2	1
Q7A6J9	LQLHGACGTCPSSTITLK	7.678	8.7	4E-16	0.01		0	9
Q7A6K4	NGATFISTNPDVSIPKER	5.844	10.8	2E-25	0.04		1	7
Q7A6L4	INSENMGQFER	4.463	8.4	3E-15	-0.01		0	3
Q7A6L4	SWDEVPEEIKR	4.284	7.6	2E-12	0.1		1	2
Q7A6L4	ELPMEYAVEMNR	4.046	7.3	2E-11	0.12		0	1
Q7A6L4	VSEEQLFYLSMR	4.384	8.1	3E-14	0.09		0	2
Q7A6L4	TFDKLGIPEAEQK	4.596	7	2E-10	0.02		1	3
Q7A6L4	VSKVSEEQLFYLSMR	6.081	8.8	1E-16	0.05		1	8
Q7A6L4	KAPDVGDYKYGFHDDVSIF	4.231	8.1	3E-14	0.24		-1	2
Q7A6L5	MNFNNLDQLYR	5.507	8.7	2E-16	0.05		0	5
Q7A6L5	NKGVLDNCSMTVDMNNPTCGDR	4.273	9.1	8E-18	0.16		1	2
Q7A6L5	MMLGEDYVITEEMGDIEALQGVSQFPAR	3.709	7.9	3E-13	0.15		0	1
Q7A6L6	ELPIEDVKR	4.456	6.1	2E-08	0.07		1	3
Q7A6L6	LVIHGFLDPVVR	6.772	7.6	5E-13	-0.04		0	9
Q7A6L6	AHNPSWMTCLR	5.389	7.3	8E-12	0.04		0	5
Q7A6L6	GDVYQSLSQLPESVR	4.193	6.5	4E-09	0.16		0	1
Q7A6L6	EAERLVIHGFLDPVVR	5.352	7.6	7E-13	0.09		1	5
Q7A6L7	YLNFGFSGGEK	4.434	6.376	0	0.069		0	3
Q7A6L7	RNEILQLMMLEPK	5.711	6.8	1E-09	0.04		1	6
Q7A6L7	KLDKNMDFLDIDKDMAQR	4.562	7.9	2E-13	0.03		3	4
Q7A6L7	RLEEEGYEWWKEEFGSAE	4.063	9	1E-17	0.24		2	1
Q7A6L7	SAINAKREEGQEINLMQFIK	5.825	10.2	2E-22	0.06		2	6

Q7A6L7	AGLFLAMQYPSEITGVTNADFMR	4.246	9.6	7E-20	0.12		0	2
Q7A6L9	ADESKFEQAK	4.454	7.4	4E-12	0.1		-2	3
Q7A6L9	AKEFVENAKEK	6.192	8.7	2E-16	-0.05		2	7
Q7A6L9	ATDFIDKVKGNKGE	6.102	8	9E-14	-0.26		3	7
Q7A6L9	ADESKFEQAKGNVK	6.114	10.6	8E-25	-0.39		-2	8
Q7A6L9	ETVGNVTDNKNLENEGKEDKASGK	4.449	11.1	1E-26	-0.04		3	3
Q7A6L9	GNVKETVGNVTDNKNLENEGKEDK	4.528	6.8	1E-09	-0.02		3	3
Q7A6L9	ADESKFEQAKGNVKETVGNVTDNK	4.755	7.9	3E-13	0.03		-2	4
Q7A6M7	FEAGWCPDCR	4.16	9.4	3E-19	0.08		0	1
Q7A6M7	SPEQVESFLAETFK	4.179	11.3	8E-28	0.12		0	1
Q7A6M7	SIINSDTPVIVKFEAGWCPDCR	4.444	9.2	1E-18	0.15	Cys_CAM::Cys_CAM::	1	3
Q7A6M7	NGDKIAHLHSANAKSPEQVESFLAETFK	6.081	11.3	8E-28	0.04		2	6
Q7A6T1	ALSNLGFEPYFEER	4.243	8.3	7E-15	0.13		0	2
Q7A6T1	KILLDESIHGVFTGLDAQHLR	5.976	9.1	8E-18	0.01		1	5
Q7A6T4	LMNHDLYPEKIDNR	5.352	10.1	2E-22	0.05		1	5
Q7A6V8	NLISFTGDTLDHLWR	5.17	6.4	2E-08	0.05		0	4
Q7A6V8	GMPEGEYDLGGQKVTVQSQQAR	4.618	7.1	1E-10	0.01		1	3
Q7A6X5	MLDEHEITSQR	4.497	8.7	2E-16	-0		0	3
Q7A6X5	ESLIESILNFKPLGTR	5.909	9	2E-17	-0.11		1	7
Q7A6X5	ALAPLCDTKESLIESILNFKPLGTR	6.148	10.6	3E-24	-0.19		2	8
Q7A6X7	LNHQQDFIDATFTALKSDR	5.275	11.6	3E-29	0.05		1	5
Q7A6X7	VIAHLPNFESD TDFVATYR	4.521	8	1E-13	-0.01		0	3
Q7A6X7	RLNHQQDFIDATFTALKSDR	6.43	7.3	2E-11	0.1		-2	8
Q7A742	EAFEFAAENKVTPK	4.596	8.3	7E-15	0.01		1	3
Q7A742	LVLGDIEVVGSLVGTR	4.253	6.8	8E-10	0.09		0	2
Q7A742	VVAVGLPVDKMNLDIPR	5.866	10.4	2E-23	0.05		1	7
Q7A742	QDLREAFEFAAENKVTPK	4.709	8.6	8E-16	0.06		2	4
Q7A742	KLEEINDIFEEMEKG TITGR	4.357	13.8	3E-41	0.13		2	2
Q7A742	ALKPGEALVQTEYCGVCHTDLHVK	6.081	7.7	1E-12	0.01	Cys_CAM::Cys_CAM::	1	8
Q7A759	ADLLLWFLRPEMK	5.993	6.9	8E-11	-0.18		1	7
Q7A759	DALVTEFQS FLENTATVR	3.831	8.2	2E-14	0.14		0	1
Q7A759	IVPKDERDALVTEFQS FLENTATVR	4.39	6.1	3E-08	0.13		2	2
Q7A783	ILAESPNI AISSSR	5.94	10.4	1E-23	0.03		0	7
Q7A788	LMLEAIEQKDTVKNNN	4.593	8.9	2E-17	0.01		2	3
Q7A788	TYNLHFFTPSSIGA FGDSTPK	6.551	11.2	1E-27	0.01		0	8
Q7A7B3	TVEVPVQLVGEAVGAK	4.408	8.749	0	0.178		0	3
Q7A7B5	DIAHPINS DMR	5.07	9.7	2E-20	0.04		0	4
Q7A7B5	TPDGEFRDIAHPINS DMR	4.485	8.1	3E-14	0.15		1	3
Q7A7B5	VYDETDEVVPDKNATSE DSEA	3.568	6.1	7E-08	0.19		1	1

Q7A7I6	YNLAPDELEKYK	4.629	8.2	2E-14	0.01		1	3
Q7A7I6	LLTGEDGEHAVLSR	4.559	9.8	1E-20	-0		0	3
Q7A7I6	LLTGEDGEHAVLSRY	4.572	10.4	2E-23	0.01		-1	3
Q7A7I6	ADITVVNDTGELYNVINQK	3.856	11.6	2E-29	0.25		-2	1
Q7A7I6	SKLHLNDLHDSEISLISTSGTF	5.213	6.9	3E-10	0.06		-1	4
Q7A7I6	LHLNDLHDSEISLISTSGTFSDR	4.53	8.628	0	0.238		0	3
Q7A7I6	SKLHLNDLHDSEISLISTSGTFSDR	5.232	11.6	6E-29	0.1		1	4
Q7A7I6	SKLHLNDLHDSEISLISTSGTFSDRMTK	6.013	8.1	5E-14	0.08		2	6
Q7A7J7	MNMHILY	6.531	6.1	6E-08	0.06		-1	8
Q7A7J7	MNMHILYNLR	8.414	8	8E-14	-0.26		0	9
Q7A7J8	TSPEDAVKKAETYKGQK	5.952	11.3	4E-28	0.03		3	6
Q7A7J8	GISFENSNGEWAYKVTQQK	6.104	9.5	6E-20	-0.27		1	7
Q7A7K2	QQNEFQDYGGQFGGQQSGQNNSYNSSNTK	4.273	8.8	5E-17	0.19		0	2
Q7A7K4	ALTAGIVGLPNVGK	8.941	8.6	3E-16	0.03		-2	10
Q7A7K4	AGALAANYPFATIDPNVGIVEVPDAR	3.92	8.9	3E-17	0.2		0	1
Q7A7L2	AQQNGEFDSEIVPVSIQR	4.085	11.6	1E-29	0.17		0	1
Q7A7L2	KGEPILVTKDEGVRENVSVEK	4.813	6.3	8E-09	0.03		3	4
Q7A7L2	GEPILVTKDEGVRENVSVEKLSR	4.805	6.4	5E-09	0.03		3	4
Q7A7T9	FFFPDVQVR	5.518	8.5	8E-16	0.03		0	5
Q7A7U9	MINQVYQLVAPR	8.385	8.2	2E-14	0.01		0	9
Q7A7W3	GTEITSIFYPK	5.883	7.4	7E-12	0.04		0	7
Q7A7W3	AHPELLNMFNQTNQK	6.833	7.3	9E-12	-0.29		0	9
Q7A7W3	AHPELLNMFNQTNQKR	8.674	9.1	5E-18	0.01		1	10
Q7A7W3	SLNYDMDRVHYETFIPR	5.357	9.3	6E-19	0.1		1	5
Q7A7W3	LGSIGVTPLVAMYEAASAK	5.996	12.4	1E-33	0.03		-2	7
Q7A7X1	MQEAYIVAYGR	5.678	8.8	8E-17	0.03		0	6
Q7A7X6	SMQPFGGIR	8.83	6.7	7E-10	0	::Oxidation_M:.....	0	10
Q7A7X6	LREELSEQYR	4.584	6.4	3E-09	0		1	3
Q7A7X6	THNQGVFDAYS	6.553	11.2	2E-27	-0.01		0	8
Q7A7X6	LTREQQLDVISR	5.89	7.7	5E-13	0.03		1	7
Q7A7X6	AGVITGLPDAYGR	5.799	7.9	9E-14	0.03		0	7
Q7A7X6	LWEQVMQLSKEERER	4.747	7.5	2E-12	0.05		2	4
Q7A7X6	KAGEPFAPGANPMHGR	8.476	7.1	7E-11	-0.01		1	10
Q7A7X6	THNQGVFDAYSREMLNCR	6.536	7.7	4E-13	0.02	:Cys_CAM::	1	8
Q7A7X6	ETLIDAMEHPPEEYPQLTIR	4.106	8.9	2E-17	0.19		0	1
Q7A7X6	AACEAYGYELDEETEKIFTDYR	3.967	9.2	5E-19	0.21		1	1
Q7A7X6	AACEAYGYELDEETEKIFTDYRK	4.202	6.7	8E-10	0.14		2	2
Q7A7X6	VASTITSHDAGYLDKDLETIVGVQTEKPFKR	5.495	10.8	9E-26	0.04		3	5
Q7A7X6	TPDYNELFSGDPTWVTESIGGVGIDGRPLVTK	3.93	6.7	9E-10	0.22		1	1

Q7A808	ALPAVFGGK	8.941	8.5	5E-16	0.01		0	10
Q7A808	LINTAIAER	5.976	6.4	4E-09	0.03		0	7
Q7A808	IGAYLIDAFHR	6.782	8.1	6E-15	0.01		0	9
Q7A808	VINNDGYTVER	4.29	6.4	5E-09	0.1		-2	2
Q7A808	GAFNEENPYMGIYDGK	4.097	9.1	1E-18	0.19		0	1
Q7A808	QHIKPVLFVINNDGYTVER	6.418	6.9	9E-11	0.05		1	8
Q7A808	MFAHITVAQGYITPENATTEIPR	5.377	8.6	1E-16	0.07		0	5
Q7A808	AVEQAGKYVHHSLGEGTFDDYRK	6.095	9.4	6E-20	0.05		2	5
Q7A808	KMFAHITVAQGYITPENATTEIPR	6.394	7.5	6E-13	0.04		1	8
Q7A821	NSVHYEEVPEVEFKR	4.861	11.3	1E-27	0.04		1	4
Q7A821	CICLYNAPDEEAVRR	4.66	8.1	5E-14	0.01		1	3
Q7A825	IYDQLVPR	5.717	7	8E-11	0.02		0	6
Q7A825	LQEAFSNIK	5.924	6.6	2E-09	0.02		0	7
Q7A825	TGRIWINTY	8.676	6.102	0	0.052		-1	10
Q7A825	NIYIDTSNALK	5.637	8.103	0	0.083		0	6
Q7A825	ETTAIDIPFAAR	4.111	8.4	2E-15	0.11		0	1
Q7A825	ESDAQILAGGHR	5.177	8.7	2E-16	0.04		0	4
Q7A825	HLVPATLELGK	6.136	8.6	4E-16	0.1		0	8
Q7A825	AVNVRDYIAENY	4.311	8.6	2E-16	0.15		-1	2
Q7A825	IAMIETLNNGKPIR	8.618	6.5	3E-09	0.01		1	10
Q7A825	NIYIDTSNALKGLY	5.664	11.4	2E-28	0.05		1	6
Q7A825	LAQEEIFGPVLTVIK	4.494	7.1	7E-11	0.03		0	3
Q7A825	AVNVRDYIAENYGLF	4.398	8.88	0	0.064		-1	3
Q7A825	GFFFEPTLIAVPDNNHK	6.078	10.2	6E-23	0.01		0	5
Q7A825	VAQEAFESWSLTSKSER	4.736	10.2	6E-23	0.04		1	4
Q7A825	IWINTYNQVPEGAPFGGYKK	8.373	9.3	9E-19	-0.07		1	9
Q7A825	VAQEAFESWSLTSKSERAQMLR	6.17	10.2	7E-23	-0.04		2	8
Q7A825	TGRIWINTYNQVPEGAPFGGYK	8.236	8.3	9E-15	-0.23		1	9
Q7A825	GSSDETIEVTNPATGETLSHITR	4.301	10.5	8E-24	0.22		0	2
Q7A825	VKDDQEAIANDSEYGLAGGVFSQNITR	3.856	10.4	2E-23	0.28		1	1
Q7A8D0	AIGVYGS�GR	8.684	7.8	2E-13	-0.33		0	10
Q7A8D0	HGYIVDVSKRIPF	8.342	10.7	8E-25	-0.17		2	9
Q7A8D0	ILDKYGDDVKAIGVYGS�GR	5.934	13.8	2E-41	-0.02		2	7
Q7A8D1	IHLWEASDEGWR	4.607	9.4	2E-19	-0		0	3
Q7A8D1	IHLWEASDEGWRSR	5.456	7	2E-10	0.04		1	5
Q7A8D1	SNDSPVCTGAESFIAGTASCR	4.214	10.1	3E-22	0.17	Cys_CAM:.....Cys_CAM::	0	2
Q7A8E9	WFLQDVEVLINGVR	4.333	9.2	2E-18	0.15		0	2
Q7A8E9	WFLQDVEVLINGVRETR	4.519	6.5	4E-09	0.04		1	3
Q820A6	LQAQFDAVK	5.776	7.3	6E-12	0.03		0	7

Q820A6	PKLQAQFDAVK	9.002	10.1	2E-22	0.01		-2	10
Q820A6	APKLQAQFDAVK	8.623	7.715	0	0.079		-2	10
Q820A6	YGPHTMAGDDPTR	5.155	7.5	2E-12	0.02		0	4
Q820A6	ALEKEDYILPGYR	4.554	9.7	5E-21	0		-2	3
Q820A6	AEQYEIYKEKESK	4.786	9.9	6E-22	0.04		-2	4
Q820A6	GLWNEDKENEVIER	4.193	8.1	2E-14	0.12	:::Oxidation_HW:::.....	1	2
Q820A6	YGPHTMAGDDPTRYR	6.461	6.1	4E-08	0.02		1	8
Q820A6	AVAGEGPTLIETMTYR	4.494	7.1	3E-11	-0.02		0	3
Q820A6	TSDEDAEWEKKDPLVR	4.193	11.9	1E-31	0.12		2	2
Q820A6	GLWNEDKENEVIERAK	4.502	9.6	2E-20	0		2	3
Q820A6	RTSDEDAEWEKKDPLVR	4.502	9.1	1E-18	-0		-2	3
Q820A6	APAIFVIQNNNYAISTPR	8.684	10.079	0	0.113		0	10
Q820A6	DRAVAGEGPTLIETMTYR	4.526	9.9	9E-22	-0.01		1	3
Q820A6	TSDEDAEWEKKDPLVRFR	4.489	7.8	1E-13	-0		3	3
Q820A6	YRTSDEDAEWEKKDPLVR	4.516	11.8	5E-31	0.01		3	3
Q820A6	FLENKGLWNEDKENEVIER	4.328	11.8	6E-31	0.18		2	2
Q820A6	DVPQIIWHGLPLTEAFLFSR	5.307	11.4	4E-29	0.04		0	5
Q820A6	KFLENKGLWNEDKENEVIER	4.613	12.6	3E-35	0.04		3	4
Q820A6	FLENKGLWNEDKENEVIERAK	4.603	6.3	6E-09	0.05		3	4
Q820A6	AIAVGIPGIQVDGMDALAVYQATKEAR	4.422	10.9	1E-26	0.24		1	3
Q820A6	SKQTA AETLAQKAIAVGIPGIQVDGMDALAVYQATK	5.788	7.3	4E-12	0.03		2	7
Q931E9	NKIDFSKDFNFK	8.317	9.293	0	0.078		2	9
Q99RW4	IDWDREHPR	5.271	6.6	3E-09	0.04		1	5
Q99RW4	FSWGHINS DQR	6.522	8.3	2E-14	0.09		0	8
Q99RW4	ATNEESYLMQK	4.485	7.8	4E-13	0.09		0	3
Q99RW4	YDPNQCILCGR	5.299	8.3	7E-15	0.04		0	5
Q99RW4	AFVEISPELAEDR	3.944	7.7	7E-13	0.12		0	1
Q99RW4	GKFSWGHINS DQR	8.636	7.585	0	0.089		1	10
Q99RW4	AFVEISPELAEDRGIHEGAEVK	4.336	7.6	2E-12	0.22		1	2
Q99RZ3	NADIKFNYGGSGALR	8.349	8.183	0	0.098		1	9
Q99S93	DNNEVRIQWR	6.046	6.9	3E-10	0.02		1	8
Q99S93	VADIKIPTSEIK	5.96	7.6	8E-13	0.02		1	7
Q99S93	TQNDQKVYNELTK	5.758	8.3	8E-15	0.12		-2	5
Q99S93	NITQDQDIHAVPKLDSK	5.259	7.6	2E-12	0.06		1	5
Q99S93	VIIDTEDHEYIIYTQNDQK	4.027	11	2E-26	0.17		0	1
Q99S93	NITQDQDIHAVPKLDSKD VSR	5.295	11.8	1E-30	0.06		2	5
Q99S93	VADIKIPTSEIKNITQDQDIHAVPK	5.389	7.3	1E-11	0.08		2	5
Q99S93	VIIDTEDHEYIIYTQNDQKVYNELTK	4.193	6.3	1E-08	0.33		1	1
Q99S93	VADIKIPTSEIKNITQDQDIHAVPKLDSK	5.427	9.8	5E-21	0.11		3	5

Q99TF4	LQQLDDDLFGGR	4.157	9.1	2E-18	0.13		0	1
Q99TF4	GVAEAFEMEYK	4.219	8.8	5E-17	0.12		0	2
Q99TF4	RLQQLDDDLFGGR	5.586	9.021	0	0.061		1	6
Q99TF4	MSAQVGAEFLQK	5.712	8.3	6E-15	0.03		0	5
Q99TF4	VISIAYETVQLPDR	4.309	9.3	5E-19	0.16		0	2
Q99TF4	VTIIGGGQAGTNAAK	8.87	7.2	2E-11	0		0	10
Q99TF4	LNGGMGILLGGVPGVPK	8.881	7.6	9E-13	0		0	10
Q99TF4	HGVVHYAVANMPGAVPR	8.505	8.642	0	0.101		0	10
Q99TF4	GHVTNKGVAEAFEMEYK	5.543	7.9	1E-13	0.05		1	5
Q99TF4	QSDLVIGAVLIPGAKAPR	8.243	11.056	0	0.112		1	10
Q99TF4	GVAEAFEMEYKSVEEALQL	3.947	9.5	1E-19	0.2		1	1
Q99TF4	TYLHLANEKLTQALIDRK	6.568	13.2	6E-38	0.13		-2	8
Q99TF4	KVISIAYETVQLPDRSSPLLSPMSEVAGR	5.76	7.2	2E-11	0.02		2	6
Q99TJ8	ASWPEVR	5.962	6.7	2E-09	-0.27		0	7
Q99TJ8	TVILPIVGR	8.91	6.4	4E-09	0.01		0	10
Q99TJ8	EVEAGRYEEWVK	4.301	6.7	1E-09	0.1		1	2
Q99TJ8	YFLATGSSSPGHDLR	6.457	7.3	7E-12	0.1		0	8
Q99TJ8	VTPAHDPNDFEIGQR	4.473	8.6	4E-16	-0		0	3
Q99TJ8	SGAVVEPYLSTQWFVR	5.709	9.3	2E-18	0.05		0	6
Q99TM6	EYAMAMER	4.302	7.6	2E-12	0.06		0	2
Q99TM6	MQPVQPPTHDLQNILTPR	6.533	8.5	3E-15	0.19		0	8
Q99TM6	NVPLYILGSSTDSAHLAAR	6.652	8	4E-14	0.06		0	8
Q99TM6	AYPAVGKNVPLYILGSSTDSAHLAAR	8.445	8.205	0	0.168		1	10
Q99TM6	DQHDGVYKFP EEVSLLQQYFGPAHQQAYVR	5.287	8.4	2E-15	0.07		1	5
Q99TM6	RDQHDGVYKFP EEVSLLQQYFGPAHQQAYVR	6.003	6.7	6E-10	-0.34		2	5
Q99TM8	AFLDHAMNLGADYVATGHYAR	6.066	9.7	3E-20	0.1		0	5
Q99TT5	TLEEVGKVFGVTR	5.84	10	3E-22	0.04		1	6
Q99TT5	TLEEVGKVFGVTRER	5.89	6.6	1E-09	0.03		2	7
Q99TW4	QAPNYEIINR	5.622	7.002	0	0.047		0	6
Q99TW4	AINEIRPGMTGAEADAISR	4.574	8.4	3E-15	0		1	3
Q99TW4	EFGHSLGHGIGLEIHEGPMLAR	5.806	9.3	6E-19	-0.03		0	5
Q99TW4	GYGKEFGHSLGHGIGLEIHEGPMLAR	6.355	11.5	5E-29	-0.34		1	7
Q99TW4	NYLESKGYGKEFGHSLGHGIGLEIHEGPMLAR	6.331	6.4	9E-09	0.05		2	7
Q99U74	IGFTTEPIDAR	4.32	8.3	9E-15	0.09		0	2
Q99U74	FSIEGVDALVPMLQR	4.231	6.2	6E-08	0.09		0	2
Q99U74	RFSIEGVDALVPMLQR	5.673	7	2E-10	0.05		1	6
Q99U74	IALANNPSHLEIVAPVVEGR	5.376	11.7	1E-29	0.09		0	5
Q99U74	AQAASLDSEQMRPLVVMSPK	6.081	6.3	1E-08	-0.38		1	7
Q99U74	LVNEGVISEDEMHSFIEQVQKELR	4.33	7.2	4E-11	0.13		1	2

Q99U74	SGLTLFLPHAYEGQGPEHSSARLER	6.025	8.6	8E-16	-0.05		1	5
Q99UT4	TDELFENFR	3.979	8.6	2E-16	0.09		0	1
Q99UT4	NIEGHDVLLWKP	5.282	6.4	4E-09	0.06		1	5
Q99UT4	RLEINYKTDELFENFR	4.742	9.1	2E-18	0.04		2	4
Q99UT4	NDSKDFFLHHGFTDVEAK	5.23	11.1	6E-27	0.04		1	4
Q99UT4	AIGRNSKDFFLHHGFTDVEAK	6.088	9.5	5E-20	0.01		2	8
Q99UT4	SFNMPIKAIGRNSKDFFLHHGFTDVEAK	6.69	6.9	1E-10	-0.16		3	9
Q99V08	YQHNRDEVIVR	6.464	7.1	7E-11	0.12		-2	8
Q99V08	AVFKVIFYQHNRDEVIVR	8.532	9.22	0	0.094		-2	10
Q99V14	AADIRDVSKR	8.665	7.7	8E-13	-0		2	10
Q99V14	LYQPYNPSILR	8.477	6.327	0	0.07		-2	10
Q99V14	ECYFADKKELQK	5.868	6.7	1E-09	0.04		2	7
Q99V14	EFVQGFATNIGGR	5.617	8.94	0	0.068		0	6
Q99V14	IMFPMVATINEFR	5.953	6.7	2E-09	0.03		-2	7
Q99V14	VSYLEYQPYNPSILR	8.377	7.768	0	0.101		0	10
Q99V14	LNIMFPMVATINEFR	5.943	7	1E-10	0.04		0	7
Q99V14	QINGLSKNEMTELNR	5.74	10.6	1E-24	0.03		1	6
Q99V14	RQINGLSKNEMTELNR	8.24	7.8	3E-13	0.3		2	9
Q99V14	LNIMFPMVATINEFREAK	6.025	8.5	1E-15	-0.25		1	8
Q99V14	ASVYGKLNIMFPMVATINEFR	8.525	7.4	1E-11	-0.13		1	9
Q99V14	ASVYGKLNIMFPMVATINEFREAK	8.5	7	2E-10	-0.32		2	9
Q99V14	TLDIGGDKELSYLNLPEEMNPFLGYR	4.055	11.5	7E-29	0.16		1	1
Q99V14	AVDCATQEEVIELVNNYVK	3.938	9.4	3E-19	0.16	Cys_CAM:.....	0	1
Q99V41	YKPQVNSSINDYIR	8.074	8.62	0	0.098		1	9
Q99V41	FINVEIVHTHDYASFAR	6.016	8.3	3E-15	-0.01		0	5
Q99VJ4	STFYGYDSNFIWR	5.435	9.9	2E-21	0.04		0	5
Q99W05	VADFEPTIESAAEHR	4.321	9.3	6E-19	0.12		0	2
Q99W05	EYYINDAGNQITNLAR	4.104	8	4E-14	0.15		0	1
Q99W05	KVADFEPTIESAAEHR	4.767	11.4	2E-28	0.03		1	4
Q99W05	NAAVGDALANILTAAGYNVTR	5.61	11.357	0	0.139		0	6
Q99W05	GNDILIDLFGADHHGYINRLK	6.066	7.5	6E-12	0.01		1	8
Q99W05	GQNVLLLEYVSANPTGDLHIGHAR	6.076	11.7	5E-30	0.01		0	8
Q99W73	NSYQLIEER	4.53	7	1E-10	-0		0	3
Q99W73	MITLYNTLTR	8.385	6.4	5E-09	-0.06		0	9
Q99W73	SQNIILEDTPQGVR	4.331	10	4E-22	0.11		0	2
Q99W73	YIAAFHEDVGALNVR	5.283	9.3	3E-19	0.06		0	5